

DAVID: Database for Annotation, Visualization, and Int

Genome Biology

4, 1

DOI: [10.1186/gb-2003-4-5-p3](https://doi.org/10.1186/gb-2003-4-5-p3)

Citation Report

#	ARTICLE	IF	CITATIONS
1	The NIA cDNA Project in mouse stem cells and early embryos. <i>Comptes Rendus - Biologies</i> , 2003, 326, 931-940.	0.1	12
2	POCUS: mining genomic sequence annotation to predict disease genes. <i>Genome Biology</i> , 2003, 4, R75.	13.9	199
3	Identifying biological themes within lists of genes with EASE. <i>Genome Biology</i> , 2003, 4, R70.	3.8	1,664
4	GeneAnnot: Interfacing GeneCards with high-throughput gene expression compendia. <i>Briefings in Bioinformatics</i> , 2003, 4, 349-360.	3.2	17
5	Inhibition of Heme Biosynthesis Prevents Transcription of Iron Uptake Genes in Yeast. <i>Journal of Biological Chemistry</i> , 2003, 278, 45499-45506.	1.6	77
6	Annotation and cross-indexing of array elements on multiple platforms.. <i>Environmental Health Perspectives</i> , 2004, 112, 506-510.	2.8	19
7	A Serial Analysis of Gene Expression (SAGE) Database Analysis of Chemosensitivity. <i>Cancer Research</i> , 2004, 64, 2805-2816.	0.4	108
8	Gender-Specific Gene Expression in Post-Mortem Human Brain: Localization to Sex Chromosomes. <i>Neuropsychopharmacology</i> , 2004, 29, 373-384.	2.8	206
9	GFINDER: Genome Function INtegrated Discoverer through dynamic annotation, statistical analysis, and mining. <i>Nucleic Acids Research</i> , 2004, 32, W293-W300.	6.5	72
10	Expression profiling of the developing and mature Nrl $\hat{\wedge}$ / $\hat{\wedge}$ mouse retina: identification of retinal disease candidates and transcriptional regulatory targets of Nrl. <i>Human Molecular Genetics</i> , 2004, 13, 1487-1503.	1.4	157
11	GOstat: find statistically overrepresented Gene Ontologies within a group of genes. <i>Bioinformatics</i> , 2004, 20, 1464-1465.	1.8	1,125
12	<i>Saccharomyces cerevisiae</i> Engineered for Xylose Metabolism Exhibits a Respiratory Response. <i>Applied and Environmental Microbiology</i> , 2004, 70, 6816-6825.	1.4	146
13	From Mice to Humans. <i>Cancer Research</i> , 2004, 64, 7748-7755.	0.4	77
14	Gene Expression Profiling of Host Response in Models of Acute HIV Infection. <i>Journal of Immunology</i> , 2004, 173, 6858-6863.	0.4	97
15	ArrayXPath: mapping and visualizing microarray gene-expression data with integrated biological pathway resources using Scalable Vector Graphics. <i>Nucleic Acids Research</i> , 2004, 32, W460-W464.	6.5	57
16	The Yeast Mitochondrial Proteome, a Study of Fermentative and Respiratory Growth. <i>Journal of Biological Chemistry</i> , 2004, 279, 3956-3979.	1.6	149
17	Onto-Tools: an ensemble of web-accessible, ontology-based tools for the functional design and interpretation of high-throughput gene expression experiments. <i>Nucleic Acids Research</i> , 2004, 32, W449-W456.	6.5	139
18	Toward a Definition of Self: Proteomic Evaluation of the Class I Peptide Repertoire. <i>Journal of Immunology</i> , 2004, 172, 2944-2952.	0.4	104

#	ARTICLE	IF	CITATIONS
19	Gene and Protein Expression Changes in Human Trabecular Meshwork Cells Treated with Transforming Growth Factor- $\beta$ . <i>Investigative Ophthalmology and Visual Science</i> , 2004, 45, 4023-4034.	3.3	147
20	Na <sup>+</sup> /H <sup>+</sup> exchanger 1 deficiency alters gene expression in mouse brain. <i>Physiological Genomics</i> , 2004, 18, 331-339.	1.0	24
21	Neuroendocrine Transcriptome in Genetic Hypertension. <i>Hypertension</i> , 2004, 43, 1301-1311.	1.3	37
22	Lineage-Specific Gene Duplication and Loss in Human and Great Ape Evolution. <i>PLoS Biology</i> , 2004, 2, e207.	2.6	263
23	Mutation of GATA3 in human breast tumors. <i>Oncogene</i> , 2004, 23, 7669-7678.	2.6	250
24	Bioinformatics tools to understand human diseases. <i>Surgery</i> , 2004, 135, 579-585.	1.0	5
25	Functional genomics of UV radiation responses in human cells. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2004, 549, 65-78.	0.4	51
26	Gene expression profiling of adipose tissue. <i>Nutrition</i> , 2004, 20, 115-120.	1.1	42
27	Handling multiple testing while interpreting microarrays with the Gene Ontology Database. <i>BMC Bioinformatics</i> , 2004, 5, 124.	1.2	28
28	Gene expression profiling of individual cases reveals consistent transcriptional changes in alcoholic human brain. <i>Journal of Neurochemistry</i> , 2004, 90, 1050-1058.	2.1	120
29	Applications of Machine Learning and High-Dimensional Visualization in Cancer Detection, Diagnosis, and Management. <i>Annals of the New York Academy of Sciences</i> , 2004, 1020, 239-262.	1.8	103
30	Gene expression profiling of parkinsonian substantia nigra pars compacta; alterations in ubiquitin-proteasome, heat shock protein, iron and oxidative stress regulated proteins, cell adhesion/cellular matrix and vesicle trafficking genes. <i>Journal of Neural Transmission</i> , 2004, 111, 1543-1573.	1.4	326
31	Class Discovery Analysis of the Lung Cancer Gene Expression Data. <i>DNA and Cell Biology</i> , 2004, 23, 715-721.	0.9	6
32	Profiling of microdissected gastric epithelial cells reveals a cell type-specific response to <i>Helicobacter pylori</i> infection. <i>Gastroenterology</i> , 2004, 127, 1446-1462.	0.6	55
33	Consensus clustering and functional interpretation of gene-expression data. <i>Genome Biology</i> , 2004, 5, R94.	13.9	122
34	A survey of ovary-, testis-, and soma-biased gene expression in <i>Drosophila melanogaster</i> adults. <i>Genome Biology</i> , 2004, 5, R40.	13.9	273
35	Gene Expression in Prostate Cancer Cells Treated With the Dual 5 Alpha- $\alpha$ -Reductase Inhibitor Dutasteride. <i>Journal of Andrology</i> , 2004, 25, 944-953.	2.0	35
37	Tissue-specific transcriptome responses in rats with early streptozotocin-induced diabetes. <i>Physiological Genomics</i> , 2005, 21, 222-229.	1.0	55

#	ARTICLE	IF	CITATIONS
38	"Promoter Array" Studies Identify Cohorts of Genes Directly Regulated by Methylation, Copy Number Change, or Transcription Factor Binding in Human Cancer Cells. <i>Annals of the New York Academy of Sciences</i> , 2005, 1058, 162-185.	1.8	20
39	Issues for Consideration in the Analysis of Microarray Data in Behavioural Studies. <i>Addiction Biology</i> , 2005, 10, 15-21.	1.4	5
40	ALCOHOL AND GENE EXPRESSION IN THE CENTRAL NERVOUS SYSTEM. <i>Alcohol and Alcoholism</i> , 2005, 40, 63-75.	0.9	36
41	Transcriptional analysis of the molecular basis of human kidney aging using cDNA microarray profiling. <i>Kidney International</i> , 2005, 68, 2667-2679.	2.6	88
42	Gene expression profile identifies a rare epithelioid variant case of pleomorphic liposarcoma carrying FUS-CHOP transcript. <i>Histopathology</i> , 2005, 46, 334-341.	1.6	21
43	Target RNA motif and target mRNAs of the Quaking STAR protein. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 691-698.	3.6	240
44	Data integration: challenges for drug discovery. <i>Nature Reviews Drug Discovery</i> , 2005, 4, 45-58.	21.5	161
45	Identification of a proliferation gene cluster associated with HPV E6/E7 expression level and viral DNA load in invasive cervical carcinoma. <i>Oncogene</i> , 2005, 24, 7094-7104.	2.6	122
46	Profiling estrogen-regulated gene expression changes in normal and malignant human ovarian surface epithelial cells. <i>Oncogene</i> , 2005, 24, 8128-8143.	2.6	33
47	Patient-based cross-platform comparison of oligonucleotide microarray expression profiles. <i>Laboratory Investigation</i> , 2005, 85, 1024-1039.	1.7	56
48	Bioinformatic methods for integrating whole-genome expression results into cellular networks. <i>Drug Discovery Today</i> , 2005, 10, 727-734.	3.2	42
49	Searching for biomarkers of developmental toxicity with microarrays: normal eye morphogenesis in rodent embryos. <i>Toxicology and Applied Pharmacology</i> , 2005, 206, 219-228.	1.3	15
50	Multievidence microarray mining. <i>Trends in Genetics</i> , 2005, 21, 553-558.	2.9	33
51	Comparison of supervised clustering methods to discriminate genotoxic from non-genotoxic carcinogens by gene expression profiling. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2005, 575, 17-33.	0.4	64
52	A database for tracking toxicogenomic samples and procedures. <i>Reproductive Toxicology</i> , 2005, 19, 411-419.	1.3	17
53	Computational systems analysis of developmental toxicity: design, development and implementation of a Birth Defects Systems Manager (BDSM). <i>Reproductive Toxicology</i> , 2005, 19, 421-439.	1.3	25
54	PAGE: parametric analysis of gene set enrichment. <i>BMC Bioinformatics</i> , 2005, 6, 144.	1.2	649
55	FACT—a framework for the functional interpretation of high-throughput experiments. <i>BMC Bioinformatics</i> , 2005, 6, 161.	1.2	6

#	ARTICLE	IF	CITATIONS
56	Storing, linking, and mining microarray databases using SRS. <i>BMC Bioinformatics</i> , 2005, 6, 192.	1.2	12
57	A TNF-induced gene expression program under oscillatory NF- $\kappa$ B control. <i>BMC Genomics</i> , 2005, 6, 137.	1.2	159
58	cGMP-independent nitric oxide signaling and regulation of the cell cycle. <i>BMC Genomics</i> , 2005, 6, 151.	1.2	45
59	Gene expression signature of estrogen receptor $\pm$ status in breast cancer. <i>BMC Genomics</i> , 2005, 6, 37.	1.2	126
60	PathwayVoyager: pathway mapping using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database. <i>BMC Genomics</i> , 2005, 6, 60.	1.2	286
61	Gene expression profile of cervical tissue compared to exfoliated cells: Impact on biomarker discovery. <i>BMC Genomics</i> , 2005, 6, 64.	1.2	18
62	Laboratory variability does not preclude identification of biological functions impacted by hydroxyurea. <i>Environmental and Molecular Mutagenesis</i> , 2005, 46, 221-235.	0.9	10
63	Identification and validation of novel ERBB2 (HER2, NEU) targets including genes involved in angiogenesis. <i>International Journal of Cancer</i> , 2005, 114, 590-597.	2.3	53
64	Differential gene expression in epidermis of mice sensitive and resistant to phorbol ester skin tumor promotion. <i>Molecular Carcinogenesis</i> , 2005, 44, 122-136.	1.3	29
65	Large-scale identification of proteins expressed in mouse embryonic stem cells. <i>Proteomics</i> , 2005, 5, 1346-1361.	1.3	89
66	Wound Site Neutrophil Transcriptome in Response to Psychological Stress in Young Men. <i>Gene Expression</i> , 2005, 12, 273-287.	0.5	30
68	ADAPT: a database of affymetrix probesets and transcripts. <i>Bioinformatics</i> , 2005, 21, 2552-2553.	1.8	31
69	Effects of ADMA upon Gene Expression: An Insight into the Pathophysiological Significance of Raised Plasma ADMA. <i>PLoS Medicine</i> , 2005, 2, e264.	3.9	52
70	Effectors of mammalian telomere dysfunction: a comparative transcriptome analysis using mouse models. <i>Carcinogenesis</i> , 2005, 26, 1613-1626.	1.3	13
71	Molecular Dissection of Mesenchymal-Epithelial Interactions in the Hair Follicle. <i>PLoS Biology</i> , 2005, 3, e331.	2.6	405
72	Ageing-associated changes in cardiac gene expression. <i>Cardiovascular Research</i> , 2005, 66, 194-204.	1.8	37
73	GOChase: correcting errors from Gene Ontology-based annotations for gene products. <i>Bioinformatics</i> , 2005, 21, 829-831.	1.8	16
74	Novel Regulatory Function for the CCAAT-Binding Factor in <i>Candida albicans</i> . <i>Eukaryotic Cell</i> , 2005, 4, 1662-1676.	3.4	31

#	ARTICLE	IF	CITATIONS
75	Genetic and genomic studies of <i>Drosophila parkin</i> mutants implicate oxidative stress and innate immune responses in pathogenesis. <i>Human Molecular Genetics</i> , 2005, 14, 799-811.	1.4	178
76	Expression Profiling of Murine Double-Negative Regulatory T Cells Suggest Mechanisms for Prolonged Cardiac Allograft Survival. <i>Journal of Immunology</i> , 2005, 174, 4535-4544.	0.4	32
77	Assembly of the Hap2p/Hap3p/Hap4p/Hap5p-DNA Complex in <i>Saccharomyces cerevisiae</i> . <i>Eukaryotic Cell</i> , 2005, 4, 1829-1839.	3.4	74
78	Disruption of Cooperation Between Ras and MycN in Human Neuroblastoma Cells Promotes Growth Arrest. <i>Clinical Cancer Research</i> , 2005, 11, 4321-4330.	3.2	61
79	Identification of Transcriptional Networks during Liver Regeneration. <i>Journal of Biological Chemistry</i> , 2005, 280, 3715-3722.	1.6	107
80	Candidate Gene Discovery in Cardiovascular Disease. <i>Circulation Research</i> , 2005, 96, 605-606.	2.0	5
81	Gene Expression Profiling Following In Utero Exposure to Phthalate Esters Reveals New Gene Targets in the Etiology of Testicular Dysgenesis <sup>1</sup> . <i>Biology of Reproduction</i> , 2005, 73, 180-192.	1.2	190
82	Recent additions and improvements to the Onto-Tools. <i>Nucleic Acids Research</i> , 2005, 33, W762-W765.	6.5	106
83	Whipple Disease: Intestinal Infiltrating Cells Exhibit a Transcriptional Pattern of M2/Alternatively Activated Macrophages. <i>Journal of Infectious Diseases</i> , 2005, 192, 1642-1646.	1.9	77
84	Human Genome Screen to Identify the Genetic Basis of the Anti-inflammatory Effects of Boswellia in Microvascular Endothelial Cells. <i>DNA and Cell Biology</i> , 2005, 24, 244-255.	0.9	72
85	Gene Expression Profiling Reveals Multiple Protective Influences of the Peptide $\alpha$ -Melanocyte-Stimulating Hormone in Experimental Heart Transplantation. <i>Journal of Immunology</i> , 2005, 175, 3391-3401.	0.4	23
86	PBK/TOPK, a Proliferating Neural Progenitor-Specific Mitogen-Activated Protein Kinase Kinase. <i>Journal of Neuroscience</i> , 2005, 25, 10773-10785.	1.7	90
87	Global gene expression profiles reveal significant nuclear reprogramming by the blastocyst stage after cloning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 17582-17587.	3.3	184
88	Improvement of Galactose Uptake in <i>Saccharomyces cerevisiae</i> through Overexpression of Phosphoglucomutase: Example of Transcript Analysis as a Tool in Inverse Metabolic Engineering. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6465-6472.	1.4	116
89	The promoters of human cell cycle genes integrate signals from two tumor suppressive pathways during cellular transformation. <i>Molecular Systems Biology</i> , 2005, 1, 2005.0022.	3.2	64
90	Inactivation of Myc in Murine Two-Hit B lymphomas Causes Dormancy with Elevated Levels of Interleukin 10 Receptor and CD20: Implications for Adjuvant Therapies. <i>Cancer Research</i> , 2005, 65, 5454-5461.	0.4	29
91	OntologyTraverser: an R package for GO analysis. <i>Bioinformatics</i> , 2005, 21, 275-276.	1.8	42
92	A Gene Expression Signature for Relapse of Primary Wilms Tumors. <i>Cancer Research</i> , 2005, 65, 2592-2601.	0.4	56

#	ARTICLE	IF	CITATIONS
93	Gene expression in Huntington's disease skeletal muscle: a potential biomarker. <i>Human Molecular Genetics</i> , 2005, 14, 1863-1876.	1.4	150
94	Transcriptional Profiling Reveals Complex Regulation of the Monocyte IL-1 $\beta$ System by IL-13. <i>Journal of Immunology</i> , 2005, 174, 834-845.	0.4	132
95	ArrayXPath II: mapping and visualizing microarray gene-expression data with biomedical ontologies and integrated biological pathway resources using Scalable Vector Graphics. <i>Nucleic Acids Research</i> , 2005, 33, W621-W626.	6.5	52
96	Differential Gene Expression in Human Peripheral Blood Mononuclear Cells Induced by Cigarette Smoke and Its Constituents. <i>Toxicological Sciences</i> , 2005, 86, 200-210.	1.4	79
97	Gene expression profile in the muscles of patients with inflammatory myopathies: effect of therapy with IVIg and biological validation of clinically relevant genes. <i>Brain</i> , 2005, 128, 1887-1896.	3.7	144
98	GFINDER: genetic disease and phenotype location statistical analysis and mining of dynamically annotated gene lists. <i>Nucleic Acids Research</i> , 2005, 33, W717-W723.	6.5	61
99	RACE: Remote Analysis Computation for gene Expression data. <i>Nucleic Acids Research</i> , 2005, 33, W638-W643.	6.5	53
100	Isolation of mRNA from specific tissues of <i>Drosophila</i> by mRNA tagging. <i>Nucleic Acids Research</i> , 2005, 33, e148-e148.	6.5	71
101	Gene Expression Pattern in Spontaneously Hypertensive Rats Exposed to Urban Particulate Matter (EHC-93). <i>Inhalation Toxicology</i> , 2005, 17, 53-65.	0.8	35
102	Bioinformatic Analysis of Circadian Gene Oscillation in Mouse Aorta. <i>Circulation</i> , 2005, 112, 2716-2724.	1.6	141
103	Autophagy promotes MHC class II presentation of peptides from intracellular source proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7922-7927.	3.3	573
104	Computational prediction of human drug metabolism. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , 2005, 1, 303-324.	1.5	78
105	WebGestalt: an integrated system for exploring gene sets in various biological contexts. <i>Nucleic Acids Research</i> , 2005, 33, W741-W748.	6.5	1,630
106	A microarray study of post-mortem mRNA degradation in mouse brain tissue. <i>Molecular Brain Research</i> , 2005, 138, 164-177.	2.5	95
107	Gene profiling in muscle of severely burned children: Age- and sex-dependent changes1. <i>Journal of Surgical Research</i> , 2005, 123, 144-152.	0.8	6
108	Transcriptional changes during neuronal death and replacement in the olfactory epithelium. <i>Molecular and Cellular Neurosciences</i> , 2005, 30, 90-107.	1.0	49
109	List of lists-annotated (LOLA): A database for annotation and comparison of published microarray gene lists. <i>Gene</i> , 2005, 360, 78-82.	1.0	54
110	Individual histone deacetylases in <i>Drosophila</i> modulate transcription of distinct genes. <i>Genomics</i> , 2005, 86, 606-617.	1.3	67

#	ARTICLE	IF	CITATIONS
111	Molecular dynamics of the compensatory response to myocardial infarct. <i>Journal of Molecular and Cellular Cardiology</i> , 2005, 38, 103-117.	0.9	44
112	Genomic profiling of acquired resistance to apoptosis in cells derived from human atherosclerotic lesions: Potential role of STATs, cyclinD1, BAD, and Bcl-X. <i>Journal of Molecular and Cellular Cardiology</i> , 2005, 39, 453-465.	0.9	28
113	Carotid atherosclerotic plaques from symptomatic stroke patients share the molecular fingerprints to develop in a neoplastic fashion: A microarray analysis study. <i>Neuroscience</i> , 2005, 131, 359-374.	1.1	38
114	CD133-Positive Hematopoietic Stem Cell "Stemness" Genes Contain Many Genes Mutated or Abnormally Expressed in Leukemia. <i>Stem Cells</i> , 2005, 23, 1142-1153.	1.4	73
115	A novel method for generation of signature networks as biomarkers from complex high throughput data. <i>Toxicology Letters</i> , 2005, 158, 20-29.	0.4	129
116	Random Walk Models for Bayesian Clustering of Gene Expression Profiles. <i>Applied Bioinformatics</i> , 2005, 4, 263-276.	1.7	14
117	BioCloneDB. <i>Applied Bioinformatics</i> , 2005, 4, 277-280.	1.7	2
118	Genomic analysis of metabolic pathway gene expression in mice. <i>Genome Biology</i> , 2005, 6, R59.	13.9	70
119	Dissection of a DNA-damage-induced transcriptional network using a combination of microarrays, RNA interference and computational promoter analysis. <i>Genome Biology</i> , 2005, 6, R43.	13.9	71
120	Promoter features related to tissue specificity as measured by Shannon entropy. <i>Genome Biology</i> , 2005, 6, R33.	3.8	377
121	Breast cancer prognosis by combinatorial analysis of gene expression data. <i>Breast Cancer Research</i> , 2006, 8, R41.	2.2	53
122	Genome-wide identification of functionally distinct subsets of cellular mRNAs associated with two nucleocytoplasmic-shuttling mammalian splicing factors. <i>Genome Biology</i> , 2006, 7, R113.	13.9	68
123	Shuffling of cis-regulatory elements is a pervasive feature of the vertebrate lineage. <i>Genome Biology</i> , 2006, 7, R56.	13.9	41
124	PI3K signaling and miRNA expression during the response of quiescent human fibroblasts to distinct proliferative stimuli. <i>Genome Biology</i> , 2006, 7, R42.	13.9	54
125	Deciphering cellular states of innate tumor drug responses. <i>Genome Biology</i> , 2006, 7, R19.	13.9	110
126	Integration and mining of malaria molecular, functional and pharmacological data: how far are we from a chemogenomic knowledge space?. <i>Malaria Journal</i> , 2006, 5, 110.	0.8	18
127	Cellular, Molecular Consequences of Peroxisome Proliferator- Activated Receptor- $\gamma$ Activation in Ovarian Cancer Cells. <i>Neoplasia</i> , 2006, 8, 851-1N12.	2.3	48
128	Methamphetamine Modulates Gene Expression Patterns in Monocyte Derived Mature Dendritic Cells. <i>Molecular Diagnosis and Therapy</i> , 2006, 10, 257-269.	1.6	45



#	ARTICLE	IF	CITATIONS
129	Gene Lethality Detection and Characterization via Topological Analysis of Regulatory Networks. IEEE Transactions on Circuits and Systems Part 1: Regular Papers, 2006, 53, 2438-2443.	0.1	3
130	Meta-Analysis and Meta-Review of Thyroid Cancer Gene Expression Profiling Studies Identifies Important Diagnostic Biomarkers. Journal of Clinical Oncology, 2006, 24, 5043-5051.	0.8	279
131	A Genomic Approach to Identify Regulatory Nodes in the Transcriptional Network of Systemic Acquired Resistance in Plants. PLoS Pathogens, 2006, 2, e123.	2.1	651
132	Transcriptome changes in a colon adenocarcinoma cell line in response to photochemical treatment as used in photochemical internalisation (PCI). FEBS Letters, 2006, 580, 5739-5746.	1.3	15
133	Hepatic Gene Expression Response to Acute Indomethacin Exposure. Molecular Diagnosis and Therapy, 2006, 10, 187-196.	1.6	6
134	Transcriptional Profiling of the Human Monocyte-to-Macrophage Differentiation and Polarization: New Molecules and Patterns of Gene Expression. Journal of Immunology, 2006, 177, 7303-7311.	0.4	2,062
135	Involvement of HTLV-I Tax and CREB in aneuploidy: a bioinformatics approach. Retrovirology, 2006, 3, 43.	0.9	14
136	Genome Wide Gene Expression Studies in Mood Disorders. OMICS A Journal of Integrative Biology, 2006, 10, 444-454.	1.0	53
137	Quantitative relationship of dioxin-responsive gene expression to dioxin response element in Hep3B and HepG2 human hepatocarcinoma cell lines. Toxicology Letters, 2006, 165, 174-181.	0.4	18
138	Global Identification of O-GlcNAc-Modified Proteins. Analytical Chemistry, 2006, 78, 452-458.	3.2	153
139	Integrated analysis of regulatory and metabolic networks reveals novel regulatory mechanisms in Saccharomyces cerevisiae. Genome Research, 2006, 16, 627-635.	2.4	202
140	Data merging for integrated microarray and proteomic analysis. Briefings in Functional Genomics & Proteomics, 2006, 5, 261-272.	3.8	95
141	BMI1 is a target gene of E2F-1 and is strongly expressed in primary neuroblastomas. Nucleic Acids Research, 2006, 34, 1745-1754.	6.5	127
142	Sepsis Plasma Protein Profiling with Immunodepletion, Three-Dimensional Liquid Chromatography Tandem Mass Spectrometry, and Spectrum Counting. Journal of Proteome Research, 2006, 5, 3154-3160.	1.8	58
143	PIGOK: Linking Protein Identity to Gene Ontology and Function. Journal of Proteome Research, 2006, 5, 3429-3432.	1.8	10
144	The search for factors in human feeders that support the derivation and propagation of human embryonic stem cells: preliminary studies using transcriptome profiling by serial analysis of gene expression. Fertility and Sterility, 2006, 85, 1843-1846.	0.5	27
145	Secretome analysis of microarray data reveals extracellular events associated with proliferative potential in a cell line model of breast disease. Cancer Letters, 2006, 241, 49-58.	3.2	12
146	Intrahepatic gene expression in human alcoholic hepatitis. Journal of Hepatology, 2006, 45, 306-320.	1.8	65

#	ARTICLE	IF	CITATIONS
147	The Grainyhead-like epithelial transactivator Get-1/Grh3 regulates epidermal terminal differentiation and interacts functionally with LMO4. <i>Developmental Biology</i> , 2006, 299, 122-136.	0.9	153
148	Genomic dissection of mucosal immunobiology in the porcine small intestine. <i>Physiological Genomics</i> , 2006, 28, 5-14.	1.0	16
149	Bioinformatics Resources for Cancer Research with an Emphasis on Gene Function and Structure Prediction Tools. <i>Cancer Informatics</i> , 2006, 2, 117693510600200.	0.9	8
150	Genomic analysis of the impact of fescue toxicosis on hepatic function1. <i>Journal of Animal Science</i> , 2006, 84, 1279-1294.	0.2	32
151	Analysing Microarray Data using the Multi-functional Immune Ontologiser. <i>Journal of Integrative Bioinformatics</i> , 2006, 3, 14-36.	1.0	2
152	Effect of fescue toxicosis on hepatic gene expression in mice1. <i>Journal of Animal Science</i> , 2006, 84, 1600-1612.	0.2	14
153	Analysis of Microarray Gene Expression Data. <i>Current Bioinformatics</i> , 2006, 1, 37-53.	0.7	35
154	Alteration in the Transcriptional Profile of Livers from Brain-dead Organ Donors. <i>Transplantation</i> , 2006, 82, 69-79.	0.5	20
155	Multiple mechanisms limit the duration of wakefulness in <i>Drosophila</i> brain. <i>Physiological Genomics</i> , 2006, 27, 337-350.	1.0	97
156	Transcriptome analysis of the ischemia-reperfused remodeling myocardium: temporal changes in inflammation and extracellular matrix. <i>Physiological Genomics</i> , 2006, 25, 364-374.	1.0	86
157	Preliminary evidence of mitochondrial dysfunction associated with post-infective fatigue after acute infection with Epstein Barr Virus. <i>BMC Infectious Diseases</i> , 2006, 6, 15.	1.3	58
158	Gene expression profiles in developing nephrons using Lim1 metanephric mesenchyme-specific conditional mutant mice. <i>BMC Nephrology</i> , 2006, 7, 1.	0.8	23
159	Cytogenetic and expression profiles associated with transformation to androgen-resistant prostate cancer. <i>Prostate</i> , 2006, 66, 157-172.	1.2	18
160	Optimized proteomic analysis of a mouse model of cerebellar dysfunction using amine-specific isobaric tags. <i>Proteomics</i> , 2006, 6, 4321-4334.	1.3	77
161	Chipping into the human genome: novel insights for transplantation. <i>Immunological Reviews</i> , 2006, 210, 138-155.	2.8	12
163	Subcellular Localization of Mammalian Type II Membrane Proteins. <i>Traffic</i> , 2006, 7, 613-625.	1.3	19
164	FACS-array profiling of striatal projection neuron subtypes in juvenile and adult mouse brains. <i>Nature Neuroscience</i> , 2006, 9, 443-452.	7.1	396
165	Deregulated stress system in non-obese diabetic lymphocyte. <i>Genes and Immunity</i> , 2006, 7, 352-358.	2.2	1

#	ARTICLE	IF	CITATIONS
166	Gene expression profiles of AML derived stem cells; similarity to hematopoietic stem cells. <i>Leukemia</i> , 2006, 20, 2147-2154.	3.3	153
167	Mitochondrial-related gene expression changes are sensitive to agonal-pH state: implications for brain disorders. <i>Molecular Psychiatry</i> , 2006, 11, 663-679.	4.1	162
168	The UVB-induced gene expression profile of human epidermis in vivo is different from that of cultured keratinocytes. <i>Oncogene</i> , 2006, 25, 2601-2614.	2.6	80
169	ST7-mediated suppression of tumorigenicity of prostate cancer cells is characterized by remodeling of the extracellular matrix. <i>Oncogene</i> , 2006, 25, 3924-3933.	2.6	22
170	Reference profiling of the genomic response induced by an antimicrotubule agent, TZT-1027 (Soblidotin), in vitro. <i>Pharmacogenomics Journal</i> , 2006, 6, 388-396.	0.9	8
171	Strategies for comparing gene expression profiles from different microarray platforms: Application to a case-control experiment. <i>Analytical Biochemistry</i> , 2006, 353, 43-56.	1.1	40
172	Algorithms for network analysis in systems-ADME/Tox using the MetaCore and MetaDrug platforms. <i>Xenobiotica</i> , 2006, 36, 877-901.	0.5	125
173	Gene Expression Profiles in Murine Hematopoietic Stem Cells Revisited: Analysis of cDNA Libraries Reveals High Levels of Translational and Metabolic Activities. <i>Stem Cells</i> , 2006, 24, 1719-1727.	1.4	11
174	Gene Expression Alterations in Immune System Pathways following Exposure to Immunosuppressive Chemicals. <i>Annals of the New York Academy of Sciences</i> , 2006, 1076, 718-727.	1.8	13
175	Gene expression profiles of vitrified in vivo derived 8-cell stage mouse embryos detected by high density oligonucleotide microarrays. <i>Molecular Reproduction and Development</i> , 2006, 73, 1380-1392.	1.0	45
176	Microarray Analysis of the Effects of a $\beta$ -protein Kinase C Null Mutation on Gene Expression in Striatum: A Role for Transthyretin in Mutant Phenotypes. <i>Behavior Genetics</i> , 2006, 36, 869-881.	1.4	9
177	Evaluating HapMap SNP data transferability in a large-scale genotyping project involving 175 cancer-associated genes. <i>Human Genetics</i> , 2006, 118, 669-679.	1.8	92
178	Associating phenotypes with molecular events: recent statistical advances and challenges underpinning microarray experiments. <i>Functional and Integrative Genomics</i> , 2006, 6, 1-13.	1.4	29
179	Gene expression profiling in <i>Salmonella Choleraesuis</i> -infected porcine lung using a long oligonucleotide microarray. <i>Mammalian Genome</i> , 2006, 17, 777-789.	1.0	41
180	A multiplexed proteomics approach to differentiate neurite outgrowth patterns. <i>Journal of Neuroscience Methods</i> , 2006, 158, 22-29.	1.3	18
181	Splenic CD4+ T Cells Have a Distinct Transcriptional Response Six Hours after the Onset of Sepsis. <i>Journal of the American College of Surgeons</i> , 2006, 203, 375.e1-375.e39.	0.2	21
182	U18666A-mediated apoptosis in cultured murine cortical neurons: Role of caspases, calpains and kinases. <i>Cellular Signalling</i> , 2006, 18, 1572-1583.	1.7	20
183	Partially Degraded RNA from Bladder Washing is a Suitable Sample for Studying Gene Expression Profiles in Bladder Cancer. <i>European Urology</i> , 2006, 50, 1347-1356.	0.9	19

#	ARTICLE	IF	CITATIONS
184	Chondrocyte genomics: implications for disease modification in osteoarthritis. <i>Drug Discovery Today</i> , 2006, 11, 825-832.	3.2	10
185	Utilization of two sample t-test statistics from redundant probe sets to evaluate different probe set algorithms in GeneChip studies. <i>BMC Bioinformatics</i> , 2006, 7, 12.	1.2	16
186	K-SPMM: a database of murine spermatogenic promoters modules & motifs. <i>BMC Bioinformatics</i> , 2006, 7, 238.	1.2	6
187	Integrated functional visualization of eukaryotic genomes. <i>BMC Bioinformatics</i> , 2006, 7, 348.	1.2	3
188	CROPPER: a metagene creator resource for cross-platform and cross-species compendium studies. <i>BMC Bioinformatics</i> , 2006, 7, 418.	1.2	3
189	Analysis with respect to instrumental variables for the exploration of microarray data structures. <i>BMC Bioinformatics</i> , 2006, 7, 422.	1.2	55
190	Mining expressed sequence tags identifies cancer markers of clinical interest. <i>BMC Bioinformatics</i> , 2006, 7, 481.	1.2	23
191	Transcriptomic response to differentiation induction. <i>BMC Bioinformatics</i> , 2006, 7, 81.	1.2	1
192	Gene expression alterations in brains of mice infected with three strains of scrapie. <i>BMC Genomics</i> , 2006, 7, 114.	1.2	80
193	Alu elements contain many binding sites for transcription factors and may play a role in regulation of developmental processes. <i>BMC Genomics</i> , 2006, 7, 133.	1.2	193
194	Gene expression profiling in the striatum of inbred mouse strains with distinct opioid-related phenotypes. <i>BMC Genomics</i> , 2006, 7, 146.	1.2	48
195	An annotated cDNA library of juvenile <i>Euprymna scolopes</i> with and without colonization by the symbiont <i>Vibrio fischeri</i> . <i>BMC Genomics</i> , 2006, 7, 154.	1.2	43
196	Defining the gene expression signature of rhabdomyosarcoma by meta-analysis. <i>BMC Genomics</i> , 2006, 7, 287.	1.2	37
197	Comparison of gene coverage of mouse oligonucleotide microarray platforms. <i>BMC Genomics</i> , 2006, 7, 58.	1.2	24
198	An online database for brain disease research. <i>BMC Genomics</i> , 2006, 7, 70.	1.2	101
199	Incorporating genetic analyses into birth defects cluster investigations: Strategies for identifying candidate genes. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2006, 76, 798-810.	1.6	8
200	A pathway analysis of poly(I:C)-induced global gene expression change in human peripheral blood mononuclear cells. <i>Physiological Genomics</i> , 2006, 26, 125-133.	1.0	75
201	Cross-species comparative toxicogenomics as an aid to safety assessment. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , 2006, 2, 859-874.	1.5	16

#	ARTICLE	IF	CITATIONS
202	PAGE: phase-shifted analysis of gene expression. <i>Bioinformatics</i> , 2006, 22, 367-368.	1.8	6
203	Identification of gene expression signatures in autoimmune disease without the influence of familial resemblance. <i>Human Molecular Genetics</i> , 2006, 15, 501-509.	1.4	19
204	Absolute enrichment: gene set enrichment analysis for homeostatic systems. <i>Nucleic Acids Research</i> , 2006, 34, e151-e151.	6.5	55
205	A systematic approach to infer biological relevance and biases of gene network structures. <i>Nucleic Acids Research</i> , 2006, 34, e6-e6.	6.5	15
206	Gene Expression Profiles Distinguish Idiopathic Pulmonary Fibrosis from Hypersensitivity Pneumonitis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2006, 173, 188-198.	2.5	431
207	Induction of the Plasminogen Activator System by Mechanical Stimulation of Human Bronchial Epithelial Cells. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2006, 35, 628-638.	1.4	72
208	GeneChips in Stem Cell Research. <i>Methods in Enzymology</i> , 2006, 420, 162-224.	0.4	4
209	C/EBP $\beta$ is required for lung maturation at birth. <i>Development (Cambridge)</i> , 2006, 133, 1155-1164.	1.2	122
210	A Genome-Wide Screen for Promoter Methylation in Lung Cancer Identifies Novel Methylation Markers for Multiple Malignancies. <i>PLoS Medicine</i> , 2006, 3, e486.	3.9	228
211	Microarray data on gene modulation by HIV-1 in immune cells: 2000-2006. <i>Journal of Leukocyte Biology</i> , 2006, 80, 1031-1043.	1.5	99
212	Integrating Genetic and Network Analysis to Characterize Genes Related to Mouse Weight. <i>PLoS Genetics</i> , 2006, 2, e130.	1.5	419
213	A multivariate approach for integrating genome-wide expression data and biological knowledge. <i>Bioinformatics</i> , 2006, 22, 2373-2380.	1.8	122
214	Assembly of mitochondrial cytochrome c-oxidase, a complicated and highly regulated cellular process. <i>American Journal of Physiology - Cell Physiology</i> , 2006, 291, C1129-C1147.	2.1	214
215	Meta-Analysis of Differentiating Mouse Embryonic Stem Cell Gene Expression Kinetics Reveals Early Change of a Small Gene Set. <i>PLoS Computational Biology</i> , 2006, 2, e158.	1.5	33
216	Filaria-Induced Monocyte Dysfunction and Its Reversal following Treatment. <i>Infection and Immunity</i> , 2006, 74, 4409-4417.	1.0	55
217	Diminished Production of Monocyte Proinflammatory Cytokines during Human Immunodeficiency Virus Viremia Is Mediated by Type I Interferons. <i>Journal of Virology</i> , 2006, 80, 11486-11497.	1.5	63
218	Regulation of myogenic progenitor proliferation in human fetal skeletal muscle by BMP4 and its antagonist Gremlin. <i>Journal of Cell Biology</i> , 2006, 175, 99-110.	2.3	61
219	A computational genomics approach to identify cis-regulatory modules from chromatin immunoprecipitation microarray data—A case study using E2F1. <i>Genome Research</i> , 2006, 16, 1585-1595.	2.4	59

#	ARTICLE	IF	CITATIONS
220	Biological characterization of gene response in Rpe65 <sup>-/-</sup> mouse model of Leber's congenital amaurosis during progression of the disease. <i>FASEB Journal</i> , 2006, 20, 2036-2049.	0.2	46
221	Identification of an NF- $\kappa$ B-Dependent Gene Network in Cells Infected by Mammalian Reovirus. <i>Journal of Virology</i> , 2006, 80, 1077-1086.	1.5	54
222	Repression and loss of gene expression outpaces activation and gain in recently duplicated fly genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11637-11641.	3.3	49
223	Nell1-deficient mice have reduced expression of extracellular matrix proteins causing cranial and vertebral defects. <i>Human Molecular Genetics</i> , 2006, 15, 1329-1341.	1.4	96
224	Gene Expression Profiling Separates Chromophobe Renal Cell Carcinoma from Oncocytoma and Identifies Vesicular Transport and Cell Junction Proteins as Differentially Expressed Genes. <i>Clinical Cancer Research</i> , 2006, 12, 6937-6945.	3.2	79
225	Adaptation and increased susceptibility to infection associated with constitutive expression of misfolded SP-C. <i>Journal of Cell Biology</i> , 2006, 172, 395-407.	2.3	111
226	Osteopontin is a downstream effector of the PI3-kinase pathway in melanomas that is inversely correlated with functional PTEN. <i>Carcinogenesis</i> , 2006, 27, 1778-1786.	1.3	55
227	A COMBINED APPROACH TO DRUG METABOLISM AND TOXICITY ASSESSMENT. <i>Drug Metabolism and Disposition</i> , 2006, 34, 495-503.	1.7	108
228	Gene Expression Differences in Normal Esophageal Mucosa Associated with Regression and Progression of Mild and Moderate Squamous Dysplasia in a High-Risk Chinese Population. <i>Cancer Research</i> , 2006, 66, 6851-6860.	0.4	27
229	A central regulatory role for eosinophils and the eotaxin/CCR3 axis in chronic experimental allergic airway inflammation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 16418-16423.	3.3	188
230	Suz12 binds to silenced regions of the genome in a cell-type-specific manner. <i>Genome Research</i> , 2006, 16, 890-900.	2.4	276
231	Inhibition of Growth and Metastasis of Mouse Mammary Carcinoma by Selective Inhibitor of Transforming Growth Factor- $\beta$ Type I Receptor Kinase In vivo. <i>Clinical Cancer Research</i> , 2006, 12, 4315-4330.	3.2	137
232	Hypoxia Modifies the Transcriptome of Primary Human Monocytes: Modulation of Novel Immune-Related Genes and Identification Of CC-Chemokine Ligand 20 as a New Hypoxia-Inducible Gene. <i>Journal of Immunology</i> , 2006, 177, 1941-1955.	0.4	189
233	Functional Interpretation of Microarray Experiments. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 398-410.	1.0	74
234	Integration of genomic data for pharmacology and toxicology using Internet resources. <i>SAR and QSAR in Environmental Research</i> , 2006, 17, 25-36.	1.0	4
235	Application of Bioinformatics in the Design of Gene Expression Microarrays. , 2006, , .		4
236	NOTCH1 directly regulates c-MYC and activates a feed-forward-loop transcriptional network promoting leukemic cell growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18261-18266.	3.3	745
237	CLUSTERING BIOLOGICAL ANNOTATIONS AND GENE EXPRESSION DATA TO IDENTIFY PUTATIVELY CO-REGULATED BIOLOGICAL PROCESSES. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 833-852.	0.3	21

#	ARTICLE	IF	CITATIONS
238	Stat3 Is Required for Cytoprotection of the Respiratory Epithelium during Adenoviral Infection. <i>Journal of Immunology</i> , 2006, 177, 527-537.	0.4	51
239	Lithium Administration to Preadolescent Rats Causes Long-Lasting Increases in Anxiety-Like Behavior and Has Molecular Consequences. <i>Journal of Neuroscience</i> , 2006, 26, 6031-6039.	1.7	39
240	Global Transcriptome Analysis of Genetically Identified Neurons in the Adult Cortex. <i>Journal of Neuroscience</i> , 2006, 26, 9956-9966.	1.7	88
241	A Comprehensive Structure-Function Analysis of Arabidopsis SNI1 Defines Essential Regions and Transcriptional Repressor Activity. <i>Plant Cell</i> , 2006, 18, 1750-1765.	3.1	130
242	Functional Annotation of IFN- $\lambda$ -Stimulated Gene Expression Profiles from Sensitive and Resistant Renal Cell Carcinoma Cell Lines. <i>Journal of Interferon and Cytokine Research</i> , 2006, 26, 534-547.	0.5	13
243	A System-Based Approach to Interpret Dose- and Time-Dependent Microarray Data: Quantitative Integration of Gene Ontology Analysis for Risk Assessment. <i>Toxicological Sciences</i> , 2006, 92, 560-577.	1.4	50
244	Transcriptional profiling of myostatin-knockout mice implicates Wnt signaling in postnatal skeletal muscle growth and hypertrophy. <i>FASEB Journal</i> , 2006, 20, 580-582.	0.2	115
245	Histamine signaling through the H2 receptor in the Peyer's patch is important for controlling <i>Yersinia enterocolitica</i> infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9268-9273.	3.3	48
246	A molecular-properties-based approach to understanding PDZ domain proteins and PDZ ligands. <i>Genome Research</i> , 2006, 16, 1056-1072.	2.4	45
247	[18] Interpreting Experimental Results Using Gene Ontologies. <i>Methods in Enzymology</i> , 2006, 411, 340-352.	0.4	52
248	DAVID Bioinformatics Resources: expanded annotation database and novel algorithms to better extract biology from large gene lists. <i>Nucleic Acids Research</i> , 2007, 35, W169-W175.	6.5	1,934
249	Changes in Gene Expression in Experimental Glaucoma and Optic Nerve Transection: The Equilibrium between Protective and Detrimental Mechanisms. , 2007, 48, 5539.		157
250	Kidney Gene Expression Analysis in a Rat Model of Intrauterine Growth Restriction Reveals Massive Alterations of Coagulation Genes. <i>Endocrinology</i> , 2007, 148, 5549-5557.	1.4	38
251	Functional Genomic Studies of the Intestinal Response to a Foodborne Enteropathogen in a Humanized Gnotobiotic Mouse Model. <i>Journal of Biological Chemistry</i> , 2007, 282, 15065-15072.	1.6	75
252	Identification of Genes Selectively Regulated by IFNs in Endothelial Cells. <i>Journal of Immunology</i> , 2007, 178, 1122-1135.	0.4	152
253	Identification of Genes Directly Regulated by the Oncogene ZNF217 Using Chromatin Immunoprecipitation (ChIP)-Chip Assays. <i>Journal of Biological Chemistry</i> , 2007, 282, 9703-9712.	1.6	71
254	dlr1/FA1 Regulates the Function of Human Bone Marrow Mesenchymal Stem Cells by Modulating Gene Expression of Pro-inflammatory Cytokines and Immune Response-related Factors. <i>Journal of Biological Chemistry</i> , 2007, 282, 7339-7351.	1.6	82
255	Graph-based identification of cancer signaling pathways from published gene expression signatures using PubLiME. <i>Nucleic Acids Research</i> , 2007, 35, 2343-2355.	6.5	17

#	ARTICLE	IF	CITATIONS
256	Genome-wide analyses of human perisylvian cerebral cortical patterning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17849-17854.	3.3	175
257	A microarray analysis for genes regulated by interferon- $\gamma$ , in ovine luminal epithelial cells. <i>Reproduction</i> , 2007, 134, 123-135.	1.1	37
258	Distinctive patterns of microRNA expression in primary muscular disorders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17016-17021.	3.3	458
259	Comparative analysis of gene expression between renal cortex and papilla in nedaplatin-induced nephrotoxicity in rats. <i>Human and Experimental Toxicology</i> , 2007, 26, 767-780.	1.1	23
260	Annotation-based distance measures for patient subgroup discovery in clinical microarray studies. <i>Bioinformatics</i> , 2007, 23, 2256-2264.	1.8	12
261	Gene expression profile in rat adrenal zona glomerulosa cells stimulated with aldosterone secretagogues. <i>Physiological Genomics</i> , 2007, 32, 117-127.	1.0	28
262	Differential brain transcriptome of $\alpha 4$ nAChR subunit-deficient mice: is it the effect of the null mutation or the background strain?. <i>Physiological Genomics</i> , 2007, 28, 213-222.	1.0	12
263	The (In)dependence of Alternative Splicing and Gene Duplication. <i>PLoS Computational Biology</i> , 2007, 3, e33.	1.5	66
264	A genome-wide approach identifies distinct but overlapping subsets of cellular mRNAs associated with Staufen1- and Staufen2-containing ribonucleoprotein complexes. <i>Rna</i> , 2008, 14, 324-335.	1.6	104
265	Impact of Antiretroviral Treatment on Gene Expression in Peripheral Blood Mononuclear Cells from SIVmac251-Infected Macaques. <i>Journal of Infectious Diseases</i> , 2007, 196, 384-393.	1.9	3
266	Fetal Mouse Phthalate Exposure Shows that Gonocyte Multinucleation is Not Associated with Decreased Testicular Testosterone. <i>Toxicological Sciences</i> , 2007, 97, 491-503.	1.4	110
268	Regulatory Pathway Analysis by High-Throughput In Situ Hybridization. <i>PLoS Genetics</i> , 2007, 3, e178.	1.5	55
269	Exposure to Arsenic at Levels Found in U.S. Drinking Water Modifies Expression in the Mouse Lung. <i>Toxicological Sciences</i> , 2007, 100, 75-87.	1.4	47
270	Genome-level expression profiles in pediatric septic shock indicate a role for altered zinc homeostasis in poor outcome. <i>Physiological Genomics</i> , 2007, 30, 146-155.	1.0	221
271	Expression changes in mouse brains following nicotine-induced seizures: the modulation of transcription factor networks. <i>Physiological Genomics</i> , 2007, 30, 242-252.	1.0	10
272	Challenges and Solutions in Proteomics. <i>Current Genomics</i> , 2007, 8, 21-28.	0.7	12
273	A High-Resolution Map of Segmental DNA Copy Number Variation in the Mouse Genome. <i>PLoS Genetics</i> , 2007, 3, e3.	1.5	196
274	Unbiased Gene Expression Analysis Implicates the huntingtin Polyglutamine Tract in Extra-mitochondrial Energy Metabolism. <i>PLoS Genetics</i> , 2007, 3, e135.	1.5	72



#	ARTICLE	IF	CITATIONS
275	FatiGO +: a functional profiling tool for genomic data. Integration of functional annotation, regulatory motifs and interaction data with microarray experiments. <i>Nucleic Acids Research</i> , 2007, 35, W91-W96.	6.5	248
276	Intraovarian Activins Are Required for Female Fertility. <i>Molecular Endocrinology</i> , 2007, 21, 2458-2471.	3.7	120
277	Genome-wide expression profiling of placentas in the p57Kip2 model of pre-eclampsia. <i>Molecular Human Reproduction</i> , 2007, 13, 251-263.	1.3	30
278	The Early Developmental Gene Semaphorin 5c Contributes to Olfactory Behavior in Adult <i>Drosophila</i> . <i>Genetics</i> , 2007, 176, 947-956.	1.2	18
279	Investigating the Genetic Circuitry of Mastermind in <i>Drosophila</i> , a Notch Signal Effector. <i>Genetics</i> , 2007, 177, 2493-2505.	1.2	57
280	GO PaD: the Gene Ontology Partition Database. <i>Nucleic Acids Research</i> , 2007, 35, D322-D327.	6.5	113
281	Differential Gene Expression of p27Kip1 and Rb Knockout Pituitary Tumors Associated with Altered Growth and Angiogenesis. <i>Cell Cycle</i> , 2007, 6, 750-757.	1.3	22
282	Comparison of HIV-derived Lentiviral and MLV-based Gammaretroviral Vector Integration Sites in Primate Repopulating Cells. <i>Molecular Therapy</i> , 2007, 15, 1356-1365.	3.7	104
283	Cytomegalovirus Infection of Human Syncytiotrophoblast Cells Strongly Interferes with Expression of Genes Involved in Placental Differentiation and Tissue Integrity. <i>Pediatric Research</i> , 2007, 61, 565-571.	1.1	28
284	HIV Protease Inhibitors Selectively Induce Gene Expression Alterations Associated with Reduced Calcium Deposition in Primary Human Osteoblasts. <i>AIDS Research and Human Retroviruses</i> , 2007, 23, 243-250.	0.5	54
285	Leukocyte gene expression signatures in antineutrophil cytoplasmic autoantibody and lupus glomerulonephritis. <i>Kidney International</i> , 2007, 72, 853-864.	2.6	48
286	Positive Adaptive State: Microarray Evaluation of Gene Expression in <i>Salmonella enterica</i> Typhimurium Exposed to Nalidixic Acid. <i>Foodborne Pathogens and Disease</i> , 2007, 4, 187-200.	0.8	20
287	Microarray Analyses of Newborn Mouse Ovaries Lacking Nobox1. <i>Biology of Reproduction</i> , 2007, 77, 312-319.	1.2	113
288	Transcription factor modularity in a gene-centered <i>C. elegans</i> core neuronal protein-DNA interaction network. <i>Genome Research</i> , 2007, 17, 1061-1071.	2.4	87
289	Transcriptional profiling of human monocytes reveals complex changes in the expression pattern of inflammation-related genes in response to the annexin A1-derived peptide Ac1-25. <i>Journal of Leukocyte Biology</i> , 2007, 82, 1592-1604.	1.5	20
290	A novel view of the transcriptome revealed from gene trapping in mouse embryonic stem cells. <i>Genome Research</i> , 2007, 17, 1051-1060.	2.4	13
291	The Rat Epididymal Transcriptome: Comparison of Segmental Gene Expression in the Rat and Mouse Epididymides1. <i>Biology of Reproduction</i> , 2007, 76, 561-570.	1.2	169
292	Reduced PDEF Expression Increases Invasion and Expression of Mesenchymal Genes in Prostate Cancer Cells. <i>Cancer Research</i> , 2007, 67, 4219-4226.	0.4	86

#	ARTICLE	IF	CITATIONS
293	Down-regulation of the dopamine receptor D2 in mice lacking ataxin 1. <i>Human Molecular Genetics</i> , 2007, 16, 2122-2134.	1.4	61
294	Thiocyanate Transport in Resting and IL-4-Stimulated Human Bronchial Epithelial Cells: Role of Pendrin and Anion Channels. <i>Journal of Immunology</i> , 2007, 178, 5144-5153.	0.4	133
295	A Method to Integrate Benchmark Dose Estimates with Genomic Data to Assess the Functional Effects of Chemical Exposure. <i>Toxicological Sciences</i> , 2007, 98, 240-248.	1.4	174
296	The Proteome of the Mouse Photoreceptor Sensory Cilium Complex. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1299-1317.	2.5	310
297	Conserved molecular portraits of bovine and human blastocysts as a consequence of the transition from maternal to embryonic control of gene expression. <i>Physiological Genomics</i> , 2007, 31, 315-327.	1.0	57
298	Functional genomics of human pre-implantation development. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2007, 6, 120-132.	3.8	17
299	Success and failure in human spermatogenesis as revealed by teratozoospermic RNAs. <i>Human Molecular Genetics</i> , 2007, 16, 763-773.	1.4	223
300	Effects of Phenylethyl Isothiocyanate on Early Molecular Events in <i>N</i> -Nitrosomethylbenzylamine-Induced Cytotoxicity in Rat Esophagus. <i>Cancer Research</i> , 2007, 67, 6484-6492.	0.4	13
301	Breast Cancer Molecular Signatures as Determined by SAGE: Correlation with Lymph Node Status. <i>Molecular Cancer Research</i> , 2007, 5, 881-890.	1.5	99
302	Smoking and alcoholism target genes associated with plasticity and glutamate transmission in the human ventral tegmental area. <i>Human Molecular Genetics</i> , 2007, 17, 38-51.	1.4	66
303	AgBase: a unified resource for functional analysis in agriculture. <i>Nucleic Acids Research</i> , 2007, 35, D599-D603.	6.5	94
304	Histones associated with downregulated genes are hypo-acetylated in Huntington's disease models. <i>Human Molecular Genetics</i> , 2007, 16, 1293-1306.	1.4	203
305	Interferon-Mediated Immunopathological Events Are Associated with Atypical Innate and Adaptive Immune Responses in Patients with Severe Acute Respiratory Syndrome. <i>Journal of Virology</i> , 2007, 81, 8692-8706.	1.5	353
306	Role of Pituitary Hormones on 17 $\beta$ -Ethinylestradiol-Induced Cholestasis in Rat. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2007, 320, 695-705.	1.3	31
307	Meta-analysis of gene expression data: a predictor-based approach. <i>Bioinformatics</i> , 2007, 23, 1599-1606.	1.8	43
308	Application of Genomic Biomarkers to Predict Increased Lung Tumor Incidence in 2-Year Rodent Cancer Bioassays. <i>Toxicological Sciences</i> , 2007, 97, 55-64.	1.4	65
309	Gene Expression Profiles Differentiate Between Sterile SIRS and Early Sepsis. <i>Annals of Surgery</i> , 2007, 245, 611-621.	2.1	100
310	Proteasome-independent HLA-B27 Ligands Arise Mainly from Small Basic Proteins. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 923-938.	2.5	25

#	ARTICLE	IF	CITATIONS
311	g:Profiler—a web-based toolset for functional profiling of gene lists from large-scale experiments. <i>Nucleic Acids Research</i> , 2007, 35, W193-W200.	6.5	1,203
312	Macrophage Scavenger Receptor-A—Deficient Mice Are Resistant Against Diabetic Nephropathy Through Amelioration of Microinflammation. <i>Diabetes</i> , 2007, 56, 363-372.	0.3	86
313	Identification of mRNAs that continue to associate with polysomes during hypoxia. <i>Rna</i> , 2007, 13, 1116-1131.	1.6	83
314	Expression Profiling of Heat Stress Effects on Mice Fed Ergot Alkaloids. <i>Toxicological Sciences</i> , 2007, 95, 89-97.	1.4	18
315	Molecular mechanisms underlying anti-inflammatory phenotype of neonatal splenic macrophages. <i>Journal of Leukocyte Biology</i> , 2007, 82, 403-416.	1.5	27
316	Functional genomics studies of oocyte competence: evidence that reduced transcript abundance for follistatin is associated with poor developmental competence of bovine oocytes. <i>Reproduction</i> , 2007, 133, 95-106.	1.1	108
317	Individual Matrix Metalloproteinases Control Distinct Transcriptional Responses in Airway Epithelial Cells Infected with <i>Pseudomonas aeruginosa</i> . <i>Infection and Immunity</i> , 2007, 75, 5640-5650.	1.0	63
318	GENE EXPRESSION PROFILING OF RAT LIVER TREATED WITH SERUM TRIGLYCERIDE-DECREASING COMPOUNDS. <i>Journal of Toxicological Sciences</i> , 2007, 32, 387-399.	0.7	14
319	Genetic effects of a titanium surface on osteoblasts: a meta-analysis. <i>Journal of Oral Science</i> , 2007, 49, 299-309.	0.7	15
320	Life Style-Related Diseases of the Digestive System: Gene Expression in Nonalcoholic Steatohepatitis Patients and Treatment Strategies. <i>Journal of Pharmacological Sciences</i> , 2007, 105, 151-156.	1.1	17
321	Transcriptional profiling of genes that are regulated by the endoplasmic reticulum-bound transcription factor AlbZIP/CREB3L4 in prostate cells. <i>Physiological Genomics</i> , 2007, 31, 295-305.	1.0	37
323	Classification of Patients. , 0, , 957-991.		2
324	Hot spots of retroviral integration in human CD34+ hematopoietic cells. <i>Blood</i> , 2007, 110, 1770-1778.	0.6	248
325	Dietary carbohydrate modification induces alterations in gene expression in abdominal subcutaneous adipose tissue in persons with the metabolic syndrome: the FUNGENUT Study. <i>American Journal of Clinical Nutrition</i> , 2007, 85, 1417-1427.	2.2	121
326	Inadequate protein intake affects skeletal muscle transcript profiles in older humans. <i>American Journal of Clinical Nutrition</i> , 2007, 85, 1344-1352.	2.2	63
327	Coagulation and Complement Protein Differences Between Septic and Uninfected Systemic Inflammatory Response Syndrome Patients. <i>Journal of Trauma</i> , 2007, 62, 1082-1094.	2.3	20
328	Effects of glucose metabolism on the regulation of genes of fatty acid synthesis and triglyceride secretion in the liver. <i>Journal of Lipid Research</i> , 2007, 48, 1499-1510.	2.0	43
329	Gene expression microarrays and respiratory muscles. <i>Respiratory Physiology and Neurobiology</i> , 2007, 156, 103-115.	0.7	8

#	ARTICLE	IF	CITATIONS
330	Co-factors of LIM domains (Clims/Ldb/Nli) regulate corneal homeostasis and maintenance of hair follicle stem cells. <i>Developmental Biology</i> , 2007, 312, 484-500.	0.9	25
331	Gene expression profiling in livers of mice after acute inhibition of $\beta^2$ -oxidation. <i>Genomics</i> , 2007, 90, 680-689.	1.3	36
332	Pleiotropic effects and compensation mechanisms determine tissue specificity in mitochondrial myopathy and sideroblastic anemia (MLASA). <i>Molecular Genetics and Metabolism</i> , 2007, 91, 148-156.	0.5	18
333	Caloric restriction suppresses apoptotic cell death in the mammalian cochlea and leads to prevention of presbycusis. <i>Neurobiology of Aging</i> , 2007, 28, 1613-1622.	1.5	122
334	Gene Expression Profiles in Human Lymphocytes Irradiated In Vitro with Low Doses of Gamma Rays. <i>Radiation Research</i> , 2007, 168, 650.	0.7	59
335	Transactivation of miR-34a by p53 Broadly Influences Gene Expression and Promotes Apoptosis. <i>Molecular Cell</i> , 2007, 26, 745-752.	4.5	1,844
336	Salmonid host response to infectious hematopoietic necrosis (IHN) virus: Cellular receptors, viral control, and novel pathways of defence. <i>Aquaculture</i> , 2007, 272, S217-S237.	1.7	27
337	Screen for genes in periaqueductal grey of male Wistar rats related to reduced exploratory activity in the elevated plus-maze. <i>Behavioural Brain Research</i> , 2007, 183, 8-17.	1.2	3
338	Microarray analysis reveals that Type I interferon strongly increases the expression of immune-response related genes in Ubp43 (Usp18) deficient macrophages. <i>Biochemical and Biophysical Research Communications</i> , 2007, 356, 193-199.	1.0	49
339	Transcriptional profiling of stress response in cultured porcine islets. <i>Biochemical and Biophysical Research Communications</i> , 2007, 357, 118-125.	1.0	5
340	Multiple tissue gene expression analyses in Japanese medaka ( <i>Oryzias latipes</i> ) exposed to hypoxia. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2007, 145, 134-144.	1.3	57
341	Bicaudal-C Recruits CCR4-NOT Deadenylase to Target mRNAs and Regulates Oogenesis, Cytoskeletal Organization, and Its Own Expression. <i>Developmental Cell</i> , 2007, 13, 691-704.	3.1	135
342	Repetitive sequence environment distinguishes housekeeping genes. <i>Gene</i> , 2007, 390, 153-165.	1.0	47
343	Novel candidate targets of Wnt/ $\beta^2$ -catenin signaling in hepatoma cells. <i>Life Sciences</i> , 2007, 80, 690-698.	2.0	46
344	A study of $17\beta$ -estradiol-regulated genes in the vagina of postmenopausal women with vaginal atrophy. <i>Maturitas</i> , 2007, 58, 366-376.	1.0	28
345	Evolutionarily Conserved Multisubunit RBL2/p130 and E2F4 Protein Complex Represses Human Cell Cycle-Dependent Genes in Quiescence. <i>Molecular Cell</i> , 2007, 26, 539-551.	4.5	347
346	The MicroRNA miR-124 Promotes Neuronal Differentiation by Triggering Brain-Specific Alternative Pre-mRNA Splicing. <i>Molecular Cell</i> , 2007, 27, 435-448.	4.5	1,235
347	Transcriptional profiling of whole blood and serum protein analysis of mice exposed to the neurotoxin Pacific Ciguatoxin-1. <i>NeuroToxicology</i> , 2007, 28, 1099-1109.	1.4	24

#	ARTICLE	IF	CITATIONS
348	Gene expression profiling of nasopharyngeal carcinoma reveals the abnormally regulated Wnt signaling pathway. <i>Human Pathology</i> , 2007, 38, 120-133.	1.1	135
349	Whole genome microarray analysis of <i>C. elegans</i> $\beta$ and $\epsilon$ mutants. <i>FEBS Letters</i> , 2007, 581, 5050-5054.	1.3	17
350	Identification of the Transcriptional Targets of FOXP2, a Gene Linked to Speech and Language, in Developing Human Brain. <i>American Journal of Human Genetics</i> , 2007, 81, 1144-1157.	2.6	262
351	High-Throughput Analysis of Promoter Occupancy Reveals Direct Neural Targets of FOXP2, a Gene Mutated in Speech and Language Disorders. <i>American Journal of Human Genetics</i> , 2007, 81, 1232-1250.	2.6	232
352	RiceDB: A Web-Based Integrated Database for Annotating Rice Microarray. <i>Rice Science</i> , 2007, 14, 256-264.	1.7	1
353	Premature Estrogen Exposure Alters Endometrial Gene Expression to Disrupt Pregnancy in the Pig. <i>Endocrinology</i> , 2007, 148, 4761-4773.	1.4	48
354	MYC2 Differentially Modulates Diverse Jasmonate-Dependent Functions in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2007, 19, 2225-2245.	3.1	947
355	THE MECHANISMS AND APPLICATIONS OF SYMBIOTIC OPPORTUNISTIC PLANT SYMBIONTS. , 2007, , 131-155.		25
356	Aging impacts transcriptomes but not genomes of hormone-dependent breast cancers. <i>Breast Cancer Research</i> , 2007, 9, R59.	2.2	64
357	Prediction of synergistic transcription factors by function conservation. <i>Genome Biology</i> , 2007, 8, R257.	13.9	24
358	Broad network-based predictability of <i>Saccharomyces cerevisiae</i> gene loss-of-function phenotypes. <i>Genome Biology</i> , 2007, 8, R258.	13.9	87
359	GeneChip analysis of human embryonic stem cell differentiation into hemangioblasts: an in silico dissection of mixed phenotypes. <i>Genome Biology</i> , 2007, 8, R240.	13.9	23
360	Genome-wide expression profiling and bioinformatics analysis of diurnally regulated genes in the mouse prefrontal cortex. <i>Genome Biology</i> , 2007, 8, R247.	13.9	37
361	Gene expression profiling of Hfe <sup>-/-</sup> liver and duodenum in mouse strains with differing susceptibilities to iron loading: identification of transcriptional regulatory targets of Hfe and potential hemochromatosis modifiers. <i>Genome Biology</i> , 2007, 8, R221.	13.9	16
362	Simplified ontologies allowing comparison of developmental mammalian gene expression. <i>Genome Biology</i> , 2007, 8, R229.	13.9	12
363	The DAVID Gene Functional Classification Tool: a novel biological module-centric algorithm to functionally analyze large gene lists. <i>Genome Biology</i> , 2007, 8, R183.	13.9	2,105
364	Regional differences in dosage compensation on the chicken Z chromosome. <i>Genome Biology</i> , 2007, 8, R202.	13.9	98
365	Transcriptomic and phenotypic analysis of murine embryonic stem cell derived BMP2 <sup>+</sup> lineage cells: an insight into mesodermal patterning. <i>Genome Biology</i> , 2007, 8, R184.	13.9	22

#	ARTICLE	IF	CITATIONS
366	The roles of binding site arrangement and combinatorial targeting in microRNA repression of gene expression. <i>Genome Biology</i> , 2007, 8, R166.	13.9	131
367	A functional map of NF $\kappa$ B signaling identifies novel modulators and multiple system controls. <i>Genome Biology</i> , 2007, 8, R104.	13.9	20
368	Morphine effects on striatal transcriptome in mice. <i>Genome Biology</i> , 2007, 8, R128.	13.9	74
369	Revealing signaling pathway deregulation by using gene expression signatures and regulatory motif analysis. <i>Genome Biology</i> , 2007, 8, R77.	13.9	18
370	Global transcriptome analysis of murine embryonic stem cell-derived cardiomyocytes. <i>Genome Biology</i> , 2007, 8, R56.	13.9	54
371	microRNA expression in the prefrontal cortex of individuals with schizophrenia and schizoaffective disorder. <i>Genome Biology</i> , 2007, 8, R27.	13.9	489
372	DiscoverySpace: an interactive data analysis application. <i>Genome Biology</i> , 2007, 8, R6.	13.9	41
373	GENECODIS: a web-based tool for finding significant concurrent annotations in gene lists. <i>Genome Biology</i> , 2007, 8, R3.	13.9	554
374	Expression and regulation of CCL18 in synovial fluid neutrophils of patients with rheumatoid arthritis. <i>Arthritis Research and Therapy</i> , 2007, 9, R94.	1.6	48
375	Genome-wide expression profiling of lymphoblastoid cell lines distinguishes different forms of autism and reveals shared pathways. <i>Human Molecular Genetics</i> , 2007, 16, 1682-1698.	1.4	290
376	Macromolecule biosynthesis: a key function of sleep. <i>Physiological Genomics</i> , 2007, 31, 441-457.	1.0	322
377	Gene Expression Profile of Bioreactor-Cultured Cardiac Cells: Activation of Morphogenetic Pathways for Tissue Engineering. <i>DNA and Cell Biology</i> , 2007, 26, 425-434.	0.9	11
378	Multiplicity adjustment for intersection-union test: detecting overlapping genes from multiple microarray gene lists. , 2007, , .		1
379	An Information Theoretic Framework for Ontology-based Bioinformatics. , 2007, , .		4
380	DURATION-DEPENDENT CYTOPROTECTIVE VERSUS INFLAMMATORY EFFECTS OF LUNG EPITHELIAL FIBROBLAST GROWTH FACTOR-7 EXPRESSION. <i>Experimental Lung Research</i> , 2007, 33, 385-417.	0.5	9
381	Strategies for Identifying Statistically Significant Dense Regions in Microarray Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 415-429.	1.9	5
382	Hepatic Transcriptional Networks Induced by Exposure to 2,3,7,8-Tetrachlorodibenzo-p-dioxin. <i>Chemical Research in Toxicology</i> , 2007, 20, 1573-1581.	1.7	34
383	A Resource Allocation Control for Wireless Ad Hoc Networks. , 2007, , .		1

#	ARTICLE	IF	CITATIONS
384	Comparison of the Cytotoxicity of the Nitroaromatic Drug Flutamide to Its Cyano Analogue in the Hepatocyte Cell Line TAMH: Evidence for Complex I Inhibition and Mitochondrial Dysfunction Using Toxicogenomic Screening. <i>Chemical Research in Toxicology</i> , 2007, 20, 1277-1290.	1.7	56
385	Cell- and gene-specific regulation of primary target genes by the androgen receptor. <i>Genes and Development</i> , 2007, 21, 2005-2017.	2.7	302
386	Sexually Dimorphic Gene Expression in Mammalian Somatic Tissue. <i>Gender Medicine</i> , 2007, 4, S75-S95.	1.4	64
387	Preventive effect of d-psicose, one of rare ketohexoses, on di-(2-ethylhexyl) phthalate (DEHP)-induced testicular injury in rat. <i>Toxicology Letters</i> , 2007, 173, 107-117.	0.4	70
388	PCR-verified microarray analysis and functional in vitro studies indicate a role of $\alpha$ -tocopherol in vesicular transport. <i>Free Radical Research</i> , 2007, 41, 930-942.	1.5	21
389	Genomic analysis of human lung fibroblasts exposed to vanadium pentoxide to identify candidate genes for occupational bronchitis. <i>Respiratory Research</i> , 2007, 8, 34.	1.4	30
390	Transforming Growth Factor- $\beta$ 2 and microRNA:mRNA Regulatory Networks in Epithelial Plasticity. <i>Cells Tissues Organs</i> , 2007, 185, 157-161.	1.3	144
391	Diesel Exhaust Inhalation and Assessment of Peripheral Blood Mononuclear Cell Gene Transcription Effects: An Exploratory Study of Healthy Human Volunteers. <i>Inhalation Toxicology</i> , 2007, 19, 1107-1119.	0.8	84
392	Gene ontology analysis of human hair follicle bulge molecular signature. <i>Journal of Dermatological Science</i> , 2007, 45, 147-150.	1.0	12
393	Interpreting physiological responses to environmental change through gene expression profiling. <i>Journal of Experimental Biology</i> , 2007, 210, 1584-1592.	0.8	103
394	Genomic and Functional Studies of Drosophila Sex Hierarchy Regulated Gene Expression in Adult Head and Nervous System Tissues. <i>PLoS Genetics</i> , 2007, 3, e216.	1.5	111
395	Differential Cerebral Cortex Transcriptomes of Baboon Neonates Consuming Moderate and High Docosahexaenoic Acid Formulas. <i>PLoS ONE</i> , 2007, 2, e370.	1.1	49
396	Public Databases and Software for the Pathway Analysis of Cancer Genomes. <i>Cancer Informatics</i> , 2007, 3, 117693510700300.	0.9	9
397	Identification and Characterization of Renal Cell Carcinoma Gene Markers. <i>Cancer Informatics</i> , 2007, 3, 117693510700300.	0.9	27
398	Up-regulation of Tissue Factor in Human Pulmonary Artery Endothelial Cells after Ultrafine Particle Exposure. <i>Environmental Health Perspectives</i> , 2007, 115, 535-540.	2.8	56
399	GSMA: Gene Set Matrix Analysis, An Automated Method for Rapid Hypothesis Testing of Gene Expression Data. <i>Bioinformatics and Biology Insights</i> , 2007, 1, 117793220700100.	1.0	2
400	Ozone induces clear cellular and molecular responses in the mouse lung independently of the transcription-coupled repair status. <i>Journal of Applied Physiology</i> , 2007, 102, 1185-1192.	1.2	10
401	Genome-Level Longitudinal Expression of Signaling Pathways and Gene Networks in Pediatric Septic Shock. <i>Molecular Medicine</i> , 2007, 13, 495-508.	1.9	114

#	ARTICLE	IF	CITATIONS
402	Integrative database management for mouse development: Systems and concepts. Birth Defects Research Part C: Embryo Today Reviews, 2007, 81, 1-19.	3.6	5
403	Comparative proteomic characterization of articular cartilage tissue from normal donors and patients with osteoarthritis. Arthritis and Rheumatism, 2007, 56, 3675-3684.	6.7	146
404	Dysregulation of X-linked gene expression in Klinefelter's syndrome and association with verbal cognition. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2007, 144B, 728-734.	1.1	68
405	Reprogramming of genetic networks during initiation of the Fetal Alcohol Syndrome. Developmental Dynamics, 2007, 236, 613-631.	0.8	122
406	Elf5 is an epithelium-specific, fibroblast growth factor-sensitive transcription factor in the embryonic lung. Developmental Dynamics, 2007, 236, 1175-1192.	0.8	66
407	Mouse olfactory sensory neurons express 10,000 genes. Journal of Comparative Neurology, 2007, 502, 1138-1156.	0.9	72
408	Diverging mechanisms for TNF-Î± receptors in normal mouse brains and in functional recovery after injury: From gene to behavior. Journal of Neuroscience Research, 2007, 85, 2668-2685.	1.3	21
409	Statistical methods for the analysis of high-throughput data based on functional profiles derived from the Gene Ontology. Journal of Statistical Planning and Inference, 2007, 137, 3975-3989.	0.4	16
410	Silencing of core transcription factors in human EC cells highlights the importance of autocrine FGF signaling for self-renewal. BMC Developmental Biology, 2007, 7, 46.	2.1	62
411	Characterization of the effect of sample quality on high density oligonucleotide microarray data using progressively degraded rat liver RNA. BMC Biotechnology, 2007, 7, 57.	1.7	72
412	Common molecular pathways involved in human CD133+/CD34+ progenitor cell expansion and cancer. Cancer Cell International, 2007, 7, 11.	1.8	15
413	Modulation by decitabine of gene expression and growth of osteosarcoma U2OS cells in vitro and in xenografts: Identification of apoptotic genes as targets for demethylation. Cancer Cell International, 2007, 7, 14.	1.8	48
414	OCPAT: an online codon-preserved alignment tool for evolutionary genomic analysis of protein coding sequences. Source Code for Biology and Medicine, 2007, 2, 5.	1.7	11
415	A hierarchical analysis of transcriptome alterations in intrauterine growth restriction (IUGR) reveals common pathophysiological pathways in mammals. Journal of Pathology, 2007, 213, 337-346.	2.1	39
416	Nine steps to proteomic wisdom: A practical guide to using protein-protein interaction networks and molecular pathways as a framework for interpreting disease proteomic profiles. Proteomics - Clinical Applications, 2007, 1, 1156-1168.	0.8	6
417	Proteomic analysis of protein expression changes in a model of gliomagenesis. Proteomics - Clinical Applications, 2007, 1, 1485-1498.	0.8	3
418	A multivariate analysis approach to the integration of proteomic and gene expression data. Proteomics, 2007, 7, 2162-2171.	1.3	70
419	Diabetes-induced changes in the renal cortical proteome assessed with two-dimensional gel electrophoresis and mass spectrometry. Proteomics, 2007, 7, 1729-1742.	1.3	53



#	ARTICLE	IF	CITATIONS
420	Combination of peptide OFFGEL fractionation and label-free quantitation facilitated proteomics profiling of extraocular muscle. <i>Proteomics</i> , 2007, 7, 3404-3416.	1.3	42
421	The LIM-only factor LMO4 regulates expression of the BMP7 gene through an HDAC2-dependent mechanism, and controls cell proliferation and apoptosis of mammary epithelial cells. <i>Oncogene</i> , 2007, 26, 6431-6441.	2.6	58
422	Gene expression and the biological phenotype of papillary thyroid carcinomas. <i>Oncogene</i> , 2007, 26, 7894-7903.	2.6	71
423	MMTV insertional mutagenesis identifies genes, gene families and pathways involved in mammary cancer. <i>Nature Genetics</i> , 2007, 39, 759-769.	9.4	184
424	A critical developmental switch defines the kinetics of kidney cyst formation after loss of Pkd1. <i>Nature Medicine</i> , 2007, 13, 1490-1495.	15.2	370
425	The Near-Naked Hairless (Hr) Mutation Disrupts Hair Formation but Is Not Due to a Mutation in the Hairless Coding Region. <i>Journal of Investigative Dermatology</i> , 2007, 127, 1605-1614.	0.3	8
426	Aplidin synergizes with cytosine arabinoside: functional relevance of mitochondria in Aplidin-induced cytotoxicity. <i>Leukemia</i> , 2007, 21, 2399-2405.	3.3	14
427	Expression profiling in monozygotic twins discordant for bipolar disorder reveals dysregulation of the WNT signalling pathway. <i>Molecular Psychiatry</i> , 2007, 12, 815-825.	4.1	97
428	Genome-wide atlas of gene expression in the adult mouse brain. <i>Nature</i> , 2007, 445, 168-176.	13.7	4,863
429	Expression profiling of the mouse prostate after castration and hormone replacement: implication of H-cadherin in prostate tumorigenesis. <i>Differentiation</i> , 2007, 75, 219-234.	1.0	59
430	Molecular markers distinguishing supragranular and infragranular layers in the human prefrontal cortex. <i>European Journal of Neuroscience</i> , 2007, 25, 1843-1854.	1.2	52
431	Using gene chips to identify organ-specific, smooth muscle responses to experimental diabetes: potential applications to urological diseases. <i>BJU International</i> , 2007, 99, 418-430.	1.3	28
432	Microarray analysis of exstrophic human bladder smooth muscle. <i>BJU International</i> , 2007, 101, 070916224627009-???	1.3	18
433	General and specific host responses to bacterial infection in Peyer's patches: a role for stromelysin-1 (matrix metalloproteinase-3) during <i>Salmonella enterica</i> infection. <i>Molecular Microbiology</i> , 2007, 64, 94-110.	1.2	28
434	Anxiety induced by prenatal stress is associated with suppression of hippocampal genes involved in synaptic function. <i>Journal of Neurochemistry</i> , 2007, 101, 1018-1030.	2.1	66
435	An integrated analysis of genes and pathways exhibiting metabolic differences between estrogen receptor positive breast cancer cells. <i>BMC Cancer</i> , 2007, 7, 181.	1.1	14
436	Novel markers for differentiation of lobular and ductal invasive breast carcinomas by laser microdissection and microarray analysis. <i>BMC Cancer</i> , 2007, 7, 55.	1.1	341
437	Gene expression analysis in human osteoblasts exposed to dexamethasone identifies altered developmental pathways as putative drivers of osteoporosis. <i>BMC Musculoskeletal Disorders</i> , 2007, 8, 12.	0.8	78

#	ARTICLE	IF	CITATIONS
438	Understanding network concepts in modules. <i>BMC Systems Biology</i> , 2007, 1, 24.	3.0	385
439	Genome Expression Pathway Analysis Tool – Analysis and visualization of microarray gene expression data under genomic, proteomic and metabolic context. <i>BMC Bioinformatics</i> , 2007, 8, 179.	1.2	19
440	Joint mapping of genes and conditions via multidimensional unfolding analysis. <i>BMC Bioinformatics</i> , 2007, 8, 181.	1.2	10
441	Post hoc pattern matching: assigning significance to statistically defined expression patterns in single channel microarray data. <i>BMC Bioinformatics</i> , 2007, 8, 240.	1.2	19
442	Portraits of breast cancer progression. <i>BMC Bioinformatics</i> , 2007, 8, 291.	1.2	32
443	EDISA: extracting biclusters from multiple time-series of gene expression profiles. <i>BMC Bioinformatics</i> , 2007, 8, 334.	1.2	52
444	Linking microarray reporters with protein functions. <i>BMC Bioinformatics</i> , 2007, 8, 360.	1.2	12
445	Improved human disease candidate gene prioritization using mouse phenotype. <i>BMC Bioinformatics</i> , 2007, 8, 392.	1.2	232
446	DAVID Knowledgebase: a gene-centered database integrating heterogeneous gene annotation resources to facilitate high-throughput gene functional analysis. <i>BMC Bioinformatics</i> , 2007, 8, 426.	1.2	510
447	The Firegoose: two-way integration of diverse data from different bioinformatics web resources with desktop applications. <i>BMC Bioinformatics</i> , 2007, 8, 456.	1.2	30
448	Including probe-level uncertainty in model-based gene expression clustering. <i>BMC Bioinformatics</i> , 2007, 8, 98.	1.2	16
449	Statistical analysis of genomic protein family and domain controlled annotations for functional investigation of classified gene lists. <i>BMC Bioinformatics</i> , 2007, 8, S14.	1.2	3
450	EasyGO: Gene Ontology-based annotation and functional enrichment analysis tool for agronomical species. <i>BMC Genomics</i> , 2007, 8, 246.	1.2	137
451	Integrated analysis of independent gene expression microarray datasets improves the predictability of breast cancer outcome. <i>BMC Genomics</i> , 2007, 8, 331.	1.2	22
452	Characterization of oligopeptide patterns in large protein sets. <i>BMC Genomics</i> , 2007, 8, 346.	1.2	11
453	Proteomics reveals multiple routes to the osteogenic phenotype in mesenchymal stem cells. <i>BMC Genomics</i> , 2007, 8, 380.	1.2	24
454	BMDEExpress: a software tool for the benchmark dose analyses of genomic data. <i>BMC Genomics</i> , 2007, 8, 387.	1.2	171
455	Computational selection and prioritization of candidate genes for Fetal Alcohol Syndrome. <i>BMC Genomics</i> , 2007, 8, 389.	1.2	36

#	ARTICLE	IF	CITATIONS
456	Large-scale analysis by SAGE reveals new mechanisms of v-erbA oncogene action. <i>BMC Genomics</i> , 2007, 8, 390.	1.2	15
457	Suicide candidate genes associated with bipolar disorder and schizophrenia: An exploratory gene expression profiling analysis of post-mortem prefrontal cortex. <i>BMC Genomics</i> , 2007, 8, 413.	1.2	91
458	Gene expression and biological processes influenced by deletion of Stat3 in pulmonary type II epithelial cells. <i>BMC Genomics</i> , 2007, 8, 455.	1.2	48
459	The molecular signature of therapeutic mesenchymal stem cells exposes the architecture of the hematopoietic stem cell niche synapse. <i>BMC Genomics</i> , 2007, 8, 65.	1.2	61
460	Transcriptional profiling of C57 and DBA strains of mice in the absence and presence of morphine. <i>BMC Genomics</i> , 2007, 8, 76.	1.2	39
461	Expression profiling of genes regulated by TGF-beta: Differential regulation in normal and tumour cells. <i>BMC Genomics</i> , 2007, 8, 98.	1.2	105
462	Comparative gene expression profiling in two congenic mouse strains following <i>Bordetella pertussis</i> infection. <i>BMC Microbiology</i> , 2007, 7, 88.	1.3	5
463	Role of IKK and ERK pathways in intrinsic inflammation of cystic fibrosis airways. <i>Biochemical Pharmacology</i> , 2007, 73, 1982-1994.	2.0	83
464	Genes encoding mitochondrial respiratory chain components are profoundly down-regulated with aging in the cochlea of DBA/2J mice. <i>Brain Research</i> , 2007, 1182, 26-33.	1.1	38
465	A novel approach of proteomics and transcriptomics to study the mechanism of action of the antioxidant iron chelator green tea polyphenol (-)-epigallocatechin-3-gallate. <i>Free Radical Biology and Medicine</i> , 2007, 43, 546-556.	1.3	71
466	Integration of statistical inference methods and a novel control measure to improve sensitivity and specificity of data analysis in expression profiling studies. <i>Journal of Biomedical Informatics</i> , 2007, 40, 552-560.	2.5	24
467	The <i>C. elegans</i> TGF- $\beta$ Dauer Pathway Regulates Longevity via Insulin Signaling. <i>Current Biology</i> , 2007, 17, 1635-1645.	1.8	242
468	Changes in gene-expression during development of the murine molar tooth germ. <i>Archives of Oral Biology</i> , 2007, 52, 803-813.	0.8	21
469	Differential gene expression in CD8+ cells from HIV-1-infected subjects showing suppression of HIV replication. <i>Virology</i> , 2007, 362, 217-225.	1.1	14
470	Transcriptional profile of Rous Sarcoma Virus transformed chicken embryo fibroblasts reveals new signaling targets of viral-src. <i>Virology</i> , 2007, 364, 10-20.	1.1	13
471	In vitro gene expression data supporting a DNA non-reactive genotoxic mechanism for ochratoxin A. <i>Toxicology and Applied Pharmacology</i> , 2007, 220, 216-224.	1.3	55
472	Time course investigation of PPAR $\alpha$ - and Kupffer cell-dependent effects of WY-14,643 in mouse liver using microarray gene expression. <i>Toxicology and Applied Pharmacology</i> , 2007, 225, 267-277.	1.3	19
473	Activation of tyrosine kinase receptor signaling pathway by rasagiline facilitates neurorescue and restoration of nigrostriatal dopamine neurons in post-MPTP-induced parkinsonism. <i>Neurobiology of Disease</i> , 2007, 25, 35-44.	2.1	123

#	ARTICLE	IF	CITATIONS
474	Microarray Analysis Reveals Overexpression of CD163 and HO-1 in Symptomatic Carotid Plaques. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2007, 27, 154-160.	1.1	50
475	Fibroblast Growth Factor 2 Modulates Transforming Growth Factor $\beta$ Signaling in Mouse Embryonic Fibroblasts and Human ESCs (hESCs) to Support hESC Self-Renewal. <i>Stem Cells</i> , 2007, 25, 455-464.	1.4	212
476	Pretreatment Gene Expression Profiles Can Be Used to Predict Response to Neoadjuvant Chemoradiotherapy in Esophageal Cancer. <i>Annals of Surgical Oncology</i> , 2007, 14, 3602-3609.	0.7	58
477	Neonatal dopamine depletion induces changes in morphogenesis and gene expression in the developing cortex. <i>Neurotoxicity Research</i> , 2007, 11, 107-130.	1.3	26
478	Lung response to Bordetella pertussis infection in mice identified by gene-expression profiling. <i>Immunogenetics</i> , 2007, 59, 555-564.	1.2	19
479	Weighted gene coexpression network analysis strategies applied to mouse weight. <i>Mammalian Genome</i> , 2007, 18, 463-472.	1.0	337
480	Metastasis signatures: genes regulating tumor-microenvironment interactions predict metastatic behavior. <i>Cancer and Metastasis Reviews</i> , 2008, 27, 75-83.	2.7	76
481	Sexually dimorphic gene expression in the heart of mice and men. <i>Journal of Molecular Medicine</i> , 2008, 86, 61-74.	1.7	135
482	Sex-specific pathways in early cardiac response to pressure overload in mice. <i>Journal of Molecular Medicine</i> , 2008, 86, 1013-1024.	1.7	115
483	Renewal and preliminary study of expressed sequence tags database on human fetal liver aged 22 wk of gestation. <i>Science Bulletin</i> , 2008, 53, 3204-3210.	4.3	0
484	Integrative decomposition procedure and Kappa statistics set up ATF2 ion binding module in malignant pleural mesothelioma (MPM). <i>Frontiers of Electrical and Electronic Engineering in China: Selected Publications From Chinese Universities</i> , 2008, 3, 381-387.	0.6	23
485	$^{18}\text{O}$ Labeling for a Quantitative Proteomic Analysis of Glycoproteins in Hepatocellular Carcinoma. <i>Clinical Proteomics</i> , 2008, 4, 137-155.	1.1	18
486	Stemming Cancer: Functional Genomics of Cancer Stem Cells in Solid Tumors. <i>Stem Cell Reviews and Reports</i> , 2008, 4, 319-328.	5.6	56
487	Herpes simplex virus type 1 modulates cellular gene expression during quiescent infection of neuronal cells. <i>Archives of Virology</i> , 2008, 153, 1335-1345.	0.9	13
488	Inactivation of the 3-phosphoglycerate dehydrogenase gene in mice: changes in gene expression and associated regulatory networks resulting from serine deficiency. <i>Functional and Integrative Genomics</i> , 2008, 8, 235-249.	1.4	18
489	Mutant huntingtin activates Nrf2-responsive genes and impairs dopamine synthesis in a PC12 model of Huntington's disease. <i>BMC Molecular Biology</i> , 2008, 9, 84.	3.0	66
490	Association between PPARGC1A polymorphisms and the occurrence of nonalcoholic fatty liver disease (NAFLD). <i>BMC Gastroenterology</i> , 2008, 8, 27.	0.8	59
491	The estrogen hypothesis of Schizophrenia implicates glucose metabolism: Association study in three independent samples. <i>BMC Medical Genetics</i> , 2008, 9, 39.	2.1	31

#	ARTICLE	IF	CITATIONS
492	Putative psychosis genes in the prefrontal cortex: combined analysis of gene expression microarrays. <i>BMC Psychiatry</i> , 2008, 8, 87.	1.1	48
493	Regulatory subunits of PKA define an axis of cellular proliferation/differentiation in ovarian cancer cells. <i>BMC Medical Genomics</i> , 2008, 1, 43.	0.7	28
494	Monocytes of patients with familial hypercholesterolemia show alterations in cholesterol metabolism. <i>BMC Medical Genomics</i> , 2008, 1, 60.	0.7	52
495	Modeling gene-by-environment interaction in comorbid depression with alcohol use disorders via an integrated bioinformatics approach. <i>BioData Mining</i> , 2008, 1, 2.	2.2	39
496	Maternal Oct-4 is a potential key regulator of the developmental competence of mouse oocytes. <i>BMC Developmental Biology</i> , 2008, 8, 97.	2.1	70
497	Comparative proteome analysis of three mouse lung adenocarcinoma CMT cell lines with different metastatic potential by two-dimensional gel electrophoresis and mass spectrometry. <i>Proteomics</i> , 2008, 8, 4932-4945.	1.3	10
498	Exploration of the normal human bronchoalveolar lavage fluid proteome. <i>Proteomics - Clinical Applications</i> , 2008, 2, 585-595.	0.8	51
499	Alpha <sub>1</sub> -antitrypsin and complement component C7 are involved in asthma exacerbation. <i>Proteomics - Clinical Applications</i> , 2008, 2, 46-54.	0.8	16
500	Analysis of the human testis proteome by mass spectrometry and bioinformatics. <i>Proteomics - Clinical Applications</i> , 2008, 2, 1651-1657.	0.8	31
501	Gene profiling approaches help to define the specific functions of retinoblastoma family in epidermis. <i>Molecular Carcinogenesis</i> , 2008, 47, 209-221.	1.3	29
502	Effect of astrocyte-targeted production of IL-6 on traumatic brain injury and its impact on the cortical transcriptome. <i>Developmental Neurobiology</i> , 2008, 68, 195-208.	1.5	33
503	FACS-array gene expression analysis during early development of mouse telencephalic interneurons. <i>Developmental Neurobiology</i> , 2008, 68, 434-445.	1.5	33
504	A meta-analysis of nonsense mutations causing human genetic disease. <i>Human Mutation</i> , 2008, 29, 1037-1047.	1.1	348
505	Protective effects of dietary curcumin in mouse model of chemically induced colitis are strain dependent. <i>Inflammatory Bowel Diseases</i> , 2008, 14, 780-793.	0.9	63
506	E-selectin regulates gene expression in metastatic colorectal carcinoma cells and enhances HMGB1 release. <i>International Journal of Cancer</i> , 2008, 123, 1741-1750.	2.3	32
507	Transcriptional profiling identifies an interferon-associated host immune response in invasive squamous cell carcinoma of the skin. <i>International Journal of Cancer</i> , 2008, 123, 2605-2615.	2.3	27
508	Modulation of several waves of gene expression during FGF <sub>1</sub> induced epithelial-mesenchymal transition of carcinoma cells. <i>Journal of Cellular Biochemistry</i> , 2008, 104, 826-839.	1.2	56
509	Genome-wide expression analysis of cells expressing gain of function mutant D374Y-PCSK9. <i>Journal of Cellular Physiology</i> , 2008, 217, 459-467.	2.0	34

#	ARTICLE	IF	CITATIONS
510	Transcriptional profiling defines the effects of nickel in human epidermal keratinocytes. <i>Journal of Cellular Physiology</i> , 2008, 217, 686-692.	2.0	13
511	C-Myc and its target FoxM1 are critical downstream effectors of constitutive androstane receptor (CAR) mediated direct liver hyperplasia. <i>Hepatology</i> , 2008, 48, 1302-1311.	3.6	121
512	Bone marrow glycophorin <sup>a</sup> -positive erythroid cells of myelodysplastic patients responding to high-dose rHuEPO therapy have a different gene expression pattern from those of nonresponders. <i>American Journal of Hematology</i> , 2008, 83, 531-539.	2.0	11
514	Interactive data analysis and clustering of genomic data. <i>Neural Networks</i> , 2008, 21, 368-378.	3.3	31
515	Assessing CMT cell line stability by two dimensional polyacrylamide gel electrophoresis and mass spectrometry based proteome analysis. <i>Journal of Proteomics</i> , 2008, 71, 160-167.	1.2	10
516	Transcriptional profiling of mouse liver in response to chronic heat stress. <i>Journal of Thermal Biology</i> , 2008, 33, 157-167.	1.1	17
517	Large-scale estimates of cellular origins of mRNAs: Enhancing the yield of transcriptome analyses. <i>Journal of Neuroscience Methods</i> , 2008, 167, 198-206.	1.3	13
518	Bioinformatics applications for pathway analysis of microarray data. <i>Current Opinion in Biotechnology</i> , 2008, 19, 50-54.	3.3	158
519	Gene expression profiles of murine fatty liver induced by the administration of methotrexate. <i>Toxicology</i> , 2008, 249, 75-84.	2.0	17
520	High glucose downregulates endothelial progenitor cell number via SIRT1. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 936-945.	1.1	103
521	Defining Pancreatic Endocrine Precursors and Their Descendants. <i>Diabetes</i> , 2008, 57, 654-668.	0.3	73
522	The Molecular Basis of Shoot Responses of Maize Seedlings to <i>Trichoderma harzianum</i> T22 Inoculation of the Root: A Proteomic Approach. <i>Plant Physiology</i> , 2008, 147, 2147-2163.	2.3	271
523	Differential placental gene expression in preeclampsia. <i>American Journal of Obstetrics and Gynecology</i> , 2008, 199, 566.e1-566.e11.	0.7	131
524	Differential gene expression profiles of normal human parotid and submandibular glands. <i>Oral Diseases</i> , 2008, 14, 500-509.	1.5	16
525	Induction of Cerebral Arteriogenesis Leads to Early-Phase Expression of Protease Inhibitors in Growing Collaterals of the Brain. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2008, 28, 1811-1823.	2.4	24
526	The fibromatosis signature defines a robust stromal response in breast carcinoma. <i>Laboratory Investigation</i> , 2008, 88, 591-601.	1.7	100
527	Cell cycle and immune-related processes are significantly altered in chronic GVHD. <i>Bone Marrow Transplantation</i> , 2008, 41, 1047-1057.	1.3	11
528	Wild-type p53 and p73 negatively regulate expression of proliferation related genes. <i>Oncogene</i> , 2008, 27, 2583-2593.	2.6	64

#	ARTICLE	IF	CITATIONS
529	The MYCN oncogene is a direct target of miR-34a. <i>Oncogene</i> , 2008, 27, 5204-5213.	2.6	273
530	Microarray Analysis of the Global Alterations in the Gene Expression in the Placentas From Cigarette-smoking Mothers. <i>Clinical Pharmacology and Therapeutics</i> , 2008, 83, 542-550.	2.3	73
531	Haplotype patterns in cancer-related genes with long-range linkage disequilibrium: no evidence of association with breast cancer or positive selection. <i>European Journal of Human Genetics</i> , 2008, 16, 252-260.	1.4	7
532	Innate immune response gene expression profiles characterize primary antiphospholipid syndrome. <i>Genes and Immunity</i> , 2008, 9, 38-46.	2.2	47
533	Microarray Analysis Demonstrates a Role for Slug in Epidermal Homeostasis. <i>Journal of Investigative Dermatology</i> , 2008, 128, 361-369.	0.3	21
534	UV Radiation-Induced Immunosuppression Is Greater in Men and Prevented by Topical Nicotinamide. <i>Journal of Investigative Dermatology</i> , 2008, 128, 447-454.	0.3	167
535	Superficial, Nodular, and Morpheiform Basal-Cell Carcinomas Exhibit Distinct Gene Expression Profiles. <i>Journal of Investigative Dermatology</i> , 2008, 128, 1797-1805.	0.3	48
536	Gene Expression Profiling of Sporadic Parkinson's Disease Substantia Nigra Pars Compacta Reveals Impairment of Ubiquitin-Proteasome Subunits, SKP1A, Aldehyde Dehydrogenase, and Chaperone HSC70. <i>Annals of the New York Academy of Sciences</i> , 2005, 1053, 356-375.	1.8	2
537	Prg1 is regulated by the basic helix-loop-helix transcription factor Math2. <i>Journal of Neurochemistry</i> , 2008, 106, 2375-2384.	2.1	13
538	Evaluation of gene expression profiles of immature dendritic cells prepared from peripheral blood mononuclear cells. <i>Transfusion</i> , 2008, 48, 647-657.	0.8	13
539	The proteome of red cell membranes and vesicles during storage in blood bank conditions. <i>Transfusion</i> , 2008, 48, 827-835.	0.8	64
540	Serial analysis of gene expression in a rat lung model of asthma. <i>Respirology</i> , 2008, 13, 972-982.	1.3	16
541	Microarray analysis of bladder smooth muscle from patients with myelomeningocele. <i>BJU International</i> , 2008, 102, 741-746.	1.3	30
542	Haploinsufficiency of <i>RPS14</i> in 5q <sup>+</sup> syndrome is associated with deregulation of ribosomal and translation-related genes. <i>British Journal of Haematology</i> , 2008, 142, 57-64.	1.2	91
543	Coordinated expression of cytoskeleton regulating genes in the accelerated neurite outgrowth of P19 embryonic carcinoma cells. <i>Experimental Cell Research</i> , 2008, 314, 677-690.	1.2	9
544	Variation of the genetic expression pattern after exposure to estradiol-17 $\beta$ and 4-nonylphenol in male zebrafish ( <i>Danio rerio</i> ). <i>General and Comparative Endocrinology</i> , 2008, 158, 138-144.	0.8	55
545	Simple integrative preprocessing preserves what is shared in data sources. <i>BMC Bioinformatics</i> , 2008, 9, 111.	1.2	12
546	Merging microarray data from separate breast cancer studies provides a robust prognostic test. <i>BMC Bioinformatics</i> , 2008, 9, 125.	1.2	82

#	ARTICLE	IF	CITATIONS
547	Stability of gene contributions and identification of outliers in multivariate analysis of microarray data. <i>BMC Bioinformatics</i> , 2008, 9, 289.	1.2	15
548	Literature-aided meta-analysis of microarray data: a compendium study on muscle development and disease. <i>BMC Bioinformatics</i> , 2008, 9, 291.	1.2	21
549	Combining Shapley value and statistics to the analysis of gene expression data in children exposed to air pollution. <i>BMC Bioinformatics</i> , 2008, 9, 361.	1.2	29
550	SQUAT: A web tool to mine human, murine and avian SAGE data. <i>BMC Bioinformatics</i> , 2008, 9, 378.	1.2	7
551	Presenting and exploring biological pathways with PathVisio. <i>BMC Bioinformatics</i> , 2008, 9, 399.	1.2	305
552	Meta-analysis of breast cancer microarray studies in conjunction with conserved cis-elements suggest patterns for coordinate regulation. <i>BMC Bioinformatics</i> , 2008, 9, 63.	1.2	41
553	Improving the power for detecting overlapping genes from multiple DNA microarray-derived gene lists. <i>BMC Bioinformatics</i> , 2008, 9, S14.	1.2	14
554	From microarray to biology: an integrated experimental, statistical and in silico analysis of how the extracellular matrix modulates the phenotype of cancer cells. <i>BMC Bioinformatics</i> , 2008, 9, S4.	1.2	15
555	Coordinated evolution of co-expressed gene clusters in the <i>Drosophila</i> transcriptome. <i>BMC Evolutionary Biology</i> , 2008, 8, 2.	3.2	30
556	MADIBA: A web server toolkit for biological interpretation of <i>Plasmodium</i> and plant gene clusters. <i>BMC Genomics</i> , 2008, 9, 105.	1.2	21
557	Transcriptome analysis identifies pathways associated with enhanced maternal performance in QSi5 mice. <i>BMC Genomics</i> , 2008, 9, 197.	1.2	18
558	In vivo gene expression profiling of human intestinal epithelial cells: analysis by laser microdissection of formalin fixed tissues. <i>BMC Genomics</i> , 2008, 9, 209.	1.2	45
559	Genomic analysis of post-mating changes in the honey bee queen ( <i>Apis mellifera</i> ). <i>BMC Genomics</i> , 2008, 9, 232.	1.2	116
560	Transcriptome profiling of developmental and xenobiotic responses in a keystone soil animal, the oligochaete annelid <i>Lumbricus rubellus</i> . <i>BMC Genomics</i> , 2008, 9, 266.	1.2	93
561	Functional characterization of endogenous siRNA target genes in <i>Caenorhabditis elegans</i> . <i>BMC Genomics</i> , 2008, 9, 270.	1.2	19
562	Sources of variation in baseline gene expression levels from toxicogenomics study control animals across multiple laboratories. <i>BMC Genomics</i> , 2008, 9, 285.	1.2	76
563	Meta-analysis of nasopharyngeal carcinoma microarray data explores mechanism of EBV-regulated neoplastic transformation. <i>BMC Genomics</i> , 2008, 9, 322.	1.2	17
564	Evolutionary conservation of zinc finger transcription factor binding sites in promoters of genes co-expressed with WT1 in prostate cancer. <i>BMC Genomics</i> , 2008, 9, 337.	1.2	21



#	ARTICLE	IF	CITATIONS
565	Development of a human mitochondrial oligonucleotide microarray (h-MitoArray) and gene expression analysis of fibroblast cell lines from 13 patients with isolated F1Fo ATP synthase deficiency. <i>BMC Genomics</i> , 2008, 9, 38.	1.2	22
566	Prioritizing genes of potential relevance to diseases affected by sex hormones: an example of Myasthenia Gravis. <i>BMC Genomics</i> , 2008, 9, 481.	1.2	8
567	Transcriptional response of Mexican axolotls to <i>Ambystoma tigrinum</i> virus (ATV) infection. <i>BMC Genomics</i> , 2008, 9, 493.	1.2	40
568	Gene expression profiling in chicken heterophils with <i>Salmonella enteritidis</i> stimulation using a chicken 44 K Agilent microarray. <i>BMC Genomics</i> , 2008, 9, 526.	1.2	73
569	Transcriptional response of rat frontal cortex following acute In Vivo exposure to the pyrethroid insecticides permethrin and deltamethrin. <i>BMC Genomics</i> , 2008, 9, 546.	1.2	19
570	Characterization of a newly developed chicken 44K Agilent microarray. <i>BMC Genomics</i> , 2008, 9, 60.	1.2	68
571	Activation of counter-regulatory mechanisms in a rat renal acute rejection model. <i>BMC Genomics</i> , 2008, 9, 71.	1.2	24
572	Analysis of the retinal gene expression profile after hypoxic preconditioning identifies candidate genes for neuroprotection. <i>BMC Genomics</i> , 2008, 9, 73.	1.2	56
573	Effect of thyroid hormone concentration on the transcriptional response underlying induced metamorphosis in the Mexican axolotl ( <i>Ambystoma</i> ). <i>BMC Genomics</i> , 2008, 9, 78.	1.2	37
574	Divergence of canonical danger signals: The genome-level expression patterns of human mononuclear cells subjected to heat shock or lipopolysaccharide. <i>BMC Immunology</i> , 2008, 9, 24.	0.9	16
575	Persistent changes in spinal cord gene expression after recovery from inflammatory hyperalgesia: A preliminary study on pain memory. <i>BMC Neuroscience</i> , 2008, 9, 32.	0.8	23
576	Different gene-expression profiles for the poorly differentiated carcinoma and the highly differentiated papillary adenocarcinoma in mammary glands support distinct metabolic pathways. <i>BMC Cancer</i> , 2008, 8, 270.	1.1	10
577	Differential gene expression associated with postnatal equine articular cartilage maturation. <i>BMC Musculoskeletal Disorders</i> , 2008, 9, 149.	0.8	38
578	Constructing disease-specific gene networks using pair-wise relevance metric: Application to colon cancer identifies interleukin 8, desmin and enolase 1 as the central elements. <i>BMC Systems Biology</i> , 2008, 2, 72.	3.0	64
579	Global gene expression profiling of oral cavity cancers suggests molecular heterogeneity within anatomic subsites. <i>BMC Research Notes</i> , 2008, 1, 113.	0.6	46
580	Using support vector regression to model the correlation between the clinical metastases time and gene expression profile for breast cancer. <i>Artificial Intelligence in Medicine</i> , 2008, 44, 221-231.	3.8	16
581	Role of copper,zinc-superoxide dismutase in catalyzing nitrotyrosine formation in murine liver. <i>Free Radical Biology and Medicine</i> , 2008, 45, 611-618.	1.3	36
582	BioLattice: A framework for the biological interpretation of microarray gene expression data using concept lattice analysis. <i>Journal of Biomedical Informatics</i> , 2008, 41, 232-241.	2.5	13

#	ARTICLE	IF	CITATIONS
583	Temporal Profiling of the Chromatin Proteome Reveals System-wide Responses to Replication Inhibition. <i>Current Biology</i> , 2008, 18, 838-843.	1.8	36
584	Nexus Between Epidermolysis Bullosa and Transcriptional Regulation by Thyroid Hormone in Epidermal Keratinocytes. <i>Clinical and Translational Science</i> , 2008, 1, 45-49.	1.5	9
585	Genomic effects of once-weekly, intramuscular interferon- $\beta$ 1a treatment after the first dose and on chronic dosing: Relationships to 5-year clinical outcomes in multiple sclerosis patients. <i>Journal of Neuroimmunology</i> , 2008, 205, 113-125.	1.1	34
586	Diabetic neuropathy: Mechanisms to management. , 2008, 120, 1-34.		588
587	Response of human renal tubular cells to cyclosporine and sirolimus: A toxicogenomic study. <i>Toxicology and Applied Pharmacology</i> , 2008, 229, 184-196.	1.3	51
588	Gene expression profiling in rat liver treated with compounds inducing phospholipidosis. <i>Toxicology and Applied Pharmacology</i> , 2008, 229, 290-299.	1.3	54
589	Gene expression profiles modulated by the human carcinogen aristolochic acid I in human cancer cells and their dependence on TP53. <i>Toxicology and Applied Pharmacology</i> , 2008, 232, 86-98.	1.3	32
590	Mutation of miRNA target sequences during human evolution. <i>Trends in Genetics</i> , 2008, 24, 262-265.	2.9	23
591	Transcriptional dysregulation in a transgenic model of Parkinson disease. <i>Neurobiology of Disease</i> , 2008, 29, 515-528.	2.1	62
593	p66Shc Deletion Confers Vascular Protection in Advanced Atherosclerosis in Hypercholesterolemic Apolipoprotein E Knockout Mice. <i>Endothelium: Journal of Endothelial Cell Research</i> , 2008, 15, 276-287.	1.7	49
594	The chemokine interleukin-8 and the surface activation protein CD69 are markers for Bcr-Abl activity in chronic myeloid leukemia. <i>Molecular Oncology</i> , 2008, 2, 272-281.	2.1	27
595	Altered Expression of Muscle- and Cytoskeleton-Related Genes in a Rat Strain With Inherited Cryptorchidism. <i>Journal of Andrology</i> , 2008, 29, 352-366.	2.0	36
596	WGCNA: an R package for weighted correlation network analysis. <i>BMC Bioinformatics</i> , 2008, 9, 559.	1.2	17,294
597	Comprehensive analysis of the mouse renal cortex using two-dimensional HPLC tandem mass spectrometry. <i>Proteome Science</i> , 2008, 6, 15.	0.7	21
598	Identification of differentially expressed proteins in spontaneous thymic lymphomas from knockout mice with deletion of p53. <i>Proteome Science</i> , 2008, 6, 18.	0.7	13
599	Differentiation of two types of mobilized peripheral blood stem cells by microRNA and cDNA expression analysis. <i>Journal of Translational Medicine</i> , 2008, 6, 39.	1.8	77
600	On the necessity of different statistical treatment for Illumina BeadChip and Affymetrix GeneChip data and its significance for biological interpretation. <i>Biology Direct</i> , 2008, 3, 23.	1.9	14
601	In silico regulatory analysis for exploring human disease progression. <i>Biology Direct</i> , 2008, 3, 24.	1.9	6

#	ARTICLE	IF	CITATIONS
602	Comparative Transcriptional Analysis of Embryoid Body Versus Two-Dimensional Differentiation of Murine Embryonic Stem Cells. <i>Tissue Engineering - Part A</i> , 2008, 14, 1603-1614.	1.6	11
603	Protein Expression Profile of the Mouse Metaphase-II Oocyte. <i>Journal of Proteome Research</i> , 2008, 7, 4821-4830.	1.8	56
604	Spectral Index for Assessment of Differential Protein Expression in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2008, 7, 845-854.	1.8	97
605	Network-based global inference of human disease genes. <i>Molecular Systems Biology</i> , 2008, 4, 189.	3.2	583
606	Boolean implication networks derived from large scale, whole genome microarray datasets. <i>Genome Biology</i> , 2008, 9, R157.	13.9	108
607	Variations in the transcriptome of Alzheimer's disease reveal molecular networks involved in cardiovascular diseases. <i>Genome Biology</i> , 2008, 9, R148.	13.9	94
608	Systematic bioinformatic analysis of expression levels of 17,330 human genes across 9,783 samples from 175 types of healthy and pathological tissues. <i>Genome Biology</i> , 2008, 9, R139.	13.9	234
609	Histone deacetylase inhibition accelerates the early events of stem cell differentiation: transcriptomic and epigenetic analysis. <i>Genome Biology</i> , 2008, 9, R65.	13.9	86
610	A sequence-based survey of the complex structural organization of tumor genomes. <i>Genome Biology</i> , 2008, 9, R59.	13.9	31
611	Novel insights into the relationships between dendritic cell subsets in human and mouse revealed by genome-wide expression profiling. <i>Genome Biology</i> , 2008, 9, R17.	13.9	472
612	Genomic chart guiding embryonic stem cell cardiopoiesis. <i>Genome Biology</i> , 2008, 9, R6.	13.9	66
613	Application of a Global Proteomic Approach to Archival Precursor Lesions: Deleted in Malignant Brain Tumors 1 and Tissue Transglutaminase 2 Are Upregulated in Pancreatic Cancer Precursors. <i>Pancreatology</i> , 2008, 8, 608-616.	0.5	48
614	A Comprehensive Negative Regulatory Program Controlled by Brn3b to Ensure Ganglion Cell Specification from Multipotential Retinal Precursors. <i>Journal of Neuroscience</i> , 2008, 28, 3392-3403.	1.7	80
615	Effects of the Proteasome Inhibitor Bortezomib on Gene Expression Profiles of Pancreatic Cancer Cells. <i>Journal of Surgical Research</i> , 2008, 145, 111-123.	0.8	30
616	MicroRNA-10a Binds the 5'UTR of Ribosomal Protein mRNAs and Enhances Their Translation. <i>Molecular Cell</i> , 2008, 30, 460-471.	4.5	1,168
617	A Role for Mammalian Sin3 in Permanent Gene Silencing. <i>Molecular Cell</i> , 2008, 32, 359-370.	4.5	112
618	Transcriptome of retrovirally transduced CD4+ lymphocytes: Influence of cell activation, transgene integration, and selection process. <i>Molecular Immunology</i> , 2008, 45, 1112-1125.	1.0	7
619	Exposure to brominated flame retardant PBDE-99 affects cytoskeletal protein expression in the neonatal mouse cerebral cortex. <i>NeuroToxicology</i> , 2008, 29, 628-637.	1.4	62

#	ARTICLE	IF	CITATIONS
620	The application of proteomics for studying the neurorescue activity of the polyphenol (âˆ™)-epigallocatechin-3-gallate. <i>Archives of Biochemistry and Biophysics</i> , 2008, 476, 152-160.	1.4	34
621	Exploring functional genomics for drug target and therapeutics discovery in Plasmodia. <i>Acta Tropica</i> , 2008, 105, 113-123.	0.9	17
622	Microarray analysis of gene expression in granulosa cells from persistent follicles in cattle. <i>Animal Reproduction Science</i> , 2008, 104, 405-413.	0.5	8
623	The role of mtDNA mutations in the pathogenesis of age-related hearing loss in mice carrying a mutator DNA polymerase Î³. <i>Neurobiology of Aging</i> , 2008, 29, 1080-1092.	1.5	83
624	Genomic Anatomy of the Hippocampus. <i>Neuron</i> , 2008, 60, 1010-1021.	3.8	337
625	Sequential and concerted gene expression changes in a chronic in vitro model of parkinsonism. <i>Neuroscience</i> , 2008, 152, 198-207.	1.1	10
626	Microarray analysis of mdx mice expressing high levels of utrophin: Therapeutic implications for dystrophin deficiency. <i>Neuromuscular Disorders</i> , 2008, 18, 239-247.	0.3	25
627	Contrast between cardiac left ventricle and diaphragm muscle in expression of genes involved in carbohydrate and lipid metabolism. <i>Respiratory Physiology and Neurobiology</i> , 2008, 161, 41-53.	0.7	9
628	Challenges in plant cellular pathway reconstruction based on gene expression profiling. <i>Trends in Plant Science</i> , 2008, 13, 44-50.	4.3	20
629	Misexpression of MIA disrupts lung morphogenesis and causes neonatal death. <i>Developmental Biology</i> , 2008, 316, 441-455.	0.9	13
630	High-Throughput Screening Assay for the Identification of Compounds Regulating Self-Renewal and Differentiation in Human Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2008, 2, 602-612.	5.2	211
631	Characterization of Dental Pulp Stem Cells of Human Tooth Germs. <i>Journal of Dental Research</i> , 2008, 87, 676-681.	2.5	117
632	Nutrition-induced catch-up growth increases hypoxia inducible factor 1Î± RNA levels in the growth plate. <i>Bone</i> , 2008, 42, 505-515.	1.4	35
633	Gene expression in women conceiving spontaneously over the age of 45 years. <i>Fertility and Sterility</i> , 2008, 89, 1641-1650.	0.5	15
634	Celecoxib pre-treatment in human colorectal adenocarcinoma patients is associated with gene expression alterations suggestive of diminished cellular proliferation. <i>European Journal of Cancer</i> , 2008, 44, 1754-1760.	1.3	28
635	Modulation of expression of RA-regulated genes by the oncoprotein v-erbA. <i>Gene</i> , 2008, 425, 23-27.	1.0	7
636	Analysis of Sus scrofa liver proteome and identification of proteins differentially expressed between genders, and conventional and genetically enhanced lines. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2008, 3, 234-242.	0.4	19
637	Genome-Wide Identification of Smad/Foxh1 Targets Reveals a Role for Foxh1 in Retinoic Acid Regulation and Forebrain Development. <i>Developmental Cell</i> , 2008, 14, 411-423.	3.1	51

#	ARTICLE	IF	CITATIONS
638	Heterogeneity of Human Macrophages in Culture and in Atherosclerotic Plaques. American Journal of Pathology, 2008, 172, 1112-1126.	1.9	213
639	Cross-Species Comparison of Human and Mouse Intestinal Polyps Reveals Conserved Mechanisms in Adenomatous Polyposis Coli (APC)-Driven Tumorigenesis. American Journal of Pathology, 2008, 172, 1363-1380.	1.9	71
640	Gene expression profiling of nonalcoholic steatohepatitis using gene set enrichment analysis. Hepatology Research, 2008, 38, 1204-1212.	1.8	29
641	New Two-Photon Activated Photodynamic Therapy Sensitizers Induce Xenograft Tumor Regressions after Near-IR Laser Treatment through the Body of the Host Mouse. Clinical Cancer Research, 2008, 14, 6564-6573.	3.2	229
642	Effect of Dietary Calcium and Dairy Proteins on the Adipose Tissue Gene Expression Profile in Diet-Induced Obesity. Journal of Nutrigenetics and Nutrigenomics, 2008, 1, 240-251.	1.8	24
643	Genetic Network Analysis of Human CD34+ Hematopoietic Stem/Precursor Cells. Taiwanese Journal of Obstetrics and Gynecology, 2008, 47, 422-430.	0.5	5
644	Chromosomal Instability Is Associated with Higher Expression of Genes Implicated in Epithelial-Mesenchymal Transition, Cancer Invasiveness, and Metastasis and with Lower Expression of Genes Involved in Cell Cycle Checkpoints, DNA Repair, and Chromatin Maintenance. Neoplasia, 2008, 10, 1222-IN26.	2.3	37
645	GOMA: Web utility for direct finding of enriched Gene Ontology terms from gene expression profile. , 2008, , .		0
646	Age-Dependent Signature of Metallothionein Expression in Primary CD4 T Cell Responses Is Due to Sustained Zinc Signaling. Rejuvenation Research, 2008, 11, 1001-1011.	0.9	39
647	Expression profiling reveals specific gene expression signatures in gastric MALT lymphomas. Leukemia and Lymphoma, 2008, 49, 974-983.	0.6	20
648	Gene Expression Profiling of Porcine Alveolar Macrophages After Antibody-Mediated Cross-Linking of Sialoadhesin (Sn, Siglec-1). Journal of Receptor and Signal Transduction Research, 2008, 28, 185-243.	1.3	8
649	Gene network dynamics controlling keratinocyte migration. Molecular Systems Biology, 2008, 4, 199.	3.2	52
650	Significance Analysis of Spectral Count Data in Label-free Shotgun Proteomics. Molecular and Cellular Proteomics, 2008, 7, 2373-2385.	2.5	344
651	E2F in vivo binding specificity: Comparison of consensus versus nonconsensus binding sites. Genome Research, 2008, 18, 1763-1777.	2.4	121
652	Chondrogenic Differentiation of Human Mesenchymal Stem Cells in Three-Dimensional Alginate Gels. Tissue Engineering - Part A, 2008, 14, 667-680.	1.6	181
653	Evaluation of Gene Expression in a Single Antibiotic Exposure—Derived Isolate of <i>Salmonella enterica</i> Typhimurium 14028 Possessing Resistance to Multiple Antibiotics. Foodborne Pathogens and Disease, 2008, 5, 205-221.	0.8	16
654	Genomic evolution of the placenta using co-option and duplication and divergence. Genome Research, 2008, 18, 695-705.	2.4	108
655	Using ChIP-chip technology to reveal common principles of transcriptional repression in normal and cancer cells. Genome Research, 2008, 18, 521-532.	2.4	44

#	ARTICLE	IF	CITATIONS
656	Methylmercury Activates Enhancer-of-Split and Bearded Complex Genes Independent of the Notch Receptor. <i>Toxicological Sciences</i> , 2008, 104, 163-176.	1.4	29
657	Specific DNA-binding by Apicomplexan AP2 transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8393-8398.	3.3	216
658	Glucocorticoid Signaling Defines a Novel Commitment State during Adipogenesis <i>In Vitro</i> . <i>Molecular Biology of the Cell</i> , 2008, 19, 4032-4041.	0.9	120
659	Annotation-Modules: a tool for finding significant combinations of multisource annotations for gene lists. <i>Bioinformatics</i> , 2008, 24, 1386-1393.	1.8	32
660	Transcriptome Profile of the Vascular Endothelial Cell Response to <i>Candida albicans</i> . <i>Journal of Infectious Diseases</i> , 2008, 198, 193-202.	1.9	39
661	Gene Expression of Endothelial Cells due to Interleukin-1 Beta Stimulation and Neutrophil Transmigration. <i>Endothelium: Journal of Endothelial Cell Research</i> , 2008, 15, 73-84.	1.7	32
662	Variations in the progranulin gene affect global gene expression in frontotemporal lobar degeneration. <i>Human Molecular Genetics</i> , 2008, 17, 1349-1362.	1.4	121
663	Dissection of a QTL Hotspot on Mouse Distal Chromosome 1 that Modulates Neurobehavioral Phenotypes and Gene Expression. <i>PLoS Genetics</i> , 2008, 4, e1000260.	1.5	98
664	Epithelial-to-Mesenchymal Transition in Early Transplant Tubulointerstitial Damage. <i>Journal of the American Society of Nephrology: JASN</i> , 2008, 19, 1571-1583.	3.0	47
665	Genomic Analysis of Drosophila Neuronal Remodeling: A Role for the RNA-Binding Protein Boule as a Negative Regulator of Axon Pruning. <i>Journal of Neuroscience</i> , 2008, 28, 6092-6103.	1.7	46
666	Conditional Deletion of <i>Smad1</i> and <i>Smad5</i> in Somatic Cells of Male and Female Gonads Leads to Metastatic Tumor Development in Mice. <i>Molecular and Cellular Biology</i> , 2008, 28, 248-257.	1.1	189
667	Sex and Age Dimorphism of Myocardial Gene Expression in Nonischemic Human Heart Failure. <i>Circulation: Cardiovascular Genetics</i> , 2008, 1, 117-125.	5.1	48
668	Regulation of liver regeneration and hepatocarcinogenesis by suppressor of cytokine signaling 3. <i>Journal of Experimental Medicine</i> , 2008, 205, 91-103.	4.2	165
669	MassNet: a functional annotation service for protein mass spectrometry data. <i>Nucleic Acids Research</i> , 2008, 36, W491-W495.	6.5	9
670	Genome-Wide Profiling of Antigen-Induced Time Course Expression Using Murine Models for Acute and Chronic Asthma. <i>International Archives of Allergy and Immunology</i> , 2008, 146, 44-56.	0.9	17
671	Proteomic and Computational Analysis of Bronchoalveolar Proteins during the Course of the Acute Respiratory Distress Syndrome. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2008, 178, 701-709.	2.5	73
672	Peripheral Blood Gene Expression Profile Associated with Sustained Virologic Response after Peginterferon Plus Ribavirin Therapy for Chronic Hepatitis-C Genotype 1. <i>Journal of the National Medical Association</i> , 2008, 100, 1425-1433.	0.6	8
673	Antioxidants increase number of progenitor endothelial cells through multiple gene expression pathways. <i>Free Radical Research</i> , 2008, 42, 754-762.	1.5	38

#	ARTICLE	IF	CITATIONS
674	Molecular Basis for Cold-Intolerant Yang-Deficient Constitution of Traditional Chinese Medicine. <i>The American Journal of Chinese Medicine</i> , 2008, 36, 827-834.	1.5	45
675	Effects of a Black Raspberry Diet on Gene Expression in the Rat Esophagus. <i>Nutrition and Cancer</i> , 2008, 60, 61-69.	0.9	45
676	Reduced Nicotinamide Adenine Dinucleotide Phosphate Oxidase-Independent Resistance to <i>Aspergillus fumigatus</i> in Alveolar Macrophages. <i>Journal of Immunology</i> , 2008, 180, 6854-6867.	0.4	45
677	Genome-wide analysis reveals Sall4 to be a major regulator of pluripotency in murine-embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 19756-19761.	3.3	179
678	PPAR $\alpha$ and C/EBP factors orchestrate adipocyte biology via adjacent binding on a genome-wide scale. <i>Genes and Development</i> , 2008, 22, 2941-2952.	2.7	690
679	Expression Analysis of Barrett's Esophagus-Associated High-Grade Dysplasia in Laser Capture Microdissected Archival Tissue. <i>Clinical Cancer Research</i> , 2008, 14, 6440-6448.	3.2	30
680	Comparisons of tyrosine phosphorylated proteins in cells expressing lung cancer-specific alleles of EGFR and KRAS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14112-14117.	3.3	113
681	Transcriptome of Hypoxic Immature Dendritic Cells: Modulation of Chemokine/Receptor Expression. <i>Molecular Cancer Research</i> , 2008, 6, 175-185.	1.5	94
682	Promoter CHIP-chip analysis in mouse testis reveals Y chromosome occupancy by HSF2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 11224-11229.	3.3	66
683	Mutation of ERBB2 Provides a Novel Alternative Mechanism for the Ubiquitous Activation of RAS-MAPK in Ovarian Serous Low Malignant Potential Tumors. <i>Molecular Cancer Research</i> , 2008, 6, 1678-1690.	1.5	108
684	Identification of cancer genes using a statistical framework for multiexperiment analysis of nondiscretized array CGH data. <i>Nucleic Acids Research</i> , 2008, 36, e13-e13.	6.5	62
685	Global Gene Expression as a Function of the Iron Status of the Bacterial Cell: Influence of Differentially Expressed Genes in the Virulence of the Human Pathogen <i>Vibrio vulnificus</i> . <i>Infection and Immunity</i> , 2008, 76, 4019-4037.	1.0	78
686	Pleiotropic Effects of <i>Drosophila</i> neuralized on Complex Behaviors and Brain Structure. <i>Genetics</i> , 2008, 179, 1327-1336.	1.2	32
687	Dysregulation of miRNA 181b in the temporal cortex in schizophrenia. <i>Human Molecular Genetics</i> , 2008, 17, 1156-1168.	1.4	312
688	Distinct genomic signatures of adaptation in pre- and postnatal environments during human evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3215-3220.	3.3	61
689	Aquaporin-1 knockout mice and polycystic kidney disease animals share a common mechanism of cyst formation. <i>FASEB Journal</i> , 2008, 22, 3672-3684.	0.2	47
690	Exon-Level Expression Profiling: A Comprehensive Transcriptome Analysis of Oral Fluids. <i>Clinical Chemistry</i> , 2008, 54, 824-832.	1.5	66
691	Label-free Quantitative Analysis of One-dimensional PAGE LC/MS/MS Proteome. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2399-2409.	2.5	87

#	ARTICLE	IF	CITATIONS
692	Kruppel-like factor 5 is required for perinatal lung morphogenesis and function. <i>Development (Cambridge)</i> , 2008, 135, 2563-2572.	1.2	113
693	Comparative hepatic gene expression profiling of rats treated with 1H,1H,2H,2H-heptadecafluorodecan-1-ol or with pentadecafluorooctanoic acid. <i>Physiological Genomics</i> , 2008, 34, 285-303.	1.0	8
694	Liver Genomic Responses to Ciguatoxin: Evidence for Activation of Phase I and Phase II Detoxification Pathways following an Acute Hypothermic Response in Mice. <i>Toxicological Sciences</i> , 2008, 103, 298-310.	1.4	29
695	An Integrated Approach for the Analysis of Biological Pathways using Mixed Models. <i>PLoS Genetics</i> , 2008, 4, e1000115.	1.5	59
696	Integrating Global Gene Expression Analysis and Genetics. <i>Advances in Genetics</i> , 2008, 60, 571-601.	0.8	48
697	Gene expression profile in labouring and non-labouring human placenta near term. <i>Molecular Human Reproduction</i> , 2008, 14, 61-65.	1.3	29
698	Comparative Toxicogenomic Examination of the Hepatic Effects of PCB126 and TCDD in Immature, Ovariectomized C57BL/6 Mice. <i>Toxicological Sciences</i> , 2008, 102, 61-75.	1.4	32
699	Molecular properties of side population-sorted cells from mouse small intestine. <i>American Journal of Physiology - Renal Physiology</i> , 2008, 294, G286-G294.	1.6	29
700	TERT Promotes Epithelial Proliferation through Transcriptional Control of a Myc- and Wnt-Related Developmental Program. <i>PLoS Genetics</i> , 2008, 4, e10.	1.5	283
701	Global gene expression profiles of ovarian surface epithelial cells in vivo. <i>Journal of Molecular Endocrinology</i> , 2008, 40, 281-296.	1.1	13
702	Chondroitin sulfate disaccharide stimulates microglia to adopt a novel regulatory phenotype. <i>Journal of Leukocyte Biology</i> , 2008, 84, 736-740.	1.5	38
703	Gene microarray analysis of human renal cell carcinoma: The effects of HDAC inhibition and retinoid treatment. <i>Cancer Biology and Therapy</i> , 2008, 7, 1607-1618.	1.5	32
704	Validating the genomic signature of pediatric septic shock. <i>Physiological Genomics</i> , 2008, 34, 127-134.	1.0	94
705	Carcinogen-Altered Genes in Rat Esophagus Positively Modulated to Normal Levels of Expression by Both Black Raspberries and Phenylethyl Isothiocyanate. <i>Cancer Research</i> , 2008, 68, 6460-6467.	0.4	48
706	The Mediator Subunit MDT-15 Confers Metabolic Adaptation to Ingested Material. <i>PLoS Genetics</i> , 2008, 4, e1000021.	1.5	100
707	AML1/ETO Oncoprotein Is Directed to AML1 Binding Regions and Co-Localizes with AML1 and HEB on Its Targets. <i>PLoS Genetics</i> , 2008, 4, e1000275.	1.5	67
708	Transcriptome response of enterocytes to dietary lipids: impact on cell architecture, signaling, and metabolism genes. <i>American Journal of Physiology - Renal Physiology</i> , 2008, 295, G942-G952.	1.6	13
709	Immune responses to <i>Pneumocystis murina</i> are robust in healthy mice but largely absent in CD40 ligand-deficient mice. <i>Journal of Leukocyte Biology</i> , 2008, 84, 420-430.	1.5	35



#	ARTICLE	IF	CITATIONS
710	Effect of destrin mutations on the gene expression profile in vivo. <i>Physiological Genomics</i> , 2008, 34, 9-21.	1.0	32
711	An Evolutionarily Conserved Sexual Signature in the Primate Brain. <i>PLoS Genetics</i> , 2008, 4, e1000100.	1.5	81
712	Regulatory Network Analyses Reveal Genome-Wide Potentiation of LIF Signaling by Glucocorticoids and Define an Innate Cell Defense Response. <i>PLoS Genetics</i> , 2008, 4, e1000224.	1.5	43
713	Defective signal transduction in B lymphocytes lacking presenilin proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 979-984.	3.3	21
714	Runx2 Regulates G Protein-coupled Signaling Pathways to Control Growth of Osteoblast Progenitors. <i>Journal of Biological Chemistry</i> , 2008, 283, 27585-27597.	1.6	114
715	Human neural crest cells display molecular and phenotypic hallmarks of stem cells. <i>Human Molecular Genetics</i> , 2008, 17, 3411-3425.	1.4	87
716	Termination of damaged protein repair defines the occurrence of symptoms in carriers of the m.3243A>G tRNA <sup>Leu</sup> mutation. <i>Journal of Medical Genetics</i> , 2008, 45, 525-534.	1.5	11
717	Babelomics: advanced functional profiling of transcriptomics, proteomics and genomics experiments. <i>Nucleic Acids Research</i> , 2008, 36, W341-W346.	6.5	73
718	o,pâ€²-DDT Elicits PXR/CAR-, Not ER-, Mediated Responses in the Immature Ovariectomized Rat Liver. <i>Toxicological Sciences</i> , 2008, 101, 350-363.	1.4	29
719	Patterns and changes in gene expression following neo-adjuvant anti-estrogen treatment in estrogen receptor-positive breast cancer. <i>Endocrine-Related Cancer</i> , 2008, 15, 439-449.	1.6	16
720	Ascorbate Peroxidase 1 Plays a Key Role in the Response of Arabidopsis thaliana to Stress Combination. <i>Journal of Biological Chemistry</i> , 2008, 283, 34197-34203.	1.6	357
721	Toxicogenomic Analysis of Gender, Chemical, and Dose Effects in Livers of TCDD- or Aroclor 1254â€™Exposed Rats Using a Multifactor Linear Model. <i>Toxicological Sciences</i> , 2008, 102, 291-309.	1.4	35
722	ERdj4 and ERdj5 Are Required for Endoplasmic Reticulum-associated Protein Degradation of Misfolded Surfactant Protein C. <i>Molecular Biology of the Cell</i> , 2008, 19, 2620-2630.	0.9	140
723	Differential Effects of Interleukin-2 and Interleukin-15 versus Interleukin-21 on CD4+ Cutaneous T-Cell Lymphoma Cells. <i>Cancer Research</i> , 2008, 68, 1083-1091.	0.4	79
724	Rapid Onset of Intestinal Epithelial Barrier Dysfunction in Primary Human Immunodeficiency Virus Infection Is Driven by an Imbalance between Immune Response and Mucosal Repair and Regeneration. <i>Journal of Virology</i> , 2008, 82, 538-545.	1.5	183
725	Phenotype of the <i>Cyp1a1</i> / <i>1a2</i> / <i>1b1</i> (-/-) Triple-Knockout Mouse. <i>Molecular Pharmacology</i> , 2008, 73, 1844-1856.	1.0	61
726	MADNet: microarray database network web server. <i>Nucleic Acids Research</i> , 2008, 36, W332-W335.	6.5	8
727	A hidden spatial-temporal Markov random field model for network-based analysis of time course gene expression data. <i>Annals of Applied Statistics</i> , 2008, 2, .	0.5	51

#	ARTICLE	IF	CITATIONS
728	Acute Rejection Modulates Gene Expression in the Collecting Duct. <i>Journal of the American Society of Nephrology: JASN</i> , 2008, 19, 538-546.	3.0	23
729	GeneChips in Regenerative Medicine. , 2008, , 562-578.		2
730	A quantitative atlas of mitotic phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10762-10767.	3.3	1,435
731	Dynamic changes in messenger RNA profiles of bovine endometrium during the oestrous cycle. <i>Reproduction</i> , 2008, 135, 225-240.	1.1	105
732	Gene Expression Changes Following Acute Hydrogen Sulfide (H <sub>2</sub> S)-induced Nasal Respiratory Epithelial Injury. <i>Toxicologic Pathology</i> , 2008, 36, 560-567.	0.9	28
733	Antagonism of microRNA-122 in mice by systemically administered LNA-anti-miR leads to up-regulation of a large set of predicted target mRNAs in the liver. <i>Nucleic Acids Research</i> , 2008, 36, 1153-1162.	6.5	630
734	Quantitative gene expression profiling of mouse brain regions reveals differential transcripts conserved in human and affected in disease models. <i>Physiological Genomics</i> , 2008, 33, 170-179.	1.0	40
735	Loss of E-Cadherin Promotes Metastasis via Multiple Downstream Transcriptional Pathways. <i>Cancer Research</i> , 2008, 68, 3645-3654.	0.4	1,298
736	Comparison of the Effects of <i>Leishmania major</i> or <i>Leishmania donovani</i> Infection on Macrophage Gene Expression. <i>Infection and Immunity</i> , 2008, 76, 1186-1192.	1.0	81
737	Identification of the TFII-I family target genes in the vertebrate genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9006-9010.	3.3	38
738	GOEAST: a web-based software toolkit for Gene Ontology enrichment analysis. <i>Nucleic Acids Research</i> , 2008, 36, W358-W363.	6.5	569
739	Constitutively Active Akt Induces Ectodermal Defects and Impaired Bone Morphogenetic Protein Signaling. <i>Molecular Biology of the Cell</i> , 2008, 19, 137-149.	0.9	27
740	Mitochondrial processes are impaired in hereditary inclusion body myopathy. <i>Human Molecular Genetics</i> , 2008, 17, 3663-3674.	1.4	49
741	Analysis of the Mechanisms Mediating Tumor-Specific Changes in Gene Expression in Human Liver Tumors. <i>Cancer Research</i> , 2008, 68, 2641-2651.	0.4	47
742	Sex-Specific Early Growth Hormone Response Genes in Rat Liver. <i>Molecular Endocrinology</i> , 2008, 22, 1962-1974.	3.7	69
743	Rosiglitazone Treatment Reduces Diabetic Neuropathy in Streptozotocin-Treated DBA/2J Mice. <i>Endocrinology</i> , 2008, 149, 4928-4937.	1.4	53
744	Direct targets of the TRP63 transcription factor revealed by a combination of gene expression profiling and reverse engineering. <i>Genome Research</i> , 2008, 18, 939-948.	2.4	72
745	Effects of Prenatal Tobacco Exposure on Gene Expression Profiling in Umbilical Cord Tissue. <i>Pediatric Research</i> , 2008, 64, 147-153.	1.1	11

#	ARTICLE	IF	CITATIONS
746	MicroRNA in Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2008, 359, 653-654.	13.9	2
747	Evidence of Key Role of Cdk2 Overexpression in Pemphigus Vulgaris. <i>Journal of Biological Chemistry</i> , 2008, 283, 8736-8745.	1.6	44
748	Curcumin downregulates the inflammatory cytokines CXCL1 and -2 in breast cancer cells via NF $\kappa$ B. <i>Carcinogenesis</i> , 2008, 29, 779-789.	1.3	196
749	Alveolar epithelial cell injury with Epstein-Barr virus upregulates TGF $\beta$ 1 expression. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2008, 295, L451-L460.	1.3	39
750	Translating the COPD Transcriptome: Insights into Pathogenesis and Tools for Clinical Management. <i>Proceedings of the American Thoracic Society</i> , 2008, 5, 834-841.	3.5	36
751	Acute appendicitis is characterized by a uniform and highly selective pattern of inflammatory gene expression. <i>Mucosal Immunology</i> , 2008, 1, 297-308.	2.7	34
752	Predominance of Interferon-Related Responses in the Brain during Murine Malaria, as Identified by Microarray Analysis. <i>Infection and Immunity</i> , 2008, 76, 1812-1824.	1.0	28
753	Colonic gene expression profile in NHE3-deficient mice: evidence for spontaneous distal colitis. <i>American Journal of Physiology - Renal Physiology</i> , 2008, 295, G63-G77.	1.6	78
754	Prioritization of candidate disease genes for metabolic syndrome by computational analysis of its defining phenotypes. <i>Physiological Genomics</i> , 2008, 35, 55-64.	1.0	21
755	Transcriptomic analysis of PPAR $\alpha$ -dependent alterations during cardiac hypertrophy. <i>Physiological Genomics</i> , 2008, 36, 15-23.	1.0	33
756	A novel inhibitor of glucose uptake sensitizes cells to FAS-induced cell death. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 3546-3555.	1.9	155
757	CD4 <sup>+</sup> T-Cell Decline after the Interruption of Antiretroviral Therapy in ACTG A5170 Is Predicted by Differential Expression of Genes in the Ras Signaling Pathway. <i>AIDS Research and Human Retroviruses</i> , 2008, 24, 1047-1066.	0.5	9
758	Broad Modulation of Gene Expression in CD4 <sup>+</sup> Lymphocyte Subpopulations in Response to Low Doses of Ionizing Radiation. <i>Radiation Research</i> , 2008, 170, 335-344.	0.7	32
759	Genome-wide profiling of PPAR $\gamma$ :RXR and RNA polymerase II occupancy reveals temporal activation of distinct metabolic pathways and changes in RXR dimer composition during adipogenesis. <i>Genes and Development</i> , 2008, 22, 2953-2967.	2.7	475
760	The MHC class I peptide repertoire is molded by the transcriptome. <i>Journal of Experimental Medicine</i> , 2008, 205, 595-610.	4.2	174
761	Network-Constrained Support Vector Machine for Classification. , 2008, , .		0
762	Phenotype reversion in fetal human liver epithelial cells identifies the role of an intermediate meso-endodermal stage before hepatic maturation. <i>Journal of Cell Science</i> , 2008, 121, 1002-1013.	1.2	35
763	Safety Evaluation of the Aqueous Extract Kothala Himbutu ( <i>Salacia reticulata</i> ) Stem in the Hepatic Gene Expression Profile of Normal Mice Using DNA Microarrays. <i>Bioscience, Biotechnology and Biochemistry</i> , 2008, 72, 3075-3083.	0.6	14

#	ARTICLE	IF	CITATIONS
764	Goat $\alpha$ S1-casein polymorphism affects gene expression profile of lactating mammary gland. <i>Animal</i> , 2008, 2, 566-573.	1.3	26
765	Microarray Analysis of Distinct Gene Transcription Profiles in Non-eosinophilic Chronic Sinusitis with Nasal Polyps. <i>American Journal of Rhinology &amp; Allergy</i> , 2008, 22, 568-581.	2.3	35
766	Zinc-controlled gene expression by metal-regulatory transcription factor 1 (MTF1) in a model vertebrate, the zebrafish. <i>Biochemical Society Transactions</i> , 2008, 36, 1252-1257.	1.6	60
767	Mutation of C/EBP $\beta$ predisposes to the development of myeloid leukemia in a retroviral insertional mutagenesis screen. <i>Blood</i> , 2008, 111, 4309-4321.	0.6	11
768	Discovery of agents that eradicate leukemia stem cells using an in silico screen of public gene expression data. <i>Blood</i> , 2008, 111, 5654-5662.	0.6	175
769	Genetic associations with thalidomide mediated venous thrombotic events in myeloma identified using targeted genotyping. <i>Blood</i> , 2008, 112, 4924-4934.	0.6	65
770	Iron regulates phosphorylation of Smad1/5/8 and gene expression of Bmp6, Smad7, Id1, and Atoh8 in the mouse liver. <i>Blood</i> , 2008, 112, 1503-1509.	0.6	401
771	MicroRNA expression profiling in classic Hodgkin lymphoma. <i>Blood</i> , 2008, 111, 2825-2832.	0.6	161
772	Gene Expression Profiling Reveals Complex Changes in the Olfactory Bulbectomy Model of Depression After Chronic Treatment With Antidepressants. <i>Journal of Pharmacological Sciences</i> , 2008, 108, 320-334.	1.1	12
773	p53 repressed miRNAs are involved with E2F in a feed-forward loop promoting proliferation. <i>Molecular Systems Biology</i> , 2008, 4, 229.	3.2	138
774	Improved Xenogenic Hepatocyte Implantation into Nude Mouse Liver Parenchyma with Acute Liver Failure when Followed by Repeated Anti-Fas Antibody (Jo2) Treatment. <i>Cell Transplantation</i> , 2008, 17, 507-524.	1.2	14
775	Genetic Expression Profile During Acute Cellular Rejection in Clinical Intestinal Transplantation. <i>Transplantation</i> , 2008, 86, 998-1001.	0.5	9
776	Topological Properties of Co-Occurrence Networks in Published Gene Expression Signatures. <i>Bioinformatics and Biology Insights</i> , 2008, 2, BBI.S518.	1.0	3
777	Tracking Differential Gene Expression in MRL/MpJ versus C57BL/6 Anergic B Cells: Molecular Markers of Autoimmunity. <i>Biomarker Insights</i> , 2008, 3, BMI.S840.	1.0	4
778	Macrophage and T-Cell Gene Expression in a Model of Early Infection with the Protozoan <i>Leishmania chagasi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e252.	1.3	45
779	Plasticity of the Systemic Inflammatory Response to Acute Infection during Critical Illness: Development of the Riboleukogram. <i>PLoS ONE</i> , 2008, 3, e1564.	1.1	68
780	Concordant Gene Expression in Leukemia Cells and Normal Leukocytes Is Associated with Germline cis-SNPs. <i>PLoS ONE</i> , 2008, 3, e2144.	1.1	8
781	Genome-Wide Analysis of Natural Selection on Human Cis-Elements. <i>PLoS ONE</i> , 2008, 3, e3137.	1.1	24

#	ARTICLE	IF	CITATIONS
782	Identification and Analysis of Co-Occurrence Networks with NetCutter. PLoS ONE, 2008, 3, e3178.	1.1	20
783	STOX1 Overexpression in Choriocarcinoma Cells Mimics Transcriptional Alterations Observed in Preeclamptic Placentas. PLoS ONE, 2008, 3, e3905.	1.1	60
784	Comparison and Identification of Estrogen-Receptor Related Gene Expression Profiles in Breast Cancer of Different Ethnic Origins. Breast Cancer: Basic and Clinical Research, 2008, 1, BCBCR.S626.	0.6	4
785	Bioinformatic Tools for Inferring Functional Information from Plant Microarray Data: Tools for the First Steps. International Journal of Plant Genomics, 2008, 2008, 1-9.	2.2	5
786	Bioinformatics Tools for Plant Genomics. International Journal of Plant Genomics, 2008, 2008, 1-2.	2.2	4
787	Hedgehog signaling regulates epithelial-mesenchymal transition during biliary fibrosis in rodents and humans. Journal of Clinical Investigation, 2008, 118, 3331-42.	3.9	284
788	Yeast Features: Identifying Significant Features Shared Among Yeast Proteins for Functional Genomics. Nature Precedings, 2008, , .	0.1	0
789	Î±- and Î³-Tocopherol Prevent Age-Related Transcriptional Alterations in the Heart and Brain of Mice <sup>3</sup> . Journal of Nutrition, 2008, 138, 1010-1018.	1.3	45
790	Identification of candidate genes for congenital splay leg in piglets by alternative analysis of DNA microarray data. International Journal of Biological Sciences, 2009, 5, 331-337.	2.6	13
791	Microarray gene expression profiles of fasting induced changes in liver and adipose tissues of pigs expressing the melanocortin-4 receptor D298N variant. Physiological Genomics, 2009, 38, 98-111.	1.0	44
792	Identification of differential gene expression during porcine conceptus rapid trophoblastic elongation and attachment to uterine luminal epithelium. Physiological Genomics, 2009, 36, 140-148.	1.0	81
793	GaGa: A parsimonious and flexible model for differential expression analysis. Annals of Applied Statistics, 2009, 3, .	0.5	14
794	Effects of short-term heat stress on endophytic ergot alkaloid-induced alterations in rat hepatic gene expression. Journal of Animal Science, 2009, 87, 3142-3155.	0.2	15
795	Differential Gene Expression in <i>Ndph</i> -Knockout Mice in Retinal Development. , 2009, 50, 906.		45
796	Modulated Modularity Clustering as an Exploratory Tool for Functional Genomic Inference. PLoS Genetics, 2009, 5, e1000479.	1.5	118
797	Overexpression of Myocilin in the Drosophila Eye Activates the Unfolded Protein Response: Implications for Glaucoma. PLoS ONE, 2009, 4, e4216.	1.1	41
798	Comparison of Proteomic and Transcriptomic Profiles in the Bronchial Airway Epithelium of Current and Never Smokers. PLoS ONE, 2009, 4, e5043.	1.1	66
799	Transcriptome-Wide Prediction of miRNA Targets in Human and Mouse Using FASTH. PLoS ONE, 2009, 4, e5745.	1.1	27

#	ARTICLE	IF	CITATIONS
800	Impact of the TCR Signal on Regulatory T Cell Homeostasis, Function, and Trafficking. PLoS ONE, 2009, 4, e6580.	1.1	52
801	Genome-Wide mRNA Expression Analysis of Hepatic Adaptation to High-Fat Diets Reveals Switch from an Inflammatory to Steatotic Transcriptional Program. PLoS ONE, 2009, 4, e6646.	1.1	52
802	Induction of Epithelial Mesenchymal Transition and Vasculogenesis in the Lenses of Dbl Oncogene Transgenic Mice. PLoS ONE, 2009, 4, e7058.	1.1	3
803	Global Transcriptional Response to Hfe Deficiency and Dietary Iron Overload in Mouse Liver and Duodenum. PLoS ONE, 2009, 4, e7212.	1.1	10
804	Transcriptional Profiling of Rats Subjected to Gestational Undernourishment: Implications for the Developmental Variations in Metabolic Traits. PLoS ONE, 2009, 4, e7271.	1.1	33
805	Alternative Splicing and Transcriptome Profiling of Experimental Autoimmune Encephalomyelitis Using Genome-Wide Exon Arrays. PLoS ONE, 2009, 4, e7773.	1.1	20
806	Gender Differences in a Drosophila Transcriptomic Model of Chronic Pentylentetrazole Induced Behavioral Deficit. PLoS ONE, 2009, 4, e8136.	1.1	7
807	Global MYCN Transcription Factor Binding Analysis in Neuroblastoma Reveals Association with Distinct E-Box Motifs and Regions of DNA Hypermethylation. PLoS ONE, 2009, 4, e8154.	1.1	72
808	Transcriptomic analysis implicates ribosomal and energy metabolic pathways in antiepileptic drug action in a Drosophila model. Nature Precedings, 2009, , .	0.1	0
809	Investigating Gene and MicroRNA Expression in Glioblastoma. , 2009, , .		0
810	Earthworm genomes, genes and proteins: the (re)discovery of Darwin's worms. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 789-797.	1.2	38
811	Selenoprotein T deficiency alters cell adhesion and elevates selenoprotein W expression in murine fibroblast cells. Biochemistry and Cell Biology, 2009, 87, 953-961.	0.9	53
812	Genome-wide strategies for discovering genetic influences on cognition and cognitive disorders: Methodological considerations. Cognitive Neuropsychiatry, 2009, 14, 391-418.	0.7	93
813	From disease ontology to disease-ontology lite: statistical methods to adapt a general-purpose ontology for the test of gene-ontology associations. Bioinformatics, 2009, 25, i63-i68.	1.8	99
814	Co-inhibition of Plasmodium falciparum S-Adenosylmethionine Decarboxylase/Ornithine Decarboxylase Reveals Perturbation-specific Compensatory Mechanisms by Transcriptome, Proteome, and Metabolome Analyses. Journal of Biological Chemistry, 2009, 284, 4635-4646.	1.6	73
815	Transcriptome Profile and Cytogenetic Analysis of Immortalized Neuronally Restricted Progenitor Cells Derived from the Porcine Olfactory Bulb. Animal Biotechnology, 2009, 20, 186-215.	0.7	1
816	Characterization of a Naturally Occurring Breast Cancer Subset Enriched in Epithelial-to-Mesenchymal Transition and Stem Cell Characteristics. Cancer Research, 2009, 69, 4116-4124.	0.4	768
817	Dysregulated gene expression networks in human acute myelogenous leukemia stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3396-3401.	3.3	253

#	ARTICLE	IF	CITATIONS
818	Immune Gene and Cell Enrichment Is Associated with a Good Prognosis in Ependymoma. <i>Journal of Immunology</i> , 2009, 183, 7428-7440.	0.4	54
819	Large-scale detection of ubiquitination substrates using cell extracts and protein microarrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2543-2548.	3.3	87
820	CLUSTERING OF GENE EXPRESSION DATA AND END-POINT MEASUREMENTS BY SIMULATED ANNEALING. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 193-215.	0.3	6
821	Discovery of candidate genes and pathways in the endometrium regulating ovine blastocyst growth and conceptus elongation. <i>Physiological Genomics</i> , 2009, 39, 85-99.	1.0	76
822	Hippocampal and Cognitive Aging across the Lifespan: A Bioenergetic Shift Precedes and Increased Cholesterol Trafficking Parallels Memory Impairment. <i>Journal of Neuroscience</i> , 2009, 29, 1805-1816.	1.7	139
823	Impact of nose-only exposure system on pulmonary gene expression. <i>Inhalation Toxicology</i> , 2009, 21, 74-82.	0.8	16
824	X-Chromosome Gene Dosage and the Risk of Diabetes in Turner Syndrome. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2009, 94, 3289-3296.	1.8	95
825	Systems biology of autosomal dominant polycystic kidney disease (ADPKD): computational identification of gene expression pathways and integrated regulatory networks. <i>Human Molecular Genetics</i> , 2009, 18, 2328-2343.	1.4	208
826	The conserved NAD(H)-dependent corepressor CTBP-1 regulates <i>Caenorhabditis elegans</i> life span. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1496-1501.	3.3	60
827	Immune dysregulation in severe influenza. <i>Journal of Leukocyte Biology</i> , 2009, 85, 1036-1043.	1.5	106
828	Functional genomic analysis of amniotic fluid cell-free mRNA suggests that oxidative stress is significant in Down syndrome fetuses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9425-9429.	3.3	106
829	The Thioxotriazole Copper(II) Complex AO Induces Endoplasmic Reticulum Stress and Paraptotic Death in Human Cancer Cells. <i>Journal of Biological Chemistry</i> , 2009, 284, 24306-24319.	1.6	115
830	The deacetylase HDAC4 controls myocyte enhancing factor $\alpha$ -dependent structural gene expression in response to neural activity. <i>FASEB Journal</i> , 2009, 23, 99-106.	0.2	75
831	Overexpressed vs mutated Kras in murine fibroblasts: a molecular phenotyping study. <i>British Journal of Cancer</i> , 2009, 100, 656-662.	2.9	28
832	Analysis of differential gene expression in colorectal cancer and stroma using fluorescence-activated cell sorting purification. <i>British Journal of Cancer</i> , 2009, 100, 1452-1464.	2.9	33
833	COFECO: composite function annotation enriched by protein complex data. <i>Nucleic Acids Research</i> , 2009, 37, W350-W355.	6.5	19
834	Overlapping promoter targeting by Elk-1 and other divergent ETS-domain transcription factor family members. <i>Nucleic Acids Research</i> , 2009, 37, 7368-7380.	6.5	36
835	The Prion Disease Database: a comprehensive transcriptome resource for systems biology research in prion diseases. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap011.	1.4	18

#	ARTICLE	IF	CITATIONS
836	Blocking the Metabolism of Starch Breakdown Products in Arabidopsis Leaves Triggers Chloroplast Degradation. <i>Molecular Plant</i> , 2009, 2, 1233-1246.	3.9	127
837	Thymic OX40 Expression Discriminates Cells Undergoing Strong Responses to Selection Ligands. <i>Journal of Immunology</i> , 2009, 182, 4581-4589.	0.4	60
838	Mouse models of human AML accurately predict chemotherapy response. <i>Genes and Development</i> , 2009, 23, 877-889.	2.7	235
839	Global Gene Expression in the Human Fetal Testis and Ovary1. <i>Biology of Reproduction</i> , 2009, 81, 438-443.	1.2	100
840	Polymorphic mature microRNAs from passenger strand of pre-miR-146a contribute to thyroid cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1502-1505.	3.3	311
841	Genome-wide analysis of SREBP-1 binding in mouse liver chromatin reveals a preference for promoter proximal binding to a new motif. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13765-13769.	3.3	85
842	High frequency of hotspot mutations in core genes of <i>Escherichia coli</i> due to short-term positive selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12412-12417.	3.3	95
843	Global Analysis of Transcriptional Regulation by Poly(ADP-ribose) Polymerase-1 and Poly(ADP-ribose) Glycohydrolase in MCF-7 Human Breast Cancer Cells. <i>Journal of Biological Chemistry</i> , 2009, 284, 33926-33938.	1.6	102
844	Genomic Analyses of Musashi1 Downstream Targets Show a Strong Association with Cancer-related Processes. <i>Journal of Biological Chemistry</i> , 2009, 284, 12125-12135.	1.6	79
845	Genome-wide Association of Hypoxia-inducible Factor (HIF)-1 $\alpha$ and HIF-2 $\alpha$ DNA Binding with Expression Profiling of Hypoxia-inducible Transcripts. <i>Journal of Biological Chemistry</i> , 2009, 284, 16767-16775.	1.6	516
846	The organization of the transcriptional network in specific neuronal classes. <i>Molecular Systems Biology</i> , 2009, 5, 291.	3.2	114
847	Dengue Virus Infection Differentially Regulates Endothelial Barrier Function over Time through Type I Interferon Effects. <i>Journal of Infectious Diseases</i> , 2009, 200, 191-201.	1.9	40
848	Transmigration across activated endothelium induces transcriptional changes, inhibits apoptosis, and decreases antimicrobial protein expression in human monocytes. <i>Journal of Leukocyte Biology</i> , 2009, 86, 1331-1343.	1.5	26
849	Gene expression profiling of bovine preovulatory follicles: gonadotropin surge and prostanoid-dependent up-regulation of genes potentially linked to the ovulatory process. <i>Reproduction</i> , 2009, 137, 297-307.	1.1	35
850	Enrichment constrained time-dependent clustering analysis for finding meaningful temporal transcription modules. <i>Bioinformatics</i> , 2009, 25, 1521-1527.	1.8	18
851	Integration of heterogeneous expression data sets extends the role of the retinol pathway in diabetes and insulin resistance. <i>Bioinformatics</i> , 2009, 25, 3121-3127.	1.8	20
852	Cardiac Resynchronization Therapy Corrects Dyssynchrony-Induced Regional Gene Expression Changes on a Genomic Level. <i>Circulation: Cardiovascular Genetics</i> , 2009, 2, 371-378.	5.1	78
853	An Integrated Systems Analysis Implicates EGR1 Downregulation in Simian Immunodeficiency Virus Encephalitis-Induced Neural Dysfunction. <i>Journal of Neuroscience</i> , 2009, 29, 12467-12476.	1.7	37



#	ARTICLE	IF	CITATIONS
854	Alcohol Sensitivity in <i>Drosophila</i> : Translational Potential of Systems Genetics. <i>Genetics</i> , 2009, 183, 733-745.	1.2	45
855	Gene Profiling of Human Adipose Tissue During Evoked Inflammation In Vivo. <i>Diabetes</i> , 2009, 58, 2211-2219.	0.3	57
856	The Effects of Dairy Components on Energy Partitioning and Metabolic Risk in Mice: A Microarray Study. <i>Journal of Nutrigenetics and Nutrigenomics</i> , 2009, 2, 64-77.	1.8	16
857	MitoMiner, an Integrated Database for the Storage and Analysis of Mitochondrial Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1324-1337.	2.5	74
858	Modulated expression of WFDC1 during carcinogenesis and cellular senescence. <i>Carcinogenesis</i> , 2009, 30, 20-27.	1.3	76
859	Comparative prion disease gene expression profiling using the prion disease mimetic, cuprizone. <i>Prion</i> , 2009, 3, 99-109.	0.9	17
860	Gene Expression Profiles in Radiation Workers Occupationally Exposed to Ionizing Radiation. <i>Journal of Radiation Research</i> , 2009, 50, 61-71.	0.8	73
861	<i>Rac1</i> Is a Critical Mediator of Endothelium-Derived Neurotrophic Activity. <i>Science Signaling</i> , 2009, 2, ra10.	1.6	26
862	Only a Subset of Met-Activated Pathways Are Required to Sustain Oncogene Addiction. <i>Science Signaling</i> , 2009, 2, ra80.	1.6	84
863	Corticolimbic Transcriptome Changes are State-Dependent and Region-Specific in a Rodent Model of Depression and of Antidepressant Reversal. <i>Neuropsychopharmacology</i> , 2009, 34, 1363-1380.	2.8	173
864	Massively parallel resequencing of the isogenic <i>Drosophila melanogaster</i> strain w1118; iso-2; iso-3 identifies hotspots for mutations in sensory perception genes. <i>Fly</i> , 2009, 3, 192-204.	0.9	13
865	Glucocorticoid- and Protein Kinase A-Dependent Transcriptome Regulation in Airway Smooth Muscle. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2009, 41, 24-39.	1.4	39
866	DNA Replication Licensing and Progenitor Numbers Are Increased by Progesterone in Normal Human Breast. <i>Endocrinology</i> , 2009, 150, 3318-3326.	1.4	122
867	Thyroid Gene Expression in Familial Nonautoimmune Hyperthyroidism Shows Common Characteristics with Hyperfunctioning Autonomous Adenomas. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2009, 94, 2602-2609.	1.8	19
868	Longitudinal system-based analysis of transcriptional responses to type I interferons. <i>Physiological Genomics</i> , 2009, 38, 362-371.	1.0	32
869	Oct-4 regulates the expression of <i>Stella</i> and <i>Foxj2</i> at the <i>Nanog</i> locus: implications for the developmental competence of mouse oocytes. <i>Human Reproduction</i> , 2009, 24, 2225-2237.	0.4	37
870	Elucidation of the ELK1 target gene network reveals a role in the coordinate regulation of core components of the gene regulation machinery. <i>Genome Research</i> , 2009, 19, 1963-1973.	2.4	119
871	Influence of fatty acid diets on gene expression in rat mammary epithelial cells. <i>Physiological Genomics</i> , 2009, 38, 80-88.	1.0	15

#	ARTICLE	IF	CITATIONS
872	Influence of hyperthyroid conditions on gene expression in extraocular muscles of rats. <i>Physiological Genomics</i> , 2009, 37, 231-238.	1.0	6
873	Gene expression endpoints following chronic waterborne copper exposure in a genomic model organism, the zebrafish, <i>Danio rerio</i> . <i>Physiological Genomics</i> , 2009, 40, 23-33.	1.0	45
874	<i>C. elegans</i> dysferlin homolog <i>fer-1</i> is expressed in muscle, and <i>fer-1</i> mutations initiate altered gene expression of muscle enriched genes. <i>Physiological Genomics</i> , 2009, 40, 8-14.	1.0	14
875	Pleiotropic effects of negative energy balance in the postpartum dairy cow on splenic gene expression: repercussions for innate and adaptive immunity. <i>Physiological Genomics</i> , 2009, 39, 28-37.	1.0	50
876	Molecular Distinctions between Stasis and Telomere Attrition Senescence Barriers Shown by Long-term Culture of Normal Human Mammary Epithelial Cells. <i>Cancer Research</i> , 2009, 69, 7557-7568.	0.4	144
877	Fine Ambient Particles Induce Oxidative Stress and Metal Binding Genes in Human Alveolar Macrophages. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2009, 41, 544-552.	1.4	54
878	Molecular Biomarkers for Quantitative and Discrete COPD Phenotypes. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2009, 40, 359-367.	1.4	94
879	Elucidating the Role of Gonadal Hormones in Sexually Dimorphic Gene Coexpression Networks. <i>Endocrinology</i> , 2009, 150, 1235-1249.	1.4	224
880	Retinoblastoma Protein Plays Multiple Essential Roles in the Terminal Differentiation of Sertoli Cells. <i>Molecular Endocrinology</i> , 2009, 23, 1900-1913.	3.7	39
881	Induction of Cytokine Gene Expression in Human Thyroid Epithelial Cells Irradiated with HZE Particles (Iron Ions). <i>Radiation Research</i> , 2009, 172, 437.	0.7	18
882	Genome-Wide Innate Immune Responses in HIV-1-Infected Macrophages Are Preserved Despite Attenuation of the NF- $\kappa$ B Activation Pathway. <i>Journal of Immunology</i> , 2009, 182, 319-328.	0.4	28
883	Colony-stimulating factor-1 (CSF-1) delivers a proatherogenic signal to human macrophages. <i>Journal of Leukocyte Biology</i> , 2009, 85, 278-288.	1.5	69
884	Perturbation of Defense Pathways by Low-Dose Arsenic Exposure in Zebrafish Embryos. <i>Environmental Health Perspectives</i> , 2009, 117, 981-987.	2.8	49
885	Genome-Wide Analyses of Exonic Copy Number Variants in a Family-Based Study Point to Novel Autism Susceptibility Genes. <i>PLoS Genetics</i> , 2009, 5, e1000536.	1.5	374
886	Discovery and Annotation of Functional Chromatin Signatures in the Human Genome. <i>PLoS Computational Biology</i> , 2009, 5, e1000566.	1.5	143
887	Host Cell Factors in HIV Replication: Meta-Analysis of Genome-Wide Studies. <i>PLoS Pathogens</i> , 2009, 5, e1000437.	2.1	396
888	Simultaneous Model Selection via Rate-Distortion Theory, With Applications to Cluster and Significance Analysis of Gene Expression Data. <i>Journal of Computational and Graphical Statistics</i> , 2009, 18, 613-639.	0.9	1
889	Conserved Expression Patterns Predict microRNA Targets. <i>PLoS Computational Biology</i> , 2009, 5, e1000513.	1.5	49

#	ARTICLE	IF	CITATIONS
890	Exon Array Analysis of Head and Neck Cancers Identifies a Hypoxia Related Splice Variant of LAMA3 Associated with a Poor Prognosis. <i>PLoS Computational Biology</i> , 2009, 5, e1000571.	1.5	37
891	An Abundance of Ubiquitously Expressed Genes Revealed by Tissue Transcriptome Sequence Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000598.	1.5	777
892	Expression Quantitative Trait Loci Are Highly Sensitive to Cellular Differentiation State. <i>PLoS Genetics</i> , 2009, 5, e1000692.	1.5	85
893	Differential Gene Expression Patterns of EBV Infected EBNA-3A Positive and Negative Human B Lymphocytes. <i>PLoS Pathogens</i> , 2009, 5, e1000506.	2.1	66
894	Comparative Analysis of AhR-Mediated TCDD-Elicited Gene Expression in Human Liver Adult Stem Cells. <i>Toxicological Sciences</i> , 2009, 112, 229-244.	1.4	56
895	Gene expression in the human mammary epithelium during lactation: the milk fat globule transcriptome. <i>Physiological Genomics</i> , 2009, 37, 12-22.	1.0	136
896	Diffuse-Type Gastric Carcinoma: Progression, Angiogenesis, and Transforming Growth Factor $\beta^2$ Signaling. <i>Journal of the National Cancer Institute</i> , 2009, 101, 592-604.	3.0	66
897	Acute molecular response of mouse hindlimb muscles to chronic stimulation. <i>American Journal of Physiology - Cell Physiology</i> , 2009, 297, C556-C570.	2.1	10
898	The <i>Drosophila</i> foraging Gene Mediates Adult Plasticity and Gene-Environment Interactions in Behaviour, Metabolites, and Gene Expression in Response to Food Deprivation. <i>PLoS Genetics</i> , 2009, 5, e1000609.	1.5	89
899	Chronic Dietary Exposure to a Low-Dose Mixture of Genistein and Vinclozolin Modifies the Reproductive Axis, Testis Transcriptome, and Fertility. <i>Environmental Health Perspectives</i> , 2009, 117, 1272-1279.	2.8	107
900	Coordinated activation of the secretory pathway during notochord formation in the <i>Xenopus</i> embryo. <i>Development (Cambridge)</i> , 2009, 136, 3543-3548.	1.2	20
901	Genome-Wide Promoter Analysis of the <i>SOX4</i> Transcriptional Network in Prostate Cancer Cells. <i>Cancer Research</i> , 2009, 69, 709-717.	0.4	176
902	Thalamic transcriptome screening in three psychiatric states. <i>Journal of Human Genetics</i> , 2009, 54, 665-675.	1.1	49
903	SimCT: a generic tool to visualize ontology-based relationships for biological objects. <i>Bioinformatics</i> , 2009, 25, 3197-3198.	1.8	11
904	Pscan: finding over-represented transcription factor binding site motifs in sequences from co-regulated or co-expressed genes. <i>Nucleic Acids Research</i> , 2009, 37, W247-W252.	6.5	377
905	Phenobarbital Elicits Unique, Early Changes in the Expression of Hepatic Genes that Affect Critical Pathways in Tumor-Prone B6C3F1 Mice. <i>Toxicological Sciences</i> , 2009, 109, 193-205.	1.4	31
906	ZBED6, a Novel Transcription Factor Derived from a Domesticated DNA Transposon Regulates IGF2 Expression and Muscle Growth. <i>PLoS Biology</i> , 2009, 7, e1000256.	2.6	149
907	Align human interactome with phenome to identify causative genes and networks underlying disease families. <i>Bioinformatics</i> , 2009, 25, 98-104.	1.8	90

#	ARTICLE	IF	CITATIONS
908	Zebrafish miR-1 and miR-133 shape muscle gene expression and regulate sarcomeric actin organization. <i>Genes and Development</i> , 2009, 23, 619-632.	2.7	149
909	Multi-Organ Expression Profiling Uncovers a Gene Module in Coronary Artery Disease Involving Transendothelial Migration of Leukocytes and LIM Domain Binding 2: The Stockholm Atherosclerosis Gene Expression (STAGE) Study. <i>PLoS Genetics</i> , 2009, 5, e1000754.	1.5	118
910	Aging Mice Show a Decreasing Correlation of Gene Expression within Genetic Modules. <i>PLoS Genetics</i> , 2009, 5, e1000776.	1.5	157
911	GeneCodis: interpreting gene lists through enrichment analysis and integration of diverse biological information. <i>Nucleic Acids Research</i> , 2009, 37, W317-W322.	6.5	391
912	Widespread cleavage of A-to-I hyperediting substrates. <i>Rna</i> , 2009, 15, 1632-1639.	1.6	41
913	Large-scale analysis of DNA methylation in chronic lymphocytic leukemia. <i>Epigenomics</i> , 2009, 1, 39-61.	1.0	57
914	FSH and FOXO1 Regulate Genes in the Sterol/Steroid and Lipid Biosynthetic Pathways in Granulosa Cells. <i>Molecular Endocrinology</i> , 2009, 23, 649-661.	3.7	134
915	Identification of Modulated Genes by Three Classes of Chemopreventive Agents at Preneoplastic Stages in a p53-Null Mouse Mammary Tumor Model. <i>Cancer Prevention Research</i> , 2009, 2, 175-184.	0.7	7
916	Effect of Leptin on Mouse Trophoblast Giant Cells1. <i>Biology of Reproduction</i> , 2009, 80, 415-424.	1.2	23
917	Intrinsic Gene Expression Profiles of Gliomas Are a Better Predictor of Survival than Histology. <i>Cancer Research</i> , 2009, 69, 9065-9072.	0.4	575
918	ChIP-Seq of transcription factors predicts absolute and differential gene expression in embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21521-21526.	3.3	312
919	Chemical Genomics Identifies the Unfolded Protein Response as a Target for Selective Cancer Cell Killing during Glucose Deprivation. <i>Cancer Research</i> , 2009, 69, 4225-4234.	0.4	148
920	The Macrophage Colony-Stimulating Factor 1 Response Signature in Breast Carcinoma. <i>Clinical Cancer Research</i> , 2009, 15, 778-787.	3.2	177
921	Deletion of Scap in Alveolar Type II Cells Influences Lung Lipid Homeostasis and Identifies a Compensatory Role for Pulmonary Lipofibroblasts. <i>Journal of Biological Chemistry</i> , 2009, 284, 4018-4030.	1.6	61
922	Hub genes with positive feedbacks function as master switches in developmental gene regulatory networks. <i>Bioinformatics</i> , 2009, 25, 1898-1904.	1.8	48
923	Gene expression profiling in rat liver treated with compounds inducing elevation of bilirubin. <i>Human and Experimental Toxicology</i> , 2009, 28, 231-244.	1.1	15
924	Triplet repeat length bias and variation in the human transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17095-17100.	3.3	33
925	The Human Cytomegalovirus-Encoded Chemokine Receptor US28 Promotes Angiogenesis and Tumor Formation via Cyclooxygenase-2. <i>Cancer Research</i> , 2009, 69, 2861-2869.	0.4	139

#	ARTICLE	IF	CITATIONS
926	High-Throughput Cell-Based Screening of 4910 Known Drugs and Drug-like Small Molecules Identifies Disulfiram as an Inhibitor of Prostate Cancer Cell Growth. <i>Clinical Cancer Research</i> , 2009, 15, 6070-6078.	3.2	185
927	Automated Brain Tumor Biopsy Prediction Using Single-labeling cDNA Microarrays-based Gene Expression Profiling. <i>Diagnostic Molecular Pathology</i> , 2009, 18, 206-218.	2.1	17
928	Comprehensive Proteome Analysis of an Apc Mouse Model Uncovers Proteins Associated with Intestinal Tumorigenesis. <i>Cancer Prevention Research</i> , 2009, 2, 224-233.	0.7	47
929	MMP-9 Sheds the $\beta 2$ Integrin Subunit (CD18) from Macrophages. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1044-1060.	2.5	76
930	Genomic Profiles Associated with Early Micrometastasis in Lung Cancer: Relevance of 4q Deletion. <i>Clinical Cancer Research</i> , 2009, 15, 1566-1574.	3.2	87
931	A conserved CCCH-type zinc finger protein regulates mRNA nuclear adenylation and export. <i>Journal of Cell Biology</i> , 2009, 185, 265-277.	2.3	40
932	Gene expression profile of rat ovarian tissue following xenotransplantation into immune-deficient mice. <i>Reproduction</i> , 2009, 137, 957-967.	1.1	12
933	Regulation of Gene Expression by Estrogen and Testosterone in the Proximal Mouse Reproductive Tract1. <i>Biology of Reproduction</i> , 2009, 81, 707-716.	1.2	38
934	Chronic Endoplasmic Reticulum Stress Activates Unfolded Protein Response in Arterial Endothelium in Regions of Susceptibility to Atherosclerosis. <i>Circulation Research</i> , 2009, 105, 453-461.	2.0	182
935	Genetic evidence for shared mechanisms of epimorphic regeneration in zebrafish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9310-9315.	3.3	141
936	Parathyroid Hormone-Related Protein Protects against Mammary Tumor Emergence and Is Associated with Monocyte Infiltration in Ductal Carcinoma <i>in situ</i> . <i>Cancer Research</i> , 2009, 69, 7473-7479.	0.4	41
937	Toxicological and gene expression analysis of the impact of aflatoxin B1 on hepatic function of male broiler chicks. <i>Poultry Science</i> , 2009, 88, 360-371.	1.5	80
938	Over-expression and localization of a host protein on the membrane of <i>Cryptosporidium parvum</i> infected epithelial cells. <i>Molecular and Biochemical Parasitology</i> , 2009, 168, 95-101.	0.5	20
939	microRNA expression in the eyes and their significance in relation to functions. <i>Progress in Retinal and Eye Research</i> , 2009, 28, 87-116.	7.3	96
940	Age-related gene expression in Tourette syndrome. <i>Journal of Psychiatric Research</i> , 2009, 43, 319-330.	1.5	25
941	Re-evaluation of the role of STOX1 transcription factor in placental development and preeclampsia. <i>Journal of Reproductive Immunology</i> , 2009, 82, 174-181.	0.8	18
942	Regression of pressure-induced left ventricular hypertrophy is characterized by a distinct gene expression profile. <i>Journal of Thoracic and Cardiovascular Surgery</i> , 2009, 137, 232-238.e8.	0.4	30
943	Early gene expression changes during embryonic stem cell differentiation into cardiomyocytes and their modulation by monobutyl phthalate. <i>Reproductive Toxicology</i> , 2009, 27, 93-102.	1.3	69

#	ARTICLE	IF	CITATIONS
944	Gene expression profiling in the liver and lung of perfluorooctane sulfonate-exposed mouse fetuses: Comparison to changes induced by exposure to perfluorooctanoic acid. <i>Reproductive Toxicology</i> , 2009, 27, 278-288.	1.3	66
945	Dose-dependent transitions in Nrf2-mediated adaptive response and related stress responses to hypochlorous acid in mouse macrophages. <i>Toxicology and Applied Pharmacology</i> , 2009, 238, 27-36.	1.3	76
946	Determination of the key innate genes related to individual variation in carbon tetrachloride-induced hepatotoxicity using a pre-biopsy procedure. <i>Toxicology and Applied Pharmacology</i> , 2009, 239, 55-63.	1.3	14
947	Genomic approaches in the identification of hypoxia biomarkers in model fish species. <i>Journal of Experimental Marine Biology and Ecology</i> , 2009, 381, S180-S187.	0.7	42
948	Seeking unique and common biological themes in multiple gene lists or datasets: pathway pattern extraction pipeline for pathway-level comparative analysis. <i>BMC Bioinformatics</i> , 2009, 10, 200.	1.2	16
949	OHMM: a Hidden Markov Model accurately predicting the occupancy of a transcription factor with a self-overlapping binding motif. <i>BMC Bioinformatics</i> , 2009, 10, 208.	1.2	11
950	Genephony: a knowledge management tool for genome-wide research. <i>BMC Bioinformatics</i> , 2009, 10, 278.	1.2	8
951	ArrayDer: automated structural re-annotation pipeline for DNA microarrays. <i>BMC Bioinformatics</i> , 2009, 10, 30.	1.2	11
952	Robust extraction of functional signals from gene set analysis using a generalized threshold free scoring function. <i>BMC Bioinformatics</i> , 2009, 10, 307.	1.2	35
953	Illumina WG-6 BeadChip strips should be normalized separately. <i>BMC Bioinformatics</i> , 2009, 10, 372.	1.2	19
954	GORilla: a tool for discovery and visualization of enriched GO terms in ranked gene lists. <i>BMC Bioinformatics</i> , 2009, 10, 48.	1.2	3,032
955	ContDist: a tool for the analysis of quantitative gene and promoter properties. <i>BMC Bioinformatics</i> , 2009, 10, 7.	1.2	8
956	Site-specific impacts on gene expression and behavior in fathead minnows ( <i>Pimephales promelas</i> ) exposed in situ to streams adjacent to sewage treatment plants. <i>BMC Bioinformatics</i> , 2009, 10, S11.	1.2	33
957	Comparing gene annotation enrichment tools for functional modeling of agricultural microarray data. <i>BMC Bioinformatics</i> , 2009, 10, S9.	1.2	21
958	Human microRNA target analysis and gene ontology clustering by GOMir, a novel stand-alone application. <i>BMC Bioinformatics</i> , 2009, 10, S20.	1.2	34
959	Natural genetic variation in transcriptome reflects network structure inferred with major effect mutations: insulin/TOR and associated phenotypes in <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2009, 10, 124.	1.2	19
960	Transcription and splicing regulation in human umbilical vein endothelial cells under hypoxic stress conditions by exon array. <i>BMC Genomics</i> , 2009, 10, 126.	1.2	47
961	Reconstruction and functional analysis of altered molecular pathways in human atherosclerotic arteries. <i>BMC Genomics</i> , 2009, 10, 13.	1.2	80

#	ARTICLE	IF	CITATIONS
962	Functional annotation of the human retinal pigment epithelium transcriptome. BMC Genomics, 2009, 10, 164.	1.2	52
963	Distinct patterns of gene and protein expression elicited by organophosphorus pesticides in <i>Caenorhabditis elegans</i> . BMC Genomics, 2009, 10, 202.	1.2	40
964	Distinct gene-expression profiles characterize mammary tumors developed in transgenic mice expressing constitutively active and C-terminally truncated variants of STAT5. BMC Genomics, 2009, 10, 231.	1.2	7
965	Gene expression profiling within the spleen of <i>Clostridium perfringens</i> -challenged Broilers fed antibiotic-medicated and non-medicated diets. BMC Genomics, 2009, 10, 260.	1.2	32
966	Discernment of possible mechanisms of hepatotoxicity via biological processes over-represented by co-expressed genes. BMC Genomics, 2009, 10, 272.	1.2	9
967	Genome wide analysis of human genes transcriptionally and post-transcriptionally regulated by the HTLV-I protein p30. BMC Genomics, 2009, 10, 311.	1.2	26
968	In silico identification of a core regulatory network of OCT4 in human embryonic stem cells using an integrated approach. BMC Genomics, 2009, 10, 314.	1.2	41
969	Detection of differentially expressed genes between Erhualian and Large White placentas on day 75 and 90 of gestation. BMC Genomics, 2009, 10, 337.	1.2	34
970	The steady-state transcriptome of the four major life-cycle stages of <i>Trypanosoma cruzi</i> . BMC Genomics, 2009, 10, 370.	1.2	125
971	Combined genome-wide expression profiling and targeted RNA interference in primary mouse macrophages reveals perturbation of transcriptional networks associated with interferon signalling. BMC Genomics, 2009, 10, 372.	1.2	22
972	Weighted gene co-expression network analysis of the peripheral blood from Amyotrophic Lateral Sclerosis patients. BMC Genomics, 2009, 10, 405.	1.2	156
973	Expulsion of <i>Trichuris muris</i> is associated with increased expression of angiogenin 4 in the gut and increased acidity of mucins within the goblet cell. BMC Genomics, 2009, 10, 492.	1.2	46
974	Transcriptome analysis of differentiating trypanosomes reveals the existence of multiple post-transcriptional regulons. BMC Genomics, 2009, 10, 495.	1.2	127
975	Identification of differentially expressed miRNAs in chicken lung and trachea with avian influenza virus infection by a deep sequencing approach. BMC Genomics, 2009, 10, 512.	1.2	113
976	RNA profiles of rat olfactory epithelia: individual and age related variations. BMC Genomics, 2009, 10, 572.	1.2	25
977	Deciphering the transcriptional circuitry of microRNA genes expressed during human monocytic differentiation. BMC Genomics, 2009, 10, 595.	1.2	65
978	Increased epithelial stem cell traits in advanced endometrial endometrioid carcinoma. BMC Genomics, 2009, 10, 613.	1.2	18
979	Transcriptional adaptations following exercise in Thoroughbred horse skeletal muscle highlights molecular mechanisms that lead to muscle hypertrophy. BMC Genomics, 2009, 10, 638.	1.2	57

#	ARTICLE	IF	CITATIONS
980	Understanding Haemophilus parasuis infection in porcine spleen through a transcriptomics approach. BMC Genomics, 2009, 10, 64.	1.2	59
981	Identification of genes differentially expressed as result of adenovirus type 5- and adenovirus type 12-transformation. BMC Genomics, 2009, 10, 67.	1.2	6
982	Somatic, germline and sex hierarchy regulated gene expression during Drosophila metamorphosis. BMC Genomics, 2009, 10, 80.	1.2	49
983	Rapid evolution of mammalian X-linked testis microRNAs. BMC Genomics, 2009, 10, 97.	1.2	98
984	Annotating the human genome with Disease Ontology. BMC Genomics, 2009, 10, S6.	1.2	204
985	A Candida albicans early stage biofilm detachment event in rich medium. BMC Microbiology, 2009, 9, 25.	1.3	43
986	Integrating microRNA and mRNA expression profiles of neuronal progenitors to identify regulatory networks underlying the onset of cortical neurogenesis. BMC Neuroscience, 2009, 10, 98.	0.8	65
987	DDEC: Dragon database of genes implicated in esophageal cancer. BMC Cancer, 2009, 9, 219.	1.1	24
988	Gene expression down-regulation in CD90+prostate tumor-associated stromal cells involves potential organ-specific genes. BMC Cancer, 2009, 9, 317.	1.1	39
989	Identification of pediatric septic shock subclasses based on genome-wide expression profiling. BMC Medicine, 2009, 7, 34.	2.3	216
990	A Drosophila systems model of pentylene tetrazole induced locomotor plasticity responsive to antiepileptic drugs. BMC Systems Biology, 2009, 3, 11.	3.0	25
991	Migration potential and gene expression profile of human mesenchymal stem cells induced by CCL25. Experimental Cell Research, 2009, 315, 1468-1479.	1.2	52
992	Transcriptional signature of human adipose tissue-derived stem cells (hASCs) preconditioned for chondrogenesis in hypoxic conditions. Experimental Cell Research, 2009, 315, 1937-1952.	1.2	46
993	CUX1/Wnt signaling regulates Epithelial Mesenchymal Transition in EBV infected epithelial cells. Experimental Cell Research, 2009, 315, 1819-1831.	1.2	31
994	QTL for traits related to humoral immune response estimated from data of a porcine F2 resource population. International Journal of Immunogenetics, 2009, 36, 141-151.	0.8	33
995	A pro-inflammatory signature mediates FGF2-induced angiogenesis. Journal of Cellular and Molecular Medicine, 2009, 13, 2083-2108.	1.6	66
996	Differential expression profiling of the synaptosome proteome in a rat model of antipsychotic resistance. Brain Research, 2009, 1295, 170-178.	1.1	14
997	Formulating and testing hypotheses in functional genomics. Artificial Intelligence in Medicine, 2009, 45, 97-107.	3.8	21



#	ARTICLE	IF	CITATIONS
998	MicroRNA expression changes during human leukemic HL-60 cell differentiation induced by 4-hydroxynonenal, a product of lipid peroxidation. <i>Free Radical Biology and Medicine</i> , 2009, 46, 282-288.	1.3	55
999	A Gene Expression Signature Associated with $\alpha$ -K-Ras Addiction Reveals Regulators of EMT and Tumor Cell Survival. <i>Cancer Cell</i> , 2009, 15, 489-500.	7.7	735
1000	Down-regulation of miR-17 family expression in response to retinoic acid induced neuronal differentiation. <i>Cellular Signalling</i> , 2009, 21, 1837-1845.	1.7	98
1001	Rational drug design. <i>European Journal of Pharmacology</i> , 2009, 625, 90-100.	1.7	217
1002	Chronic wound healing by fetal cell therapy may be explained by differential gene profiling observed in fetal versus old skin cells. <i>Experimental Gerontology</i> , 2009, 44, 208-218.	1.2	65
1003	Microarray analysis of liver gene expression in iron overloaded patients with sickle cell anemia and beta-thalassemia. <i>American Journal of Hematology</i> , 2009, 84, 328-334.	2.0	14
1004	Single-cell expression profiling of dopaminergic neurons combined with association analysis identifies pyridoxal kinase as Parkinson's disease gene. <i>Annals of Neurology</i> , 2009, 66, 792-798.	2.8	49
1005	Age-related decrease in proteasome expression contributes to defective nuclear factor- $\kappa$ B activation during hepatic ischemia/reperfusion. <i>Hepatology</i> , 2009, 49, 1718-1728.	3.6	38
1006	Extracellular matrix modulates sensitivity of hepatocytes to fibroblastoid dedifferentiation and transforming growth factor $\beta$ -induced apoptosis. <i>Hepatology</i> , 2009, 49, 2031-2043.	3.6	217
1007	Quantitative transcriptional neuroanatomy of the rat hippocampus: Evidence for wide-ranging, pathway-specific heterogeneity among three principal cell layers. <i>Hippocampus</i> , 2009, 19, 253-264.	0.9	48
1008	Pharmacogenomics and analogues of the antitumour agent N <sup>6</sup> -isopentenyladenosine. <i>International Journal of Cancer</i> , 2009, 124, 2179-2185.	2.3	25
1009	Alterations in miRNA processing and expression in pleomorphic adenomas of the salivary gland. <i>International Journal of Cancer</i> , 2009, 124, 2855-2863.	2.3	87
1010	Gene signatures of pulmonary metastases of renal cell carcinoma reflect the disease-free interval and the number of metastases per patient. <i>International Journal of Cancer</i> , 2009, 125, 474-482.	2.3	93
1011	Housekeeping genes in prostate tumorigenesis. <i>International Journal of Cancer</i> , 2009, 125, 2603-2608.	2.3	14
1012	Gene expression-based analysis of local and metastatic neuroblastoma variants reveals a set of genes associated with tumor progression in neuroblastoma patients. <i>International Journal of Cancer</i> , 2010, 126, 1570-1581.	2.3	17
1013	Focal amplifications are associated with high grade and recurrences in stage Ta bladder carcinoma. <i>International Journal of Cancer</i> , 2010, 126, 1390-1402.	2.3	54
1014	Cellular expression of <i>Midkine<sup>a</sup></i> and <i>Midkine<sup>b</sup></i> during retinal development and photoreceptor regeneration in zebrafish. <i>Journal of Comparative Neurology</i> , 2009, 514, 1-10.	0.9	42
1015	Analysis of Rex1 (zfp42) function in embryonic stem cell differentiation. <i>Developmental Dynamics</i> , 2009, 238, 1863-1877.	0.8	61

#	ARTICLE	IF	CITATIONS
1016	Dynamic patterning at the pylorus: Formation of an epithelial intestine-stomach boundary in late fetal life. <i>Developmental Dynamics</i> , 2009, 238, 3205-3217.	0.8	36
1017	Oncogene expression profiles in K6/ODC mouse skin and papillomas following a chronic exposure to monomethylarsonous acid. <i>Journal of Biochemical and Molecular Toxicology</i> , 2009, 23, 406-418.	1.4	9
1018	The osteogenic transcription factor Runx2 regulates components of the fibroblast growth factor/proteoglycan signaling axis in osteoblasts. <i>Journal of Cellular Biochemistry</i> , 2009, 107, 144-154.	1.2	87
1019	FGF-8b induces growth and rich vascularization in an orthotopic PC-3 model of prostate cancer. <i>Journal of Cellular Biochemistry</i> , 2009, 107, 769-784.	1.2	27
1020	Retinoid-responsive transcriptional changes in epidermal keratinocytes. <i>Journal of Cellular Physiology</i> , 2009, 220, 427-439.	2.0	96
1021	Human cell toxicogenomic analysis of bromoacetic acid: A regulated drinking water disinfection by-product. <i>Environmental and Molecular Mutagenesis</i> , 2010, 51, 205-214.	0.9	31
1022	Genomic imbalances in rhabdomyosarcoma cell lines affect expression of genes frequently altered in primary tumors: An approach to identify candidate genes involved in tumor development. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 455-467.	1.5	98
1023	AML/MDS with 11q/MLL amplification show characteristic gene expression signature and interplay of DNA copy number changes. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 510-520.	1.5	29
1024	Comprehensive gene expression profiling in lungs of mice infected with <i>Mycobacterium tuberculosis</i> following DNAhsp65 immunotherapy. <i>Journal of Gene Medicine</i> , 2009, 11, 66-78.	1.4	22
1025	Genomic landscape of developing male germ cells. <i>Birth Defects Research Part C: Embryo Today Reviews</i> , 2009, 87, 43-63.	3.6	40
1026	Incomplete penetrance and variable expressivity: is there a microRNA connection?. <i>BioEssays</i> , 2009, 31, 981-992.	1.2	28
1027	Dynamic culture of droplet-confined cell arrays. <i>Biotechnology Progress</i> , 2010, 26, 220-231.	1.3	6
1028	Detection of low-abundant novel transcripts in mouse hematopoietic stem cells. <i>Molecular Genetics and Genomics</i> , 2009, 282, 363-370.	1.0	0
1029	Identification of common genetic variants that account for transcript isoform variation between human populations. <i>Human Genetics</i> , 2009, 125, 81-93.	1.8	75
1030	In vitro multipotent differentiation and barrier function of a human mammary epithelium. <i>Cell and Tissue Research</i> , 2009, 335, 383-395.	1.5	29
1031	Porcine muscle sensory attributes associate with major changes in gene networks involving CAPZB, ANKRD1, and CTBP2. <i>Functional and Integrative Genomics</i> , 2009, 9, 455-471.	1.4	39
1032	Gene expression profiles of dental follicle cells before and after osteogenic differentiation in vitro. <i>Clinical Oral Investigations</i> , 2009, 13, 383-391.	1.4	58
1033	HIF-1-Dependent Gene Expression Program During the Nucleic Acid-Triggered Antiviral Innate Immune Responses. <i>Molecules and Cells</i> , 2009, 27, 243-250.	1.0	12

#	ARTICLE	IF	CITATIONS
1034	Genomic and proteomic study to survey the mechanism of action of the anti-Parkinson's disease drug, rasagiline compared with selegiline, in the rat midbrain. <i>Journal of Neural Transmission</i> , 2009, 116, 1457-1472.	1.4	24
1035	Insights into the molecular basis of the microaerophily of three Campylobacterales: a comparative study. <i>Antonie Van Leeuwenhoek</i> , 2009, 96, 545-557.	0.7	8
1036	Meiotic behavior of aneuploid chromatin in mouse models of Down syndrome. <i>Chromosoma</i> , 2009, 118, 723-736.	1.0	20
1037	Spatial Mapping of Thymic Stromal Microenvironments Reveals Unique Features Influencing T Lymphoid Differentiation. <i>Immunity</i> , 2009, 31, 999-1009.	6.6	76
1038	Microarray Analysis of Gene Expression in Rat Cortical Neurons Exposed to Hyperbaric Air and Oxygen. <i>Neurochemical Research</i> , 2009, 34, 1047-1056.	1.6	26
1039	Selenoprotein W Modulates Control of Cell Cycle Entry. <i>Biological Trace Element Research</i> , 2009, 131, 229-244.	1.9	35
1040	Differential gene expression in the developing human macula: microarray analysis using rare tissue samples. <i>Journal of Ocular Biology, Diseases, and Informatics</i> , 2009, 2, 176-189.	0.2	8
1041	Identification of human sperm transcripts as candidate markers of male fertility. <i>Journal of Molecular Medicine</i> , 2009, 87, 735-748.	1.7	76
1042	d-Serine exposure resulted in gene expression changes implicated in neurodegenerative disorders and neuronal dysfunction in male Fischer 344 rats. <i>Archives of Toxicology</i> , 2009, 83, 747-762.	1.9	22
1043	Insights into Mesenchymal Stem Cell Aging: Involvement of Antioxidant Defense and Actin Cytoskeleton. <i>Stem Cells</i> , 2009, 27, 1288-1297.	1.4	203
1044	Proteomics analysis of two mice hepatocarcinoma ascites syngeneic cell lines with high and low lymph node metastasis rates provide potential protein markers for tumor malignancy attributes to lymphatic metastasis. <i>Proteomics</i> , 2009, 9, 3285-3302.	1.3	49
1045	Comparative proteomic analysis of the insulin-induced L6 myotube secretome. <i>Proteomics</i> , 2009, 9, 51-60.	1.3	82
1046	Role of translation by mitochondrial-type ribosomes during sperm capacitation: An analysis based on a proteomic approach. <i>Proteomics</i> , 2009, 9, 1385-1399.	1.3	62
1047	Genome-wide analysis and proteomic studies reveal APE1/Ref1 multifunctional role in mammalian cells. <i>Proteomics</i> , 2009, 9, 1058-1074.	1.3	90
1048	Phosphoproteomic analysis of distinct tumor cell lines in response to nocodazole treatment. <i>Proteomics</i> , 2009, 9, 2861-2874.	1.3	27
1049	Application of iTRAQ to catalogue the skeletal muscle proteome in pigs and assessment of effects of gender and diet dephytinization. <i>Proteomics</i> , 2009, 9, 4000-4016.	1.3	51
1050	LC-MS/MS as an alternative for SDS-PAGE in blue native analysis of protein complexes. <i>Proteomics</i> , 2009, 9, 4221-4228.	1.3	80
1051	Gene expression associations with the growth inhibitory effects of small molecules on live cells: Specificity of effects and uniformity of mechanisms. <i>Statistical Analysis and Data Mining</i> , 2009, 2, 175-185.	1.4	0

#	ARTICLE	IF	CITATIONS
1052	Proteins that underlie neoplastic progression of ulcerative colitis. <i>Proteomics - Clinical Applications</i> , 2009, 3, 1326-1337.	0.8	47
1053	Unique patterns of molecular profiling between human prostate cancer LNCaP and PCa cells. <i>Prostate</i> , 2009, 69, 1077-1090.	1.2	82
1054	Temporal expression profiling of the effects of secreted factors from prostate stromal cells on embryonal carcinoma stem cells. <i>Prostate</i> , 2009, 69, 1353-1365.	1.2	15
1055	Use of serial analysis of gene expression to reveal the specific regulation of gene expression profile in asthmatic rats treated by acupuncture. <i>Journal of Biomedical Science</i> , 2009, 16, 46.	2.6	28
1056	Global transcriptional response after exposure of fission yeast cells to ultraviolet light. <i>BMC Cell Biology</i> , 2009, 10, 87.	3.0	5
1057	Gene expression profiling of human alveolar macrophages infected by <i>B. anthracis</i> spores demonstrates TNF- $\alpha$ and NF- $\kappa$ B are key components of the innate immune response to the pathogen. <i>BMC Infectious Diseases</i> , 2009, 9, 152.	1.3	27
1058	Effects of typical and atypical antipsychotic drugs on gene expression profiles in the liver of schizophrenia subjects. <i>BMC Psychiatry</i> , 2009, 9, 57.	1.1	34
1059	Gene expression profiling predicts a three-gene expression signature of endometrial adenocarcinoma in a rat model. <i>Cancer Cell International</i> , 2009, 9, 12.	1.8	9
1060	Microarray and cDNA sequence analysis of transcription during nerve-dependent limb regeneration. <i>BMC Biology</i> , 2009, 7, 1.	1.7	203
1061	Mutations in many genes affect aggressive behavior in <i>Drosophila melanogaster</i> . <i>BMC Biology</i> , 2009, 7, 29.	1.7	85
1062	Toxicogenomic analysis of susceptibility to inhaled urban particulate matter in mice with chronic lung inflammation. <i>Particle and Fibre Toxicology</i> , 2009, 6, 6.	2.8	27
1063	Prediction of HIV-1 virus-host protein interactions using virus and host sequence motifs. <i>BMC Medical Genomics</i> , 2009, 2, 27.	0.7	85
1064	Integrated analysis of DNA methylation and gene expression reveals specific signaling pathways associated with platinum resistance in ovarian cancer. <i>BMC Medical Genomics</i> , 2009, 2, 34.	0.7	192
1065	Candidate pathways and genes for prostate cancer: a meta-analysis of gene expression data. <i>BMC Medical Genomics</i> , 2009, 2, 48.	0.7	45
1066	Early over expression of messenger RNA for multiple genes, including insulin, in the Pancreatic Lymph Nodes of NOD mice is associated with Islet Autoimmunity. <i>BMC Medical Genomics</i> , 2009, 2, 63.	0.7	12
1067	A taxonomy of epithelial human cancer and their metastases. <i>BMC Medical Genomics</i> , 2009, 2, 69.	0.7	19
1068	Genome-wide Gene Expression Profiling of SCID Mice with T cell-mediated Colitis. <i>Scandinavian Journal of Immunology</i> , 2009, 69, 437-446.	1.3	4
1069	Transcriptional profiling of CD31 <sup>+</sup> cells isolated from murine embryonic stem cells. <i>Genes To Cells</i> , 2009, 14, 243-260.	0.5	15

#	ARTICLE	IF	CITATIONS
1070	Expression profiling of genes related to asthma exacerbations. <i>Clinical and Experimental Allergy</i> , 2009, 39, 213-221.	1.4	63
1071	Gene expression profiles in human nasal polyp tissues and identification of genetic susceptibility in aspirin-intolerant asthma. <i>Clinical and Experimental Allergy</i> , 2009, 39, 972-981.	1.4	37
1072	The epidermal differentiation-associated Grainyhead gene <i>Get1/Grhl3</i> also regulates urothelial differentiation. <i>EMBO Journal</i> , 2009, 28, 1890-1903.	3.5	70
1073	Pten in stromal fibroblasts suppresses mammary epithelial tumours. <i>Nature</i> , 2009, 461, 1084-1091.	13.7	475
1074	Targeted bisulfite sequencing reveals changes in DNA methylation associated with nuclear reprogramming. <i>Nature Biotechnology</i> , 2009, 27, 353-360.	9.4	458
1075	The proteomic analysis of human neonatal umbilical cord serum by mass spectrometry. <i>Acta Pharmacologica Sinica</i> , 2009, 30, 1550-1558.	2.8	17
1076	Large histone H3 lysine 9 dimethylated chromatin blocks distinguish differentiated from embryonic stem cells. <i>Nature Genetics</i> , 2009, 41, 246-250.	9.4	540
1077	Systems genetics of complex traits in <i>Drosophila melanogaster</i> . <i>Nature Genetics</i> , 2009, 41, 299-307.	9.4	490
1078	Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. <i>Nature Protocols</i> , 2009, 4, 44-57.	5.5	31,831
1079	Network visualization and analysis of gene expression data using BioLayout Express3D. <i>Nature Protocols</i> , 2009, 4, 1535-1550.	5.5	443
1080	The histone variant macroH2A is an epigenetic regulator of key developmental genes. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1074-1079.	3.6	166
1081	ORIGINAL ARTICLE: Cytokine Array Comparisons of Plasma from Cycling Fertile Women on Cycle Day 5 and Ovulation. <i>American Journal of Reproductive Immunology</i> , 2009, 62, 158-164.	1.2	6
1082	Gene expression demonstrates increased resilience toward harmful inflammatory stimuli in the proliferating epidermis of human skin wounds. <i>Experimental Dermatology</i> , 2010, 19, e329-32.	1.4	14
1083	Massive induction of innate immune response to <i>Candida albicans</i> in the kidney in a murine intravenous challenge model. <i>FEMS Yeast Research</i> , 2009, 9, 1111-1122.	1.1	49
1084	Gene expression in the detection of autologous blood transfusion in sports – a pilot study. <i>Vox Sanguinis</i> , 2009, 96, 333-336.	0.7	26
1085	Gene expression profiling to define host response to baculoviral transduction in the brain. <i>Journal of Neurochemistry</i> , 2009, 109, 1203-1214.	2.1	25
1086	Oxidative stress and longevity in <i>Caenorhabditis elegans</i> as mediated by SKN-1. <i>Aging Cell</i> , 2009, 8, 258-269.	3.0	202
1087	Condition-adapted stress and longevity gene regulation by <i>Caenorhabditis elegans</i> SKN-1/Nrf. <i>Aging Cell</i> , 2009, 8, 524-541.	3.0	302

#	ARTICLE	IF	CITATIONS
1088	<i>Caenorhabditis elegans</i> PI3K mutants reveal novel genes underlying exceptional stress resistance and lifespan. <i>Aging Cell</i> , 2009, 8, 706-725.	3.0	34
1089	Mucosal gene expression profiles following the colonization of immunocompetent defined-flora C3H mice with <i>Helicobacter bilis</i> : a prelude to typhlocolitis. <i>Microbes and Infection</i> , 2009, 11, 374-383.	1.0	15
1090	The molecular basis of prostate cancer cell escape from protoporphyrin IX-based photodynamic therapy. <i>Medical Laser Application: International Journal for Laser Treatment and Research</i> , 2009, 24, 237-246.	0.4	3
1091	Alterations in gene expression of glutamate receptors and exocytosis-related factors by a hydroxylated-polychlorinated biphenyl in the developing rat brain. <i>Toxicology</i> , 2009, 257, 17-24.	2.0	14
1092	Comparison of gene expression responses to hypoxia in viviparous ( <i>Xiphophorus</i> ) and oviparous ( <i>Oryzias</i> ) fishes using a medaka microarray. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2009, 149, 258-265.	1.3	36
1093	Gene expression profiling of single bovine embryos uncovers significant effects of in vitro maturation, fertilization and culture. <i>Molecular Reproduction and Development</i> , 2009, 76, 38-47.	1.0	66
1094	Molecular mechanisms regulating bovine ovarian follicular selection. <i>Molecular Reproduction and Development</i> , 2009, 76, 351-366.	1.0	28
1095	Profile of estrogen-responsive genes in an estrogen-specific mammary gland outgrowth model. <i>Molecular Reproduction and Development</i> , 2009, 76, 733-750.	1.0	30
1096	Meta-analysis of age-related gene expression profiles identifies common signatures of aging. <i>Bioinformatics</i> , 2009, 25, 875-881.	1.8	651
1097	SWI/SNF-Brg1 Regulates Self-Renewal and Occupies Core Pluripotency-Related Genes in Embryonic Stem Cells. <i>Stem Cells</i> , 2009, 27, 317-328.	1.4	221
1098	BAC Transgenesis in Human Embryonic Stem Cells as a Novel Tool to Define the Human Neural Lineage. <i>Stem Cells</i> , 2009, 27, 521-532.	1.4	75
1099	Evaluation of 3 Clinical Dendritic Cell Maturation Protocols Containing Lipopolysaccharide and Interferon- $\beta$ . <i>Journal of Immunotherapy</i> , 2009, 32, 399-407.	1.2	58
1100	Functional Profiling Methods in Cancer. <i>Methods in Molecular Biology</i> , 2009, 576, 363-374.	0.4	2
1101	A Genome-wide Survey of the Prevalence and Evolutionary Forces Acting on Human Nonsense SNPs. <i>American Journal of Human Genetics</i> , 2009, 84, 224-234.	2.6	69
1102	Genetic Control of Human Brain Transcript Expression in Alzheimer Disease. <i>American Journal of Human Genetics</i> , 2009, 84, 445-458.	2.6	290
1103	Global placental gene expression in gestational diabetes mellitus. <i>American Journal of Obstetrics and Gynecology</i> , 2009, 200, 206.e1-206.e13.	0.7	68
1104	Stable Isotope Labeling and Label-Free Proteomics of <i>Drosophila parkin</i> Null Mutants. <i>Journal of Proteome Research</i> , 2009, 8, 4500-4510.	1.8	17
1105	Three subclasses of a <i>Drosophila</i> insulator show distinct and cell type-specific genomic distributions. <i>Genes and Development</i> , 2009, 23, 1338-1350.	2.7	171

#	ARTICLE	IF	CITATIONS
1106	2â€²-Benzoyloxycinnamaldehyde Inhibits Tumor Growth in H- <i>ras</i> 12V Transgenic Mice via Downregulation of Metallothionein. <i>Nutrition and Cancer</i> , 2009, 61, 723-734.	0.9	7
1107	Integrating Gene Expression and Phenotypic Information to Analyze Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2009, 16, 73-84.	1.2	10
1108	Bioinformatics enrichment tools: paths toward the comprehensive functional analysis of large gene lists. <i>Nucleic Acids Research</i> , 2009, 37, 1-13.	6.5	13,313
1109	Establishment of Intestinal Identity and Epithelial-Mesenchymal Signaling by Cdx2. <i>Developmental Cell</i> , 2009, 16, 588-599.	3.1	332
1110	Gene expression signatures of a fibroblastoid preosteoblast and cuboidal osteoblast cell model compared to the MLO-Y4 osteocyte cell model. <i>Bone</i> , 2009, 44, 32-45.	1.4	43
1111	Modified titanium surfaces promote accelerated osteogenic differentiation of mesenchymal stromal cells in vitro. <i>Bone</i> , 2009, 45, 17-26.	1.4	253
1112	Comparison of rat olfactory mucosal responses to carcinogenic and non-carcinogenic chloracetanilides. <i>Food and Chemical Toxicology</i> , 2009, 47, 1051-1057.	1.8	3
1113	A Genome-wide RNAi Screen for Modifiers of the Circadian Clock in Human Cells. <i>Cell</i> , 2009, 139, 199-210.	13.5	437
1114	Induction of Intestinal Th17 Cells by Segmented Filamentous Bacteria. <i>Cell</i> , 2009, 139, 485-498.	13.5	3,818
1115	Jumonji Modulates Polycomb Activity and Self-Renewal versus Differentiation of Stem Cells. <i>Cell</i> , 2009, 139, 1303-1314.	13.5	398
1116	Non-CpG Methylation of the PGC-1 $\beta$ Promoter through DNMT3B Controls Mitochondrial Density. <i>Cell Metabolism</i> , 2009, 10, 189-198.	7.2	530
1117	Global gene expression changes including drug metabolism and disposition induced by three-dimensional culture of HepG2 cells-Involvement of microtubules. <i>Biochemical and Biophysical Research Communications</i> , 2009, 378, 558-562.	1.0	21
1118	Transcriptomic profiling identifies a PU.1 regulatory network in macrophages. <i>Biochemical and Biophysical Research Communications</i> , 2009, 380, 308-312.	1.0	31
1119	DNA Methyltransferase 1 Is Essential for and Uniquely Regulates Hematopoietic Stem and Progenitor Cells. <i>Cell Stem Cell</i> , 2009, 5, 442-449.	5.2	318
1120	Functional and Evolutionary Insights into Human Brain Development through Global Transcriptome Analysis. <i>Neuron</i> , 2009, 62, 494-509.	3.8	555
1121	Analysis of biomarkers after intramuscular injection of Vaxfectin $\text{\textcircled{R}}$ -formulated hCMV gB plasmid DNA. <i>Vaccine</i> , 2009, 27, 7409-7417.	1.7	10
1122	Human immunodeficiency virus type 1 chronic infection is associated with different gene expression in MT-4, H9 and U937 cell lines. <i>Virus Research</i> , 2009, 139, 22-31.	1.1	16
1123	Forkhead box M1 transcriptional factor is required for smooth muscle cells during embryonic development of blood vessels and esophagus. <i>Developmental Biology</i> , 2009, 336, 266-279.	0.9	63

#	ARTICLE	IF	CITATIONS
1124	Tissue specific differentially methylated regions (TDMR): Changes in DNA methylation during development. <i>Genomics</i> , 2009, 93, 130-139.	1.3	116
1125	SNP-based prediction of the human germ cell methylation landscape. <i>Genomics</i> , 2009, 93, 434-440.	1.3	17
1126	Finding disease-specific coordinated functions by multi-function genes: Insight into the coordination mechanisms in diseases. <i>Genomics</i> , 2009, 94, 94-100.	1.3	17
1127	Candidate <i>Agtr2</i> influenced genes and pathways identified by expression profiling in the developing brain of <i>Agtr2</i> <sup>+/y</sup> mice. <i>Genomics</i> , 2009, 94, 188-195.	1.3	14
1128	Technical considerations in using DNA microarrays to define regulons. <i>Methods</i> , 2009, 47, 63-72.	1.9	12
1129	Phenotypic expression of maternally inherited deafness is affected by RNA modification and cytoplasmic ribosomal proteins. <i>Molecular Genetics and Metabolism</i> , 2009, 97, 297-304.	0.5	9
1130	Progesterone receptor A-regulated gene expression in mammary organoid cultures. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2009, 115, 161-172.	1.2	31
1131	Identification of neuronal target genes for CCAAT/Enhancer Binding Proteins. <i>Molecular and Cellular Neurosciences</i> , 2009, 40, 313-327.	1.0	40
1132	Primary biliary cirrhosis is associated with altered hepatic microRNA expression. <i>Journal of Autoimmunity</i> , 2009, 32, 246-253.	3.0	191
1133	A Genome-wide siRNA Screen Reveals Diverse Cellular Processes and Pathways that Mediate Genome Stability. <i>Molecular Cell</i> , 2009, 35, 228-239.	4.5	482
1134	Insights into GATA-1-Mediated Gene Activation versus Repression via Genome-wide Chromatin Occupancy Analysis. <i>Molecular Cell</i> , 2009, 36, 682-695.	4.5	278
1135	A Reconfigured Pattern of MLL Occupancy within Mitotic Chromatin Promotes Rapid Transcriptional Reactivation Following Mitotic Exit. <i>Molecular Cell</i> , 2009, 36, 970-983.	4.5	173
1136	Specificity of the zebrafish host transcriptome response to acute and chronic mycobacterial infection and the role of innate and adaptive immune components. <i>Molecular Immunology</i> , 2009, 46, 2317-2332.	1.0	112
1137	Effects of lithium chloride on the gene expression profiles in <i>Drosophila</i> heads. <i>Neuroscience Research</i> , 2009, 64, 413-420.	1.0	20
1138	Genetical toxicogenomics in <i>Drosophila</i> identifies master-modulatory loci that are regulated by developmental exposure to lead. <i>NeuroToxicology</i> , 2009, 30, 898-914.	1.4	45
1139	Transcriptome Profiling Reveals TGF- $\beta$ Signaling Involvement in Epileptogenesis. <i>Journal of Neuroscience</i> , 2009, 29, 8927-8935.	1.7	317
1140	Differential Testicular Gene Expression in Seasonal Fertility. <i>Journal of Biological Rhythms</i> , 2009, 24, 114-125.	1.4	10
1141	Chromatin Immunoprecipitation on Microarray Analysis of Smad2/3 Binding Sites Reveals Roles of ETS1 and TFAP2A in Transforming Growth Factor $\beta$ Signaling. <i>Molecular and Cellular Biology</i> , 2009, 29, 172-186.	1.1	179



#	ARTICLE	IF	CITATIONS
1142	Downregulation of oligodendrocyte transcripts is associated with impaired prefrontal cortex function in rats. <i>Schizophrenia Research</i> , 2009, 113, 277-287.	1.1	54
1143	Comparison of gene expression profiles in mice liver following intravenous injection of 4 and 100nm-sized PEG-coated gold nanoparticles. <i>Toxicology Letters</i> , 2009, 191, 96-102.	0.4	100
1144	Changes in transcriptome after in vivo exposure to ionising radiation reveal a highly specialised liver response. <i>International Journal of Radiation Biology</i> , 2009, 85, 656-671.	1.0	12
1145	Bioinformatics Analysis of Microarray Data. <i>Methods in Molecular Biology</i> , 2009, 573, 259-284.	0.4	63
1146	Zinc Replenishment Reverses Overexpression of the Proinflammatory Mediator S100A8 and Esophageal Preneoplasia in the Rat. <i>Gastroenterology</i> , 2009, 136, 953-966.	0.6	44
1147	Disruption of Dicer1 Induces Dysregulated Fetal Gene Expression and Promotes Hepatocarcinogenesis. <i>Gastroenterology</i> , 2009, 136, 2304-2315.e4.	0.6	167
1148	Extracting Biological Meaning from Large Gene Lists with DAVID. <i>Current Protocols in Bioinformatics</i> , 2009, 27, Unit 13.11.	25.8	375
1149	Corticosteroid effects on blood gene expression in Duchenne muscular dystrophy. <i>Pharmacogenomics Journal</i> , 2009, 9, 411-418.	0.9	6
1150	GeneDecks: Paralog Hunting and Gene-Set Distillation with GeneCards Annotation. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 477-487.	1.0	74
1151	Expression profiling identifies genes involved in emphysema severity. <i>Respiratory Research</i> , 2009, 10, 81.	1.4	35
1152	Comprehensive proteomic analysis of human cervical-vaginal fluid using colposcopy samples. <i>Proteome Science</i> , 2009, 7, 17.	0.7	84
1153	Proteins recruited by SH3 domains of Ruk/CIN85 adaptor identified by LC-MS/MS. <i>Proteome Science</i> , 2009, 7, 21.	0.7	41
1154	GO Explorer: A gene-ontology tool to aid in the interpretation of shotgun proteomics data. <i>Proteome Science</i> , 2009, 7, 6.	0.7	35
1155	MicroRNA and gene expression patterns in the differentiation of human embryonic stem cells. <i>Journal of Translational Medicine</i> , 2009, 7, 20.	1.8	165
1156	Gene and microRNA analysis of neutrophils from patients with polycythemia vera and essential thrombocytosis: down-regulation of micro RNA-1 and -133a. <i>Journal of Translational Medicine</i> , 2009, 7, 39.	1.8	46
1157	The effect of alcohol and nicotine abuse on gene expression in the brain. <i>Nutrition Research Reviews</i> , 2009, 22, 148-162.	2.1	14
1158	Association of survival and disease progression with chromosomal instability: A genomic exploration of colorectal cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7131-7136.	3.3	326
1159	The preferentially expressed antigen in melanoma (PRAME) inhibits myeloid differentiation in normal hematopoietic and leukemic progenitor cells. <i>Blood</i> , 2009, 114, 3299-3308.	0.6	72

#	ARTICLE	IF	CITATIONS
1160	Genome-Wide Determination of DNA Methylation by Hpa II Tiny Fragment Enrichment by Ligation-Mediated PCR (HELP) for the Study of Acute Leukemias. <i>Methods in Molecular Biology</i> , 2009, 538, 395-407.	0.4	34
1161	MB49 Murine Urothelial Carcinoma: Molecular and Phenotypic Comparison to Human Cell Lines as a Model of the Direct Tumor Response to Bacillus Calmette-Guerin. <i>Journal of Urology</i> , 2009, 182, 2932-2937.	0.2	24
1162	CTCF binding site classes exhibit distinct evolutionary, genomic, epigenomic and transcriptomic features. <i>Genome Biology</i> , 2009, 10, R131.	13.9	72
1163	Molecular networks involved in mouse cerebral corticogenesis and spatio-temporal regulation of Sox4 and Sox11 novel antisense transcripts revealed by transcriptome profiling. <i>Genome Biology</i> , 2009, 10, R104.	13.9	34
1164	Studying alternative splicing regulatory networks through partial correlation analysis. <i>Genome Biology</i> , 2009, 10, R3.	13.9	49
1165	Interactions among type I and type II interferon, tumor necrosis factor, and 1 $\beta$ -estradiol in the regulation of immune response-related gene expressions in systemic lupus erythematosus. <i>Arthritis Research and Therapy</i> , 2009, 11, R1.	1.6	43
1166	Lipoproteomics: using mass spectrometry-based proteomics to explore the assembly, structure, and function of lipoproteins. <i>Journal of Lipid Research</i> , 2009, 50, 1967-1975.	2.0	81
1167	UVB Radiation Induces Persistent Activation of Ribosome and Oxidative Phosphorylation Pathways. <i>Radiation Research</i> , 2009, 171, 716.	0.7	17
1168	ArrayQ: Querying Microarray Expressions for Relevant Pathways. , 2009, , .		0
1169	Transcriptome Profiling and Functional Analyses of the Zebrafish Embryonic Innate Immune Response to <i>Salmonella</i> Infection. <i>Journal of Immunology</i> , 2009, 182, 5641-5653.	0.4	214
1170	Computational methods for discovering gene networks from expression data. <i>Briefings in Bioinformatics</i> , 2009, 10, 408-23.	3.2	185
1171	A genome-wide analysis of brain DNA methylation identifies new candidate genes for sporadic amyotrophic lateral sclerosis. <i>Amyotrophic Lateral Sclerosis and Other Motor Neuron Disorders</i> , 2009, 10, 418-429.	2.3	82
1172	Mining gene functional networks to improve mass-spectrometry-based protein identification. <i>Bioinformatics</i> , 2009, 25, 2955-2961.	1.8	34
1173	Adaptive response in embryogenesis: VI. Comparative microarray analysis of gene expressions in mouse fetuses. <i>International Journal of Radiation Biology</i> , 2009, 85, 70-86.	1.0	12
1174	FOS Proliferating Network Construction in Early Colorectal Cancer (CRC) Based on Integrative Significant Function Cluster and Inferring Analysis. <i>Cancer Investigation</i> , 2009, 27, 816-824.	0.6	42
1175	Microarray coupled to quantitative RT-PCR analysis of androgen-regulated genes in human LNCaP prostate cancer cells. <i>Oncogene</i> , 2009, 28, 2051-2063.	2.6	60
1176	Correlation between Gene Expression and Clinical Data through Linear and Nonlinear Principal Components Analyses: Muscular Dystrophies as Case Studies. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 173-184.	1.0	8
1177	Generation of Gene Ontology benchmark datasets with various types of positive signal. <i>BMC Bioinformatics</i> , 2009, 10, 319.	1.2	5

#	ARTICLE	IF	CITATIONS
1178	Dissecting the dynamics of dysregulation of cellular processes in mouse mammary gland tumor. <i>BMC Genomics</i> , 2009, 10, 601.	1.2	28
1179	Early Dysregulation of Cell Adhesion and Extracellular Matrix Pathways in Breast Cancer Progression. <i>American Journal of Pathology</i> , 2009, 175, 1292-1302.	1.9	59
1180	Transcriptome profiling of <i>Streptococcus uberis</i> -induced mastitis reveals fundamental differences between immune gene expression in the mammary gland and in a primary cell culture model. <i>Journal of Dairy Science</i> , 2009, 92, 117-129.	1.4	114
1181	Unique Biological Properties and Application Potentials of CD34+ CD38 <sup>+</sup> Stem Cells From Various Sources. <i>Taiwanese Journal of Obstetrics and Gynecology</i> , 2009, 48, 356-369.	0.5	7
1182	Protein array technology to investigate cytokine production by monocytes from patients with advanced alcoholic cirrhosis: An <i>in vivo</i> pilot study. <i>Hepatology Research</i> , 2009, 39, 706-715.	1.8	15
1183	HIV-1 infection of macrophages is dependent on evasion of innate immune cellular activation. <i>Aids</i> , 2009, 23, 2255-2263.	1.0	91
1184	Genomic expression profiling across the pediatric systemic inflammatory response syndrome, sepsis, and septic shock spectrum*. <i>Critical Care Medicine</i> , 2009, 37, 1558-1566.	0.4	285
1185	DIFFERENTIAL EXPRESSION OF TOLL-LIKE RECEPTOR GENES. <i>Shock</i> , 2009, 31, 238-244.	1.0	37
1186	Gene expression profiling in rat liver treated with various hepatotoxic-compounds inducing coagulopathy. <i>Journal of Toxicological Sciences</i> , 2009, 34, 281-293.	0.7	30
1188	Maturation of mouse NK cells is a 4-stage developmental program. <i>Blood</i> , 2009, 113, 5488-5496.	0.6	643
1189	HIV-1 <sup>+</sup> infected dendritic cells show 2 phases of gene expression changes, with lysosomal enzyme activity decreased during the second phase. <i>Blood</i> , 2009, 114, 85-94.	0.6	63
1190	The transcriptional program controlled by the stem cell leukemia gene <i>Scl/Tal1</i> during early embryonic hematopoietic development. <i>Blood</i> , 2009, 113, 5456-5465.	0.6	107
1191	Gene expression profiling of minimally differentiated acute myeloid leukemia: M0 is a distinct entity subdivided by RUNX1 mutation status. <i>Blood</i> , 2009, 114, 3001-3007.	0.6	51
1192	MicroRNA 29b functions in acute myeloid leukemia. <i>Blood</i> , 2009, 114, 5331-5341.	0.6	412
1193	Plerixafor (AMD3100) and granulocyte colony-stimulating factor (G-CSF) mobilize different CD34+ cell populations based on global gene and microRNA expression signatures. <i>Blood</i> , 2009, 114, 2530-2541.	0.6	95
1194	Identification of Mouse 8-Cell Embryo Stage-Specific Genes by Digital Differential Display. <i>Experimental Animals</i> , 2009, 58, 547-556.	0.7	2
1195	Identification of condition-specific regulatory modules through multi-level motif and mRNA expression analysis. <i>International Journal of Computational Biology and Drug Design</i> , 2009, 2, 1.	0.3	0
1197	Enhanced expression of <i>SOS1</i> is detected in prostate cancer epithelial cells from African-American men. <i>International Journal of Oncology</i> , 2009, 35, .	1.4	26

#	ARTICLE	IF	CITATIONS
1198	Transcriptome analysis of skeletal muscle tissue to identify genes involved in pre-slaughter stress response in pigs. Italian Journal of Animal Science, 2009, 8, 69-71.	0.8	2
1199	Orientation, distance, regulation and function of neighbouring genes. Human Genomics, 2009, 3, 143-56.	1.4	22
1200	Exploring the relationship between polymorphic (TG/CA) n repeats in intron 1 regions and gene expression. Human Genomics, 2009, 3, 236-45.	1.4	10
1201	Molecular Signature of HPV-Induced Carcinogenesis: pRb, p53 and Gene Expression Profiling. Current Genomics, 2009, 10, 26-34.	0.7	81
1202	Functional Annotation of Genes Overlapping Copy Number Variants in Autistic Patients: Focus on Axon Pathfinding. Current Genomics, 2010, 11, 136-145.	0.7	29
1203	Effect of mild restriction of food intake on gene expression profile in the liver of young rats: reference data for in vivo nutrigenomics study. British Journal of Nutrition, 2010, 104, 941-950.	1.2	16
1204	Quercetin supplementation and its effect on human monocyte gene expression profiles <i>in vivo</i> . British Journal of Nutrition, 2010, 104, 336-345.	1.2	39
1205	Evidence for a Novel Blood RNA Diagnostic for Pediatric Appendicitis. Pediatric Emergency Care, 2010, 26, 333-338.	0.5	13
1206	Transcriptome Changes of Chronic Tubulointerstitial Damage in Early Kidney Transplantation. Transplantation, 2010, 89, 537-547.	0.5	27
1207	An introduction to effective use of enrichment analysis software. Human Genomics, 2010, 4, 202.	1.4	60
1208	Oxidative Stress: Emerging Mitochondrial and Cellular Themes and Variations in Neuronal Injury. Journal of Alzheimer's Disease, 2010, 20, S453-S473.	1.2	129
1209	Novel systems biology insights using antifibrotic approaches for diabetic kidney disease. Expert Review of Endocrinology and Metabolism, 2010, 5, 127-135.	1.2	1
1210	MicroRNAs 15a/16-1 function as tumor suppressor genes in multiple myeloma. Blood, 2010, , .	0.6	13
1211	TNFRSF11B computational development network construction and analysis between frontal cortex of HIV encephalitis (HIVE) and HIVE-control patients. Journal of Inflammation, 2010, 7, 50.	1.5	24
1212	Integrated biochemical and computational approach identifies BCL6 direct target genes controlling multiple pathways in normal germinal center B cells. Blood, 2010, 115, 975-984.	0.6	216
1213	Down syndrome acute lymphoblastic leukemia, a highly heterogeneous disease in which aberrant expression of CRLF2 is associated with mutated JAK2: a report from the International BFM Study Group. Blood, 2010, 115, 1006-1017.	0.6	305
1214	Transactivation of the dopamine receptor 3 gene by a single provirus integration results in development of B-cell lymphoma in transgenic mice generated from retrovirally transduced embryonic stem cells. Blood, 2010, 115, 3930-3938.	0.6	0
1215	Down-regulation of GATA1 uncouples STAT5-induced erythroid differentiation from stem/progenitor cell proliferation. Blood, 2010, 115, 4367-4376.	0.6	22

#	ARTICLE	IF	CITATIONS
1216	Effects of TNF- $\alpha$ and IL-1 $\beta$ on the Activation of Genes Related to Inflammatory, Immune Responses and Cell Death in Immortalized Human HaCat Keratinocytes. <i>International Journal of Immunopathology and Pharmacology</i> , 2010, 23, 1057-1072.	1.0	7
1217	Intermittent Hypoxia Mobilizes Bone Marrow-Derived Very Small Embryonic-Like Stem Cells and Activates Developmental Transcriptional Programs in Mice. <i>Sleep</i> , 2010, 33, 1439-1446.	0.6	40
1218	Differential gene expression of ewes varying in tolerance to dietary nitrate <sup>1</sup> . <i>Journal of Animal Science</i> , 2010, 88, 3187-3197.	0.2	10
1219	Rhinovirus-induced modulation of gene expression in bronchial epithelial cells from subjects with asthma. <i>Mucosal Immunology</i> , 2010, 3, 69-80.	2.7	276
1220	Transcriptional profiling of day 12 porcine embryonic disc and trophectoderm samples using ultra-deep sequencing technologies. <i>Molecular Reproduction and Development</i> , 2010, 77, 812-819.	1.0	16
1221	Activation method does not alter abnormal placental gene expression and development in cloned pigs. <i>Molecular Reproduction and Development</i> , 2010, 77, 1016-1030.	1.0	20
1222	Gene Expression in Skin and Lymphoblastoid Cells: Refined Statistical Method Reveals Extensive Overlap in cis-eQTL Signals. <i>American Journal of Human Genetics</i> , 2010, 87, 779-789.	2.6	169
1223	Identification of LPS-inducible genes downregulated by ubiquinone in human THP-1 monocytes. <i>BioFactors</i> , 2010, 36, 222-228.	2.6	30
1224	Shotgun Proteomics Analysis of Hibernating Arctic Ground Squirrels. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 313-326.	2.5	81
1225	Early alterations in heart gene expression profiles associated with doxorubicin cardiotoxicity in rats. <i>Cancer Chemotherapy and Pharmacology</i> , 2010, 66, 303-314.	1.1	62
1226	Defining TNF- $\alpha$ - and LPS-induced gene signatures in monocytes to unravel the complexity of peripheral blood transcriptomes in health and disease. <i>Journal of Molecular Medicine</i> , 2010, 88, 1065-1079.	1.7	18
1227	Mitochondrial abnormalities in the putamen in Parkinson's disease dyskinesia. <i>Acta Neuropathologica</i> , 2010, 120, 623-631.	3.9	30
1228	Genetics of keloid scarring. <i>Archives of Dermatological Research</i> , 2010, 302, 319-339.	1.1	210
1229	Gene expression profiling for the investigation of soft tissue sarcoma pathogenesis and the identification of diagnostic, prognostic, and predictive biomarkers. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2010, 456, 141-151.	1.4	43
1230	Effect of mood stabilizers on gene expression in lymphoblastoid cells. <i>Journal of Neural Transmission</i> , 2010, 117, 155-164.	1.4	30
1231	Modulation of gene expression in endothelial cells by hyperlipaemic postprandial serum from healthy volunteers. <i>Genes and Nutrition</i> , 2010, 5, 263-274.	1.2	10
1232	Expression Profile of Rat Hippocampal Neurons Treated with the Neuroprotective Compound 2,4-Dinitrophenol: Up-Regulation of cAMP Signaling Genes. <i>Neurotoxicity Research</i> , 2010, 18, 112-123.	1.3	17
1233	Gene Expression Profiling Reveals Differentially Expressed Genes in Ovarian Cancer of the Hen: Support for Oviductal Origin?. <i>Hormones and Cancer</i> , 2010, 1, 177-186.	4.9	38

#	ARTICLE	IF	CITATIONS
1234	Comparative study on transcriptional responses of human neuronal cells to silica nanoparticles with different stabilizers. <i>Biochip Journal</i> , 2010, 4, 296-304.	2.5	1
1235	Quantitative proteomic analysis of S-nitrosated proteins in diabetic mouse liver with ICAT switch method. <i>Protein and Cell</i> , 2010, 1, 675-687.	4.8	22
1236	AFP computational secreted network construction and analysis between human hepatocellular carcinoma (HCC) and no-tumor hepatitis/cirrhotic liver tissues. <i>Tumor Biology</i> , 2010, 31, 417-425.	0.8	37
1237	A Common Neuronal Response to Alphaherpesvirus Infection. <i>Journal of NeuroImmune Pharmacology</i> , 2010, 5, 418-427.	2.1	32
1238	Identification of novel epithelial ovarian cancer biomarkers by cross-laboratory microarray analysis. <i>Journal of Huazhong University of Science and Technology [Medical Sciences]</i> , 2010, 30, 354-359.	1.0	4
1239	Characterization of the Human Cervical Mucous Proteome. <i>Clinical Proteomics</i> , 2010, 6, 18-28.	1.1	32
1240	A Functional Role of RB-Dependent Pathway in the Control of Quiescence in Adult Epidermal Stem Cells Revealed by Genomic Profiling. <i>Stem Cell Reviews and Reports</i> , 2010, 6, 162-177.	5.6	18
1241	Gene expression profiles in the PC-3 human prostate cancer cells induced by NKX3.1. <i>Molecular Biology Reports</i> , 2010, 37, 1505-1512.	1.0	12
1242	Stem cell associated gene expression in glioblastoma multiforme: relationship to survival and the subventricular zone. <i>Journal of Neuro-Oncology</i> , 2010, 96, 359-367.	1.4	86
1243	Effector T cells driving monophasic vs. relapsing/remitting experimental autoimmune uveitis show unique pathway signatures. <i>Molecular Immunology</i> , 2010, 48, 272-280.	1.0	26
1244	Temporal gene expression changes induced by a low concentration of benzo[a]pyrene diol epoxide in a normal human cell line. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2010, 684, 74-80.	0.4	12
1245	Genes regulated in MPTP-treated macaques and human Parkinson's disease suggest a common signature in prefrontal cortex. <i>Neurobiology of Disease</i> , 2010, 38, 386-394.	2.1	14
1246	Transcriptional profiling of oral squamous cell carcinoma using formalin-fixed paraffin-embedded samples. <i>Oral Oncology</i> , 2010, 46, 379-386.	0.8	30
1247	HIV-1 matrix protein p17: A candidate antigen for therapeutic vaccines against AIDS. , 2010, 128, 433-444.		39
1248	Effect of Maternal Tobacco Smoke Exposure on the Placental Transcriptome. <i>Placenta</i> , 2010, 31, 186-191.	0.7	65
1249	Global Gene Expression Changes Induced in the Human Placenta during Labor. <i>Placenta</i> , 2010, 31, 698-704.	0.7	41
1250	Trophoblast invasion: Assessment of cellular models using gene expression signatures. <i>Placenta</i> , 2010, 31, 989-996.	0.7	163
1251	Microarray analysis of Leflunomide-induced limb malformations in CD-1 mice. <i>Reproductive Toxicology</i> , 2010, 29, 42-48.	1.3	6

#	ARTICLE	IF	CITATIONS
1252	Transcriptomics analysis of retinoic acid embryotoxicity in rat postimplantation whole embryo culture. <i>Reproductive Toxicology</i> , 2010, 30, 333-340.	1.3	28
1253	The HOX Code as a "biological fingerprint" to distinguish functionally distinct stem cell populations derived from cord blood. <i>Stem Cell Research</i> , 2010, 5, 40-50.	0.3	74
1254	PCB153-elicited hepatic responses in the immature, ovariectomized C57BL/6 mice: Comparative toxicogenomic effects of dioxin and non-dioxin-like ligands. <i>Toxicology and Applied Pharmacology</i> , 2010, 243, 359-371.	1.3	47
1255	AutoSOME: a clustering method for identifying gene expression modules without prior knowledge of cluster number. <i>BMC Bioinformatics</i> , 2010, 11, 117.	1.2	92
1256	GOAL: A software tool for assessing biological significance of genes groups. <i>BMC Bioinformatics</i> , 2010, 11, 229.	1.2	27
1257	PhenoFam-gene set enrichment analysis through protein structural information. <i>BMC Bioinformatics</i> , 2010, 11, 254.	1.2	6
1258	Bayesian integrated modeling of expression data: a case study on RhoG. <i>BMC Bioinformatics</i> , 2010, 11, 295.	1.2	2
1259	PCA2GO: a new multivariate statistics based method to identify highly expressed GO-Terms. <i>BMC Bioinformatics</i> , 2010, 11, 336.	1.2	4
1260	Integration and visualization of systems biology data in context of the genome. <i>BMC Bioinformatics</i> , 2010, 11, 382.	1.2	31
1261	Uncovering packaging features of co-regulated modules based on human protein interaction and transcriptional regulatory networks. <i>BMC Bioinformatics</i> , 2010, 11, 392.	1.2	10
1262	TAM: A method for enrichment and depletion analysis of a microRNA category in a list of microRNAs. <i>BMC Bioinformatics</i> , 2010, 11, 419.	1.2	121
1263	Asymmetric microarray data produces gene lists highly predictive of research literature on multiple cancer types. <i>BMC Bioinformatics</i> , 2010, 11, 483.	1.2	13
1264	Trimming of mammalian transcriptional networks using network component analysis. <i>BMC Bioinformatics</i> , 2010, 11, 511.	1.2	14
1265	PathEx: a novel multi factors based datasets selector web tool. <i>BMC Bioinformatics</i> , 2010, 11, 528.	1.2	4
1266	Epigenetic domains found in mouse embryonic stem cells via a hidden Markov model. <i>BMC Bioinformatics</i> , 2010, 11, 557.	1.2	16
1267	Schizophrenia and vitamin D related genes could have been subject to latitude-driven adaptation. <i>BMC Evolutionary Biology</i> , 2010, 10, 351.	3.2	32
1268	Expression profiling of mouse embryonic fibroblasts with a deletion in the helicase domain of the Werner Syndrome gene homologue treated with hydrogen peroxide. <i>BMC Genomics</i> , 2010, 11, 127.	1.2	12
1269	Pediatric primary central nervous system germ cell tumors of different prognosis groups show characteristic miRNome traits and chromosome copy number variations. <i>BMC Genomics</i> , 2010, 11, 132.	1.2	45

#	ARTICLE	IF	CITATIONS
1270	Distribution of candidate genes for experimentally induced arthritis in rats. BMC Genomics, 2010, 11, 146.	1.2	2
1271	Comparative transcriptomic analysis of follicle-enclosed oocyte maturational and developmental competence acquisition in two non-mammalian vertebrates. BMC Genomics, 2010, 11, 18.	1.2	41
1272	Reciprocal regulation of metabolic and signaling pathways. BMC Genomics, 2010, 11, 197.	1.2	10
1273	Downregulation of genes with a function in axon outgrowth and synapse formation in motor neurones of the VEGF11 mouse model of amyotrophic lateral sclerosis. BMC Genomics, 2010, 11, 203.	1.2	38
1274	Whole transcriptome analysis of the hippocampus: toward a molecular portrait of epileptogenesis. BMC Genomics, 2010, 11, 230.	1.2	92
1275	Identification of copy number variations and common deletion polymorphisms in cattle. BMC Genomics, 2010, 11, 232.	1.2	126
1276	Comparison of clastogen-induced gene expression profiles in wild-type and DNA repair-deficient Rad54/Rad54B cells. BMC Genomics, 2010, 11, 24.	1.2	4
1277	Systems genetics analysis of body weight and energy metabolism traits in Drosophila melanogaster. BMC Genomics, 2010, 11, 297.	1.2	84
1278	Functional and gene network analyses of transcriptional signatures characterizing pre-weaned bovine mammary parenchyma or fat pad uncovered novel inter-tissue signaling networks during development. BMC Genomics, 2010, 11, 331.	1.2	28
1279	Benzo(a)pyrene induces similar gene expression changes in testis of DNA repair proficient and deficient mice. BMC Genomics, 2010, 11, 333.	1.2	14
1280	Bioinformatic identification and characterization of human endothelial cell-restricted genes. BMC Genomics, 2010, 11, 342.	1.2	54
1281	Transcriptomic analysis of dystrophin RNAi knockdown reveals a central role for dystrophin in muscle differentiation and contractile apparatus organization. BMC Genomics, 2010, 11, 345.	1.2	26
1282	Transcriptional regulation of gene expression clusters in motor neurons following spinal cord injury. BMC Genomics, 2010, 11, 365.	1.2	36
1283	A gene network switch enhances the oxidative capacity of ovine skeletal muscle during late fetal development. BMC Genomics, 2010, 11, 378.	1.2	27
1284	Global transcriptional response to carbonic anhydrase IX deficiency in the mouse stomach. BMC Genomics, 2010, 11, 397.	1.2	11
1285	Characterization of the equine skeletal muscle transcriptome identifies novel functional responses to exercise training. BMC Genomics, 2010, 11, 398.	1.2	81
1286	A systems approach to mapping transcriptional networks controlling surfactant homeostasis. BMC Genomics, 2010, 11, 451.	1.2	28
1287	Gene signatures in wound tissue as evidenced by molecular profiling in the chick embryo model. BMC Genomics, 2010, 11, 495.	1.2	15



#	ARTICLE	IF	CITATIONS
1288	Comparative transcriptional profiling of the limbal epithelial crypt demonstrates its putative stem cell niche characteristics. <i>BMC Genomics</i> , 2010, 11, 526.	1.2	74
1289	Identification of the Rage-dependent gene regulatory network in a mouse model of skin inflammation. <i>BMC Genomics</i> , 2010, 11, 537.	1.2	29
1290	Dynamic transcriptomic profiles of zebrafish gills in response to zinc depletion. <i>BMC Genomics</i> , 2010, 11, 548.	1.2	26
1291	Gene duplications in prokaryotes can be associated with environmental adaptation. <i>BMC Genomics</i> , 2010, 11, 588.	1.2	102
1292	Transcriptomic analysis of the temporal host response to skin infestation with the ectoparasitic mite <i>Psoroptes ovis</i> . <i>BMC Genomics</i> , 2010, 11, 624.	1.2	32
1293	Insights into metazoan evolution from <i>alvinella pompejana</i> cDNAs. <i>BMC Genomics</i> , 2010, 11, 634.	1.2	46
1294	Bovine proteins containing poly-glutamine repeats are often polymorphic and enriched for components of transcriptional regulatory complexes. <i>BMC Genomics</i> , 2010, 11, 654.	1.2	15
1295	Analysis of transcript and protein overlap in a human osteosarcoma cell line. <i>BMC Genomics</i> , 2010, 11, 684.	1.2	13
1296	Relationship between operon preference and functional properties of persistent genes in bacterial genomes. <i>BMC Genomics</i> , 2010, 11, 71.	1.2	24
1297	Investigation gene and microRNA expression in glioblastoma. <i>BMC Genomics</i> , 2010, 11, S16.	1.2	36
1298	Dynamics of dendritic cell maturation are identified through a novel filtering strategy applied to biological time-course microarray replicates. <i>BMC Immunology</i> , 2010, 11, 41.	0.9	11
1299	Gram-positive pathogenic bacteria induce a common early response in human monocytes. <i>BMC Microbiology</i> , 2010, 10, 275.	1.3	17
1300	Gene expression profiling in brain of mice exposed to the marine neurotoxin ciguatoxin reveals an acute anti-inflammatory, neuroprotective response. <i>BMC Neuroscience</i> , 2010, 11, 107.	0.8	31
1301	Meta-analysis of archived DNA microarrays identifies genes regulated by hypoxia and involved in a metastatic phenotype in cancer cells. <i>BMC Cancer</i> , 2010, 10, 176.	1.1	14
1302	Cellular processes of v-Src transformation revealed by gene profiling of primary cells - Implications for human cancer. <i>BMC Cancer</i> , 2010, 10, 41.	1.1	14
1303	Expression profiling in canine osteosarcoma: identification of biomarkers and pathways associated with outcome. <i>BMC Cancer</i> , 2010, 10, 506.	1.1	47
1304	Prioritizing genes associated with prostate cancer development. <i>BMC Cancer</i> , 2010, 10, 599.	1.1	28
1305	Proteomic analysis of prolactinoma cells by immuno-laser capture microdissection combined with online two-dimensional nano-scale liquid chromatography/mass spectrometry. <i>Proteome Science</i> , 2010, 8, 2.	0.7	24

#	ARTICLE	IF	CITATIONS
1306	A comparative genome analysis of gene expression reveals different regulatory mechanisms between mouse and human embryo pre-implantation development. <i>Reproductive Biology and Endocrinology</i> , 2010, 8, 41.	1.4	19
1307	Impact of methoxyacetic acid on mouse Leydig cell gene expression. <i>Reproductive Biology and Endocrinology</i> , 2010, 8, 65.	1.4	14
1308	A quantitative approach to study indirect effects among disease proteins in the human protein interaction network. <i>BMC Systems Biology</i> , 2010, 4, 103.	3.0	18
1309	Molecular mechanistic associations of human diseases. <i>BMC Systems Biology</i> , 2010, 4, 124.	3.0	11
1310	Noninvasive diagnosis of intraamniotic infection: proteomic biomarkers in vaginal fluid. <i>American Journal of Obstetrics and Gynecology</i> , 2010, 203, 32.e1-32.e8.	0.7	44
1311	Calcium signaling of thyrocytes is modulated by TSH through calcium binding protein expression. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2010, 1803, 352-360.	1.9	12
1312	Profiles of oxidative stress-related microRNA and mRNA expression in auditory cells. <i>Brain Research</i> , 2010, 1346, 14-25.	1.1	79
1313	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. <i>Cancer Cell</i> , 2010, 17, 98-110.	7.7	6,138
1314	From phenotype to gene: Detecting disease-specific gene functional modules via a text-based human disease phenotype network construction. <i>FEBS Letters</i> , 2010, 584, 3635-3643.	1.3	17
1315	Consequences of long-term oral administration of the mitochondria-targeted antioxidant MitoQ to wild-type mice. <i>Free Radical Biology and Medicine</i> , 2010, 48, 161-172.	1.3	193
1316	Modulation of gene expression by $\alpha$ -tocopherol and $\alpha$ -tocopheryl phosphate in THP-1 monocytes. <i>Free Radical Biology and Medicine</i> , 2010, 49, 1989-2000.	1.3	48
1317	Gene expression profiling of Pseudorabies virus (PrV) infected bovine cells by combination of transcript analysis and quantitative proteomic techniques. <i>Veterinary Microbiology</i> , 2010, 143, 14-20.	0.8	20
1318	Identification of the potential target genes of microRNA-146a induced by PMA treatment in human microvascular endothelial cells. <i>Experimental Cell Research</i> , 2010, 316, 1119-1126.	1.2	18
1319	Toxicogenomics and cancer risk assessment: A framework for key event analysis and dose-response assessment for nongenotoxic carcinogens. <i>Regulatory Toxicology and Pharmacology</i> , 2010, 58, 369-381.	1.3	31
1320	Machine learning approach identifies new pathways associated with demyelination in a viral model of multiple sclerosis. <i>Journal of Cellular and Molecular Medicine</i> , 2010, 14, 434-448.	1.6	53
1321	Significant Downregulation of Platelet Gene Expression in Metastatic Lung Cancer. <i>Clinical and Translational Science</i> , 2010, 3, 227-232.	1.5	101
1322	DNA damage and toxicogenomic analyses of hydrogen sulfide in human intestinal epithelial FHs 74 Int cells. <i>Environmental and Molecular Mutagenesis</i> , 2010, 51, 304-314.	0.9	156
1323	A systems biology approach to understanding atherosclerosis. <i>EMBO Molecular Medicine</i> , 2010, 2, 79-89.	3.3	69

#	ARTICLE	IF	CITATIONS
1324	Integrated approach for the identification of human hepatocyte nuclear factor 4 $\beta$ target genes using protein binding microarrays. <i>Hepatology</i> , 2010, 51, 642-653.	3.6	151
1325	MicroRNA-dependent regulation of DNA methyltransferase-1 and tumor suppressor gene expression by interleukin-6 in human malignant cholangiocytes. <i>Hepatology</i> , 2010, 51, NA-NA.	3.6	317
1326	Genome-wide tissue-specific farnesoid X receptor binding in mouse liver and intestine. <i>Hepatology</i> , 2010, 51, 1410-1419.	3.6	173
1327	Identification of a gene module associated with BMD through the integration of network analysis and genome-wide association data. <i>Journal of Bone and Mineral Research</i> , 2010, 25, 2359-2367.	3.1	78
1328	Enhanced differentiation of human embryonic stem cells to mesenchymal progenitors by inhibition of TGF- $\beta$ 2/activin/nodal signaling using SB-431542. <i>Journal of Bone and Mineral Research</i> , 2010, 25, 1216-1233.	3.1	102
1329	Prolonged <i>Nrf1</i> overexpression triggers adipocyte inflammation and insulin resistance. <i>Journal of Cellular Biochemistry</i> , 2010, 111, 1575-1585.	1.2	17
1330	Selective control of gene expression by CDK9 in human cells. <i>Journal of Cellular Physiology</i> , 2010, 222, 200-208.	2.0	45
1331	Gene expression in the efferent ducts, epididymis, and vas deferens during embryonic development of the mouse. <i>Developmental Dynamics</i> , 2010, 239, 2479-2491.	0.8	33
1332	Linking transcriptomic and proteomic data on the level of protein interaction networks. <i>Electrophoresis</i> , 2010, 31, 1780-1789.	1.3	28
1333	Analysis of whole genome biomarker expression in blood and brain. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2010, 153B, 919-936.	1.1	149
1334	Analysis of expressed sequence tags from a significant livestock pest, the stable fly ( <i>Stomoxys</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Archives of Insect Biochemistry and Physiology, 2010, 74, 179-204.	0.6	17
1335	Developmental microRNA expression profiling of murine embryonic orofacial tissue. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2010, 88, 511-534.	1.6	44
1336	Integrating genetic and toxicogenomic information for determining underlying susceptibility to developmental disorders. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2010, 88, 920-930.	1.6	10
1337	A systems-based approach to investigate dose- and time-dependent methylmercury-induced gene expression response in C57BL/6 mouse embryos undergoing neurulation. <i>Birth Defects Research Part B: Developmental and Reproductive Toxicology</i> , 2010, 89, 188-200.	1.4	13
1338	Microarray analysis of cutaneous squamous cell carcinomas reveals enhanced expression of epidermal differentiation complex genes. <i>Molecular Carcinogenesis</i> , 2010, 49, 619-629.	1.3	36
1339	Regulation of FGF2 by an endogenous antisense RNA: Effects on cell adhesion and cell cycle progression. <i>Molecular Carcinogenesis</i> , 2010, 49, 1031-1044.	1.3	7
1340	Proprotein convertase subtilisin/kexin type 9 (PCSK9) affects gene expression pathways beyond cholesterol metabolism in liver cells. <i>Journal of Cellular Physiology</i> , 2010, 224, 273-281.	2.0	60
1341	Tocotrienols activity in MCF7 breast cancer cells: Involvement of ER $\beta$ 2 signal transduction. <i>Molecular Nutrition and Food Research</i> , 2010, 54, 669-678.	1.5	29

#	ARTICLE	IF	CITATIONS
1342	Global gene expression profiles of ischemic preconditioning in deceased donor liver transplantation. <i>Liver Transplantation</i> , 2010, 16, NA-NA.	1.3	14
1343	Quantitative proteomic analysis of ribosomal protein L35b mutant of <i>Saccharomyces cerevisiae</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 676-683.	1.1	3
1344	Serum profile in preeclampsia and intra-uterine growth restriction revealed by iTRAQ technology. <i>Journal of Proteomics</i> , 2010, 73, 1004-1017.	1.2	55
1345	Identification of JAK-STAT pathways as important for the anti-inflammatory activity of a <i>Hypericum perforatum</i> fraction and bioactive constituents in RAW 264.7 mouse macrophages. <i>Phytochemistry</i> , 2010, 71, 716-725.	1.4	24
1346	Virus-host protein interactions in RNA viruses. <i>Microbes and Infection</i> , 2010, 12, 1134-1143.	1.0	33
1347	High density gene expression microarrays and gene ontology analysis for identifying processes in implanted tissue engineering constructs. <i>Biomaterials</i> , 2010, 31, 8299-8312.	5.7	19
1348	Genetic profiling of osteoblast-like cells cultured on a novel bone reconstructive material, consisting of poly-L-lactide, carbon nanotubes and microhydroxyapatite, in the presence of bone morphogenetic protein-2. <i>Acta Biomaterialia</i> , 2010, 6, 4352-4360.	4.1	21
1349	Fatty acid composition and gene expression profiles are altered in aryl hydrocarbon receptor-1 mutant <i>Caenorhabditis elegans</i> . <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2010, 151, 318-324.	1.3	22
1350	Assembling Ligands In Situ Using Bioorthogonal Boronate Ester Synthesis. <i>Chemistry and Biology</i> , 2010, 17, 1171-1176.	6.2	34
1351	Meta-analysis of microarray data: The case of imatinib resistance in chronic myelogenous leukemia. <i>Computational Biology and Chemistry</i> , 2010, 34, 184-192.	1.1	9
1352	Akt regulates the expression of MafK, synaptotagmin I, and syntenin-1, which play roles in neuronal function. <i>Journal of Biomedical Science</i> , 2010, 17, 18.	2.6	12
1353	A maternal low protein diet has pronounced effects on mitochondrial gene expression in offspring liver and skeletal muscle; protective effect of taurine. <i>Journal of Biomedical Science</i> , 2010, 17, S38.	2.6	43
1354	Octamer-binding factor 6 (Oct-6/Pou3f1) is induced by interferon and contributes to dsRNA-mediated transcriptional responses. <i>BMC Cell Biology</i> , 2010, 11, 61.	3.0	12
1355	Global transcriptional profiles of beating clusters derived from human induced pluripotent stem cells and embryonic stem cells are highly similar. <i>BMC Developmental Biology</i> , 2010, 10, 98.	2.1	76
1356	Modeling complex genetic and environmental influences on comorbid bipolar disorder with tobacco use disorder. <i>BMC Medical Genetics</i> , 2010, 11, 14.	2.1	26
1357	Protective effects and potential mechanisms of Pien Tze Huang on cerebral chronic ischemia and hypertensive stroke. <i>Chinese Medicine</i> , 2010, 5, 35.	1.6	14
1358	GTC: A web server for integrating systems biology data with web tools and desktop applications. <i>Source Code for Biology and Medicine</i> , 2010, 5, 7.	1.7	2
1359	Mural granulosa cell gene expression associated with oocyte developmental competence. <i>Journal of Ovarian Research</i> , 2010, 3, 6.	1.3	40

#	ARTICLE	IF	CITATIONS
1360	Human duodenal proteome modulations by glutamine and antioxidants. <i>Proteomics - Clinical Applications</i> , 2010, 4, 325-336.	0.8	5
1361	Gene expression correlation analysis predicts involvement of high- and low-confidence risk genes in different stages of prostate carcinogenesis. <i>Prostate</i> , 2010, 70, 1746-1759.	1.2	2
1362	A proteome map of the pituitary melanotrope cell activated by black background adaptation of <i>Xenopus laevis</i> . <i>Proteomics</i> , 2010, 10, 574-580.	1.3	4
1363	From proteome lists to biological impact: tools and strategies for the analysis of large MS data sets. <i>Proteomics</i> , 2010, 10, 1270-1283.	1.3	54
1364	Pathway analysis of dilated cardiomyopathy using global proteomic profiling and enrichment maps. <i>Proteomics</i> , 2010, 10, 1316-1327.	1.3	55
1365	Protein Information and Knowledge Extractor: Discovering biological information from proteomics data. <i>Proteomics</i> , 2010, 10, 3262-3271.	1.3	7
1366	Identification of osteocyte-selective proteins. <i>Proteomics</i> , 2010, 10, 3688-3698.	1.3	49
1367	Vitamin C Promotes Widespread Yet Specific DNA Demethylation of the Epigenome in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2010, 28, 1848-1855.	1.4	156
1368	Toward a complete <i>in silico</i> , multi-layered embryonic stem cell regulatory network. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 708-733.	6.6	21
1369	Genes Associated With Alcohol Abuse and Tobacco Smoking in the Human Nucleus Accumbens and Ventral Tegmental Area. <i>Alcoholism: Clinical and Experimental Research</i> , 2010, 34, 1291-1302.	1.4	28
1370	Ethanol Alters the Osteogenic Differentiation of Amniotic Fluid-Derived Stem Cells. <i>Alcoholism: Clinical and Experimental Research</i> , 2010, 34, 1714-1722.	1.4	11
1371	MicroRNA identity and abundance in porcine skeletal muscles determined by deep sequencing. <i>Animal Genetics</i> , 2010, 41, 159-168.	0.6	144
1372	Global transcriptomic analysis of murine embryonic stem cell-derived brachyury <sup>+</sup> (T) cells. <i>Genes To Cells</i> , 2010, 15, 209-228.	0.5	5
1373	Optimization of the culturing conditions of human umbilical cord blood-derived endothelial colony-forming cells under xeno-free conditions applying a transcriptomic approach. <i>Genes To Cells</i> , 2010, 15, 671-687.	0.5	17
1374	An oncogenic role of eIF3e/INT6 in human breast cancer. <i>Oncogene</i> , 2010, 29, 4080-4089.	2.6	53
1375	An ESRP-regulated splicing programme is abrogated during the epithelial-mesenchymal transition. <i>EMBO Journal</i> , 2010, 29, 3286-3300.	3.5	346
1376	Specific gene expression signature associated with development of autoimmune type-I diabetes using whole-blood microarray analysis. <i>Genes and Immunity</i> , 2010, 11, 269-278.	2.2	61
1377	Global H4 acetylation analysis by ChIP-chip in systemic lupus erythematosus monocytes. <i>Genes and Immunity</i> , 2010, 11, 124-133.	2.2	113

#	ARTICLE	IF	CITATIONS
1378	MHC class II-associated proteins in B cell exosomes and potential functional implications for exosome biogenesis. <i>Immunology and Cell Biology</i> , 2010, 88, 851-856.	1.0	247
1379	Blood orange juice inhibits fat accumulation in mice. <i>International Journal of Obesity</i> , 2010, 34, 578-588.	1.6	128
1380	Correlation analysis between genome-wide expression profiles and cytoarchitectural abnormalities in the prefrontal cortex of psychiatric disorders. <i>Molecular Psychiatry</i> , 2010, 15, 326-336.	4.1	118
1381	Schizophrenia is associated with an increase in cortical microRNA biogenesis. <i>Molecular Psychiatry</i> , 2010, 15, 1176-1189.	4.1	396
1382	Chromatin signature of embryonic pluripotency is established during genome activation. <i>Nature</i> , 2010, 464, 922-926.	13.7	340
1383	Widespread transcription at neuronal activity-regulated enhancers. <i>Nature</i> , 2010, 465, 182-187.	13.7	2,120
1384	Chronic high-fat diet in fathers programs $\beta$ -cell dysfunction in female rat offspring. <i>Nature</i> , 2010, 467, 963-966.	13.7	1,214
1385	Global analysis of lysine ubiquitination by ubiquitin remnant immunoaffinity profiling. <i>Nature Biotechnology</i> , 2010, 28, 868-873.	9.4	460
1386	Ontology engineering. <i>Nature Biotechnology</i> , 2010, 28, 128-130.	9.4	113
1387	Applicability of coexpression networks analysis to anticancer drug targets discovery. <i>Molecular Biology</i> , 2010, 44, 326-333.	0.4	1
1388	p53-independent upregulation of miR-34a during oncogene-induced senescence represses MYC. <i>Cell Death and Differentiation</i> , 2010, 17, 236-245.	5.0	314
1389	A map of open chromatin in human pancreatic islets. <i>Nature Genetics</i> , 2010, 42, 255-259.	9.4	515
1390	Amplification-free digital gene expression profiling from minute cell quantities. <i>Nature Methods</i> , 2010, 7, 619-621.	9.0	57
1391	Trans-SILAC: sorting out the non-cell-autonomous proteome. <i>Nature Methods</i> , 2010, 7, 923-927.	9.0	30
1392	Next-generation genomics: an integrative approach. <i>Nature Reviews Genetics</i> , 2010, 11, 476-486.	7.7	554
1393	Statistical analysis strategies for association studies involving rare variants. <i>Nature Reviews Genetics</i> , 2010, 11, 773-785.	7.7	426
1394	Glycotranscriptomics. , 2010, , 95-135.		3
1395	In Search of a Function for BCLAF1. <i>Scientific World Journal</i> , The, 2010, 10, 1450-1461.	0.8	56

#	ARTICLE	IF	CITATIONS
1396	Automated Network Analysis Identifies Core Pathways in Glioblastoma. PLoS ONE, 2010, 5, e8918.	1.1	318
1397	Individual Variation in Pheromone Response Correlates with Reproductive Traits and Brain Gene Expression in Worker Honey Bees. PLoS ONE, 2010, 5, e9116.	1.1	54
1398	A New Strategy to Identify and Annotate Human RPE-Specific Gene Expression. PLoS ONE, 2010, 5, e9341.	1.1	72
1399	Phenotypic Covariance of Longevity, Immunity and Stress Resistance in the Caenorhabditis Nematodes. PLoS ONE, 2010, 5, e9978.	1.1	36
1400	Systematic Analysis of a Novel Human Renal Glomerulus-Enriched Gene Expression Dataset. PLoS ONE, 2010, 5, e11545.	1.1	71
1401	Gene Network Disruptions and Neurogenesis Defects in the Adult Ts1Cje Mouse Model of Down Syndrome. PLoS ONE, 2010, 5, e11561.	1.1	44
1402	Gene Expression Profiling of the Local Cecal Response of Genetic Chicken Lines That Differ in Their Susceptibility to Campylobacter jejuni Colonization. PLoS ONE, 2010, 5, e11827.	1.1	69
1403	NK Cell Terminal Differentiation: Correlated Stepwise Decrease of NKG2A and Acquisition of KIRs. PLoS ONE, 2010, 5, e11966.	1.1	179
1404	Profiling and Functional Analyses of MicroRNAs and Their Target Gene Products in Human Uterine Leiomyomas. PLoS ONE, 2010, 5, e12362.	1.1	64
1405	MicroRNA-218 Is Deleted and Downregulated in Lung Squamous Cell Carcinoma. PLoS ONE, 2010, 5, e12560.	1.1	100
1406	Self-Contained Gene-Set Analysis of Expression Data: An Evaluation of Existing and Novel Methods. PLoS ONE, 2010, 5, e12693.	1.1	52
1407	QKI-7 Regulates Expression of Interferon-Related Genes in Human Astrocyte Glioma Cells. PLoS ONE, 2010, 5, e13079.	1.1	8
1408	Transcript Profiling of Elf5+ Mammary Glands during Pregnancy Identifies Novel Targets of Elf5. PLoS ONE, 2010, 5, e13150.	1.1	8
1409	A Network of Cancer Genes with Co-Occurring and Anti-Co-Occurring Mutations. PLoS ONE, 2010, 5, e13180.	1.1	31
1410	Gene Expression Profiling of U12-Type Spliceosome Mutant Drosophila Reveals Widespread Changes in Metabolic Pathways. PLoS ONE, 2010, 5, e13215.	1.1	26
1411	Bypass Mechanisms of the Androgen Receptor Pathway in Therapy-Resistant Prostate Cancer Cell Models. PLoS ONE, 2010, 5, e13500.	1.1	88
1412	Enrichment Map: A Network-Based Method for Gene-Set Enrichment Visualization and Interpretation. PLoS ONE, 2010, 5, e13984.	1.1	1,883
1413	Phosphoproteomics Profiling of Human Skin Fibroblast Cells Reveals Pathways and Proteins Affected by Low Doses of Ionizing Radiation. PLoS ONE, 2010, 5, e14152.	1.1	21

#	ARTICLE	IF	CITATIONS
1414	The Reverse Transcription Inhibitor Abacavir Shows Anticancer Activity in Prostate Cancer Cell Lines. PLoS ONE, 2010, 5, e14221.	1.1	48
1415	Chromatin Remodeling Pathways in Smooth Muscle Cell Differentiation, and Evidence for an Integral Role for p300. PLoS ONE, 2010, 5, e14301.	1.1	26
1416	ZNF274 Recruits the Histone Methyltransferase SETDB1 to the 3' Ends of ZNF Genes. PLoS ONE, 2010, 5, e15082.	1.1	147
1417	RNAi Screen of DAF-16/FOXO Target Genes in <i>C. elegans</i> Links Pathogenesis and Dauer Formation. PLoS ONE, 2010, 5, e15902.	1.1	27
1418	Longissimus muscle transcriptome profiles related to carcass and meat quality traits in fresh meat PiÅ©train carcasses1. Journal of Animal Science, 2010, 88, 4044-4055.	0.2	40
1419	Alterations in gene expression profiles correlated with cisplatin cytotoxicity in the glioma U343 cell line. Genetics and Molecular Biology, 2010, 33, 159-168.	0.6	17
1420	Association Rule Based Similarity Measures for the Clustering of Gene Expression Data. Open Medical Informatics Journal, 2010, 4, 63-73.	1.0	15
1421	Gene targeting and Calcium handling efficiencies in mouse embryonic stem cell lines. World Journal of Stem Cells, 2010, 2, 127.	1.3	6
1422	A Two-tiered compensatory response to loss of DNA repair modulates aging and stress response pathways. Aging, 2010, 2, 133-159.	1.4	23
1423	Reversal of preexisting hyperglycemia in diabetic mice by acute deletion of the <i>Men1</i> gene. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20358-20363.	3.3	44
1424	HIV-Exposed Seronegative Commercial Sex Workers Show a Quiescent Phenotype in the CD4 <sup>+</sup> T Cell Compartment and Reduced Expression of HIV-Dependent Host Factors. Journal of Infectious Diseases, 2010, 202, S339-S344.	1.9	104
1425	SAFB1 Mediates Repression of Immune Regulators and Apoptotic Genes in Breast Cancer Cells. Journal of Biological Chemistry, 2010, 285, 3608-3616.	1.6	30
1426	Expression of Genes Associated with Immunoproteasome Processing of Major Histocompatibility Complex Peptides Is Indicative of Protection with Adjuvanted RTS,S Malaria Vaccine. Journal of Infectious Diseases, 2010, 201, 580-589.	1.9	115
1427	Cell Sorting-Assisted Microarray Profiling of Host Cell Response to <i>Cryptosporidium parvum</i> Infection. Infection and Immunity, 2010, 78, 1040-1048.	1.0	17
1428	MGMT modulates glioblastoma angiogenesis and response to the tyrosine kinase inhibitor sunitinib. Neuro-Oncology, 2010, 12, 822-833.	0.6	74
1429	Gene Expression Profiles in a Rabbit Model of Systemic Lupus Erythematosus Autoantibody Production. Journal of Immunology, 2010, 185, 4446-4456.	0.4	8
1430	Genome-wide assessment of differential roles for p300 and CBP in transcription regulation. Nucleic Acids Research, 2010, 38, 5396-5408.	6.5	133
1431	A Critical Role for Ceramide Synthase 2 in Liver Homeostasis. Journal of Biological Chemistry, 2010, 285, 10911-10923.	1.6	200



#	ARTICLE	IF	CITATIONS
1432	Genomewide Association Analysis of Respiratory Syncytial Virus Infection in Mice. <i>Journal of Virology</i> , 2010, 84, 2257-2269.	1.5	15
1433	The CrebA/Creb3-like transcription factors are major and direct regulators of secretory capacity. <i>Journal of Cell Biology</i> , 2010, 191, 479-492.	2.3	127
1434	Role of microRNA-23b in flow-regulation of Rb phosphorylation and endothelial cell growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3234-3239.	3.3	160
1435	An EGFR autocrine loop encodes a slow-reacting but dominant mode of mechanotransduction in a polarized epithelium. <i>FASEB Journal</i> , 2010, 24, 1604-1615.	0.2	21
1436	Functional analysis and identification of cis-regulatory elements of human chromosome 21 gene promoters. <i>Nucleic Acids Research</i> , 2010, 38, 6112-6123.	6.5	19
1437	Immune Activation in Retinal Aging: A Gene Expression Study. , 2010, 51, 5888.		96
1438	A large-scale study of differential gene expression in monocyte-derived macrophages infected with several strains of <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> . <i>Briefings in Functional Genomics</i> , 2010, 9, 220-237.	1.3	51
1439	Molecular and phenotypic characterization of a mouse model of oculopharyngeal muscular dystrophy reveals severe muscular atrophy restricted to fast glycolytic fibres. <i>Human Molecular Genetics</i> , 2010, 19, 2191-2207.	1.4	78
1440	Integrated Pathways for Neutrophil Recruitment and Inflammation in Leprosy. <i>Journal of Infectious Diseases</i> , 2010, 201, 558-569.	1.9	65
1441	MSEA: a web-based tool to identify biologically meaningful patterns in quantitative metabolomic data. <i>Nucleic Acids Research</i> , 2010, 38, W71-W77.	6.5	582
1442	Characterization of Macaque Pulmonary Fluid Proteome during Monkeypox Infection. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2760-2771.	2.5	16
1443	Distinct roles for miRâ€1 and miRâ€133a in the proliferation and differentiation of rhabdomyosarcoma cells. <i>FASEB Journal</i> , 2010, 24, 3427-3437.	0.2	118
1444	Identification of Methylmercury Tolerance Gene Candidates in <i>Drosophila</i> . <i>Toxicological Sciences</i> , 2010, 116, 225-238.	1.4	34
1445	Proteome bioprofiles distinguish between M1 priming and activation states in human macrophages. <i>Journal of Leukocyte Biology</i> , 2010, 87, 655-662.	1.5	28
1446	Neuronal MicroRNA Deregulation in Response to Alzheimer's Disease Amyloid-Î². <i>PLoS ONE</i> , 2010, 5, e11070.	1.1	183
1447	Regulation of Cell Cycle Genes and Induction of Senescence by Overexpression of OTX2 in Medulloblastoma Cell Lines. <i>Molecular Cancer Research</i> , 2010, 8, 1344-1357.	1.5	45
1448	Transcriptional Profiling by Deep Sequencing Identifies Differences in mRNA Transcript Abundance in In Vivo-Derived Versus In Vitro-Cultured Porcine Blastocyst Stage Embryos1. <i>Biology of Reproduction</i> , 2010, 83, 791-798.	1.2	66
1449	ToppCluster: a multiple gene list feature analyzer for comparative enrichment clustering and network-based dissection of biological systems. <i>Nucleic Acids Research</i> , 2010, 38, W96-W102.	6.5	325

#	ARTICLE	IF	CITATIONS
1450	Spectral Clustering of Microarray Data Elucidates the Roles of Microenvironment Remodeling and Immune Responses in Survival of Head and Neck Squamous Cell Carcinoma. <i>Journal of Clinical Oncology</i> , 2010, 28, 2881-2888.	0.8	72
1451	Microarray Analysis of Equine Endometrium at Days 8 and 12 of Pregnancy <sup>1</sup> . <i>Biology of Reproduction</i> , 2010, 83, 874-886.	1.2	81
1452	Examination of transcriptional networks reveals an important role for TCFAP2C, SMARCA4, and EOMES in trophoblast stem cell maintenance. <i>Genome Research</i> , 2010, 20, 458-472.	2.4	118
1453	N-WASP is a novel regulator of hair-follicle cycling that controls antiproliferative TGF $\beta$ <sup>2</sup> pathways. <i>Journal of Cell Science</i> , 2010, 123, 128-140.	1.2	36
1454	ConceptGen: a gene set enrichment and gene set relation mapping tool. <i>Bioinformatics</i> , 2010, 26, 456-463.	1.8	134
1455	Differential Roles of Sall4 Isoforms in Embryonic Stem Cell Pluripotency. <i>Molecular and Cellular Biology</i> , 2010, 30, 5364-5380.	1.1	157
1456	Dynamic O-GlcNAc cycling at promoters of <i>Caenorhabditis elegans</i> genes regulating longevity, stress, and immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7413-7418.	3.3	136
1457	Differential epigenomic and transcriptomic responses in subcutaneous adipose tissue between low and high responders to caloric restriction. <i>American Journal of Clinical Nutrition</i> , 2010, 91, 309-320.	2.2	193
1458	Monensin Is a Potent Inducer of Oxidative Stress and Inhibitor of Androgen Signaling Leading to Apoptosis in Prostate Cancer Cells. <i>Molecular Cancer Therapeutics</i> , 2010, 9, 3175-3185.	1.9	80
1459	Examination of Testicular Gene Expression Patterns in Yorkshire Pigs with High and Low Levels of Boar Taint. <i>Animal Biotechnology</i> , 2010, 21, 77-87.	0.7	18
1460	Gene Expression Profiling of Mouse Oocytes and Preimplantation Embryos. <i>Methods in Enzymology</i> , 2010, 477, 457-480.	0.4	7
1461	Brain transcriptomic analysis in paper wasps identifies genes associated with behaviour across social insect lineages. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 2139-2148.	1.2	121
1462	Upstream transcription factor 1 influences plasma lipid and metabolic traits in mice. <i>Human Molecular Genetics</i> , 2010, 19, 597-608.	1.4	30
1463	Glycoprotein Capture and Quantitative Phosphoproteomics Indicate Coordinated Regulation of Cell Migration upon Lysophosphatidic Acid Stimulation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2337-2353.	2.5	13
1464	The Mammalian Sin3 Proteins Are Required for Muscle Development and Sarcomere Specification. <i>Molecular and Cellular Biology</i> , 2010, 30, 5686-5697.	1.1	59
1465	ACBP Knockdown Leads to Down-regulation of Genes Encoding Rate-limiting Enzymes in Cholesterol and Fatty Acid Metabolism. <i>Cellular Physiology and Biochemistry</i> , 2010, 25, 675-686.	1.1	22
1466	Cyclosporin-A Induced Toxicity in Rat Renal Collecting Duct Cells: Interference with Enhanced Hypertonicity Induced Apoptosis. <i>Cellular Physiology and Biochemistry</i> , 2010, 26, 887-900.	1.1	11
1467	Genetic Dependence of Central Corneal Thickness among Inbred Strains of Mice. , 2010, 51, 160.		47

#	ARTICLE	IF	CITATIONS
1468	PHF8 Targets Histone Methylation and RNA Polymerase II To Activate Transcription. <i>Molecular and Cellular Biology</i> , 2010, 30, 3286-3298.	1.1	98
1469	Distinct gene expression profiles characterize cellular responses to palmitate and oleate. <i>Journal of Lipid Research</i> , 2010, 51, 2121-2131.	2.0	29
1470	Signaling pathways coupling phenomena. , 2010, , .		4
1471	Functional Analysis of the Cdk7-Cyclin H-Mat1 Complex in Mouse Embryonic Stem Cells and Embryos. <i>Journal of Biological Chemistry</i> , 2010, 285, 15587-15598.	1.6	27
1472	Parkinson Disease-associated DJ-1 Is Required for the Expression of the Glial Cell Line-derived Neurotrophic Factor Receptor RET in Human Neuroblastoma Cells. <i>Journal of Biological Chemistry</i> , 2010, 285, 18565-18574.	1.6	37
1473	Estrogen-related Receptor $\beta$ Is a Key Regulator of Muscle Mitochondrial Activity and Oxidative Capacity. <i>Journal of Biological Chemistry</i> , 2010, 285, 22619-22629.	1.6	153
1474	Gene expression centroids that link with low intrinsic aerobic exercise capacity and complex disease risk. <i>FASEB Journal</i> , 2010, 24, 4565-4574.	0.2	56
1475	Parallel Genetic and Proteomic Screens Identify Msp as a CLASP Abl Pathway Interactor in <i>Drosophila</i> . <i>Genetics</i> , 2010, 185, 1311-1325.	1.2	49
1476	Cyclic Stretch Magnitude and Duration Affect Rat Alveolar Epithelial Gene Expression. <i>Cellular Physiology and Biochemistry</i> , 2010, 25, 113-122.	1.1	28
1477	Maternal Hyperglycemia Modifies Extracellular Matrix Signaling Pathways in Neonatal Rat Lung. <i>Neonatology</i> , 2010, 98, 387-396.	0.9	7
1478	&lt;i>RRM2&lt;/i> Computational Phosphoprotein Network Construction and Analysis between No-Tumor Hepatitis/Cirrhotic Liver Tissues and Human Hepatocellular Carcinoma (HCC). <i>Cellular Physiology and Biochemistry</i> , 2010, 26, 303-310.	1.1	35
1479	Reference Profile Correlation Reveals Estrogen-like Transcriptional Activity of Curcumin. <i>Cellular Physiology and Biochemistry</i> , 2010, 26, 471-482.	1.1	73
1480	High-Density Lipoprotein Suppresses the Type I Interferon Response, a Family of Potent Antiviral Immunoregulators, in Macrophages Challenged With Lipopolysaccharide. <i>Circulation</i> , 2010, 122, 1919-1927.	1.6	116
1481	Young™ Oral Fibroblasts Are Genotypically Distinct. <i>Journal of Dental Research</i> , 2010, 89, 1407-1413.	2.5	31
1482	Global Gene Expression Profiling of <i>Yersinia pestis</i> Replicating inside Macrophages Reveals the Roles of a Putative Stress-Induced Operon in Regulating Type III Secretion and Intracellular Cell Division. <i>Infection and Immunity</i> , 2010, 78, 3700-3715.	1.0	37
1483	Female-Biased Expression on the X Chromosome as a Key Step in Sex Chromosome Evolution in Threespine Sticklebacks. <i>Molecular Biology and Evolution</i> , 2010, 27, 1495-1503.	3.5	86
1484	Deficiency in the 15-kDa Selenoprotein Inhibits Tumorigenicity and Metastasis of Colon Cancer Cells. <i>Cancer Prevention Research</i> , 2010, 3, 630-639.	0.7	76
1485	Evolution of alternative splicing in primate brain transcriptomes. <i>Human Molecular Genetics</i> , 2010, 19, 2958-2973.	1.4	47

#	ARTICLE	IF	CITATIONS
1486	Rank hypergeometric overlap: identification of statistically significant overlap between gene-expression signatures. <i>Nucleic Acids Research</i> , 2010, 38, e169-e169.	6.5	357
1487	Female sex and estrogen receptor- $\beta$ attenuate cardiac remodeling and apoptosis in pressure overload. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2010, 298, R1597-R1606.	0.9	205
1488	<i>ATF3</i> , an adaptive-response gene, enhances TGF $\beta$ signaling and cancer-initiating cell features in breast cancer cells. <i>Journal of Cell Science</i> , 2010, 123, 3558-3565.	1.2	152
1489	Identification of Subtypes in Human Epidermal Growth Factor Receptor 2 Positive Breast Cancer Reveals a Gene Signature Prognostic of Outcome. <i>Journal of Clinical Oncology</i> , 2010, 28, 1813-1820.	0.8	145
1490	<i>Biomedical Informatics for Cancer Research.</i> , 2010, , .		13
1491	GLD-2/RNP-8 cytoplasmic poly(A) polymerase is a broad-spectrum regulator of the oogenesis program. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17445-17450.	3.3	65
1492	Exon-Level Microarray Analyses Identify Alternative Splicing Programs in Breast Cancer. <i>Molecular Cancer Research</i> , 2010, 8, 961-974.	1.5	121
1493	Macaque Proteome Response to Highly Pathogenic Avian Influenza and 1918 Reassortant Influenza Virus Infections. <i>Journal of Virology</i> , 2010, 84, 12058-12068.	1.5	36
1494	Hedgehog pathway-regulated gene networks in cerebellum development and tumorigenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9736-9741.	3.3	109
1495	Dampened activity of E2F1 and Myb transcription factors in <i>Drosophila</i> endocycling cells. <i>Journal of Cell Science</i> , 2010, 123, 4095-4106.	1.2	44
1496	Of mice and men: comparative proteomics of bronchoalveolar fluid. <i>European Respiratory Journal</i> , 2010, 35, 1388-1395.	3.1	43
1497	Intrinsic Depot-Specific Differences in the Secretome of Adipose Tissue, Preadipocytes, and Adipose Tissue-Derived Microvascular Endothelial Cells. <i>Diabetes</i> , 2010, 59, 3008-3016.	0.3	108
1498	Coordinate Interaction between IL-13 and Epithelial Differentiation Cluster Genes in Eosinophilic Esophagitis. <i>Journal of Immunology</i> , 2010, 184, 4033-4041.	0.4	257
1499	Genetic Associations of Variants in Genes Encoding HIV Dependency Factors Required for HIV Infection. <i>Journal of Infectious Diseases</i> , 2010, 202, 1836-1845.	1.9	29
1500	Immunobiological Characterization of Cancer Stem Cells Isolated from Glioblastoma Patients. <i>Clinical Cancer Research</i> , 2010, 16, 800-813.	3.2	295
1501	Differential Gene Expression in Adipose Stem Cells Cultured in Allogeneic Human Serum Versus Fetal Bovine Serum. <i>Tissue Engineering - Part A</i> , 2010, 16, 2281-2294.	1.6	82
1502	Analysis of Self-Inactivating Lentiviral Vector Integration Sites and Flanking Gene Expression in Human Peripheral Blood Progenitor Cells After Alkylator Chemotherapy. <i>Human Gene Therapy</i> , 2010, 21, 943-956.	1.4	7
1503	A Double-Layered Mixture Model for the Joint Analysis of DNA Copy Number and Gene Expression Data. <i>Journal of Computational Biology</i> , 2010, 17, 121-137.	0.8	16

#	ARTICLE	IF	CITATIONS
1504	Foxa1 and Foxa2 Maintain the Metabolic and Secretory Features of the Mature $\beta$ -Cell. <i>Molecular Endocrinology</i> , 2010, 24, 1594-1604.	3.7	105
1505	Deciphering the Mesodermal Potency of Porcine Skin-Derived Progenitors (SKP) by Microarray Analysis. <i>Cellular Reprogramming</i> , 2010, 12, 161-173.	0.5	8
1506	An Integrative Scoring Approach to Identify Transcriptional Regulations Controlling Lung Surfactant Homeostasis. , 2010, , .		0
1507	Quantitative Proteomic Analysis of Formalin-fixed and Paraffin-embedded Nasopharyngeal Carcinoma Using iTRAQ Labeling, Two-dimensional Liquid Chromatography, and Tandem Mass Spectrometry. <i>Journal of Histochemistry and Cytochemistry</i> , 2010, 58, 517-527.	1.3	80
1508	Microarray Analysis and Draft Genomes of Two <i>Escherichia coli</i> O157:H7 Lineage II Cattle Isolates FRIK966 and FRIK2000 Investigating Lack of Shiga Toxin Expression. <i>Foodborne Pathogens and Disease</i> , 2010, 7, 763-773.	0.8	15
1509	Discovery and assessment of gene-disease associations by integrated analysis of scientific literature and microarray data. , 2010, , .		2
1510	Molecular Characterization of Cultured Adult Human Liver Progenitor Cells. <i>Tissue Engineering - Part C: Methods</i> , 2010, 16, 821-834.	1.1	13
1511	Dynamics of Protein Damage in Yeast Frataxin Mutant Exposed to Oxidative Stress. <i>OMICS A Journal of Integrative Biology</i> , 2010, 14, 689-699.	1.0	15
1512	Trinucleotide repeats in human genome and exome. <i>Nucleic Acids Research</i> , 2010, 38, 4027-4039.	6.5	124
1513	In vivo actin cross-linking induced by <i>Vibrio cholerae</i> type VI secretion system is associated with intestinal inflammation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4365-4370.	3.3	197
1514	Characterization of the xenobiotic response of <i>Caenorhabditis elegans</i> to the anthelmintic drug albendazole and the identification of novel drug glucoside metabolites. <i>Biochemical Journal</i> , 2010, 432, 505-516.	1.7	59
1515	Using molecular classification to predict gains in maximal aerobic capacity following endurance exercise training in humans. <i>Journal of Applied Physiology</i> , 2010, 108, 1487-1496.	1.2	296
1516	In Situ trans Ligands of CD22 Identified by Glycan-Protein Photocross-linking-enabled Proteomics. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1339-1351.	2.5	79
1517	A Comprehensive Proteomics and Transcriptomics Analysis of <i>Bacillus subtilis</i> Salt Stress Adaptation. <i>Journal of Bacteriology</i> , 2010, 192, 870-882.	1.0	175
1518	Dietary iron-deficient anemia induces a variety of metabolic changes and even apoptosis in rat liver: a DNA microarray study. <i>Physiological Genomics</i> , 2010, 42, 149-156.	1.0	45
1519	Autoantibodies Against the Exocrine Pancreas in Autoimmune Pancreatitis: Gene and Protein Expression Profiling and Immunoassays Identify Pancreatic Enzymes as a Major Target of the Inflammatory Process. <i>American Journal of Gastroenterology</i> , 2010, 105, 2060-2071.	0.2	126
1520	Altered Gene Expression Profiles in the Brain, Kidney, and Lung of Deceased Neonatal Cloned Pigs. <i>Cellular Reprogramming</i> , 2010, 12, 589-597.	0.5	11
1521	Enhanced Function of Prefrontal Serotonin 5-HT <sub>2</sub> Receptors in a Rat Model of Psychiatric Vulnerability. <i>Journal of Neuroscience</i> , 2010, 30, 12138-12150.	1.7	78

#	ARTICLE	IF	CITATIONS
1522	Molecular Basis for Hair Loss in Mice Carrying a Novel Nonsense Mutation (Hrrh-R) in the Hairless Gene (Hr). <i>Veterinary Pathology</i> , 2010, 47, 167-176.	0.8	10
1523	Existence of CD8 $\alpha$ -Like Dendritic Cells with a Conserved Functional Specialization and a Common Molecular Signature in Distant Mammalian Species. <i>Journal of Immunology</i> , 2010, 185, 3313-3325.	0.4	107
1524	Genome-wide interrogation of hepatic FXR reveals an asymmetric IR-1 motif and synergy with LRH-1. <i>Nucleic Acids Research</i> , 2010, 38, 6007-6017.	6.5	79
1525	PathWave: discovering patterns of differentially regulated enzymes in metabolic pathways. <i>Bioinformatics</i> , 2010, 26, 1225-1231.	1.8	26
1526	Cdx2 regulates endo-lysosomal function and epithelial cell polarity. <i>Genes and Development</i> , 2010, 24, 1295-1305.	2.7	75
1527	Testosterone-induced permanent changes of hepatic gene expression in female mice sustained during <i>Plasmodium chabaudi</i> malaria infection. <i>Journal of Molecular Endocrinology</i> , 2010, 45, 379-390.	1.1	28
1528	Site-specific Phosphorylation Dynamics of the Nuclear Proteome during the DNA Damage Response. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1314-1323.	2.5	225
1529	Ablation of Indian Hedgehog in the Murine Uterus Results in Decreased Cell Cycle Progression, Aberrant Epidermal Growth Factor Signaling, and Increased Estrogen Signaling1. <i>Biology of Reproduction</i> , 2010, 82, 783-790.	1.2	62
1530	Hepatocyte Nuclear Factor-4 $\alpha$ Promotes Gut Neoplasia in Mice and Protects against the Production of Reactive Oxygen Species. <i>Cancer Research</i> , 2010, 70, 9423-9433.	0.4	89
1531	Genome-wide expression profile of LHON patients with the 11778 mutation. <i>British Journal of Ophthalmology</i> , 2010, 94, 256-259.	2.1	17
1532	Genomic Profiling of MicroRNAs and Messenger RNAs Reveals Hormonal Regulation in MicroRNA Expression in Human Endometrium1. <i>Biology of Reproduction</i> , 2010, 82, 791-801.	1.2	259
1533	The liver X-receptor gene promoter is hypermethylated in a mouse model of prenatal protein restriction. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2010, 298, R275-R282.	0.9	131
1534	A two-parameter generalized Poisson model to improve the analysis of RNA-seq data. <i>Nucleic Acids Research</i> , 2010, 38, e170-e170.	6.5	131
1535	NF $\kappa$ B-related factor 2 regulates the stress response to UVA $\alpha$ -oxidized phospholipids in skin cells. <i>FASEB Journal</i> , 2010, 24, 39-48.	0.2	71
1536	Ageing-Related Gene Expression in Hippocampus Proper Compared with Dentate Gyrus Is Selectively Associated with Metabolic Syndrome Variables in Rhesus Monkeys. <i>Journal of Neuroscience</i> , 2010, 30, 6058-6071.	1.7	53
1537	Targets of the Tal1 Transcription Factor in Erythrocytes. <i>Journal of Biological Chemistry</i> , 2010, 285, 5338-5346.	1.6	16
1538	Molecular signatures and new candidates to target the pathogenesis of rheumatoid arthritis. <i>Physiological Genomics</i> , 2010, 42A, 267-282.	1.0	114
1539	The <i>Drosophila</i> nuclear receptors DHR3 and FTZ-F1 control overlapping developmental responses in late embryos. <i>Development (Cambridge)</i> , 2010, 137, 123-131.	1.2	77

#	ARTICLE	IF	CITATIONS
1540	Strong synaptic transmission impact by copy number variations in schizophrenia. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10584-10589.	3.3	212
1541	Interactome analysis of longitudinal pharyngeal infection of cynomolgus macaques by group A <i>Streptococcus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4693-4698.	3.3	30
1542	GtLay: community structure analysis of biological networks. Bioinformatics, 2010, 26, 3135-3137.	1.8	241
1543	Inference of combinatorial Boolean rules of synergistic gene sets from cancer microarray datasets. Bioinformatics, 2010, 26, 1506-1512.	1.8	12
1544	Identification of differential protein interactors of lamin A and progerin. Nucleus, 2010, 1, 513-525.	0.6	81
1545	Cytokine-Induced Monocyte Characteristics in SLE. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-13.	3.0	21
1546	Deep SAGE analysis of the <i>Caenorhabditis elegans</i> transcriptome. Nucleic Acids Research, 2010, 38, 3252-3262.	6.5	16
1547	Cre-loxP DNA recombination is possible with only minimal unspecific transcriptional changes and without cardiomyopathy in Tg(I±MHC-MerCreMer) mice. American Journal of Physiology - Heart and Circulatory Physiology, 2010, 299, H1671-H1678.	1.5	34
1548	Pathogen Specific, IRF3-Dependent Signaling and Innate Resistance to Human Kidney Infection. PLoS Pathogens, 2010, 6, e1001109.	2.1	68
1549	Genomic Analysis Highlights the Role of the JAK-STAT Signaling in the Anti-Proliferative Effects of Dietary Flavonoid "Ashwagandha"™ in Prostate Cancer Cells. Evidence-based Complementary and Alternative Medicine, 2010, 7, 177-187.	0.5	51
1550	Capture Compound Mass Spectrometry Sheds Light on the Molecular Mechanisms of Liver Toxicity of Two Parkinson Drugs. Toxicological Sciences, 2010, 113, 243-253.	1.4	34
1551	Conditional deletion of <i>Abca3</i> in alveolar type II cells alters surfactant homeostasis in newborn and adult mice. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2010, 298, L646-L659.	1.3	58
1552	Altered Gene Expression and DNA Damage in Peripheral Blood Cells from Friedreich's Ataxia Patients: Cellular Model of Pathology. PLoS Genetics, 2010, 6, e1000812.	1.5	93
1553	Gene Expression Variability within and between Human Populations and Implications toward Disease Susceptibility. PLoS Computational Biology, 2010, 6, e1000910.	1.5	85
1554	Deciphering Normal Blood Gene Expression Variation "The NOWAC Postgenome Study. PLoS Genetics, 2010, 6, e1000873.	1.5	76
1555	Proteomic analysis of brush-border membrane vesicles isolated from purified proximal convoluted tubules. American Journal of Physiology - Renal Physiology, 2010, 298, F1323-F1331.	1.3	32
1556	Uniformly curated signaling pathways reveal tissue-specific cross-talks and support drug target discovery. Bioinformatics, 2010, 26, 2042-2050.	1.8	72
1557	Interpretation of Toxicogenomics Data. , 2010, , 663-683.		0

#	ARTICLE	IF	CITATIONS
1558	Genome-Wide mRNA Expression Correlates of Viral Control in CD4+ T-Cells from HIV-1-Infected Individuals. <i>PLoS Pathogens</i> , 2010, 6, e1000781.	2.1	158
1559	The Arf tumor suppressor protein inhibits Miz1 to suppress cell adhesion and induce apoptosis. <i>Journal of Cell Biology</i> , 2010, 188, 905-918.	2.3	37
1560	The Stanley Neuropathology Consortium Integrative Database: a Novel, Web-Based Tool for Exploring Neuropathological Markers in Psychiatric Disorders and the Biological Processes Associated with Abnormalities of Those Markers. <i>Neuropsychopharmacology</i> , 2010, 35, 473-482.	2.8	75
1561	Genome-Wide Profiling of p63 DNA-Binding Sites Identifies an Element that Regulates Gene Expression during Limb Development in the 7q21 SHFM1 Locus. <i>PLoS Genetics</i> , 2010, 6, e1001065.	1.5	169
1562	Finding the "Dark Matter" in Human and Yeast Protein Network Prediction and Modelling. <i>PLoS Computational Biology</i> , 2010, 6, e1000945.	1.5	21
1563	Transcriptional Regulation by CHIP/LDB Complexes. <i>PLoS Genetics</i> , 2010, 6, e1001063.	1.5	28
1564	Co-ordinated Gene Expression in the Liver and Spleen during <i>Schistosoma japonicum</i> Infection Regulates Cell Migration. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e686.	1.3	40
1565	A novel approach to analyze gene expression data demonstrates that the F508 mutation in CFTR downregulates the antigen presentation pathway. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2010, 298, L473-L482.	1.3	21
1566	Hyperglycemic conditions modulate connective tissue reorganization by human vascular smooth muscle cells through stimulation of hyaluronan synthesis. <i>Glycobiology</i> , 2010, 20, 1117-1126.	1.3	27
1567	Many sequence-specific chromatin modifying protein-binding motifs show strong positional preferences for potential regulatory regions in the <i>Saccharomyces cerevisiae</i> genome. <i>Nucleic Acids Research</i> , 2010, 38, 1772-1779.	6.5	21
1568	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. <i>Genome Research</i> , 2010, 20, 791-803.	2.4	84
1569	Gene expression profiling of the short-term adaptive response to acute caloric restriction in liver and adipose tissues of pigs differing in feed efficiency. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2010, 298, R494-R507.	0.9	83
1570	Electrical signals affect the cardiomyocyte transcriptome independently of contraction. <i>Physiological Genomics</i> , 2010, 42A, 283-289.	1.0	31
1571	IKK $\beta$ Leads to an Inflammatory Skin Disease Resembling Interface Dermatitis. <i>Journal of Investigative Dermatology</i> , 2010, 130, 1598-1610.	0.3	35
1572	Regulation of Human Skin Pigmentation in situ by Repetitive UV Exposure: Molecular Characterization of Responses to UVA and/or UVB. <i>Journal of Investigative Dermatology</i> , 2010, 130, 1685-1696.	0.3	80
1573	Cross-species comparison of genomewide gene expression profiles reveals induction of hypoxia-inducible factor-responsive genes in iron-deprived intestinal epithelial cells. <i>American Journal of Physiology - Cell Physiology</i> , 2010, 299, C930-C938.	2.1	22
1574	Off-pump coronary artery bypass surgery is associated with fewer gene expression changes in the human myocardium in comparison with on-pump surgery. <i>Physiological Genomics</i> , 2010, 42, 67-75.	1.0	27
1575	EPS8 upregulates FOXM1 expression, enhancing cell growth and motility. <i>Carcinogenesis</i> , 2010, 31, 1132-1141.	1.3	47



#	ARTICLE	IF	CITATIONS
1576	Gene Expression Profiling in Wild-Type and PPAR-Null Mice Exposed to Perfluorooctane Sulfonate Reveals PPAR-Independent Effects. <i>PPAR Research</i> , 2010, 2010, 1-23.	1.1	100
1577	RB-pathway disruption in breast cancer. <i>Cell Cycle</i> , 2010, 9, 4153-4163.	1.3	163
1578	The Association of Multiple Interacting Genes with Specific Phenotypes in Rice Using Gene Coexpression Networks. <i>Plant Physiology</i> , 2010, 154, 13-24.	2.3	93
1579	Urinary-Type Plasminogen Activator Receptor/Î±3Î²1 Integrin Signaling, Altered Gene Expression, and Oral Tumor Progression. <i>Molecular Cancer Research</i> , 2010, 8, 145-158.	1.5	23
1580	Therapeutic implications of down-regulation of cyclophilin D in bipolar disorder. <i>International Journal of Neuropsychopharmacology</i> , 2010, 13, 1355-1368.	1.0	26
1581	Accelerated Ovarian Aging in the Absence of the Transcription Regulator TAF4B in Mice <sup>1</sup> . <i>Biology of Reproduction</i> , 2010, 82, 23-34.	1.2	34
1582	Constitutive Activation of Smoothed Leads to Female Infertility and Altered Uterine Differentiation in the Mouse <sup>1</sup> . <i>Biology of Reproduction</i> , 2010, 82, 991-999.	1.2	47
1583	miR-125b-2 is a potential oncomiR on human chromosome 21 in megakaryoblastic leukemia. <i>Genes and Development</i> , 2010, 24, 478-490.	2.7	202
1584	Aurora kinase A as a rational target for therapy in glioblastoma. <i>Journal of Neurosurgery: Pediatrics</i> , 2010, 6, 98-105.	0.8	39
1585	The Plasma Microparticle Proteome. <i>Seminars in Thrombosis and Hemostasis</i> , 2010, 36, 845-856.	1.5	45
1586	Effects of Age on the Synergistic Interactions between Lipopolysaccharide and Mechanical Ventilation in Mice. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2010, 43, 475-486.	1.4	40
1587	Using Expression Genetics to Study the Neurobiology of Ethanol and Alcoholism. <i>International Review of Neurobiology</i> , 2010, 91, 95-128.	0.9	41
1588	Cutaneous Anaplastic Large Cell Lymphoma and Peripheral T-Cell Lymphoma NOS Show Distinct Chromosomal Alterations and Differential Expression of Chemokine Receptors and Apoptosis Regulators. <i>Journal of Investigative Dermatology</i> , 2010, 130, 563-575.	0.3	62
1589	Scalp fibroblasts have a shared expression profile in monogenic craniosynostosis. <i>Journal of Medical Genetics</i> , 2010, 47, 803-808.	1.5	15
1590	Differential Endometrial Gene Expression in Pregnant and Nonpregnant Sows <sup>1</sup> . <i>Biology of Reproduction</i> , 2010, 83, 277-285.	1.2	88
1591	Global metabolic consequences of the chromogranin A-null model of hypertension: transcriptomic detection, pathway identification, and experimental verification. <i>Physiological Genomics</i> , 2010, 40, 195-207.	1.0	16
1592	REDD1 Is a Major Target of Testosterone Action in Preventing Dexamethasone-Induced Muscle Loss. <i>Endocrinology</i> , 2010, 151, 1050-1059.	1.4	58
1593	An integrated genomic analysis of gene-function correlation on schizophrenia susceptibility genes. <i>Journal of Human Genetics</i> , 2010, 55, 285-292.	1.1	49

#	ARTICLE	IF	CITATIONS
1594	Defective erythroid differentiation in miR-451 mutant mice mediated by 14-3-3 $\sigma$ . <i>Genes and Development</i> , 2010, 24, 1614-1619.	2.7	156
1595	Forty-eight hours of unloading and 24 h of reloading lead to changes in global gene expression patterns related to ubiquitination and oxidative stress in humans. <i>Journal of Applied Physiology</i> , 2010, 109, 1404-1415.	1.2	74
1596	Gene expression in hypothalamus, liver, and adipose tissues and food intake response to melanocortin-4 receptor agonist in pigs expressing melanocortin-4 receptor mutations. <i>Physiological Genomics</i> , 2010, 41, 254-268.	1.0	16
1597	From raw materials to validated system: the construction of a genomic library and microarray to interpret systemic perturbations in Northern bobwhite. <i>Physiological Genomics</i> , 2010, 42, 219-235.	1.0	55
1598	Natural Variation, Functional Pleiotropy and Transcriptional Contexts of <i>Odorant Binding Protein</i> Genes in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2010, 186, 1475-1485.	1.2	57
1599	Equivalence testing in microarray analysis: similarities in the transcriptome of human atherosclerotic and nonatherosclerotic macrophages. <i>Physiological Genomics</i> , 2010, 41, 212-223.	1.0	16
1600	Transcriptomic Analysis of Human Lung Development. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2010, 181, 54-63.	2.5	107
1601	Utilizing Cox regression model to assess the relations between predefined gene sets and the survival outcome of lung adenocarcinoma. , 2010, , .		0
1602	Transcriptome analysis and molecular signature of human retinal pigment epithelium. <i>Human Molecular Genetics</i> , 2010, 19, 2468-2486.	1.4	249
1603	Direct Transfer of $\alpha$ -Synuclein from Neuron to Astroglia Causes Inflammatory Responses in Synucleinopathies. <i>Journal of Biological Chemistry</i> , 2010, 285, 9262-9272.	1.6	704
1604	Integrative gene-tissue microarray-based approach for identification of human disease biomarkers: application to amyotrophic lateral sclerosis. <i>Human Molecular Genetics</i> , 2010, 19, 3233-3253.	1.4	58
1605	Integrative Systems Biology for Data-Driven Knowledge Discovery. <i>Seminars in Nephrology</i> , 2010, 30, 443-454.	0.6	20
1606	Pathways and Promoter Networks Analysis Provides Systems Topology for Systems Biology Approaches. <i>Seminars in Nephrology</i> , 2010, 30, 477-486.	0.6	4
1607	Systemic Delivery of Synthetic MicroRNA-16 Inhibits the Growth of Metastatic Prostate Tumors via Downregulation of Multiple Cell-cycle Genes. <i>Molecular Therapy</i> , 2010, 18, 181-187.	3.7	399
1608	MeV: MultiExperiment Viewer. , 2010, , 267-277.		167
1609	<i>In vivo</i> nutrigenomic effects of virgin olive oil polyphenols within the frame of the Mediterranean diet: a randomized controlled trial. <i>FASEB Journal</i> , 2010, 24, 2546-2557.	0.2	243
1610	Gene Expression Profile of Hyperoxic and Hypoxic Retinas in a Mouse Model of Oxygen-Induced Retinopathy. , 2010, 51, 4307.		66
1611	An in silico analysis of microRNAs: Mining the miRNAome. <i>Molecular BioSystems</i> , 2010, 6, 1853.	2.9	42

#	ARTICLE	IF	CITATIONS
1614	Analysis of Detergent-Insoluble and Whole Cell Lysate Fractions of Resting Neutrophils Using High-Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2010, 9, 2030-2036.	1.8	20
1615	Transcriptional Profiling of Human Embryonic Stem Cells Differentiating to Definitive and Primitive Endoderm and Further Toward the Hepatic Lineage. <i>Stem Cells and Development</i> , 2010, 19, 961-978.	1.1	17
1616	Widespread Protein Aggregation as an Inherent Part of Aging in <i>C. elegans</i> . <i>PLoS Biology</i> , 2010, 8, e1000450.	2.6	551
1617	Involvement of mast cells in eosinophilic esophagitis. <i>Journal of Allergy and Clinical Immunology</i> , 2010, 126, 140-149.	1.5	261
1618	Molecular diversity in ductal carcinoma <i>in situ</i> (DCIS) and early invasive breast cancer. <i>Molecular Oncology</i> , 2010, 4, 357-368.	2.1	107
1619	From RNA-seq reads to differential expression results. <i>Genome Biology</i> , 2010, 11, 220.	13.9	603
1620	The Effect of Simulated Microgravity on Human Mesenchymal Stem Cells Cultured in an Osteogenic Differentiation System: A Bioinformatics Study. <i>Tissue Engineering - Part A</i> , 2010, 16, 3403-3412.	1.6	58
1621	Functional Differences Between Mesenchymal Stem Cell Populations Are Reflected by Their Transcriptome. <i>Stem Cells and Development</i> , 2010, 19, 481-490.	1.1	124
1622	Tasquinimod (ABR-215050), a quinoline-3-carboxamide anti-angiogenic agent, modulates the expression of thrombospondin-1 in human prostate tumors. <i>Molecular Cancer</i> , 2010, 9, 107.	7.9	77
1623	Gene expression profiling of mouse p53-deficient epidermal carcinoma defines molecular determinants of human cancer malignancy. <i>Molecular Cancer</i> , 2010, 9, 193.	7.9	22
1624	Sp1 acetylation is associated with loss of DNA binding at promoters associated with cell cycle arrest and cell death in a colon cell line. <i>Molecular Cancer</i> , 2010, 9, 275.	7.9	98
1625	A Genome-wide screen identifies frequently methylated genes in haematological and epithelial cancers. <i>Molecular Cancer</i> , 2010, 9, 44.	7.9	92
1626	Identification of 5 novel genes methylated in breast and other epithelial cancers. <i>Molecular Cancer</i> , 2010, 9, 51.	7.9	83
1627	MFSD2A is a novel lung tumor suppressor gene modulating cell cycle and matrix attachment. <i>Molecular Cancer</i> , 2010, 9, 62.	7.9	32
1628	Transcriptional responses in the adaptation to ischaemia-reperfusion injury: a study of the effect of ischaemic preconditioning in total knee arthroplasty patients. <i>Journal of Translational Medicine</i> , 2010, 8, 46.	1.8	27
1629	Copy number and gene expression differences between African American and Caucasian American prostate cancer. <i>Journal of Translational Medicine</i> , 2010, 8, 70.	1.8	50
1630	Luteolin triggers global changes in the microglial transcriptome leading to a unique anti-inflammatory and neuroprotective phenotype. <i>Journal of Neuroinflammation</i> , 2010, 7, 3.	3.1	139
1631	Investigation of Human Testis Protein Heterogeneity Using 2D-Dimensional Electrophoresis. <i>Journal of Andrology</i> , 2010, 31, 419-429.	2.0	32

#	ARTICLE	IF	CITATIONS
1632	Colorectal Cancer Cell Lines Lack the Molecular Heterogeneity of Clinical Colorectal Tumors. <i>Clinical Colorectal Cancer</i> , 2010, 9, 40-47.	1.0	20
1633	Novel Candidate Cancer Genes Identified by a Large-Scale Cross-Species Comparative Oncogenomics Approach. <i>Cancer Research</i> , 2010, 70, 883-895.	0.4	40
1634	Functional Module Analysis Reveals Differential Osteogenic and Stemness Potentials in Human Mesenchymal Stem Cells from Bone Marrow and Wharton's Jelly of Umbilical Cord. <i>Stem Cells and Development</i> , 2010, 19, 1895-1910.	1.1	158
1635	Antiproliferative Mechanisms of the Flavonoids 2,2- $\alpha$ -Dihydroxychalcone and Fisetin in Human Prostate Cancer Cells. <i>Nutrition and Cancer</i> , 2010, 62, 668-681.	0.9	33
1636	<i>In Vitro</i> Neurotoxicity of PBDE-99: Immediate and Concentration-Dependent Effects on Protein Expression in Cerebral Cortex Cells. <i>Journal of Proteome Research</i> , 2010, 9, 1226-1235.	1.8	26
1637	Activation of Aortic Endothelial Cells by Oxidized Phospholipids: A Phosphoproteomic Analysis. <i>Journal of Proteome Research</i> , 2010, 9, 2812-2824.	1.8	38
1638	Quantitative Proteome Analysis of Pluripotent Cells by iTRAQ Mass Tagging Reveals Post-transcriptional Regulation of Proteins Required for ES Cell Self-renewal. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2238-2251.	2.5	35
1639	Pro-Inflammatory CD11c+CD206+ Adipose Tissue Macrophages Are Associated With Insulin Resistance in Human Obesity. <i>Diabetes</i> , 2010, 59, 1648-1656.	0.3	521
1640	Negative energy balance and hepatic gene expression patterns in high-yielding dairy cows during the early postpartum period: a global approach. <i>Physiological Genomics</i> , 2010, 42A, 188-199.	1.0	73
1641	Endogenous Collagen Influences Differentiation of Human Multipotent Mesenchymal Stromal Cells. <i>Tissue Engineering - Part A</i> , 2010, 16, 1693-1702.	1.6	57
1642	Water Chemistry Alters Gene Expression and Physiological End Points of Chronic Waterborne Copper Exposure in Zebrafish, <i>Danio rerio</i> . <i>Environmental Science &amp; Technology</i> , 2010, 44, 2156-2162.	4.6	33
1643	Proteomic Analysis of Human Osteoblastic Cells: Relevant Proteins and Functional Categories for Differentiation. <i>Journal of Proteome Research</i> , 2010, 9, 4688-4700.	1.8	30
1644	Analysis of Secreted Proteins as an <i>in vitro</i> Model for Discovery of Liver Toxicity Markers. <i>Journal of Proteome Research</i> , 2010, 9, 5794-5802.	1.8	13
1645	Dominant Processes during Human Dendritic Cell Maturation Revealed by Integration of Proteome and Transcriptome at the Pathway Level. <i>Journal of Proteome Research</i> , 2010, 9, 1727-1737.	1.8	45
1646	Association weight matrix for the genetic dissection of puberty in beef cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13642-13647.	3.3	127
1647	Phospholipid Transfer Protein in Human Plasma Associates with Proteins Linked to Immunity and Inflammation. <i>Biochemistry</i> , 2010, 49, 7314-7322.	1.2	47
1648	Proteomic Identification of Paclitaxel-Resistance Associated hnRNP A2 and GDI 2 Proteins in Human Ovarian Cancer Cells. <i>Journal of Proteome Research</i> , 2010, 9, 5668-5676.	1.8	58
1649	Proteomic Analysis of Proteins Involved in Spermiogenesis in Mouse. <i>Journal of Proteome Research</i> , 2010, 9, 1246-1256.	1.8	65

#	ARTICLE	IF	CITATIONS
1650	Neuron Differentiation-Related Genes Are Up-regulated in the Hypothalamus of Odorant-Inhaling Rats Subjected to Acute Restraint Stress. <i>Journal of Agricultural and Food Chemistry</i> , 2010, 58, 7922-7929.	2.4	24
1651	Developmental regulation and individual differences of neuronal H3K4me3 epigenomes in the prefrontal cortex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8824-8829.	3.3	218
1652	Lidocaine inhibits epithelial chemokine secretion via inhibition of nuclear factor $\kappa$ B activation. <i>Immunobiology</i> , 2010, 215, 304-313.	0.8	30
1653	Transcriptional effects of progesterone receptor antagonist in rat granulosa cells. <i>Molecular and Cellular Endocrinology</i> , 2010, 315, 121-130.	1.6	10
1654	Naringenin chalcone improves adipocyte functions by enhancing adiponectin production. <i>Molecular and Cellular Endocrinology</i> , 2010, 323, 208-214.	1.6	42
1655	Expectations, validity, and reality in gene expression profiling. <i>Journal of Clinical Epidemiology</i> , 2010, 63, 950-959.	2.4	55
1656	Myostatin regulates glucose metabolism via the AMP-activated protein kinase pathway in skeletal muscle cells. <i>International Journal of Biochemistry and Cell Biology</i> , 2010, 42, 2072-2081.	1.2	80
1657	Effects of Salmonella on spatial-temporal processes of jejunal development in chickens. <i>Developmental and Comparative Immunology</i> , 2010, 34, 1090-1100.	1.0	19
1658	Hopx and Hdac2 Interact to Modulate Gata4 Acetylation and Embryonic Cardiac Myocyte Proliferation. <i>Developmental Cell</i> , 2010, 19, 450-459.	3.1	125
1659	The use of neuroproteomics in drug abuse research. <i>Drug and Alcohol Dependence</i> , 2010, 107, 11-22.	1.6	17
1660	Autoantibody profiling to identify biomarkers of key pathogenic pathways in mucinous ovarian cancer. <i>European Journal of Cancer</i> , 2010, 46, 170-179.	1.3	33
1661	3-Methylcholanthrene (3-MC) and 4-chlorobiphenyl (PCB3) genotoxicity is gender-related in Fischer 344 transgenic rats. <i>Environment International</i> , 2010, 36, 970-979.	4.8	16
1662	Combining suppressive subtractive hybridization and cDNA microarrays to identify dietary phosphorus-responsive genes of the rainbow trout ( <i>Oncorhynchus mykiss</i> ) kidney. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 24-35.	0.4	9
1663	Nucleoporins Directly Stimulate Expression of Developmental and Cell-Cycle Genes Inside the Nucleoplasm. <i>Cell</i> , 2010, 140, 360-371.	13.5	388
1664	Precision Mapping of an In Vivo N-Glycoproteome Reveals Rigid Topological and Sequence Constraints. <i>Cell</i> , 2010, 141, 897-907.	13.5	789
1665	An Alternative Splicing Network Links Cell-Cycle Control to Apoptosis. <i>Cell</i> , 2010, 142, 625-636.	13.5	273
1666	Quantitative Interaction Proteomics and Genome-wide Profiling of Epigenetic Histone Marks and Their Readers. <i>Cell</i> , 2010, 142, 967-980.	13.5	710
1667	Comparative Epigenomic Analysis of Murine and Human Adipogenesis. <i>Cell</i> , 2010, 143, 156-169.	13.5	460

#	ARTICLE	IF	CITATIONS
1668	A Myc Network Accounts for Similarities between Embryonic Stem and Cancer Cell Transcription Programs. <i>Cell</i> , 2010, 143, 313-324.	13.5	606
1669	TGF- $\beta$ <sup>2</sup> and Insulin Signaling Regulate Reproductive Aging via Oocyte and Germline Quality Maintenance. <i>Cell</i> , 2010, 143, 299-312.	13.5	238
1670	Pausing of RNA Polymerase II Disrupts DNA-Specified Nucleosome Organization to Enable Precise Gene Regulation. <i>Cell</i> , 2010, 143, 540-551.	13.5	369
1671	Germinal Center Dynamics Revealed by Multiphoton Microscopy with a Photoactivatable Fluorescent Reporter. <i>Cell</i> , 2010, 143, 592-605.	13.5	1,026
1672	A Tissue-Specific Atlas of Mouse Protein Phosphorylation and Expression. <i>Cell</i> , 2010, 143, 1174-1189.	13.5	1,564
1673	Integrative Genomic Approaches Highlight a Family of Parasite-Specific Kinases that Regulate Host Responses. <i>Cell Host and Microbe</i> , 2010, 8, 208-218.	5.1	238
1675	An Expanded Oct4 Interaction Network: Implications for Stem Cell Biology, Development, and Disease. <i>Cell Stem Cell</i> , 2010, 6, 382-395.	5.2	338
1676	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. <i>Cell Stem Cell</i> , 2010, 6, 479-491.	5.2	747
1677	Identification and Classification of Chromosomal Aberrations in Human Induced Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2010, 7, 521-531.	5.2	695
1678	Testosterone-induced upregulation of miRNAs in the female mouse liver. <i>Steroids</i> , 2010, 75, 998-1004.	0.8	60
1679	Differentially expressed genes associated with Staphylococcus aureus mastitis in dairy goats. <i>Veterinary Immunology and Immunopathology</i> , 2010, 135, 208-217.	0.5	31
1680	Gene expression profiling of PBMCs from Holstein and Jersey cows sub-clinically infected with Mycobacterium avium ssp. paratuberculosis. <i>Veterinary Immunology and Immunopathology</i> , 2010, 137, 1-11.	0.5	283
1681	Methods for transcriptomic analyses of the porcine host immune response: Application to Salmonella infection using microarrays. <i>Veterinary Immunology and Immunopathology</i> , 2010, 138, 280-291.	0.5	10
1682	Genomic phenotype of non-cultured pulmonary fibroblasts in idiopathic pulmonary fibrosis. <i>Genomics</i> , 2010, 96, 134-145.	1.3	70
1683	NF- $\kappa$ B driven cardioprotective gene programs; Hsp70.3 and cardioprotection after late ischemic preconditioning. <i>Journal of Molecular and Cellular Cardiology</i> , 2010, 49, 664-672.	0.9	41
1684	Curcumin Extends Life Span, Improves Health Span, and Modulates the Expression of Age-Associated Aging Genes in <i>Drosophila melanogaster</i> . <i>Rejuvenation Research</i> , 2010, 13, 561-570.	0.9	195
1685	Restriction of Receptor Movement Alters Cellular Response: Physical Force Sensing by EphA2. <i>Science</i> , 2010, 327, 1380-1385.	6.0	301
1686	Epigenetic and immune function profiles associated with posttraumatic stress disorder. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9470-9475.	3.3	452

#	ARTICLE	IF	CITATIONS
1687	<i>Porphyrromonas gingivalis</i> infection-induced tissue and bone transcriptional profiles. <i>Molecular Oral Microbiology</i> , 2010, 25, 61-74.	1.3	48
1688	p53 prevents progression of nevi to melanoma predominantly through cell cycle regulation. <i>Pigment Cell and Melanoma Research</i> , 2010, 23, 781-794.	1.5	59
1689	miR-451 enhances erythroid differentiation in K562 cells. <i>Leukemia and Lymphoma</i> , 2010, 51, 686-693.	0.6	47
1690	Molecular signatures of maturing dendritic cells: implications for testing the quality of dendritic cell therapies. <i>Journal of Translational Medicine</i> , 2010, 8, 4.	1.8	109
1691	Human Endometrial Side Population Cells Exhibit Genotypic, Phenotypic and Functional Features of Somatic Stem Cells. <i>PLoS ONE</i> , 2010, 5, e10964.	1.1	161
1692	Statistical Methods for Pathway Analysis of Genome-Wide Data for Association with Complex Genetic Traits. <i>Advances in Genetics</i> , 2010, 72, 141-179.	0.8	86
1693	Estrogen Receptor $\beta$ Controls a Gene Network in Luminal-Like Breast Cancer Cells Comprising Multiple Transcription Factors and MicroRNAs. <i>American Journal of Pathology</i> , 2010, 176, 2113-2130.	1.9	151
1694	Differential Gene Regulation by the Human and Mouse Aryl Hydrocarbon Receptor. <i>Toxicological Sciences</i> , 2010, 114, 217-225.	1.4	90
1695	U87MG Decoded: The Genomic Sequence of a Cytogenetically Aberrant Human Cancer Cell Line. <i>PLoS Genetics</i> , 2010, 6, e1000832.	1.5	229
1696	agriGO: a GO analysis toolkit for the agricultural community. <i>Nucleic Acids Research</i> , 2010, 38, W64-W70.	6.5	2,289
1697	Genome-wide analysis of mRNA targets for <i>Caenorhabditis elegans</i> FBF, a conserved stem cell regulator. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3936-3941.	3.3	108
1698	A Comparison of Whole Genome Gene Expression Profiles of HepaRG Cells and HepG2 Cells to Primary Human Hepatocytes and Human Liver Tissues. <i>Drug Metabolism and Disposition</i> , 2010, 38, 988-994.	1.7	222
1699	Disease-specific, neurosphere-derived cells as models for brain disorders. <i>DMM Disease Models and Mechanisms</i> , 2010, 3, 785-798.	1.2	175
1700	Vitreous Proteomics and Diabetic Retinopathy. <i>Seminars in Ophthalmology</i> , 2010, 25, 289-294.	0.8	27
1701	Genomic Analyses of Hormone Signaling and Gene Regulation. <i>Annual Review of Physiology</i> , 2010, 72, 191-218.	5.6	78
1702	Quantitative Expression Profiling in Formalin-Fixed Paraffin-Embedded Samples by Affymetrix Microarrays. <i>Journal of Molecular Diagnostics</i> , 2010, 12, 409-417.	1.2	81
1703	Integrative Functional Genomics Analysis of Sustained Polyploidy Phenotypes in Breast Cancer Cells Identifies an Oncogenic Profile for GINS2. <i>Neoplasia</i> , 2010, 12, 877-IN14.	2.3	44
1704	Phenotypic and molecular characterization of the claudin-low intrinsic subtype of breast cancer. <i>Breast Cancer Research</i> , 2010, 12, R68.	2.2	1,748

#	ARTICLE	IF	CITATIONS
1705	Gene expression profiling of peripheral blood cells for early detection of breast cancer. Breast Cancer Research, 2010, 12, R7.	2.2	95
1706	Quantifying the mechanisms of domain gain in animal proteins. Genome Biology, 2010, 11, R74.	13.9	93
1707	A mouse embryonic stem cell bank for inducible overexpression of human chromosome 21 genes. Genome Biology, 2010, 11, R64.	13.9	16
1708	Identification of functional modules that correlate with phenotypic difference: the influence of network topology. Genome Biology, 2010, 11, R23.	13.9	67
1709	Matrix metalloproteinase-8 deficiency increases joint inflammation and bone erosion in the K/BxN serum-transfer arthritis model. Arthritis Research and Therapy, 2010, 12, R224.	1.6	48
1710	Proteomic Profile Regulated by the Anticancer Peptide CIGB-300 in Non-Small Cell Lung Cancer (NSCLC) Cells. Journal of Proteome Research, 2010, 9, 5473-5483.	1.8	26
1711	Three-Dimensional Culture Alters Primary Cardiac Cell Phenotype. Tissue Engineering - Part A, 2010, 16, 629-641.	1.6	40
1712	Analysis of genome-wide methylation and gene expression induced by 5-aza-2-deoxycytidine identifies BCL2L10 as a frequent methylation target in acute myeloid leukemia. Leukemia and Lymphoma, 2010, 51, 2275-2284.	0.6	43
1713	Translation efficiency in humans: tissue specificity, global optimization and differences between developmental stages. Nucleic Acids Research, 2010, 38, 2964-2974.	6.5	69
1714	Heat Shock Transcription Factor 1 Localizes to Sex Chromatin during Meiotic Repression. Journal of Biological Chemistry, 2010, 285, 34469-34476.	1.6	62
1715	Bioinformatics and Systems Biology of Cancers. Progress in Molecular Biology and Translational Science, 2010, 95, 159-191.	0.9	5
1716	Systems genetics analysis of molecular pathways underlying ethanol-induced behavioral phenotypes. , 2010, , .		1
1717	Gene expression profiling of peripheral blood leukocytes identifies potential novel biomarkers of chronic obstructive pulmonary disease in current and former smokers. Biomarkers, 2010, 15, 715-730.	0.9	17
1718	Transcriptional control of the proliferation cluster by the tumor suppressor p53. Molecular BioSystems, 2010, 6, 17-29.	2.9	28
1719	Protein phosphorylation analysis in archival clinical cancer samples by shotgun and targeted proteomics approaches. Molecular BioSystems, 2011, 7, 2368.	2.9	35
1720	Investigating Neoplastic Progression of Ulcerative Colitis with Label-Free Comparative Proteomics. Journal of Proteome Research, 2011, 10, 200-209.	1.8	41
1721	Global risk transformative prioritization for prostate cancer candidate genes in molecular networks. Molecular BioSystems, 2011, 7, 2547.	2.9	4
1722	Early gene response of human brain microvascular endothelial cells to <i>Listeria monocytogenes</i> infection. Canadian Journal of Microbiology, 2011, 57, 441-446.	0.8	5



#	ARTICLE	IF	CITATIONS
1723	Histone deacetylase 3 is an epigenomic brake in macrophage alternative activation. <i>Genes and Development</i> , 2011, 25, 2480-2488.	2.7	254
1724	Mining the Bioinformation of Differentially Expressed Genes in Rats Treated by Diesel Exhaust Inhalation Based on the Bioinformatics Methods. , 2011, , .		0
1725	Correction of Sickle Cell Disease in Adult Mice by Interference with Fetal Hemoglobin Silencing. <i>Science</i> , 2011, 334, 993-996.	6.0	281
1726	Alternative translation start sites are conserved in eukaryotic genomes. <i>Nucleic Acids Research</i> , 2011, 39, 567-577.	6.5	133
1727	Networked-based Characterization of Extracellular Matrix Proteins from Adult Mouse Pulmonary and Aortic Valves. <i>Journal of Proteome Research</i> , 2011, 10, 812-823.	1.8	36
1728	Gene Expression Biomarkers in the Brain of a Mouse Model for Alzheimer's Disease: Mining of Microarray Data by Logic Classification and Feature Selection. <i>Journal of Alzheimer's Disease</i> , 2011, 24, 721-738.	1.2	104
1729	Comparison of Three Quantitative Phosphoproteomic Strategies to Study Receptor Tyrosine Kinase Signaling. <i>Journal of Proteome Research</i> , 2011, 10, 5454-5462.	1.8	26
1730	microRNAs in Early Diabetic Retinopathy in Streptozotocin-Induced Diabetic Rats. , 2011, 52, 4402.		242
1731	Proteomics and Pathway Analyses of the Milk Fat Globule in Sheep Naturally Infected by <i>Mycoplasma agalactiae</i> Provide Indications of the <i>In Vivo</i> Response of the Mammary Epithelium to Bacterial Infection. <i>Infection and Immunity</i> , 2011, 79, 3833-3845.	1.0	69
1732	Genome-Wide Association Study of the Child Behavior Checklist Dysregulation Profile. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2011, 50, 807-817.e8.	0.3	56
1733	Whole transcriptome analysis of the fasting and fed Burmese python heart: insights into extreme physiological cardiac adaptation. <i>Physiological Genomics</i> , 2011, 43, 69-76.	1.0	24
1734	Effects of dietary aflatoxin on the hepatic expression of apoptosis genes in growing barrows1. <i>Journal of Animal Science</i> , 2011, 89, 916-925.	0.2	39
1735	Hepatic Gene Expression of the Insulin Signaling Pathway Is Altered by Administration of Persimmon Peel Extract: A DNA Microarray Study Using Type 2 Diabetic Goto-Kakizaki Rats. <i>Journal of Agricultural and Food Chemistry</i> , 2011, 59, 3320-3329.	2.4	18
1736	Polycomb preferentially targets stalled promoters of coding and noncoding transcripts. <i>Genome Research</i> , 2011, 21, 216-226.	2.4	146
1737	Quantitative Proteomic Analysis of the Adipocyte Plasma Membrane. <i>Journal of Proteome Research</i> , 2011, 10, 4970-4982.	1.8	29
1738	Label-free Proteomics and Systems Biology Analysis of Mycobacterial Phagosomes in Dendritic Cells and Macrophages. <i>Journal of Proteome Research</i> , 2011, 10, 2425-2439.	1.8	19
1739	New insights into the pathogenesis of cystic follicles in cattle: Microarray analysis of gene expression in granulosa cells1. <i>Journal of Animal Science</i> , 2011, 89, 1769-1786.	0.2	39
1740	Integrated Analysis of ATM Mediated Gene and Protein Expression Impacting Cellular Metabolism. <i>Journal of Proteome Research</i> , 2011, 10, 2651-2657.	1.8	27

#	ARTICLE	IF	CITATIONS
1741	Expression Profiling of Vulvar Carcinoma: Clues for Deranged Extracellular Matrix Remodeling and Effects on Multiple Signaling Pathways Combined with Discrete Patient Subsets. <i>Translational Oncology</i> , 2011, 4, 301-IN6.	1.7	9
1742	SNAIL Regulates Interleukin-8 Expression, Stem Cell-Like Activity, and Tumorigenicity of Human Colorectal Carcinoma Cells. <i>Gastroenterology</i> , 2011, 141, 279-291.e5.	0.6	266
1743	Upregulation of Dicer and MicroRNA Expression in the Dorsolateral Prefrontal Cortex Brodmann Area 46 in Schizophrenia. <i>Biological Psychiatry</i> , 2011, 69, 180-187.	0.7	236
1744	Binge Cocaine Administration in Adolescent Rats Affects Amygdalar Gene Expression Patterns and Alters Anxiety-Related Behavior in Adulthood. <i>Biological Psychiatry</i> , 2011, 70, 583-592.	0.7	24
1745	Proteome-Wide Mapping of the <i>Drosophila</i> Acetylome Demonstrates a High Degree of Conservation of Lysine Acetylation. <i>Science Signaling</i> , 2011, 4, ra48.	1.6	243
1746	PPAR $\gamma$ disease gene network and identification of therapeutic targets for prostate cancer. <i>Journal of Drug Targeting</i> , 2011, 19, 781-796.	2.1	14
1749	Aberrant Overexpression of Satellite Repeats in Pancreatic and Other Epithelial Cancers. <i>Science</i> , 2011, 331, 593-596.	6.0	452
1750	Escitalopram modulates neuron-remodelling proteins in a rat gene-environment interaction model of depression as revealed by proteomics. Part I: genetic background. <i>International Journal of Neuropsychopharmacology</i> , 2011, 14, 796-833.	1.0	20
1751	Scriptaid Corrects Gene Expression of a Few Aberrantly Reprogrammed Transcripts in Nuclear Transfer Pig Blastocyst Stage Embryos. <i>Cellular Reprogramming</i> , 2011, 13, 191-204.	0.5	69
1752	Transcriptome Analysis in Endothelial Progenitor Cell Biology. <i>Antioxidants and Redox Signaling</i> , 2011, 15, 1029-1042.	2.5	26
1753	Joint Binding of OTX2 and MYC in Promotor Regions Is Associated with High Gene Expression in Medulloblastoma. <i>PLoS ONE</i> , 2011, 6, e26058.	1.1	24
1754	Proteomic Analysis of Acetaminophen-Induced Changes in Mitochondrial Protein Expression Using Spectral Counting. <i>Chemical Research in Toxicology</i> , 2011, 24, 549-558.	1.7	27
1755	Comparative Analysis of Human Embryonic Stem Cell and Induced Pluripotent Stem Cell-Derived Hepatocyte-Like Cells Reveals Current Drawbacks and Possible Strategies for Improved Differentiation. <i>Stem Cells and Development</i> , 2011, 20, 1259-1275.	1.1	75
1756	Methylation profiling with a panel of cancer related genes: Association with estrogen receptor, TP53 mutation status and expression subtypes in sporadic breast cancer. <i>Molecular Oncology</i> , 2011, 5, 61-76.	2.1	110
1757	Mechanisms of blast induced brain injuries, experimental studies in rats. <i>NeuroImage</i> , 2011, 54, S89-S97.	2.1	156
1758	Weighted Network Analysis. , 2011, , .		241
1759	Comparative analysis of nuclear estrogen receptor alpha and beta interactomes in breast cancer cells. <i>Molecular BioSystems</i> , 2011, 7, 667-676.	2.9	39
1760	Auxin Signaling and Transport Promote Susceptibility to the Root-Infecting Fungal Pathogen <i>Fusarium oxysporum</i> in <i>Arabidopsis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 733-748.	1.4	146

#	ARTICLE	IF	CITATIONS
1761	Intrinsic disorder of the extracellular matrix. <i>Molecular BioSystems</i> , 2011, 7, 3353.	2.9	54
1762	Transcriptome sequencing across a prostate cancer cohort identifies PCAT-1, an unannotated lincRNA implicated in disease progression. <i>Nature Biotechnology</i> , 2011, 29, 742-749.	9.4	950
1763	Endometrial receptivity is affected in women with high circulating progesterone levels at the end of the follicular phase: a functional genomics analysis. <i>Human Reproduction</i> , 2011, 26, 1813-1825.	0.4	288
1764	Systematic Approaches towards the Development of Host-Directed Antiviral Therapeutics. <i>International Journal of Molecular Sciences</i> , 2011, 12, 4027-4052.	1.8	79
1765	Genome-wide FOXO targets and topology of the transcriptomic response to stress and insulin signalling. <i>Molecular Systems Biology</i> , 2011, 7, 502.	3.2	112
1766	The autism disconnect. <i>Nature</i> , 2011, 474, 294-295.	13.7	6
1767	Proteomic Analysis of an Immortalized Mouse Pancreatic Stellate Cell Line Identifies Differentially-Expressed Proteins in Activated vs Nonproliferating Cell States. <i>Journal of Proteome Research</i> , 2011, 10, 4835-4844.	1.8	36
1768	Unraveling the Human Bone Microenvironment beyond the Classical Extracellular Matrix Proteins: A Human Bone Protein Library. <i>Journal of Proteome Research</i> , 2011, 10, 4725-4733.	1.8	39
1769	Aging Enhances the Production of Reactive Oxygen Species and Bactericidal Activity in Peritoneal Macrophages by Upregulating Classical Activation Pathways. <i>Biochemistry</i> , 2011, 50, 9911-9922.	1.2	46
1770	Cistrome: an integrative platform for transcriptional regulation studies. <i>Genome Biology</i> , 2011, 12, R83.	13.9	598
1771	Boundary distinction interpretation of microarray data via discrete correlate summation. <i>Genome Biology</i> , 2011, 12, .	13.9	0
1772	Modeling the cumulative genetic risk for multiple sclerosis from genome-wide association data. <i>Genome Medicine</i> , 2011, 3, 3.	3.6	63
1773	Proteome Profile of Zebrafish <i>Danio rerio</i> Olfactory Bulb Based on Two-Dimensional Gel Electrophoresis Matrix-Assisted Laser Desorption/Ionization MS/MS Analysis. <i>Zebrafish</i> , 2011, 8, 183-189.	0.5	7
1774	Transcriptional Modulation in a Leukocyte-Depleted Splenic Cell Population During Prion Disease. <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2011, 74, 1504-1520.	1.1	5
1775	Conceptual Thinking for In Silico Prioritization of Candidate Disease Genes. <i>Methods in Molecular Biology</i> , 2011, 760, 175-187.	0.4	9
1776	Mechanisms of stable lipid loss in a social insect. <i>Journal of Experimental Biology</i> , 2011, 214, 3808-3821.	0.8	88
1777	Body mass index-independent inflammation in omental adipose tissue associated with insulin resistance in morbid obesity. <i>Surgery for Obesity and Related Diseases</i> , 2011, 7, 60-67.	1.0	186
1778	Global transcriptome analysis of human bone marrow stromal cells (BMSC) reveals proliferative, mobile and interactive cells that produce abundant extracellular matrix proteins, some of which may affect BMSC potency. <i>Cytotherapy</i> , 2011, 13, 661-674.	0.3	59

#	ARTICLE	IF	CITATIONS
1779	Proteomic analysis of a model fish species exposed to individual pesticides and a binary mixture. <i>Aquatic Toxicology</i> , 2011, 101, 196-206.	1.9	29
1780	Lung Gene Expression in a Rhesus Allergic Asthma Model Correlates with Physiologic Parameters of Disease and Exhibits Common and Distinct Pathways with Human Asthma and a Mouse Asthma Model. <i>American Journal of Pathology</i> , 2011, 179, 1667-1680.	1.9	14
1781	Seasonal liver protein differences in a hibernator revealed by quantitative proteomics using whole animal isotopic labeling. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2011, 6, 163-170.	0.4	18
1782	Shift in chicken intestinal gene association networks after infection with <i>Salmonella</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2011, 6, 339-347.	0.4	9
1783	Responses of threespine stickleback ( <i>Gasterosteus aculeatus</i> , L) transcriptome to hypoxia. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2011, 6, 370-381.	0.4	31
1784	FMRP Stalls Ribosomal Translocation on mRNAs Linked to Synaptic Function and Autism. <i>Cell</i> , 2011, 146, 247-261.	13.5	1,864
1785	Mbd3/NURD Complex Regulates Expression of 5-Hydroxymethylcytosine Marked Genes in Embryonic Stem Cells. <i>Cell</i> , 2011, 147, 1498-1510.	13.5	424
1786	Genome-wide Localization of SREBP-2 in Hepatic Chromatin Predicts a Role in Autophagy. <i>Cell Metabolism</i> , 2011, 13, 367-375.	7.2	147
1787	Notch Initiates the Endothelial-to-Mesenchymal Transition in the Atrioventricular Canal through Autocrine Activation of Soluble Guanylyl Cyclase. <i>Developmental Cell</i> , 2011, 21, 288-300.	3.1	144
1788	ATXN1 Protein Family and CIC Regulate Extracellular Matrix Remodeling and Lung Alveolarization. <i>Developmental Cell</i> , 2011, 21, 746-757.	3.1	89
1789	A prognostic multigene classifier for squamous cell carcinomas of the larynx. <i>Cancer Letters</i> , 2011, 307, 37-46.	3.2	42
1790	Transcriptional modulation of a human monocytic cell line exposed to PM10 from an urban area. <i>Environmental Research</i> , 2011, 111, 765-774.	3.7	9
1791	Endometrial gene expression in the window of implantation is altered in obese women especially in an association with polycystic ovary syndrome. <i>Fertility and Sterility</i> , 2011, 95, 2335-2341.e8.	0.5	149
1792	Gene expression analysis of blastemal component reveals genes associated with relapse mechanism in Wilms tumour. <i>European Journal of Cancer</i> , 2011, 47, 2715-2722.	1.3	28
1793	MicroRNA changes in the mouse prefrontal cortex after inflammatory pain. <i>European Journal of Pain</i> , 2011, 15, 801.e1-12.	1.4	41
1794	Chronic alcohol exposure induced gene expression changes in the zebrafish brain. <i>Behavioural Brain Research</i> , 2011, 216, 66-76.	1.2	64
1795	Microarray analysis of differentially regulated genes in human neuronal and epithelial cell lines upon exposure to type A botulinum neurotoxin. <i>Biochemical and Biophysical Research Communications</i> , 2011, 405, 684-690.	1.0	23
1796	Proteomic Characterization of Aggregating Proteins after the Inhibition of the Ubiquitin Proteasome System. <i>Journal of Proteome Research</i> , 2011, 10, 1062-1072.	1.8	55

#	ARTICLE	IF	CITATIONS
1797	Two Phases of Mitogenic Signaling Unveil Roles for p53 and EGR1 in Elimination of Inconsistent Growth Signals. <i>Molecular Cell</i> , 2011, 42, 524-535.	4.5	93
1798	Lack of change in microRNA expression in adult mouse liver following treatment with benzo(a)pyrene despite robust mRNA transcriptional response. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2011, 722, 131-139.	0.9	42
1799	Low dose radiation response curves, networks and pathways in human lymphoblastoid cells exposed from 1 to 10cGy of acute gamma radiation. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2011, 722, 119-130.	0.9	37
1800	Illumina whole-genome complementary DNA-mediated annealing, selection, extension and ligation platform: assessing its performance in formalin-fixed, paraffin-embedded samples and identifying invasion pattern-related genes in oral squamous cell carcinoma. <i>Human Pathology</i> , 2011, 42, 1911-1922.	1.1	24
1801	Microarray and Functional Cluster Analysis Implicates Transforming Growth Factor Beta1 in Endothelial Cell Dysfunction in a Swine Hemorrhagic Shock Model. <i>Journal of Surgical Research</i> , 2011, 170, 120-132.	0.8	15
1802	Gene Pathway Analysis of Hepatocellular Carcinoma Genomic Expression Datasets. <i>Journal of Surgical Research</i> , 2011, 170, e85-e92.	0.8	7
1803	Phenotypic and molecular characterization of proliferating and differentiated GnRH-expressing GnV-3 cells. <i>Molecular and Cellular Endocrinology</i> , 2011, 332, 97-105.	1.6	12
1804	Transcriptional profiling of intrinsic PNS factors in the postnatal mouse. <i>Molecular and Cellular Neurosciences</i> , 2011, 46, 32-44.	1.0	53
1805	Oxidative stress induced carbonylation in human plasma. <i>Journal of Proteomics</i> , 2011, 74, 2395-2416.	1.2	37
1806	Proteomic analysis of 1 $\alpha$ ,25-Dihydroxyvitamin D3 action on human colon cancer cells reveals a link to splicing regulation. <i>Journal of Proteomics</i> , 2011, 75, 384-397.	1.2	37
1807	Proteomic analysis of a rat pancreatic stellate cell line using liquid chromatography tandem mass spectrometry (LC-MS/MS). <i>Journal of Proteomics</i> , 2011, 75, 708-717.	1.2	31
1808	Novel estrogen-related genes and potential biomarkers of ovarian endometriosis identified by differential expression analysis. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2011, 125, 231-242.	1.2	37
1809	Elevated Copper Remodels Hepatic RNA Processing Machinery in the Mouse Model of Wilson's Disease. <i>Journal of Molecular Biology</i> , 2011, 406, 44-58.	2.0	32
1810	The transcriptional coactivator TAZ regulates mesenchymal differentiation in malignant glioma. <i>Genes and Development</i> , 2011, 25, 2594-2609.	2.7	326
1811	Genome-wide Association: From Confounded to Confident. <i>Neuroscientist</i> , 2011, 17, 174-184.	2.6	4
1812	A search for factors specifying tonotopy implicates DNER in hair-cell development in the chick's cochlea. <i>Developmental Biology</i> , 2011, 354, 221-231.	0.9	35
1813	Genomic and transcriptomic analyses distinguish classic Rett and Rett-like syndrome and reveals shared altered pathways. <i>Genomics</i> , 2011, 97, 19-28.	1.3	28
1814	Effects of genome architecture and epigenetic factors on susceptibility of promoter CpG islands to aberrant DNA methylation induction. <i>Genomics</i> , 2011, 98, 182-188.	1.3	14

#	ARTICLE	IF	CITATIONS
1815	Mouse phenotyping. <i>Methods</i> , 2011, 53, 120-135.	1.9	128
1816	Testosterone response of hepatic gene expression in female mice having acquired testosterone-unresponsive immunity to <i>Plasmodium chabaudi</i> malaria. <i>Steroids</i> , 2011, 76, 1204-1212.	0.8	15
1817	Differential expression of porcine sperm microRNAs and their association with sperm morphology and motility. <i>Theriogenology</i> , 2011, 76, 1532-1539.	0.9	95
1818	Gene expression analysis of HUVEC in response to TF-binding. <i>Thrombosis Research</i> , 2011, 127, 259-263.	0.8	7
1819	Gene expression profiling reveals multiple differences in platelets from patients with stable angina or non-ST elevation acute coronary syndrome. <i>Thrombosis Research</i> , 2011, 128, 161-168.	0.8	27
1820	Preservation of hepatocellular functionality in cultures of primary rat hepatocytes upon exposure to 4-Me2N-BAVAH, a hydroxamate-based HDAC-inhibitor. <i>Toxicology in Vitro</i> , 2011, 25, 100-109.	1.1	2
1821	Comparative transcriptome analysis reveals a fetal origin for mesenchymal stem cells and novel fetal surface antigens for noninvasive prenatal diagnosis. <i>Taiwanese Journal of Obstetrics and Gynecology</i> , 2011, 50, 447-457.	0.5	14
1822	Genome-wide association study of blood pressure response to methylphenidate treatment of attention-deficit/hyperactivity disorder. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2011, 35, 466-472.	2.5	24
1823	Neurotrophic signaling molecules associated with cholinergic damage in young and aged rats: Environmental enrichment as potential therapeutic agent. <i>Neurobiology of Aging</i> , 2011, 32, 470-485.	1.5	30
1824	Multiple Recurrent De Novo CNVs, Including Duplications of the 7q11.23 Williams Syndrome Region, Are Strongly Associated with Autism. <i>Neuron</i> , 2011, 70, 863-885.	3.8	1,146
1825	Importance of genetic background for risk of relapse shown in altered prefrontal cortex gene expression during abstinence following chronic alcohol intoxication. <i>Neuroscience</i> , 2011, 173, 57-75.	1.1	26
1826	Regulation of cytoskeleton machinery, neurogenesis and energy metabolism pathways in a rat gene-environment model of depression revealed by proteomic analysis. <i>Neuroscience</i> , 2011, 176, 349-380.	1.1	42
1827	MicroRNA dysregulation following spinal cord contusion: implications for neural plasticity and repair. <i>Neuroscience</i> , 2011, 186, 146-160.	1.1	128
1828	Nitric oxide metabolism controlled by formaldehyde dehydrogenase (fdh, homolog of mammalian) Tj ETQq1 1 0.784314 rgBT /Overlook Chemistry, 2011, 24, 17-24.	1.2	23
1829	Polymicrobial periodontal pathogen transcriptomes in calvarial bone and soft tissue. <i>Molecular Oral Microbiology</i> , 2011, 26, 303-320.	1.3	11
1830	During hormone depletion or tamoxifen treatment of breast cancer cells the estrogen receptor apoprotein supports cell cycling through the retinoic acid receptor $\pm 1$ apoprotein. <i>Breast Cancer Research</i> , 2011, 13, R18.	2.2	22
1831	Transcriptome analysis of embryonic mammary cells reveals insights into mammary lineage establishment. <i>Breast Cancer Research</i> , 2011, 13, R79.	2.2	46
1832	Developmental influence of the cellular prion protein on the gene expression profile in mouse hippocampus. <i>Physiological Genomics</i> , 2011, 43, 711-725.	1.0	20

#	ARTICLE	IF	CITATIONS
1833	Software and Tools for Microarray Data Analysis. <i>Methods in Molecular Biology</i> , 2011, 784, 41-53.	0.4	14
1834	Development of a Neural Teratogenicity Test Based on Human Embryonic Stem Cells: Response to Retinoic Acid Exposure. <i>Toxicological Sciences</i> , 2011, 124, 370-377.	1.4	58
1835	System Level Changes in Gene Expression in Maturing Bladder Mucosa. <i>Journal of Urology</i> , 2011, 185, 1952-1958.	0.2	5
1836	Survey of the effect of genetic variations on gene expression in human prefrontal cortex and its application to genetics of psychiatric disorders. <i>Neuroscience Research</i> , 2011, 70, 238-242.	1.0	13
1837	Nortriptyline influences protein pathways involved in carbohydrate metabolism and actin-related processes in a rat geneâ€environment model of depression. <i>European Neuropsychopharmacology</i> , 2011, 21, 545-562.	0.3	21
1838	CD98 expression modulates intestinal homeostasis, inflammation, and colitis-associated cancer in mice. <i>Journal of Clinical Investigation</i> , 2011, 121, 1733-1747.	3.9	102
1839	Gene Expression and miR Profiles of Human Corneal Fibroblasts in Response to Dexamethasone. , 2011, 52, 7282.		21
1840	Genetic Risk Factors: Their Function and Comorbidities in Alzheimer's Disease. <i>International Journal of Alzheimer's Disease</i> , 2011, 2011, 1-2.	1.1	1
1841	Identification and functional analysis of novel genes expressed in the Anterior Visceral Endoderm. <i>International Journal of Developmental Biology</i> , 2011, 55, 281-295.	0.3	19
1842	Microarray Analysis of Iris Gene Expression in Mice with Mutations Influencing Pigmentation. , 2011, 52, 237.		14
1843	Analysis of Complement Expression in Light-Induced Retinal Degeneration: Synthesis and Deposition of C3 by Microglia/Macrophages Is Associated with Focal Photoreceptor Degeneration. , 2011, 52, 5347.		84
1844	Gene expression profiling identifies eleven DNA repair genes down-regulated during mouse neural crest cell migration. <i>International Journal of Developmental Biology</i> , 2011, 55, 65-72.	0.3	15
1845	Increased mRNA Levels of <i>TCF7L2</i> and <i>MYC</i> of the Wnt Pathway in Tg-ArcSwe Mice and Alzheimer's Disease Brain. <i>International Journal of Alzheimer's Disease</i> , 2011, 2011, 1-7.	1.1	15
1846	Differential Gene Expression Analysis of Placentas with Increased Vascular Resistance and Pre-Eclampsia Using Whole-Genome Microarrays. <i>Journal of Pregnancy</i> , 2011, 2011, 1-12.	1.1	48
1847	GenSensor Suite: A Web-Based Tool for the Analysis of Gene and Protein Interactions, Pathways, and Regulation. <i>Advances in Bioinformatics</i> , 2011, 2011, 1-7.	5.7	6
1848	Reproducible Isolation of Lymph Node Stromal Cells Reveals Site-Dependent Differences in Fibroblastic Reticular Cells. <i>Frontiers in Immunology</i> , 2011, 2, 35.	2.2	214
1849	On Acute Gene Expression Changes after Ventral Root Replantation. <i>Frontiers in Neurology</i> , 2011, 1, 159.	1.1	13
1850	Exploiting statistical methodologies and controlled vocabularies for prioritized functional analysis of genomic experiments: the StRAnGER web application. <i>Frontiers in Neuroscience</i> , 2011, 5, 8.	1.4	30

#	ARTICLE	IF	CITATIONS
1851	Transcriptomic Analysis in a Drosophila Model Identifies Previously Implicated and Novel Pathways in the Therapeutic Mechanism in Neuropsychiatric Disorders. <i>Frontiers in Neuroscience</i> , 2011, 5, 161.	1.4	6
1852	Cortical gene expression in spinal cord injury and repair: insight into the functional complexity of the neural regeneration program. <i>Frontiers in Molecular Neuroscience</i> , 2011, 4, 26.	1.4	17
1853	Cranberry Proanthocyanidins Mediate Growth Arrest of Lung Cancer Cells through Modulation of Gene Expression and Rapid Induction of Apoptosis. <i>Molecules</i> , 2011, 16, 2375-2390.	1.7	38
1854	Molecular Characterization of Transcriptome-wide Interactions between Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus and Porcine Alveolar Macrophages in vivo. <i>International Journal of Biological Sciences</i> , 2011, 7, 947-959.	2.6	65
1855	A Network-Based Approach to Prioritize Results from Genome-Wide Association Studies. <i>PLoS ONE</i> , 2011, 6, e24220.	1.1	64
1856	Genome-Wide and Phase-Specific DNA-Binding Rhythms of BMAL1 Control Circadian Output Functions in Mouse Liver. <i>PLoS Biology</i> , 2011, 9, e1000595.	2.6	395
1857	Genome-Wide Polymorphism and Comparative Analyses in the White-Tailed Deer ( <i>Odocoileus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502	1.1	41
1858	MicroRNAs MiR-17, MiR-20a, and MiR-106b Act in Concert to Modulate E2F Activity on Cell Cycle Arrest during Neuronal Lineage Differentiation of USSC. <i>PLoS ONE</i> , 2011, 6, e16138.	1.1	114
1859	Autism and Increased Paternal Age Related Changes in Global Levels of Gene Expression Regulation. <i>PLoS ONE</i> , 2011, 6, e16715.	1.1	91
1860	Changes in Whole Blood Gene Expression in Obese Subjects with Type 2 Diabetes Following Bariatric Surgery: a Pilot Study. <i>PLoS ONE</i> , 2011, 6, e16729.	1.1	70
1861	A Computational Method for Prediction of Excretory Proteins and Application to Identification of Gastric Cancer Markers in Urine. <i>PLoS ONE</i> , 2011, 6, e16875.	1.1	32
1862	Distinct Early Molecular Responses to Mutations Causing vLINCL and JNCL Presage ATP Synthase Subunit C Accumulation in Cerebellar Cells. <i>PLoS ONE</i> , 2011, 6, e17118.	1.1	53
1863	Identification of ER Proteins Involved in the Functional Organisation of the Early Secretory Pathway in Drosophila Cells by a Targeted RNAi Screen. <i>PLoS ONE</i> , 2011, 6, e17173.	1.1	34
1864	Genes and Gene Ontologies Common to Airflow Obstruction and Emphysema in the Lungs of Patients with COPD. <i>PLoS ONE</i> , 2011, 6, e17442.	1.1	26
1865	Identification and Replication of Loci Involved in Camptothecin-Induced Cytotoxicity Using CEPH Pedigrees. <i>PLoS ONE</i> , 2011, 6, e17561.	1.1	14
1866	GOBO: Gene Expression-Based Outcome for Breast Cancer Online. <i>PLoS ONE</i> , 2011, 6, e17911.	1.1	361
1867	Identification of a Gene Regulatory Network Necessary for the Initiation of Oligodendrocyte Differentiation. <i>PLoS ONE</i> , 2011, 6, e18088.	1.1	88
1868	Relationship between Gene Body DNA Methylation and Intragenic H3K9me3 and H3K36me3 Chromatin Marks. <i>PLoS ONE</i> , 2011, 6, e18844.	1.1	131



#	ARTICLE	IF	CITATIONS
1869	Dose-Dependent Onset of Regenerative Program in Neutron Irradiated Mouse Skin. PLoS ONE, 2011, 6, e19242.	1.1	13
1870	A Customized Pigmentation SNP Array Identifies a Novel SNP Associated with Melanoma Predisposition in the SLC45A2 Gene. PLoS ONE, 2011, 6, e19271.	1.1	18
1871	Platelets Alter Gene Expression Profile in Human Brain Endothelial Cells in an In Vitro Model of Cerebral Malaria. PLoS ONE, 2011, 6, e19651.	1.1	32
1872	GATA3 Expression Is Decreased in Psoriasis and during Epidermal Regeneration; Induction by Narrow-Band UVB and IL-4. PLoS ONE, 2011, 6, e19806.	1.1	44
1873	A High-Throughput Platform for Lentiviral Overexpression Screening of the Human ORFeome. PLoS ONE, 2011, 6, e20057.	1.1	43
1874	Increased Expression of the Dyslexia Candidate Gene DCDC2 Affects Length and Signaling of Primary Cilia in Neurons. PLoS ONE, 2011, 6, e20580.	1.1	113
1875	A Systems Level, Functional Genomics Analysis of Chronic Epilepsy. PLoS ONE, 2011, 6, e20763.	1.1	67
1876	Proteomic Analysis of Polypeptides Captured from Blood during Extracorporeal Albumin Dialysis in Patients with Cholestasis and Resistant Pruritus. PLoS ONE, 2011, 6, e21850.	1.1	14
1877	Interplay between SIN3A and STAT3 Mediates Chromatin Conformational Changes and GFAP Expression during Cellular Differentiation. PLoS ONE, 2011, 6, e22018.	1.1	48
1878	Quantitative Proteomics Identify Novel miR-155 Target Proteins. PLoS ONE, 2011, 6, e22146.	1.1	28
1879	Voluntary Wheel Running Reverses Age-Induced Changes in Hippocampal Gene Expression. PLoS ONE, 2011, 6, e22654.	1.1	61
1880	Genomic Analysis of Parent-of-Origin Allelic Expression in Arabidopsis thaliana Seeds. PLoS ONE, 2011, 6, e23687.	1.1	178
1881	Inactivation of a Single Copy of Crebbp Selectively Alters Pre-mRNA Processing in Mouse Hematopoietic Stem Cells. PLoS ONE, 2011, 6, e24153.	1.1	7
1882	Proteomic Interrogation of Human Chromatin. PLoS ONE, 2011, 6, e24747.	1.1	35
1883	Necdin, a Negative Growth Regulator, Is a Novel STAT3 Target Gene Down-Regulated in Human Cancer. PLoS ONE, 2011, 6, e24923.	1.1	16
1884	High-Throughput Analysis of Promoter Occupancy Reveals New Targets for Arx, a Gene Mutated in Mental Retardation and Interneuronopathies. PLoS ONE, 2011, 6, e25181.	1.1	36
1885	attract: A Method for Identifying Core Pathways That Define Cellular Phenotypes. PLoS ONE, 2011, 6, e25445.	1.1	37
1886	HIF-1 and SKN-1 Coordinate the Transcriptional Response to Hydrogen Sulfide in Caenorhabditis elegans. PLoS ONE, 2011, 6, e25476.	1.1	55

#	ARTICLE	IF	CITATIONS
1887	An Integrated Transcriptomic and Meta-Analysis of Hepatoma Cells Reveals Factors That Influence Susceptibility to HCV Infection. PLoS ONE, 2011, 6, e25584.	1.1	18
1888	RNA Sequencing Reveals Differential Expression of Mitochondrial and Oxidation Reduction Genes in the Long-Lived Naked Mole-Rat When Compared to Mice. PLoS ONE, 2011, 6, e26729.	1.1	91
1889	Gene Expression Profile Change and Associated Physiological and Pathological Effects in Mouse Liver Induced by Fasting and Refeeding. PLoS ONE, 2011, 6, e27553.	1.1	49
1890	Identification of Prognostic Genes for Recurrent Risk Prediction in Triple Negative Breast Cancer Patients in Taiwan. PLoS ONE, 2011, 6, e28222.	1.1	25
1891	Gene Expression Profiling of Embryonic Human Neural Stem Cells and Dopaminergic Neurons from Adult Human Substantia Nigra. PLoS ONE, 2011, 6, e28420.	1.1	30
1892	Single Cell Analysis Facilitates Staging of Blimp1-Dependent Primordial Germ Cells Derived from Mouse Embryonic Stem Cells. PLoS ONE, 2011, 6, e28960.	1.1	26
1893	Searching for a system: The quest for ovarian cancer biomarkers. Cancer Biomarkers, 2011, 8, 223-230.	0.8	8
1894	Microarray Analysis for <i>Saccharomyces cerevisiae</i> . Journal of Visualized Experiments, 2011, , .	0.2	3
1895	Proteomic Identification of Overexpressed Adenomatous Polyposis Coli and Cyclin B3 During Endoderm Differentiation From Human Embryonic Stem Cells. Pancreas, 2011, 40, 271-280.	0.5	3
1896	Analysis of the Human Pancreatic Stellate Cell Secreted Proteome. Pancreas, 2011, 40, 557-566.	0.5	83
1897	Upregulated Signaling Pathways in Ruptured Human Saccular Intracranial Aneurysm Wall: An Emerging Regulative Role of Toll-Like Receptor Signaling and Nuclear Factor- $\kappa$ B, Hypoxia-Inducible Factor-1A, and ETS Transcription Factors. Neurosurgery, 2011, 68, 1667-1676.	0.6	111
1898	CREB-mediated alterations in the amygdala transcriptome: coordinated regulation of immune response genes following cocaine. International Journal of Neuropsychopharmacology, 2011, 14, 1111-1126.	1.0	6
1899	Human Neurotrophin Receptor p75NTR Defines Differentiation-Oriented Skeletal Muscle Precursor Cells: Implications for Muscle Regeneration. Journal of Neuropathology and Experimental Neurology, 2011, 70, 133-142.	0.9	26
1900	C-terminal domain of MEIS1 converts PKNOX1 (PREP1) into a HOXA9-collaborating oncoprotein. Blood, 2011, 118, 4682-4689.	0.6	9
1901	Aberrant DNA hypermethylation signature in acute myeloid leukemia directed by EVI1. Blood, 2011, 117, 234-241.	0.6	94
1902	Genomic profiling combined with gene expression profiling in primary central nervous system lymphoma. Blood, 2011, 117, 1291-1300.	0.6	94
1903	Impact of alkylphospholipids on the gene expression profile of HaCaT cells. Pharmacogenetics and Genomics, 2011, 21, 375-387.	0.7	6
1904	Classical Hodgkin's lymphoma shows epigenetic features of abortive plasma cell differentiation. Haematologica, 2011, 96, 863-870.	1.7	20

#	ARTICLE	IF	CITATIONS
1905	A meta-analysis of single base-pair substitutions in translational termination codons ('nonstop') Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74	1.4	34
1907	Caecal transcriptome analysis of colonized and non-colonized chickens within two genetic lines that differ in caecal colonization by <i>Campylobacter jejuni</i> . <i>Animal Genetics</i> , 2011, 42, 491-500.	0.6	26
1908	Transcriptional profiling during foetal skeletal muscle development of Piau and Yorkshire-Landrace cross-bred pigs. <i>Animal Genetics</i> , 2011, 42, 600-612.	0.6	21
1909	Genome-wide analysis of brain transcriptional changes in honey bee ( <i>Apis mellifera</i> L.) queens exposed to carbon dioxide and physical manipulation. <i>Insect Molecular Biology</i> , 2011, 20, 387-398.	1.0	23
1910	Gene expression profiling in male genital lichen sclerosis. <i>International Journal of Experimental Pathology</i> , 2011, 92, 320-325.	0.6	37
1911	Functional genomics of the evolution of increased resistance to parasitism in <i>Drosophila</i> . <i>Molecular Ecology</i> , 2011, 20, 932-949.	2.0	32
1912	The effects of mitochondrial genotype on hypoxic survival and gene expression in a hybrid population of the killifish, <i>Fundulus heteroclitus</i> . <i>Molecular Ecology</i> , 2011, 20, 4503-4520.	2.0	27
1913	The Wnt/beta-catenin pathway is activated during advanced arterial aging in humans. <i>Aging Cell</i> , 2011, 10, 220-232.	3.0	109
1914	Microarray analysis of nemorosone-induced cytotoxic effects on pancreatic cancer cells reveals activation of the unfolded protein response (UPR). <i>British Journal of Pharmacology</i> , 2011, 162, 1045-1059.	2.7	31
1915	Molecular Profiles of Drinking Alcohol to Intoxication in C57BL/6J Mice. <i>Alcoholism: Clinical and Experimental Research</i> , 2011, 35, 659-670.	1.4	106
1916	Up-Regulation of MicroRNAs in Brain of Human Alcoholics. <i>Alcoholism: Clinical and Experimental Research</i> , 2011, 35, 1928-1937.	1.4	174
1917	Effects of Levosimendan on Cardiac Gene Expression Profile and Post-Infarct Cardiac Remodelling in Diabetic Goto-Kakizaki Rats. <i>Basic and Clinical Pharmacology and Toxicology</i> , 2011, 109, 387-397.	1.2	14
1918	Transcriptional profiling of osseointegration in humans. <i>Clinical Oral Implants Research</i> , 2011, 22, 373-381.	1.9	85
1919	Cartilage oligomeric matrix protein (COMP) forms part of the connective tissue of normal human hair follicles. <i>Experimental Dermatology</i> , 2011, 20, 361-366.	1.4	15
1920	MicroRNA and gene expression analysis of melatonin-exposed human breast cancer cell lines indicating involvement of the anticancer effect. <i>Journal of Pineal Research</i> , 2011, 51, 345-352.	3.4	89
1921	Recessive LAMC3 mutations cause malformations of occipital cortical development. <i>Nature Genetics</i> , 2011, 43, 590-594.	9.4	102
1922	Blood Gene Expression Reveal Pathway Differences Between Diet-Sensitive and Resistant Obese Subjects Prior to Caloric Restriction. <i>Obesity</i> , 2011, 19, 457-463.	1.5	23
1923	Integration of cap analysis of gene expression and chromatin immunoprecipitation analysis on array reveals genome-wide androgen receptor signaling in prostate cancer cells. <i>Oncogene</i> , 2011, 30, 619-630.	2.6	99

#	ARTICLE	IF	CITATIONS
1924	Efficient in vivo microRNA targeting of liver metastasis. <i>Oncogene</i> , 2011, 30, 1481-1488.	2.6	101
1925	Transforming growth factor- $\beta^2$ decreases the cancer-initiating cell population within diffuse-type gastric carcinoma cells. <i>Oncogene</i> , 2011, 30, 1693-1705.	2.6	77
1926	Genotoxic exposure: novel cause of selection for a functional $\beta^N$ -p53 isoform. <i>Oncogene</i> , 2011, 30, 1764-1772.	2.6	9
1927	Genome-wide screen reveals WNT11, a non-canonical WNT gene, as a direct target of ETS transcription factor ERG. <i>Oncogene</i> , 2011, 30, 2044-2056.	2.6	35
1928	Prdm14 initiates lymphoblastic leukemia after expanding a population of cells resembling common lymphoid progenitors. <i>Oncogene</i> , 2011, 30, 2859-2873.	2.6	52
1929	Prostate cancer gene expression signature of patients with high body mass index. <i>Prostate Cancer and Prostatic Diseases</i> , 2011, 14, 22-29.	2.0	32
1930	The unfolded protein response transducer IRE1 $\beta$ prevents ER stress-induced hepatic steatosis. <i>EMBO Journal</i> , 2011, 30, 1357-1375.	3.5	302
1931	Extensive chromatin remodelling and establishment of transcription factor "hotspots" during early adipogenesis. <i>EMBO Journal</i> , 2011, 30, 1459-1472.	3.5	300
1932	KDM5B regulates embryonic stem cell self-renewal and represses cryptic intragenic transcription. <i>EMBO Journal</i> , 2011, 30, 1473-1484.	3.5	144
1933	Human gene expression profiles of susceptibility and resistance in tuberculosis. <i>Genes and Immunity</i> , 2011, 12, 15-22.	2.2	288
1934	Characterization of the macrophage transcriptome in glomerulonephritis-susceptible and -resistant rat strains. <i>Genes and Immunity</i> , 2011, 12, 78-89.	2.2	11
1935	Therapeutic hypothermia alters microRNA responses to traumatic brain injury in rats. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2011, 31, 1897-1907.	2.4	89
1936	Somatic coding mutations in human induced pluripotent stem cells. <i>Nature</i> , 2011, 471, 63-67.	18.7	1,147
1937	$\beta^N$ p63 is an ectodermal gatekeeper of epidermal morphogenesis. <i>Cell Death and Differentiation</i> , 2011, 18, 887-896.	5.0	119
1938	Mutant p53R175H upregulates Twist1 expression and promotes epithelial "mesenchymal transition in immortalized prostate cells. <i>Cell Death and Differentiation</i> , 2011, 18, 271-281.	5.0	136
1939	Arsenic- and cadmium-induced toxicogenomic response in mouse embryos undergoing neurulation. <i>Toxicology and Applied Pharmacology</i> , 2011, 250, 117-129.	1.3	45
1940	Non-additive hepatic gene expression elicited by 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD) and 2,2',4,4',5,5'-hexachlorobiphenyl (PCB153) co-treatment in C57BL/6 mice. <i>Toxicology and Applied Pharmacology</i> , 2011, 256, 154-167.	1.3	23
1941	The effect of four non-genotoxic carcinogens and four non-carcinogens on NRK-52E cells using a transcriptomics approach. <i>Toxicology</i> , 2011, 290, 110.	2.0	2

#	ARTICLE	IF	CITATIONS
1942	Transcriptional responses of host peripheral blood cells to tuberculosis infection. <i>Tuberculosis</i> , 2011, 91, 390-399.	0.8	64
1943	Candidate genes for physical performance in the horse. <i>Veterinary Journal</i> , 2011, 190, 39-48.	0.6	35
1944	General and family-specific gene expression responses to viral hemorrhagic septicaemia virus infection in rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>Molecular Immunology</i> , 2011, 48, 1046-1058.	1.0	18
1945	Radiation-induced epigenetic alterations after low and high LET irradiations. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2011, 707, 24-33.	0.4	100
1946	Dynamics of the transcriptome response of cultured human embryonic stem cells to ionizing radiation exposure. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2011, 709-710, 40-48.	0.4	27
1947	Inhibition of Gsk3 $\beta$ in cartilage induces osteoarthritic features through activation of the canonical Wnt signaling pathway. <i>Osteoarthritis and Cartilage</i> , 2011, 19, 1363-1372.	0.6	58
1948	TGF $\beta$ 1 and Wnt-3a interact to induce unique gene expression profiles in murine embryonic palate mesenchymal cells. <i>Reproductive Toxicology</i> , 2011, 31, 128-133.	1.3	1
1949	Exposure of human fetal penile cells to different PCB mixtures: transcriptome analysis points to diverse modes of interference on external genitalia programming. <i>Reproductive Toxicology</i> , 2011, 32, 1-14.	1.3	13
1950	Comparison of MeHg-induced toxicogenomic responses across in vivo and in vitro models used in developmental toxicology. <i>Reproductive Toxicology</i> , 2011, 32, 180-188.	1.3	35
1951	Genome-wide DNA methylation patterns in IVF-conceived mice and their progeny: A putative model for ART-conceived humans. <i>Reproductive Toxicology</i> , 2011, 32, 98-105.	1.3	20
1952	Patterns of pain: Meta-analysis of microarray studies of pain. <i>Pain</i> , 2011, 152, 1888-1898.	2.0	176
1953	Effect of postharvest water deficit stress on gene expression in heads of broccoli ( <i>Brassica oleracea</i> ) Tj ETQq1 1 0.784314 rgBT /Overbo	2.9	29
1954	Mechanisms of epileptogenesis and potential treatment targets. <i>Lancet Neurology</i> , The, 2011, 10, 173-186.	4.9	490
1955	Transcriptional profiling of peripheral lymphoid tissue reveals genes and networks linked to SSBP/1 scrapie pathology in sheep. <i>Veterinary Microbiology</i> , 2011, 153, 218-228.	0.8	9
1956	Transcriptional profiling of <i>C. elegans</i> DAF-19 uncovers a ciliary base-associated protein and a CDK/CCRK/LF2p-related kinase required for intraflagellar transport. <i>Developmental Biology</i> , 2011, 357, 235-247.	0.9	65
1957	Identification of novel <i>Hoxa1</i> downstream targets regulating hindbrain, neural crest and inner ear development. <i>Developmental Biology</i> , 2011, 357, 295-304.	0.9	51
1958	Gene expression profiling at early organogenesis reveals both common and diverse mechanisms in foregut patterning. <i>Developmental Biology</i> , 2011, 359, 163-175.	0.9	52
1959	Trachealess ( <i>Trh</i> ) regulates all tracheal genes during <i>Drosophila</i> embryogenesis. <i>Developmental Biology</i> , 2011, 360, 160-172.	0.9	44

#	ARTICLE	IF	CITATIONS
1960	Wnt signalling mediates the cross-talk between bone marrow derived pre-adipocytic and pre-osteoblastic cell populations. <i>Experimental Cell Research</i> , 2011, 317, 745-756.	1.2	101
1961	Joint analysis of transcriptional and post-transcriptional brain tumor data: searching for emergent properties of cellular systems. <i>BMC Bioinformatics</i> , 2011, 12, 86.	1.2	8
1962	Limited redundancy in genes regulated by Cyclin T2 and Cyclin T1. <i>BMC Research Notes</i> , 2011, 4, 260.	0.6	16
1963	Deregulation of the ubiquitin-proteasome system is the predominant molecular pathology in OPMD animal models and patients. <i>Skeletal Muscle</i> , 2011, 1, 15.	1.9	40
1964	Gene expression evidence for off-target effects caused by RNA interference-mediated gene silencing of Ubiquitin-63E in the cattle tick <i>Rhipicephalus microplus</i> . <i>International Journal for Parasitology</i> , 2011, 41, 1001-1014.	1.3	33
1965	Molecular phenotype of monocytes at the maternal-fetal interface. <i>American Journal of Obstetrics and Gynecology</i> , 2011, 205, 265.e1-265.e8.	0.7	22
1966	A global transcriptomic view of the multifaceted role of glutathione peroxidase-1 in cerebral ischemic-reperfusion injury. <i>Free Radical Biology and Medicine</i> , 2011, 50, 736-748.	1.3	20
1967	Differential gene expression in normal and transformed human mammary epithelial cells in response to oxidative stress. <i>Free Radical Biology and Medicine</i> , 2011, 50, 1565-1574.	1.3	14
1968	Identification of differentially expressed genes in the heart precursor cells of the chick embryo. <i>Gene Expression Patterns</i> , 2011, 11, 437-447.	0.3	8
1969	The induction of epigenetic regulation of PROS1 gene in lung fibroblasts by gold nanoparticles and implications for potential lung injury. <i>Biomaterials</i> , 2011, 32, 7609-7615.	5.7	81
1970	High-frequency stimulation of the ventrolateral thalamus regulates gene expression in hippocampus, motor cortex and caudate-putamen. <i>Brain Research</i> , 2011, 1391, 1-13.	1.1	16
1971	Transcriptional profiles induced by the Aryl Hydrocarbon Receptor agonists 2,3,7,8-tetrachlorodibenzo-p-dioxin, 2,3,7,8-tetrachlorodibenzofuran and 2,3,4,7,8-pentachlorodibenzofuran in primary rat hepatocytes. <i>Chemosphere</i> , 2011, 85, 232-238.	4.2	11
1972	Large-Scale Discovery of ERK2 Substrates Identifies ERK-Mediated Transcriptional Regulation by ETV3. <i>Science Signaling</i> , 2011, 4, rs11.	1.6	125
1973	A METHODOLOGY BASED ON MOLECULAR INTERACTIONS AND PATHWAYS TO FIND CANDIDATE GENES ASSOCIATED TO DISEASES: ITS APPLICATION TO SCHIZOPHRENIA AND ALZHEIMER'S DISEASE. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 541-557.	0.3	5
1974	Breast Cancer Methylomes Establish an Epigenomic Foundation for Metastasis. <i>Science Translational Medicine</i> , 2011, 3, 75ra25.	5.8	242
1975	Regulation of male germ cell cycle arrest and differentiation by DND1 is modulated by genetic background. <i>Development (Cambridge)</i> , 2011, 138, 23-32.	1.2	89
1976	A systems biological view of intracellular pathogens. <i>Immunological Reviews</i> , 2011, 240, 117-128.	2.8	23
1977	A Qualitative and Quantitative Proteomic Study of Human Microdialysate and the Cutaneous Response to Injury. <i>AAPS Journal</i> , 2011, 13, 309-317.	2.2	19

#	ARTICLE	IF	CITATIONS
1978	Mutations in PRDM5 in Brittle Cornea Syndrome Identify a Pathway Regulating Extracellular Matrix Development and Maintenance. <i>American Journal of Human Genetics</i> , 2011, 88, 767-777.	2.6	106
1979	Recent Admixture in an Indian Population of African Ancestry. <i>American Journal of Human Genetics</i> , 2011, 89, 111-120.	2.6	32
1980	<i>Helicobacter bilis</i> Colonization Enhances Susceptibility to Typhlocolitis Following an Inflammatory Trigger. <i>Digestive Diseases and Sciences</i> , 2011, 56, 2838-2848.	1.1	26
1981	Enhanced serine production by bone metastatic breast cancer cells stimulates osteoclastogenesis. <i>Breast Cancer Research and Treatment</i> , 2011, 125, 421-430.	1.1	222
1982	Cerebral gene expression in response to single or combined gestational exposure to methylmercury and selenium through the maternal diet. <i>Cell Biology and Toxicology</i> , 2011, 27, 181-197.	2.4	14
1983	MYBPC1 Computational Phosphoprotein Network Construction and Analysis between Frontal Cortex of HIV encephalitis (HIVE) and HIVE-Control Patients. <i>Cellular and Molecular Neurobiology</i> , 2011, 31, 233-241.	1.7	22
1984	A systems view of epithelial-mesenchymal transition signaling states. <i>Clinical and Experimental Metastasis</i> , 2011, 28, 137-155.	1.7	190
1985	OLIG2 is differentially expressed in pediatric astrocytic and in ependymal neoplasms. <i>Journal of Neuro-Oncology</i> , 2011, 104, 423-438.	1.4	63
1986	Generation of a large-scale genomic resource for functional and comparative genomics in <i>Liriodendron tulipifera</i> L.. <i>Tree Genetics and Genomes</i> , 2011, 7, 941-954.	0.6	13
1987	Engineering of red cells of <i>Arabidopsis thaliana</i> and comparative genome-wide gene expression analysis of red cells versus wild-type cells. <i>Planta</i> , 2011, 233, 787-805.	1.6	40
1988	Transcriptomic analysis of cell-free fetal RNA suggests a specific molecular phenotype in trisomy 18. <i>Human Genetics</i> , 2011, 129, 295-305.	1.8	44
1989	Genetic analysis of Down syndrome-associated heart defects in mice. <i>Human Genetics</i> , 2011, 130, 623-632.	1.8	47
1990	Identification of the Target Proteins of Rosiglitazone in 3T3-L1 Adipocytes through Proteomic Analysis of Cytosolic and Secreted Proteins. <i>Molecules and Cells</i> , 2011, 31, 239-246.	1.0	26
1991	cGMP modulates responses to queen mandibular pheromone in worker honey bees. <i>Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology</i> , 2011, 197, 939-948.	0.7	15
1992	Rat neonatal beta cells lack the specialised metabolic phenotype of mature beta cells. <i>Diabetologia</i> , 2011, 54, 594-604.	2.9	111
1993	Antigens in chronic myeloid leukemia: implications for vaccine development. <i>Cancer Immunology, Immunotherapy</i> , 2011, 60, 1655-1668.	2.0	21
1994	Picoplatin overcomes resistance to cell toxicity in small-cell lung cancer cells previously treated with cisplatin and carboplatin. <i>Cancer Chemotherapy and Pharmacology</i> , 2011, 67, 1389-1400.	1.1	40
1995	Overexpression of SUMO perturbs the growth and development of <i>Caenorhabditis elegans</i> . <i>Cellular and Molecular Life Sciences</i> , 2011, 68, 3219-3232.	2.4	15

#	ARTICLE	IF	CITATIONS
1996	A two-dimensional protein fragmentation-proteomic study of neuronal ceroid lipofuscinoses: Identification and characterization of differentially expressed proteins. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2011, 879, 304-316.	1.2	8
1997	Phospho-proteomic analysis of mantle cell lymphoma cells suggests a pro-survival role of B-cell receptor signaling. <i>Cellular Oncology (Dordrecht)</i> , 2011, 34, 141-153.	2.1	65
1998	CREB5 Computational Regulation Network Construction and Analysis Between Frontal Cortex of HIV Encephalitis (HIVE) and HIVE-Control Patients. <i>Cell Biochemistry and Biophysics</i> , 2011, 60, 199-207.	0.9	24
1999	Differential Inductive Signaling of CD90+ Prostate Cancer-Associated Fibroblasts Compared to Normal Tissue Stromal Mesenchyme Cells. <i>Cancer Microenvironment</i> , 2011, 4, 51-59.	3.1	19
2000	The effects of aging vs. $\hat{1}\pm 7$ nAChR subunit deficiency on the mouse brain transcriptome: aging beats the deficiency. <i>Age</i> , 2011, 33, 1-13.	3.0	6
2001	An <i>Arabidopsis thaliana</i> (Ler) inbred line AFDL exhibiting abnormal flower development mainly caused by reduced AP1 expression. <i>Science Bulletin</i> , 2011, 56, 39-47.	1.7	5
2002	TEAD1-dependent expression of the FoxO3a gene in mouse skeletal muscle. <i>BMC Molecular Biology</i> , 2011, 12, 1.	3.0	39
2003	Dengue-2 Structural Proteins Associate with Human Proteins to Produce a Coagulation and Innate Immune Response Biased Interactome. <i>BMC Infectious Diseases</i> , 2011, 11, 34.	1.3	23
2004	Parental ages and levels of DNA methylation in the newborn are correlated. <i>BMC Medical Genetics</i> , 2011, 12, 47.	2.1	86
2005	Expression patterns of microRNAs associated with CML phases and their disease related targets. <i>Molecular Cancer</i> , 2011, 10, 41.	7.9	124
2006	Analysis of EGFR signaling pathway in nasopharyngeal carcinoma cells by quantitative phosphoproteomics. <i>Proteome Science</i> , 2011, 9, 35.	0.7	30
2007	Comparison of human glomerulus proteomic profiles obtained from low quantities of samples by different mass spectrometry with the comprehensive database. <i>Proteome Science</i> , 2011, 9, 47.	0.7	14
2008	Bioinformatic detection of E47, E2F1 and SREBP1 transcription factors as potential regulators of genes associated to acquisition of endometrial receptivity. <i>Reproductive Biology and Endocrinology</i> , 2011, 9, 14.	1.4	51
2009	15 kDa Granulysin versus GM-CSF for monocytes differentiation: analogies and differences at the transcriptome level. <i>Journal of Translational Medicine</i> , 2011, 9, 41.	1.8	11
2010	Role of adhesion molecules and inflammation in Venezuelan equine encephalitis virus infected mouse brain. <i>Virology Journal</i> , 2011, 8, 197.	1.4	31
2011	The biology of lysine acetylation integrates transcriptional programming and metabolism. <i>Nutrition and Metabolism</i> , 2011, 8, 12.	1.3	59
2012	Decreased expression of B cell related genes in leukocytes of women with Parkinson's disease. <i>Molecular Neurodegeneration</i> , 2011, 6, 66.	4.4	23
2013	WebGimm: An integrated web-based platform for cluster analysis, functional analysis, and interactive visualization of results. <i>Source Code for Biology and Medicine</i> , 2011, 6, 3.	1.7	6



#	ARTICLE	IF	CITATIONS
2014	In Silico discovery of transcription factors as potential diagnostic biomarkers of ovarian cancer. BMC Systems Biology, 2011, 5, 144.	3.0	12
2015	Regulation of the yeast metabolic cycle by transcription factors with periodic activities. BMC Systems Biology, 2011, 5, 160.	3.0	14
2016	Identifying cancer biomarkers by network-constrained support vector machines. BMC Systems Biology, 2011, 5, 161.	3.0	76
2017	Regulatory coordination of clustered microRNAs based on microRNA-transcription factor regulatory network. BMC Systems Biology, 2011, 5, 199.	3.0	57
2018	Exploring molecular links between lymph node invasion and cancer prognosis in human breast cancer. BMC Systems Biology, 2011, 5, S4.	3.0	8
2019	Jejunal gene expression patterns correlate with severity of systemic infection in chicken. BMC Proceedings, 2011, 5, S4.	1.8	4
2020	Time course analysis of gene expression identifies multiple genes with differential expression in patients with in-stent restenosis. BMC Medical Genomics, 2011, 4, 20.	0.7	6
2021	Comparative analysis of the human hepatic and adipose tissue transcriptomes during LPS-induced inflammation leads to the identification of differential biological pathways and candidate biomarkers. BMC Medical Genomics, 2011, 4, 71.	0.7	20
2022	Alignment of gene expression profiles from test samples against a reference database: New method for context-specific interpretation of microarray data. BioData Mining, 2011, 4, 5.	2.2	5
2023	Genome-wide mapping of imprinted differentially methylated regions by DNA methylation profiling of human placentas from triploidies. Epigenetics and Chromatin, 2011, 4, 10.	1.8	84
2024	Extensive epigenetic reprogramming in human somatic tissues between fetus and adult. Epigenetics and Chromatin, 2011, 4, 7.	1.8	57
2025	A noise-reduction GWAS analysis implicates altered regulation of neurite outgrowth and guidance in autism. Molecular Autism, 2011, 2, 1.	2.6	191
2026	Transcriptional landscape of bone marrow-derived very small embryonic-like stem cells during hypoxia. Respiratory Research, 2011, 12, 63.	1.4	12
2027	Expression analysis of asthma candidate genes during human and murine lung development. Respiratory Research, 2011, 12, 86.	1.4	55
2028	Pathway-based analysis using reduced gene subsets in genome-wide association studies. BMC Bioinformatics, 2011, 12, 17.	1.2	30
2029	TAFEL: Independent Enrichment Analysis of gene sets. BMC Bioinformatics, 2011, 12, 171.	1.2	1
2030	Identifier mapping performance for integrating transcriptomics and proteomics experimental results. BMC Bioinformatics, 2011, 12, 213.	1.2	73
2031	Discovering biological connections between experimental conditions based on common patterns of differential gene expression. BMC Bioinformatics, 2011, 12, 381.	1.2	21

#	ARTICLE	IF	CITATIONS
2032	Network based transcription factor analysis of regenerating axolotl limbs. BMC Bioinformatics, 2011, 12, 80.	1.2	25
2033	Integrated metabolome and transcriptome analysis of the NCI60 dataset. BMC Bioinformatics, 2011, 12, S36.	1.2	38
2034	Construction and analysis of the protein-protein interaction networks for schizophrenia, bipolar disorder, and major depression. BMC Bioinformatics, 2011, 12, S20.	1.2	46
2035	Genome-wide mapping of Sox6 binding sites in skeletal muscle reveals both direct and indirect regulation of muscle terminal differentiation by Sox6. BMC Developmental Biology, 2011, 11, 59.	2.1	46
2036	Identification of common and cell type specific LXXLL motif EcR cofactors using a bioinformatics refined candidate RNAi screen in Drosophila melanogaster cell lines. BMC Developmental Biology, 2011, 11, 66.	2.1	9
2037	Genome-wide analysis of gene expression during Xenopus tropicalis tadpole tail regeneration. BMC Developmental Biology, 2011, 11, 70.	2.1	74
2038	Sequential analysis of global gene expression profiles in immature and in vitro matured bovine oocytes: potential molecular markers of oocyte maturation. BMC Genomics, 2011, 12, 151.	1.2	70
2039	Comparative transcriptome profiling of amyloid precursor protein family members in the adult cortex. BMC Genomics, 2011, 12, 160.	1.2	39
2040	Differences in TCDD-elicited gene expression profiles in human HepG2, mouse Hepa1c1c7 and rat H4IIE hepatoma cells. BMC Genomics, 2011, 12, 193.	1.2	48
2041	Gene expression patterns in four brain areas associate with quantitative measure of estrous behavior in dairy cows. BMC Genomics, 2011, 12, 200.	1.2	16
2042	Genome-wide survey reveals dynamic widespread tissue-specific changes in DNA methylation during development. BMC Genomics, 2011, 12, 231.	1.2	121
2043	Integration of Genome-Wide Computation DRE Search, AhR ChIP-chip and Gene Expression Analyses of TCDD-Elicited Responses in the Mouse Liver. BMC Genomics, 2011, 12, 365.	1.2	112
2044	Histological and transcriptome-wide level characteristics of fetal myofiber hyperplasia during the second half of gestation in Texel and Ujumqin sheep. BMC Genomics, 2011, 12, 411.	1.2	27
2045	Differential gene expression profiling of human bone marrow-derived mesenchymal stem cells during adipogenic development. BMC Genomics, 2011, 12, 461.	1.2	92
2046	Genome-wide examination of the transcriptional response to ecdysteroids 20-hydroxyecdysone and ponasterone A in Drosophila melanogaster. BMC Genomics, 2011, 12, 475.	1.2	17
2047	Deciphering c-MYC-regulated genes in two distinct tissues. BMC Genomics, 2011, 12, 476.	1.2	16
2048	Meta-analysis and genome-wide interpretation of genetic susceptibility to drug addiction. BMC Genomics, 2011, 12, 508.	1.2	34
2049	Sex-dimorphism in Cardiac Nutrigenomics: effect of Trans fat and/or Monosodium Glutamate consumption. BMC Genomics, 2011, 12, 555.	1.2	14

#	ARTICLE	IF	CITATIONS
2050	Global assessment of genomic variation in cattle by genome resequencing and high-throughput genotyping. <i>BMC Genomics</i> , 2011, 12, 557.	1.2	74
2051	Proteomic analysis of endothelial cold-adaptation. <i>BMC Genomics</i> , 2011, 12, 630.	1.2	19
2052	Differential gene expression in liver and small intestine from lactating rats compared to age-matched virgin controls detects increased mRNA of cholesterol biosynthetic genes. <i>BMC Genomics</i> , 2011, 12, 95.	1.2	22
2053	A robust tool for discriminative analysis and feature selection in paired samples impacts the identification of the genes essential for reprogramming lung tissue to adenocarcinoma. <i>BMC Genomics</i> , 2011, 12, S24.	1.2	18
2054	Transcriptomic profiles of peripheral white blood cells in type II diabetes and racial differences in expression profiles. <i>BMC Genomics</i> , 2011, 12, S12.	1.2	12
2055	Protease-associated cellular networks in malaria parasite <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2011, 12, S9.	1.2	22
2056	Comparison of static immersion and intravenous injection systems for exposure of zebrafish embryos to the natural pathogen <i>Edwardsiella tarda</i> . <i>BMC Immunology</i> , 2011, 12, 58.	0.9	85
2057	<i>Staphylococcus aureus</i> Biofilm and Planktonic cultures differentially impact gene expression, mapk phosphorylation, and cytokine production in human keratinocytes. <i>BMC Microbiology</i> , 2011, 11, 143.	1.3	101
2058	A comparison of the <i>Giardia lamblia</i> trophozoite and cyst transcriptome using microarrays. <i>BMC Microbiology</i> , 2011, 11, 91.	1.3	24
2059	Gain of function mutant p53 but not p53 deletion promotes head and neck cancer progression in response to oncogenic KRAS. <i>Journal of Pathology</i> , 2011, 225, 479-489.	2.1	44
2060	Mass spectrometry-based proteomics of endoscopically collected pancreatic fluid in chronic pancreatitis research. <i>Proteomics - Clinical Applications</i> , 2011, 5, 109-120.	0.8	19
2061	Discovery of biomarker candidates for coronary artery disease from an APOE knock out mouse model using iTRAQ-based multiplex quantitative proteomics. <i>Proteomics</i> , 2011, 11, 2763-2776.	1.3	30
2062	Proteomic analysis of urinary exosomes from patients of early IgA nephropathy and thin basement membrane nephropathy. <i>Proteomics</i> , 2011, 11, 2459-2475.	1.3	211
2063	The Protein Information and Property Explorer 2: Goggle-like exploration of biological proteomic data within one webpage. <i>Proteomics</i> , 2011, 11, 154-158.	1.3	9
2064	Quantitative temporal proteomic analysis of human embryonic stem cell differentiation into oligodendrocyte progenitor cells. <i>Proteomics</i> , 2011, 11, 4007-4020.	1.3	39
2065	Molecular and Functional Characterizations of Gastrula Organizer Cells Derived from Human Embryonic Stem Cells. <i>Stem Cells</i> , 2011, 29, 600-608.	1.4	32
2066	Functional Characterization of Quiescent Keratinocyte Stem Cells and Their Progeny Reveals a Hierarchical Organization in Human Skin Epidermis. <i>Stem Cells</i> , 2011, 29, 1256-1268.	1.4	59
2067	Signaling pathways in early cardiac development. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 191-205.	6.6	15

#	ARTICLE	IF	CITATIONS
2068	Forced activation of Stat5 subjects mammary epithelial cells to DNA damage and preferential induction of the cellular response mechanism during proliferation. <i>Journal of Cellular Physiology</i> , 2011, 226, 616-626.	2.0	11
2069	Gene profiling reveals hydrogen sulphide recruits death signaling via the N-methyl-D-aspartate receptor identifying commonalities with excitotoxicity. <i>Journal of Cellular Physiology</i> , 2011, 226, 1308-1322.	2.0	30
2070	5-fluorouracil drug alters the microRNA expression profiles in MCF-7 breast cancer cells. <i>Journal of Cellular Physiology</i> , 2011, 226, 1868-1878.	2.0	53
2071	Similarities and differences in peripheral blood gene expression signatures of individuals with schizophrenia and their first-degree biological relatives. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2011, 156, 869-887.	1.1	53
2073	Human Î²-defensin 3 affects the activity of pro-inflammatory pathways associated with MyD88 and TRIF. <i>European Journal of Immunology</i> , 2011, 41, 3291-3300.	1.6	122
2074	Activation of interferon signaling pathways in spinal cord astrocytes from an ALS mouse model. <i>Glia</i> , 2011, 59, 946-958.	2.5	82
2075	Prenatal stress diminishes gender differences in behavior and in expression of hippocampal synaptic genes and proteins in rats. <i>Hippocampus</i> , 2011, 21, 1114-1125.	0.9	52
2076	Genomic signature of <i>BRCA1</i> deficiency in sporadic basal-like breast tumors. <i>Genes Chromosomes and Cancer</i> , 2011, 50, 71-81.	1.5	53
2077	Functional implications of microRNAs in acute myeloid leukemia by integrating microRNA and messenger RNA expression profiling. <i>Cancer</i> , 2011, 117, 4696-4706.	2.0	55
2078	Peripheral nerve graft with immunosuppression modifies gene expression in axotomized CNS neurons. <i>Journal of Comparative Neurology</i> , 2011, 519, 3433-3455.	0.9	2
2079	Characterization of copy number stable regions in the human genome. <i>Human Mutation</i> , 2011, 32, 947-955.	1.1	19
2080	Genome-wide DNA methylation analysis of neuroblastic tumors reveals clinically relevant epigenetic events and large-scale epigenomic alterations localized to telomeric regions. <i>International Journal of Cancer</i> , 2011, 128, 2296-2305.	2.3	38
2081	Tumor associated mesenchymal stem cells protects ovarian cancer cells from hyperthermia through CXCL12. <i>International Journal of Cancer</i> , 2011, 128, 715-725.	2.3	96
2082	Gene expression profiling reveals novel biomarkers in nonsmall cell lung cancer. <i>International Journal of Cancer</i> , 2011, 129, 355-364.	2.3	224
2083	Large-scale integration of microarray data reveals genes and pathways common to multiple cancer types. <i>International Journal of Cancer</i> , 2011, 128, 2881-2891.	2.3	33
2084	MED29, a component of the mediator complex, possesses both oncogenic and tumor suppressive characteristics in pancreatic cancer. <i>International Journal of Cancer</i> , 2011, 129, 2553-2565.	2.3	18
2085	Delayed response in the rat frontal lobe transcriptome to perinatal exposure to the flame retardant BDE-47. <i>Journal of Applied Toxicology</i> , 2011, 31, 477-483.	1.4	26
2086	Trans fat diet causes decreased brood size and shortened lifespan in <i>Caenorhabditis elegans</i> delta-6-desaturase mutant <i>fat-3</i> . <i>Journal of Biochemical and Molecular Toxicology</i> , 2011, 25, 269-279.	1.4	12

#	ARTICLE	IF	CITATIONS
2087	MicroRNA identity and abundance in developing swine adipose tissue as determined by solexa sequencing. <i>Journal of Cellular Biochemistry</i> , 2011, 112, 1318-1328.	1.2	128
2088	Rituximab treatment induces the expression of genes involved in healing processes in the rheumatoid arthritis synovium. <i>Arthritis and Rheumatism</i> , 2011, 63, 1246-1254.	6.7	30
2089	Racial differences in gene-specific DNA methylation levels are present at birth. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2011, 91, 728-736.	1.6	131
2090	MicroRNA gene expression signatures in the developing neural tube. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2011, 91, 744-762.	1.6	33
2091	Blood Gene Expression Profiling of Breast Cancer Survivors Experiencing Fibrosis. <i>International Journal of Radiation Oncology Biology Physics</i> , 2011, 79, 875-883.	0.4	12
2092	Shotgun proteomic analysis of microdissected postmortem human pituitary using complementary two-dimensional liquid chromatography coupled with tandem mass spectrometer. <i>Analytica Chimica Acta</i> , 2011, 688, 183-190.	2.6	13
2093	A combination method of chemical with enzyme reactions for identification of membrane proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 397-404.	1.1	7
2094	The influence of surface microroughness and hydrophilicity of titanium on the up-regulation of TGF $\beta$ 2/BMP signalling in osteoblasts.. <i>Biomaterials</i> , 2011, 32, 665-671.	5.7	184
2095	Genetic identification of unique immunological responses in mice infected with virulent and attenuated <i>Francisella tularensis</i> . <i>Microbes and Infection</i> , 2011, 13, 261-275.	1.0	14
2096	Uncovering the global host cell requirements for influenza virus replication via RNAi screening. <i>Microbes and Infection</i> , 2011, 13, 516-525.	1.0	84
2097	Proteomic analysis of formalin-fixed, paraffin-embedded lung neuroendocrine tumor samples from hospital archives. <i>Journal of Proteomics</i> , 2011, 74, 359-370.	1.2	39
2098	Rescue of the mutant CFTR chloride channel by pharmacological correctors and low temperature analyzed by gene expression profiling. <i>American Journal of Physiology - Cell Physiology</i> , 2011, 301, C872-C885.	2.1	79
2099	Airway Epithelial Transcription Factor NK2 Homeobox 1 Inhibits Mucous Cell Metaplasia and Th2 Inflammation. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011, 184, 421-429.	2.5	73
2100	Functional analysis of human whole brain regions based on gene expression. , 2011, , .		2
2101	Quantitative, high-resolution epigenetic profiling of CpG loci identifies associations with cord blood plasma homocysteine and birth weight in humans. <i>Epigenetics</i> , 2011, 6, 86-94.	1.3	123
2102	Phosphatase and tensin homologue/protein kinase B pathway linked to motor neuron survival in human superoxide dismutase 1-related amyotrophic lateral sclerosis. <i>Brain</i> , 2011, 134, 506-517.	3.7	71
2103	Gene ontology analysis of the centrosome proteomes of <i>Drosophila</i> and human. <i>Communicative and Integrative Biology</i> , 2011, 4, 308-311.	0.6	7
2104	Use of Chemical Genomics in Assessment of the UPR. <i>Methods in Enzymology</i> , 2011, 491, 327-341.	0.4	8

#	ARTICLE	IF	CITATIONS
2105	Crosstalk between c-Jun and TAp73 $\pm$ / $\beta$ 2 contributes to the apoptosis $\leftrightarrow$ survival balance. <i>Nucleic Acids Research</i> , 2011, 39, 6069-6085.	6.5	49
2106	Highly accurate and high-resolution function prediction of RNA binding proteins by fold recognition and binding affinity prediction. <i>RNA Biology</i> , 2011, 8, 988-996.	1.5	53
2107	Intestinal Injury and Endotoxemia in Children Undergoing Surgery for Congenital Heart Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011, 184, 1261-1269.	2.5	53
2108	Temporal blastemal cell gene expression analysis in the kidney reveals new Wnt and related signaling pathway genes to be essential for Wilms' tumor onset. <i>Cell Death and Disease</i> , 2011, 2, e224-e224.	2.7	23
2109	Comparison of phenotypic and transcriptomic effects of false-positive genotoxins, true genotoxins and non-genotoxins using HepG2 cells. <i>Mutagenesis</i> , 2011, 26, 593-604.	1.0	46
2110	Insertion Sites in Engrafted Cells Cluster Within a Limited Repertoire of Genomic Areas After Gammaretroviral Vector Gene Therapy. <i>Molecular Therapy</i> , 2011, 19, 2031-2039.	3.7	48
2111	Waves of early transcriptional activation and pluripotency program initiation during human preimplantation development. <i>Development (Cambridge)</i> , 2011, 138, 3699-3709.	1.2	237
2112	FoxO3A promotes metabolic adaptation to hypoxia by antagonizing Myc function. <i>EMBO Journal</i> , 2011, 30, 4554-4570.	3.5	103
2113	Serum Response Factor Utilizes Distinct Promoter- and Enhancer-Based Mechanisms To Regulate Cytoskeletal Gene Expression in Macrophages. <i>Molecular and Cellular Biology</i> , 2011, 31, 861-875.	1.1	56
2114	Skeletal Muscle Gene Expression Profile Is Modified by Dietary Protein Source and Calcium during Energy Restriction. <i>Journal of Nutrigenetics and Nutrigenomics</i> , 2011, 4, 49-62.	1.8	7
2115	Network-Like Impact of MicroRNAs on Neuronal Lineage Differentiation of Unrestricted Somatic Stem Cells from Human Cord Blood. <i>Stem Cells and Development</i> , 2011, 20, 1383-1394.	1.1	20
2116	Reprogramming of Mouse Fibroblasts to an Intermediate State of Differentiation by Chemical Induction. <i>Cellular Reprogramming</i> , 2011, 13, 121-131.	0.5	15
2117	Interval Trees for Detection of Overlapping Genetic Entities. , 2011, , .		1
2118	Experiment Specific Expression Patterns. <i>Journal of Computational Biology</i> , 2011, 18, 1423-1435.	0.8	0
2119	Altered Gene Expression Profiles in the Brain, Kidney, and Lung of One-Month-Old Cloned Pigs. <i>Cellular Reprogramming</i> , 2011, 13, 215-223.	0.5	14
2120	Mesenchymal Stromal Cells from Neonatal Tracheal Aspirates Demonstrate a Pattern of Lung-Specific Gene Expression. <i>Stem Cells and Development</i> , 2011, 20, 1995-2007.	1.1	45
2121	The Reduced Form of Coenzyme Q <sub>10</sub> Decreases the Expression of Lipopolysaccharide-Sensitive Genes in Human THP-1 Cells. <i>Journal of Medicinal Food</i> , 2011, 14, 391-397.	0.8	8
2122	Complement Protein C1q-Mediated Neuroprotection Is Correlated with Regulation of Neuronal Gene and MicroRNA Expression. <i>Journal of Neuroscience</i> , 2011, 31, 3459-3469.	1.7	129

#	ARTICLE	IF	CITATIONS
2123	Induction of Mucin and MUC5AC Expression by the Protease Activity of <i>Aspergillus fumigatus</i> in Airway Epithelial Cells. <i>Journal of Immunology</i> , 2011, 187, 999-1005.	0.4	50
2124	Phosphoinositide 3-Kinase (PI3K(p110 $\alpha$ )) Directly Regulates Key Components of the Z-disc and Cardiac Structure*. <i>Journal of Biological Chemistry</i> , 2011, 286, 30837-30846.	1.6	32
2125	The Gut Mucosal Viral Reservoir in HIV-Infected Patients Is Not the Major Source of Rebound Plasma Viremia following Interruption of Highly Active Antiretroviral Therapy. <i>Journal of Virology</i> , 2011, 85, 4772-4782.	1.5	70
2126	microRNA-Seq reveals cocaine-regulated expression of striatal microRNAs. <i>Rna</i> , 2011, 17, 1529-1543.	1.6	113
2127	Genomewide Analysis of Rat Barrel Cortex Reveals Time- and Layer-Specific mRNA Expression Changes Related to Experience-Dependent Plasticity. <i>Journal of Neuroscience</i> , 2011, 31, 6140-6158.	1.7	40
2128	Transcriptional Profiling of Diabetic Neuropathy in the BKS <i>db/db</i> Mouse. <i>Diabetes</i> , 2011, 60, 1981-1989.	0.3	107
2129	seqMINER: an integrated ChIP-seq data interpretation platform. <i>Nucleic Acids Research</i> , 2011, 39, e35-e35.	6.5	377
2130	Paraoxonase-2 Modulates Stress Response of Endothelial Cells to Oxidized Phospholipids and a Bacterial Quorum-Sensing Molecule. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2011, 31, 2624-2633.	1.1	35
2131	Mechanisms of Urokinase Plasminogen Activator (uPA)-mediated Atherosclerosis. <i>Journal of Biological Chemistry</i> , 2011, 286, 22665-22677.	1.6	51
2132	SigReannot-mart: a query environment for expression microarray probe re-annotations. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar025-bar025.	1.4	6
2133	Maternal Undernourished Fetal Kidneys Exhibit Differential Regulation of Nephrogenic Genes Including Downregulation of the Notch Signaling Pathway. <i>Reproductive Sciences</i> , 2011, 18, 563-576.	1.1	10
2134	Deficiency of $\alpha$ -actinin-3 is associated with increased susceptibility to contraction-induced damage and skeletal muscle remodeling. <i>Human Molecular Genetics</i> , 2011, 20, 2914-2927.	1.4	95
2135	Conservation of Salmonella Infection Mechanisms in Plants and Animals. <i>PLoS ONE</i> , 2011, 6, e24112.	1.1	114
2136	A Comprehensive Expression Profile of MicroRNAs in Porcine Pituitary. <i>PLoS ONE</i> , 2011, 6, e24883.	1.1	22
2137	A Physical Interaction Network of Dengue Virus and Human Proteins. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.012187.	2.5	153
2138	P-Selectin Glycoprotein Ligand-1 Deficiency Is Protective Against Obesity-Related Insulin Resistance. <i>Diabetes</i> , 2011, 60, 189-199.	0.3	33
2139	Resection of Non-Small Cell Lung Cancers Reverses Tumor-Induced Gene Expression Changes in the Peripheral Immune System. <i>Clinical Cancer Research</i> , 2011, 17, 5867-5877.	3.2	47
2140	A <i>Drosophila</i> model of the neurodegenerative disease SCA17 reveals a role of RBP-J/Su(H) in modulating the pathological outcome. <i>Human Molecular Genetics</i> , 2011, 20, 3424-3436.	1.4	33

#	ARTICLE	IF	CITATIONS
2141	A CHOP-regulated microRNA controls rhodopsin expression. <i>Journal of Cell Biology</i> , 2011, 192, 919-927.	2.3	108
2142	Transcriptional effect of the LH surge in bovine granulosa cells during the peri-ovulation period. <i>Reproduction</i> , 2011, 141, 193-205.	1.1	46
2143	Genes and pathways affected by CAG-repeat RNA-based toxicity in <i>Drosophila</i> . <i>Human Molecular Genetics</i> , 2011, 20, 4810-4821.	1.4	52
2144	ChIP-seq analysis reveals distinct H3K27me3 profiles that correlate with transcriptional activity. <i>Nucleic Acids Research</i> , 2011, 39, 7415-7427.	6.5	250
2145	Therapeutics of Ebola Hemorrhagic Fever: Whole-Genome Transcriptional Analysis of Successful Disease Mitigation. <i>Journal of Infectious Diseases</i> , 2011, 204, S1043-S1052.	1.9	38
2146	Mindbomb 1, an E3 ubiquitin ligase, forms a complex with RYK to activate Wnt/ $\beta$ -catenin signaling. <i>Journal of Cell Biology</i> , 2011, 194, 737-750.	2.3	90
2147	Foxl1-Cre-marked adult hepatic progenitors have clonogenic and bilineage differentiation potential. <i>Genes and Development</i> , 2011, 25, 1185-1192.	2.7	138
2148	A systems biology approach sheds new light on <i>Escherichia coli</i> acid resistance. <i>Nucleic Acids Research</i> , 2011, 39, 7512-7528.	6.5	86
2149	JAG2 Induction in Hypoxic Tumor Cells Alters Notch Signaling and Enhances Endothelial Cell Tube Formation. <i>Molecular Cancer Research</i> , 2011, 9, 626-636.	1.5	56
2150	Different gene expression profiles in metastasizing midgut carcinoid tumors. <i>Endocrine-Related Cancer</i> , 2011, 18, 479-489.	1.6	24
2151	Redox Proteomics of Protein-bound Methionine Oxidation. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006866.	2.5	117
2152	Transcriptome transfer provides a model for understanding the phenotype of cardiomyocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11918-11923.	3.3	31
2153	Time-resolved Quantitative Proteome Analysis of In Vivo Intestinal Development. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.005231.	2.5	25
2154	Whole-Genome Analysis Reveals That Active Heat Shock Factor Binding Sites Are Mostly Associated with Non-Heat Shock Genes in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2011, 6, e15934.	1.1	78
2155	Prospective isolation of a bipotential clonogenic liver progenitor cell in adult mice. <i>Genes and Development</i> , 2011, 25, 1193-1203.	2.7	209
2156	Global Expression Analysis Identified a Preferentially Nerve Growth Factor-induced Transcriptional Program Regulated by Sustained Mitogen-activated Protein Kinase/Extracellular Signal-regulated Kinase (ERK) and AP-1 Protein Activation during PC12 Cell Differentiation*. <i>Journal of Biological Chemistry</i> , 2011, 286, 45131-45145.	1.6	49
2157	Systems Genetics: a Powerful Approach for Gene-Environment Interactions. <i>Journal of Nutrition</i> , 2011, 141, 515-519.	1.3	11
2158	Basal Bioenergetic Abnormalities in Skeletal Muscle from Ryanodine Receptor Malignant Hyperthermia-susceptible R163C Knock-in Mice. <i>Journal of Biological Chemistry</i> , 2011, 286, 99-113.	1.6	41



#	ARTICLE	IF	CITATIONS
2159	Targets of the Tumor Suppressor <i>miR-200</i> in Regulation of the Epithelial-Mesenchymal Transition in Cancer. <i>Cancer Research</i> , 2011, 71, 7670-7682.	0.4	126
2160	Nuclear and cytoplasmic localization of neural stem cell microRNAs. <i>Rna</i> , 2011, 17, 675-686.	1.6	105
2161	Characterization of the Core Elements of the NF- $\kappa$ B Signaling Pathway of the Sea Anemone <i>Nematostella vectensis</i> . <i>Molecular and Cellular Biology</i> , 2011, 31, 1076-1087.	1.1	56
2162	GProX, a User-Friendly Platform for Bioinformatics Analysis and Visualization of Quantitative Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2011, 10, O110.007450.	2.5	150
2163	Human Papillomavirus 16 E5 Modulates the Expression of Host MicroRNAs. <i>PLoS ONE</i> , 2011, 6, e21646.	1.1	82
2164	An integrative functional genomics approach for discovering biomarkers in schizophrenia. <i>Briefings in Functional Genomics</i> , 2011, 10, 387-399.	1.3	19
2165	Gene expression profile in mesenchymal stem cells derived from dental tissues and bone marrow. <i>Journal of Periodontal and Implant Science</i> , 2011, 41, 192.	0.9	46
2166	MicroRNAs Regulate the Timing of Embryo Maturation in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2011, 155, 1871-1884.	2.3	147
2167	Global map of physical interactions among differentially expressed genes in multiple sclerosis relapses and remissions. <i>Human Molecular Genetics</i> , 2011, 20, 3606-3619.	1.4	20
2168	A Nuclear Variant of ErbB3 Receptor Tyrosine Kinase Regulates Ezrin Distribution and Schwann Cell Myelination. <i>Journal of Neuroscience</i> , 2011, 31, 5106-5119.	1.7	39
2169	Review of Weighted Gene Coexpression Network Analysis. , 2011, , 369-388.		19
2170	Wide-ranging functions of E2F4 in transcriptional activation and repression revealed by genome-wide analysis. <i>Nucleic Acids Research</i> , 2011, 39, 3558-3573.	6.5	132
2171	An integrated transcriptomic and computational analysis for biomarker identification in gastric cancer. <i>Nucleic Acids Research</i> , 2011, 39, 1197-1207.	6.5	188
2172	Transcriptomic data-mining approach for identifying potential pharmacogenetic candidates in antiepileptic drug response. <i>Indian Journal of Human Genetics</i> , 2011, 17, 58.	0.7	0
2173	Suppression of Stra8 Expression in the Mouse Gonad by WIN 18,4461. <i>Biology of Reproduction</i> , 2011, 84, 957-965.	1.2	57
2174	Patterns of Gene Expression in <i>Drosophila</i> InsP3 Receptor Mutant Larvae Reveal a Role for InsP3 Signaling in Carbohydrate and Energy Metabolism. <i>PLoS ONE</i> , 2011, 6, e24105.	1.1	5
2175	Genome-wide RNA-seq analysis of human and mouse platelet transcriptomes. <i>Blood</i> , 2011, 118, e101-e111.	0.6	484
2176	Prognostic Significance and Tumor Biology of Regional Lymph Node Disease in Patients With Rhabdomyosarcoma: A Report From the Children's Oncology Group. <i>Journal of Clinical Oncology</i> , 2011, 29, 1304-1311.	0.8	102

#	ARTICLE	IF	CITATIONS
2177	Gene Expression following Exposure to Celecoxib in Humans: Pathways of Inflammation and Carcinogenesis Are Activated in Tumors but Not Normal Tissues. <i>Digestion</i> , 2011, 84, 169-184.	1.2	3
2178	Gene Coexpression Network Topology of Cardiac Development, Hypertrophy, and Failure. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 26-35.	5.1	88
2179	Transcription factor FOXL2 protects granulosa cells from stress and delays cell cycle: role of its regulation by the SIRT1 deacetylase. <i>Human Molecular Genetics</i> , 2011, 20, 1673-1686.	1.4	81
2180	Phosphoproteomic Analysis of <i>Salmonella</i> -Infected Cells Identifies Key Kinase Regulators and SopB-Dependent Host Phosphorylation Events. <i>Science Signaling</i> , 2011, 4, rs9.	1.6	52
2181	Proteomic and Functional Genomic Landscape of Receptor Tyrosine Kinase and Ras to Extracellular Signal-Regulated Kinase Signaling. <i>Science Signaling</i> , 2011, 4, rs10.	1.6	87
2182	Conjunctival Transcriptome in Scarring Trachoma. <i>Infection and Immunity</i> , 2011, 79, 499-511.	1.0	59
2183	Genomic Analysis Reveals Pre- and Postchallenge Differences in a Rhesus Macaque AIDS Vaccine Trial: Insights into Mechanisms of Vaccine Efficacy. <i>Journal of Virology</i> , 2011, 85, 1099-1116.	1.5	24
2184	Sequentially acting Sox transcription factors in neural lineage development. <i>Genes and Development</i> , 2011, 25, 2453-2464.	2.7	263
2185	Mining the Bioinformation of Differentially Expressed Genes in Lung Treated with the Hypoxia Based on the Bioinformatics Methods. , 2011, , .		0
2186	Circadian cycles are the dominant transcriptional rhythm in the intertidal mussel <i>Mytilus californianus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16110-16115.	3.3	127
2187	Endothelial Jarid2/Jumonji Is Required for Normal Cardiac Development and Proper Notch1 Expression. <i>Journal of Biological Chemistry</i> , 2011, 286, 17193-17204.	1.6	73
2188	Genome-wide Analysis of Transcription Factor E2F1 Mutant Proteins Reveals That N- and C-terminal Protein Interaction Domains Do Not Participate in Targeting E2F1 to the Human Genome. <i>Journal of Biological Chemistry</i> , 2011, 286, 11985-11996.	1.6	45
2189	The BTB and CNC Homology 1 (BACH1) Target Genes Are Involved in the Oxidative Stress Response and in Control of the Cell Cycle. <i>Journal of Biological Chemistry</i> , 2011, 286, 23521-23532.	1.6	136
2190	Glycosaminoglycans and Glucose Prevent Apoptosis in 4-Methylumbelliferone-treated Human Aortic Smooth Muscle Cells*. <i>Journal of Biological Chemistry</i> , 2011, 286, 34497-34503.	1.6	42
2191	HLA-DR-presented Peptide Repertoires Derived From Human Monocyte-derived Dendritic Cells Pulsed With Blood Coagulation Factor VIII. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.002246.	2.5	71
2192	Bacterial genotoxin triggers FEN1-dependent RhoA activation, cytoskeleton remodeling and cell survival. <i>Journal of Cell Science</i> , 2011, 124, 2735-2742.	1.2	35
2193	Predominant Gain of Promoter TATA Box after Gene Duplication Associated with Stress Responses. <i>Molecular Biology and Evolution</i> , 2011, 28, 2893-2904.	3.5	21
2194	Functional MicroRNA Involved in Endometriosis. <i>Molecular Endocrinology</i> , 2011, 25, 821-832.	3.7	220

#	ARTICLE	IF	CITATIONS
2195	Diagnosis of Prostate Cancer Using Differentially Expressed Genes in Stroma. <i>Cancer Research</i> , 2011, 71, 2476-2487.	0.4	84
2196	Acquisition of Host-Derived CD40L by HIV-1 <i>In Vivo</i> and Its Functional Consequences in the B-Cell Compartment. <i>Journal of Virology</i> , 2011, 85, 2189-2200.	1.5	46
2197	Dynamic Changes in the MicroRNA Expression Profile Reveal Multiple Regulatory Mechanisms in the Spinal Nerve Ligation Model of Neuropathic Pain. <i>PLoS ONE</i> , 2011, 6, e17670.	1.1	123
2198	Shifting the Fermentative/Oxidative Balance in <i>Saccharomyces cerevisiae</i> by Transcriptional Deregulation of Snf1 via Overexpression of the Upstream Activating Kinase Sak1p. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1981-1989.	1.4	18
2199	Whole Transcriptome Sequencing Reveals Gene Expression and Splicing Differences in Brain Regions Affected by Alzheimer's Disease. <i>PLoS ONE</i> , 2011, 6, e16266.	1.1	266
2200	Chromatin remodeling as a mechanism for circadian prolactin transcription: rhythmic NONO and SFPQ recruitment to HLF. <i>FASEB Journal</i> , 2011, 25, 2740-2756.	0.2	36
2201	Identification and gene expression profiling of tumor-initiating cells isolated from human osteosarcoma cell lines in an orthotopic mouse model. <i>Cancer Biology and Therapy</i> , 2011, 12, 278-287.	1.5	35
2202	Gene expression profiling of the androgen independent prostate cancer cells demonstrates complex mechanisms mediating resistance to docetaxel. <i>Cancer Biology and Therapy</i> , 2011, 11, 204-212.	1.5	27
2203	Overlapping and distinct pRb pathways in the mammalian auditory and vestibular organs. <i>Cell Cycle</i> , 2011, 10, 337-351.	1.3	29
2204	Genome-wide DNA methylation patterns in CD4+ T cells from patients with systemic lupus erythematosus. <i>Epigenetics</i> , 2011, 6, 593-601.	1.3	224
2205	Protein-network modeling of prostate cancer gene signatures reveals essential pathways in disease recurrence. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2011, 18, 392-402.	2.2	27
2206	Diabetes causes multiple genetic alterations and downregulates expression of DNA repair genes in the prostate. <i>Laboratory Investigation</i> , 2011, 91, 1363-1374.	1.7	18
2207	Organelles Contribute Differentially to Reactive Oxygen Species-Related Events during Extended Darkness. <i>Plant Physiology</i> , 2011, 156, 185-201.	2.3	102
2208	Conserved and Divergent Rhythms of Crassulacean Acid Metabolism-Related and Core Clock Gene Expression in the Cactus <i>Opuntia ficus-indica</i> . <i>Plant Physiology</i> , 2011, 156, 1978-1989.	2.3	53
2209	Specific and Shared Targets of Ephrin A Signaling in Epidermal Keratinocytes. <i>Journal of Biological Chemistry</i> , 2011, 286, 9419-9428.	1.6	37
2210	A Multiprotein Binding Interface in an Intrinsically Disordered Region of the Tumor Suppressor Protein Interferon Regulatory Factor-1. <i>Journal of Biological Chemistry</i> , 2011, 286, 14291-14303.	1.6	26
2211	Endothelin-1 Increases Collagen Accumulation in Renal Mesangial Cells by Stimulating a Chemokine and Cytokine Autocrine Signaling Loop. <i>Journal of Biological Chemistry</i> , 2011, 286, 11003-11008.	1.6	59
2212	Genomic Analysis Reveals a Novel Nuclear Factor- $\kappa$ B (NF- $\kappa$ B)-binding Site in Alu-repetitive Elements. <i>Journal of Biological Chemistry</i> , 2011, 286, 38768-38782.	1.6	55

#	ARTICLE	IF	CITATIONS
2213	Combined transcriptome analysis of fetal human and mouse cerebral cortex exposed to alcohol. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4212-4217.	3.3	66
2214	Cardiac pressure overload hypertrophy is differentially regulated by $\beta^2$ -adrenergic receptor subtypes. American Journal of Physiology - Heart and Circulatory Physiology, 2011, 301, H1461-H1470.	1.5	32
2215	piRNA profiling during specific stages of mouse spermatogenesis. Rna, 2011, 17, 1191-1203.	1.6	94
2216	TLR 2 and CD14 Mediate Innate Immunity and Lung Inflammation to Staphylococcal Pantone's "Valentine" Leukocidin In Vivo. Journal of Immunology, 2011, 186, 1608-1617.	0.4	68
2217	Modulation of chromatin position and gene expression by HDAC4 interaction with nucleoporins. Journal of Cell Biology, 2011, 193, 21-29.	2.3	83
2218	Identification and Expression of Potential Regulators of the Mammalian Mitotic-to-Meiotic Transition1. Biology of Reproduction, 2011, 84, 34-42.	1.2	38
2219	Genetic and expression analysis of cattle identifies candidate genes in pathways responding to <i>Trypanosoma congolense</i> infection. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9304-9309.	3.3	92
2220	Functional Analysis of KAP1 Genomic Recruitment. Molecular and Cellular Biology, 2011, 31, 1833-1847.	1.1	99
2221	mRNA and microRNA Expression Profiles in Circulating Tumor Cells and Primary Tumors of Metastatic Breast Cancer Patients. Clinical Cancer Research, 2011, 17, 3600-3618.	3.2	207
2222	The Virulence of 1997 H5N1 Influenza Viruses in the Mouse Model Is Increased by Correcting a Defect in Their NS1 Proteins. Journal of Virology, 2011, 85, 7048-7058.	1.5	71
2223	NOA: a novel Network Ontology Analysis method. Nucleic Acids Research, 2011, 39, e87-e87.	6.5	101
2224	Medusa structure of the gene regulatory network: dominance of transcription factors in cancer subtype classification. Experimental Biology and Medicine, 2011, 236, 628-636.	1.1	20
2225	MAP Kinase-Interacting Kinase 1 Regulates SMAD2-Dependent TGF- $\beta^2$ Signaling Pathway in Human Glioblastoma. Cancer Research, 2011, 71, 2392-2402.	0.4	135
2226	Fibroblast growth factor 9 delivery during angiogenesis produces durable, vasoresponsive microvessels wrapped by smooth muscle cells. Nature Biotechnology, 2011, 29, 421-427.	9.4	107
2227	CD140a identifies a population of highly myelinogenic, migration-competent and efficiently engrafting human oligodendrocyte progenitor cells. Nature Biotechnology, 2011, 29, 934-941.	9.4	185
2228	Genetic regulation of Nrx1 expression: an integrative cross-species analysis of schizophrenia candidate genes. Translational Psychiatry, 2011, 1, e25-e25.	2.4	26
2229	Resolution of infection promotes a state of dormancy and long survival of CD4 memory T cells. Immunology and Cell Biology, 2011, 89, 870-881.	1.0	22
2230	Functional Homogeneity in microRNA Target Heterogeneity—a New Sight into Human microRNomics. OMICS A Journal of Integrative Biology, 2011, 15, 25-35.	1.0	10

#	ARTICLE	IF	CITATIONS
2231	An integrative clustering and modeling algorithm for dynamical gene expression data. <i>Bioinformatics</i> , 2011, 27, i392-i400.	1.8	26
2232	Wide-ranging DNA methylation differences of primary trophoblast cell populations and derived cell lines: implications and opportunities for understanding trophoblast function. <i>Molecular Human Reproduction</i> , 2011, 17, 344-353.	1.3	76
2233	The Evolutionarily Conserved Longevity Determinants HCF-1 and SIR-2.1/SIRT1 Collaborate to Regulate DAF-16/FOXO. <i>PLoS Genetics</i> , 2011, 7, e1002235.	1.5	106
2234	Discovering Transcription Factor Binding Sites in Highly Repetitive Regions of Genomes with Multi-Read Analysis of ChIP-Seq Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002111.	1.5	73
2235	Towards a System Level Understanding of Non-Model Organisms Sampled from the Environment: A Network Biology Approach. <i>PLoS Computational Biology</i> , 2011, 7, e1002126.	1.5	83
2236	Identifying Causal Genes and Dysregulated Pathways in Complex Diseases. <i>PLoS Computational Biology</i> , 2011, 7, e1001095.	1.5	163
2237	Nuclear Accumulation of Stress Response mRNAs Contributes to the Neurodegeneration Caused by Fragile X Premutation rCGG Repeats. <i>PLoS Genetics</i> , 2011, 7, e1002102.	1.5	56
2238	Alterations in the <i>Aedes aegypti</i> Transcriptome during Infection with West Nile, Dengue and Yellow Fever Viruses. <i>PLoS Pathogens</i> , 2011, 7, e1002189.	2.1	180
2239	Biologicals and Fetal Cell Therapy for Wound and Scar Management. <i>ISRN Dermatology</i> , 2011, 2011, 1-16.	1.9	21
2240	A Systems Biology Approach Identifies Molecular Networks Defining Skeletal Muscle Abnormalities in Chronic Obstructive Pulmonary Disease. <i>PLoS Computational Biology</i> , 2011, 7, e1002129.	1.5	66
2241	Interferon Regulatory Factor 8 Regulates Pathways for Antigen Presentation in Myeloid Cells and during Tuberculosis. <i>PLoS Genetics</i> , 2011, 7, e1002097.	1.5	85
2242	Genome-Wide Analysis Reveals PADI4 Cooperates with Elk-1 to Activate c-Fos Expression in Breast Cancer Cells. <i>PLoS Genetics</i> , 2011, 7, e1002112.	1.5	107
2243	Interactions between Glucocorticoid Treatment and Cis-Regulatory Polymorphisms Contribute to Cellular Response Phenotypes. <i>PLoS Genetics</i> , 2011, 7, e1002162.	1.5	103
2244	Over-Expression of DSCAM and COL6A2 Cooperatively Generates Congenital Heart Defects. <i>PLoS Genetics</i> , 2011, 7, e1002344.	1.5	79
2245	<i>Candida albicans</i> Infection of <i>Caenorhabditis elegans</i> Induces Antifungal Immune Defenses. <i>PLoS Pathogens</i> , 2011, 7, e1002074.	2.1	131
2246	Short-Time Gene Expression Response to Valproic Acid and Valproic Acid Analogs in Mouse Embryonic Stem Cells. <i>Toxicological Sciences</i> , 2011, 121, 328-342.	1.4	45
2247	Dynamic molecular and histopathological changes in the extracellular matrix and inflammation in the transition to heart failure in isolated volume overload. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2011, 300, H2251-H2260.	1.5	64
2248	The Epithelial-Mesenchymal Transition Mediator S100A4 Maintains Cancer-Initiating Cells in Head and Neck Cancers. <i>Cancer Research</i> , 2011, 71, 1912-1923.	0.4	123

#	ARTICLE	IF	CITATIONS
2249	Prolyl Endopeptidase Is Involved in Cellular Signalling in Human Neuroblastoma SH-SY5Y Cells. <i>NeuroSignals</i> , 2011, 19, 97-109.	0.5	25
2250	RNA-Seq analysis in MeV. <i>Bioinformatics</i> , 2011, 27, 3209-3210.	1.8	461
2251	<i>GO-Module</i> : functional synthesis and improved interpretation of Gene Ontology patterns. <i>Bioinformatics</i> , 2011, 27, 1444-1446.	1.8	97
2252	Early Patterns of Gene Expression Correlate With the Humoral Immune Response to Influenza Vaccination in Humans. <i>Journal of Infectious Diseases</i> , 2011, 203, 921-929.	1.9	208
2253	Adipose tissue transcriptome changes during obesity development in female dogs. <i>Physiological Genomics</i> , 2011, 43, 295-307.	1.0	50
2254	Fenfluramine-Induced Gene Dysregulation in Human Pulmonary Artery Smooth Muscle and Endothelial Cells. <i>Pulmonary Circulation</i> , 2011, 1, 405-418.	0.8	7
2255	Use of transcriptional signatures induced in lymphoid and myeloid cell lines as an inflammatory biomarker in Type 1 diabetes. <i>Physiological Genomics</i> , 2011, 43, 697-709.	1.0	11
2256	Reciprocal Transcriptional Regulation of Metabolic and Signaling Pathways Correlates With Disease Severity in Heart Failure. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 475-483.	5.1	57
2257	Effective Treatment of Psoriasis with Narrow-Band UVB Phototherapy Is Linked to Suppression of the IFN and Th17 Pathways. <i>Journal of Investigative Dermatology</i> , 2011, 131, 1547-1558.	0.3	129
2258	Gene Expression Profiling in Human High-Grade Astrocytomas. <i>Comparative and Functional Genomics</i> , 2011, 2011, 1-10.	2.0	25
2259	Nerve Growth Factor Partially Recovers Inflamed Skin from Stress-Induced Worsening in Allergic Inflammation. <i>Journal of Investigative Dermatology</i> , 2011, 131, 735-743.	0.3	47
2260	In silico Analysis of Combinatorial microRNA Activity Reveals Target Genes and Pathways Associated with Breast Cancer Metastasis. <i>Cancer Informatics</i> , 2011, 10, CIN.S6631.	0.9	16
2261	Gene Coexpression Network Alignment and Conservation of Gene Modules between Two Grass Species: Maize and Rice. <i>Plant Physiology</i> , 2011, 156, 1244-1256.	2.3	141
2262	High expression of BMP pathway genes distinguishes a subset of atypical teratoid/rhabdoid tumors associated with shorter survival. <i>Neuro-Oncology</i> , 2011, 13, 1296-1307.	0.6	52
2263	Genetic Factors Underlying the Risk of Thalidomide-Related Neuropathy in Patients With Multiple Myeloma. <i>Journal of Clinical Oncology</i> , 2011, 29, 797-804.	0.8	95
2264	Temporal Coordination of Gene Networks by Zelda in the Early Drosophila Embryo. <i>PLoS Genetics</i> , 2011, 7, e1002339.	1.5	222
2265	A single nucleotide polymorphism-derived regulatory gene network underlying puberty in 2 tropical breeds of beef cattle. <i>Journal of Animal Science</i> , 2011, 89, 1669-1683.	0.2	90
2266	Distinct protein degradation profiles are induced by different disuse models of skeletal muscle atrophy. <i>Physiological Genomics</i> , 2011, 43, 1075-1086.	1.0	57

#	ARTICLE	IF	CITATIONS
2267	Retinoic acid inhibits endometrial cancer cell growth via multiple genomic mechanisms. <i>Journal of Molecular Endocrinology</i> , 2011, 46, 139-153.	1.1	34
2268	Degenerate T-cell Recognition of Peptides on MHC Molecules Creates Large Holes in the T-cell Repertoire. <i>PLoS Computational Biology</i> , 2012, 8, e1002412.	1.5	73
2269	Exon Level Transcriptomic Profiling of HIV-1-Infected CD4+ T Cells Reveals Virus-Induced Genes and Host Environment Favorable for Viral Replication. <i>PLoS Pathogens</i> , 2012, 8, e1002861.	2.1	46
2270	ELK1 Uses Different DNA Binding Modes to Regulate Functionally Distinct Classes of Target Genes. <i>PLoS Genetics</i> , 2012, 8, e1002694.	1.5	66
2271	Rapid Turnover of Long Noncoding RNAs and the Evolution of Gene Expression. <i>PLoS Genetics</i> , 2012, 8, e1002841.	1.5	284
2272	The renal transcriptome of <i>db/db</i> mice identifies putative urinary biomarker proteins in patients with type 2 diabetes: a pilot study. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 302, F820-F829.	1.3	33
2273	Transcriptomic Analysis of Neurulation and Early Organogenesis in Rat Embryos: An In Vivo and Ex Vivo Comparison. <i>Toxicological Sciences</i> , 2012, 126, 255-266.	1.4	18
2274	A Comparison of Gene Expression Responses in Rat Whole Embryo Culture and In Vivo: Time-Dependent Retinoic Acid-Induced Teratogenic Response. <i>Toxicological Sciences</i> , 2012, 126, 242-254.	1.4	34
2275	Comparative Proteome Analysis of Human Lung Squamous Carcinoma using Two Different Methods: Two-Dimensional Gel Electrophoresis and iTRAQ Analysis. <i>Technology in Cancer Research and Treatment</i> , 2012, 11, 395-408.	0.8	10
2276	Tools for managing and analyzing microarray data. <i>Briefings in Bioinformatics</i> , 2012, 13, 46-60.	3.2	28
2277	Quantifying the white blood cell transcriptome as an accessible window to the multiorgan transcriptome. <i>Bioinformatics</i> , 2012, 28, 538-545.	1.8	52
2278	Neuroendocrine Mechanisms of Acupuncture. <i>Evidence-based Complementary and Alternative Medicine</i> , 2012, 2012, 1-2.	0.5	9
2279	An Unbiased Assessment of the Role of Imprinted Genes in an Intergenerational Model of Developmental Programming. <i>PLoS Genetics</i> , 2012, 8, e1002605.	1.5	105
2280	Time-course network analysis reveals TNF- $\alpha$ can promote G1/S transition of cell cycle in vascular endothelial cells. <i>Bioinformatics</i> , 2012, 28, 1-4.	1.8	39
2281	Large-scale phosphotyrosine proteomic profiling of rat renal collecting duct epithelium reveals predominance of proteins involved in cell polarity determination. <i>American Journal of Physiology - Cell Physiology</i> , 2012, 302, C27-C45.	2.1	11
2282	Enhancing the Prioritization of Disease-Causing Genes through Tissue Specific Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2012, 8, e1002690.	1.5	145
2283	PHYSIOLOGY AND ENDOCRINOLOGY SYMPOSIUM: How single nucleotide polymorphism chips will advance our knowledge of factors controlling puberty and aid in selecting replacement beef females <sup>1,2,3,4</sup> . <i>Journal of Animal Science</i> , 2012, 90, 1152-1165.	0.2	43
2284	An Integrated Regulatory Network Reveals Pervasive Cross-Regulation among Transcription and Splicing Factors. <i>PLoS Computational Biology</i> , 2012, 8, e1002603.	1.5	14

#	ARTICLE	IF	CITATIONS
2285	MOfinder: A Novel Algorithm for Detecting Overlapping Modules from Protein-Protein Interaction Network. <i>Journal of Biomedicine and Biotechnology</i> , 2012, 2012, 1-10.	3.0	7
2286	Overactivation of Hedgehog Signaling Alters Development of the Ovarian Vasculature in Mice <sup>1</sup> . <i>Biology of Reproduction</i> , 2012, 86, 174.	1.2	34
2287	The Cortical and Striatal Gene Expression Profile of 100%Hz Electroacupuncture Treatment in 6-Hydroxydopamine-Induced Parkinson's Disease Model. <i>Evidence-based Complementary and Alternative Medicine</i> , 2012, 2012, 1-14.	0.5	17
2288	The human phosphotyrosine signaling network: Evolution and hotspots of hijacking in cancer. <i>Genome Research</i> , 2012, 22, 1222-1230.	2.4	72
2289	DNA Methylation and Gene Expression Changes in Monozygotic Twins Discordant for Psoriasis: Identification of Epigenetically Dysregulated Genes. <i>PLoS Genetics</i> , 2012, 8, e1002454.	1.5	145
2290	Interleukin-1 $\beta$ modulates smooth muscle cell phenotype to a distinct inflammatory state relative to PDGF-DD via NF- $\kappa$ B-dependent mechanisms. <i>Physiological Genomics</i> , 2012, 44, 417-429.	1.0	106
2291	Transcriptomic Characterization of Temperature Stress Responses in Larval Zebrafish. <i>PLoS ONE</i> , 2012, 7, e37209.	1.1	171
2292	A genome-wide analysis of open chromatin in human tracheal epithelial cells reveals novel candidate regulatory elements for lung function. <i>Thorax</i> , 2012, 67, 385-391.	2.7	20
2293	Telmisartan improves kidney function through inhibition of the oxidative phosphorylation pathway in diabetic rats. <i>Journal of Molecular Endocrinology</i> , 2012, 49, 35-46.	1.1	20
2294	A promoter DNA demethylation landscape of human hematopoietic differentiation. <i>Nucleic Acids Research</i> , 2012, 40, 116-131.	6.5	97
2295	GenomeRunner: automating genome exploration. <i>Bioinformatics</i> , 2012, 28, 419-420.	1.8	41
2296	DNA Microarray Analysis and Functional Profile of Pituitary Transcriptome Under Core-Clock Protein BMAL1 Control. <i>Chronobiology International</i> , 2012, 29, 103-130.	0.9	16
2297	Discovering the hidden sub-network component in a ranked list of genes or proteins derived from genomic experiments. <i>Nucleic Acids Research</i> , 2012, 40, e158-e158.	6.5	22
2298	A microRNA network regulates expression and biosynthesis of wild-type and F508 mutant cystic fibrosis transmembrane conductance regulator. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13362-13367.	3.3	111
2299	Abnormal p38 $\beta$ mitogen-activated protein kinase signaling in dilated cardiomyopathy caused by lamin A/C gene mutation. <i>Human Molecular Genetics</i> , 2012, 21, 4325-4333.	1.4	114
2300	Shifting of Immune Responsiveness to House Dust Mite by Influenza A Infection: Genomic Insights. <i>Journal of Immunology</i> , 2012, 188, 832-843.	0.4	17
2301	A Quantitative Spatial Proteomics Analysis of Proteome Turnover in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011429.	2.5	332
2302	Alpha 1-antitrypsin reduces inflammation and enhances mouse pancreatic islet transplant survival. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15443-15448.	3.3	56



#	ARTICLE	IF	CITATIONS
2303	IDENTIFICATION OF SHORTENED 3' UNTRANSLATED REGIONS FROM EXPRESSION ARRAYS. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1241001.	0.3	3
2304	Gene-Expression Changes Caused by Inbreeding Protect Against Inbreeding Depression in <i>Drosophila</i> . <i>Genetics</i> , 2012, 192, 161-172.	1.2	18
2305	Comparison of the Effects of Early Pregnancy with Human Interferon, Alpha 2 (IFNA2), on Gene Expression in Bovine Endometrium. <i>Biology of Reproduction</i> , 2012, 86, 46.	1.2	86
2306	Convergent Molecular Evolution of Genomic Cores in <i>Salmonella enterica</i> and <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2012, 194, 5002-5011.	1.0	40
2307	Differences in the early response of hatchlings of different chicken breeding lines to <i>Salmonella enterica</i> serovar Enteritidis infection. <i>Poultry Science</i> , 2012, 91, 346-353.	1.5	21
2308	Cholesterol Accumulation Regulates Expression of Macrophage Proteins Implicated in Proteolysis and Complement Activation. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2012, 32, 2910-2918.	1.1	14
2309	Transcriptome analysis reveals specific changes in osteoarthritis synovial fibroblasts. <i>Annals of the Rheumatic Diseases</i> , 2012, 71, 275-280.	0.5	36
2310	GeneWeaver: a web-based system for integrative functional genomics. <i>Nucleic Acids Research</i> , 2012, 40, D1067-D1076.	6.5	112
2311	Identification of Candidate Biomarkers for Early Detection of Human Lung Squamous Cell Cancer by Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013946.	2.5	67
2312	Protein Kinase C (PKC) $\delta$ -mediated G $\beta$ q Stimulation of ERK5 Protein Pathway in Cardiomyocytes and Cardiac Fibroblasts. <i>Journal of Biological Chemistry</i> , 2012, 287, 7792-7802.	1.6	27
2313	The Effect of Long Term Calorie Restriction on in Vivo Hepatic Proteostasis: A Novel Combination of Dynamic and Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1801-1814.	2.5	65
2314	FoxO6 regulates memory consolidation and synaptic function. <i>Genes and Development</i> , 2012, 26, 2780-2801.	2.7	116
2315	Gene Expression Analysis of the Embryonic Subplate. <i>Cerebral Cortex</i> , 2012, 22, 1343-1359.	1.6	83
2316	Silencing of enzymes involved in ceramide biosynthesis causes distinct global alterations of lipid homeostasis and gene expression. <i>Journal of Lipid Research</i> , 2012, 53, 1459-1471.	2.0	28
2317	Adipose Genes Down-Regulated During Experimental Endotoxemia Are Also Suppressed in Obesity. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2012, 97, E2152-E2159.	1.8	12
2318	Nonpathogenic <i>Lactobacillus rhamnosus</i> activates the inflammasome and antiviral responses in human macrophages. <i>Gut Microbes</i> , 2012, 3, 510-522.	4.3	49
2319	Autotaxin and Its Product Lysophosphatidic Acid Suppress Brown Adipose Differentiation and Promote Diet-Induced Obesity in Mice. <i>Molecular Endocrinology</i> , 2012, 26, 786-797.	3.7	59
2320	CTGR-Span: Efficient mining of cross-timepoint gene regulation sequential patterns from microarray datasets. , 2012, , .		0

#	ARTICLE	IF	CITATIONS
2321	Overexpression of <i>S100B</i> , <i>TM4SF4</i> , and <i>OLFM4</i> Genes Is Correlated with Liver Metastasis in Taiwanese Colorectal Cancer Patients. <i>DNA and Cell Biology</i> , 2012, 31, 43-49.	0.9	45
2322	Global transcriptional profiling reveals similarities and differences between human stem cell-derived cardiomyocyte clusters and heart tissue. <i>Physiological Genomics</i> , 2012, 44, 245-258.	1.0	65
2323	DAVID-WS: a stateful web service to facilitate gene/protein list analysis. <i>Bioinformatics</i> , 2012, 28, 1805-1806.	1.8	955
2324	Genome-wide mapping of Myc binding and gene regulation in serum-stimulated fibroblasts. <i>Oncogene</i> , 2012, 31, 1695-1709.	2.6	90
2325	Overexpressing the CCL2 chemokine in an epithelial ovarian cancer cell line results in latency of in vivo tumourigenicity. <i>Oncogenesis</i> , 2012, 1, e27-e27.	2.1	13
2326	Genetic mapping of habitual substance use, obesity-related traits, responses to mental and physical stress, and heart rate and blood pressure measurements reveals shared genes that are overrepresented in the neural synapse. <i>Hypertension Research</i> , 2012, 35, 585-591.	1.5	37
2327	Gene Expression Profile Changes After Short-activating RNA-mediated Induction of Endogenous Pluripotency Factors in Human Mesenchymal Stem Cells. <i>Molecular Therapy - Nucleic Acids</i> , 2012, 1, e35.	2.3	28
2328	Gene expression profiling of placentae from women with early- and late-onset pre-eclampsia: down-regulation of the angiogenesis-related genes <i>ACVRL1</i> and <i>EGFL7</i> in early-onset disease. <i>Molecular Human Reproduction</i> , 2012, 18, 146-155.	1.3	63
2329	Differential Gene Expression Responses Distinguish Contact and Respiratory Sensitizers and Nonsensitizing Irritants in the Local Lymph Node Assay. <i>Toxicological Sciences</i> , 2012, 126, 413-425.	1.4	24
2330	Myc, Aurora Kinase A, and mutant p53R172H co-operate in a mouse model of metastatic skin carcinoma. <i>Oncogene</i> , 2012, 31, 2680-2690.	2.6	27
2331	Gene expression profiling in glomeruli of diabetic nephropathy rat. <i>Experimental Biology and Medicine</i> , 2012, 237, 903-911.	1.1	13
2332	Association between SNPs and gene expression in multiple regions of the human brain. <i>Translational Psychiatry</i> , 2012, 2, e113-e113.	2.4	40
2333	Identifying Grade/Stage-Related Active Modules in Human Co-regulatory Networks: A Case Study for Breast Cancer. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 681-689.	1.0	1
2334	Advanced Bone Formation in Mice with a Dominant-negative Mutation in the Thyroid Hormone Receptor $\beta^2$ Gene due to Activation of Wnt/ $\beta^2$ -Catenin Protein Signaling. <i>Journal of Biological Chemistry</i> , 2012, 287, 17812-17822.	1.6	37
2335	Comprehensive Gene Expression Profiling in the Prefrontal Cortex Links Immune Activation and Neutrophil Infiltration to Antinociception. <i>Journal of Neuroscience</i> , 2012, 32, 35-45.	1.7	35
2336	Human Adipose Tissue Macrophages Display Activation of Cancer-related Pathways. <i>Journal of Biological Chemistry</i> , 2012, 287, 21904-21913.	1.6	60
2337	Differential Ly-6C expression identifies the recruited macrophage phenotype, which orchestrates the regression of murine liver fibrosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3186-95.	3.3	793
2338	The genomic response to courtship song stimulation in female <i>Drosophila melanogaster</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 1359-1365.	1.2	50

#	ARTICLE	IF	CITATIONS
2339	Oncogenic Kras Expression in Postmitotic Neurons Leads to S100A8-S100A9 Protein Overexpression and Gliosis. <i>Journal of Biological Chemistry</i> , 2012, 287, 22948-22958.	1.6	14
2340	RBF Binding to both Canonical E2F Targets and Noncanonical Targets Depends on Functional dE2F/dDP Complexes. <i>Molecular and Cellular Biology</i> , 2012, 32, 4375-4387.	1.1	60
2341	Widespread Polymorphism in the Positions of Stop Codons in <i>Drosophila melanogaster</i> . <i>Genome Biology and Evolution</i> , 2012, 4, 533-549.	1.1	25
2342	Exploration of Global Gene Expression Changes During the Estrous Cycle in Equine Endometrium1. <i>Biology of Reproduction</i> , 2012, 87, 136.	1.2	33
2343	Increased Immune Gene Expression and Immune Cell Infiltration in High-Grade Astrocytoma Distinguish Long-Term from Short-Term Survivors. <i>Journal of Immunology</i> , 2012, 189, 1920-1927.	0.4	62
2344	H3K4 demethylation by Jarid1a and Jarid1b contributes to retinoblastoma-mediated gene silencing during cellular senescence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8971-8976.	3.3	141
2345	Cardiopulmonary dysfunction in the Osteogenesis imperfecta mouse model <i>Aga2</i> and human patients are caused by bone-independent mechanisms. <i>Human Molecular Genetics</i> , 2012, 21, 3535-3545.	1.4	57
2346	Pancreas-enriched miRNA refines endocrine cell differentiation. <i>Development (Cambridge)</i> , 2012, 139, 3021-3031.	1.2	92
2347	Identification and Pathway Mapping of Furan Target Proteins Reveal Mitochondrial Energy Production and Redox Regulation as Critical Targets of Furan Toxicity. <i>Toxicological Sciences</i> , 2012, 126, 336-352.	1.4	37
2348	Leptin-Induced mTOR Activation Defines a Specific Molecular and Transcriptional Signature Controlling CD4+ Effector T Cell Responses. <i>Journal of Immunology</i> , 2012, 189, 2941-2953.	0.4	121
2349	A program for annotating and predicting the effects of single nucleotide polymorphisms, SnpEff. <i>Fly</i> , 2012, 6, 80-92.	0.9	8,643
2350	Different Gene Expression Patterns in Human Papillary and Reticular Fibroblasts. <i>Journal of Investigative Dermatology</i> , 2012, 132, 2565-2572.	0.3	133
2351	The atypical E2F family member E2F7 couples the p53 and RB pathways during cellular senescence. <i>Genes and Development</i> , 2012, 26, 1546-1557.	2.7	100
2352	Tissue-Selective Regulation of Androgen-Responsive Genes. <i>Endocrine Research</i> , 2012, 37, 203-215.	0.6	14
2353	ReLiance: a machine learning and literature-based prioritization of receptor-ligand pairings. <i>Bioinformatics</i> , 2012, 28, i569-i574.	1.8	5
2354	Complement C3 is a novel plasma clot component with anti-fibrinolytic properties. <i>Diabetes and Vascular Disease Research</i> , 2012, 9, 216-225.	0.9	79
2355	Novel Loci Associated With PR Interval in a Genome-Wide Association Study of 10 African American Cohorts. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 639-646.	5.1	48
2356	BEYOND COMPARING MEANS: THE USEFULNESS OF ANALYZING INTERINDIVIDUAL VARIATION IN GENE EXPRESSION FOR IDENTIFYING GENES ASSOCIATED WITH CANCER DEVELOPMENT. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1241013.	0.3	11

#	ARTICLE	IF	CITATIONS
2357	Mining the Bioinformation of Differentially Expressed Genes in Obese Mice Treated with Chronic Intermittent Hypoxia Based on the Bioinformatics Methods. <i>Applied Mechanics and Materials</i> , 0, 195-196, 429-434.	0.2	0
2358	Integrated Analysis of Multiple Gene Expression Profiling Datasets Revealed Novel Gene Signatures and Molecular Markers in Nasopharyngeal Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 166-175.	1.1	16
2359	Penetrance of biallelic SMARCAL1 mutations is associated with environmental and genetic disturbances of gene expression. <i>Human Molecular Genetics</i> , 2012, 21, 2572-2587.	1.4	57
2360	Progesterone Inhibits Uterine Gland Development in the Neonatal Mouse Uterus1. <i>Biology of Reproduction</i> , 2012, 86, 146, 1-9.	1.2	66
2362	Forkhead box N4 (Foxn4) activates Dll4-Notch signaling to suppress photoreceptor cell fates of early retinal progenitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E553-62.	3.3	73
2363	Integrated Analysis Reveals hsa-miR-142 as a Representative of a Lymphocyte-Specific Gene Expression and Methylation Signature. <i>Cancer Informatics</i> , 2012, 11, CIN.S9037.	0.9	20
2364	Comprehensive Characterization of Mesenchymal Stem Cells from Human Placenta and Fetal Membrane and Their Response to Osteoactivin Stimulation. <i>Stem Cells International</i> , 2012, 2012, 1-13.	1.2	61
2365	CUX1 transcription factor is required for optimal ATM/ATR-mediated responses to DNA damage. <i>Nucleic Acids Research</i> , 2012, 40, 4483-4495.	6.5	47
2366	Genome-wide analysis of p63 binding sites identifies AP-2 factors as co-regulators of epidermal differentiation. <i>Nucleic Acids Research</i> , 2012, 40, 7190-7206.	6.5	87
2367	Novel Proteomic Tools Reveal Essential Roles of SRP and Importance of Proper Membrane Protein Biogenesis. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011585.	2.5	18
2368	Annexin A2 Silencing Induces G2 Arrest of Non-small Cell Lung Cancer Cells through p53-dependent and -independent Mechanisms. <i>Journal of Biological Chemistry</i> , 2012, 287, 32512-32524.	1.6	64
2369	Down-regulation of NF- $\kappa$ B Transcriptional Activity in HIV-associated Kidney Disease by BRD4 Inhibition. <i>Journal of Biological Chemistry</i> , 2012, 287, 28840-28851.	1.6	172
2370	Morphine Produces Immunosuppressive Effects in Nonhuman Primates at the Proteomic and Cellular Levels. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 605-618.	2.5	45
2371	Single-cell analysis of population context advances RNAi screening at multiple levels. <i>Molecular Systems Biology</i> , 2012, 8, 579.	3.2	153
2372	Microtubule stability, Golgi organization, and transport flux require dystonin-a-MAP1B interaction. <i>Journal of Cell Biology</i> , 2012, 196, 727-742.	2.3	60
2373	Quantifying the white blood cell transcriptome as an accessible window to the multiorgan transcriptome. <i>Bioinformatics</i> , 2012, 28, 905-905.	1.8	22
2374	Elephant Transcriptome Provides Insights into the Evolution of Eutherian Placentation. <i>Genome Biology and Evolution</i> , 2012, 4, 713-725.	1.1	27
2375	A systematic characterization of genes underlying both complex and Mendelian diseases. <i>Human Molecular Genetics</i> , 2012, 21, 1611-1624.	1.4	35

#	ARTICLE	IF	CITATIONS
2376	Mice Lacking the $\beta_2$ Adrenergic Receptor Have a Unique Genetic Profile before and after Focal Brain Ischaemia. <i>ASN Neuro</i> , 2012, 4, AN20110020.	1.5	20
2377	Centrosome loss or amplification does not dramatically perturb global gene expression in <i>Drosophila</i> . <i>Biology Open</i> , 2012, 1, 983-993.	0.6	10
2378	Sertoli-cell-specific knockout of connexin 43 leads to multiple alterations in testicular gene expression in prepubertal mice. <i>DMM Disease Models and Mechanisms</i> , 2012, 5, 895-913.	1.2	37
2379	Changes in Brain Transcripts Related to Alzheimer's Disease in a Model of HFE Hemochromatosis are not Consistent with Increased Alzheimer's Disease Risk. <i>Journal of Alzheimer's Disease</i> , 2012, 30, 791-803.	1.2	11
2380	CUGBP1 and MBNL1 preferentially bind to 3' UTRs and facilitate mRNA decay. <i>Scientific Reports</i> , 2012, 2, 209.	1.6	150
2381	A Novel Tumor suppressor network in squamous malignancies. <i>Scientific Reports</i> , 2012, 2, 828.	1.6	11
2382	Proteomic Identification of RREB1, PDE6B, and CD209 Up-Regulated in Primitive Gut Tube Differentiated From Human Embryonic Stem Cells. <i>Pancreas</i> , 2012, 41, 65-73.	0.5	11
2383	Proteomic Analysis of Formalin-Fixed Paraffin-Embedded Pancreatic Tissue Using Liquid Chromatography Tandem Mass Spectrometry. <i>Pancreas</i> , 2012, 41, 175-185.	0.5	30
2384	Lipid metabolic pathways as lung cancer therapeutic targets: A computational study. <i>International Journal of Molecular Medicine</i> , 2012, 29, 519-529.	1.8	14
2385	Clinical utility and implementation of gene-expression profiling in myeloma: current status and challenges. <i>International Journal of Hematologic Oncology</i> , 2012, 1, 133-146.	0.7	0
2386	3T3 Cell Lines Stably Expressing Pax6 or Pax6(5a) – A New Tool Used for Identification of Common and Isoform Specific Target Genes. <i>PLoS ONE</i> , 2012, 7, e31915.	1.1	34
2387	Hepatic gene expression analysis of 2-aminoanthracene exposed Fisher-344 rats reveal patterns indicative of liver carcinoma and type 2 diabetes. <i>Journal of Toxicological Sciences</i> , 2012, 37, 1001-1016.	0.7	13
2388	Analysis of candidate genes of spontaneous arthritis in mice deficient for interleukin-1 receptor antagonist. <i>Genes and Genetic Systems</i> , 2012, 87, 107-113.	0.2	2
2389	Network Biology of Tumor Stem-like Cells Identified a Regulatory Role of CBX5 in Lung Cancer. <i>Scientific Reports</i> , 2012, 2, 584.	1.6	52
2390	Mitochondrial function, fatty acid metabolism, and immune system are relevant features of pig adipose tissue development. <i>Physiological Genomics</i> , 2012, 44, 1116-1124.	1.0	13
2391	Redefining interferon-producing killer dendritic cells as a novel intermediate in NK-cell differentiation. <i>Blood</i> , 2012, 119, 4349-4357.	0.6	30
2392	KAP1 regulates gene networks controlling mouse B-lymphoid cell differentiation and function. <i>Blood</i> , 2012, 119, 4675-4685.	0.6	39
2393	HIV-1 infection of human macrophages directly induces viperin which inhibits viral production. <i>Blood</i> , 2012, 120, 778-788.	0.6	184

#	ARTICLE	IF	CITATIONS
2394	Loss of mitochondrial protease OMA1 alters processing of the GTPase OPA1 and causes obesity and defective thermogenesis in mice. <i>EMBO Journal</i> , 2012, 31, 2117-2133.	3.5	230
2395	An environmental analysis of genes associated with schizophrenia: hypoxia and vascular factors as interacting elements in the neurodevelopmental model. <i>Molecular Psychiatry</i> , 2012, 17, 1194-1205.	4.1	95
2396	Nutritional Control of Growth and Development in Yeast. <i>Genetics</i> , 2012, 192, 73-105.	1.2	560
2397	Gene Expression Changes in C57BL/6J and DBA/2J Mice Following Prenatal Alcohol Exposure. <i>Alcoholism: Clinical and Experimental Research</i> , 2012, 36, 1519-1529.	1.4	47
2398	A Hierarchical Semiparametric Model for Incorporating Intergene Information for Analysis of Genomic Data. <i>Biometrics</i> , 2012, 68, 1168-1177.	0.8	2
2399	Microbiome and immunological interactions. <i>Nutrition Reviews</i> , 2012, 70, S18-S30.	2.6	96
2400	mrhl RNA, a Long Noncoding RNA, Negatively Regulates Wnt Signaling through Its Protein Partner Ddx5/p68 in Mouse Spermatogonial Cells. <i>Molecular and Cellular Biology</i> , 2012, 32, 3140-3152.	1.1	148
2401	Interleukin-17 Signaling in Inflammatory, Kupffer Cells, and Hepatic Stellate Cells Exacerbates Liver Fibrosis in Mice. <i>Gastroenterology</i> , 2012, 143, 765-776.e3.	0.6	536
2402	Retroelement Demethylation Associated with Abnormal Placentation in Mus musculus × Mus caroli Hybrids. <i>Biology of Reproduction</i> , 2012, 86, 88.	1.2	18
2403	EnrichNet: network-based gene set enrichment analysis. <i>Bioinformatics</i> , 2012, 28, i451-i457.	1.8	269
2404	A Novel Regulatory Factor Recruits the Nucleosome Remodeling Complex to Wingless Integrated (Wnt) Signaling Gene Promoters in Mouse Embryonic Stem Cells. <i>Journal of Biological Chemistry</i> , 2012, 287, 41103-41117.	1.6	12
2405	Host Response Signature to Staphylococcus aureus Alpha-Hemolysin Implicates Pulmonary Th17 Response. <i>Infection and Immunity</i> , 2012, 80, 3161-3169.	1.0	44
2406	Metscape 2 bioinformatics tool for the analysis and visualization of metabolomics and gene expression data. <i>Bioinformatics</i> , 2012, 28, 373-380.	1.8	392
2407	Step-Wise Methylation of Histone H3K9 Positions Heterochromatin at the Nuclear Periphery. <i>Cell</i> , 2012, 150, 934-947.	13.5	524
2408	The Cytokines Interleukin 27 and Interferon- $\gamma$ Promote Distinct Treg Cell Populations Required to Limit Infection-Induced Pathology. <i>Immunity</i> , 2012, 37, 511-523.	6.6	340
2409	Alkylation Sensitivity Screens Reveal a Conserved Cross-species Functionome. <i>Molecular Cancer Research</i> , 2012, 10, 1580-1596.	1.5	35
2410	Transcriptomic analysis of postmortem brain identifies dysregulated splicing events in novel candidate genes for schizophrenia. <i>Schizophrenia Research</i> , 2012, 142, 188-199.	1.1	28
2411	Regulated Accumulation of Desmosterol Integrates Macrophage Lipid Metabolism and Inflammatory Responses. <i>Cell</i> , 2012, 151, 138-152.	13.5	487

#	ARTICLE	IF	CITATIONS
2412	Early Alterations of the Immune Transcriptome in Cultured Progenitor Cells From Obese African-American Women. <i>Obesity</i> , 2012, 20, 1481-1490.	1.5	5
2413	Lack of dystrophin in <i>mdx</i> mice modulates the expression of genes involved in neuron survival and differentiation. <i>European Journal of Neuroscience</i> , 2012, 35, 691-701.	1.2	13
2414	Implications for health and disease in the genetic signature of the Ashkenazi Jewish population. <i>Genome Biology</i> , 2012, 13, R2.	13.9	48
2415	Genome-wide distribution of 5-formylcytosine in embryonic stem cells is associated with transcription and depends on thymine DNA glycosylase. <i>Genome Biology</i> , 2012, 13, R69.	13.9	205
2416	Muscle Gene Expression Is a Marker of Amyotrophic Lateral Sclerosis Severity. <i>Neurodegenerative Diseases</i> , 2012, 9, 38-52.	0.8	41
2417	Direct regulation of microRNA biogenesis and expression by estrogen receptor beta in hormone-responsive breast cancer. <i>Oncogene</i> , 2012, 31, 4196-4206.	2.6	87
2418	Inositol phosphatase regulation of gene expression in preadipocytes and adipocytes. <i>BioFactors</i> , 2012, 38, 450-457.	2.6	22
2419	Systems-level analysis of clinically different phenotypes of juvenile nasopharyngeal angiofibromas. <i>Laryngoscope</i> , 2012, 122, 2728-2735.	1.1	7
2420	Novel neurodevelopmental information revealed in amniotic fluid supernatant transcripts from fetuses with trisomies 18 and 21. <i>Human Genetics</i> , 2012, 131, 1751-1759.	1.8	32
2421	Gene expression profiling in rat kidney after intratracheal exposure to cadmium-doped nanoparticles. <i>Journal of Nanoparticle Research</i> , 2012, 14, 1.	0.8	15
2422	Transcriptome Analysis of the Planarian Eye Identifies ovo as a Specific Regulator of Eye Regeneration. <i>Cell Reports</i> , 2012, 2, 294-307.	2.9	174
2423	Three Distinct Patterns of Histone H3Y41 Phosphorylation Mark Active Genes. <i>Cell Reports</i> , 2012, 2, 470-477.	2.9	54
2424	Effects of heat shock protein 72 (Hsp72) on evolution of astrocyte activation following stroke in the mouse. <i>Experimental Neurology</i> , 2012, 238, 284-296.	2.0	53
2425	Finding disease similarity based on implicit semantic similarity. <i>Journal of Biomedical Informatics</i> , 2012, 45, 363-371.	2.5	122
2426	Protein indicators for HaCaT cell damage induced by UVB irradiation. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2012, 114, 94-101.	1.7	15
2427	Identification of Flotillin-1 as a novel biomarker for lymph node metastasis and prognosis of lung adenocarcinoma by quantitative plasma membrane proteome analysis. <i>Journal of Proteomics</i> , 2012, 77, 202-214.	1.2	27
2428	Early Activation of the Inflammatory Response in the Liver of Brain-Dead Non-Human Primates. <i>Journal of Surgical Research</i> , 2012, 176, 639-648.	0.8	25
2429	Genomic analysis of sleep deprivation reveals translational regulation in the hippocampus. <i>Physiological Genomics</i> , 2012, 44, 981-991.	1.0	123

#	ARTICLE	IF	CITATIONS
2430	Peripheral blood gene expression profile of atherosclerotic coronary artery disease in patients of different ethnicity in Malaysia. <i>Journal of Cardiology</i> , 2012, 60, 192-203.	0.8	19
2431	Transcriptional responses to loss of RNase H2 in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2012, 11, 933-941.	1.3	20
2432	Early life stage trimethyltin exposure induces ADP-ribosylation factor expression and perturbs the vascular system in zebrafish. <i>Toxicology</i> , 2012, 302, 129-139.	2.0	11
2433	Identification of novel NRF2-regulated genes by ChIP-Seq: influence on retinoid X receptor alpha. <i>Nucleic Acids Research</i> , 2012, 40, 7416-7429.	6.5	459
2434	Gene expression profiling of bovine periparturient placentomes: detection of molecular pathways potentially involved in the release of foetal membranes. <i>Reproduction</i> , 2012, 143, 85-105.	1.1	50
2435	MultiFacTV: Finding modules from higher-order gene expression profiles with time dimension. , 2012, , .		1
2436	Live-cell monitoring of periodic gene expression in synchronous human cells identifies Forkhead genes involved in cell cycle control. <i>Molecular Biology of the Cell</i> , 2012, 23, 3079-3093.	0.9	33
2437	A frequency-based gene selection method to identify robust biomarkers for radiation dose prediction. <i>International Journal of Radiation Biology</i> , 2012, 88, 267-276.	1.0	44
2438	Gene Expression in Low- and High-Dose-Irradiated Human Peripheral Blood Lymphocytes: Possible Applications for Biodosimetry. <i>Radiation Research</i> , 2012, 178, 304.	0.7	64
2439	Global alteration in gene expression profiles of deciduas from women with idiopathic recurrent pregnancy loss. <i>Molecular Human Reproduction</i> , 2012, 18, 442-450.	1.3	69
2440	Controlled reoxygenation cardiopulmonary bypass is associated with reduced transcriptomic changes in cyanotic tetralogy of Fallot patients undergoing surgery. <i>Physiological Genomics</i> , 2012, 44, 1098-1106.	1.0	18
2441	A transcriptomics-based in vitro assay for predicting chemical genotoxicity in vivo. <i>Carcinogenesis</i> , 2012, 33, 1421-1429.	1.3	80
2442	Response of Primary Human Airway Epithelial Cells to Influenza Infection: A Quantitative Proteomic Study. <i>Journal of Proteome Research</i> , 2012, 11, 4132-4146.	1.8	65
2443	Discovery of Novel Glucose-Regulated Proteins in Isolated Human Pancreatic Islets Using LC-MS/MS-Based Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 3520-3532.	1.8	69
2444	Evolution and function of CAG/polyglutamine repeats in protein-protein interaction networks. <i>Nucleic Acids Research</i> , 2012, 40, 4273-4287.	6.5	166
2445	Clinical and molecular characteristics of congenital glioblastoma. <i>Neuro-Oncology</i> , 2012, 14, 931-941.	0.6	45
2446	Identification of Targets of c-Src Tyrosine Kinase by Chemical Complementation and Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 355-369.	2.5	47
2447	Transcriptional signatures as a disease-specific and predictive inflammatory biomarker for type 1 diabetes. <i>Genes and Immunity</i> , 2012, 13, 593-604.	2.2	67



#	ARTICLE	IF	CITATIONS
2448	Spleen transcriptome profiles of BALB/c mouse in response to egg ovomucoid sensitisation and challenge. <i>Food and Agricultural Immunology</i> , 2012, 23, 227-246.	0.7	2
2449	Comprehensive Identification of Substrates for F-box Proteins by Differential Proteomics Analysis. <i>Journal of Proteome Research</i> , 2012, 11, 3175-3185.	1.8	28
2450	Two-Dimensional Liquid Chromatography-Tandem Mass Spectrometry Coupled with Isobaric Tags for Relative and Absolute Quantification (iTRAQ) Labeling Approach Revealed First Proteome Profiles of Pulmonary Alveolar Macrophages Infected with Porcine Reproductive and Respiratory Syndrome Virus. <i>Journal of Proteome Research</i> , 2012, 11, 2890-2903.	1.8	50
2451	Global Analysis of Phosphoproteome Regulation by the Ser/Thr Phosphatase Ppt1 in <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2012, 11, 2397-2408.	1.8	22
2452	Patterns of Gene and Metabolite Define the Effects of Extracellular Osmolality on Kidney Collecting Duct. <i>Journal of Proteome Research</i> , 2012, 11, 3816-3828.	1.8	17
2453	Transcriptome analysis of subcutaneous adipose tissues in beef cattle using 3 $\times$ digital gene expression-tag profiling. <i>Journal of Animal Science</i> , 2012, 90, 171-183.	0.2	28
2454	Renin mRNA is upregulated in testes and testicular cells in response to treatment with aflatoxin B1. <i>Theriogenology</i> , 2012, 77, 331-337.e7.	0.9	15
2455	A genomics-based approach to assessment of vaccine safety and immunogenicity in children. <i>Vaccine</i> , 2012, 30, 1865-1874.	1.7	21
2456	Genome-wide dynamic changes of DNA methylation of repetitive elements in human embryonic stem cells and fetal fibroblasts. <i>Genomics</i> , 2012, 99, 10-17.	1.3	45
2457	GFOLD: a generalized fold change for ranking differentially expressed genes from RNA-seq data. <i>Bioinformatics</i> , 2012, 28, 2782-2788.	1.8	376
2458	Differential Modulation of the Oligodendrocyte Transcriptome by Sonic Hedgehog and Bone Morphogenetic Protein 4 via Opposing Effects on Histone Acetylation. <i>Journal of Neuroscience</i> , 2012, 32, 6651-6664.	1.7	77
2459	Wnt5a Potentiates TGF- $\beta$ 2 Signaling to Promote Colonic Crypt Regeneration After Tissue Injury. <i>Science</i> , 2012, 338, 108-113.	6.0	402
2460	SIRT7 links H3K18 deacetylation to maintenance of oncogenic transformation. <i>Nature</i> , 2012, 487, 114-118.	13.7	503
2461	Inhibition of serine palmitoyltransferase delays the onset of radiation-induced pulmonary fibrosis through the negative regulation of sphingosine kinase-1 expression. <i>Journal of Lipid Research</i> , 2012, 53, 1553-1568.	2.0	43
2462	Microarray Meta-Analysis: From Data to Expression to Biological Relationships. , 2012, , 59-77.		11
2463	Transcriptome-wide Analysis of Exosome Targets. <i>Molecular Cell</i> , 2012, 48, 422-433.	4.5	184
2464	Temporal Profiling and Pulsed SILAC Labeling Identify Novel Secreted Proteins During Ex Vivo Osteoblast Differentiation of Human Stromal Stem Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 989-1007.	2.5	75
2465	Interspecies Comparison of Human and Murine Scleroderma Reveals IL-13 and CCL2 as Disease Subset-Specific Targets. <i>American Journal of Pathology</i> , 2012, 180, 1080-1094.	1.9	78

#	ARTICLE	IF	CITATIONS
2466	Overexpression of Tumor Necrosis Factor- $\alpha$ in the Lungs Alters Immune Response, Matrix Remodeling, and Repair and Maintenance Pathways. <i>American Journal of Pathology</i> , 2012, 180, 1413-1430.	1.9	46
2467	Histone modification profiles characterize function-specific gene regulation. <i>Journal of Theoretical Biology</i> , 2012, 310, 132-142.	0.8	12
2468	Valproic acid reversed pathologic endothelial cell gene expression profile associated with ischemia-reperfusion injury in a swine hemorrhagic shock model. <i>Journal of Vascular Surgery</i> , 2012, 55, 1096-1103.e51.	0.6	53
2469	Polycomb Protein Ezh1 Promotes RNA Polymerase II Elongation. <i>Molecular Cell</i> , 2012, 45, 255-262.	4.5	163
2470	Direct Recruitment of Polycomb Repressive Complex 1 to Chromatin by Core Binding Transcription Factors. <i>Molecular Cell</i> , 2012, 45, 330-343.	4.5	188
2471	Oligomeric amyloid- $\beta$ peptide affects the expression of genes involved in steroid and lipid metabolism in primary neurons. <i>Neurochemistry International</i> , 2012, 61, 321-333.	1.9	21
2472	PDX1 regulation of FABP1 and novel target genes in human intestinal epithelial Caco-2 cells. <i>Biochemical and Biophysical Research Communications</i> , 2012, 423, 183-187.	1.0	5
2473	Down-regulation of the PTTG1 proto-oncogene contributes to the melanoma suppressive effects of the cyclin-dependent kinase inhibitor PHA-848125. <i>Biochemical Pharmacology</i> , 2012, 84, 598-611.	2.0	26
2474	Cerebral gene expression and neurobehavioural responses in mice pups exposed to methylmercury and docosahexaenoic acid through the maternal diet. <i>Environmental Toxicology and Pharmacology</i> , 2012, 33, 26-38.	2.0	10
2475	Identification and characterization of the human leiomyoma side population as putative tumor-initiating cells. <i>Fertility and Sterility</i> , 2012, 98, 741-751.e6.	0.5	101
2476	Microarray expression analysis of genes and pathways involved in growth plate cartilage injury responses and bony repair. <i>Bone</i> , 2012, 50, 1081-1091.	1.4	52
2477	The multi-reference contrast method: Facilitating set enrichment analysis. <i>Computers in Biology and Medicine</i> , 2012, 42, 188-194.	3.9	5
2478	Cell-Surface Proteomics Identifies Lineage-Specific Markers of Embryo-Derived Stem Cells. <i>Developmental Cell</i> , 2012, 22, 887-901.	3.1	134
2479	Transcription factors TP53 and SP1 and the osteogenic differentiation of dental stem cells. <i>Differentiation</i> , 2012, 83, 10-16.	1.0	17
2480	RYBP-PRC1 Complexes Mediate H2A Ubiquitylation at Polycomb Target Sites Independently of PRC2 and H3K27me3. <i>Cell</i> , 2012, 148, 664-678.	13.5	513
2481	TAK1 Inhibition Promotes Apoptosis in KRAS-Dependent Colon Cancers. <i>Cell</i> , 2012, 148, 639-650.	13.5	245
2482	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. <i>Cell</i> , 2012, 148, 1293-1307.	13.5	1,134
2483	Cloning and expression of porcine Dicer and the impact of developmental stage and culture conditions on MicroRNA expression in porcine embryos. <i>Gene</i> , 2012, 501, 198-205.	1.0	33

#	ARTICLE	IF	CITATIONS
2484	Reconstructing Models from Proteomics Data. , 2012, , 23-80.		0
2485	Quantitative Proteomic Profiling Identifies Protein Correlates to EGFR Kinase Inhibition. <i>Molecular Cancer Therapeutics</i> , 2012, 11, 1071-1081.	1.9	6
2486	CLIP-seq of eIF4AIII reveals transcriptome-wide mapping of the human exon junction complex. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1124-1131.	3.6	197
2487	Proteomic analysis of mitochondria from infantile hemangioma endothelial cells treated with sodium morrhuate and its liposomal formulation. <i>Journal of Biochemical and Molecular Toxicology</i> , 2012, 26, 374-380.	1.4	4
2488	AbsIDconvert: An absolute approach for converting genetic identifiers at different granularities. <i>BMC Bioinformatics</i> , 2012, 13, 229.	1.2	8
2489	Transcriptome landscape of the human placenta. <i>BMC Genomics</i> , 2012, 13, 115.	1.2	83
2490	Gene expression analysis of <i>Drosophila</i> Manf mutants reveals perturbations in membrane traffic and major metabolic changes. <i>BMC Genomics</i> , 2012, 13, 134.	1.2	49
2491	Characterization of the transcriptome profiles related to globin gene switching during in vitro erythroid maturation. <i>BMC Genomics</i> , 2012, 13, 153.	1.2	23
2492	Transcriptome analysis of a long-lived natural <i>Drosophila</i> variant: a prominent role of stress- and reproduction-genes in lifespan extension. <i>BMC Genomics</i> , 2012, 13, 167.	1.2	43
2493	Postmortem cardiac tissue maintains gene expression profile even after late harvesting. <i>BMC Genomics</i> , 2012, 13, 26.	1.2	39
2494	Integrated analysis of microRNA expression and mRNA transcriptome in lungs of avian influenza virus infected broilers. <i>BMC Genomics</i> , 2012, 13, 278.	1.2	99
2495	Distinct and overlapping gene regulatory networks in BMP- and HDAC-controlled cell fate determination in the embryonic forebrain. <i>BMC Genomics</i> , 2012, 13, 298.	1.2	11
2496	An unbiased approach to identify genes involved in development in a turtle with temperature-dependent sex determination. <i>BMC Genomics</i> , 2012, 13, 308.	1.2	8
2497	<i>Burkholderia pseudomallei</i> transcriptional adaptation in macrophages. <i>BMC Genomics</i> , 2012, 13, 328.	1.2	52
2498	Medulla oblongata transcriptome changes during presymptomatic natural scrapie and their association with prion-related lesions. <i>BMC Genomics</i> , 2012, 13, 399.	1.2	12
2499	Genome-wide landscape of liver X receptor chromatin binding and gene regulation in human macrophages. <i>BMC Genomics</i> , 2012, 13, 50.	1.2	69
2500	Genome-wide analysis of hepatic LRH-1 reveals a promoter binding preference and suggests a role in regulating genes of lipid metabolism in concert with FXR. <i>BMC Genomics</i> , 2012, 13, 51.	1.2	40
2501	LRpath analysis reveals common pathways dysregulated via DNA methylation across cancer types. <i>BMC Genomics</i> , 2012, 13, 526.	1.2	65

#	ARTICLE	IF	CITATIONS
2502	Effects of immunostimulation on social behavior, chemical communication and genome-wide gene expression in honey bee workers ( <i>Apis mellifera</i> ). <i>BMC Genomics</i> , 2012, 13, 558.	1.2	97
2503	Factors regulated by interferon gamma and hypoxia-inducible factor 1A contribute to responses that protect mice from <i>Coccidioides immitis</i> infection. <i>BMC Microbiology</i> , 2012, 12, 218.	1.3	17
2504	Fluoxetine prevents development of an early stress-related molecular signature in the rat infralimbic medial prefrontal cortex. Implications for depression?. <i>BMC Neuroscience</i> , 2012, 13, 125.	0.8	29
2505	Transcriptome analysis of amoeboid and ramified microglia isolated from the corpus callosum of rat brain. <i>BMC Neuroscience</i> , 2012, 13, 64.	0.8	90
2506	Systems analysis of inflammatory bowel disease based on comprehensive gene information. <i>BMC Medical Genetics</i> , 2012, 13, 25.	2.1	8
2507	Genistein cooperates with the histone deacetylase inhibitor vorinostat to induce cell death in prostate cancer cells. <i>BMC Cancer</i> , 2012, 12, 145.	1.1	53
2508	NF- $\kappa$ B2 mutation targets survival, proliferation and differentiation pathways in the pathogenesis of plasma cell tumors. <i>BMC Cancer</i> , 2012, 12, 203.	1.1	4
2509	The database of chromosome imbalance regions and genes resided in lung cancer from Asian and Caucasian identified by array-comparative genomic hybridization. <i>BMC Cancer</i> , 2012, 12, 235.	1.1	42
2510	Role of aldo-keto reductases and other doxorubicin pharmacokinetic genes in doxorubicin resistance, DNA binding, and subcellular localization. <i>BMC Cancer</i> , 2012, 12, 381.	1.1	79
2511	An update on the strategies in multicomponent activity monitoring within the phytopharmaceutical field. <i>BMC Complementary and Alternative Medicine</i> , 2012, 12, 18.	3.7	17
2512	Efficient algorithms for fast integration on large data sets from multiple sources. <i>BMC Medical Informatics and Decision Making</i> , 2012, 12, 59.	1.5	10
2513	An antibody microarray analysis of serum cytokines in neurodegenerative Parkinsonian syndromes. <i>Proteome Science</i> , 2012, 10, 71.	0.7	22
2514	Plasma proteomics shows an elevation of the anti-inflammatory protein APOA-IV in chronic equine laminitis. <i>BMC Veterinary Research</i> , 2012, 8, 179.	0.7	14
2515	Identification of estrogen responsive genes using esophageal squamous cell carcinoma (ESCC) as a model. <i>BMC Systems Biology</i> , 2012, 6, 135.	3.0	2
2516	Genomic signatures for predicting survival and adjuvant chemotherapy benefit in patients with non-small-cell lung cancer. <i>BMC Medical Genomics</i> , 2012, 5, 30.	0.7	34
2517	Impact of Collection and Storage of Lung Tumor Tissue on Whole Genome Expression Profiling. <i>Journal of Molecular Diagnostics</i> , 2012, 14, 140-148.	1.2	36
2519	Hepatitis B Virus Encoded X Protein Suppresses Apoptosis by Inhibition of the Caspase-Independent Pathway. <i>Journal of Proteome Research</i> , 2012, 11, 4803-4813.	1.8	25
2520	Gene network analyses of first service conception in Brangus heifers: Use of genome and trait associations, hypothalamic-transcriptome information, and transcription factors1. <i>Journal of Animal Science</i> , 2012, 90, 2894-2906.	0.2	66

#	ARTICLE	IF	CITATIONS
2521	Recurrent mutations in the U2AF1 splicing factor in myelodysplastic syndromes. <i>Nature Genetics</i> , 2012, 44, 53-57.	9.4	513
2522	Deep brain stimulation induces rapidly reversible transcript changes in Parkinson's leucocytes. <i>Journal of Cellular and Molecular Medicine</i> , 2012, 16, 1496-1507.	1.6	15
2523	Genome-Wide Bacterial Toxicity Screening Uncovers the Mechanisms of Toxicity of a Cationic Polystyrene Nanomaterial. <i>Environmental Science &amp; Technology</i> , 2012, 46, 2398-2405.	4.6	54
2524	Noncanonical MicroRNAs and Endogenous siRNAs in Lytic Infection of Murine Gammaherpesvirus. <i>PLoS ONE</i> , 2012, 7, e47863.	1.1	20
2525	The Human Pancreatic Islet Transcriptome: Expression of Candidate Genes for Type 1 Diabetes and the Impact of Pro-Inflammatory Cytokines. <i>PLoS Genetics</i> , 2012, 8, e1002552.	1.5	398
2526	Using the Bioconductor GeneAnswers Package to Interpret Gene Lists. <i>Methods in Molecular Biology</i> , 2012, 802, 101-112.	0.4	22
2527	Relationship between pro- and anti-inflammatory cytokines profiles and some haematological parameters in some Cameroonians infected with <i>Onchocerca volvulus</i> . <i>Asian Pacific Journal of Tropical Medicine</i> , 2012, 5, 713-717.	0.4	2
2528	Clinical, molecular, and cellular immunologic findings in patients with SP110-associated veno-occlusive disease with immunodeficiency syndrome. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 130, 735-742.e6.	1.5	49
2529	Divergent Whole-Genome Methylation Maps of Human and Chimpanzee Brains Reveal Epigenetic Basis of Human Regulatory Evolution. <i>American Journal of Human Genetics</i> , 2012, 91, 455-465.	2.6	147
2530	A Noncoding, Regulatory Mutation Implicates HCFC1 in Nonsyndromic Intellectual Disability. <i>American Journal of Human Genetics</i> , 2012, 91, 694-702.	2.6	89
2531	Four day inhibition of prolyl oligopeptidase causes significant changes in the peptidome of rat brain, liver and kidney. <i>Biochimie</i> , 2012, 94, 1849-1859.	1.3	20
2532	Administration of botanicals with the diet regulates gene expression in peripheral blood cells of Sarda sheep during ACTH challenge. <i>Domestic Animal Endocrinology</i> , 2012, 43, 213-226.	0.8	24
2533	Prediction of gene network models in limb muscle precursors. <i>Gene</i> , 2012, 509, 16-23.	1.0	8
2534	Dose-response analysis of phthalate effects on gene expression in rat whole embryo culture. <i>Toxicology and Applied Pharmacology</i> , 2012, 264, 32-41.	1.3	22
2535	Comparative analysis of the invasion-associated genes expression pattern in first trimester trophoblastic (HTR-8/SVneo) and JEG-3 choriocarcinoma cells. <i>Placenta</i> , 2012, 33, 874-877.	0.7	38
2536	Stromal galectin-1 expression is associated with long-term survival in resectable pancreatic ductal adenocarcinoma. <i>Cancer Biology and Therapy</i> , 2012, 13, 899-907.	1.5	56
2537	Clonal Architecture of Secondary Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2012, 366, 1090-1098.	13.9	688
2538	Systems-pharmacology dissection of a drug synergy in imatinib-resistant CML. <i>Nature Chemical Biology</i> , 2012, 8, 905-912.	3.9	96

#	ARTICLE	IF	CITATIONS
2539	Linking Variants from Genome-Wide Association Analysis to Function via Transcriptional Network Analysis. <i>Methods in Molecular Biology</i> , 2012, 910, 297-308.	0.4	0
2540	Detection and Phylogenetic Assessment of Conserved Synteny Derived from Whole Genome Duplications. <i>Methods in Molecular Biology</i> , 2012, 855, 385-395.	0.4	23
2541	Gene expression during long-term culture of mesenchymal stem cells obtained from patients with amyotrophic lateral sclerosis. <i>Biochip Journal</i> , 2012, 6, 342-353.	2.5	2
2542	Gold nanoparticle-mediated gene delivery induces widespread changes in the expression of innate immunity genes. <i>Gene Therapy</i> , 2012, 19, 347-353.	2.3	53
2543	New Insight on the Mechanisms of Epileptogenesis in the Developing Brain. <i>Advances and Technical Standards in Neurosurgery</i> , 2012, 39, 3-44.	0.2	20
2544	Dysregulation of Uterine Signaling Pathways in Progesterone Receptor-Cre Knockout of Dicer. <i>Molecular Endocrinology</i> , 2012, 26, 1552-1566.	3.7	28
2546	Hypothesis-driven candidate genes for schizophrenia compared to genome-wide association results. <i>Psychological Medicine</i> , 2012, 42, 607-616.	2.7	83
2547	Genome-wide copy number variation study associates metabotropic glutamate receptor gene networks with attention deficit hyperactivity disorder. <i>Nature Genetics</i> , 2012, 44, 78-84.	9.4	334
2548	Benzothiadiazole-elicited defense priming and systemic acquired resistance against bacterial and viral pathogens of pepper under field conditions. <i>Plant Biotechnology Reports</i> , 2012, 6, 373-380.	0.9	21
2549	Application of a systems approach to study developmental gene regulation. <i>Biophysical Reviews</i> , 2012, 4, 245-253.	1.5	2
2550	The Development and Research of Bioinformatics in Neuroscience. <i>AASRI Procedia</i> , 2012, 1, 359-364.	0.6	4
2551	Identification of Cell Surface Targets through Meta-analysis of Microarray Data. <i>Neoplasia</i> , 2012, 14, 666-669.	2.3	17
2552	Human Induced Pluripotent Stem Cells Derived Under Feeder-Free Conditions Display Unique Cell Cycle and DNA Replication Gene Profiles. <i>Stem Cells and Development</i> , 2012, 21, 206-216.	1.1	23
2553	Molecular basis of acquired epileptogenesis. <i>Handbook of Clinical Neurology</i> / Edited By P J Vinken and C W Bruyn, 2012, 107, 3-12.	1.0	9
2554	A genome-wide association study of Alzheimer's disease using random forests and enrichment analysis. <i>Science China Life Sciences</i> , 2012, 55, 618-625.	2.3	12
2555	Mapping of lamin A- and progerin-interacting genome regions. <i>Chromosoma</i> , 2012, 121, 447-464.	1.0	86
2557	Hypoxia Regulated Gene Transcription in Human Optic Nerve Lamina Cribrosa Cells in Culture. , 2012, 53, 2243.		24
2558	Position-dependent FUS-RNA interactions regulate alternative splicing events and transcriptions. <i>Scientific Reports</i> , 2012, 2, 529.	1.6	180

#	ARTICLE	IF	CITATIONS
2559	Proteomic Analysis (GeLCâ€‘MS/MS) of ePFT-Collected Pancreatic Fluid in Chronic Pancreatitis. <i>Journal of Proteome Research</i> , 2012, 11, 1897-1912.	1.8	25
2560	Blood-Based Gene Expression Signatures of Infants and Toddlers With Autism. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2012, 51, 934-944.e2.	0.3	98
2561	Proteomic Analysis of Eccrine Sweat: Implications for the Discovery of Schizophrenia Biomarker Proteins. <i>Journal of Proteome Research</i> , 2012, 11, 2127-2139.	1.8	119
2562	In vivo skin leptin modulation after 14 MeV neutron irradiation: a molecular and FT-IR spectroscopic study. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 1317-1326.	1.9	41
2563	Quantitative biomedical annotation using medical subject heading over-representation profiles (MeSHOPs). <i>BMC Bioinformatics</i> , 2012, 13, 249.	1.2	24
2564	Probing the <i>Xenopus laevis</i> inner ear transcriptome for biological function. <i>BMC Genomics</i> , 2012, 13, 225.	1.2	11
2565	Cliques for the identification of gene signatures for colorectal cancer across population. <i>BMC Systems Biology</i> , 2012, 6, S17.	3.0	44
2566	Computational gene network analysis reveals TNF-induced angiogenesis. <i>BMC Systems Biology</i> , 2012, 6, S12.	3.0	16
2567	Detection of biomarkers for Hepatocellular Carcinoma using a hybrid univariate gene selection methods. <i>Theoretical Biology and Medical Modelling</i> , 2012, 9, 34.	2.1	14
2568	A gene expression signature of emphysema-related lung destruction and its reversal by the tripeptide GHK. <i>Genome Medicine</i> , 2012, 4, 67.	3.6	94
2569	Gene expression profiling of peripheral blood mononuclear cells in the setting of peripheral arterial disease. <i>Journal of Clinical Bioinformatics</i> , 2012, 2, 6.	1.2	39
2570	AP-1 Transcription Factors, Mucin-Type Molecules and MMPs Regulate the IL-11 Mediated Invasiveness of JEG-3 and HTR-8/SVneo Trophoblastic Cells. <i>PLoS ONE</i> , 2012, 7, e29745.	1.1	26
2571	Microarray Analysis of HIV Resistant Female Sex Workers Reveal a Gene Expression Signature Pattern Reminiscent of a Lowered Immune Activation State. <i>PLoS ONE</i> , 2012, 7, e30048.	1.1	51
2572	The Transcriptional Response of <i>Caenorhabditis elegans</i> to Ivermectin Exposure Identifies Novel Genes Involved in the Response to Reduced Food Intake. <i>PLoS ONE</i> , 2012, 7, e31367.	1.1	31
2573	The Gene Expression Analysis of Blood Reveals S100A11 and AQP9 as Potential Biomarkers of Infective Endocarditis. <i>PLoS ONE</i> , 2012, 7, e31490.	1.1	46
2574	Integrative Genomic Analysis Reveals Extended Germline Homozygosity with Lung Cancer Risk in the PLCO Cohort. <i>PLoS ONE</i> , 2012, 7, e31975.	1.1	13
2575	Knockdown of SF-1 and RNF31 Affects Components of Steroidogenesis, TGFÎ², and Wnt/Î²-catenin Signaling in Adrenocortical Carcinoma Cells. <i>PLoS ONE</i> , 2012, 7, e32080.	1.1	24
2576	PTRF/Cavin-1 and MIF Proteins Are Identified as Non-Small Cell Lung Cancer Biomarkers by Label-Free Proteomics. <i>PLoS ONE</i> , 2012, 7, e33752.	1.1	60

#	ARTICLE	IF	CITATIONS
2577	HDL Proteome in Hemodialysis Patients: A Quantitative Nanoflow Liquid Chromatography-Tandem Mass Spectrometry Approach. PLoS ONE, 2012, 7, e34107.	1.1	67
2578	Gene Regulation of Intestinal Porcine Epithelial Cells IPEC-J2 Is Dependent on the Site of Deoxynivalenol Toxicological Action. PLoS ONE, 2012, 7, e34136.	1.1	28
2579	Focused Examination of the Intestinal lamina Propria Yields Greater Molecular Insight into Mechanisms Underlying SIV Induced Immune Dysfunction. PLoS ONE, 2012, 7, e34561.	1.1	21
2580	Experimental Verification of a Predicted Intronic MicroRNA in Human NGFR Gene with a Potential Pro-Apoptotic Function. PLoS ONE, 2012, 7, e35561.	1.1	29
2581	Linking Proteins to Signaling Pathways for Experiment Design and Evaluation. PLoS ONE, 2012, 7, e36202.	1.1	28
2582	Transcriptional Programs Controlling Perinatal Lung Maturation. PLoS ONE, 2012, 7, e37046.	1.1	67
2583	Expression Profiling Reveals Novel Hypoxic Biomarkers in Peripheral Blood of Adult Mice Exposed to Chronic Hypoxia. PLoS ONE, 2012, 7, e37497.	1.1	16
2584	Oligonucleotide Microarray Analysis of Dietary-Induced Hyperlipidemia Gene Expression Profiles in Miniature Pigs. PLoS ONE, 2012, 7, e37581.	1.1	16
2585	Circadian Rhythm-Dependent Alterations of Gene Expression in Drosophila Brain Lacking Fragile X Mental Retardation Protein. PLoS ONE, 2012, 7, e37937.	1.1	19
2586	Role of MXD3 in Proliferation of DAOY Human Medulloblastoma Cells. PLoS ONE, 2012, 7, e38508.	1.1	24
2587	Intra- and Inter-Individual Variance of Gene Expression in Clinical Studies. PLoS ONE, 2012, 7, e38650.	1.1	35
2588	High-Throughput Transcriptomic and RNAi Analysis Identifies AIM1, ERGIC1, TMED3 and TPX2 as Potential Drug Targets in Prostate Cancer. PLoS ONE, 2012, 7, e39801.	1.1	54
2589	CD28 Costimulation Regulates Genome-Wide Effects on Alternative Splicing. PLoS ONE, 2012, 7, e40032.	1.1	51
2590	Dynamic Changes in Ezh2 Gene Occupancy Underlie Its Involvement in Neural Stem Cell Self-Renewal and Differentiation towards Oligodendrocytes. PLoS ONE, 2012, 7, e40399.	1.1	59
2591	Twist1 Transcriptional Targets in the Developing Atrio-Ventricular Canal of the Mouse. PLoS ONE, 2012, 7, e40815.	1.1	10
2592	IKAROS Deletions Dictate a Unique Gene Expression Signature in Patients with Adult B-Cell Acute Lymphoblastic Leukemia. PLoS ONE, 2012, 7, e40934.	1.1	73
2593	Cre-Mediated Stress Affects Sirtuin Expression Levels, Peroxisome Biogenesis and Metabolism, Antioxidant and Proinflammatory Signaling Pathways. PLoS ONE, 2012, 7, e41097.	1.1	26
2594	Measuring the Maturity of the Fast-Spiking Interneuron Transcriptional Program in Autism, Schizophrenia, and Bipolar Disorder. PLoS ONE, 2012, 7, e41215.	1.1	64



#	ARTICLE	IF	CITATIONS
2595	Prion Protein and Shadoo Are Involved in Overlapping Embryonic Pathways and Trophoblastic Development. PLoS ONE, 2012, 7, e41959.	1.1	22
2596	The B-MYB Transcriptional Network Guides Cell Cycle Progression and Fate Decisions to Sustain Self-Renewal and the Identity of Pluripotent Stem Cells. PLoS ONE, 2012, 7, e42350.	1.1	35
2597	Phosphoproteome of Human Glioblastoma Initiating Cells Reveals Novel Signaling Regulators Encoded by the Transcriptome. PLoS ONE, 2012, 7, e43398.	1.1	34
2598	miRNA Regulation of Gene Expression: A Predictive Bioinformatics Analysis in the Postnatally Developing Monkey Hippocampus. PLoS ONE, 2012, 7, e43435.	1.1	13
2599	Diversity and Complexity in Chromatin Recognition by TFII-I Transcription Factors in Pluripotent Embryonic Stem Cells and Embryonic Tissues. PLoS ONE, 2012, 7, e44443.	1.1	23
2600	Analysis of the Transcriptomes Downstream of Eyeless and the Hedgehog, Decapentaplegic and Notch Signaling Pathways in <i>Drosophila melanogaster</i> . PLoS ONE, 2012, 7, e44583.	1.1	12
2601	Peripheral Blood Gene Expression as a Novel Genomic Biomarker in Complicated Sarcoidosis. PLoS ONE, 2012, 7, e44818.	1.1	73
2602	Multi-Edge Gene Set Networks Reveal Novel Insights into Global Relationships between Biological Themes. PLoS ONE, 2012, 7, e45211.	1.1	10
2603	Inhibition of AKT with the Orally Active Allosteric AKT Inhibitor, MK-2206, Sensitizes Endometrial Cancer Cells to Progestin. PLoS ONE, 2012, 7, e41593.	1.1	45
2604	Exploring the Transcriptome of Ciliated Cells Using In Silico Dissection of Human Tissues. PLoS ONE, 2012, 7, e35618.	1.1	73
2605	Elongation Factor 1 alpha1 and Genes Associated with Usher Syndromes Are Downstream Targets of GBX2. PLoS ONE, 2012, 7, e47366.	1.1	13
2606	DNA Hypomethylation Affects Cancer-Related Biological Functions and Genes Relevant in Neuroblastoma Pathogenesis. PLoS ONE, 2012, 7, e48401.	1.1	31
2607	Structural, Genetic, and Functional Signatures of Disordered Neuro-Immunological Development in Autism Spectrum Disorder. PLoS ONE, 2012, 7, e48835.	1.1	15
2608	Building a Statistical Model for Predicting Cancer Genes. PLoS ONE, 2012, 7, e49175.	1.1	2
2609	Characteristics and Predictive Value of Blood Transcriptome Signature in Males with Autism Spectrum Disorders. PLoS ONE, 2012, 7, e49475.	1.1	151
2610	Micro-Scale Genomic DNA Copy Number Aberrations as Another Means of Mutagenesis in Breast Cancer. PLoS ONE, 2012, 7, e51719.	1.1	13
2611	Transcriptomic profiles of Japanese medaka ( <i>Oryzias latipes</i> ) in response to alkalinity stress. Genetics and Molecular Research, 2012, 11, 2200-2246.	0.3	25
2612	Genome-Wide Identification and Quantification of cis- and trans-Regulated Genes Responding to Marek's Disease Virus Infection via Analysis of Allele-Specific Expression. Frontiers in Genetics, 2012, 2, 113.	1.1	20

#	ARTICLE	IF	CITATIONS
2613	Global Approaches to the Role of miRNAs in Drug-Induced Changes in Gene Expression. <i>Frontiers in Genetics</i> , 2012, 3, 109.	1.1	21
2614	Non-Biased Enrichment Does Not Improve Quantitative Proteomic Delineation of Reovirus T3D-Infected HeLa Cell Protein Alterations. <i>Frontiers in Microbiology</i> , 2012, 3, 310.	1.5	6
2615	Cortical Auditory Deafferentation Induces Long-Term Plasticity in the Inferior Colliculus of Adult Rats: Microarray and qPCR Analysis. <i>Frontiers in Neural Circuits</i> , 2012, 6, 86.	1.4	9
2616	Sex-Specific Modulation of Gene Expression Networks in Murine Hypothalamus. <i>Frontiers in Neuroscience</i> , 2012, 6, 63.	1.4	49
2617	Comparative molecular portraits of human unfertilized oocytes and primordial germ cells at 10 weeks of gestation. <i>International Journal of Developmental Biology</i> , 2012, 56, 789-797.	0.3	9
2618	In Vivo Topoisomerase I Inhibition Attenuates the Expression of Hypoxia-Inducible Factor 1 $\alpha$ Target Genes and Decreases Tumor Angiogenesis. <i>Molecular Medicine</i> , 2012, 18, 83-94.	1.9	36
2619	MaskedPainter: Feature selection for microarray data analysis. <i>Intelligent Data Analysis</i> , 2012, 16, 717-737.	0.4	10
2620	Expression profiling based on coexpressed modules in obese prepubertal children. <i>Genetics and Molecular Research</i> , 2012, 11, 3077-3085.	0.3	5
2621	Mechanisms of $\beta$ 3 Biogenesis in the Megakaryocyte: A Proteomics Approach. , 0, , .		0
2622	Comparative Analysis of Nuclear Transfer Embryo-Derived Mouse Embryonic Stem Cells. Part II: Gene Regulation. <i>Cellular Reprogramming</i> , 2012, 14, 68-78.	0.5	1
2623	Improving ChIP-seq peak-calling for functional co-regulator binding by integrating multiple sources of biological information. <i>BMC Genomics</i> , 2012, 13, S1.	1.2	4
2624	Suppression of cancer stemness p21-regulating mRNA and microRNA signatures in recurrent ovarian cancer patient samples. <i>Journal of Ovarian Research</i> , 2012, 5, 2.	1.3	11
2625	15 $\alpha$ -Hydroxyprostaglandin dehydrogenase associates with poor prognosis in breast cancer, induces epithelial $\rightarrow$ mesenchymal transition, and promotes cell migration in cultured breast cancer cells. <i>Journal of Pathology</i> , 2012, 226, 674-686.	2.1	32
2626	Mass spectrometry $\rightarrow$ based proteomics: qualitative identification to activity $\rightarrow$ based protein profiling. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2012, 4, 141-162.	6.6	12
2627	Serum $\rightarrow$ autoantibodies for discovery of prostate cancer specific biomarkers. <i>Prostate</i> , 2012, 72, 427-436.	1.2	33
2628	cAMP-induced Mitochondrial Compartment Biogenesis. <i>Journal of Biological Chemistry</i> , 2012, 287, 14569-14578.	1.6	17
2629	Chromatin state signatures associated with tissue-specific gene expression and enhancer activity in the embryonic limb. <i>Genome Research</i> , 2012, 22, 1069-1080.	2.4	121
2630	A gene expression signature distinguishes normal tissues of sporadic and radiation-induced papillary thyroid carcinomas. <i>British Journal of Cancer</i> , 2012, 107, 994-1000.	2.9	111

#	ARTICLE	IF	CITATIONS
2631	Gene expression profiles of vitrified in vitro and in vivo derived bovine blastocysts. <i>Molecular Reproduction and Development</i> , 2012, 79, 613-625.	1.0	43
2632	Genetic identification and functional validation of Fc $\gamma$ RIV as key molecule in autoantibody induced tissue injury. <i>Journal of Pathology</i> , 2012, 228, 8-19.	2.1	89
2633	Bone marrow of neuroblastoma patients shows downregulation of CXCL12 expression and presence of IFN signature. <i>Pediatric Blood and Cancer</i> , 2012, 59, 44-51.	0.8	22
2634	Pediatric brainstem gangliogliomas show overexpression of neuropeptide prepronociceptin (PNOC) by microarray and immunohistochemistry. <i>Pediatric Blood and Cancer</i> , 2012, 59, 1173-1179.	0.8	18
2635	<i>Lactobacillus casei</i> Zhang stimulates lipid metabolism in hypercholesterolemic rats by affecting gene expression in the liver. <i>European Journal of Lipid Science and Technology</i> , 2012, 114, 244-252.	1.0	28
2636	Genetic toxicology and toxicogenomic analysis of three cigarette smoke condensates in vitro reveals few differences among full flavor, blonde, and light products. <i>Environmental and Molecular Mutagenesis</i> , 2012, 53, 281-296.	0.9	22
2637	Molecular perturbations restrict potential for liver repopulation of hepatocytes isolated from non-heart-beating donor rats. <i>Hepatology</i> , 2012, 55, 1182-1192.	3.6	4
2638	Bioinformatics analysis reveals transcriptome and microRNA signatures and drug repositioning targets for IBD and other autoimmune diseases. <i>Inflammatory Bowel Diseases</i> , 2012, 18, 2315-2333.	0.9	47
2639	OTX2 directly activates cell cycle genes and inhibits differentiation in medulloblastoma cells. <i>International Journal of Cancer</i> , 2012, 131, E21-32.	2.3	74
2640	Histological and molecular evaluation of iron as degradable medical implant material in a murine animal model. <i>Journal of Biomedical Materials Research - Part A</i> , 2012, 100A, 2881-2889.	2.1	55
2641	The MuvB complex sequentially recruits B-Myb and FoxM1 to promote mitotic gene expression. <i>Genes and Development</i> , 2012, 26, 474-489.	2.7	264
2642	Hormonal and molecular characterization of follicular fluid, cumulus cells and oocytes from pre-ovulatory follicles in stimulated and unstimulated cycles. <i>Human Reproduction</i> , 2012, 27, 1596-1605.	0.4	44
2643	Generation of human vascular smooth muscle subtypes provides insight into embryological origin dependent disease susceptibility. <i>Nature Biotechnology</i> , 2012, 30, 165-173.	9.4	321
2644	Differential Expression for RNA Sequencing (RNA-Seq) Data: Mapping, Summarization, Statistical Analysis, and Experimental Design. , 2012, , 169-190.		4
2645	Dynamic mRNA and miRNA profiling of CHO K1 suspension cell cultures. <i>Biotechnology Journal</i> , 2012, 7, 500-515.	1.8	83
2646	Confined 3D microenvironment regulates early differentiation in human pluripotent stem cells. <i>Biotechnology and Bioengineering</i> , 2012, 109, 3119-3132.	1.7	44
2647	MicroRNA microarray analysis of human umbilical vein endothelial cells exposed to benzo(a)pyrene. <i>Biochip Journal</i> , 2012, 6, 191-196.	2.5	9
2648	Intermittent hypoxia activates temporally coordinated transcriptional programs in visceral adipose tissue. <i>Journal of Molecular Medicine</i> , 2012, 90, 435-445.	1.7	33

#	ARTICLE	IF	CITATIONS
2649	Time-dependent transcriptional profiling links gene expression to mitogen-activated protein kinase kinase 4 (MKK4)-mediated suppression of omental metastatic colonization. <i>Clinical and Experimental Metastasis</i> , 2012, 29, 397-408.	1.7	4
2650	Genome-wide identification of palmitate-regulated immediate early genes and target genes in pancreatic beta-cells reveals a central role of NF- $\kappa$ B. <i>Molecular Biology Reports</i> , 2012, 39, 6781-6789.	1.0	20
2651	Effects of Oestrogen on MicroRNA Expression in Hormone-Responsive Breast Cancer Cells. <i>Hormones and Cancer</i> , 2012, 3, 65-78.	4.9	51
2652	Functional roles for redox genes in ethanol sensitivity in <i>Drosophila</i> . <i>Functional and Integrative Genomics</i> , 2012, 12, 305-315.	1.4	14
2653	A Genetic Analysis of the Stinging and Guarding Behaviors of the Honey Bee. <i>Behavior Genetics</i> , 2012, 42, 663-674.	1.4	11
2654	DNA Methylation Signatures in Development and Aging of the Human Prefrontal Cortex. <i>American Journal of Human Genetics</i> , 2012, 90, 260-272.	2.6	350
2655	Differential coexpression analysis of obesity-associated networks in human subcutaneous adipose tissue. <i>International Journal of Obesity</i> , 2012, 36, 137-147.	1.6	42
2656	Gene expression analysis of an epidermolysis bullosa simplex Dowling-Meara cell line by subtractive hybridization: recapitulation of cellular differentiation, migration and wound healing. <i>Experimental Dermatology</i> , 2012, 21, 111-117.	1.4	22
2657	Benzo[a]pyrene exposure influences the cardiac development and the expression of cardiovascular relative genes in zebrafish ( <i>Danio rerio</i> ) embryos. <i>Chemosphere</i> , 2012, 87, 369-375.	4.2	64
2658	Detecting disease genes based on semi-supervised learning and protein-protein interaction networks. <i>Artificial Intelligence in Medicine</i> , 2012, 54, 63-71.	3.8	59
2659	The cytotoxic and immunogenic hurdles associated with non-viral mRNA-mediated reprogramming of human fibroblasts. <i>Biomaterials</i> , 2012, 33, 4059-4068.	5.7	41
2660	Inducing healing-like human primary macrophage phenotypes by 3D hydrogel coated nanofibres. <i>Biomaterials</i> , 2012, 33, 4136-4146.	5.7	112
2661	Molecular profiling of functional interactions between pre-osteoblastic and breast carcinoma cells. <i>Genes To Cells</i> , 2012, 17, 302-315.	0.5	1
2662	Pathophysiology of asthma: lessons from genetic research with particular focus on severe asthma. <i>Journal of Internal Medicine</i> , 2012, 272, 108-120.	2.7	24
2663	Active and passive MDMA (ecstasy™) intake induces differential transcriptional changes in the mouse brain. <i>Genes, Brain and Behavior</i> , 2012, 11, 38-51.	1.1	20
2664	GENOMIC BASIS OF AGING AND LIFE-HISTORY EVOLUTION IN <i>DROSOPHILA MELANOGASTER</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 3390-3403.	1.1	134
2665	Multifaceted role of nitric oxide in an <i>in vitro</i> , mouse neuronal injury model: transcriptomic profiling defines the temporal recruitment of death signalling cascades. <i>Journal of Cellular and Molecular Medicine</i> , 2012, 16, 41-58.	1.6	4
2666	Triazole induced concentration-related gene signatures in rat whole embryo culture. <i>Reproductive Toxicology</i> , 2012, 34, 275-283.	1.3	47

#	ARTICLE	IF	CITATIONS
2667	Investigation of autoantibody profiles for cerebrospinal fluid biomarker discovery in patients with relapsingâ€“remitting multiple sclerosis. <i>Journal of Neuroimmunology</i> , 2012, 242, 26-32.	1.1	18
2668	10E12Z CLA alters adipocyte differentiation and adipocyte cytokine expression and induces macrophage proliferation. <i>Journal of Nutritional Biochemistry</i> , 2012, 23, 510-518.	1.9	8
2669	Dual phosphoproteomics and chemical proteomics analysis of erlotinib and gefitinib interference in acute myeloid leukemia cells. <i>Journal of Proteomics</i> , 2012, 75, 1343-1356.	1.2	79
2670	Unraveling the human dendritic cell phagosome proteome by organellar enrichment ranking. <i>Journal of Proteomics</i> , 2012, 75, 1547-1562.	1.2	27
2671	Mitochondria, oligodendrocytes and inflammation in bipolar disorder: Evidence from transcriptome studies points to intriguing parallels with multiple sclerosis. <i>Neurobiology of Disease</i> , 2012, 45, 37-47.	2.1	130
2672	Gene expression profiling of the brain: Pondering facts and fiction. <i>Neurobiology of Disease</i> , 2012, 45, 3-7.	2.1	13
2673	Meta-analysis of genetic and environmental Parkinson's disease models reveals a common role of mitochondrial protection pathways. <i>Neurobiology of Disease</i> , 2012, 45, 1018-1030.	2.1	34
2674	MicroRNA dysregulation in schizophrenia. <i>Neurobiology of Disease</i> , 2012, 46, 263-271.	2.1	180
2675	DRPLA transgenic mouse substrains carrying single copy of full-length mutant human DRPLA gene with variable sizes of expanded CAG repeats exhibit CAG repeat length- and age-dependent changes in behavioral abnormalities and gene expression profiles. <i>Neurobiology of Disease</i> , 2012, 46, 336-350.	2.1	23
2676	Genome-wide gene expression effects in B6C3F1 mouse intestinal epithelia following 7 and 90 days of exposure to hexavalent chromium in drinking water. <i>Toxicology and Applied Pharmacology</i> , 2012, 259, 13-26.	1.3	45
2677	Comparative toxicogenomic analysis of oral Cr(VI) exposure effects in rat and mouse small intestinal epithelia. <i>Toxicology and Applied Pharmacology</i> , 2012, 262, 124-138.	1.3	29
2678	Transcriptomic profile of host response in mouse brain after exposure to plant toxin abrin. <i>Toxicology</i> , 2012, 299, 33-43.	2.0	14
2679	Post-fasting olfactory, transcriptional, and feeding responses in <i>Drosophila</i> . <i>Physiology and Behavior</i> , 2012, 105, 544-553.	1.0	60
2680	Genome-wide association analysis for feed efficiency in Angus cattle. <i>Animal Genetics</i> , 2012, 43, 367-374.	0.6	110
2681	Identification and comparison of microRNA<sc>s from skeletal muscle and adipose tissues from two porcine breeds. <i>Animal Genetics</i> , 2012, 43, 704-713.	0.6	44
2682	Combining quantitative trait loci and heterogeneous microarray data analyses reveals putative candidate pathways affecting mastitis in cattle. <i>Animal Genetics</i> , 2012, 43, 793-799.	0.6	13
2683	Hydroxycarbamide alters erythroid gene expression in children with sickle cell anaemia. <i>British Journal of Haematology</i> , 2012, 157, 240-248.	1.2	26
2684	<sc><i>Ex vivo</i></sc> expansion of cord blood progenitors impairs their short-term and long-term repopulating activity associated with transcriptional dysregulation of signalling networks. <i>Cell Proliferation</i> , 2012, 45, 266-278.	2.4	17

#	ARTICLE	IF	CITATIONS
2685	Genome-wide microarray comparison reveals downstream genes of Pax6 in the developing mouse cerebellum. <i>European Journal of Neuroscience</i> , 2012, 36, 2888-2898.	1.2	15
2686	A systematic comparison of genome-scale clustering algorithms. <i>BMC Bioinformatics</i> , 2012, 13, S7.	1.2	55
2687	Downregulation of HuR as a new mechanism of doxorubicin resistance in breast cancer cells. <i>Molecular Cancer</i> , 2012, 11, 13.	7.9	63
2688	Gene expression profiling of primary male breast cancers reveals two unique subgroups and identifies N-acetyltransferase-1 (NAT1) as a novel prognostic biomarker. <i>Breast Cancer Research</i> , 2012, 14, R31.	2.2	100
2689	Transcriptomic profiling of astrocytes treated with the Rho kinase inhibitor Fasudil reveals cytoskeletal and pro-survival responses. <i>Journal of Cellular Physiology</i> , 2012, 227, 1199-1211.	2.0	47
2690	EphA2B, acting as an extracellular ligand, induces differentiation markers in epidermal keratinocytes. <i>Journal of Cellular Physiology</i> , 2012, 227, 2330-2340.	2.0	11
2691	Microarray analysis reveals age-related differences in gene expression during the development of osteoarthritis in mice. <i>Arthritis and Rheumatism</i> , 2012, 64, 705-717.	6.7	190
2692	Application of microarray technology in <i>Drosophila</i> ethanol behavioral research. <i>Frontiers in Biology</i> , 2012, 7, 65-72.	0.7	2
2693	Systemic response to <i>Campylobacter jejuni</i> infection by profiling gene transcription in the spleens of two genetic lines of chickens. <i>Immunogenetics</i> , 2012, 64, 59-69.	1.2	26
2694	INS GFP/w human embryonic stem cells facilitate isolation of in vitro derived insulin-producing cells. <i>Diabetologia</i> , 2012, 55, 694-706.	2.9	113
2695	Microarray Profiling of Diaphyseal Bone of Rats Suffering from Hypervitaminosis A. <i>Calcified Tissue International</i> , 2012, 90, 219-229.	1.5	10
2696	The curcuminoid CLEFMA selectively induces cell death in H441 lung adenocarcinoma cells via oxidative stress. <i>Investigational New Drugs</i> , 2012, 30, 558-567.	1.2	24
2697	Transcription profiling of Prss16 (Tssp) can be used to find additional peptidase genes that are candidates for self-peptide generation in the thymus. <i>Molecular Biology Reports</i> , 2012, 39, 4051-4058.	1.0	6
2698	Novel amplifications in pediatric medulloblastoma identified by genome-wide copy number profiling. <i>Journal of Neuro-Oncology</i> , 2012, 107, 37-49.	1.4	3
2699	The application of quantification techniques in proteomics for biomedical research. <i>Mass Spectrometry Reviews</i> , 2013, 32, 1-26.	2.8	60
2700	Transcriptome profiling of mice testes following low dose irradiation. <i>Reproductive Biology and Endocrinology</i> , 2013, 11, 50.	1.4	11
2701	Progressive morphological changes and impaired retinal function associated with temporal regulation of gene expression after retinal ischemia/reperfusion injury in mice. <i>Molecular Neurodegeneration</i> , 2013, 8, 21.	4.4	75
2702	Embryonic mammary signature subsets are activated in <i>Brca1</i> <sup>-/-</sup> and basal-like breast cancers. <i>Breast Cancer Research</i> , 2013, 15, R25.	2.2	52

#	ARTICLE	IF	CITATIONS
2703	A randomised controlled phase II trial of pre-operative celecoxib treatment reveals anti-tumour transcriptional response in primary breast cancer. <i>Breast Cancer Research</i> , 2013, 15, R29.	2.2	55
2704	RNA sequencing reveals sexually dimorphic gene expression before gonadal differentiation in chicken and allows comprehensive annotation of the W-chromosome. <i>Genome Biology</i> , 2013, 14, R26.	13.9	98
2705	Genome-wide analysis reveals downregulation of miR-379/miR-656 cluster in human cancers. <i>Biology Direct</i> , 2013, 8, 10.	1.9	69
2706	Smchd1 regulates a subset of autosomal genes subject to monoallelic expression in addition to being critical for X inactivation. <i>Epigenetics and Chromatin</i> , 2013, 6, 19.	1.8	88
2707	MeCP2 modulates gene expression pathways in astrocytes. <i>Molecular Autism</i> , 2013, 4, 3.	2.6	74
2708	Genomic analysis of the ecdysone steroid signal at metamorphosis onset using ecdysoneless and EcRnull <i>Drosophila melanogaster</i> mutants. <i>Genes and Genomics</i> , 2013, 35, 21-46.	0.5	10
2709	Semantic networks for genome-wide CNV associated with AST and ALT in Korean cohorts. <i>Molecular and Cellular Toxicology</i> , 2013, 9, 103-111.	0.8	1
2710	An integrated analysis of microRNA and mRNA expression in salvianolic acid B-treated human umbilical vein endothelial cells. <i>Molecular and Cellular Toxicology</i> , 2013, 9, 1-7.	0.8	6
2711	Novel differential transcript expression identified by LongSAGE in the mouse endometrium during the implantation window. <i>Molecular Biology Reports</i> , 2013, 40, 651-663.	1.0	1
2712	Comparison and optimization of strategies for a more profound profiling of the sialylated N-glycoproteomics in human plasma using metal oxide enrichment. <i>Analytical and Bioanalytical Chemistry</i> , 2013, 405, 5519-5529.	1.9	18
2713	Hepatocyte Nuclear Factor 4 Alpha and Farnesoid X Receptor Co-regulates Gene Transcription in Mouse Livers on a Genome-Wide Scale. <i>Pharmaceutical Research</i> , 2013, 30, 2188-2198.	1.7	27
2714	A global toxicogenomic analysis investigating the mechanistic differences between tobacco and marijuana smoke condensates in vitro. <i>Toxicology</i> , 2013, 308, 60-73.	2.0	32
2715	Analysis of the combined action of miR-143 and miR-145 on oncogenic pathways in colorectal cancer cells reveals a coordinate program of gene repression. <i>Oncogene</i> , 2013, 32, 4806-4813.	2.6	159
2716	Empirical Bayes estimation of posterior probabilities of enrichment: A comparative study of five estimators of the local false discovery rate. <i>BMC Bioinformatics</i> , 2013, 14, 87.	1.2	17
2717	Genome-wide association study of antibody response to Newcastle disease virus in chicken. <i>BMC Genetics</i> , 2013, 14, 42.	2.7	32
2718	Deep brain stimulation modulates nonsense-mediated RNA decay in Parkinson's patients leukocytes. <i>BMC Genomics</i> , 2013, 14, 478.	1.2	14
2719	Coexpression analysis of large cancer datasets provides insight into the cellular phenotypes of the tumour microenvironment. <i>BMC Genomics</i> , 2013, 14, 469.	1.2	39
2720	Detection of selective sweeps in cattle using genome-wide SNP data. <i>BMC Genomics</i> , 2013, 14, 382.	1.2	102

#	ARTICLE	IF	CITATIONS
2721	Alterations in gene expression in <i>Caenorhabditis elegans</i> associated with organophosphate pesticide intoxication and recovery. <i>BMC Genomics</i> , 2013, 14, 291.	1.2	34
2722	Dynamic regulation of epigenomic landscapes during hematopoiesis. <i>BMC Genomics</i> , 2013, 14, 193.	1.2	41
2723	The transcript catalogue of the short-lived fish <i>Nothobranchius furzeri</i> provides insights into age-dependent changes of mRNA levels. <i>BMC Genomics</i> , 2013, 14, 185.	1.2	52
2724	Profiling and metaanalysis of epidermal keratinocytes responses to epidermal growth factor. <i>BMC Genomics</i> , 2013, 14, 85.	1.2	29
2725	Microarray analysis of MicroRNA expression in peripheral blood mononuclear cells of critically ill patients with influenza A (H1N1). <i>BMC Infectious Diseases</i> , 2013, 13, 257.	1.3	66
2726	Nuclear entrapment and extracellular depletion of PCOLCE is associated with muscle degeneration in oculopharyngeal muscular dystrophy. <i>BMC Neurology</i> , 2013, 13, 70.	0.8	15
2727	Microarray gene expression profiling of neural tissues in bovine spastic paresis. <i>BMC Veterinary Research</i> , 2013, 9, 122.	0.7	8
2728	Maximizing capture of gene co-expression relationships through pre-clustering of input expression samples: an <i>Arabidopsis</i> case study. <i>BMC Systems Biology</i> , 2013, 7, 44.	3.0	22
2729	Integrative analysis of congenital muscular torticollis: from gene expression to clinical significance. <i>BMC Medical Genomics</i> , 2013, 6, S10.	0.7	17
2730	Validation of microarray data in human lymphoblasts shows a role of the ubiquitin-proteasome system and NF- $\kappa$ B in the pathogenesis of Down syndrome. <i>BMC Medical Genomics</i> , 2013, 6, 24.	0.7	22
2731	Genome-wide expression profiling and functional characterization of SCA28 lymphoblastoid cell lines reveal impairment in cell growth and activation of apoptotic pathways. <i>BMC Medical Genomics</i> , 2013, 6, 22.	0.7	14
2732	Genome-wide prediction and analysis of human tissue-selective genes using microarray expression data. <i>BMC Medical Genomics</i> , 2013, 6, S10.	0.7	11
2733	Changes in transcriptome of native nasal epithelium expressing F508del-CFTR and intersecting data from comparable studies. <i>Respiratory Research</i> , 2013, 14, 38.	1.4	61
2734	Extracellular matrix of adipogenically differentiated mesenchymal stem cells reveals a network of collagen filaments, mostly interwoven by hexagonal structural units. <i>Matrix Biology</i> , 2013, 32, 452-465.	1.5	25
2735	Personal genomes, quantitative dynamic omics and personalized medicine. <i>Quantitative Biology</i> , 2013, 1, 71-90.	0.3	29
2736	Altered miRNA Expression is Associated with Differentiation, Invasion, and Metastasis of Esophageal Squamous Cell Carcinoma (ESCC) in Patients from Huaian, China. <i>Cell Biochemistry and Biophysics</i> , 2013, 67, 657-668.	0.9	74
2737	Identification of circulating microRNAs in HNF1A-MODY carriers. <i>Diabetologia</i> , 2013, 56, 1743-1751.	2.9	26
2738	Research Resource: Progesterone Receptor Targetome Underlying Mammary Gland Branching Morphogenesis. <i>Molecular Endocrinology</i> , 2013, 27, 1743-1761.	3.7	37



#	ARTICLE	IF	CITATIONS
2739	Whole-Genome Expression Analysis of Human Mesenchymal Stromal Cells Exposed to Ultrasmooth Tantalum vs. Titanium Oxide Surfaces. <i>Cellular and Molecular Bioengineering</i> , 2013, 6, 199-209.	1.0	4
2740	Influence of Oxygen in the Cultivation of Human Mesenchymal Stem Cells in Simulated Microgravity: An Explorative Study. <i>Microgravity Science and Technology</i> , 2013, 25, 59-66.	0.7	8
2741	LGR5 is a Proneural Factor and is Regulated by OLIG2 in Glioma Stem-Like Cells. <i>Cellular and Molecular Neurobiology</i> , 2013, 33, 851-865.	1.7	15
2742	A decision theory paradigm for evaluating identifier mapping and filtering methods using data integration. <i>BMC Bioinformatics</i> , 2013, 14, 223.	1.2	18
2743	All-trans retinoic acid and basic fibroblast growth factor synergistically direct pluripotent human embryonic stem cells to extraembryonic lineages. <i>Stem Cell Research</i> , 2013, 10, 228-240.	0.3	15
2744	Defining the RGG/RC Motif. <i>Molecular Cell</i> , 2013, 50, 613-623.	4.5	512
2745	An Interactive Approach to Multiobjective Clustering of Gene Expression Patterns. <i>IEEE Transactions on Biomedical Engineering</i> , 2013, 60, 35-41.	2.5	38
2746	Early Growth Response 3 (Egr-3) Is Induced by Transforming Growth Factor- $\beta^2$ and Regulates Fibrogenic Responses. <i>American Journal of Pathology</i> , 2013, 183, 1197-1208.	1.9	48
2747	Transcriptomic analysis of inbreeding depression in cold-sensitive <i>Drosophila melanogaster</i> shows upregulation of the immune response. <i>Journal of Evolutionary Biology</i> , 2013, 26, 1890-1902.	0.8	49
2748	Functional Genomics, Proteomics, Metabolomics and Bioinformatics for Systems Biology. , 2013, , 3-41.		5
2749	DAX1 regulatory networks unveil conserved and potentially new functions. <i>Gene</i> , 2013, 530, 66-74.	1.0	10
2750	Neurodevelopmental alcohol exposure elicits long-term changes to gene expression that alter distinct molecular pathways dependent on timing of exposure. <i>Journal of Neurodevelopmental Disorders</i> , 2013, 5, 6.	1.5	66
2751	An Aberrant Transcription Factor Network Essential for Wnt Signaling and Stem Cell Maintenance in Glioblastoma. <i>Cell Reports</i> , 2013, 3, 1567-1579.	2.9	236
2752	Sensory-Neuron Subtype-Specific Transcriptional Programs Controlling Dendrite Morphogenesis: Genome-wide Analysis of Abrupt and Knot/Collier. <i>Developmental Cell</i> , 2013, 27, 530-544.	3.1	60
2753	PainNetworks: A web-based resource for the visualisation of pain-related genes in the context of their network associations. <i>Pain</i> , 2013, 154, 2586e1-2586e12.	2.0	50
2754	A simulation to analyze feature selection methods utilizing gene ontology for gene expression classification. <i>Journal of Biomedical Informatics</i> , 2013, 46, 1044-1059.	2.5	13
2755	Ionizing radiation-induced gene expression changes in TP53 proficient and deficient glioblastoma cell lines. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2013, 756, 46-55.	0.9	24
2756	Pediatric rhabdoid tumors of kidney and brain show many differences in gene expression but share dysregulation of cell cycle and epigenetic effector genes. <i>Pediatric Blood and Cancer</i> , 2013, 60, 1095-1102.	0.8	40

#	ARTICLE	IF	CITATIONS
2757	Nicotine Alters MicroRNA Expression and Hinders Human Adult Stem Cell Regenerative Potential. <i>Stem Cells and Development</i> , 2013, 22, 781-790.	1.1	55
2758	Semantic extraction of geographic data from web tables for big data integration. , 2013, , .		10
2759	In vivo regulation of gene transcription by alpha- and gamma-tocopherol in murine T lymphocytes. <i>Archives of Biochemistry and Biophysics</i> , 2013, 538, 111-119.	1.4	31
2760	Genetic Mapping with Multiple Levels of Phenotypic Information Reveals Determinants of Lymphocyte Glucocorticoid Sensitivity. <i>American Journal of Human Genetics</i> , 2013, 93, 735-743.	2.6	23
2761	Integrative Mechanisms of Oriented Neuronal Migration in the Developing Brain. <i>Annual Review of Cell and Developmental Biology</i> , 2013, 29, 299-353.	4.0	134
2762	Proteogenomic Analysis of Human Colon Carcinoma Cell Lines LIM1215, LIM1899, and LIM2405. <i>Journal of Proteome Research</i> , 2013, 12, 1732-1742.	1.8	30
2763	Differential L1 regulation in pluripotent stem cells of humans and apes. <i>Nature</i> , 2013, 503, 525-529.	13.7	220
2764	The challenging environment on board the International Space Station affects endothelial cell function by triggering oxidative stress through thioredoxin interacting protein overexpression: the ESAâ€™SPHINX experiment. <i>FASEB Journal</i> , 2013, 27, 4466-4475.	0.2	110
2765	Transgenic 6F tomatoes act on the small intestine to prevent systemic inflammation and dyslipidemia caused by Western diet and intestinally derived lysophosphatidic acid. <i>Journal of Lipid Research</i> , 2013, 54, 3403-3418.	2.0	60
2766	Association of AMD-like retinopathy development with an Alzheimerâ€™s disease metabolic pathway in OXYS rats. <i>Biogerontology</i> , 2013, 14, 753-762.	2.0	34
2767	Gene expression changes associated with erlotinib response in glioma cell lines. <i>European Journal of Cancer</i> , 2013, 49, 1641-1653.	1.3	35
2768	Tissue and circulating microRNA influence reproductive function in endometrial disease. <i>Reproductive BioMedicine Online</i> , 2013, 27, 515-529.	1.1	70
2769	Extended Self-Renewal and Accelerated Reprogramming in the Absence of Kdm5b. <i>Molecular and Cellular Biology</i> , 2013, 33, 4793-4810.	1.1	58
2770	Transcriptional Profiling of <i>Neisseria meningitidis</i> Interacting with Human Epithelial Cells in a Long-Term <i>In Vitro</i> Colonization Model. <i>Infection and Immunity</i> , 2013, 81, 4149-4159.	1.0	25
2771	Thymic Stromal Lymphopoietin-Mediated Extramedullary Hematopoiesis Promotes Allergic Inflammation. <i>Immunity</i> , 2013, 39, 1158-1170.	6.6	64
2772	The N and C Termini of ZO-1 Are Surrounded by Distinct Proteins and Functional Protein Networks. <i>Journal of Biological Chemistry</i> , 2013, 288, 13775-13788.	1.6	110
2773	The molecular diversity of Luminal A breast tumors. <i>Breast Cancer Research and Treatment</i> , 2013, 141, 409-420.	1.1	120
2774	Comprehensive high-resolution genomic profiling and cytogenetics of two pediatric and one adult medulloblastoma. <i>Pathology Research and Practice</i> , 2013, 209, 541-547.	1.0	1

#	ARTICLE	IF	CITATIONS
2775	Dietary Selenium Supplementation and Whole Blood Gene Expression in Healthy North American Men. <i>Biological Trace Element Research</i> , 2013, 155, 201-208.	1.9	15
2776	Differential proteomic profiling in human spermatozoa that did or did not result in pregnancy via IVF and AID. <i>Proteomics - Clinical Applications</i> , 2013, 7, 850-858.	0.8	44
2777	SHANK3 overexpression causes manic-like behaviour with unique pharmacogenetic properties. <i>Nature</i> , 2013, 503, 72-77.	13.7	323
2778	Transcriptome-wide identification of RNA binding sites by CLIP-seq. <i>Methods</i> , 2013, 63, 32-40.	1.9	28
2779	Microarray-Based Transcriptome Profiling of Ovarian Cancer Cells. <i>Methods in Molecular Biology</i> , 2013, 1049, 119-137.	0.4	0
2780	Metastasis tumor-associated protein 2 enhances metastatic behavior and is associated with poor outcomes in estrogen receptor-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2013, 141, 375-384.	1.1	38
2781	Gene expression analysis of induced pluripotent stem cells from aneuploid chromosomal syndromes. <i>BMC Genomics</i> , 2013, 14, S8.	1.2	30
2782	Intronic Non-CG DNA hydroxymethylation and alternative mRNA splicing in honey bees. <i>BMC Genomics</i> , 2013, 14, 666.	1.2	62
2783	MultiFacTV: module detection from higher-order time series biological data. <i>BMC Genomics</i> , 2013, 14, S2.	1.2	5
2784	An efficient method for mining cross-timepoint gene regulation sequential patterns from time course gene expression datasets. <i>BMC Bioinformatics</i> , 2013, 14, S3.	1.2	4
2786	PKIS: computational identification of protein kinases for experimentally discovered protein phosphorylation sites. <i>BMC Bioinformatics</i> , 2013, 14, 247.	1.2	43
2787	MicroRNAs implicated in dysregulation of gene expression following human lung transplantation. <i>Translational Respiratory Medicine</i> , 2013, 1, .	3.8	22
2788	Exploring signatures of positive selection in pigmentation candidate genes in populations of East Asian ancestry. <i>BMC Evolutionary Biology</i> , 2013, 13, 150.	3.2	54
2789	Mining differential top-k co-expression patterns from time course comparative gene expression datasets. <i>BMC Bioinformatics</i> , 2013, 14, 230.	1.2	27
2790	Label-free mass spectrometry proteome quantification of human embryonic kidney cells following 24 hours of sialic acid overproduction. <i>Proteome Science</i> , 2013, 11, 38.	0.7	13
2791	Prediabetic changes in gene expression induced by aspartame and monosodium glutamate in Trans fat-fed C57Bl/6AJ mice. <i>Nutrition and Metabolism</i> , 2013, 10, 44.	1.3	13
2792	PROGRESS IN COMPUTATIONAL STUDIES OF HOST-“PATHOGEN INTERACTIONS. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1230001.	0.3	54
2793	The early phase transcriptome of bovine monocyte-derived macrophages infected with <i>Staphylococcus aureus</i> in vitro. <i>BMC Genomics</i> , 2013, 14, 891.	1.2	46

#	ARTICLE	IF	CITATIONS
2794	Transcriptome analysis of primary monocytes from HIV-positive patients with differential responses to antiretroviral therapy. <i>Virology Journal</i> , 2013, 10, 361.	1.4	17
2795	A flexible statistical model for alignment of label-free proteomics data - incorporating ion mobility and product ion information. <i>BMC Bioinformatics</i> , 2013, 14, 364.	1.2	6
2796	Integrating human omics data to prioritize candidate genes. <i>BMC Medical Genomics</i> , 2013, 6, 57.	0.7	36
2797	Stringent DDI-based Prediction of <i>H. sapiens</i> - <i>M. tuberculosis</i> H37Rv Protein-Protein Interactions. <i>BMC Systems Biology</i> , 2013, 7, S6.	3.0	34
2798	HOXC9 directly regulates distinct sets of genes to coordinate diverse cellular processes during neuronal differentiation. <i>BMC Genomics</i> , 2013, 14, 830.	1.2	24
2799	Gene Expression Profiling Reveals Regulation of ERK Phosphorylation by Androgen-Induced Tumor Suppressor U19/EAF2 in the Mouse Prostate. <i>Cancer Microenvironment</i> , 2013, 6, 247-261.	3.1	14
2800	A transcriptomic approach to elucidate the physiological significance of human cytochrome P450 2S1 in bronchial epithelial cells. <i>BMC Genomics</i> , 2013, 14, 833.	1.2	12
2801	Expression profiling of 519 kinase genes in matched malignant peripheral nerve sheath tumor/plexiform neurofibroma samples is discriminatory and identifies mitotic regulators BUB1B, PBK and NEK2 as overexpressed with transformation. <i>Modern Pathology</i> , 2013, 26, 930-943.	2.9	29
2802	Mesenchymal Differentiation Mediated by NF- $\kappa$ B Promotes Radiation Resistance in Glioblastoma. <i>Cancer Cell</i> , 2013, 24, 331-346.	7.7	856
2803	Chromosome 7-Centric Analysis of Proteomics Data from a Panel of Human Colon Carcinoma Cell Lines. <i>Journal of Proteome Research</i> , 2013, 12, 89-96.	1.8	6
2804	The Grainyhead transcription factor Grhl3/Get1 suppresses miR-21 expression and tumorigenesis in skin: modulation of the miR-21 target MSH2 by RNA-binding protein DND1. <i>Oncogene</i> , 2013, 32, 1497-1507.	2.6	66
2805	Common and specific signatures of gene expression and protein-protein interactions in autoimmune diseases. <i>Genes and Immunity</i> , 2013, 14, 67-82.	2.2	89
2806	Chd4 and associated proteins function as corepressors of Sox9 expression during BMP-2-induced chondrogenesis. <i>Journal of Bone and Mineral Research</i> , 2013, 28, 1950-1961.	3.1	15
2807	Global versus Local Hubs in Human Protein-Protein Interaction Network. <i>Journal of Proteome Research</i> , 2013, 12, 5436-5446.	1.8	24
2808	The experimental renal cell carcinoma model in the chick embryo. <i>Angiogenesis</i> , 2013, 16, 181-194.	3.7	46
2809	CDK-mediated activation of the SCF <sup>FBXO</sup> ubiquitin ligase promotes MYC-driven transcription and tumorigenesis and predicts poor survival in breast cancer. <i>EMBO Molecular Medicine</i> , 2013, 5, 1067-1086.	3.3	61
2810	Integrative genomics of gene and metabolic regulation by estrogen receptors $\alpha$ and $\beta$ , and their coregulators. <i>Molecular Systems Biology</i> , 2013, 9, 676.	3.2	81
2811	The histone H3K27 methylation mark regulates intestinal epithelial cell density-dependent proliferation and the inflammatory response. <i>Journal of Cellular Biochemistry</i> , 2013, 114, 1203-1215.	1.2	20

#	ARTICLE	IF	CITATIONS
2812	25-Hydroxycholesterol Activates the Integrated Stress Response to Reprogram Transcription and Translation in Macrophages. <i>Journal of Biological Chemistry</i> , 2013, 288, 35812-35823.	1.6	64
2813	MicroRNA 218 Acts as a Tumor Suppressor by Targeting Multiple Cancer Phenotype-associated Genes in Medulloblastoma. <i>Journal of Biological Chemistry</i> , 2013, 288, 1918-1928.	1.6	100
2814	Th-MYCN Mice with Caspase-8 Deficiency Develop Advanced Neuroblastoma with Bone Marrow Metastasis. <i>Cancer Research</i> , 2013, 73, 4086-4097.	0.4	57
2815	Trelliscope: A system for detailed visualization in the deep analysis of large complex data. , 2013, , .		10
2816	Ontogeny of erythroid gene expression. <i>Blood</i> , 2013, 121, e5-e13.	0.6	150
2817	Gene profiling identifies commonalities in neuronal pathways in excitotoxicity: Evidence favouring cell cycle re-activation in concert with oxidative stress. <i>Neurochemistry International</i> , 2013, 62, 719-730.	1.9	13
2818	Detection and interpretation of genomic structural variation in health and disease. <i>Expert Review of Molecular Diagnostics</i> , 2013, 13, 61-82.	1.5	13
2819	Transcriptome Analysis in Patients with Progressive Coronary Artery Disease: Identification of Differential Gene Expression in Peripheral Blood. <i>Journal of Cardiovascular Translational Research</i> , 2013, 6, 81-93.	1.1	33
2820	Genome-wide profiling in melatonin-exposed human breast cancer cell lines identifies differentially methylated genes involved in the anticancer effect of melatonin. <i>Journal of Pineal Research</i> , 2013, 54, 80-88.	3.4	55
2821	The Impact of Cell Source, Culture Methodology, Culture Location, and Individual Donors on Gene Expression Profiles of Bone Marrow-Derived and Adipose-Derived Stromal Cells. <i>Stem Cells and Development</i> , 2013, 22, 1086-1096.	1.1	45
2822	Glycoproteomics enabled by tagging sialic acid- or galactose-terminated glycans. <i>Glycobiology</i> , 2013, 23, 211-221.	1.3	81
2823	Unravelling the enigma of selective vulnerability in neurodegeneration: motor neurons resistant to degeneration in ALS show distinct gene expression characteristics and decreased susceptibility to excitotoxicity. <i>Acta Neuropathologica</i> , 2013, 125, 95-109.	3.9	133
2824	Attenuating effect of Fufang Xueshuantong Capsule on kidney function in diabetic nephropathy model. <i>Journal of Natural Medicines</i> , 2013, 67, 86-97.	1.1	14
2825	RNA Targets and Specificity of Staufen, a Double-stranded RNA-binding Protein in <i>Caenorhabditis elegans</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 2532-2545.	1.6	45
2826	Global expression profiling of globose basal cells and neurogenic progression within the olfactory epithelium. <i>Journal of Comparative Neurology</i> , 2013, 521, 833-859.	0.9	44
2827	Proteomic snapshot of breast cancer cell cycle: G <sub>1</sub> /S transition point. <i>Proteomics</i> , 2013, 13, 48-60.	1.3	19
2828	Comparative proteomic analysis of the ATP-sensitive K <sup>+</sup> channel complex in different tissue types. <i>Proteomics</i> , 2013, 13, 368-378.	1.3	16
2829	Endothelial cells provide a niche for placental hematopoietic stem/progenitor cell expansion through broad transcriptomic modification. <i>Stem Cell Research</i> , 2013, 11, 1074-1090.	0.3	25

#	ARTICLE	IF	CITATIONS
2830	Analysis of the STAT3 interactome using in-situ biotinylation and SILAC. <i>Journal of Proteomics</i> , 2013, 94, 370-386.	1.2	10
2831	Placental invasion, preeclampsia risk and adaptive molecular evolution at the origin of the great apes: Evidence from genome-wide analyses. <i>Placenta</i> , 2013, 34, 127-132.	0.7	55
2832	PPAR $\alpha$ -mediated responses in human adult liver stem cells: In vivo/in vitro and cross-species comparisons. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2013, 138, 236-247.	1.2	11
2833	Acute prenatal exposure to a moderate dose of valproic acid increases social behavior and alters gene expression in rats. <i>International Journal of Developmental Neuroscience</i> , 2013, 31, 740-750.	0.7	44
2834	Thrombopoietin improved ventricular function and regulated remodeling genes in a rat model of myocardial infarction. <i>International Journal of Cardiology</i> , 2013, 167, 2546-2554.	0.8	7
2835	Insulin/IGF-1 Controls Epidermal Morphogenesis via Regulation of FoxO-Mediated p63 Inhibition. <i>Developmental Cell</i> , 2013, 26, 176-187.	3.1	41
2836	A dynamic and complex monochloramine stress response in <i>Escherichia coli</i> revealed by transcriptome analysis. <i>Water Research</i> , 2013, 47, 4978-4985.	5.3	26
2837	Obesity and airway responsiveness: Role of TNFR2. <i>Pulmonary Pharmacology and Therapeutics</i> , 2013, 26, 444-454.	1.1	44
2838	Sost and its paralog Sostdc1 coordinate digit number in a Gli3-dependent manner. <i>Developmental Biology</i> , 2013, 383, 90-105.	0.9	47
2839	The TGR5 gene is expressed in human subcutaneous adipose tissue and is associated with obesity, weight loss and resting metabolic rate. <i>Biochemical and Biophysical Research Communications</i> , 2013, 433, 563-566.	1.0	35
2840	Induced CYP3A4 Expression in Confluent Huh7 Hepatoma Cells as a Result of Decreased Cell Proliferation and Subsequent Pregnane X Receptor Activation. <i>Molecular Pharmacology</i> , 2013, 83, 659-670.	1.0	34
2841	The atypical mechanosensitive microRNA-712 derived from pre-ribosomal RNA induces endothelial inflammation and atherosclerosis. <i>Nature Communications</i> , 2013, 4, 3000.	5.8	198
2842	Basal Splicing Factors Regulate the Stability of Mature mRNAs in Trypanosomes. <i>Journal of Biological Chemistry</i> , 2013, 288, 4991-5006.	1.6	33
2843	Analysis and Meta-analysis of Transcriptional Profiling in Human Epidermis. <i>Methods in Molecular Biology</i> , 2013, 1195, 61-97.	0.4	12
2844	Genome-wide DNA methylation patterns in discordant sib pairs with alcohol dependence. <i>Asia-Pacific Psychiatry</i> , 2013, 5, 39-50.	1.2	47
2845	Assessment of gene expression in peripheral blood using RNAseq before and after weight restoration in anorexia nervosa. <i>Psychiatry Research</i> , 2013, 210, 287-293.	1.7	9
2846	Dual Pten/Tp53 Suppression Promotes Sarcoma Progression by Activating Notch Signaling. <i>American Journal of Pathology</i> , 2013, 182, 2015-2027.	1.9	21
2847	Neonatal mesenchymal-like cells adapt to surrounding cells. <i>Stem Cell Research</i> , 2013, 11, 634-646.	0.3	9

#	ARTICLE	IF	CITATIONS
2848	Spatial transcriptional profile of the chick and mouse endocardial cushions identify novel regulators of endocardial EMT in vitro. <i>Journal of Molecular and Cellular Cardiology</i> , 2013, 59, 196-204.	0.9	37
2849	Family-wide Investigation of PDZ Domain-Mediated Protein-Protein Interactions Implicates $\beta$ -Catenin in Maintaining the Integrity of Tight Junctions. <i>Chemistry and Biology</i> , 2013, 20, 816-827.	6.2	33
2850	Transcriptional effects of inhibiting epidermal growth factor receptor in keratinocytes. <i>Dermatologica Sinica</i> , 2013, 31, 107-119.	0.2	7
2851	Integrating GWASs and Human Protein Interaction Networks Identifies a Gene Subnetwork Underlying Alcohol Dependence. <i>American Journal of Human Genetics</i> , 2013, 93, 1027-1034.	2.6	72
2852	Dietary supplementation with resveratrol and/or docosahexaenoic acid alters hippocampal gene expression in adult C57Bl/6 mice. <i>Journal of Nutritional Biochemistry</i> , 2013, 24, 1735-1740.	1.9	16
2853	Screening Preeclamptic Cord Plasma for Proteins Associated with Decreased Breast Cancer Susceptibility. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 335-344.	3.0	7
2854	Identification of Molecular Subtypes of Gastric Cancer With Different Responses to PI3-Kinase Inhibitors and 5-Fluorouracil. <i>Gastroenterology</i> , 2013, 145, 554-565.	0.6	381
2855	Gender differences in the bronchoalveolar lavage cell proteome of patients with chronic obstructive pulmonary disease. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 131, 743-751.e9.	1.5	58
2856	Associations between muscle gene expression pattern and technological and sensory meat traits highlight new biomarkers for pork quality assessment. <i>Meat Science</i> , 2013, 95, 744-754.	2.7	29
2857	Evolutionary conservation of the polyproline II conformation surrounding intrinsically disordered phosphorylation sites. <i>Protein Science</i> , 2013, 22, 405-417.	3.1	50
2858	Transcriptome analysis reveals upregulation of bitter taste receptors in severe asthmatics. <i>European Respiratory Journal</i> , 2013, 42, 65-78.	3.1	130
2859	Comparison of Whole-Genome DNA Methylation Patterns in Whole Blood, Saliva, and Lymphoblastoid Cell Lines. <i>Behavior Genetics</i> , 2013, 43, 168-176.	1.4	68
2860	Identification of human plasma proteins associated with the cell wall of the pathogenic fungus <i>Paracoccidioides brasiliensis</i> . <i>FEMS Microbiology Letters</i> , 2013, 341, 87-95.	0.7	8
2861	Accelerated gene evolution through replication-transcription conflicts. <i>Nature</i> , 2013, 495, 512-515.	13.7	120
2862	The neuron-specific chromatin regulatory subunit BAF53b is necessary for synaptic plasticity and memory. <i>Nature Neuroscience</i> , 2013, 16, 552-561.	7.1	213
2863	The $\beta$ Crystallin Domain of Small Heat Shock Protein b8 (Hspb8) Acts as Survival and Differentiation Factor in Adult Hippocampal Neurogenesis. <i>Journal of Neuroscience</i> , 2013, 33, 5785-5796.	1.7	27
2864	The formation of an organic coat and the release of corrosion microparticles from metallic magnesium implants. <i>Acta Biomaterialia</i> , 2013, 9, 7580-7589.	4.1	42
2865	A Dynamic Bronchial Airway Gene Expression Signature of Chronic Obstructive Pulmonary Disease and Lung Function Impairment. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013, 187, 933-942.	2.5	142

#	ARTICLE	IF	CITATIONS
2866	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013, 9, 652.	3.2	61
2867	Mapping the Human miRNA Interactome by CLASH Reveals Frequent Noncanonical Binding. <i>Cell</i> , 2013, 153, 654-665.	13.5	1,164
2868	The Disruption of <i>Celf6</i> , a Gene Identified by Translational Profiling of Serotonergic Neurons, Results in Autism-Related Behaviors. <i>Journal of Neuroscience</i> , 2013, 33, 2732-2753.	1.7	88
2869	Comparison of TCDD-elicited genome-wide hepatic gene expression in Sprague-Dawley rats and C57BL/6 mice. <i>Toxicology and Applied Pharmacology</i> , 2013, 267, 184-191.	1.3	22
2870	Global Proteomic Profiling and Enrichment Maps of Dilated Cardiomyopathy. <i>Methods in Molecular Biology</i> , 2013, 1005, 53-66.	0.4	1
2871	Influenza A Infection of Primary Human Airway Epithelial Cells Up-Regulates Proteins Related to Purine Metabolism and Ubiquitin-Related Signaling. <i>Journal of Proteome Research</i> , 2013, 12, 3139-3151.	1.8	35
2872	Skeletal muscle transcriptome profiles related to different training intensities and detraining in Standardbred horses: A search for overtraining biomarkers. <i>Veterinary Journal</i> , 2013, 197, 717-723.	0.6	5
2873	Adult ovarian granulosa cell tumor transcriptomics: prevalence of FOXL2 target genes misregulation gives insights into the pathogenic mechanism of the p.Cys134Trp somatic mutation. <i>Oncogene</i> , 2013, 32, 2739-2746.	2.6	49
2874	Proteomic analysis of balding and non-balding mesenchyme-derived dermal papilla cells from androgenetic alopecia patients using on-line two-dimensional reversed phase-reversed phase LC-MS/MS. <i>Journal of Proteomics</i> , 2013, 85, 174-191.	1.2	13
2875	Transdifferentiation of mesenchymal stem cells-derived adipogenic-differentiated cells into osteogenic- or chondrogenic-differentiated cells proceeds via dedifferentiation and have a correlation with cell cycle arresting and driving genes. <i>Differentiation</i> , 2013, 85, 78-90.	1.0	51
2876	Impaired Transcriptional Response of the Murine Heart to Cigarette Smoke in the Setting of High Fat Diet and Obesity. <i>Chemical Research in Toxicology</i> , 2013, 26, 1034-1042.	1.7	11
2877	Comparison of the differentiation potential of neural crest derived progenitor cells from apical papilla (dNC-PCs) and stem cells from exfoliated deciduous teeth (SHED) into mineralising cells. <i>Archives of Oral Biology</i> , 2013, 58, 699-706.	0.8	27
2878	The Evolution of Lineage-Specific Regulatory Activities in the Human Embryonic Limb. <i>Cell</i> , 2013, 154, 185-196.	13.5	202
2879	Regulation of IRS1/Akt insulin signaling by microRNA-128a during myogenesis. <i>Journal of Cell Science</i> , 2013, 126, 2678-91.	1.2	105
2880	TFEB controls cellular lipid metabolism through a starvation-induced autoregulatory loop. <i>Nature Cell Biology</i> , 2013, 15, 647-658.	4.6	796
2881	Glucocorticoid-Dependent Hippocampal Transcriptome in Male Rats: Pathway-Specific Alterations With Aging. <i>Endocrinology</i> , 2013, 154, 2807-2820.	1.4	30
2882	Escherichia coli- and Staphylococcus aureus-induced mastitis differentially modulate transcriptional responses in neighbouring uninfected bovine mammary gland quarters. <i>BMC Genomics</i> , 2013, 14, 36.	1.2	125
2883	Deep Sequencing of the Porcine Endometrial Transcriptome on Day 14 of Pregnancy <sup>1</sup> . <i>Biology of Reproduction</i> , 2013, 88, 84.	1.2	70



#	ARTICLE	IF	CITATIONS
2884	Network-Based Multiple Sclerosis Pathway Analysis with GWAS Data from 15,000 Cases and 30,000 Controls. <i>American Journal of Human Genetics</i> , 2013, 92, 854-865.	2.6	164
2885	Differences in gene expression profiles and carcinogenesis pathways involved in cisplatin resistance of four types of cancer. <i>Oncology Reports</i> , 2013, 30, 596-614.	1.2	5
2886	Methylomics of gene expression in human monocytes. <i>Human Molecular Genetics</i> , 2013, 22, 5065-5074.	1.4	95
2887	A NETWORK VIEW ON PARKINSON'S DISEASE. <i>Computational and Structural Biotechnology Journal</i> , 2013, 7, e201304004.	1.9	48
2888	Potential antitumor mechanisms of phenothiazine drugs. <i>Science China Life Sciences</i> , 2013, 56, 1020-1027.	2.3	21
2889	Wood chemistry analysis and expression profiling of a poplar clone expressing a tyrosine-rich peptide. <i>Plant Cell Reports</i> , 2013, 32, 1827-1841.	2.8	5
2890	Transcriptional profiling identifies genes induced by hepatocyte-derived extracellular matrix in metastatic human colorectal cancer cell lines. <i>Clinical and Experimental Metastasis</i> , 2013, 30, 189-200.	1.7	19
2891	Elevated Concentrations of Milk Î²2-Microglobulin Are Associated with Increased Risk of Breastfeeding Transmission of HIV-1 (Vertical Transmission Study). <i>Journal of Proteome Research</i> , 2013, 12, 5616-5625.	1.8	8
2892	Cancer-related marketing centrality motifs acting as pivot units in the human signaling network and mediating cross-talk between biological pathways. <i>Molecular BioSystems</i> , 2013, 9, 3026.	2.9	13
2893	Tracking recent adaptive evolution in microbial species using TimeZone. <i>Nature Protocols</i> , 2013, 8, 652-665.	5.5	23
2894	<i>Orientia tsutsugamushi</i> , the causative agent of scrub typhus, induces an inflammatory program in human macrophages. <i>Microbial Pathogenesis</i> , 2013, 55, 55-63.	1.3	36
2895	Loss of Phosphatase and Tensin Homolog (PTEN) Induces Leptin-mediated Leptin Gene Expression. <i>Journal of Biological Chemistry</i> , 2013, 288, 29821-29835.	1.6	32
2896	Brain-Derived Neurotrophic Factor Signaling Rewrites the Glucocorticoid Transcriptome via Glucocorticoid Receptor Phosphorylation. <i>Molecular and Cellular Biology</i> , 2013, 33, 3700-3714.	1.1	93
2897	Transcriptome Changes in the Porcine Endometrium During the Preattachment Phase1. <i>Biology of Reproduction</i> , 2013, 89, 134.	1.2	67
2898	Changes in Eutopic Endometrial Gene Expression During the Progression of Experimental Endometriosis in the Baboon, <i>Papio Anubis</i> 1. <i>Biology of Reproduction</i> , 2013, 88, 44.	1.2	62
2899	Prioritising risk pathways of complex human diseases based on functional profiling. <i>European Journal of Human Genetics</i> , 2013, 21, 666-672.	1.4	1
2900	Hepatic Differentiation and Maturation of Human Embryonic Stem Cells Cultured in a Perfused Three-Dimensional Bioreactor. <i>Stem Cells and Development</i> , 2013, 22, 581-594.	1.1	56
2901	Transcriptome Profiling Following Neuronal and Glial Expression of ALS-Linked SOD1 in <i>Drosophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 695-708.	0.8	23

#	ARTICLE	IF	CITATIONS
2902	Systems biology of Ewing sarcoma: a network model of EWS-FLI1 effect on proliferation and apoptosis. <i>Nucleic Acids Research</i> , 2013, 41, 8853-8871.	6.5	45
2903	Analysis of the cartilage proteome from three different mouse models of genetic skeletal diseases reveals common and discrete disease signatures. <i>Biology Open</i> , 2013, 2, 802-811.	0.6	12
2904	Expression and Functional Pathway Analysis of Nuclear Receptor NR2F2 in Ovarian Cancer. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2013, 98, E1152-E1162.	1.8	37
2905	Rat retinal transcriptome: Effects of aging and AMD-like retinopathy. <i>Cell Cycle</i> , 2013, 12, 1745-1761.	1.3	62
2906	Next-Generation Sequencing of Small RNAs from HIV-Infected Cells Identifies Phased microRNA Expression Patterns and Candidate Novel microRNAs Differentially Expressed upon Infection. <i>MBio</i> , 2013, 4, e00549-12.	1.8	48
2907	Age-Specific Signatures of Glioblastoma at the Genomic, Genetic, and Epigenetic levels. , 2013, , .		0
2908	Identification of gene sets and pathways associated with lactation performance in mice. <i>Physiological Genomics</i> , 2013, 45, 171-181.	1.0	15
2909	Matrix Metalloproteinase-7 Coordinates Airway Epithelial Injury Response and Differentiation of Ciliated Cells. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2013, 48, 390-396.	1.4	36
2910	p-Cresol sulfate and indoxyl sulfate induce similar cellular inflammatory gene expressions in cultured proximal renal tubular cells. <i>Nephrology Dialysis Transplantation</i> , 2013, 28, 70-78.	0.4	141
2911	Oncogenic ETS fusions deregulate E2F3 target genes in Ewing sarcoma and prostate cancer. <i>Genome Research</i> , 2013, 23, 1797-1809.	2.4	99
2912	Characterization of the rat developmental liver transcriptome. <i>Physiological Genomics</i> , 2013, 45, 301-311.	1.0	21
2913	iBAG: integrative Bayesian analysis of high-dimensional multiplatform genomics data. <i>Bioinformatics</i> , 2013, 29, 149-159.	1.8	115
2914	Divergent Protein Motifs Direct Elongation Factor P-Mediated Translational Regulation in <i>Salmonella enterica</i> and <i>Escherichia coli</i> . <i>MBio</i> , 2013, 4, e00180-13.	1.8	83
2915	Chronic Hepatitis E Virus Infection Is Specifically Associated With an Interferon-Related Transcriptional Program. <i>Journal of Infectious Diseases</i> , 2013, 207, 125-132.	1.9	42
2916	A Systems Biology-Based Investigation into the Pharmacological Mechanisms of Wu Tou Tang Acting on Rheumatoid Arthritis by Integrating Network Analysis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2013, 2013, 1-12.	0.5	25
2917	Dynamics of the <i>Saccharomyces cerevisiae</i> Transcriptome during Bread Dough Fermentation. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7325-7333.	1.4	24
2918	Transcriptional Profiling of Hilar Nodes from Pigs after Experimental Infection with <i>Actinobacillus Pleuropneumoniae</i> . <i>International Journal of Molecular Sciences</i> , 2013, 14, 23516-23532.	1.8	9
2919	EV11 oncoprotein interacts with a large and complex network of proteins and integrates signals through protein phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2885-94.	3.3	44

#	ARTICLE	IF	CITATIONS
2920	FUS-regulated region- and cell-type-specific transcriptome is associated with cell selectivity in ALS/FTLD. <i>Scientific Reports</i> , 2013, 3, 2388.	1.6	41
2921	Post-transcriptional regulation of myotube elongation and myogenesis by Hoi Polloi. <i>Development (Cambridge)</i> , 2013, 140, 3645-3656.	1.2	41
2922	Phylogeny, Functional Annotation, and Protein Interaction Network Analyses of the <i>Xenopus tropicalis</i> Basic Helix-Loop-Helix Transcription Factors. <i>BioMed Research International</i> , 2013, 2013, 1-15.	0.9	3
2923	Genes Related to Mitochondrial Functions, Protein Degradation, and Chromatin Folding Are Differentially Expressed in Lymphomonocytes of Rett Syndrome Patients. <i>Mediators of Inflammation</i> , 2013, 2013, 1-18.	1.4	62
2924	Sequential Waves of Gene Expression in Patients with Clinically Defined Dengue Illnesses Reveal Subtle Disease Phases and Predict Disease Severity. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2298.	1.3	64
2925	The Conserved SKN-1/Nrf2 Stress Response Pathway Regulates Synaptic Function in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2013, 9, e1003354.	1.5	61
2926	The Interactomes of Influenza Virus NS1 and NS2 Proteins Identify New Host Factors and Provide Insights for ADAR1 Playing a Supportive Role in Virus Replication. <i>PLoS Pathogens</i> , 2013, 9, e1003440.	2.1	91
2927	Multifunctional Double-negative T Cells in Sooty Mangabeys Mediate T-helper Functions Irrespective of SIV Infection. <i>PLoS Pathogens</i> , 2013, 9, e1003441.	2.1	29
2928	Network-Based Inference Framework for Identifying Cancer Genes from Gene Expression Data. <i>BioMed Research International</i> , 2013, 2013, 1-12.	0.9	10
2929	Significant Overexpression of DVL1 in Taiwanese Colorectal Cancer Patients with Liver Metastasis. <i>International Journal of Molecular Sciences</i> , 2013, 14, 20492-20507.	1.8	16
2930	Serum-free culture success of glial tumors is related to specific molecular profiles and expression of extracellular matrix-associated gene modules. <i>Neuro-Oncology</i> , 2013, 15, 1684-1695.	0.6	55
2931	Decoding a Signature-Based Model of Transcription Cofactor Recruitment Dictated by Cardinal Cis-Regulatory Elements in Proximal Promoter Regions. <i>PLoS Genetics</i> , 2013, 9, e1003906.	1.5	38
2932	Genome-wide Analysis of Immune System Genes by Expressed Sequence Tag Profiling. <i>Journal of Immunology</i> , 2013, 190, 5578-5587.	0.4	14
2933	The <i>Escherichia coli</i> Cpx Envelope Stress Response Regulates Genes of Diverse Function That Impact Antibiotic Resistance and Membrane Integrity. <i>Journal of Bacteriology</i> , 2013, 195, 2755-2767.	1.0	152
2934	The histone H3.3K27M mutation in pediatric glioma reprograms H3K27 methylation and gene expression. <i>Genes and Development</i> , 2013, 27, 985-990.	2.7	570
2935	A Genome-Wide Analysis of Open Chromatin in Human Epididymis Epithelial Cells Reveals Candidate Regulatory Elements for Genes Coordinating Epididymal Function1. <i>Biology of Reproduction</i> , 2013, 89, 104.	1.2	18
2936	A meta-analysis study of gene expression datasets in mouse liver under PPAR $\alpha$ knockout. <i>Genetical Research</i> , 2013, 95, 78-88.	0.3	1
2937	Lipids as Tumoricidal Components of Human $\alpha$ -Lactalbumin Made Lethal to Tumor Cells (HAMLET). <i>Journal of Biological Chemistry</i> , 2013, 288, 17460-17471.	1.6	19

#	ARTICLE	IF	CITATIONS
2938	Delay and Impairment in Brain Development and Function in Rat Offspring After Maternal Exposure to Methylmercury. <i>Toxicological Sciences</i> , 2013, 133, 112-124.	1.4	25
2939	A Synthetic TLR3 Ligand Mitigates Profibrotic Fibroblast Responses by Inducing Autocrine IFN Signaling. <i>Journal of Immunology</i> , 2013, 191, 2956-2966.	0.4	46
2940	MicroRNA-16 affects key functions of human endothelial progenitor cells. <i>Journal of Leukocyte Biology</i> , 2013, 93, 645-655.	1.5	38
2941	Identification of cell cycle-regulated genes periodically expressed in U2OS cells and their regulation by FOXM1 and E2F transcription factors. <i>Molecular Biology of the Cell</i> , 2013, 24, 3634-3650.	0.9	154
2942	The WASH complex, an endosomal Arp2/3 activator, interacts with the Hermansky-Pudlak syndrome complex BLOC-1 and its cargo phosphatidylinositol-4-kinase type II $\alpha$ . <i>Molecular Biology of the Cell</i> , 2013, 24, 2269-2284.	0.9	101
2943	NF-E2 p45 Is Important for Establishing Normal Function of Platelets. <i>Molecular and Cellular Biology</i> , 2013, 33, 2659-2670.	1.1	35
2944	Computational Translation of Nonmammalian Species Data to Mammalian Species to Meet REACH and Next Generation Risk Assessment Needs. , 2013, , 113-136.		1
2945	Influenza-Induced Inflammation Drives Pneumococcal Otitis Media. <i>Infection and Immunity</i> , 2013, 81, 645-652.	1.0	58
2946	The search for biomarkers of human embryo developmental potential in IVF: a comprehensive proteomic approach. <i>Molecular Human Reproduction</i> , 2013, 19, 250-263.	1.3	34
2947	Translational profiling of hypocretin neurons identifies candidate molecules for sleep regulation. <i>Genes and Development</i> , 2013, 27, 565-578.	2.7	87
2948	Determination of Molecular Markers for BRCA1 and BRCA2 Heterozygosity Using Gene Expression Profiling. <i>Cancer Prevention Research</i> , 2013, 6, 82-90.	0.7	9
2949	Graphite Web: web tool for gene set analysis exploiting pathway topology. <i>Nucleic Acids Research</i> , 2013, 41, W89-W97.	6.5	49
2950	Depletion of FOXP3+ regulatory T cells promotes hypercholesterolemia and atherosclerosis. <i>Journal of Clinical Investigation</i> , 2013, 123, 1323-1334.	3.9	304
2951	Different Patterns of Epstein-Barr Virus Latency in Endemic Burkitt Lymphoma (BL) Lead to Distinct Variants within the BL-Associated Gene Expression Signature. <i>Journal of Virology</i> , 2013, 87, 2882-2894.	1.5	45
2952	CDKN2B expression in adipose tissue of familial combined hyperlipidemia patients. <i>Journal of Lipid Research</i> , 2013, 54, 3491-3505.	2.0	23
2953	Effects on Gene Expression in Rat Liver after Administration of RXR Agonists: UAB30, 4-Methyl-UAB30, and Targretin (Bexarotene). <i>Molecular Pharmacology</i> , 2013, 83, 698-708.	1.0	28
2954	Meta-analysis of interspecies microarray sets of cardiac diseases revealed common and disease-specific signatures. <i>Animal Cells and Systems</i> , 2013, 17, 388-396.	0.8	0
2955	Reverse engineering a mouse embryonic stem cell-specific transcriptional network reveals a new modulator of neuronal differentiation. <i>Nucleic Acids Research</i> , 2013, 41, 711-726.	6.5	24

#	ARTICLE	IF	CITATIONS
2956	Analysis of disease-associated objects at the Rat Genome Database. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat046.	1.4	11
2957	Autophagy and Cellular Senescence Mediated by Sox2 Suppress Malignancy of Cancer Cells. PLoS ONE, 2013, 8, e57172.	1.1	42
2958	Peeling Back the Evolutionary Layers of Molecular Mechanisms Responsive to Exercise-Stress in the Skeletal Muscle of the Racing Horse. DNA Research, 2013, 20, 287-298.	1.5	20
2959	Germinal centre protein HGAL promotes lymphoid hyperplasia and amyloidosis via BCR-mediated Syk activation. Nature Communications, 2013, 4, 1338.	5.8	37
2960	Enhanced Tissue Regeneration Potential of Juvenile Articular Cartilage. American Journal of Sports Medicine, 2013, 41, 2658-2667.	1.9	42
2961	Identification of Two Distinct Carcinoma-Associated Fibroblast Subtypes with Differential Tumor-Promoting Abilities in Oral Squamous Cell Carcinoma. Cancer Research, 2013, 73, 3888-3901.	0.4	133
2962	Reduced Insulin/Insulin-like Growth Factor-1 Signaling and Dietary Restriction Inhibit Translation but Preserve Muscle Mass in Caenorhabditis elegans. Molecular and Cellular Proteomics, 2013, 12, 3624-3639.	2.5	79
2963	Brain-Derived Neurotrophic Factor Signaling Rewrites the Glucocorticoid Transcriptome via Glucocorticoid Receptor Phosphorylation. Molecular and Cellular Biology, 2013, 33, 4138-4138.	1.1	42
2964	A high-content, high-throughput siRNA screen identifies cyclin D2 as a potent regulator of muscle progenitor cell fusion and a target to enhance muscle regeneration. Human Molecular Genetics, 2013, 22, 3283-3295.	1.4	15
2965	STAT3 promotes motor neuron differentiation by collaborating with motor neuron-specific LIM complex. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11445-11450.	3.3	35
2966	A strategy to capture and characterize the synaptic transcriptome. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7464-7469.	3.3	49
2967	Identifying Natural Substrates for Dipeptidyl Peptidases 8 and 9 Using Terminal Amine Isotopic Labeling of Substrates (TAILS) Reveals in Vivo Roles in Cellular Homeostasis and Energy Metabolism. Journal of Biological Chemistry, 2013, 288, 13936-13949.	1.6	73
2968	Collaborative Regulation of Development but Independent Control of Metabolism by Two Epidermis-specific Transcription Factors in Caenorhabditis elegans. Journal of Biological Chemistry, 2013, 288, 33411-33426.	1.6	29
2969	Activin A Suppresses Osteoblast Mineralization Capacity by Altering Extracellular Matrix (ECM) Composition and Impairing Matrix Vesicle (MV) Production. Molecular and Cellular Proteomics, 2013, 12, 2890-2900.	2.5	57
2970	Release of Severe Acute Respiratory Syndrome Coronavirus Nuclear Import Block Enhances Host Transcription in Human Lung Cells. Journal of Virology, 2013, 87, 3885-3902.	1.5	140
2971	Metabolomic Dynamic Analysis of Hypoxia in MDA-MB-231 and the Comparison with Inferred Metabolites from Transcriptomics Data. Cancers, 2013, 5, 491-510.	1.7	14
2972	Evaluation of Different Normalization and Analysis Procedures for Illumina Gene Expression Microarray Data Involving Small Changes. Microarrays (Basel, Switzerland), 2013, 2, 131-152.	1.4	12
2973	Bioinformatics and Gene Network Analyses of the Swine Mammary Gland Transcriptome during Late Gestation. Bioinformatics and Biology Insights, 2013, 7, BBI.S12205.	1.0	13

#	ARTICLE	IF	CITATIONS
2974	A Mycâ€“microRNA network promotes exit from quiescence by suppressing the interferon response and cell-cycle arrest genes. <i>Nucleic Acids Research</i> , 2013, 41, 2239-2254.	6.5	49
2975	E2F2 and CREB cooperatively regulate transcriptional activity of cell cycle genes. <i>Nucleic Acids Research</i> , 2013, 41, 10185-10198.	6.5	45
2976	Expression Patterns and Regulatory Functions of MicroRNAs During the Initiation of Primordial Follicle Development in the Neonatal Mouse Ovary1. <i>Biology of Reproduction</i> , 2013, 89, 126.	1.2	72
2977	Sequential Binary Gene Ratio Tests Define a Novel Molecular Diagnostic Strategy for Malignant Pleural Mesothelioma. <i>Clinical Cancer Research</i> , 2013, 19, 2493-2502.	3.2	27
2978	Dissection of the Human Multipotent Adult Progenitor Cell Secretome by Proteomic Analysis. <i>Stem Cells Translational Medicine</i> , 2013, 2, 745-757.	1.6	35
2979	Toxicogenomic Evaluation of Long-term Hepatic Effects of TCDD in Immature, Ovariectomized C57BL/6 Mice. <i>Toxicological Sciences</i> , 2013, 135, 465-475.	1.4	21
2980	Tissue Inhibitor of Metalloproteinasesâ€“3 Moderates the Proinflammatory Status of Macrophages. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2013, 49, 768-777.	1.4	41
2981	Review of Biological Network Data and Its Applications. <i>Genomics and Informatics</i> , 2013, 11, 200.	0.4	79
2982	Modeling competing endogenous RNA regulatory networks in glioblastoma multiforme. , 2013, , .		5
2983	CD8+Lymphocytes Suppress Human Immunodeficiency Virus 1 Replication by Secreting Type I Interferons. <i>Journal of Interferon and Cytokine Research</i> , 2013, 33, 632-645.	0.5	8
2984	Subcutaneous and gonadal adipose tissue transcriptome differences in lean and obese female dogs. <i>Animal Genetics</i> , 2013, 44, 728-735.	0.6	4
2985	Noncanonical microRNAs and endogenous siRNAs in normal and psoriatic human skin. <i>Human Molecular Genetics</i> , 2013, 22, 737-748.	1.4	43
2986	Skeletal muscle tissue transcriptome differences in lean and obese female beagle dogs. <i>Animal Genetics</i> , 2013, 44, 560-568.	0.6	7
2987	Coordinated dysregulation of mRNAs and microRNAs in the rat medial prefrontal cortex following a history of alcohol dependence. <i>Pharmacogenomics Journal</i> , 2013, 13, 286-296.	0.9	87
2988	The identification of genetic pathways involved in vascular adaptations after physical deconditioning <i>versus</i> exercise training in humans. <i>Experimental Physiology</i> , 2013, 98, 710-721.	0.9	16
2989	An Overview of Synergistic Data Tools for Biological Scrutiny. <i>Israel Journal of Chemistry</i> , 2013, 53, 185-198.	1.0	5
2990	Draft genome sequence of the Tibetan antelope. <i>Nature Communications</i> , 2013, 4, 1858.	5.8	229
2991	Nonâ€“trisomic homeobox gene expression during craniofacial development in the Ts65Dn mouse model of Down syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2013, 161, 1866-1874.	0.7	11

#	ARTICLE	IF	CITATIONS
2992	Pathogenic mechanisms of influenza A(H1N1)pdm09 infection elucidated on gene expression profiling. <i>Pediatrics International</i> , 2013, 55, 572-577.	0.2	6
2993	Alkaline Phosphatase ALPPL-2 Is a Novel Pancreatic Carcinoma-Associated Protein. <i>Cancer Research</i> , 2013, 73, 1934-1945.	0.4	80
2994	Blood-based gene expression predictors of PTSD risk and resilience among deployed marines: A pilot study. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2013, 162, 313-326.	1.1	63
2995	Integrative Proteomic and Transcriptomic Analyses Reveal Multiple Post-transcriptional Regulatory Mechanisms of Mouse Spermatogenesis. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1144-1157.	2.5	70
2996	Transcriptional response to stress in the dynamic chromatin environment of cycling and mitotic cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3388-97.	3.3	134
2997	The Trithorax Group Protein Ash2 Is Essential for Pluripotency and Maintaining Open Chromatin in Embryonic Stem Cells. <i>Journal of Biological Chemistry</i> , 2013, 288, 5039-5048.	1.6	67
2998	Coordinate Changes in Histone Modifications, mRNA Levels, and Metabolite Profiles in Clonal INS-1 832/13 Î²-Cells Accompany Functional Adaptations to Lipotoxicity. <i>Journal of Biological Chemistry</i> , 2013, 288, 11973-11987.	1.6	66
2999	MicroRNAs miR-30b, miR-30d, and miR-494 Regulate Human Endometrial Receptivity. <i>Reproductive Sciences</i> , 2013, 20, 308-317.	1.1	169
3000	Profiling of T helper cell-derived small RNAs reveals unique antisense transcripts and differential association of miRNAs with argonaute proteins 1 and 2. <i>Nucleic Acids Research</i> , 2013, 41, 1164-1177.	6.5	20
3001	Concise Review: New Paradigms for Down Syndrome Research Using Induced Pluripotent Stem Cells: Tackling Complex Human Genetic Disease. <i>Stem Cells Translational Medicine</i> , 2013, 2, 175-184.	1.6	13
3002	Male-specific region of the bovine Y chromosome is gene rich with a high transcriptomic activity in testis development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12373-12378.	3.3	73
3003	Comparative Expression Analysis Reveals Lineage Relationships between Human and Murine Gliomas and a Dominance of Glial Signatures during Tumor Propagation <i>In Vitro</i> . <i>Cancer Research</i> , 2013, 73, 5834-5844.	0.4	28
3004	E2F1 loss induces spontaneous tumour development in Rb-deficient epidermis. <i>Oncogene</i> , 2013, 32, 2937-2951.	2.6	19
3005	Gene expression profiling by mRNA sequencing reveals increased expression of immune/inflammation-related genes in the hippocampus of individuals with schizophrenia. <i>Translational Psychiatry</i> , 2013, 3, e321-e321.	2.4	162
3006	Inter-ethnic differences in lymphocyte sensitivity to glucocorticoids reflect variation in transcriptional response. <i>Pharmacogenomics Journal</i> , 2013, 13, 121-129.	0.9	26
3007	ER stress-mediated apoptosis induced by celastrol in cancer cells and important role of glycogen synthase kinase-3Î² in the signal network. <i>Cell Death and Disease</i> , 2013, 4, e715-e715.	2.7	48
3008	In serum veritasâ€”in serum sanitas? Cell non-autonomous aging compromises differentiation and survival of mesenchymal stromal cells via the oxidative stress pathway. <i>Cell Death and Disease</i> , 2013, 4, e970-e970.	2.7	45
3009	3,4-Dimethoxyphenyl Bis-benzimidazole Derivative, Mitigates Radiation-Induced DNA Damage. <i>Radiation Research</i> , 2013, 179, 647.	0.7	5

#	ARTICLE	IF	CITATIONS
3010	Surface functionalities of gold nanoparticles impact embryonic gene expression responses. <i>Nanotoxicology</i> , 2013, 7, 192-201.	1.6	64
3011	Reconstruction of novel transcription factor regulons through inference of their binding sites. , 2013, , .		0
3012	PQBP1, a factor linked to intellectual disability, affects alternative splicing associated with neurite outgrowth. <i>Genes and Development</i> , 2013, 27, 615-626.	2.7	65
3013	New Levels of Transcriptome Complexity at Upper Thermal Limits in Wild <i>Drosophila</i> Revealed by Exon Expression Analysis. <i>Genetics</i> , 2013, 195, 809-830.	1.2	38
3014	Molecular Signatures in Skin Associated with Clinical Improvement during Mycophenolate Treatment in Systemic Sclerosis. <i>Journal of Investigative Dermatology</i> , 2013, 133, 1979-1989.	0.3	150
3015	Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. <i>Genome Research</i> , 2013, 23, 1422-1433.	2.4	457
3016	Network as biomarker. <i>Systems Biomedicine (Austin, Tex )</i> , 2013, 1, 35-41.	0.7	15
3017	Gene-expression signatures differ between different clinical forms of familial hemophagocytic lymphohistiocytosis. <i>Blood</i> , 2013, 121, e14-e24.	0.6	20
3018	Genome-scale expression and transcription factor binding profiles reveal therapeutic targets in transgenic ERG myeloid leukemia. <i>Blood</i> , 2013, 122, 2694-2703.	0.6	44
3019	Co-Culture of Human Bone Marrow Stromal Cells with Endothelial Cells Alters Gene Expression Profiles. <i>International Journal of Artificial Organs</i> , 2013, 36, 650-662.	0.7	22
3020	Metabolite and transcriptome analysis during fasting suggest a role for the p53-Ddit4 axis in major metabolic tissues. <i>BMC Genomics</i> , 2013, 14, 758.	1.2	65
3021	Significant modulation of the hepatic proteome induced by exposure to low temperature in <i>Xenopus laevis</i> . <i>Biology Open</i> , 2013, 2, 1057-1069.	0.6	19
3022	Global Gene Expression Analysis of Term Amniotic Fluid Cell-Free Fetal RNA. <i>Obstetrics and Gynecology</i> , 2013, 121, 1248-1254.	1.2	28
3023	Integrative analysis of time course microarray data and DNA sequence data via log-linear models for identifying dynamic transcriptional regulatory networks. <i>International Journal of Data Mining and Bioinformatics</i> , 2013, 7, 38.	0.1	1
3024	FGFR2 signaling underlies p63 oncogenic function in squamous cell carcinoma. <i>Journal of Clinical Investigation</i> , 2013, 123, 3525-3538.	3.9	111
3025	Neuron-Enriched Gene Expression Patterns are Regionally Anti-Correlated with Oligodendrocyte-Enriched Patterns in the Adult Mouse and Human Brain. <i>Frontiers in Neuroscience</i> , 2013, 7, 5.	1.4	23
3026	An analysis and validation pipeline for large-scale RNAi-based screens. <i>Scientific Reports</i> , 2013, 3, 1076.	1.6	5
3027	Mitigating effects of L-selenomethionine on low-dose iron ion radiation-induced changes in gene expression associated with cellular stress. <i>Oncology Letters</i> , 2013, 6, 35-42.	0.8	5



#	ARTICLE	IF	CITATIONS
3028	Analysis of protein expression regulated by lumican in PANC-1 cells using shotgun proteomics. <i>Oncology Reports</i> , 2013, 30, 1609-1621.	1.2	10
3029	Hypoxia Alters MicroRNA Expression in Rat Cortical Pericytes. <i>MicroRNA (Sharjah, United Arab)</i> Tj ETQq1 1 0.784314 rgBT /Overlock 10 0.6 35		
3030	Endometrial Receptivity: A Revisit to Functional Genomics Studies on Human Endometrium and Creation of HGEx-ERdb. <i>PLoS ONE</i> , 2013, 8, e58419.	1.1	59
3031	Pathogen Induced Changes in the Protein Profile of Human Tears from Fusarium Keratitis Patients. <i>PLoS ONE</i> , 2013, 8, e53018.	1.1	48
3032	DNA Methylation Dynamics in Blood after Hematopoietic Cell Transplant. <i>PLoS ONE</i> , 2013, 8, e56931.	1.1	24
3033	Focused Examination of the Intestinal Epithelium Reveals Transcriptional Signatures Consistent with Disturbances in Enterocyte Maturation and Differentiation during the Course of SIV Infection. <i>PLoS ONE</i> , 2013, 8, e60122.	1.1	18
3034	Striatal Molecular Signature of Subchronic Subthalamic Nucleus High Frequency Stimulation in Parkinsonian Rat. <i>PLoS ONE</i> , 2013, 8, e60447.	1.1	18
3035	RNA Profiles of Porcine Embryos during Genome Activation Reveal Complex Metabolic Switch Sensitive to In Vitro Conditions. <i>PLoS ONE</i> , 2013, 8, e61547.	1.1	21
3036	Proteomic Characterization of Inbreeding-Related Cold Sensitivity in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2013, 8, e62680.	1.1	5
3037	Age-Specific Signatures of Glioblastoma at the Genomic, Genetic, and Epigenetic Levels. <i>PLoS ONE</i> , 2013, 8, e62982.	1.1	49
3038	Reduce Manual Curation by Combining Gene Predictions from Multiple Annotation Engines, a Case Study of Start Codon Prediction. <i>PLoS ONE</i> , 2013, 8, e63523.	1.1	12
3039	Global Gene Expression Profiling of Individual Human Oocytes and Embryos Demonstrates Heterogeneity in Early Development. <i>PLoS ONE</i> , 2013, 8, e64192.	1.1	33
3040	Influence of a Short-Term Iron-Deficient Diet on Hepatic Gene Expression Profiles in Rats. <i>PLoS ONE</i> , 2013, 8, e65732.	1.1	14
3041	A Systems-Genetics Approach and Data Mining Tool to Assist in the Discovery of Genes Underlying Complex Traits in <i>Oryza sativa</i> . <i>PLoS ONE</i> , 2013, 8, e68551.	1.1	26
3042	Effects of Fertility on Gene Expression and Function of the Bovine Endometrium. <i>PLoS ONE</i> , 2013, 8, e69444.	1.1	58
3043	Proteomic and Systems Biology Analysis of the Monocyte Response to <i>Coxiella burnetii</i> Infection. <i>PLoS ONE</i> , 2013, 8, e69558.	1.1	7
3044	Reverse Differentiation as a Gene Filtering Tool in Genome Expression Profiling of Adipogenesis for Fat Marker Gene Selection and Their Analysis. <i>PLoS ONE</i> , 2013, 8, e69754.	1.1	23
3045	Partial Restoration of Macrophage Alteration from Diet-Induced Obesity in Response to <i>Porphyromonas gingivalis</i> Infection. <i>PLoS ONE</i> , 2013, 8, e70320.	1.1	5

#	ARTICLE	IF	CITATIONS
3046	Prioritizing Disease Candidate Proteins in Cardiomyopathy-Specific Protein-Protein Interaction Networks Based on $\alpha$ -Guilt by Association Analysis. PLoS ONE, 2013, 8, e71191.	1.1	14
3047	Mesenchymal Stem Cells from Human Umbilical Cord Express Preferentially Secreted Factors Related to Neuroprotection, Neurogenesis, and Angiogenesis. PLoS ONE, 2013, 8, e72604.	1.1	252
3048	HDAC1 and HDAC2 Restrain the Intestinal Inflammatory Response by Regulating Intestinal Epithelial Cell Differentiation. PLoS ONE, 2013, 8, e73785.	1.1	84
3049	Transcriptional Profiling of Human Monocytes Identifies the Inhibitory Receptor CD300a as Regulator of Transendothelial Migration. PLoS ONE, 2013, 8, e73981.	1.1	7
3050	The Genome-Wide Early Temporal Response of <i>Saccharomyces cerevisiae</i> to Oxidative Stress Induced by Cumene Hydroperoxide. PLoS ONE, 2013, 8, e74939.	1.1	29
3051	Genome-Wide Promoter Methylome of Small Renal Masses. PLoS ONE, 2013, 8, e77309.	1.1	13
3052	The Human Placental Sexome Differs between Trophoblast Epithelium and Villous Vessel Endothelium. PLoS ONE, 2013, 8, e79233.	1.1	96
3053	Computational Prediction of Human Salivary Proteins from Blood Circulation and Application to Diagnostic Biomarker Identification. PLoS ONE, 2013, 8, e80211.	1.1	29
3054	Urinary Prognostic Biomarkers and Classification of IgA Nephropathy by High Resolution Mass Spectrometry Coupled with Liquid Chromatography. PLoS ONE, 2013, 8, e80830.	1.1	73
3055	Distinct MicroRNAs Expression Profile in Primary Biliary Cirrhosis and Evaluation of miR 505-3p and miR197-3p as Novel Biomarkers. PLoS ONE, 2013, 8, e66086.	1.1	77
3056	Infection with a Virulent Strain of <i>Wolbachia</i> Disrupts Genome Wide-Patterns of Cytosine Methylation in the Mosquito <i>Aedes aegypti</i> . PLoS ONE, 2013, 8, e66482.	1.1	57
3057	Machine-Based Morphologic Analysis of Glioblastoma Using Whole-Slide Pathology Images Uncovers Clinically Relevant Molecular Correlates. PLoS ONE, 2013, 8, e81049.	1.1	91
3058	Anticancer Agent Shikonin Is an Incompetent Inducer of Cancer Drug Resistance. PLoS ONE, 2013, 8, e52706.	1.1	51
3059	A Genome-Wide Screen of CREB Occupancy Identifies the RhoA Inhibitors Par6C and Rnd3 as Regulators of BDNF-Induced Synaptogenesis. PLoS ONE, 2013, 8, e64658.	1.1	57
3060	Maximal information component analysis: a novel non-linear network analysis method. <i>Frontiers in Genetics</i> , 2013, 4, 28.	1.1	22
3061	Construction and Analysis of the Cell Surface's Protein Network for Human Sperm-Egg Interaction. , 2013, 2013, 1-8.		8
3062	Phosphoproteomics-Based Characterization of Cancer Cell Signaling Networks. , 2013, , .		0
3063	Protection Genes in Nucleus Accumbens Shell Affect Vulnerability to Nicotine Self-Administration across Isogenic Strains of Adolescent Rat. PLoS ONE, 2014, 9, e86214.	1.1	10

#	ARTICLE	IF	CITATIONS
3064	Investigating the Different Mechanisms of Genotoxic and Non-Genotoxic Carcinogens by a Gene Set Analysis. PLoS ONE, 2014, 9, e86700.	1.1	11
3065	Model Steatogenic Compounds (Amiodarone, Valproic Acid, and Tetracycline) Alter Lipid Metabolism by Different Mechanisms in Mouse Liver Slices. PLoS ONE, 2014, 9, e86795.	1.1	47
3066	Differential Induction of TLR3-Dependent Innate Immune Signaling by Closely Related Parasite Species. PLoS ONE, 2014, 9, e88398.	1.1	57
3067	Meta-Analysis of Pathway Enrichment: Combining Independent and Dependent Omics Data Sets. PLoS ONE, 2014, 9, e89297.	1.1	44
3068	A Method for Predicting Protein-Protein Interaction Types. PLoS ONE, 2014, 9, e90904.	1.1	18
3069	Integrated Analysis of DNA Methylation and RNA Transcriptome during In Vitro Differentiation of Human Pluripotent Stem Cells into Retinal Pigment Epithelial Cells. PLoS ONE, 2014, 9, e91416.	1.1	19
3070	Studying the System-Level Involvement of MicroRNAs in Parkinson's Disease. PLoS ONE, 2014, 9, e93751.	1.1	21
3071	Genes Influenced by the Non-Muscle Isoform of Myosin Light Chain Kinase Impact Human Cancer Prognosis. PLoS ONE, 2014, 9, e94325.	1.1	17
3072	Systemic Inflammatory Response to Smoking in Chronic Obstructive Pulmonary Disease: Evidence of a Gender Effect. PLoS ONE, 2014, 9, e97491.	1.1	40
3073	Human Endogenous Retrovirus-K(II) Envelope Induction Protects Neurons during HIV/AIDS. PLoS ONE, 2014, 9, e97984.	1.1	41
3074	Intracellular Bacteria Interfere with Dendritic Cell Functions: Role of the Type I Interferon Pathway. PLoS ONE, 2014, 9, e99420.	1.1	64
3075	Differential Transcriptional Effects of EGFR Inhibitors. PLoS ONE, 2014, 9, e102466.	1.1	12
3076	SILAC-Based Proteomic Profiling of the Human MDA-MB-231 Metastatic Breast Cancer Cell Line in Response to the Two Antitumoral Lactoferrin Isoforms: The Secreted Lactoferrin and the Intracellular Delta-Lactoferrin. PLoS ONE, 2014, 9, e104563.	1.1	11
3077	Dynamic Modularity of Host Protein Interaction Networks in Salmonella Typhi Infection. PLoS ONE, 2014, 9, e104911.	1.1	6
3078	Genetic and Epigenetic Changes in Chromosomally Stable and Unstable Progeny of Irradiated Cells. PLoS ONE, 2014, 9, e107722.	1.1	19
3079	Transcriptomic Characterization of C57BL/6 Mouse Embryonic Stem Cell Differentiation and Its Modulation by Developmental Toxicants. PLoS ONE, 2014, 9, e108510.	1.1	14
3080	Computational Surprisal Analysis Speeds-Up Genomic Characterization of Cancer Processes. PLoS ONE, 2014, 9, e108549.	1.1	3
3081	Genome-Wide Microarray Expression and Genomic Alterations by Array-CGH Analysis in Neuroblastoma Stem-Like Cells. PLoS ONE, 2014, 9, e113105.	1.1	5

#	ARTICLE	IF	CITATIONS
3082	Kismet Positively Regulates Glutamate Receptor Localization and Synaptic Transmission at the <i>Drosophila</i> Neuromuscular Junction. <i>PLoS ONE</i> , 2014, 9, e113494.	1.1	18
3083	Transcriptome Analysis of <i>Enterococcus faecalis</i> during Mammalian Infection Shows Cells Undergo Adaptation and Exist in a Stringent Response State. <i>PLoS ONE</i> , 2014, 9, e115839.	1.1	35
3084	Differential Network Analyses of Alzheimer's Disease Identify Early Events in Alzheimer's Disease Pathology. <i>International Journal of Alzheimer's Disease</i> , 2014, 2014, 1-18.	1.1	12
3085	Cyclin D activates the Rb tumor suppressor by mono-phosphorylation. <i>ELife</i> , 2014, 3, .	2.8	332
3086	Docetaxel-loaded solid lipid nanoparticles suppress breast cancer cells growth with reduced myelosuppression toxicity. <i>International Journal of Nanomedicine</i> , 2014, 9, 4829.	3.3	38
3087	Myeloid decidual dendritic cells and immunoregulation of pregnancy: defective responsiveness to <i>Coxiella burnetii</i> and <i>Brucella abortus</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2014, 4, 179.	1.8	17
3088	Comparison of gene regulatory networks of benign and malignant breast cancer samples with normal samples. <i>Genetics and Molecular Research</i> , 2014, 13, 9453-9462.	0.3	3
3089	Oligonucleotide microarray analysis reveals dysregulation of energy-related metabolism in insulin-sensitive tissues of type 2 diabetes patients. <i>Genetics and Molecular Research</i> , 2014, 13, 4494-4504.	0.3	8
3090	Functional analysis of differentially expressed genes associated with glaucoma from DNA microarray data. <i>Genetics and Molecular Research</i> , 2014, 13, 9421-9428.	0.3	5
3091	Changes in Rat Spinal Cord Gene Expression After Inflammatory Hyperalgesia of the Joint and Manual Therapy. <i>Journal of Osteopathic Medicine</i> , 2014, 114, 768-776.	0.4	7
3092	Transduction motif analysis of gastric cancer based on a human signaling network. <i>Brazilian Journal of Medical and Biological Research</i> , 2014, 47, 369-375.	0.7	2
3093	Proteomics-Based Identification of Differentially Abundant Proteins from Human Keratinocytes Exposed to Arsenic Trioxide. <i>Journal of Proteomics and Bioinformatics</i> , 2014, 07, 166-178.	0.4	17
3094	A Systems Biology View of the Spliceosome Component Phf5a in Relation to Estrogen and Cancer. <i>Journal of Computer Science and Systems Biology</i> , 2014, 07, .	0.0	0
3095	Increased Survival despite Failure of Transplanted Human Hepatocyte Implantation into Liver Parenchyma of Nude Mice with Repeated Lethal Jo2-Induced Liver Deficiency. <i>Cell Transplantation</i> , 2014, 23, 1557-1572.	1.2	2
3096	Deep sequencing analysis of microRNA expression in porcine serum-induced hepatic fibrosis rats. <i>Annals of Hepatology</i> , 2014, 13, 439-449.	0.6	8
3097	CGG repeats in RNA modulate expression of TDP-43 in mouse and fly models of fragile X tremor ataxia syndrome. <i>Human Molecular Genetics</i> , 2014, 23, 5906-5915.	1.4	21
3098	A genome-wide scan for selection signatures in Yorkshire and Landrace pigs based on sequencing data. <i>Animal Genetics</i> , 2014, 45, 808-816.	0.6	19
3099	Lipid Droplet Protein LID-1 Mediates ATGL-1-Dependent Lipolysis during Fasting in <i>Caenorhabditis elegans</i> . <i>Molecular and Cellular Biology</i> , 2014, 34, 4165-4176.	1.1	82

#	ARTICLE	IF	CITATIONS
3100	Epigenome-wide analysis of piRNAs in gene-specific DNA methylation. <i>RNA Biology</i> , 2014, 11, 1301-1312.	1.5	55
3101	Proteomic alteration of PK-15 cells after infection by porcine circovirus type 2. <i>Virus Genes</i> , 2014, 49, 400-416.	0.7	10
3102	Human Cytomegalovirus Modulates Monocyte-Mediated Innate Immune Responses during Short-Term Experimental Latency <i>in Vitro</i> . <i>Journal of Virology</i> , 2014, 88, 9391-9405.	1.5	41
3103	Network-based analysis identifies epigenetic biomarkers of esophageal squamous cell carcinoma progression. <i>Bioinformatics</i> , 2014, 30, 3054-3061.	1.8	15
3104	Discovery of new glomerular disease-relevant genes by translational profiling of podocytes in vivo. <i>Kidney International</i> , 2014, 86, 1116-1129.	2.6	36
3105	Identifying candidate genes for discrimination of ulcerative colitis and Crohn's disease. <i>Molecular Biology Reports</i> , 2014, 41, 6349-6355.	1.0	7
3106	Calcifying vascular smooth muscle cells and osteoblasts: independent cell types exhibiting extracellular matrix and biomineralization-related mimics. <i>BMC Genomics</i> , 2014, 15, 965.	1.2	87
3107	Identifying and mapping cell-type-specific chromatin programming of gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E645-54.	3.3	31
3108	Proteomic analysis of human plasma in chronic rheumatic mitral stenosis reveals proteins involved in the complement and coagulation cascade. <i>Clinical Proteomics</i> , 2014, 11, 35.	1.1	17
3109	Proteomic study reveals a functional network of cancer markers in the G1-Stage of the breast cancer cell cycle. <i>BMC Cancer</i> , 2014, 14, 710.	1.1	13
3111	Liver transcriptome analysis in gilthead sea bream upon exposure to low temperature. <i>BMC Genomics</i> , 2014, 15, 765.	1.2	96
3112	De novo prediction of cis-regulatory elements and modules through integrative analysis of a large number of ChIP datasets. <i>BMC Genomics</i> , 2014, 15, 1047.	1.2	11
3113	Changes in renal medulla gene expression in a pre-clinical model of post cardiopulmonary bypass acute kidney injury. <i>BMC Genomics</i> , 2014, 15, 916.	1.2	12
3115	Understanding disease mechanisms with models of signaling pathway activities. <i>BMC Systems Biology</i> , 2014, 8, 121.	3.0	42
3116	Early transcriptional changes in the reef-building coral <i>Acropora aspera</i> in response to thermal and nutrient stress. <i>BMC Genomics</i> , 2014, 15, 1052.	1.2	67
3117	ChIP-Enrich: gene set enrichment testing for ChIP-seq data. <i>Nucleic Acids Research</i> , 2014, 42, e105-e105.	6.5	136
3118	Comprehensive analysis of microRNA-regulated protein interaction network reveals the tumor suppressive role of microRNA-149 in human hepatocellular carcinoma via targeting AKT-mTOR pathway. <i>Molecular Cancer</i> , 2014, 13, 253.	7.9	85
3119	Divergence of RNA localization between rat and mouse neurons reveals the potential for rapid brain evolution. <i>BMC Genomics</i> , 2014, 15, 883.	1.2	22

#	ARTICLE	IF	CITATIONS
3120	Integrative genomics and transcriptomics analysis of human embryonic and induced pluripotent stem cells. <i>BioData Mining</i> , 2014, 7, 32.	2.2	2
3121	Patterns of gene expression associated with recovery and injury in heat-stressed rats. <i>BMC Genomics</i> , 2014, 15, 1058.	1.2	34
3122	The forkhead transcription factor FOXM1 promotes endocrine resistance and invasiveness in estrogen receptor-positive breast cancer by expansion of stem-like cancer cells. <i>Breast Cancer Research</i> , 2014, 16, 436.	2.2	102
3123	Expression profile of <i>Caenorhabditis elegans</i> mutant for the Werner syndrome gene ortholog reveals the impact of vitamin C on development to increase life span. <i>BMC Genomics</i> , 2014, 15, 940.	1.2	15
3124	Integrative analysis of young genes, positively selected genes and lncRNAs in the development of <i>Drosophila melanogaster</i> . <i>BMC Evolutionary Biology</i> , 2014, 14, 241.	3.2	11
3125	E2F1 Coregulates Cell Cycle Genes and Chromatin Components during the Transition of Oligodendrocyte Progenitors from Proliferation to Differentiation. <i>Journal of Neuroscience</i> , 2014, 34, 1481-1493.	1.7	64
3126	Uncoupling reproduction from metabolism extends chronological lifespan in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1538-47.	3.3	40
3127	Kinome-wide screening of HER2+ breast cancer cells for molecules that mediate cell proliferation or sensitize cells to trastuzumab therapy. <i>Oncogenesis</i> , 2014, 3, e133-e133.	2.1	18
3128	Impact of Hospital Variables on Case Mix Index as a Marker of Disease Severity. <i>Population Health Management</i> , 2014, 17, 28-34.	0.8	85
3129	Finding Novel Molecular Connections between Developmental Processes and Disease. <i>PLoS Computational Biology</i> , 2014, 10, e1003578.	1.5	10
3130	Gene expression profile analysis for different idiopathic interstitial pneumonias subtypes. <i>Experimental Lung Research</i> , 2014, 40, 367-379.	0.5	13
3131	Identification of overexpressed genes in <i>Sodalis glossinidius</i> inhabiting trypanosome-infected self-cured tsetse flies. <i>Frontiers in Microbiology</i> , 2014, 5, 255.	1.5	6
3132	Pivotal role of IL-6 in the hyperinflammatory responses to subacute ozone in adiponectin-deficient mice. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2014, 306, L508-L520.	1.3	22
3133	Regulation of Synaptic nlg-1/Neuroigin Abundance by the skn-1/Nrf Stress Response Pathway Protects against Oxidative Stress. <i>PLoS Genetics</i> , 2014, 10, e1004100.	1.5	45
3134	Dopamine Signaling Leads to Loss of Polycomb Repression and Aberrant Gene Activation in Experimental Parkinsonism. <i>PLoS Genetics</i> , 2014, 10, e1004574.	1.5	49
3135	Immunology of Bats and Their Viruses: Challenges and Opportunities. <i>Viruses</i> , 2014, 6, 4880-4901.	1.5	87
3136	Tungstate promotes $\beta$ -cell survival in <i>Irs2<sup>+/+</sup></i> mice. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2014, 306, E36-E47.	1.8	17
3137	Urinary Prognostic Biomarkers in Patients With Focal Segmental Glomerulosclerosis. <i>Nephro-Urology Monthly</i> , 2014, 6, e16806.	0.0	24

#	ARTICLE	IF	CITATIONS
3138	Long Non-Coding RNA and Alternative Splicing Modulations in Parkinson's Leukocytes Identified by RNA Sequencing. <i>PLoS Computational Biology</i> , 2014, 10, e1003517.	1.5	167
3139	The Genomic Architecture of Population Divergence between Subspecies of the European Rabbit. <i>PLoS Genetics</i> , 2014, 10, e1003519.	1.5	82
3140	Pathogenesis analysis of pituitary adenoma based on gene expression profiling. <i>Oncology Letters</i> , 2014, 8, 2423-2430.	0.8	10
3141	Learning Dysregulated Pathways in Cancers from Differential Variability Analysis. <i>Cancer Informatics</i> , 2014, 13s5, CIN.S14066.	0.9	37
3142	Deep Sequencing-Based Identification of Small Regulatory RNAs in <i>Synechocystis</i> sp. PCC 6803. <i>PLoS ONE</i> , 2014, 9, e92711.	1.1	28
3143	Molecular Mechanisms of Hypoxic Responses via Unique Roles of Ras1, Cdc24 and Ptp3 in a Human Fungal Pathogen <i>Cryptococcus neoformans</i> . <i>PLoS Genetics</i> , 2014, 10, e1004292.	1.5	14
3144	Selective nuclear export of specific classes of mRNA from mammalian nuclei is promoted by GANP. <i>Nucleic Acids Research</i> , 2014, 42, 5059-5071.	6.5	64
3145	Epigenome-Guided Analysis of the Transcriptome of Plaque Macrophages during Atherosclerosis Regression Reveals Activation of the Wnt Signaling Pathway. <i>PLoS Genetics</i> , 2014, 10, e1004828.	1.5	31
3146	COE Loss-of-Function Analysis Reveals a Genetic Program Underlying Maintenance and Regeneration of the Nervous System in Planarians. <i>PLoS Genetics</i> , 2014, 10, e1004746.	1.5	43
3147	â€™Omics-Based Testing for Direct Immunotoxicity. , 2014, , 89-124.		1
3148	Optimization and Analysis of Seriation Algorithm for Ordering Protein Networks. , 2014, , .		3
3149	Drug-induced liver injury classification model based on in vitro human transcriptomics and in vivo rat clinical chemistry data. <i>Systems Biomedicine (Austin, Tex )</i> , 2014, 2, 63-70.	0.7	10
3150	Transcriptional profiling of the postnatal brain of the Ts1Cje mouse model of Down syndrome. <i>Genomics Data</i> , 2014, 2, 314-317.	1.3	3
3151	Common Mechanisms Underlying Refractive Error Identified in Functional Analysis of Gene Lists From Genome-Wide Association Study Results in 2 European British Cohorts. <i>JAMA Ophthalmology</i> , 2014, 132, 50.	1.4	23
3152	Inactivation of the budding yeast cohesin loader Scc2 alters gene expression both globally and in response to a single DNA double strand break. <i>Cell Cycle</i> , 2014, 13, 3645-3658.	1.3	11
3153	Integrated Omic Analysis of Oropharyngeal Carcinomas Reveals Human Papillomavirus (HPV)â€™dependent Regulation of the Activator Protein 1 (AP-1) Pathway. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3572-3584.	2.5	19
3154	Biological pathway selection through Bayesian integrative modeling. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 435-57.	0.2	1
3155	Genetic Factors Involved in Susceptibility to Lung Disease. , 2014, , 369-384.		0

#	ARTICLE	IF	CITATIONS
3156	Cell-type specific transcriptomic profiling to dissect mechanisms of differential dendritogenesis. <i>Genomics Data</i> , 2014, 2, 378-381.	1.3	5
3157	Muscle ring finger 1 and muscle ring finger 2 are necessary but functionally redundant during developmental cardiac growth and regulate E2F1-mediated gene expression <i>in vivo</i> . <i>Cell Biochemistry and Function</i> , 2014, 32, 39-50.	1.4	36
3158	Establishment of a proteomic profile associated with gonocyte and spermatogonial stem cell maturation and differentiation in neonatal mice. <i>Proteomics</i> , 2014, 14, 274-285.	1.3	25
3159	Fam40b is required for lineage commitment of murine embryonic stem cells. <i>Cell Death and Disease</i> , 2014, 5, e1320-e1320.	2.7	19
3160	Constructing protein-protein interaction network of hypertension with blood stasis syndrome via digital gene expression sequencing and database mining. <i>Journal of Integrative Medicine</i> , 2014, 12, 476-482.	1.4	5
3161	Dexmedetomidine preconditioning ameliorates kidney ischemia-reperfusion injury. <i>Pharmacology Research and Perspectives</i> , 2014, 2, e00045.	1.1	61
3162	A systematic review of microRNA expression profiling studies in human gastric cancer. <i>Cancer Medicine</i> , 2014, 3, 878-888.	1.3	125
3163	Molecular Aspects of Adipoepithelial Transdifferentiation in Mouse Mammary Gland. <i>Stem Cells</i> , 2014, 32, 2756-2766.	1.4	47
3164	Transcriptional profiling predicts overwhelming homology of schwann cells, olfactory ensheathing cells, and schwann cell-like glia. <i>Glia</i> , 2014, 62, 1559-1581.	2.5	32
3165	Upregulation of MMP12 and Its Activity by UVA1 in Human Skin: Potential Implications for Photoaging. <i>Journal of Investigative Dermatology</i> , 2014, 134, 2598-2609.	0.3	62
3166	Melatonin prevents maternal fructose intake-induced programmed hypertension in the offspring: roles of nitric oxide and arachidonic acid metabolites. <i>Journal of Pineal Research</i> , 2014, 57, 80-89.	3.4	80
3167	In-Depth Quantitative Proteomic Analysis of de Novo Protein Synthesis Induced by Brain-Derived Neurotrophic Factor. <i>Journal of Proteome Research</i> , 2014, 13, 5707-5714.	1.8	45
3168	Identifying progression related disease risk modules based on the human subcellular signaling networks. <i>Molecular BioSystems</i> , 2014, 10, 3298-3309.	2.9	2
3169	A system-level model for the microbial regulatory genome. <i>Molecular Systems Biology</i> , 2014, 10, 740.	3.2	64
3170	Expression differences between African American and Caucasian prostate cancer tissue reveals that stroma is the site of aggressive changes. <i>International Journal of Cancer</i> , 2014, 134, 81-91.	2.3	67
3171	Alpha-mangostin promotes myoblast differentiation by modulating the gene-expression profile in C2C12 cells. <i>Bioscience, Biotechnology and Biochemistry</i> , 2014, 78, 1923-1929.	0.6	3
3172	Profiling human protein degradome delineates cellular responses to proteasomal inhibition and reveals a feedback mechanism in regulating proteasome homeostasis. <i>Cell Research</i> , 2014, 24, 1214-1230.	5.7	13
3173	Extensive Differences in Gene Expression Between Symbiotic and Aposymbiotic Cnidarians. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 277-295.	0.8	150



#	ARTICLE	IF	CITATIONS
3174	Transcriptomic signatures of peroxisome proliferator-activated receptor $\hat{\pm}$ (PPAR $\hat{\pm}$ ) in different mouse liver models identify novel aspects of its biology. <i>BMC Genomics</i> , 2014, 15, 1106.	1.2	33
3175	Benzo "Equation missing" <!-- No EquationSource Format="TEX", only image -->pyrene-induced DNA adducts and gene expression profiles in target and non-target organs for carcinogenesis in mice. <i>BMC Genomics</i> , 2014, 15, 880.	1.2	44
3176	Predictive urinary biomarkers for steroid-resistant and steroid-sensitive focal segmental glomerulosclerosis using high resolution mass spectrometry and multivariate statistical analysis. <i>BMC Nephrology</i> , 2014, 15, 141.	0.8	30
3177	A whole genomic scan to detect selection signatures between Berkshire and Korean native pig breeds. <i>Journal of Animal Science and Technology</i> , 2014, 56, 23.	0.8	19
3178	Identification of skin-expressed genes possibly associated with wool growth regulation of Aohan fine wool sheep. <i>BMC Genetics</i> , 2014, 15, 144.	2.7	16
3179	Differential microRNA expression following infection with a mouse-adapted, highly virulent avian H5N2 virus. <i>BMC Microbiology</i> , 2014, 14, 252.	1.3	42
3180	Comparative iron oxide nanoparticle cellular dosimetry and response in mice by the inhalation and liquid cell culture exposure routes. <i>Particle and Fibre Toxicology</i> , 2014, 11, 46.	2.8	49
3181	Cell Type-Specific Expression Analysis to Identify Putative Cellular Mechanisms for Neurogenetic Disorders. <i>Journal of Neuroscience</i> , 2014, 34, 1420-1431.	1.7	261
3182	A proof-of-concept study. <i>Psychiatric Genetics</i> , 2014, 24, 1-9.	0.6	16
3183	Ischemic postconditioning alters the gene expression pattern of the ischemic heart. <i>Experimental Biology and Medicine</i> , 2014, 239, 141-150.	1.1	7
3184	<i>miR-125b</i> can enhance skin tumor initiation and promote malignant progression by repressing differentiation and prolonging cell survival. <i>Genes and Development</i> , 2014, 28, 2532-2546.	2.7	52
3185	Selective Activity of the Histone Deacetylase Inhibitor AR-42 against Leukemia Stem Cells: A Novel Potential Strategy in Acute Myelogenous Leukemia. <i>Molecular Cancer Therapeutics</i> , 2014, 13, 1979-1990.	1.9	49
3186	The analysis of functional modules in primary cardiomyopathies. , 2014, , .		0
3187	Natural variation in the histone demethylase, <i>KDM4C</i> , influences expression levels of specific genes including those that affect cell growth. <i>Genome Research</i> , 2014, 24, 52-63.	2.4	29
3188	Noise exposure immediately activates cochlear mitogen-activated protein kinase signaling. <i>Noise and Health</i> , 2014, 16, 400.	0.4	25
3189	Nox1 is a master regulator of alternative splicing in pancreatic beta cells. <i>Nucleic Acids Research</i> , 2014, 42, 11818-11830.	6.5	71
3190	Pharmacogenomic predictors of citalopram treatment outcome in major depressive disorder. <i>World Journal of Biological Psychiatry</i> , 2014, 15, 135-144.	1.3	23
3191	Analysis of microRNAs in patients with systemic lupus erythematosus, using Solexa deep sequencing. <i>Connective Tissue Research</i> , 2014, 55, 187-196.	1.1	9

#	ARTICLE	IF	CITATIONS
3192	Dysferlin Mediates the Cytoprotective Effects of TRAF2 Following Myocardial Ischemia Reperfusion Injury. <i>Journal of the American Heart Association</i> , 2014, 3, e000662.	1.6	30
3193	Ets homologous factor regulates pathways controlling response to injury in airway epithelial cells. <i>Nucleic Acids Research</i> , 2014, 42, 13588-13598.	6.5	38
3194	The Novel Diagnostic Biomarkers for Focal Segmental Glomerulosclerosis. <i>International Journal of Nephrology</i> , 2014, 2014, 1-10.	0.7	23
3195	Comparison of Metabolic Network between Muscle and Intramuscular Adipose Tissues in Hanwoo Beef Cattle Using a Systems Biology Approach. <i>International Journal of Genomics</i> , 2014, 2014, 1-6.	0.8	19
3196	Conditional Genetic Interactions of <i>RTT107</i> , <i>SLX4</i> , and <i>HRQ1</i> Reveal Dynamic Networks upon DNA Damage in <i>S. cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1059-1069.	0.8	13
3197	Identification of molecular sub-networks associated with cell survival in a chronically SIVmac-infected human CD4+ T cell line. <i>Virology Journal</i> , 2014, 11, 152.	1.4	5
3198	Stress-induced changes in gene interactions in human cells. <i>Nucleic Acids Research</i> , 2014, 42, 1757-1771.	6.5	20
3199	Cell cycle-dependent regulation of the RNA-binding protein Stauf1. <i>Nucleic Acids Research</i> , 2014, 42, 7867-7883.	6.5	35
3200	Gene expression of peripheral blood cells reveals pathways downstream of glucocorticoid receptor antagonism and nab-paclitaxel treatment. <i>Pharmacogenetics and Genomics</i> , 2014, 24, 451-458.	0.7	1
3201	Complete Dosage Compensation and Sex-Biased Gene Expression in the Moth <i>Manduca sexta</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 526-537.	1.1	52
3202	Wnt signalling in an <i>in vitro</i> niche model for conjunctival progenitor cells. <i>Journal of Tissue Engineering and Regenerative Medicine</i> , 2014, 8, 969-977.	1.3	10
3203	Random forest fishing: a novel approach to identifying organic group of risk factors in genome-wide association studies. <i>European Journal of Human Genetics</i> , 2014, 22, 254-259.	1.4	6
3204	Mutations in <i>USP9X</i> Are Associated with X-Linked Intellectual Disability and Disrupt Neuronal Cell Migration and Growth. <i>American Journal of Human Genetics</i> , 2014, 94, 470-478.	2.6	117
3205	The transcriptional signatures of <i>Sodalis glossinidius</i> in the <i>Glossina palpalis gambiense</i> flies negative for <i>Trypanosoma brucei gambiense</i> contrast with those of this symbiont in tsetse flies positive for the parasite: Possible involvement of a <i>Sodalis</i> -hosted prophage in fly <i>Trypanosoma</i> refractoriness?. <i>Infection, Genetics and Evolution</i> , 2014, 24, 41-56.	1.0	24
3206	Gestational diabetes mellitus alters apoptotic and inflammatory gene expression of trophoblasts from human term placenta. <i>Journal of Diabetes and Its Complications</i> , 2014, 28, 448-459.	1.2	61
3207	Comprehensive DNA methylation analysis of human neuroblastoma cells treated with blonanserin. <i>Neuroscience Letters</i> , 2014, 563, 123-128.	1.0	20
3208	Impact of final oocyte maturation using gonadotropin-releasing hormone agonist triggering and different luteal support protocols on endometrial gene expression. <i>Fertility and Sterility</i> , 2014, 101, 138-146.e3.	0.5	25
3209	Pathway-based Analysis of the Hidden Genetic Heterogeneities in Cancers. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 31-38.	3.0	6

#	ARTICLE	IF	CITATIONS
3210	Early life perfluorooctanesulphonic acid (PFOS) exposure impairs zebrafish organogenesis. <i>Aquatic Toxicology</i> , 2014, 150, 124-132.	1.9	53
3211	Integration of gene expression data with network-based analysis to identify signaling and metabolic pathways regulated during the development of osteoarthritis. <i>Gene</i> , 2014, 542, 38-45.	1.0	47
3212	COL11A1 promotes tumor progression and predicts poor clinical outcome in ovarian cancer. <i>Oncogene</i> , 2014, 33, 3432-3440.	2.6	176
3213	Sho-saiko-to, a traditional herbal medicine, regulates gene expression and biological function by way of microRNAs in primary mouse hepatocytes. <i>BMC Complementary and Alternative Medicine</i> , 2014, 14, 14.	3.7	13
3214	Differentially expressed microRNAs in the serum of cervical squamous cell carcinoma patients before and after surgery. <i>Journal of Hematology and Oncology</i> , 2014, 7, 6.	6.9	51
3215	FUT11 as a potential biomarker of clear cell renal cell carcinoma progression based on meta-analysis of gene expression data. <i>Tumor Biology</i> , 2014, 35, 2607-2617.	0.8	34
3216	Identification of Differentially Coexpressed Genes in Gonadotrope Tumors and Normal Pituitary Using Bioinformatics Methods. <i>Pathology and Oncology Research</i> , 2014, 20, 375-380.	0.9	7
3217	Discovery of Consensus Gene Signature and Intermodular Connectivity Defining Self-Renewal of Human Embryonic Stem Cells. <i>Stem Cells</i> , 2014, 32, 1468-1479.	1.4	22
3218	Differential Transcriptomic Analysis by RNA-Seq of GSNO-Responsive Genes Between Arabidopsis Roots and Leaves. <i>Plant and Cell Physiology</i> , 2014, 55, 1080-1095.	1.5	124
3219	RNA-seq analysis revealed novel genes and signaling pathway associated with disease resistance to avian influenza virus infection in chickens. <i>Poultry Science</i> , 2014, 93, 485-493.	1.5	97
3220	Toxicity assessment of chlorinated wastewater effluents by using transcriptome-based bioassays and Fourier transform mass spectrometry (FT-MS) analysis. <i>Water Research</i> , 2014, 52, 73-82.	5.3	25
3221	Regulation network and expression profiles of Epstein-Barr virus-encoded microRNAs and their potential target host genes in nasopharyngeal carcinomas. <i>Science China Life Sciences</i> , 2014, 57, 315-326.	2.3	66
3222	Unique features of the transcriptional response to model aneuploidy in human cells. <i>BMC Genomics</i> , 2014, 15, 139.	1.2	87
3223	DFLAT: functional annotation for human development. <i>BMC Bioinformatics</i> , 2014, 15, 45.	1.2	27
3224	Induction of polyploidy by nuclear fusion mechanism upon decreased expression of the nuclear envelope protein LAP2 <sup>12</sup> in the human osteosarcoma cell line U2OS. <i>Molecular Cytogenetics</i> , 2014, 7, 9.	0.4	9
3225	Genome-wide methylation profiling of ADPKD identified epigenetically regulated genes associated with renal cyst development. <i>Human Genetics</i> , 2014, 133, 281-297.	1.8	52
3226	Gene expression profiling of mesenteric lymph nodes from sheep with natural scrapie. <i>BMC Genomics</i> , 2014, 15, 59.	1.2	27
3227	PRMT5 is Required for Human Embryonic Stem Cell Proliferation But Not Pluripotency. <i>Stem Cell Reviews and Reports</i> , 2014, 10, 230-239.	5.6	34

#	ARTICLE	IF	CITATIONS
3228	Molecular sub-group-specific immunophenotypic changes are associated with outcome in recurrent posterior fossa ependymoma. <i>Acta Neuropathologica</i> , 2014, 127, 731-745.	3.9	73
3229	Comprehensive analysis of gene expression in human retina and supporting tissues. <i>Human Molecular Genetics</i> , 2014, 23, 4001-4014.	1.4	109
3230	Computational gene network study on antibiotic resistance genes of <i>Acinetobacter baumannii</i> . <i>Computers in Biology and Medicine</i> , 2014, 48, 17-27.	3.9	27
3231	Impact of gestational chronodisruption on fetal cardiac genomics. <i>Journal of Molecular and Cellular Cardiology</i> , 2014, 66, 1-11.	0.9	23
3232	Review on statistical methods for gene network reconstruction using expression data. <i>Journal of Theoretical Biology</i> , 2014, 362, 53-61.	0.8	160
3233	c-Myc-dependent transcriptional regulation of cell cycle and nucleosomal histones during oligodendrocyte differentiation. <i>Neuroscience</i> , 2014, 276, 72-86.	1.1	35
3234	Integrative analysis of histone ChIP-seq and transcription data using Bayesian mixture models. <i>Bioinformatics</i> , 2014, 30, 1154-1162.	1.8	31
3235	Expression analysis of genes and pathways associated with liver metastases of the uveal melanoma. <i>BMC Medical Genetics</i> , 2014, 15, 29.	2.1	35
3236	ATF3 attenuates cyclosporin A-induced nephrotoxicity by downregulating CHOP in HK-2 cells. <i>Biochemical and Biophysical Research Communications</i> , 2014, 448, 182-188.	1.0	13
3237	The Transcription Factor Gata6 Links Tissue Macrophage Phenotype and Proliferative Renewal. <i>Science</i> , 2014, 344, 645-648.	6.0	317
3238	Activin A supplement in the hESCs culture enhances the endoderm differentiation efficiency. <i>Cell Biology International</i> , 2014, 38, 849-856.	1.4	10
3239	The impact of using the combined oral contraceptive pill for cycle scheduling on gene expression related to endometrial receptivity. <i>Human Reproduction</i> , 2014, 29, 1271-1278.	0.4	18
3240	Comparison of Reprogramming Genes in Induced Pluripotent Stem Cells and Nuclear Transfer Cloned Embryos. <i>Stem Cell Reviews and Reports</i> , 2014, 10, 548-560.	5.6	4
3241	Comparative analysis of viral protein interaction networks in Hepatitis B Virus and Hepatitis C Virus infected HCC. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 271-279.	1.1	8
3242	Clustering longitudinal profiles using P-splines and mixed effects models applied to time-course gene expression data. <i>Computational Statistics and Data Analysis</i> , 2014, 71, 14-29.	0.7	33
3243	A genome-wide association study identifies major loci affecting the immune response against infectious bronchitis virus in chicken. <i>Infection, Genetics and Evolution</i> , 2014, 21, 351-358.	1.0	16
3244	Genomic changes under rapid evolution: selection for parasitoid resistance. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132303.	1.2	41
3245	The ALS/FTLD-related RNA-binding proteins TDP43 and FUS have common downstream RNA targets in cortical neurons. <i>FEBS Open Bio</i> , 2014, 4, 1-10.	1.0	50

#	ARTICLE	IF	CITATIONS
3246	Proteome analysis of the effects of all-trans retinoic acid on human germ cell tumor cell lines. <i>Journal of Proteomics</i> , 2014, 96, 300-313.	1.2	14
3247	Toxicity Mechanisms in <i>Escherichia coli</i> Vary for Silver Nanoparticles and Differ from Ionic Silver. <i>ACS Nano</i> , 2014, 8, 374-386.	7.3	458
3248	Lens specific RLIP76 transgenic mice show a phenotype similar to microphthalmia. <i>Experimental Eye Research</i> , 2014, 118, 125-134.	1.2	2
3249	Identification of Enriched PTM Crosstalk Motifs from Large-Scale Experimental Data Sets. <i>Journal of Proteome Research</i> , 2014, 13, 249-259.	1.8	40
3251	PIWI proteins and PIWI-interacting RNAs function in <i>Hydra</i> somatic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 337-342.	3.3	140
3252	A systems biology analysis for the whole genome sequencing data. , 2014, , .		0
3253	Resources for Functional Genomics Studies in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2014, 197, 1-18.	1.2	61
3254	The <i>Arabidopsis</i> Mediator CDK8 module genes <i>CCT</i> ( <i>MED12</i> ) and <i>GCT</i> ( <i>MED13</i> ) are global regulators of developmental phase transitions. <i>Development (Cambridge)</i> , 2014, 141, 4580-4589.	1.2	50
3255	Genomic analysis of the interaction between pesticide exposure and nutrition in honey bees ( <i>Apis</i> )	0.9	158
3256	A Notch-dependent transcriptional hierarchy promotes mesenchymal transdifferentiation in the cardiac cushion. <i>Developmental Dynamics</i> , 2014, 243, 894-905.	0.8	21
3257	Exploration of salivary proteins in buffalo: an approach to find marker proteins for estrus. <i>FASEB Journal</i> , 2014, 28, 4700-4709.	0.2	17
3258	Age-related variations in the methylome associated with gene expression in human monocytes and T cells. <i>Nature Communications</i> , 2014, 5, 5366.	5.8	168
3259	Endometrial gene expression reveals compromised progesterone signaling in women refractory to embryo implantation. <i>Reproductive Biology and Endocrinology</i> , 2014, 12, 92.	1.4	34
3260	Mating system variation drives rapid evolution of the female transcriptome in <i>Drosophila pseudoobscura</i> . <i>Ecology and Evolution</i> , 2014, 4, 2186-2201.	0.8	38
3261	Shotgun MS proteomic analysis of bronchoalveolar lavage fluid in normal subjects. <i>Proteomics - Clinical Applications</i> , 2014, 8, 737-747.	0.8	17
3262	The effects of PPAR- $\beta$ inhibition on gene expression and the progression of induced osteogenic differentiation of human mesenchymal stem cells. <i>Connective Tissue Research</i> , 2014, 55, 262-274.	1.1	12
3263	Discovery of Novel Disease-specific and Membrane-associated Candidate Markers in a Mouse Model of Multiple Sclerosis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 679-700.	2.5	10
3264	Research Resource: Genome-Wide Identification of AR-Regulated Genes Translated in Sertoli Cells In Vivo Using the RiboTag Approach. <i>Molecular Endocrinology</i> , 2014, 28, 575-591.	3.7	51

#	ARTICLE	IF	CITATIONS
3265	p21 suppresses inflammation and tumorigenesis on pRB-deficient stratified epithelia. <i>Oncogene</i> , 2014, 33, 4599-4612.	2.6	13
3266	An algorithm for identifying differentially expressed genes in multiclass RNA-seq samples. , 2014, , .		1
3267	MetalImprint: an information repository of mammalian imprinted genes. <i>Development (Cambridge)</i> , 2014, 141, 2516-2523.	1.2	68
3268	Integrative analysis of transcriptomic and metabolomic profiling of ascites syndrome in broiler chickens induced by low temperature. <i>Molecular BioSystems</i> , 2014, 10, 2984-2993.	2.9	9
3269	Molecular mechanism underlying the impact of vitamin D on disease activity of MS. <i>Annals of Clinical and Translational Neurology</i> , 2014, 1, 605-617.	1.7	44
3270	Microarray analysis of tick-infested skin in resistant and susceptible cattle confirms the role of inflammatory pathways in immune activation and larval rejection. <i>Veterinary Parasitology</i> , 2014, 205, 307-317.	0.7	16
3271	Proteomic analysis of human substantia nigra identifies novel candidates involved in <scp>P</scp>arkinson's disease pathogenesis. <i>Proteomics</i> , 2014, 14, 784-794.	1.3	85
3272	Sexual Dimorphism in Developmental Programming of the Bovine Preimplantation Embryo Caused by Colony-Stimulating Factor 21. <i>Biology of Reproduction</i> , 2014, 91, 80.	1.2	42
3274	Asymmetric mRNA localization contributes to fidelity and sensitivity of spatially localized systems. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 833-839.	3.6	57
3275	Muscle Biological Characteristics of Differentially Expressed Genes in Wujin and Landrace Pigs. <i>Journal of Integrative Agriculture</i> , 2014, 13, 2236-2242.	1.7	2
3276	A Drosophila Genetic Resource of Mutants to Study Mechanisms Underlying Human Genetic Diseases. <i>Cell</i> , 2014, 159, 200-214.	13.5	322
3277	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. <i>Nature Communications</i> , 2014, 5, 3365.	5.8	123
3278	mi<scp>RN</scp>ome of <scp>I</scp>talian <scp>L</scp>arge <scp>W</scp>hite pig subcutaneous fat tissue: new mi<scp>RNA</scp>s, isomi<scp>R</scp>s and mo<scp>RNA</scp>s. <i>Animal Genetics</i> , 2014, 45, 685-698.	0.6	17
3279	Integrated transcriptome analysis reveals miRNAâ€™mRNA crosstalk in laryngeal squamous cell carcinoma. <i>Genomics</i> , 2014, 104, 249-256.	1.3	20
3280	MspA-Mycobacterium tuberculosis-transformant with reduced virulence: The â€™unbirthday paradigmâ€™. <i>Microbial Pathogenesis</i> , 2014, 76, 10-18.	1.3	7
3281	Comparative proteomic profiling reveals aberrant cell proliferation in the brain of embryonic Ts1Cje, a mouse model of Down syndrome. <i>Neuroscience</i> , 2014, 281, 1-15.	1.1	24
3282	DegPack: A web package using a non-parametric and information theoretic algorithm to identify differentially expressed genes in multiclass RNA-seq samples. <i>Methods</i> , 2014, 69, 306-314.	1.9	5
3283	Correlation between <scp>DNA</scp> methylation and gene expression in the brains of patients with bipolar disorder and schizophrenia. <i>Bipolar Disorders</i> , 2014, 16, 790-799.	1.1	94

#	ARTICLE	IF	CITATIONS
3284	Prioritizing candidate disease miRNAs by integrating phenotype associations of multiple diseases with matched miRNA and mRNA expression profiles. <i>Molecular BioSystems</i> , 2014, 10, 2800-2809.	2.9	67
3285	Chromium-containing traditional Chinese medicine, Tianmai Xiaoke Tablet improves blood glucose through activating insulin-signaling pathway and inhibiting PTP1B and PCK2 in diabetic rats. <i>Journal of Integrative Medicine</i> , 2014, 12, 162-170.	1.4	19
3286	Dynamic expression of microRNAs in M2b polarized macrophages associated with systemic lupus erythematosus. <i>Gene</i> , 2014, 547, 300-309.	1.0	20
3287	Enrichment Analysis for Discovering Biological Associations in Phenotypic Screens. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 377-386.	2.5	12
3288	A genome-wide scan for selection signatures in Holstein cattle. <i>Animal Genetics</i> , 2014, 45, 771-781.	0.6	15
3290	Elucidating Novel Hepatitis C Virus-Host Interactions Using Combined Mass Spectrometry and Functional Genomics Approaches. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 184-203.	2.5	61
3291	IL-17A Mediates a Selective Gene Expression Profile in Asthmatic Human Airway Smooth Muscle Cells. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2014, 50, 1053-1063.	1.4	19
3292	MiningABs: mining associated biomarkers across multi-connected gene expression datasets. <i>BMC Bioinformatics</i> , 2014, 15, 173.	1.2	1
3293	Characterization of the kidney transcriptome of the South American olive mouse <i>Abrothrix olivacea</i> . <i>BMC Genomics</i> , 2014, 15, 446.	1.2	15
3294	Liver transcriptome analysis of Atlantic cod ( <i>Gadus morhua</i> ) exposed to PCB 153 indicates effects on cell cycle regulation and lipid metabolism. <i>BMC Genomics</i> , 2014, 15, 481.	1.2	35
3295	Functional transcriptome analysis of the postnatal brain of the Ts1Cje mouse model for Down syndrome reveals global disruption of interferon-related molecular networks. <i>BMC Genomics</i> , 2014, 15, 624.	1.2	61
3296	A network-based approach to dissect the cilia/centrosome complex interactome. <i>BMC Genomics</i> , 2014, 15, 658.	1.2	19
3297	Human immunodeficiency virus Tat associates with a specific set of cellular RNAs. <i>Retrovirology</i> , 2014, 11, 53.	0.9	9
3298	Selecting biologically informative genes in co-expression networks with a centrality score. <i>Biology Direct</i> , 2014, 9, 12.	1.9	49
3299	Differential effects of selective frankincense (Ru Xiang) essential oil versus non-selective sandalwood (Tan Xiang) essential oil on cultured bladder cancer cells: a microarray and bioinformatics study. <i>Chinese Medicine</i> , 2014, 9, 18.	1.6	27
3300	Transcriptional profiling of <i>Arabidopsis</i> root hairs and pollen defines an apical cell growth signature. <i>BMC Plant Biology</i> , 2014, 14, 197.	1.6	49
3301	A Smad3 and TTF-1/NKX2-1 complex regulates Smad4-independent gene expression. <i>Cell Research</i> , 2014, 24, 994-1008.	5.7	45
3302	Efficient sequential and parallel algorithms for record linkage. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2014, 21, 252-262.	2.2	17

#	ARTICLE	IF	CITATIONS
3303	LincRNA-p21 Regulates Neointima Formation, Vascular Smooth Muscle Cell Proliferation, Apoptosis, and Atherosclerosis by Enhancing p53 Activity. <i>Circulation</i> , 2014, 130, 1452-1465.	1.6	425
3304	Comparative transcriptomic analysis to identify differentially expressed genes in fat tissue of adult Berkshire and Jeju Native Pig using RNA-seq. <i>Molecular Biology Reports</i> , 2014, 41, 6305-6315.	1.0	29
3305	A comparative transcriptomic study on the effects of valproic acid on two different hESCs lines in a neural teratogenicity test system. <i>Toxicology Letters</i> , 2014, 231, 38-44.	0.4	14
3306	MicroRNA expression signature for Satb2-induced osteogenic differentiation in bone marrow stromal cells. <i>Molecular and Cellular Biochemistry</i> , 2014, 387, 227-239.	1.4	53
3307	Cisplatin associated with LY294002 increases cytotoxicity and induces changes in transcript profiles of glioblastoma cells. <i>Molecular Biology Reports</i> , 2014, 41, 165-177.	1.0	16
3308	Differential expression of genes and proteins associated with wool follicle cycling. <i>Molecular Biology Reports</i> , 2014, 41, 5343-5349.	1.0	25
3309	Interactions among mitochondrial proteins altered in glioblastoma. <i>Journal of Neuro-Oncology</i> , 2014, 118, 247-256.	1.4	57
3310	Hippocampal HDAC4 Contributes to Postnatal Fluoxetine-Evoked Depression-Like Behavior. <i>Neuropsychopharmacology</i> , 2014, 39, 2221-2232.	2.8	65
3311	Synovial phenotypes in rheumatoid arthritis correlate with response to biologic therapeutics. <i>Arthritis Research and Therapy</i> , 2014, 16, R90.	1.6	292
3312	DNA methylome profiling of human tissues identifies global and tissue-specific methylation patterns. <i>Genome Biology</i> , 2014, 15, r54.	3.8	325
3313	Proteomic analysis of adipose tissue: informing diabetes research. <i>Expert Review of Proteomics</i> , 2014, 11, 491-502.	1.3	9
3314	Quantitative Proteomic Profiling Reveals Differentially Regulated Proteins in Cystic Fibrosis Cells. <i>Journal of Proteome Research</i> , 2014, 13, 4668-4675.	1.8	25
3315	A Comprehensive Analysis of MicroProteins Reveals Their Potentially Widespread Mechanism of Transcriptional Regulation. <i>Plant Physiology</i> , 2014, 165, 149-159.	2.3	21
3316	Developmental transcriptome analysis of human erythropoiesis. <i>Human Molecular Genetics</i> , 2014, 23, 4528-4542.	1.4	45
3317	Peripheral nerve morphogenesis induced by scaffold micropatterning. <i>Biomaterials</i> , 2014, 35, 4035-4045.	5.7	39
3318	UTX and MLL4 Coordinately Regulate Transcriptional Programs for Cell Proliferation and Invasiveness in Breast Cancer Cells. <i>Cancer Research</i> , 2014, 74, 1705-1717.	0.4	198
3319	Identification and bioinformatics analysis of microRNAs associated with stress and immune response in serum of heat-stressed and normal Holstein cows. <i>Cell Stress and Chaperones</i> , 2014, 19, 973-981.	1.2	119
3320	Transcriptome profiling of the cancer and normal tissues from gastric cancer patients by deep sequencing. <i>Tumor Biology</i> , 2014, 35, 7423-7427.	0.8	8



#	ARTICLE	IF	CITATIONS
3321	GO2MSIG, an automated GO based multi-species gene set generator for gene set enrichment analysis. BMC Bioinformatics, 2014, 15, 146.	1.2	49
3322	DNA methylation subgroups and the CpG island methylator phenotype in gastric cancer: a comprehensive profiling approach. BMC Gastroenterology, 2014, 14, 55.	0.8	34
3323	Berberine moderates glucose metabolism through the GnRH-GLP-1 and MAPK pathways in the intestine. BMC Complementary and Alternative Medicine, 2014, 14, 188.	3.7	44
3324	Stringent homology-based prediction of H. sapiens-M. tuberculosis H37Rv protein-protein interactions. Biology Direct, 2014, 9, 5.	1.9	74
3325	Optic nerve crush induces spatial and temporal gene expression patterns in retina and optic nerve of BALB/c mice. Molecular Neurodegeneration, 2014, 9, 14.	4.4	26
3326	Transcriptional and Physiological Responses Induced by Binary Mixtures of Drospirenone and Progesterone in Zebrafish ( <i>Danio rerio</i> ). Environmental Science & Technology, 2014, 48, 3523-3531.	4.6	91
3327	Impact of MLL5 expression on decitabine efficacy and DNA methylation in acute myeloid leukemia. Haematologica, 2014, 99, 1456-1464.	1.7	26
3328	Integrative analysis of independent transcriptome data for rare diseases. Methods, 2014, 69, 315-325.	1.9	6
3329	Buffalo Cervico-Vaginal Fluid Proteomics with Special Reference to Estrous Cycle: Heat Shock Protein (Hsp)-70 Appears to Be an Estrus Indicator <sup>1</sup> . Biology of Reproduction, 2014, 90, 97.	1.2	19
3330	Genome-Wide DNA Methylation Patterns in Naive CD4+ T Cells From Patients With Primary Sjögren's Syndrome. Arthritis and Rheumatology, 2014, 66, 731-739.	2.9	147
3331	A Phase I Study of the First-in-Class Antimitochondrial Metabolism Agent, CPI-613, in Patients with Advanced Hematologic Malignancies. Clinical Cancer Research, 2014, 20, 5255-5264.	3.2	82
3332	Gene expression profile based classification models of psoriasis. Genomics, 2014, 103, 48-55.	1.3	102
3333	Prioritization of Candidate Genes for Periodontitis Using Multiple Computational Tools. Journal of Periodontology, 2014, 85, 1059-1069.	1.7	37
3334	rClca2 is associated with epidermal differentiation and is strongly downregulated by ultraviolet radiation. British Journal of Dermatology, 2014, 171, 376-387.	1.4	12
3335	Novel markers of osteogenic and adipogenic differentiation of human bone marrow stromal cells identified using a quantitative proteomics approach. Stem Cell Research, 2014, 12, 153-165.	0.3	155
3336	Heparin-protein interactions: From affinity and kinetics to biological roles. Application to an interaction network regulating angiogenesis. Matrix Biology, 2014, 35, 73-81.	1.5	103
3337	Tumor resistance to anti-VEGF therapy through up-regulation of VEGF-C expression. Cancer Letters, 2014, 346, 45-52.	3.2	46
3338	Use of toxicogenomics to predict the potential toxic effect of Benzo(a)pyrene on zebrafish embryos: Ocular developmental toxicity. Chemosphere, 2014, 108, 55-61.	4.2	51

#	ARTICLE	IF	CITATIONS
3339	The effects of actin cytoskeleton perturbation on keratin intermediate filament formation in mesenchymal stem/stromal cells. <i>Biomaterials</i> , 2014, 35, 3934-3944.	5.7	29
3340	A genome-wide association study of calf birth weight in Holstein cattle using single nucleotide polymorphisms and phenotypes predicted from auxiliary traits. <i>Journal of Dairy Science</i> , 2014, 97, 3156-3172.	1.4	38
3341	Identifying colon cancer risk modules with better classification performance based on human signaling network. <i>Genomics</i> , 2014, 104, 242-248.	1.3	7
3342	Mapping genomic markers to closest feature using the R package Map2NCBI. <i>Livestock Science</i> , 2014, 162, 59-65.	0.6	18
3343	Proteomics reveal energy metabolism and mitogen-activated protein kinase signal transduction perturbation in human Borna disease virus Hu-H1-infected oligodendroglial cells. <i>Neuroscience</i> , 2014, 268, 284-296.	1.1	17
3344	Mouse SCNT ESCs Have Lower Somatic Mutation Load Than Syngeneic iPSCs. <i>Stem Cell Reports</i> , 2014, 2, 399-405.	2.3	20
3345	A distinctive ovarian cancer molecular subgroup characterized by poor prognosis and somatic focal copy number amplifications at chromosome 19. <i>Gynecologic Oncology</i> , 2014, 132, 343-350.	0.6	17
3346	Dietary resveratrol supplementation normalizes gene expression in the hippocampus of streptozotocin-induced diabetic C57Bl/6 mice. <i>Journal of Nutritional Biochemistry</i> , 2014, 25, 313-318.	1.9	30
3347	Abnormal gene expression and gene fusion in lung adenocarcinoma with high-throughput RNA sequencing. <i>Cancer Gene Therapy</i> , 2014, 21, 74-82.	2.2	27
3348	The combination of transcriptomics and informatics identifies pathways targeted by miR-204 during neurogenesis and axon guidance. <i>Nucleic Acids Research</i> , 2014, 42, 7793-7806.	6.5	31
3349	Integrated microRNA-mRNA analysis of coronary artery disease. <i>Molecular Biology Reports</i> , 2014, 41, 5505-5511.	1.0	19
3350	Characterization of brown adipose tissue in the human perirenal depot. <i>Obesity</i> , 2014, 22, 1830-1837.	1.5	45
3351	The toxicological application of transcriptomics and epigenomics in zebrafish and other teleosts. <i>Briefings in Functional Genomics</i> , 2014, 13, 157-171.	1.3	62
3352	Aberrant Expression of Long Noncoding RNAs in Early Diabetic Retinopathy. , 2014, 55, 941.		170
3353	Comparative transcriptomic analysis by RNA-seq to discern differential expression of genes in liver and muscle tissues of adult Berkshire and Jeju Native Pig. <i>Gene</i> , 2014, 546, 233-242.	1.0	26
3354	Overexpression of SMARCE1 is associated with CD8+ T-cell infiltration in early stage ovarian cancer. <i>International Journal of Biochemistry and Cell Biology</i> , 2014, 53, 389-398.	1.2	15
3355	A bi-Poisson model for clustering gene expression profiles by RNA-seq. <i>Briefings in Bioinformatics</i> , 2014, 15, 534-541.	3.2	6
3356	The acetylome regulators Hdac1 and Hdac2 differently modulate intestinal epithelial cell dependent homeostatic responses in experimental colitis. <i>American Journal of Physiology - Renal Physiology</i> , 2014, 306, G594-G605.	1.6	55

#	ARTICLE	IF	CITATIONS
3357	Proteome profiling of virus-host interactions of wild type and attenuated measles virus strains. <i>Journal of Proteomics</i> , 2014, 108, 325-336.	1.2	5
3358	Transcriptomic effects of estradiol treatment on cultured human uterine smooth muscle cells. <i>Molecular and Cellular Endocrinology</i> , 2014, 393, 16-23.	1.6	9
3359	Pathway and network analysis in proteomics. <i>Journal of Theoretical Biology</i> , 2014, 362, 44-52.	0.8	98
3360	Plasma-based proteomics reveals lipid metabolic and immunoregulatory dysregulation in post-stroke depression. <i>European Psychiatry</i> , 2014, 29, 307-315.	0.1	48
3361	Identifying arsenic trioxide (ATO) functions in leukemia cells by using time series gene expression profiles. <i>Gene</i> , 2014, 535, 312-317.	1.0	2
3362	Genome-Wide Analysis of Long Noncoding RNA (lncRNA) Expression in Hepatoblastoma Tissues. <i>PLoS ONE</i> , 2014, 9, e85599.	1.1	78
3363	Analysis of protein-protein interaction network and functional modules on primary osteoporosis. <i>European Journal of Medical Research</i> , 2014, 19, 15.	0.9	4
3364	Identification of copy number variation-driven genes for liver cancer via bioinformatics analysis. <i>Oncology Reports</i> , 2014, 32, 1845-1852.	1.2	14
3365	Expression and clinical significance of estrogen-regulated long non-coding RNAs in estrogen receptor $\beta$ -positive ovarian cancer progression. <i>Oncology Reports</i> , 2014, 31, 1613-1622.	1.2	29
3366	DNA methylation temporal profiling following peripheral versus central nervous system axotomy. <i>Scientific Data</i> , 2014, 1, 140038.	2.4	16
3367	A Bayesian Integrative Model for Genetical Genomics with Spatially Informed Variable Selection. <i>Cancer Informatics</i> , 2014, 13s2, CIN.S13784.	0.9	3
3368	Genome-wide Expression Profiles of Necrotizing Enterocolitis Versus Spontaneous Intestinal Perforation in Human Intestinal Tissues. <i>Annals of Surgery</i> , 2014, 260, 1128-1137.	2.1	64
3369	Application of quantitative trait locus mapping and transcriptomics to studies of the senescence-accelerated phenotype in rats. <i>BMC Genomics</i> , 2014, 15, S3.	1.2	11
3370	Complex-based analysis of dysregulated cellular processes in cancer. <i>BMC Systems Biology</i> , 2014, 8, S1.	3.0	19
3371	Sex-related gene expression profiles in the adrenal cortex in the mature rat: Microarray analysis with emphasis on genes involved in steroidogenesis. <i>International Journal of Molecular Medicine</i> , 2015, 35, 702-714.	1.8	34
3372	Genetic architecture of early pre-inflammatory stage transcription signatures of autoimmune diabetes in the pancreatic lymph nodes of the NOD mouse reveals significant gene enrichment on chromosomes 6 and 7. <i>Meta Gene</i> , 2015, 6, 96-104.	0.3	0
3373	A comparison of human and mouse gene co-expression networks reveals conservation and divergence at the tissue, pathway and disease levels. <i>BMC Evolutionary Biology</i> , 2015, 15, 259.	3.2	89
3374	Multiple sources of bias confound functional enrichment analysis of global -omics data. <i>Genome Biology</i> , 2015, 16, 186.	3.8	131

#	ARTICLE	IF	CITATIONS
3375	Gene expression profiling of brakeless mutant <i>Drosophila</i> embryos. <i>Data in Brief</i> , 2015, 5, 134-137.	0.5	2
3376	Analysis of differences in the molecular mechanism of rheumatoid arthritis and osteoarthritis based on integration of gene expression profiles. <i>Immunology Letters</i> , 2015, 168, 246-253.	1.1	20
3377	Deletion of low molecular weight protein tyrosine phosphatase ( <i>Acp1</i> ) protects against stress-induced cardiomyopathy. <i>Journal of Pathology</i> , 2015, 237, 482-494.	2.1	12
3378	Gene expression during the first 28 days of axolotl limb regeneration I: Experimental design and global analysis of gene expression. <i>Regeneration (Oxford, England)</i> , 2015, 2, 120-136.	6.3	72
3379	Genomewide identification of target genes of histone methyltransferase <i>dG9a</i> during <i>Drosophila</i> embryogenesis. <i>Genes To Cells</i> , 2015, 20, 902-914.	0.5	12
3380	Comparative two-dimensional polyacrylamide gel electrophoresis of the salivary proteome of children with autism spectrum disorder. <i>Journal of Cellular and Molecular Medicine</i> , 2015, 19, 2664-2678.	1.6	39
3381	Toxicogenomic responses of human liver HepG2 cells to silver nanoparticles. <i>Journal of Applied Toxicology</i> , 2015, 35, 1160-1168.	1.4	37
3382	Evolving transcriptomic fingerprint based on genome-wide data as prognostic tools in prostate cancer. <i>Biology of the Cell</i> , 2015, 107, 232-244.	0.7	6
3383	Establishment of a proteome profile and identification of molecular markers for mouse spermatogonial stem cells. <i>Journal of Cellular and Molecular Medicine</i> , 2015, 19, 521-534.	1.6	27
3384	Vaccinia Virus Infection Requires Maturation of Macropinosomes. <i>Traffic</i> , 2015, 16, 814-831.	1.3	44
3385	An integrated analysis of the effects of microRNA and mRNA on esophageal squamous cell carcinoma. <i>Molecular Medicine Reports</i> , 2015, 12, 945-952.	1.1	17
3386	Prediction of Scaffold Proteins based on Protein Interaction and Domain Architectures. , 2015, , .		0
3387	Autophagic degradation of aquaporin-2 is an early event in hypokalemia-induced nephrogenic diabetes insipidus. <i>Scientific Reports</i> , 2015, 5, 18311.	1.6	53
3388	Chronic acidosis in the tumour microenvironment selects for overexpression of LAMP2 in the plasma membrane. <i>Nature Communications</i> , 2015, 6, 8752.	5.8	151
3389	Adaptation of <i>Lactococcus lactis</i> to high growth temperature leads to a dramatic increase in acidification rate. <i>Scientific Reports</i> , 2015, 5, 14199.	1.6	63
3390	miR-34a screened by miRNA profiling negatively regulates Wnt/ $\beta$ 2-catenin signaling pathway in Aflatoxin B1 induced hepatotoxicity. <i>Scientific Reports</i> , 2015, 5, 16732.	1.6	65
3391	Identification of the differentially expressed genes associated with familial combined hyperlipidemia using bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2015, 11, 4032-4038.	1.1	6
3392	MicroRNA profiling of CD3+CD56+ cytokine-induced killer cells. <i>Scientific Reports</i> , 2015, 5, 9571.	1.6	8

#	ARTICLE	IF	CITATIONS
3393	Identifying miRNA/mRNA negative regulation pairs in colorectal cancer. <i>Scientific Reports</i> , 2015, 5, 12995.	1.6	43
3394	The exosome controls alternative splicing by mediating the gene expression and assembly of the spliceosome complex. <i>Scientific Reports</i> , 2015, 5, 13403.	1.6	18
3395	Co-expression analysis of differentially expressed genes in hepatitis C virus-induced hepatocellular carcinoma. <i>Molecular Medicine Reports</i> , 2015, 11, 21-28.	1.1	4
3396	Aberrant expression of long noncoding RNAs in chronic thromboembolic pulmonary hypertension. <i>Molecular Medicine Reports</i> , 2015, 11, 2631-2643.	1.1	33
3397	Network-based survival-associated module biomarker and its crosstalk with cell death genes in ovarian cancer. <i>Scientific Reports</i> , 2015, 5, 11566.	1.6	36
3398	Computational networks of activating transcription factor 3 gene in Huh7 cell lines and hepatitis C virus-infected Huh7 cell lines. <i>Molecular Medicine Reports</i> , 2015, 12, 1239-1246.	1.1	3
3399	Transcriptomic Analysis of Drosophila Mushroom Body Neurons Lacking Amyloid- $\beta^2$ Precursor-Like Protein Activity. <i>Journal of Alzheimer's Disease</i> , 2015, 46, 913-928.	1.2	2
3400	Integrated analysis of miRNA/mRNA network in placenta identifies key factors associated with labor onset of Large White and Qingping sows. <i>Scientific Reports</i> , 2015, 5, 13074.	1.6	12
3401	Integrative proteomics to understand the transmission mechanism of Barley yellow dwarf virus-GPV by its insect vector <i>Rhopalosiphum padi</i> . <i>Scientific Reports</i> , 2015, 5, 10971.	1.6	56
3402	Transdifferentiation of periodontal ligament-derived stem cells into retinal ganglion-like cells and its microRNA signature. <i>Scientific Reports</i> , 2015, 5, 16429.	1.6	47
3404	Identification of Genes Associated with Smad3-dependent Renal Injury by RNA-seq-based Transcriptome Analysis. <i>Scientific Reports</i> , 2015, 5, 17901.	1.6	20
3405	Transcription factor p63 bookmarks and regulates dynamic enhancers during epidermal differentiation. <i>EMBO Reports</i> , 2015, 16, 863-878.	2.0	134
3406	Gene co-expression network and function modules in three types of glioma. <i>Molecular Medicine Reports</i> , 2015, 11, 3055-3063.	1.1	4
3407	Somatic deletions implicated in functional diversity of brain cells of individuals with schizophrenia and unaffected controls. <i>Scientific Reports</i> , 2015, 4, 3807.	1.6	25
3408	Network-assisted analysis of primary Sjögren's syndrome GWAS data in Han Chinese. <i>Scientific Reports</i> , 2015, 5, 18855.	1.6	13
3409	Unique Toll-Like Receptor 4 Activation by NAMPT/PBEF Induces NF- $\kappa$ B Signaling and Inflammatory Lung Injury. <i>Scientific Reports</i> , 2015, 5, 13135.	1.6	126
3410	Discrete domains of gene expression in germinal layers distinguish the development of gyrencephaly. <i>EMBO Journal</i> , 2015, 34, 1859-1874.	3.5	146
3411	miR-95p suppresses pro-fibrogenic transformation of fibroblasts and prevents organ fibrosis by targeting <i>NOX4</i> and <i>TGFBR2</i> . <i>EMBO Reports</i> , 2015, 16, 1358-1377.	2.0	87

#	ARTICLE	IF	CITATIONS
3412	Expression analysis of the estrogen receptor target genes in renal cell carcinoma. <i>Molecular Medicine Reports</i> , 2015, 11, 75-82.	1.1	6
3413	Advanced Applications of RNA Sequencing and Challenges. <i>Bioinformatics and Biology Insights</i> , 2015, 9s1, BBI.S28991.	1.0	178
3414	CpG island erosion, polycomb occupancy and sequence motif enrichment at bivalent promoters in mammalian embryonic stem cells. <i>Scientific Reports</i> , 2015, 5, 16791.	1.6	24
3415	Identification of novel trans-crosstalk between histone modifications via genome-wide analysis of maximal deletion effect. <i>Genes and Genomics</i> , 2015, 37, 693-701.	0.5	1
3416	A machine learning heuristic to identify biologically relevant and minimal biomarker panels from omics data. <i>BMC Genomics</i> , 2015, 16, S2.	1.2	43
3417	Copy number variations in the genome of the Qatari population. <i>BMC Genomics</i> , 2015, 16, 834.	1.2	9
3418	Blood transcriptomics of drug-naïve sporadic Parkinson's disease patients. <i>BMC Genomics</i> , 2015, 16, 876.	1.2	64
3419	Gene expression profiling of the human natural killer cell response to Fc receptor activation: unique enhancement in the presence of interleukin-12. <i>BMC Medical Genomics</i> , 2015, 8, 66.	0.7	15
3420	A survey of computational tools for downstream analysis of proteomic and other omic datasets. <i>Human Genomics</i> , 2015, 9, 28.	1.4	16
3421	Chronic binge alcohol administration dysregulates global regulatory gene networks associated with skeletal muscle wasting in simian immunodeficiency virus-infected macaques. <i>BMC Genomics</i> , 2015, 16, 1097.	1.2	21
3422	Bioinformatics identification of potentially involved microRNAs in Tibetan with gastric cancer based on microRNA profiling. <i>Cancer Cell International</i> , 2015, 15, 115.	1.8	16
3423	PTTG1 expression is associated with hyperproliferative disease and poor prognosis in multiple myeloma. <i>Journal of Hematology and Oncology</i> , 2015, 8, 106.	6.9	29
3424	Total variation based tensor decomposition for multi-dimensional data with time dimension. <i>Numerical Linear Algebra With Applications</i> , 2015, 22, 999-1019.	0.9	8
3425	Splenic gene expression profiling in White Leghorn layer inoculated with the <i>Salmonella enterica</i> serovar <i>Enteritidis</i> . <i>Animal Genetics</i> , 2015, 46, 617-626.	0.6	22
3426	The relative vertex clustering value - a new criterion for the fast discovery of functional modules in protein interaction networks. <i>BMC Bioinformatics</i> , 2015, 16, S3.	1.2	3
3427	Parameter optimization for constructing competing endogenous RNA regulatory network in glioblastoma multiforme and other cancers. <i>BMC Genomics</i> , 2015, 16, S1.	1.2	43
3428	Integrative network-based approach identifies key genetic elements in breast invasive carcinoma. <i>BMC Genomics</i> , 2015, 16, S2.	1.2	30
3429	Memory acquisition and retrieval impact different epigenetic processes that regulate gene expression. <i>BMC Genomics</i> , 2015, 16, S5.	1.2	50

#	ARTICLE	IF	CITATIONS
3430	Reconstruction of novel transcription factor regulons through inference of their binding sites. BMC Bioinformatics, 2015, 16, 299.	1.2	3
3431	Identification of candidate gonadal sex differentiation genes in the chicken embryo using RNA-seq. BMC Genomics, 2015, 16, 704.	1.2	54
3432	Helveticoside is a biologically active component of the seed extract of <i>Descurainia sophia</i> and induces reciprocal gene regulation in A549 human lung cancer cells. BMC Genomics, 2015, 16, 713.	1.2	16
3433	Cyclosporin A-induced toxicity in mouse liver slices is only slightly aggravated by Fxr-deficiency and co-occurs with upregulation of pro-inflammatory genes and downregulation of genes involved in mitochondrial functions. BMC Genomics, 2015, 16, 822.	1.2	6
3434	Genome-wide DNA methylome variation in two genetically distinct chicken lines using MethylC-seq. BMC Genomics, 2015, 16, 851.	1.2	39
3435	Reconstruction of temporal activity of microRNAs from gene expression data in breast cancer cell line. BMC Genomics, 2015, 16, 1077.	1.2	5
3436	Transfection of Sertoli cells with androgen receptor alters gene expression without androgen stimulation. BMC Molecular Biology, 2015, 16, 23.	3.0	4
3437	Association between in vivo bone formation and ex vivo migratory capacity of human bone marrow stromal cells. Stem Cell Research and Therapy, 2015, 6, 196.	2.4	17
3438	Transcriptional profiling of differentially vulnerable motor neurons at pre-symptomatic stage in the <i>Smn 2b</i> <sup>-/-</sup> mouse model of spinal muscular atrophy. Acta Neuropathologica Communications, 2015, 3, 55.	2.4	61
3439	Screening Feature Genes of Venous Thromboembolism with <sc>DNA</sc> Microarray. Chemical Biology and Drug Design, 2015, 86, 821-828.	1.5	3
3440	Discovering All Transcriptome Single-Nucleotide Polymorphisms and Scanning for Selection Signatures in Ducks ( <i>Anas platyrhynchos</i> ). Evolutionary Bioinformatics, 2015, 11s1, EBO.S21545.	0.6	5
3441	Regulation of monocyte/macrophage polarisation by extracellular RNA. Thrombosis and Haemostasis, 2015, 113, 473-481.	1.8	36
3442	Exogenous retinoic acid induces digit reduction in opossums ( <i>Monodelphis domestica</i> ) by disrupting cell death and proliferation, and apical ectodermal ridge and zone of polarizing activity function. Birth Defects Research Part A: Clinical and Molecular Teratology, 2015, 103, 225-234.	1.6	7
3443	Identification of a mitochondrial defect gene signature reveals NUPR1 as a key regulator of liver cancer progression. Hepatology, 2015, 62, 1174-1189.	3.6	50
3444	Bisphenol A affects placental layers morphology and angiogenesis during early pregnancy phase in mice. Journal of Applied Toxicology, 2015, 35, 1278-1291.	1.4	74
3445	Gene expression profiles and protein&ndash;protein interaction network analysis in AIDS patients with HIV-associated encephalitis and dementia. HIV/AIDS - Research and Palliative Care, 2015, 7, 265.	0.4	12
3446	Novel prognostic genes of diffuse large B-cell lymphoma revealed by survival analysis of gene expression data. OncoTargets and Therapy, 2015, 8, 3407.	1.0	10
3447	Critical genes in head and neck squamous cell carcinoma revealed by bioinformatic analysis of gene expression data. Genetics and Molecular Research, 2015, 14, 17406-17415.	0.3	8

#	ARTICLE	IF	CITATIONS
3448	Microarray data analysis reveals differentially expressed genes in prolactinoma. <i>Neoplasma</i> , 2015, 62, 53-60.	0.7	2
3449	NOB1 is essential for the survival of RKO colorectal cancer cells. <i>World Journal of Gastroenterology</i> , 2015, 21, 868.	1.4	17
3450	ATF4 licenses C/EBP $\beta$ activity in human mesenchymal stem cells primed for adipogenesis. <i>ELife</i> , 2015, 4, e06821.	2.8	45
3451	Lipid-mediated regulation of SKN-1/Nrf in response to germ cell absence. <i>ELife</i> , 2015, 4, .	2.8	171
3452	Comparative proteomic analyses demonstrate enhanced interferon and STAT-1 activation in reovirus T3D-infected HeLa cells. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 30.	1.8	10
3453	Differential Occurrence of Interactions and Interaction Domains in Proteins Containing Homopolymeric Amino Acid Repeats. <i>Frontiers in Genetics</i> , 2015, 6, 345.	1.1	21
3454	Nitric oxide as a regulator of <i>B. anthracis</i> pathogenicity. <i>Frontiers in Microbiology</i> , 2015, 6, 921.	1.5	12
3455	Noncoding RNA in the transcriptional landscape of human neural progenitor cell differentiation. <i>Frontiers in Neuroscience</i> , 2015, 9, 392.	1.4	11
3456	The Wnt signaling network in cancer. , 0, , 222-255.		0
3457	Construction of gene/protein interaction networks for primary myelofibrosis and KEGG pathway-enrichment analysis of molecular compounds. <i>Genetics and Molecular Research</i> , 2015, 14, 16126-16132.	0.3	2
3458	Bovine Milk Proteome in the First 9 Days: Protein Interactions in Maturation of the Immune and Digestive System of the Newborn. <i>PLoS ONE</i> , 2015, 10, e0116710.	1.1	79
3459	Expression Profiling of Preadipocyte MicroRNAs by Deep Sequencing on Chicken Lines Divergently Selected for Abdominal Fatness. <i>PLoS ONE</i> , 2015, 10, e0117843.	1.1	24
3460	Functional Genomic Analysis Identifies Indoxyl Sulfate as a Major, Poorly Dialyzable Uremic Toxin in End-Stage Renal Disease. <i>PLoS ONE</i> , 2015, 10, e0118703.	1.1	14
3461	Characterization of the Kidney Transcriptome of the Long-Haired Mouse <i>Abrothrix hirta</i> (Rodentia,) Tj ETQq1 1 0.784314 rgBI /Overl	1.1	7
3462	Identification of MicroRNAs and their Targets Associated with Embryo Abortion during Chrysanthemum Cross Breeding via High-Throughput Sequencing. <i>PLoS ONE</i> , 2015, 10, e0124371.	1.1	19
3463	Effects of Valproic Acid and Dexamethasone Administration on Early Bio-Markers and Gene Expression Profile in Acute Kidney Ischemia-Reperfusion Injury in the Rat. <i>PLoS ONE</i> , 2015, 10, e0126622.	1.1	30
3464	The Orphan Nuclear Receptor TLX Is an Enhancer of STAT1-Mediated Transcription and Immunity to <i>Toxoplasma gondii</i> . <i>PLoS Biology</i> , 2015, 13, e1002200.	2.6	25
3465	Integration Analysis of Three Omics Data Using Penalized Regression Methods: An Application to Bladder Cancer. <i>PLoS Genetics</i> , 2015, 11, e1005689.	1.5	68



#	ARTICLE	IF	CITATIONS
3466	Disruption of Mitochondrion-To-Nucleus Interaction in Deceased Cloned Piglets. PLoS ONE, 2015, 10, e0129378.	1.1	7
3467	Immunological Response to Single Pathogen Challenge with Agents of the Bovine Respiratory Disease Complex: An RNA-Sequence Analysis of the Bronchial Lymph Node Transcriptome. PLoS ONE, 2015, 10, e0131459.	1.1	51
3468	Comparing Two Intestinal Porcine Epithelial Cell Lines (IPECs): Morphological Differentiation, Function and Metabolism. PLoS ONE, 2015, 10, e0132323.	1.1	48
3469	Functional Analysis of Chicken IRF7 in Response to dsRNA Analog Poly(I:C) by Integrating Overexpression and Knockdown. PLoS ONE, 2015, 10, e0133450.	1.1	45
3470	Meta-Analysis of Microarray Data of Rainbow Trout Fry Gonad Differentiation Modulated by Ethynylestradiol. PLoS ONE, 2015, 10, e0135799.	1.1	10
3471	Social Regulation of Gene Expression in Threespine Sticklebacks. PLoS ONE, 2015, 10, e0137726.	1.1	32
3472	Recurrent Glioblastomas Reveal Molecular Subtypes Associated with Mechanistic Implications of Drug-Resistance. PLoS ONE, 2015, 10, e0140528.	1.1	38
3473	Analysis of Stage-Specific Gene Expression Profiles in the Uterine Endometrium during Pregnancy in Pigs. PLoS ONE, 2015, 10, e0143436.	1.1	20
3474	Functional Cross-Talking between Differentially Expressed and Alternatively Spliced Genes in Human Liver Cancer Cells Treated with Berberine. PLoS ONE, 2015, 10, e0143742.	1.1	11
3475	Expression Profiling after Prolonged Experimental Febrile Seizures in Mice Suggests Structural Remodeling in the Hippocampus. PLoS ONE, 2015, 10, e0145247.	1.1	13
3476	Size of the Ovulatory Follicle Dictates Spatial Differences in the Oviductal Transcriptome in Cattle. PLoS ONE, 2015, 10, e0145321.	1.1	29
3477	Maternal Melatonin Therapy Rescues Prenatal Dexamethasone and Postnatal High-Fat Diet Induced Programmed Hypertension in Male Rat Offspring. Frontiers in Physiology, 2015, 6, 377.	1.3	41
3479	Identification of potential therapeutic targets for melanoma using gene expression analysis. Neoplasma, 2015, 62, 733-739.	0.7	10
3480	Comprehensive Screening of Gene Function and Networks by DNA Microarray Analysis in Japanese Patients with Idiopathic Portal Hypertension. Mediators of Inflammation, 2015, 2015, 1-10.	1.4	17
3481	Detecting Key Genes Regulated by miRNAs in Dysfunctional Crosstalk Pathway of Myasthenia Gravis. BioMed Research International, 2015, 2015, 1-10.	0.9	12
3482	Embryonic attenuated Wnt/ $\beta$ -catenin signaling defines niche location and long-term stem cell fate in hair follicle. ELife, 2015, 4, e10567.	2.8	57
3483	Lysosome and Cytoskeleton Pathways Are Robustly Enriched in the Blood of Septic Patients: A Meta-Analysis of Transcriptomic Data. Mediators of Inflammation, 2015, 2015, 1-15.	1.4	24
3484	Improving the Understanding of Pathogenesis of Human Papillomavirus 16 via Mapping Protein-Protein Interaction Network. BioMed Research International, 2015, 2015, 1-10.	0.9	8

#	ARTICLE	IF	CITATIONS
3485	Discover the Molecular Biomarker Associated with Cell Death and Extracellular Matrix Module in Ovarian Cancer. <i>BioMed Research International</i> , 2015, 2015, 1-6.	0.9	1
3486	Whole-transcriptome analysis of flow-sorted cervical cancer samples reveals that B cell expressed TCL1A is correlated with improved survival. <i>Oncotarget</i> , 2015, 6, 38681-38694.	0.8	15
3487	Network-based approach to identify prognostic biomarkers for estrogen receptor- $\alpha$ positive breast cancer treatment with tamoxifen. <i>Cancer Biology and Therapy</i> , 2015, 16, 317-324.	1.5	72
3488	Copy number variations and genetic admixtures in three Xinjiang ethnic minority groups. <i>European Journal of Human Genetics</i> , 2015, 23, 536-542.	1.4	22
3489	Evidence that MHC I-E dampens thyroid autoantibodies and prevents spreading to a second thyroid autoantigen in I-Ak NOD mice. <i>Genes and Immunity</i> , 2015, 16, 268-274.	2.2	25
3490	Prmt5 is a regulator of muscle stem cell expansion in adult mice. <i>Nature Communications</i> , 2015, 6, 7140.	5.8	98
3491	Biochemical and bioinformatic methods for elucidating the role of RNA-protein interactions in posttranscriptional regulation. <i>Briefings in Functional Genomics</i> , 2015, 14, 102-114.	1.3	10
3492	From Raw Data to Biological Discoveries: A Computational Analysis Pipeline for Mass Spectrometry-Based Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1820-1826.	1.2	17
3493	Position-specific binding of FUS to nascent RNA regulates mRNA length. <i>Genes and Development</i> , 2015, 29, 1045-1057.	2.7	98
3494	Differential expression and alternative splicing of cell cycle genes in imatinib-treated K562 cells. <i>Tumor Biology</i> , 2015, 36, 8127-8136.	0.8	3
3495	Deciphering the pharmacological mechanism of the Chinese formula Huanglian-Jie-Du decoction in the treatment of ischemic stroke using a systems biology-based strategy. <i>Acta Pharmacologica Sinica</i> , 2015, 36, 724-733.	2.8	36
3496	A systematic investigation based on microRNA-mediated gene regulatory network reveals that dysregulation of microRNA-19a/Cyclin D1 axis confers an oncogenic potential and a worse prognosis in human hepatocellular carcinoma. <i>RNA Biology</i> , 2015, 12, 643-657.	1.5	33
3497	Transcriptional changes associated with resistance to inhibitors of epidermal growth factor receptor revealed using metaanalysis. <i>BMC Cancer</i> , 2015, 15, 369.	1.1	4
3498	Inferring data-specific micro-RNA function through the joint ranking of micro-RNA and pathways from matched micro-RNA and gene expression data. <i>Bioinformatics</i> , 2015, 31, 2822-2828.	1.8	4
3499	A fluorescent bimolecular complementation screen reveals MAF1, RNF7 and SETD3 as PCNA-associated proteins in human cells. <i>Cell Cycle</i> , 2015, 14, 2509-2519.	1.3	19
3500	Genome-wide DNA methylation analysis in dermal fibroblasts from patients with diffuse and limited systemic sclerosis reveals common and subset-specific DNA methylation aberrancies. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, 1612-1620.	0.5	148
3501	Scoring Large-Scale Affinity Purification Mass Spectrometry Datasets with MiST. <i>Current Protocols in Bioinformatics</i> , 2015, 49, 8.19.1-8.19.16.	25.8	58
3502	Maternal fructose-intake-induced renal programming in adult male offspring. <i>Journal of Nutritional Biochemistry</i> , 2015, 26, 642-650.	1.9	57

#	ARTICLE	IF	CITATIONS
3503	Integration of gene expression and GWAS results supports involvement of calcium signaling in Schizophrenia. <i>Schizophrenia Research</i> , 2015, 164, 92-99.	1.1	31
3504	Prenatal dexamethasone-induced programmed hypertension and renal programming. <i>Life Sciences</i> , 2015, 132, 41-48.	2.0	40
3505	Transcriptomic profiles of aging in purified human immune cells. <i>BMC Genomics</i> , 2015, 16, 333.	1.2	58
3506	Wilms's tumor gene 1 regulates p63 and promotes cell proliferation in squamous cell carcinoma of the head and neck. <i>BMC Cancer</i> , 2015, 15, 342.	1.1	11
3507	Transcriptional profiling of PRKG2-null growth plate identifies putative down-stream targets of PRKG2. <i>BMC Research Notes</i> , 2015, 8, 177.	0.6	9
3508	Dysregulated mechanisms underlying Duchenne muscular dystrophy from co-expression network preservation analysis. <i>BMC Research Notes</i> , 2015, 8, 182.	0.6	24
3509	Ascorbic Acid-Induced Cardiac Differentiation of Murine Pluripotent Stem Cells: Transcriptional Profiling and Effect of a Small Molecule Synergist of Wnt/ $\beta$ 2-Catenin Signaling Pathway. <i>Cellular Physiology and Biochemistry</i> , 2015, 36, 810-830.	1.1	23
3510	Transcriptomic profiling of linolenic acid-responsive genes in ROS signaling from RNA-seq data in Arabidopsis. <i>Frontiers in Plant Science</i> , 2015, 6, 122.	1.7	51
3511	Transcriptome Analysis of Porphyrin-Accumulated and X-Ray-Irradiated Cell Cultures under Limited Proliferation and Non-Lethal Conditions. <i>Microarrays (Basel, Switzerland)</i> , 2015, 4, 25-40.	1.4	11
3512	The Role of DNA Insertions in Phenotypic Differentiation between Humans and Other Primates. <i>Genome Biology and Evolution</i> , 2015, 7, 1168-1178.	1.1	5
3513	Profiling of promoter occupancy by the SND1 transcriptional coactivator identifies downstream glycerolipid metabolic genes involved in TNF $\alpha$ response in human hepatoma cells. <i>Nucleic Acids Research</i> , 2015, 43, 10673-10688.	6.5	27
3514	Retinoblastoma protein promotes oxidative phosphorylation through upregulation of glycolytic genes in oncogene-induced senescent cells. <i>Aging Cell</i> , 2015, 14, 689-697.	3.0	53
3515	Comparative proteomic analysis of plasma from bipolar depression and depressive disorder: identification of proteins associated with immune regulatory. <i>Protein and Cell</i> , 2015, 6, 908-911.	4.8	22
3516	Transcriptome profile of liver at different physiological stages reveals potential mode for lipid metabolism in laying hens. <i>BMC Genomics</i> , 2015, 16, 763.	1.2	89
3517	MVDA: a multi-view genomic data integration methodology. <i>BMC Bioinformatics</i> , 2015, 16, 261.	1.2	62
3518	A simplicial complex-based approach to unmixing tumor progression data. <i>BMC Bioinformatics</i> , 2015, 16, 254.	1.2	11
3519	Selective Coregulator Function and Restriction of Steroid Receptor Chromatin Occupancy by Hic-5. <i>Molecular Endocrinology</i> , 2015, 29, 716-729.	3.7	19
3520	A Search for Parent-of-Origin Effects on Honey Bee Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1657-1662.	0.8	41

#	ARTICLE	IF	CITATIONS
3521	PAGER: constructing PAGs and new PAGâ€PAG relationships for network biology. <i>Bioinformatics</i> , 2015, 31, i250-i257.	1.8	21
3522	Genome-wide gene expression analysis for target genes to differentiate patients with intestinal tuberculosis and Crohnâ€™s disease and discriminative value of FOXP3 mRNA expression. <i>Gastroenterology Report</i> , 2016, 4, gov015.	0.6	11
3523	EvoTol: a protein-sequence based evolutionary intolerance framework for disease-gene prioritization. <i>Nucleic Acids Research</i> , 2015, 43, e33-e33.	6.5	33
3524	The impact of genetic variation and cigarette smoke on DNA methylation in current and former smokers from the COPD Gene study. <i>Epigenetics</i> , 2015, 10, 1064-1073.	1.3	31
3525	Acute Cellular Rejection Elicits Distinct MicroRNA Signatures in Airway Epithelium of Lung Transplant Patients. <i>Transplantation Direct</i> , 2015, 1, e44.	0.8	8
3526	Integrative analysis of miRNA and mRNA profiles in response to myricetin in human endothelial cells. <i>Biochip Journal</i> , 2015, 9, 239-246.	2.5	5
3527	Distributed processing of biological interactions using Hadoop. , 2015, , .		0
3528	Quantitative dynamic imaging of immune cell signalling using lentiviral gene transfer. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 713-725.	0.6	40
3529	Response and survival of breast cancer intrinsic subtypes following multi-agent neoadjuvant chemotherapy. <i>BMC Medicine</i> , 2015, 13, 303.	2.3	113
3530	Pathways related to PMA-differentiated THP1 human monocytic leukemia cells revealed by RNA-Seq. <i>Science China Life Sciences</i> , 2015, 58, 1282-1287.	2.3	33
3531	Cognitive Computing: A Brief Survey and Open Research Challenges. , 2015, , .		22
3532	Bioinformatics Analysis of Proteome Changes in Calu-3 Cell Infected by Influenza A Virus (H5N1). <i>Journal of Molecular Microbiology and Biotechnology</i> , 2015, 25, 311-319.	1.0	1
3533	The organic osmolyte betaine induces keratin 2 expression in rat epidermal keratinocytes â€” A genome-wide study in UVB irradiated organotypic 3D cultures. <i>Toxicology in Vitro</i> , 2015, 30, 462-475.	1.1	5
3534	High-throughput alternative splicing detection using dually constrained correspondence analysis (DCCA). <i>Journal of Biomedical Informatics</i> , 2015, 58, 175-185.	2.5	8
3535	In-depth analysis of the critical genes and pathways in colorectal cancer. <i>International Journal of Molecular Medicine</i> , 2015, 36, 923-930.	1.8	20
3536	Identification of biomarkers with a tumor stage-dependent expression and exploration of the mechanism involved in laryngeal squamous cell carcinoma. <i>Oncology Reports</i> , 2015, 34, 2627-2635.	1.2	9
3537	iTRAQ-based quantitative proteomic analysis of cerebrospinal fluid reveals NELL2 as a potential diagnostic biomarker of tuberculous meningitis. <i>International Journal of Molecular Medicine</i> , 2015, 35, 1323-1332.	1.8	19
3538	Understanding the molecular aspects of oriental obesity pattern differentiation using DNA microarray. <i>Journal of Translational Medicine</i> , 2015, 13, 331.	1.8	1

#	ARTICLE	IF	CITATIONS
3539	The homeobox gene <i>DLX4</i> regulates erythro-megakaryocytic differentiation by stimulating IL-1/NF- $\kappa$ B signaling. <i>Journal of Cell Science</i> , 2015, 128, 3055-67.	1.2	12
3540	Identification of Key Genes and Pathways in Renal Cell Carcinoma Through Expression Profiling Data. <i>Kidney and Blood Pressure Research</i> , 2015, 40, 288-297.	0.9	42
3541	Comprehensive Transcriptome Analysis Reveals Accelerated Genic Evolution in a Tibet Fish, <i>Gymnodiptychus pachycheilus</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 251-261.	1.1	112
3542	Stage-specific signaling pathways during murine testis development and spermatogenesis: A pathway-based analysis to quantify developmental dynamics. <i>Reproductive Toxicology</i> , 2015, 51, 31-39.	1.3	5
3543	Frequent involvement of chromatin remodeler alterations in gastric field cancerization. <i>Cancer Letters</i> , 2015, 357, 328-338.	3.2	55
3544	Zic2 Is an Enhancer-Binding Factor Required for Embryonic Stem Cell Specification. <i>Molecular Cell</i> , 2015, 57, 685-694.	4.5	92
3545	mRNA expression profiles in circulating tumor cells of metastatic colorectal cancer patients. <i>Molecular Oncology</i> , 2015, 9, 920-932.	2.1	37
3546	The Amniotic Fluid Transcriptome as a Guide to Understanding Fetal Disease. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2015, 5, a023101-a023101.	2.9	32
3547	The over-expression of aquaporin-1 alters erythroid gene expression in human erythroleukemia K562 cells. <i>Tumor Biology</i> , 2015, 36, 291-302.	0.8	7
3548	In silico identification of conserved microRNAs and their targets in bovine fat tissue. <i>Gene</i> , 2015, 559, 119-128.	1.0	13
3549	Identification of proteins associated with Aha1 in HeLa cells by quantitative proteomics. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 365-380.	1.1	10
3550	DNA microarray analysis of the antihypertensive effect of milk fermented by <i>Lactobacillus helveticus</i> H9 on spontaneously hypertensive rats. <i>Dairy Science and Technology</i> , 2015, 95, 321-330.	2.2	2
3551	Loss of Cdh1 and Trp53 in the uterus induces chronic inflammation with modification of tumor microenvironment. <i>Oncogene</i> , 2015, 34, 2471-2482.	2.6	24
3552	Characterization of the nasopharyngeal carcinoma methylome identifies aberrant disruption of key signaling pathways and methylated tumor suppressor genes. <i>Epigenomics</i> , 2015, 7, 155-173.	1.0	52
3553	Human PrimPol is a highly error-prone polymerase regulated by single-stranded DNA binding proteins. <i>Nucleic Acids Research</i> , 2015, 43, 1056-1068.	6.5	93
3554	Zebrafish liver (ZFL) cells are able to mount an anti-viral response after stimulation with Poly (I:C). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2015, 182, 55-63.	0.7	18
3555	The gene expression profile of porcine alveolar macrophages infected with a highly pathogenic porcine reproductive and respiratory syndrome virus indicates overstimulation of the innate immune system by the virus. <i>Archives of Virology</i> , 2015, 160, 649-662.	0.9	16
3556	Inference on differences between classes using cluster-specific contrasts of mixed effects. <i>Biostatistics</i> , 2015, 16, 98-112.	0.9	14

#	ARTICLE	IF	CITATIONS
3557	Automatic Teaching—Learning-Based Optimization: A Novel Clustering Method for Gene Functional Enrichments. SpringerBriefs in Applied Sciences and Technology, 2015, , 17-35.	0.2	7
3558	Resistin-Like Molecule $\pm$ in Allergen-Induced Pulmonary Vascular Remodeling. American Journal of Respiratory Cell and Molecular Biology, 2015, 53, 303-313.	1.4	18
3559	Analysis of gene expression identifies candidate markers and pathways in pre-eclampsia. Journal of Obstetrics and Gynaecology, 2015, 35, 578-584.	0.4	33
3560	The clinicopathological and gene expression patterns associated with ulceration of primary melanoma. Pigment Cell and Melanoma Research, 2015, 28, 94-104.	1.5	26
3561	The Novel Small Leucine-rich Protein Chondroadherin-like (CHADL) Is Expressed in Cartilage and Modulates Chondrocyte Differentiation. Journal of Biological Chemistry, 2015, 290, 918-925.	1.6	30
3562	Identification of copy number variations in Qinchuan cattle using BovineHD Genotyping Beadchip array. Molecular Genetics and Genomics, 2015, 290, 319-327.	1.0	48
3563	A search for protein biomarkers links olfactory signal transduction to social immunity. BMC Genomics, 2015, 16, 63.	1.2	45
3564	A Systems Biology Perspective on the Molecular Mechanisms Underlying the Therapeutic Effects of Buyang Huanwu Decoction on Ischemic Stroke. Rejuvenation Research, 2015, 18, 313-325.	0.9	31
3565	Integrative analysis of lung development—cancer expression associations reveals the roles of signatures with inverse expression patterns. Molecular BioSystems, 2015, 11, 1271-1284.	2.9	9
3566	Mutations in early follicular lymphoma progenitors are associated with suppressed antigen presentation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1116-25.	3.3	307
3567	Time-restricted feeding attenuates age-related cardiac decline in <i>Drosophila</i> . Science, 2015, 347, 1265-1269.	6.0	223
3568	Peripheral blood mononuclear cell gene expression profile in obese boys who followed a moderate energy-restricted diet: differences between high and low responders at baseline and after the intervention. British Journal of Nutrition, 2015, 113, 331-342.	1.2	25
3569	Oscillatory Shear Stress Mediates Directional Reorganization of Actin Cytoskeleton and Alters Differentiation Propensity of Mesenchymal Stem Cells. Stem Cells, 2015, 33, 429-442.	1.4	50
3570	Effects of an 11-nm DMSA-coated iron nanoparticle on the gene expression profile of two human cell lines, THP-1 and HepG2. Journal of Nanobiotechnology, 2015, 13, 3.	4.2	16
3571	Identification of potential genomic biomarkers for Sjögren's syndrome using data pooling of gene expression microarrays. Rheumatology International, 2015, 35, 829-836.	1.5	55
3572	Identification and validation of gene module associated with lung cancer through coexpression network analysis. Gene, 2015, 563, 56-62.	1.0	37
3573	Identification of targets for rational pharmacological therapy in childhood craniopharyngioma. Acta Neuropathologica Communications, 2015, 3, 30.	2.4	85
3574	Epigenetic and in vivo comparison of diverse MSC sources reveals an endochondral signature for human hematopoietic niche formation. Blood, 2015, 125, 249-260.	0.6	201

#	ARTICLE	IF	CITATIONS
3575	Tracking global gene expression responses in T cell differentiation. <i>Gene</i> , 2015, 569, 259-266.	1.0	20
3576	Transcriptomic changes in mouse embryonic stem cells exposed to thalidomide during spontaneous differentiation. <i>Data in Brief</i> , 2015, 4, 199-202.	0.5	4
3577	Profiling signaling proteins in human spermatozoa: biomarker identification for sperm quality evaluation. <i>Fertility and Sterility</i> , 2015, 104, 845-856.e8.	0.5	36
3578	Comparative transcriptome analysis reveals that the extracellular matrix receptor interaction contributes to the venous metastases of hepatocellular carcinoma. <i>Cancer Genetics</i> , 2015, 208, 482-491.	0.2	52
3579	Transcriptomic analysis provides insight into high-altitude acclimation in domestic goats. <i>Gene</i> , 2015, 567, 208-216.	1.0	26
3580	Prediction of feature genes in trauma patients with the TNF rs1800629 A allele using support vector machine. <i>Computers in Biology and Medicine</i> , 2015, 64, 24-29.	3.9	4
3581	Analysis of copy number variations by SNP50 BeadChip array in Chinese sheep. <i>Genomics</i> , 2015, 106, 295-300.	1.3	18
3582	A new mib allele with a chromosomal deletion covering foxc1a exhibits anterior somite specification defect. <i>Scientific Reports</i> , 2015, 5, 10673.	1.6	10
3583	An epigenomic role of Fe65 in the cellular response to DNA damage. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2015, 776, 40-47.	0.4	6
3584	Maternal diabetes induces changes in the umbilical cord gene expression. <i>Placenta</i> , 2015, 36, 767-774.	0.7	10
3585	Gene expression profiling by high throughput sequencing to determine signatures for the bovine receptive uterus at early gestation. <i>Genomics Data</i> , 2015, 5, 94-96.	1.3	2
3586	Role of the anti-glioma drug AT13148 in the inhibition of Notch signaling pathway. <i>Gene</i> , 2015, 573, 153-159.	1.0	4
3587	Systematic investigation of hierarchical phosphorylation by protein kinase CK2. <i>Journal of Proteomics</i> , 2015, 118, 49-62.	1.2	64
3588	Quantitative Proteomics Reveals the Essential Roles of Stromal Interaction Molecule 1 (STIM1) in the Testicular Cord Formation in Mouse Testis. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2682-2691.	2.5	23
3589	ABCG2 Localizes to the Nucleus and Modulates CDH1 Expression in Lung Cancer Cells. <i>Neoplasia</i> , 2015, 17, 265-278.	2.3	45
3590	Blood-based gene-expression biomarkers of post-traumatic stress disorder among deployed marines: A pilot study. <i>Psychoneuroendocrinology</i> , 2015, 51, 472-494.	1.3	54
3591	Microbial Forensics: Predicting Phenotypic Characteristics and Environmental Conditions from Large-Scale Gene Expression Profiles. <i>PLoS Computational Biology</i> , 2015, 11, e1004127.	1.5	26
3592	Combined Metabolomics and Proteomics Analysis of Major Depression in an Animal Model: Perturbed Energy Metabolism in the Chronic Mild Stressed Rat Cerebellum. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 383-392.	1.0	80

#	ARTICLE	IF	CITATIONS
3593	A feature analysis of lower solubility proteins in three eukaryotic systems. <i>Journal of Proteomics</i> , 2015, 118, 21-38.	1.2	15
3594	Genome-wide burden of deleterious coding variants increased in schizophrenia. <i>Nature Communications</i> , 2015, 6, 7501.	5.8	22
3595	Thalidomide induced early gene expression perturbations indicative of human embryopathy in mouse embryonic stem cells. <i>Toxicology and Applied Pharmacology</i> , 2015, 287, 43-51.	1.3	10
3596	Identifying influential nodes in a wound healing-related network of biological processes using mean first-passage time. <i>New Journal of Physics</i> , 2015, 17, 025002.	1.2	14
3597	Vitamin B <sub>12</sub> modulates the transcriptome of the skin microbiota in acne pathogenesis. <i>Science Translational Medicine</i> , 2015, 7, 293ra103.	5.8	138
3598	Identification of adenine modulating AMPK activation in NIH/3T3 cells by proteomic approach. <i>Journal of Proteomics</i> , 2015, 120, 204-214.	1.2	14
3599	Genes involved in keratinization, keratinocyte and epithelium differentiation are aberrantly regulated in oral lichen planus. <i>Genes and Genomics</i> , 2015, 37, 751-757.	0.5	0
3600	Bioinformatic analysis of specific genes in diabetic nephropathy. <i>Renal Failure</i> , 2015, 37, 1219-1224.	0.8	6
3601	How data analysis affects power, reproducibility and biological insight of RNA-seq studies in complex datasets. <i>Nucleic Acids Research</i> , 2015, 43, 7664-7674.	6.5	90
3602	Parallel Gene Expression Changes in Sarcoidosis Involving the Lacrimal Gland, Orbital Tissue, or Blood. <i>JAMA Ophthalmology</i> , 2015, 133, 770.	1.4	31
3603	Extracts from presumed "reduced harm" cigarettes induce equivalent or greater toxicity in antigen-presenting cells. <i>Toxicology</i> , 2015, 335, 46-54.	2.0	2
3604	Orbital pseudotumor can be a localized form of granulomatosis with polyangiitis as revealed by gene expression profiling. <i>Experimental and Molecular Pathology</i> , 2015, 99, 271-278.	0.9	33
3605	Divergence of dim-light vision among bats (order: Chiroptera) as estimated by molecular and electrophysiological methods. <i>Scientific Reports</i> , 2015, 5, 11531.	1.6	12
3606	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015, 6, 7866.	5.8	676
3607	Alterations of a Cellular Cholesterol Metabolism Network Are a Molecular Feature of Obesity-Related Type 2 Diabetes and Cardiovascular Disease. <i>Diabetes</i> , 2015, 64, 3464-3474.	0.3	82
3608	Identification of lncRNA MEG3 Binding Protein Using MS2-Tagged RNA Affinity Purification and Mass Spectrometry. <i>Applied Biochemistry and Biotechnology</i> , 2015, 176, 1834-1845.	1.4	18
3609	FOXG1-Dependent Dysregulation of GABA/Glutamate Neuron Differentiation in Autism Spectrum Disorders. <i>Cell</i> , 2015, 162, 375-390.	13.5	894
3610	Acute Targeting of General Transcription Factor IIB Restricts Cardiac Hypertrophy via Selective Inhibition of Gene Transcription. <i>Circulation: Heart Failure</i> , 2015, 8, 138-148.	1.6	22



#	ARTICLE	IF	CITATIONS
3611	Highly Constrained Intergenic Drosophila Ultraconserved Elements Are Candidate ncRNAs. <i>Genome Biology and Evolution</i> , 2015, 7, 689-698.	1.1	16
3612	Genomic characteristics of miscarriage copy number variants. <i>Molecular Human Reproduction</i> , 2015, 21, 655-661.	1.3	28
3613	Identifying genes related with rheumatoid arthritis via system biology analysis. <i>Gene</i> , 2015, 571, 97-106.	1.0	8
3614	Loss of NFIX Transcription Factor Biases Postnatal Neural Stem/Progenitor Cells Toward Oligodendrogenesis. <i>Stem Cells and Development</i> , 2015, 24, 2114-2126.	1.1	21
3615	A proteomic perspective on the changes in milk proteins due to high somatic cell count. <i>Journal of Dairy Science</i> , 2015, 98, 5339-5351.	1.4	33
3616	Ataxin-2 Regulates RGS8 Translation in a New BAC-SCA2 Transgenic Mouse Model. <i>PLoS Genetics</i> , 2015, 11, e1005182.	1.5	70
3617	Identification and characterization of MicroRNAs in acrolein-stimulated endothelial cells: Implications for vascular disease. <i>Biochip Journal</i> , 2015, 9, 144-155.	2.5	7
3618	Label-free quantitative proteomic analysis reveals strong involvement of complement alternative and terminal pathways in human glomerular sclerotic lesions. <i>Journal of Proteomics</i> , 2015, 123, 89-100.	1.2	5
3619	Unraveling regulatory mechanisms of atrial remodeling of mitral regurgitation pigs by gene expression profiling analysis: role of type I angiotensin II receptor antagonist. <i>Translational Research</i> , 2015, 165, 599-620.	2.2	10
3620	Destabilization of pluripotency in the absence of Mad2l2. <i>Cell Cycle</i> , 2015, 14, 1596-1610.	1.3	13
3621	Knockdown of transcription factor forkhead box O3 (FOXO3) suppresses erythroid differentiation in human cells and zebrafish. <i>Biochemical and Biophysical Research Communications</i> , 2015, 460, 923-930.	1.0	13
3622	Uncovering pharmacological mechanisms of Wu-tou decoction acting on rheumatoid arthritis through systems approaches: drug-target prediction, network analysis and experimental validation. <i>Scientific Reports</i> , 2015, 5, 9463.	1.6	91
3623	Insights into protein interaction networks reveal non-receptor kinases as significant druggable targets for psoriasis. <i>Gene</i> , 2015, 566, 138-147.	1.0	8
3624	Transcription-Dependent Generation of a Specialized Chromatin Structure at the TCR $\beta$ Locus. <i>Journal of Immunology</i> , 2015, 194, 3432-3443.	0.4	10
3625	MPTP's Pathway of Toxicity Indicates Central Role of Transcription Factor SP1. <i>Archives of Toxicology</i> , 2015, 89, 743-755.	1.9	33
3626	Identification of biological processes and genes for gestational diabetes mellitus. <i>Archives of Gynecology and Obstetrics</i> , 2015, 292, 635-640.	0.8	10
3627	Exome sequencing as a tool for short stature gene discovery: analysis of a Korean family with pseudohypoparathyroidism. <i>Genes and Genomics</i> , 2015, 37, 339-346.	0.5	0
3628	Transcriptional response of human umbilical vein endothelial cell to H9N2 influenza virus infection. <i>Virology</i> , 2015, 482, 117-127.	1.1	8

#	ARTICLE	IF	CITATIONS
3629	Technical data of the transcriptomic analysis performed on tsetse fly symbionts, <i>Sodalis glossinidius</i> and <i>Wigglesworthia glossinidia</i> , harbored, respectively by non-infected, <i>Trypanosoma brucei</i> gambiense infected and self-cured <i>Glossina palpalis gambiensis</i> tsetse flies. <i>Genomics Data</i> , 2015, 4, 133-136.	1.3	1
3630	BACA: bubble chArt to compare annotations. <i>BMC Bioinformatics</i> , 2015, 16, 37.	1.2	16
3631	Genome-wide detection and characterization of positive selection in Korean Native Black Pig from Jeju Island. <i>BMC Genetics</i> , 2015, 16, 3.	2.7	18
3632	Global liver gene expression differences in Nelore steers with divergent residual feed intake phenotypes. <i>BMC Genomics</i> , 2015, 16, 242.	1.2	109
3633	Human non-small cell lung cancer expresses putative cancer stem cell markers and exhibits the transcriptomic profile of multipotent cells. <i>BMC Cancer</i> , 2015, 15, 84.	1.1	103
3634	Identification of Pivotal Markers in Vascular Dementia Based on Proteomics Data. <i>Dementia and Geriatric Cognitive Disorders</i> , 2015, 39, 312-320.	0.7	5
3635	Integration of transcriptome and methylome analysis of aldosterone-producing adenomas. <i>European Journal of Endocrinology</i> , 2015, 173, 185-195.	1.9	46
3636	DNA methylation changes in the placenta are associated with fetal manganese exposure. <i>Reproductive Toxicology</i> , 2015, 57, 43-49.	1.3	43
3637	Argonaute 2 Binds Directly to tRNA Genes and Promotes Gene Repression in <i>C. elegans</i> . <i>Molecular and Cellular Biology</i> , 2015, 35, 2278-2294.	1.1	31
3638	Mapping Genetic Contributions to Cardiac Pathology Induced by Beta-Adrenergic Stimulation in Mice. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 40-49.	5.1	71
3639	Comprehensive transcriptome analysis of mesenchymal stem cells in elderly patients with osteoporosis. <i>Aging Clinical and Experimental Research</i> , 2015, 27, 595-601.	1.4	16
3640	Cigarette smoking hinders human periodontal ligament-derived stem cell proliferation, migration and differentiation potentials. <i>Scientific Reports</i> , 2015, 5, 7828.	1.6	73
3641	Differential Gene Expression in Uterine Endometrium During Implantation in Pigs1. <i>Biology of Reproduction</i> , 2015, 92, 52.	1.2	31
3642	Alteration of Cell-Cell and Cell-Matrix Adhesion in Urothelial Cells: An Oncogenic Mechanism for Mutant FGFR3. <i>Molecular Cancer Research</i> , 2015, 13, 138-148.	1.5	18
3643	Mitochondrial and Nuclear Accumulation of the Transcription Factor ATFS-1 Promotes OXPHOS Recovery during the UPRmt. <i>Molecular Cell</i> , 2015, 58, 123-133.	4.5	354
3644	Hippocampal transcriptional and neurogenic changes evoked by combination yohimbine and imipramine treatment. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2015, 61, 1-9.	2.5	5
3646	Host Response to the Lung Microbiome in Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015, 192, 438-445.	2.5	195
3647	Interactions between horizontally acquired genes create a fitness cost in <i>Pseudomonas aeruginosa</i> . <i>Nature Communications</i> , 2015, 6, 6845.	5.8	147

#	ARTICLE	IF	CITATIONS
3648	Gene expression microarray analysis of the sciatic nerve of mice with diabetic neuropathy. <i>International Journal of Molecular Medicine</i> , 2015, 35, 333-339.	1.8	8
3649	Biological pathways and networks implicated in psychiatric disorders. <i>Current Opinion in Behavioral Sciences</i> , 2015, 2, 58-68.	2.0	21
3650	Screening for characteristic microRNAs between pre-invasive and invasive stages of cervical cancer. <i>Molecular Medicine Reports</i> , 2015, 12, 55-62.	1.1	7
3651	The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.	6.0	1,127
3652	Quantification of Extracellular Matrix Proteins from a Rat Lung Scaffold to Provide a Molecular Readout for Tissue Engineering. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 961-973.	2.5	131
3653	Network-based proteomic approaches reveal the neurodegenerative, neuroprotective and pain-related mechanisms involved after retrograde axonal damage. <i>Scientific Reports</i> , 2015, 5, 9185.	1.6	29
3654	Constraints, independence, and evolution of thermal plasticity: Probing genetic architecture of long- and short-term thermal acclimation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4399-4404.	3.3	144
3655	Direct Involvement of Retinoblastoma Family Proteins in DNA Repair by Non-homologous End-Joining. <i>Cell Reports</i> , 2015, 10, 2006-2018.	2.9	62
3656	KPC1-Mediated Ubiquitination and Proteasomal Processing of NF- $\kappa$ B1 p105 to p50 Restricts Tumor Growth. <i>Cell</i> , 2015, 161, 333-347.	13.5	89
3657	Controlled induction of DNA double-strand breaks in the mouse liver induces features of tissue ageing. <i>Nature Communications</i> , 2015, 6, 6790.	5.8	90
3658	Chronic toxicity evaluation of the flame retardant tris (2-butoxyethyl) phosphate (TBOEP) using <i>Daphnia magna</i> transcriptomic response. <i>Chemosphere</i> , 2015, 132, 159-165.	4.2	41
3659	Storage time does not modify the gene expression profile of cryopreserved human metaphase II oocytes. <i>Human Reproduction</i> , 2015, 30, 2519-2526.	0.4	39
3660	Graph-based unsupervised feature selection and multiview clustering for microarray data. <i>Journal of Biosciences</i> , 2015, 40, 755-767.	0.5	11
3661	SILAC-based quantification of changes in protein tyrosine phosphorylation induced by Interleukin-2 (IL-2) and IL-15 in T-lymphocytes. <i>Data in Brief</i> , 2015, 5, 53-58.	0.5	16
3662	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. <i>Neuron</i> , 2015, 87, 1215-1233.	3.8	1,219
3663	The DNA damage response induces inflammation and senescence by inhibiting autophagy of GATA4. <i>Science</i> , 2015, 349, aaa5612.	6.0	693
3664	mRIN for direct assessment of genome-wide and gene-specific mRNA integrity from large-scale RNA-sequencing data. <i>Nature Communications</i> , 2015, 6, 7816.	5.8	59
3665	RNA-Seq versus oligonucleotide array assessment of dose-dependent TCDD-elicited hepatic gene expression in mice. <i>BMC Genomics</i> , 2015, 16, 373.	1.2	31

#	ARTICLE	IF	CITATIONS
3666	Gene expression profiling can predict the fate of HeLa cells exposed to X-ray irradiation with or without protoporphyrin accumulation. <i>Genomics Data</i> , 2015, 5, 192-194.	1.3	1
3667	A comparative analysis of host responses to avian influenza infection in ducks and chickens highlights a role for the interferon-induced transmembrane proteins in viral resistance. <i>BMC Genomics</i> , 2015, 16, 574.	1.2	92
3668	Transcriptome Analysis of Pig <i>In Vivo</i> , <i>In Vitro</i> Fertilized, and Nuclear Transfer Blastocyst-Stage Embryos Treated with Histone Deacetylase Inhibitors Postfusion and Activation Reveals Changes in the Lysosomal Pathway. <i>Cellular Reprogramming</i> , 2015, 17, 243-258.	0.5	21
3669	A mutation profile for top-k patient search exploiting Gene-Ontology and orthogonal non-negative matrix factorization. <i>Bioinformatics</i> , 2015, 31, 3653-3659.	1.8	12
3670	Quality Control and Analysis of NGS RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2015, 1326, 217-232.	0.4	1
3671	High-fat diet caused widespread epigenomic differences on hepatic methylome in rat. <i>Physiological Genomics</i> , 2015, 47, 514-523.	1.0	26
3673	The autism-associated gene chromodomain helicase DNA-binding protein 8 (CHD8) regulates noncoding RNAs and autism-related genes. <i>Translational Psychiatry</i> , 2015, 5, e568-e568.	2.4	104
3675	Ribosome profiling reveals translation control as a key mechanism generating differential gene expression in <i>Trypanosoma cruzi</i> . <i>BMC Genomics</i> , 2015, 16, 443.	1.2	121
3676	Variation analysis of transcriptome changes reveals cochlear genes and their associated functions in cochlear susceptibility to acoustic overstimulation. <i>Hearing Research</i> , 2015, 330, 78-89.	0.9	19
3677	Genome-wide identification of microRNAs regulating cholesterol and triglyceride homeostasis. <i>Nature Medicine</i> , 2015, 21, 1290-1297.	15.2	214
3678	Causal Biological Network Database: A Comprehensive Platform of Causal Biological Network Models Focused on the Pulmonary and Vascular Systems. <i>Methods in Pharmacology and Toxicology</i> , 2015, , 65-93.	0.1	8
3679	A new approach for investigating venom function applied to venom calreticulin in a parasitoid wasp. <i>Toxicon</i> , 2015, 107, 304-316.	0.8	32
3680	Monocyte enhancers are highly altered in systemic lupus erythematosus. <i>Epigenomics</i> , 2015, 7, 921-935.	1.0	27
3682	Combined serial analysis of gene expression and transcription factor binding site prediction identifies novel-candidate-target genes of Nr2e1 in neocortex development. <i>BMC Genomics</i> , 2015, 16, 545.	1.2	9
3684	KnowEnG: a knowledge engine for genomics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1115-1119.	2.2	13
3685	Bifidobacteria grown on human milk oligosaccharides downregulate the expression of inflammation-related genes in Caco-2 cells. <i>BMC Microbiology</i> , 2015, 15, 172.	1.3	67
3686	Integration of Proteomics and Transcriptomics Data Sets for the Analysis of a Lymphoma B-Cell Line in the Context of the Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 3530-3540.	1.8	16
3687	Molecular insight into thiopurine resistance: transcriptomic signature in lymphoblastoid cell lines. <i>Genome Medicine</i> , 2015, 7, 37.	3.6	19

#	ARTICLE	IF	CITATIONS
3688	Genome-Wide Analysis of ChREBP Binding Sites on Male Mouse Liver and White Adipose Chromatin. <i>Endocrinology</i> , 2015, 156, 1982-1994.	1.4	78
3689	Global Proteomic Analysis of Functional Compartments in Immature Avian Follicles Using Laser Microdissection Coupled to LC-MS/MS. <i>Journal of Proteome Research</i> , 2015, 14, 3912-3923.	1.8	8
3690	Elevated host lipid metabolism revealed by iTRAQ-based quantitative proteomic analysis of cerebrospinal fluid of tuberculous meningitis patients. <i>Biochemical and Biophysical Research Communications</i> , 2015, 466, 689-695.	1.0	18
3691	Effects of dietary supplementation with docosahexaenoic acid (DHA) on hippocampal gene expression in streptozotocin induced diabetic C57Bl/6 mice. <i>Journal of Nutrition &amp; Intermediary Metabolism</i> , 2015, 2, 2-7.	1.7	1
3692	Microarray profiling of long non-coding RNA (lncRNA) associated with hypertrophic cardiomyopathy. <i>BMC Cardiovascular Disorders</i> , 2015, 15, 62.	0.7	49
3694	Identifying the biological pathways underlying human focal epilepsy: from complexity to coherence to centrality. <i>Human Molecular Genetics</i> , 2015, 24, 4306-4316.	1.4	45
3695	Extraction of relations between genes and diseases from text and large-scale data analysis: implications for translational research. <i>BMC Bioinformatics</i> , 2015, 16, 55.	1.2	170
3696	Biological processes and pathway changes in isoflurane-induced anesthesia revealed by bioinformatics analysis of gene expression profiles. <i>Journal of Anesthesia</i> , 2015, 29, 912-919.	0.7	2
3697	Structural and biochemical changes underlying a keratoderma-like phenotype in mice lacking suprabasal AP1 transcription factor function. <i>Cell Death and Disease</i> , 2015, 6, e1647-e1647.	2.7	17
3698	Defining the phospho-adesome through the phosphoproteomic analysis of integrin signalling. <i>Nature Communications</i> , 2015, 6, 6265.	5.8	150
3699	New Perspectives for the Rescue of Cognitive Disability in Down Syndrome. <i>Journal of Neuroscience</i> , 2015, 35, 13843-13852.	1.7	28
3700	Exposure of mice to secondhand smoke elicits both transient and long-lasting transcriptional changes in cancer-related functional networks. <i>International Journal of Cancer</i> , 2015, 136, 2253-2263.	2.3	11
3701	Potential anti-cancer effect of curcumin in human lung squamous cell carcinoma. <i>Thoracic Cancer</i> , 2015, 6, 508-516.	0.8	25
3702	Temporal gene expression profiling of the rat knee joint capsule during immobilization-induced joint contractures. <i>BMC Musculoskeletal Disorders</i> , 2015, 16, 125.	0.8	20
3703	Evidence for Adaptation to the Tibetan Plateau Inferred from Tibetan Loach Transcriptomes. <i>Genome Biology and Evolution</i> , 2015, 7, 2970-2982.	1.1	70
3704	Gene expression profiling of ovarian carcinomas and prognostic analysis of outcome. <i>Journal of Ovarian Research</i> , 2015, 8, 50.	1.3	10
3705	A novel method for predicting post-translational modifications on serine and threonine sites by using site-modification network profiles. <i>Molecular BioSystems</i> , 2015, 11, 3092-3100.	2.9	16
3706	The mRNA expression of soluble urokinase plasminogen activator surface receptor in human adipose tissue is positively correlated with body mass index. <i>Genome</i> , 2015, 58, 315-321.	0.9	5

#	ARTICLE	IF	CITATIONS
3707	Prioritization of rheumatoid arthritis risk subpathways based on global immune subpathway interaction network and random walk strategy. <i>Molecular BioSystems</i> , 2015, 11, 2986-2997.	2.9	8
3709	Ageing-Dependent Demethylation of Regulatory Elements Correlates with Chromatin State and Improved $\beta$ Cell Function. <i>Cell Metabolism</i> , 2015, 22, 619-632.	7.2	172
3710	Larger aggregates of mutant seipin in Celia's Encephalopathy, a new protein misfolding neurodegenerative disease. <i>Neurobiology of Disease</i> , 2015, 83, 44-53.	2.1	14
3711	The Receptive Endometrial Transcriptomic Signature Indicates an Earlier Shift from Proliferation to Metabolism at Early Diestrus in the Cow1. <i>Biology of Reproduction</i> , 2015, 93, 52.	1.2	40
3712	Potential role of differentially expressed lncRNAs in the pathogenesis of oral squamous cell carcinoma. <i>Archives of Oral Biology</i> , 2015, 60, 1581-1587.	0.8	40
3713	MiRNA-TF-gene network analysis through ranking of biomolecules for multi-informative uterine leiomyoma dataset. <i>Journal of Biomedical Informatics</i> , 2015, 57, 308-319.	2.5	27
3714	Identification of stable reference genes in differentiating human pluripotent stem cells. <i>Physiological Genomics</i> , 2015, 47, 232-239.	1.0	18
3715	SPINK1 promotes colorectal cancer progression by downregulating Metallothioneins expression. <i>Oncogenesis</i> , 2015, 4, e162-e162.	2.1	50
3716	Recent studies of ovine neuronal ceroid lipofuscinoses from BARN, the Batten Animal Research Network. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2015, 1852, 2279-2286.	1.8	29
3717	Sympatric speciation revealed by genome-wide divergence in the blind mole rat <i>Spalax</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11905-11910.	3.3	53
3718	Protein-protein interaction network analysis and identifying regulation microRNAs in asthmatic children. <i>Allergologia Et Immunopathologia</i> , 2015, 43, 584-592.	1.0	13
3719	Interaction of CDCP1 with HER2 Enhances HER2-Driven Tumorigenesis and Promotes Trastuzumab Resistance in Breast Cancer. <i>Cell Reports</i> , 2015, 11, 564-576.	2.9	52
3720	Impact of vitamin C on the cardiometabolic and inflammatory profiles of mice lacking a functional Werner syndrome protein helicase. <i>Experimental Gerontology</i> , 2015, 72, 192-203.	1.2	14
3721	Peripheral challenge with a viral mimic upregulates expression of the complement genes in the hippocampus. <i>Journal of Neuroimmunology</i> , 2015, 285, 137-142.	1.1	15
3722	A genome wide scan highlights differences in the genetic architecture of fat and protein contents in dairy sheep. <i>Small Ruminant Research</i> , 2015, 131, 21-28.	0.6	0
3723	Isolated Rat Epididymal Basal Cells Share Common Properties with Adult Stem Cells1. <i>Biology of Reproduction</i> , 2015, 93, 115.	1.2	39
3724	The Brakeless co-regulator can directly activate and repress transcription in early <i>Drosophila</i> embryos. <i>Developmental Biology</i> , 2015, 407, 173-181.	0.9	6
3725	Recurrent internal tandem duplications of BCOR in clear cell sarcoma of the kidney. <i>Nature Communications</i> , 2015, 6, 8891.	5.8	126

#	ARTICLE	IF	CITATIONS
3726	Diet and endocrine effects on behavioral maturation-related gene expression in the <i>pars intercerebralis</i> of the honey bee brain. <i>Journal of Experimental Biology</i> , 2015, 218, 4005-14.	0.8	17
3727	Systems toxicology identifies mechanistic impacts of 2-amino-4,6-dinitrotoluene (2A-DNT) exposure in Northern Bobwhite. <i>BMC Genomics</i> , 2015, 16, 587.	1.2	9
3728	Therapeutic concentration of lithium stimulates complement C3 production in dendritic cells and microglia via GSK $\beta$ inhibition. <i>Glia</i> , 2015, 63, 257-270.	2.5	19
3729	Impaired alveolarization and intrauterine growth restriction in rats: a postnatal genome-wide analysis. <i>Journal of Pathology</i> , 2015, 235, 420-430.	2.1	33
3730	Expression profiling of circulating tumor cells in metastatic breast cancer. <i>Breast Cancer Research and Treatment</i> , 2015, 149, 121-131.	1.1	48
3731	Analysis of Differentially Expressed Genes Associated With Alzheimer's Disease Based on Bioinformatics Methods. <i>American Journal of Alzheimer's Disease and Other Dementias</i> , 2015, 30, 746-751.	0.9	5
3732	Transcriptome organization for chronic alcohol abuse in human brain. <i>Molecular Psychiatry</i> , 2015, 20, 1438-1447.	4.1	111
3733	Identification of nuclear hormone receptor pathways causing insulin resistance by transcriptional and epigenomic analysis. <i>Nature Cell Biology</i> , 2015, 17, 44-56.	4.6	61
3734	TRIM24 links glucose metabolism with transformation of human mammary epithelial cells. <i>Oncogene</i> , 2015, 34, 2836-2845.	2.6	50
3735	Quantitative Proteomics of the Human Skin Secretome Reveal a Reduction in Immune Defense Mediators in Ectodermal Dysplasia Patients. <i>Journal of Investigative Dermatology</i> , 2015, 135, 759-767.	0.3	28
3736	Dauer-independent insulin/IGF-1-signalling implicates collagen remodelling in longevity. <i>Nature</i> , 2015, 519, 97-101.	13.7	251
3737	Identification of coexistence of DNA methylation and H3K27me3 specifically in cancer cells as a promising target for epigenetic therapy. <i>Carcinogenesis</i> , 2015, 36, 192-201.	1.3	64
3738	Stressor-induced proteome alterations in zebrafish: A meta-analysis of response patterns. <i>Aquatic Toxicology</i> , 2015, 159, 1-12.	1.9	25
3739	Disruption of microRNA-21 by TALEN leads to diminished cell transformation and increased expression of cell-environment interaction genes. <i>Cancer Letters</i> , 2015, 356, 506-516.	3.2	31
3740	CbGRiTS: Cerebellar gene regulation in time and space. <i>Developmental Biology</i> , 2015, 397, 18-30.	0.9	22
3742	Alzheimer's disease is associated with altered expression of genes involved in immune response and mitochondrial processes in astrocytes. <i>Neurobiology of Aging</i> , 2015, 36, 583-591.	1.5	156
3743	Proteins associated with pancreatic cancer survival in patients with resectable pancreatic ductal adenocarcinoma. <i>Laboratory Investigation</i> , 2015, 95, 43-55.	1.7	44
3744	Insight into the primary mode of action of TiO <sub>2</sub> nanoparticles on <i>Escherichia coli</i> in the dark. <i>Proteomics</i> , 2015, 15, 98-113.	1.3	104

#	ARTICLE	IF	CITATIONS
3745	Interferon Regulatory Factor 1 Marks Activated Genes and Can Induce Target Gene Expression in Systemic Lupus Erythematosus. <i>Arthritis and Rheumatology</i> , 2015, 67, 785-796.	2.9	31
3746	PEGylation of ORMOSIL nanoparticles differently modulates the in vitro toxicity toward human lung cells. <i>Archives of Toxicology</i> , 2015, 89, 607-620.	1.9	17
3747	Identification of disease-related miRNAs based on co-expression network in spinal cord injury. <i>International Journal of Neuroscience</i> , 2015, 125, 270-276.	0.8	9
3748	GLUT12 deficiency during early development results in heart failure and a diabetic phenotype in zebrafish. <i>Journal of Endocrinology</i> , 2015, 224, 1-15.	1.2	32
3749	Toxicogenomic analysis in the combined effect of tributyltin and benzo[a]pyrene on the development of zebrafish embryos. <i>Aquatic Toxicology</i> , 2015, 158, 157-164.	1.9	34
3750	Genome-wide gene expression profiles of dental follicle stem cells. <i>Acta Odontologica Scandinavica</i> , 2015, 73, 93-100.	0.9	11
3751	Functional annotation and biological interpretation of proteomics data. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 46-54.	1.1	45
3752	Global Transcriptome Profiling of Genes that Are Differentially Regulated During Differentiation of Mouse Embryonic Neural Stem Cells into Astrocytes. <i>Journal of Molecular Neuroscience</i> , 2015, 55, 109-125.	1.1	31
3753	Molecular classification of basal cell carcinoma of skin by gene expression profiling. <i>Molecular Carcinogenesis</i> , 2015, 54, 1605-1612.	1.3	22
3754	The <i>Vibrio cholerae</i> Cpx Envelope Stress Response Senses and Mediates Adaptation to Low Iron. <i>Journal of Bacteriology</i> , 2015, 197, 262-276.	1.0	41
3755	Response of NBS encoding resistance genes linked to both heat and fungal stress in <i>Brassica oleracea</i> . <i>Plant Physiology and Biochemistry</i> , 2015, 86, 130-136.	2.8	21
3756	Identification of key genes affecting disease free survival time of pediatric acute lymphoblastic leukemia based on bioinformatic analysis. <i>Blood Cells, Molecules, and Diseases</i> , 2015, 54, 38-43.	0.6	10
3757	Qualitative and quantitative peptidomic and proteomic approaches to phenotyping chicken semen. <i>Journal of Proteomics</i> , 2015, 112, 313-335.	1.2	80
3758	Diet-dependent gene expression in honey bees: honey vs. sucrose or high fructose corn syrup. <i>Scientific Reports</i> , 2014, 4, 5726.	1.6	67
3759	Argonaute CLIP-Seq reveals miRNA targetome diversity across tissue types. <i>Scientific Reports</i> , 2014, 4, 5947.	1.6	88
3760	How to learn about gene function: text-mining or ontologies?. <i>Methods</i> , 2015, 74, 3-15.	1.9	24
3761	High Quality RNA in Semen and Sperm: Isolation, Analysis and Potential Application in Clinical Testing. <i>Journal of Urology</i> , 2015, 193, 352-359.	0.2	35
3762	H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells. <i>Genome Research</i> , 2015, 25, 27-40.	2.4	119



#	ARTICLE	IF	CITATIONS
3763	Myostatin/activin blocking combined with exercise reconditions skeletal muscle expression profile of mdx mice. <i>Molecular and Cellular Endocrinology</i> , 2015, 399, 131-142.	1.6	21
3764	A systems biology-based investigation into the therapeutic effects of Gansui Banxia Tang on reversing the imbalanced network of hepatocellular carcinoma. <i>Scientific Reports</i> , 2014, 4, 4154.	1.6	52
3765	The limitations of simple gene set enrichment analysis assuming gene independence. <i>Statistical Methods in Medical Research</i> , 2016, 25, 472-487.	0.7	86
3767	Identification of differentially expressed genes affecting hair and cashmere growth in the Laiwu black goat by microarray. <i>Molecular Medicine Reports</i> , 2016, 14, 3823-3831.	1.1	4
3768	Small-Molecule Inhibition of Rho/MKL/SRF Transcription in Prostate Cancer Cells: Modulation of Cell Cycle, ER Stress, and Metastasis Gene Networks. <i>Microarrays (Basel, Switzerland)</i> , 2016, 5, 13.	1.4	21
3769	Screening of biomarkers for prediction of response to and prognosis after chemotherapy for breast cancers. <i>OncoTargets and Therapy</i> , 2016, 9, 2593.	1.0	12
3770	Inferring the progression of multifocal liver cancer from spatial and temporal genomic heterogeneity. <i>Oncotarget</i> , 2016, 7, 2867-2877.	0.8	38
3771	Expression of myogenes in longissimus dorsi muscle during prenatal development in commercial and local Piau pigs. <i>Genetics and Molecular Biology</i> , 2016, 39, 589-599.	0.6	8
3772	Bioinformatics analysis of differentially expressed proteins in prostate cancer based on proteomics data. <i>OncoTargets and Therapy</i> , 2016, 9, 1545.	1.0	21
3773	Molecular crosstalk between tumour and brain parenchyma instructs histopathological features in glioblastoma. <i>Oncotarget</i> , 2016, 7, 31955-31971.	0.8	69
3774	Practical aspects of NGS-based pathways analysis for personalized cancer science and medicine. <i>Oncotarget</i> , 2016, 7, 52493-52516.	0.8	15
3775	LINC00520 is induced by Src, STAT3, and PI3K and plays a functional role in breast cancer. <i>Oncotarget</i> , 2016, 7, 81981-81994.	0.8	48
3776	Pericyte MyD88 and IRAK4 control inflammatory and fibrotic responses to tissue injury. <i>Journal of Clinical Investigation</i> , 2016, 127, 321-334.	3.9	113
3777	Identification of Molecular Targets for Predicting Colon Adenocarcinoma. <i>Medical Science Monitor</i> , 2016, 22, 460-468.	0.5	13
3778	DNA Microarray Analysis in Screening Features of Genes Involved in Spinal Cord Injury. <i>Medical Science Monitor</i> , 2016, 22, 1571-1581.	0.5	4
3779	Leveraging Comparative Genomics to Identify and Functionally Characterize Genes Associated with Sperm Phenotypes in <i>Python bivittatus</i> (Burmese Python). <i>Genetics Research International</i> , 2016, 2016, 1-16.	2.0	0
3780	A Transcriptomic Signature of Mouse Liver Progenitor Cells. <i>Stem Cells International</i> , 2016, 2016, 1-15.	1.2	5
3781	Human Epithelial Cells Discriminate between Commensal and Pathogenic Interactions with <i>Candida albicans</i> . <i>PLoS ONE</i> , 2016, 11, e0153165.	1.1	16

#	ARTICLE	IF	CITATIONS
3782	Transcriptomic Profiling Using Next Generation Sequencing - Advances, Advantages, and Challenges. , O, , .		8
3783	Construction of a protein-protein interaction network of Wilms's™ tumor and pathway prediction of molecular complexes. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	2
3784	Induction of Macrophage Function in Human THP-1 Cells Is Associated with Rewiring of MAPK Signaling and Activation of MAP3K7 (TAK1) Protein Kinase. <i>Frontiers in Cell and Developmental Biology</i> , 2016, 4, 21.	1.8	54
3785	<i>Mycobacterium bovis</i> BCG Interferes with miR-3619-5p Control of Cathepsin S in the Process of Autophagy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 27.	1.8	26
3786	Immunosenescence-Related Transcriptomic and Immunologic Changes in Older Individuals Following Influenza Vaccination. <i>Frontiers in Immunology</i> , 2016, 7, 450.	2.2	40
3787	Aging Shapes the Population-Mean and -Dispersion of Gene Expression in Human Brains. <i>Frontiers in Aging Neuroscience</i> , 2016, 8, 183.	1.7	31
3788	Long Non-coding RNA in Neurons: New Players in Early Response to BDNF Stimulation. <i>Frontiers in Molecular Neuroscience</i> , 2016, 9, 15.	1.4	14
3789	Maternal Chromium Restriction Leads to Glucose Metabolism Imbalance in Mice Offspring through Insulin Signaling and Wnt Signaling Pathways. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1767.	1.8	22
3790	Systematic Analysis of Protein Interaction Network Associated with Azoospermia. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1857.	1.8	14
3791	The Pleiotropic Antibacterial Mechanisms of Ursolic Acid against Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA). <i>Molecules</i> , 2016, 21, 884.	1.7	26
3792	Effects of Maternal Chromium Restriction on the Long-Term Programming in MAPK Signaling Pathway of Lipid Metabolism in Mice. <i>Nutrients</i> , 2016, 8, 488.	1.7	16
3793	Differential effect of mild and severe pulmonary embolism on the rat lung transcriptome. <i>Respiratory Research</i> , 2016, 17, 86.	1.4	9
3794	Behavioral and molecular studies of quantitative differences in hygienic behavior in honeybees. <i>BMC Research Notes</i> , 2016, 9, 474.	0.6	11
3795	Low expression levels of putative HPV encoded microRNAs in cervical samples. <i>SpringerPlus</i> , 2016, 5, 1856.	1.2	17
3796	Network Topology Analysis of Post-Mortem Brain Microarrays Identifies More Alzheimer's™ Related Genes and MicroRNAs and Points to Novel Routes for Fighting with the Disease. <i>PLoS ONE</i> , 2016, 11, e0144052.	1.1	25
3797	Context Specific and Differential Gene Co-expression Networks via Bayesian Biclustering. <i>PLoS Computational Biology</i> , 2016, 12, e1004791.	1.5	46
3798	Comparative Transcriptomic and Epigenomic Analyses Reveal New Regulators of Murine Brown Adipogenesis. <i>PLoS Genetics</i> , 2016, 12, e1006474.	1.5	44
3799	Low Dose Iron Treatments Induce a DNA Damage Response in Human Endothelial Cells within Minutes. <i>PLoS ONE</i> , 2016, 11, e0147990.	1.1	39

#	ARTICLE	IF	CITATIONS
3800	Association of MicroRNA-196a2 Variant with Response to Short-Acting $\beta_2$ -Agonist in COPD: An Egyptian Pilot Study. <i>PLoS ONE</i> , 2016, 11, e0152834.	1.1	31
3801	WDR76 Co-Localizes with Heterochromatin Related Proteins and Rapidly Responds to DNA Damage. <i>PLoS ONE</i> , 2016, 11, e0155492.	1.1	27
3802	Gene Expression Differences in Peripheral Blood of Parkinson's Disease Patients with Distinct Progression Profiles. <i>PLoS ONE</i> , 2016, 11, e0157852.	1.1	36
3803	Microdialysis Sampling from Wound Fluids Enables Quantitative Assessment of Cytokines, Proteins, and Metabolites Reveals Bone Defect-Specific Molecular Profiles. <i>PLoS ONE</i> , 2016, 11, e0159580.	1.1	17
3804	Transcriptional Profiling of Cultured, Embryonic Epicardial Cells Identifies Novel Genes and Signaling Pathways Regulated by TGF $\beta$ 3 In Vitro. <i>PLoS ONE</i> , 2016, 11, e0159710.	1.1	19
3805	Endothelial-Specific EphA4 Negatively Regulates Native Pial Collateral Formation and Re-Perfusion following Hindlimb Ischemia. <i>PLoS ONE</i> , 2016, 11, e0159930.	1.1	17
3806	DNA Damage Response Is Involved in the Developmental Toxicity of Mebendazole in Zebrafish Retina. <i>Frontiers in Pharmacology</i> , 2016, 7, 57.	1.6	31
3807	Aliskiren Administration during Early Postnatal Life Sex-Specifically Alleviates Hypertension Programmed by Maternal High Fructose Consumption. <i>Frontiers in Physiology</i> , 2016, 7, 299.	1.3	36
3808	Circadian Oscillation of the Lettuce Transcriptome under Constant Light and Light-Dark Conditions. <i>Frontiers in Plant Science</i> , 2016, 7, 1114.	1.7	23
3809	Epigenetics in Schizophrenia: A Pilot Study of Global DNA Methylation in Different Brain Regions Associated with Higher Cognitive Functions. <i>Frontiers in Psychology</i> , 2016, 7, 1496.	1.1	35
3810	Epigenetic Profiling of H3K4Me3 Reveals Herbal Medicine Jinfukang-Induced Epigenetic Alteration Is Involved in Anti-Lung Cancer Activity. <i>Evidence-based Complementary and Alternative Medicine</i> , 2016, 1-13.	0.5	16
3811	Network pharmacology-based identification of key pharmacological pathways of Yin-Huang-Qing-Fei capsule acting on chronic bronchitis. <i>International Journal of COPD</i> , 2017, Volume 12, 85-94.	0.9	80
3812	Calcineurin complex isolated from T-cell acute lymphoblastic leukemia (T-ALL) cells identifies new signaling pathways including mTOR/AKT/S6K whose inhibition synergize with calcineurin inhibition to promote T-ALL cell death. <i>Oncotarget</i> , 2016, 7, 45715-45729.	0.8	16
3813	Functional Genomic Analyses Identify Pathways Dysregulated in Animal Model of Autism. <i>CNS Neuroscience and Therapeutics</i> , 2016, 22, 845-853.	1.9	22
3814	Genetic and epigenetic methylation defects and implication of the ERMN gene in autism spectrum disorders. <i>Translational Psychiatry</i> , 2016, 6, e855-e855.	2.4	36
3815	Using PSEA-Quant for Protein Set Enrichment Analysis of Quantitative Mass Spectrometry-Based Proteomics. <i>Current Protocols in Bioinformatics</i> , 2016, 53, 13.28.1-13.28.16.	25.8	8
3816	Suppression of SPIN1-mediated PI3K-Akt pathway by miR-489 increases chemosensitivity in breast cancer. <i>Journal of Pathology</i> , 2016, 239, 459-472.	2.1	97
3817	Interaction and localization diversities of global and local hubs in human protein-protein interaction networks. <i>Molecular BioSystems</i> , 2016, 12, 2875-2882.	2.9	10

#	ARTICLE	IF	CITATIONS
3818	Transcriptomic investigation of meat tenderness in two Italian cattle breeds. <i>Animal Genetics</i> , 2016, 47, 273-287.	0.6	37
3819	Multipronged functional proteomics approaches for global identification of altered cell signalling pathways in B cell chronic lymphocytic leukaemia. <i>Proteomics</i> , 2016, 16, 1193-1203.	1.3	15
3820	Investigation of potential molecular biomarkers and small molecule drugs for hepatocellular carcinoma transformed from cirrhosis. <i>Oncology Letters</i> , 2016, 12, 495-503.	0.8	1
3821	Extracellular microvesicle microRNA in children with sickle cell anaemia with divergent clinical phenotypes. <i>British Journal of Haematology</i> , 2016, 174, 786-798.	1.2	44
3822	MicroRNA signatures characterizing caste-independent ovarian activity in queen and worker honeybees ( <i>Apis mellifera</i> L.). <i>Insect Molecular Biology</i> , 2016, 25, 216-226.	1.0	39
3823	Feature Subset Selection for Cancer Classification Using Weight Local Modularity. <i>Scientific Reports</i> , 2016, 6, 34759.	1.6	17
3824	Tocotrienols induce endoplasmic reticulum stress and apoptosis in cervical cancer cells. <i>Genes and Nutrition</i> , 2016, 11, 32.	1.2	23
3825	hTERT promotes cell adhesion and migration independent of telomerase activity. <i>Scientific Reports</i> , 2016, 6, 22886.	1.6	45
3826	Nucleolin interacts with influenza A nucleoprotein and contributes to viral ribonucleoprotein complexes nuclear trafficking and efficient influenza viral replication. <i>Scientific Reports</i> , 2016, 6, 29006.	1.6	29
3827	Functional genomics analyses of RNA-binding proteins reveal the splicing regulator SNRPB as an oncogenic candidate in glioblastoma. <i>Genome Biology</i> , 2016, 17, 125.	3.8	83
3828	Transcriptome sequencing of the choroid plexus in schizophrenia. <i>Translational Psychiatry</i> , 2016, 6, e964-e964.	2.4	50
3829	Microarray analysis of differentially-expressed genes and linker genes associated with the molecular mechanism of colorectal cancer. <i>Oncology Letters</i> , 2016, 12, 3250-3258.	0.8	19
3830	Microbiota Diurnal Rhythmicity Programs Host Transcriptome Oscillations. <i>Cell</i> , 2016, 167, 1495-1510.e12.	13.5	591
3831	Comprehensive genomic characterization of five canine lymphoid tumor cell lines. <i>BMC Veterinary Research</i> , 2016, 12, 207.	0.7	5
3832	Gene-set-based inference of biological network topologies from big molecular profiling data. , 0, 391-408.		0
3833	Large-scale correlation mining for biomolecular network discovery. , 2016, , 409-436.		1
3834	Isoform switching and exon skipping induced by the DNA methylation inhibitor 5-Aza-2'-deoxycytidine. <i>Scientific Reports</i> , 2016, 6, 24545.	1.6	15
3835	Var2GO: a web-based tool for gene variants selection. <i>BMC Bioinformatics</i> , 2016, 17, 376.	1.2	7

#	ARTICLE	IF	CITATIONS
3836	Vascular smooth muscle cell contractile protein expression is increased through protein kinase G-dependent and -independent pathways by glucose-6-phosphate dehydrogenase inhibition and deficiency. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2016, 311, H904-H912.	1.5	22
3837	Elucidation of the molecular mechanisms of anaplastic thyroid carcinoma by integrated miRNA and mRNA analysis. <i>Oncology Reports</i> , 2016, 36, 3005-3013.	1.2	11
3838	The genome-wide role of HSF-1 in the regulation of gene expression in <i>Caenorhabditis elegans</i> . <i>BMC Genomics</i> , 2016, 17, 559.	1.2	133
3839	Cross-tissue Analysis of Gene and Protein Expression in Normal and Cancer Tissues. <i>Scientific Reports</i> , 2016, 6, 24799.	1.6	155
3840	Lrrc75b is a novel negative regulator of C2C12 myogenic differentiation. <i>International Journal of Molecular Medicine</i> , 2016, 38, 1411-1418.	1.8	4
3841	Gene expression differences in Longissimus muscle of Nelore steers genetically divergent for residual feed intake. <i>Scientific Reports</i> , 2016, 6, 39493.	1.6	57
3842	An Atlas of annotations of <i>Hydra vulgaris</i> transcriptome. <i>BMC Bioinformatics</i> , 2016, 17, 360.	1.2	1
3843	Prediction of key genes and miRNAs responsible for loss of muscle force in patients during an acute exacerbation of chronic obstructive pulmonary disease. <i>International Journal of Molecular Medicine</i> , 2016, 38, 1450-1462.	1.8	15
3844	Design of pathway preferential estrogens that provide beneficial metabolic and vascular effects without stimulating reproductive tissues. <i>Science Signaling</i> , 2016, 9, ra53.	1.6	81
3845	Differentially expressed genes in iron-induced prion protein conversion. <i>Biochemical and Biophysical Research Communications</i> , 2016, 480, 734-740.	1.0	1
3846	Patient survival and tumor characteristics associated with CHEK2:p.I157T " findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016, 18, 98.	2.2	39
3847	Dynamic changes in the gene expression profile during rat oral carcinogenesis induced by 4-nitroquinoline 1-oxide. <i>Molecular Medicine Reports</i> , 2016, 13, 2561-2569.	1.1	5
3848	Systematic analysis of the regulatory functions of microRNAs in chicken hepatic lipid metabolism. <i>Scientific Reports</i> , 2016, 6, 31766.	1.6	36
3849	Co-expression analysis and identification of fecundity-related long non-coding RNAs in sheep ovaries. <i>Scientific Reports</i> , 2016, 6, 39398.	1.6	74
3850	Interactomic analysis of REST/NRSF and implications of its functional links with the transcription suppressor TRIM28 during neuronal differentiation. <i>Scientific Reports</i> , 2016, 6, 39049.	1.6	20
3851	Quantitative extracellular matrix proteomics to study mammary and liver tissue microenvironments. <i>International Journal of Biochemistry and Cell Biology</i> , 2016, 81, 223-232.	1.2	89
3852	Genome-wide Long Non-coding RNA Analysis Identified Circulating LncRNAs as Novel Non-invasive Diagnostic Biomarkers for Gynecological Disease. <i>Scientific Reports</i> , 2016, 6, 23343.	1.6	93
3853	Bioinformatics Tools for Proteomics Data Interpretation. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 281-341.	0.8	20

#	ARTICLE	IF	CITATIONS
3854	Genome-wide analysis of DNA methylation in hepatoblastoma tissues. <i>Oncology Letters</i> , 2016, 12, 1529-1534.	0.8	23
3855	A SILAC-Based Method for Quantitative Proteomic Analysis of Intestinal Organoids. <i>Scientific Reports</i> , 2016, 6, 38195.	1.6	24
3856	Towards constructing "Super Gene Sets" regulatory networks. , 2016, , .		1
3857	Identification of novel noncoding transcripts in telomerase-negative yeast using RNA-seq. <i>Scientific Reports</i> , 2016, 6, 19376.	1.6	8
3858	Gene markers of fracture healing in early stage and the regulatory mechanism during the process using microarray analysis. <i>Acta Orthopaedica Et Traumatologica Turcica</i> , 2016, 50, 681-685.	0.3	3
3859	Large-scale rewiring of innate immunity circuitry and microRNA regulation during initial rice blast infection. <i>Scientific Reports</i> , 2016, 6, 25493.	1.6	27
3860	Generation of 2,000 breast cancer metabolic landscapes reveals a poor prognosis group with active serotonin production. <i>Scientific Reports</i> , 2016, 6, 19771.	1.6	30
3861	Integrating network, sequence and functional features using machine learning approaches towards identification of novel Alzheimer genes. <i>BMC Genomics</i> , 2016, 17, 807.	1.2	30
3862	Functional analysis of keratinocyte and fibroblast gene expression in skin and keloid scar tissue based on deviation analysis of dynamic capabilities. <i>Experimental and Therapeutic Medicine</i> , 2016, 12, 3633-3641.	0.8	13
3863	Network analysis of human post-mortem microarrays reveals novel genes, microRNAs, and mechanistic scenarios of potential importance in fighting huntington's disease. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 117-130.	1.9	24
3864	Biostatistics, Data Mining and Computational Modeling. <i>Translational Bioinformatics</i> , 2016, , 23-57.	0.0	2
3865	HSPA6 is an ulcerative colitis susceptibility factor that is induced by cigarette smoke and protects intestinal epithelial cells by stabilizing anti-apoptotic Bcl-XL. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 788-796.	1.8	16
3866	Bioinformatics Based Approaches to Study Virus-Host Interactions During Chikungunya Virus Infection. <i>Methods in Molecular Biology</i> , 2016, 1426, 195-200.	0.4	1
3867	Common integration sites of published datasets identified using a graph-based framework. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 87-90.	1.9	2
3868	An examination of the regulatory mechanism of Pxdn mutation-induced eye disorders using microarray analysis. <i>International Journal of Molecular Medicine</i> , 2016, 37, 1449-1456.	1.8	5
3869	Characterization of the Antigen Processing Machinery and Endogenous Peptide Presentation of a Bat MHC Class I Molecule. <i>Journal of Immunology</i> , 2016, 196, 4468-4476.	0.4	30
3870	Genomic Landscape of Colorectal Mucosa and Adenomas. <i>Cancer Prevention Research</i> , 2016, 9, 417-427.	0.7	65
3871	Altered gene expression in the lower respiratory tract of Car6 <sup>+/+</sup> mice. <i>Transgenic Research</i> , 2016, 25, 649-664.	1.3	7

#	ARTICLE	IF	CITATIONS
3872	Endometrial transcriptional profiling of a bovine fertility model by Next-Generation Sequencing. <i>Genomics Data</i> , 2016, 7, 26-28.	1.3	4
3873	Megakaryocytic Maturation in Response to Shear Flow Is Mediated by the Activator Protein 1 (AP-1) Transcription Factor via Mitogen-activated Protein Kinase (MAPK) Mechanotransduction. <i>Journal of Biological Chemistry</i> , 2016, 291, 7831-7843.	1.6	21
3874	Evolution of a transcriptional regulator from a transmembrane nucleoporin. <i>Genes and Development</i> , 2016, 30, 1155-1171.	2.7	34
3875	Interactive Visualization of Large Data Sets. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2016, 28, 2142-2157.	4.0	54
3876	Skeletal muscle transcriptional profiles in two Italian beef breeds, Chianina and Maremmana, reveal breed specific variation. <i>Molecular Biology Reports</i> , 2016, 43, 253-268.	1.0	16
3877	The tumor microenvironment underlies acquired resistance to CSF-1R inhibition in gliomas. <i>Science</i> , 2016, 352, aad3018.	6.0	477
3878	Evidence for embryonic stem-like signature and epithelial-mesenchymal transition features in the spheroid cells derived from lung adenocarcinoma. <i>Tumor Biology</i> , 2016, 37, 11843-11859.	0.8	19
3879	Whole Transcriptome Screening Reveals Myelination Deficits in Dysplastic Human Temporal Neocortex. <i>Cerebral Cortex</i> , 2017, 27, bhv346.	1.6	16
3880	Adipose tissue RNASeq reveals novel gene-nutrient interactions following n-3 PUFA supplementation and evoked inflammation in humans. <i>Journal of Nutritional Biochemistry</i> , 2016, 30, 126-132.	1.9	30
3881	Sevoflurane exerts a more marked influence compared with propofol on gene expression in patients undergoing coronary artery bypass graft surgery. <i>Experimental and Therapeutic Medicine</i> , 2016, 11, 448-454.	0.8	1
3882	Spatio-temporal coordination of cell cycle exit, fusion and differentiation of adult muscle precursors by <i>Drosophila</i> Erect wing (Ewg). <i>Mechanisms of Development</i> , 2016, 141, 109-118.	1.7	5
3883	Using biological networks to integrate, visualize and analyze genomics data. <i>Genetics Selection Evolution</i> , 2016, 48, 27.	1.2	86
3884	Oncomirs miRNA-221/222 and Tumor Suppressors miRNA-199a/195 Are Crucial miRNAs in Liver Cancer: A Systematic Analysis. <i>Digestive Diseases and Sciences</i> , 2016, 61, 2315-2327.	1.1	33
3885	Immunogenic Subtypes of Breast Cancer Delineated by Gene Classifiers of Immune Responsiveness. <i>Cancer Immunology Research</i> , 2016, 4, 600-610.	1.6	86
3886	Understanding the progression of atherosclerosis through gene profiling and co-expression network analysis in Apob tm2Sgy Ldlr tm1Her double knockout mice. <i>Genomics</i> , 2016, 107, 239-247.	1.3	14
3887	The landscape of viral proteomics and its potential to impact human health. <i>Expert Review of Proteomics</i> , 2016, 13, 579-591.	1.3	9
3888	Co-clustering of diseases, genes, and drugs for identification of their related gene modules. , 2016, , .		0
3889	ISL1 and JMJD3 synergistically control cardiac differentiation of embryonic stem cells. <i>Nucleic Acids Research</i> , 2016, 44, 6741-6755.	6.5	40

#	ARTICLE	IF	CITATIONS
3890	The Chromatin Remodeling Complex Chd4/NuRD Controls Striated Muscle Identity and Metabolic Homeostasis. <i>Cell Metabolism</i> , 2016, 23, 881-892.	7.2	68
3891	Transcriptome differences in the rumen of beef steers with variation in feed intake and gain. <i>Gene</i> , 2016, 586, 12-26.	1.0	45
3892	Calcineurin Orchestrates Lateral Transfer of <i>Aspergillus fumigatus</i> during Macrophage Cell Death. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 1127-1139.	2.5	54
3893	Identification of potential therapeutic targets for papillary thyroid carcinoma by bioinformatics analysis. <i>Oncology Letters</i> , 2016, 11, 51-58.	0.8	15
3894	Screening genes associated with melanoma using a combined analysis of mRNA and methylation microarray. <i>Gene Reports</i> , 2016, 4, 53-59.	0.4	1
3895	Altered global gene expression profiles in human gastrointestinal epithelial Caco2 cells exposed to nanosilver. <i>Toxicology Reports</i> , 2016, 3, 262-268.	1.6	6
3896	Transcriptomic profiling of <i>Chamelea gallina</i> from sites along the Abruzzo coast (Italy), subject to periodic localized mortality events. <i>Marine Biology</i> , 2016, 163, 1.	0.7	6
3897	Combined treatment with X-ray irradiation and 5-aminolevulinic acid elicits better transcriptomic response of cell cycle-related factors than X-ray irradiation alone. <i>International Journal of Radiation Biology</i> , 2016, 92, 774-789.	1.0	20
3898	Co-expression network analysis of Down's syndrome based on microarray data. <i>Experimental and Therapeutic Medicine</i> , 2016, 12, 1503-1508.	0.8	25
3899	Identification of key pathways and genes in colorectal cancer using bioinformatics analysis. <i>Medical Oncology</i> , 2016, 33, 111.	1.2	112
3900	Whole blood transcriptional profiling comparison between different milk yield of Chinese Holstein cows using RNA-seq data. <i>BMC Genomics</i> , 2016, 17, 512.	1.2	22
3901	Identification of hub genes and regulatory factors of glioblastoma multiforme subgroups by RNA-seq data analysis. <i>International Journal of Molecular Medicine</i> , 2016, 38, 1170-1178.	1.8	13
3902	The differential expression of alternatively polyadenylated transcripts is a common stress-induced response mechanism that modulates mammalian mRNA expression in a quantitative and qualitative fashion. <i>Rna</i> , 2016, 22, 1441-1453.	1.6	36
3903	Sex differences in renal transcriptome and programmed hypertension in offspring exposed to prenatal dexamethasone. <i>Steroids</i> , 2016, 115, 40-46.	0.8	19
3904	Identification of genes involved in Epstein-Barr virus-associated nasopharyngeal carcinoma. <i>Oncology Letters</i> , 2016, 12, 2375-2380.	0.8	8
3905	Nicosamide As a Potential Nonsteroidal Therapy for Endometriosis That Preserves Reproductive Function in an Experimental Mouse Model. <i>Biology of Reproduction</i> , 2016, 95, 74-74.	1.2	25
3906	Improved pose and affinity predictions using different protocols tailored on the basis of data availability. <i>Journal of Computer-Aided Molecular Design</i> , 2016, 30, 817-828.	1.3	6
3907	SPIRE, a modular pipeline for eQTL analysis of RNA-Seq data, reveals a regulatory hotspot controlling miRNA expression in <i>C. elegans</i> . <i>Molecular BioSystems</i> , 2016, 12, 3447-3458.	2.9	4



#	ARTICLE	IF	CITATIONS
3908	Functional and cellular consequences of covalent target protein modification by furan in rat liver. <i>Toxicology</i> , 2016, 361-362, 49-61.	2.0	11
3909	Advancing Clinical Proteomics via Analysis Based on Biological Complexes: A Tale of Five Paradigms. <i>Journal of Proteome Research</i> , 2016, 15, 3167-3179.	1.8	37
3910	Endochondral Growth Defect and Deployment of Transient Chondrocyte Behaviors Underlie Osteoarthritis Onset in a Natural Murine Model. <i>Arthritis and Rheumatology</i> , 2016, 68, 880-891.	2.9	37
3911	Caspase-related apoptosis genes in gliomas by RNA-seq and bioinformatics analysis. <i>Journal of Clinical Neuroscience</i> , 2016, 33, 259-263.	0.8	6
3912	A chromatin modifier integrates insulin/IGF-1 signalling and dietary restriction to regulate longevity. <i>Aging Cell</i> , 2016, 15, 694-705.	3.0	15
3913	Identification of aldolase A as a potential diagnostic biomarker for colorectal cancer based on proteomic analysis using formalin-fixed paraffin-embedded tissue. <i>Tumor Biology</i> , 2016, 37, 13595-13606.	0.8	40
3914	Multi-scale modeling of <i>Arabidopsis thaliana</i> response to different CO <sub>2</sub> conditions: From gene expression to metabolic flux. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 2-11.	4.1	20
3915	Maternal melatonin or N-acetylcysteine therapy regulates hydrogen sulfide-generating pathway and renal transcriptome to prevent prenatal NG-Nitro-L-arginine-methyl ester (L-NAME)-induced fetal programming of hypertension in adult male offspring. <i>American Journal of Obstetrics and Gynecology</i> , 2016, 215, 636.e1-636.e72.	0.7	59
3916	Comparison of muscle characteristics and underpinning mechanisms between Texel and Ujumqin sheep aged from day 70 to 135 of gestation. <i>Livestock Science</i> , 2016, 192, 8-16.	0.6	0
3917	Application of network construction to estimate functional changes to insulin receptor substrates 1 and 2 in Huh7 cells following infection with the hepatitis C virus. <i>Molecular Medicine Reports</i> , 2016, 14, 2379-2388.	1.1	1
3918	Detection of selection signatures of population-specific genomic regions selected during domestication process in Jinhua pigs. <i>Animal Genetics</i> , 2016, 47, 672-681.	0.6	17
3919	Integrin-10 Dependency Identifies RAC and RICTOR as Therapeutic Targets in High-Grade Myxofibrosarcoma. <i>Cancer Discovery</i> , 2016, 6, 1148-1165.	7.7	62
3920	Comprehensive characterization of tissue-specific circular RNAs in the human and mouse genomes. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw081.	3.2	251
3921	A small molecule inhibitor of mutant IDH2 rescues cardiomyopathy in a 2-hydroxyglutaric aciduria type II mouse model. <i>Journal of Inherited Metabolic Disease</i> , 2016, 39, 807-820.	1.7	11
3922	Foxn1 regulates key target genes essential for T cell development in postnatal thymic epithelial cells. <i>Nature Immunology</i> , 2016, 17, 1206-1215.	7.0	142
3923	Effects of muscular dystrophy, exercise and blocking activin receptor IIB ligands on the unfolded protein response and oxidative stress. <i>Free Radical Biology and Medicine</i> , 2016, 99, 308-322.	1.3	27
3924	Carbonic anhydrase enzymes regulate mast cell-mediated inflammation. <i>Journal of Experimental Medicine</i> , 2016, 213, 1663-1673.	4.2	26
3925	The Spectrum and Regulatory Landscape of Intestinal Innate Lymphoid Cells Are Shaped by the Microbiome. <i>Cell</i> , 2016, 166, 1231-1246.e13.	13.5	465

#	ARTICLE	IF	CITATIONS
3926	Different responses of Caco-2 and MCF-7 cells to silver nanoparticles are based on highly similar mechanisms of action. <i>Nanotoxicology</i> , 2016, 10, 1431-1441.	1.6	49
3927	Insights into the human mesenchymal stromal/stem cell identity through integrative transcriptomic profiling. <i>BMC Genomics</i> , 2016, 17, 944.	1.2	55
3928	Candidate methylated genes in osteoarthritis explored by bioinformatics analysis. <i>Knee</i> , 2016, 23, 1035-1043.	0.8	5
3929	Differentially expressed circulating lncRNAs and mRNA identified by microarray analysis in obese patients. <i>Scientific Reports</i> , 2016, 6, 35421.	1.6	42
3930	The bronchial epithelial cell bacterial microbiome and host response in patients infected with human immunodeficiency virus. <i>BMC Pulmonary Medicine</i> , 2016, 16, 142.	0.8	8
3931	Macrophage Ontogeny Underlies Differences in Tumor-Specific Education in Brain Malignancies. <i>Cell Reports</i> , 2016, 17, 2445-2459.	2.9	450
3932	Diet-Microbiota Interactions Mediate Global Epigenetic Programming in Multiple Host Tissues. <i>Molecular Cell</i> , 2016, 64, 982-992.	4.5	405
3933	Systems-Pharmacology Dissection of Traditional Chinese Medicine Compound Saffron Formula Reveals Multi-scale Treatment Strategy for Cardiovascular Diseases. <i>Scientific Reports</i> , 2016, 6, 19809.	1.6	56
3934	v-Src Oncogene Induces Trop2 Proteolytic Activation via Cyclin D1. <i>Cancer Research</i> , 2016, 76, 6723-6734.	0.4	22
3935	Transcriptome analysis of paired primary colorectal carcinoma and liver metastases reveals fusion transcripts and similar gene expression profiles in primary carcinoma and liver metastases. <i>BMC Cancer</i> , 2016, 16, 539.	1.1	30
3936	FOXO/DAF-16 Activation Slows Down Turnover of the Majority of Proteins in <i>C.Âelegans</i> . <i>Cell Reports</i> , 2016, 16, 3028-3040.	2.9	44
3937	A mouse model of alcoholic liver fibrosis-associated acute kidney injury identifies key molecular pathways. <i>Toxicology and Applied Pharmacology</i> , 2016, 310, 129-139.	1.3	14
3938	The human <i>RHOX</i> gene cluster: target genes and functional analysis of gene variants in infertile men. <i>Human Molecular Genetics</i> , 2016, 25, ddw313.	1.4	25
3939	Reactive Oxygen Species-Associated Molecular Signature Predicts Survival in Patients with Sepsis. <i>Pulmonary Circulation</i> , 2016, 6, 196-201.	0.8	25
3940	Effects of Pharmacological Agents on Human Amniotic Fluid-Derived Stem Cells in Culture. <i>Stem Cells and Development</i> , 2016, 25, 1570-1579.	1.1	2
3941	Expression Profiling Elucidates a Molecular Gene Signature for Pulmonary Hypertension in Sarcoidosis. <i>Pulmonary Circulation</i> , 2016, 6, 465-471.	0.8	10
3942	Analysis of MicroRNA and Transcription Factor Regulation. <i>Lecture Notes in Computer Science</i> , 2016, , 278-284.	1.0	0
3943	Identification of potential therapeutic targets for lung cancer by bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2016, 13, 1975-1982.	1.1	15

#	ARTICLE	IF	CITATIONS
3944	Activation of AIFM2 enhances apoptosis of human lung cancer cells undergoing toxicological stress. <i>Toxicology Letters</i> , 2016, 258, 227-236.	0.4	34
3945	Epigenetic Plasticity Drives Adipogenic and Osteogenic Differentiation of Marrow-derived Mesenchymal Stem Cells. <i>Journal of Biological Chemistry</i> , 2016, 291, 17829-17847.	1.6	150
3946	Chromatin remodeling inactivates activity genes and regulates neural coding. <i>Science</i> , 2016, 353, 300-305.	6.0	96
3947	5-azacytidine induces transcriptome changes in <i>Escherichia coli</i> via DNA methylation-dependent and DNA methylation-independent mechanisms. <i>BMC Microbiology</i> , 2016, 16, 130.	1.3	7
3948	Generation and characterization of rat liver stem cell lines and their engraftment in a rat model of liver failure. <i>Scientific Reports</i> , 2016, 6, 22154.	1.6	50
3949	Differential expression of TGF- $\beta$ 2 superfamily members and role of Smad1/5/9-signalling in chondral versus endochondral chondrocyte differentiation. <i>Scientific Reports</i> , 2016, 6, 36655.	1.6	72
3950	Systemic inoculation of <i>Escherichia coli</i> causes emergency myelopoiesis in zebrafish larval caudal hematopoietic tissue. <i>Scientific Reports</i> , 2016, 6, 36853.	1.6	17
3951	Identification of potential therapeutic targets for colorectal cancer by bioinformatics analysis. <i>Oncology Letters</i> , 2016, 12, 5092-5098.	0.8	23
3952	SOX7 co-regulates Wnt/ $\beta$ -catenin signaling with Axin-2: both expressed at low levels in breast cancer. <i>Scientific Reports</i> , 2016, 6, 26136.	1.6	25
3953	Toward a Reference Gene Catalog of Human Primary Monocytes. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 627-634.	1.0	11
3954	MuSK is a BMP co-receptor that shapes BMP responses and calcium signaling in muscle cells. <i>Science Signaling</i> , 2016, 9, ra87.	1.6	26
3955	Analysis of the molecular mechanism of osteosarcoma using a bioinformatics approach. <i>Oncology Letters</i> , 2016, 12, 3075-3080.	0.8	13
3956	Single-Cell Analysis Uncovers Clonal Acinar Cell Heterogeneity in the Adult Pancreas. <i>Developmental Cell</i> , 2016, 39, 289-301.	3.1	82
3957	Telomere shortening and metabolic compromise underlie dystrophic cardiomyopathy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13120-13125.	3.3	60
3958	Serum microRNA microarray analysis identifies miR-4429 and miR-4689 are potential diagnostic biomarkers for biliary atresia. <i>Scientific Reports</i> , 2016, 6, 21084.	1.6	38
3959	A YY1-dependent increase in aerobic metabolism is indispensable for intestinal organogenesis. <i>Development (Cambridge)</i> , 2016, 143, 3711-3722.	1.2	22
3960	Mechanistic evaluation and transcriptional signature of a glutathione S-transferase omega 1 inhibitor. <i>Nature Communications</i> , 2016, 7, 13084.	5.8	53
3961	Pathogenic landscape of idiopathic male infertility: new insight towards its regulatory networks. <i>Npj Genomic Medicine</i> , 2016, 1, 16023.	1.7	35

#	ARTICLE	IF	CITATIONS
3962	RYR2, PTDSS1 and AREG genes are implicated in a Lebanese population-based study of copy number variation in autism. Scientific Reports, 2016, 6, 19088.	1.6	27
3963	SYVN1, NEDD8, and FBXO2 Proteins Regulate Î”F508 Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) Ubiquitin-mediated Proteasomal Degradation. Journal of Biological Chemistry, 2016, 291, 25489-25504.	1.6	27
3964	Genome-wide DNA methylation analysis identifies candidate epigenetic markers and drivers of hepatocellular carcinoma. Briefings in Bioinformatics, 2018, 19, bbw094.	3.2	53
3965	Discover Mouse Gene Coexpression Landscape Using Dictionary Learning and Sparse Coding. Lecture Notes in Computer Science, 2016, , 63-71.	1.0	0
3966	Transcriptome Analysis on Monocytes from Patients with Neovascular Age-Related Macular Degeneration. Scientific Reports, 2016, 6, 29046.	1.6	32
3967	Identification of circulating protein biomarkers in patients with hepatocellular carcinoma concomitantly infected with chronic hepatitis C virus. Biomarkers, 2016, 22, 1-8.	0.9	14
3968	A restricted period for formation of outer subventricular zone defined by Cdh1 and Trnp1 levels. Nature Communications, 2016, 7, 11812.	5.8	108
3969	Identification of Changes in Gene expression of rats after Sensory and Motor Nerves Injury. Scientific Reports, 2016, 6, 26579.	1.6	6
3970	Long noncoding RNA linc00598 regulates CCND2 transcription and modulates the G1 checkpoint. Scientific Reports, 2016, 6, 32172.	1.6	13
3971	Injury-induced <i>ctgfa</i> directs glial bridging and spinal cord regeneration in zebrafish. Science, 2016, 354, 630-634.	6.0	196
3972	Transcriptional Mechanisms Regulating Pulmonary Epithelial Maturation: A Systems Biology Approach. , 0, , 58-76.		0
3973	iTRAQ-based quantitative proteomic analysis reveals potential early diagnostic markers of clear-cell Renal cell carcinoma. BioScience Trends, 2016, 10, 210-219.	1.1	21
3974	A new strategy for exploring the hierarchical structure of cancers by adaptively partitioning functional modules from gene expression network. Scientific Reports, 2016, 6, 28720.	1.6	13
3975	Mammalian Brain Development is Accompanied by a Dramatic Increase in Bipolar DNA Methylation. Scientific Reports, 2016, 6, 32298.	1.6	13
3976	Transcriptomic signature of high dietary organic selenium supplementation in sheep: A nutrigenomic insight using a custom microarray platform and gene set enrichment analysis <sup>1,2</sup> . Journal of Animal Science, 2016, 94, 3169-3184.	0.2	27
3977	Proposal of Chance Index in Co-occurrence Network. Electronics and Communications in Japan, 2016, 99, 65-73.	0.3	0
3978	Genome-wide association studies of immune, disease and production traits in indigenous chicken ecotypes. Genetics Selection Evolution, 2016, 48, 74.	1.2	36
3979	Most of the tight positional conservation of transcription factor binding sites near the transcription start site reflects their co-localization within regulatory modules. BMC Bioinformatics, 2016, 17, 479.	1.2	1

#	ARTICLE	IF	CITATIONS
3980	Coordinated regulation of hepatic and adipose tissue transcriptomes by the oral administration of an amino acid mixture simulating the larval saliva of <i>Vespa</i> species. <i>Genes and Nutrition</i> , 2016, 11, 21.	1.2	4
3981	Prediction of scaffold proteins based on protein interaction and domain architectures. <i>BMC Bioinformatics</i> , 2016, 17, 220.	1.2	6
3982	Integrated analysis of omics data using microRNA-target mRNA network and PPI network reveals regulation of <i>Gnai1</i> function in the spinal cord of <i>Ews/Ewsr1</i> KO mice. <i>BMC Medical Genomics</i> , 2016, 9, 33.	0.7	4
3983	Potential molecular characteristics in situ in response to repetitive UVB irradiation. <i>Diagnostic Pathology</i> , 2016, 11, 129.	0.9	8
3984	Transcriptomic Profiling of Extracellular RNAs Present in Cerebrospinal Fluid Identifies Differentially Expressed Transcripts in Parkinson's Disease. <i>Journal of Parkinson's Disease</i> , 2016, 6, 109-117.	1.5	40
3985	Focal exposure of limited lung volumes to high-dose irradiation down-regulated organ development-related functions and up-regulated the immune response in mouse pulmonary tissues. <i>BMC Genetics</i> , 2016, 17, 29.	2.7	6
3986	SOHSite: incorporating evolutionary information and physicochemical properties to identify protein S-sulfonylation sites. <i>BMC Genomics</i> , 2016, 17, 9.	1.2	45
3987	Differential co-expression analysis of venous thromboembolism based on gene expression profile data. <i>Experimental and Therapeutic Medicine</i> , 2016, 11, 2193-2200.	0.8	3
3988	Construction and analysis of protein-protein interaction networks based on proteomics data of prostate cancer. <i>International Journal of Molecular Medicine</i> , 2016, 37, 1576-1586.	1.8	35
3989	Identification of genes associated with renal cell carcinoma using gene expression profiling analysis. <i>Oncology Letters</i> , 2016, 12, 73-78.	0.8	18
3990	Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, W90-W97.	6.5	7,240
3991	Understanding tissue-specificity with human tissue-specific regulatory networks. <i>Science China Information Sciences</i> , 2016, 59, 1.	2.7	11
3992	Rare variants in known and novel candidate genes predisposing to statin-associated myopathy. <i>Pharmacogenomics</i> , 2016, 17, 1405-1414.	0.6	17
3993	Identification of key genes in glioblastoma-associated stromal cells using bioinformatics analysis. <i>Oncology Letters</i> , 2016, 11, 3999-4007.	0.8	11
3994	Chicken cecal microRNAs in the response to <i>Campylobacter jejuni</i> inoculation by Solexa sequencing. <i>Poultry Science</i> , 2016, 95, 2819-2823.	1.5	5
3995	Hypothalamic Proteomic Analysis Reveals Dysregulation of Glutamate Balance and Energy Metabolism in a Mouse Model of Chronic Mild Stress-Induced Depression. <i>Neurochemical Research</i> , 2016, 41, 2443-2456.	1.6	44
3996	A systematic exploration of the associations between amino acid variants and post-translational modifications. <i>Neurocomputing</i> , 2016, 206, 13-18.	3.5	1
3997	Microarray data on altered transcriptional program of <i>Phgdh</i> -deficient mouse embryonic fibroblasts caused by $\beta$ -serine depletion. <i>Data in Brief</i> , 2016, 7, 1598-1601.	0.5	4

#	ARTICLE	IF	CITATIONS
3998	microRNAs in the Same Clusters Evolve to Coordinately Regulate Functionally Related Genes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2232-2247.	3.5	150
3999	Key genes and pathways predicted in papillary thyroid carcinoma based on bioinformatics analysis. <i>Journal of Endocrinological Investigation</i> , 2016, 39, 1285-1293.	1.8	17
4000	Transcriptomic analysis of porcine PBMCs infected with <i>Toxoplasma gondii</i> RH strain. <i>Acta Tropica</i> , 2016, 154, 82-88.	0.9	38
4001	Identification of novel gene and pathway targets for human epilepsy treatment. <i>Biological Research</i> , 2016, 49, 3.	1.5	10
4002	A Thermodynamic-Based Interpretation of Protein Expression Heterogeneity in Different Glioblastoma Multiforme Tumors Identifies Tumor-Specific Unbalanced Processes. <i>Journal of Physical Chemistry B</i> , 2016, 120, 5990-5997.	1.2	11
4003	Medoidshift clustering applied to genomic bulk tumor data. <i>BMC Genomics</i> , 2016, 17, 6.	1.2	4
4004	MiR-210 promotes sensory hair cell formation in the organ of corti. <i>BMC Genomics</i> , 2016, 17, 309.	1.2	25
4005	Identification of biological targets of therapeutic intervention for clear cell renal cell carcinoma based on bioinformatics approach. <i>Cancer Cell International</i> , 2016, 16, 16.	1.8	17
4006	Pancreatic cancer cell-derived IGFBP-3 contributes to muscle wasting. <i>Journal of Experimental and Clinical Cancer Research</i> , 2016, 35, 46.	3.5	44
4007	Transcriptional response of porcine skeletal muscle to feeding a linseed-enriched diet to growing pigs. <i>Journal of Animal Science and Biotechnology</i> , 2016, 7, 6.	2.1	17
4008	Candidate genes and pathogenesis investigation for sepsis-related acute respiratory distress syndrome based on gene expression profile. <i>Biological Research</i> , 2016, 49, 25.	1.5	20
4009	Inhibition of MNK pathways enhances cancer cell response to chemotherapy with temozolomide and targeted radionuclide therapy. <i>Cellular Signalling</i> , 2016, 28, 1412-1421.	1.7	48
4010	KeyPathwayMinerWeb: online multi-omics network enrichment. <i>Nucleic Acids Research</i> , 2016, 44, W98-W104.	6.5	45
4011	SPATIAL: A System-level PATHway Impact Analysis approach. <i>Nucleic Acids Research</i> , 2016, 44, 5034-5044.	6.5	18
4012	A Bayesian approach for estimating allele-specific expression from RNA-Seq data with diploid genomes. <i>BMC Genomics</i> , 2016, 17, 2.	1.2	22
4013	Î² <sub>1</sub> mediates prostate cancer cell death induced by combinatorial targeting of the androgen receptor. <i>BMC Cancer</i> , 2016, 16, 141.	1.1	10
4014	The landscape of accessible chromatin in mammalian preimplantation embryos. <i>Nature</i> , 2016, 534, 652-657.	13.7	550
4015	Proteomic profiling of eccrine sweat reveals its potential as a diagnostic biofluid for active tuberculosis. <i>Proteomics - Clinical Applications</i> , 2016, 10, 547-553.	0.8	45

#	ARTICLE	IF	CITATIONS
4016	PCBP1/HNRNP E1 Protects Chromosomal Integrity by Translational Regulation of CDC27. <i>Molecular Cancer Research</i> , 2016, 14, 634-646.	1.5	22
4017	Network motif-based method for identifying coronary artery disease. <i>Experimental and Therapeutic Medicine</i> , 2016, 12, 257-261.	0.8	1
4018	Chemoproteomic Approach to Explore the Target Profile of GPCR ligands: Application to 5-HT <sub>1A</sub> and 5-HT <sub>6</sub> Receptors. <i>Chemistry - A European Journal</i> , 2016, 22, 1313-1321.	1.7	15
4019	Effect of single post-ovulatory administration of mifepristone (RU486) on transcript profile during the receptive period in human endometrium. <i>Reproduction</i> , 2016, 151, 331-349.	1.1	14
4020	Identifying molecular subtypes in human colon cancer using gene expression and DNA methylation microarray data. <i>International Journal of Oncology</i> , 2016, 48, 690-702.	1.4	21
4021	An essential role for UTX in resolution and activation of bivalent promoters. <i>Nucleic Acids Research</i> , 2016, 44, 3659-3674.	6.5	63
4022	Effects of combined progesterone and 17 $\beta$ -estradiol treatment on the transcriptome of cultured human myometrial smooth muscle cells. <i>Physiological Genomics</i> , 2016, 48, 50-61.	1.0	13
4023	Genome-wide methylation profiling identifies novel methylated genes in neuroblastoma tumors. <i>Epigenetics</i> , 2016, 11, 74-84.	1.3	63
4024	High risk of development of renal cell tumor in end-stage kidney disease: the role of microenvironment. <i>Tumor Biology</i> , 2016, 37, 9511-9519.	0.8	9
4025	Mapping the O-Mannose Glycoproteome in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1323-1337.	2.5	61
4026	Quantitative phosphoproteomic analysis of early seed development in rice ( <i>Oryza sativa</i> L.). <i>Plant Molecular Biology</i> , 2016, 90, 249-265.	2.0	38
4027	<i>Mycoplasma</i> Infection Alters Cancer Stem Cell Properties in Vitro. <i>Stem Cell Reviews and Reports</i> , 2016, 12, 156-161.	5.6	13
4028	Comprehensive Transcriptome Analysis of Six Catfish Species from an Altitude Gradient Reveals Adaptive Evolution in Tibetan Fishes. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 141-148.	0.8	49
4029	Analysis of miRNA expression profiling in mouse spleen affected by acute <i>Toxoplasma gondii</i> infection. <i>Infection, Genetics and Evolution</i> , 2016, 37, 137-142.	1.0	47
4030	The impact of oil spill to lung health—Insights from an RNA-seq study of human airway epithelial cells. <i>Gene</i> , 2016, 578, 38-51.	1.0	16
4031	Expression of mitochondria-related genes is elevated in overfeeding-induced goose fatty liver. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2016, 192, 30-37.	0.7	22
4032	Comparative transcriptome analysis of atrial septal defect identifies dysregulated genes during heart septum morphogenesis. <i>Gene</i> , 2016, 575, 303-312.	1.0	19
4033	GeneAnalytics: An Integrative Gene Set Analysis Tool for Next Generation Sequencing, RNAseq and Microarray Data. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 139-151.	1.0	187

#	ARTICLE	IF	CITATIONS
4034	Circulating microRNAs as Potential Biomarkers of Endothelial Dysfunction in Obese Children. <i>Chest</i> , 2016, 149, 786-800.	0.4	66
4035	Mutations in SMG9, Encoding an Essential Component of Nonsense-Mediated Decay Machinery, Cause a Multiple Congenital Anomaly Syndrome in Humans and Mice. <i>American Journal of Human Genetics</i> , 2016, 98, 643-652.	2.6	51
4036	Ancestral vinclozolin exposure alters the epigenetic transgenerational inheritance of sperm small noncoding RNAs. <i>Environmental Epigenetics</i> , 2016, 2, dvw001.	0.9	90
4037	Network-Based Method for Inferring Cancer Progression at the Pathway Level from Cross-Sectional Mutation Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 1036-1044.	1.9	8
4038	Integrated microRNA-gene analysis of coronary artery disease based on miRNA and gene expression profiles. <i>Molecular Medicine Reports</i> , 2016, 13, 3063-3073.	1.1	7
4039	Analysis of differentially expressed proteins in <i>Yersinia enterocolitica</i> -infected HeLa cells. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 562-569.	1.1	8
4040	Transcriptional profiling of cortical versus cancellous bone from mechanically-loaded murine tibiae reveals differential gene expression. <i>Bone</i> , 2016, 86, 22-29.	1.4	59
4041	Transcriptome of early embryonic invasion at implantation sites in a murine model. <i>Reproduction, Fertility and Development</i> , 2016, 28, 1487.	0.1	6
4042	Mood stabilizing drugs regulate transcription of immune, neuronal and metabolic pathway genes in <i>Drosophila</i> . <i>Psychopharmacology</i> , 2016, 233, 1751-1762.	1.5	6
4043	MicroRNAs as early toxicity signatures of doxorubicin in human-induced pluripotent stem cell-derived cardiomyocytes. <i>Archives of Toxicology</i> , 2016, 90, 3087-3098.	1.9	77
4044	Endogenous dendritic cells from the tumor microenvironment support T-ALL growth via IGF1R activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1016-25.	3.3	24
4045	Controlled hydrostatic pressure stress downregulates the expression of ribosomal genes in preimplantation embryos: a possible protection mechanism?. <i>Reproduction, Fertility and Development</i> , 2016, 28, 776.	0.1	4
4046	Multilevel functional genomics data integration as a tool for understanding physiology: a network biology perspective. <i>Journal of Applied Physiology</i> , 2016, 120, 297-309.	1.2	10
4047	<i>Salmonella Typhimurium</i> infection primes a nutriprive mechanism in piglets. <i>Veterinary Microbiology</i> , 2016, 186, 117-125.	0.8	2
4048	Low birth weight associates with hippocampal gene expression. <i>Neuroscience</i> , 2016, 318, 190-205.	1.1	6
4049	Chronic TCDD exposure results in the dysregulation of gene expression in splenic B-lymphocytes and in the impairments in T-cell and B-cell differentiation in mouse model. <i>Journal of Environmental Sciences</i> , 2016, 39, 218-227.	3.2	7
4050	Small RNA and RNA-IP Sequencing Identifies and Validates Novel MicroRNAs in Human Mesenchymal Stem Cells. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 191-198.	1.0	1
4051	A patient with a novel homozygous missense mutation in FTO and concomitant nonsense mutation in CETP. <i>Journal of Human Genetics</i> , 2016, 61, 395-403.	1.1	14



#	ARTICLE	IF	CITATIONS
4052	Proteomics of Urinary Vesicles Links Plakins and Complement to Polycystic Kidney Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2016, 27, 3079-3092.	3.0	58
4053	Can ecological history influence response to pollutants? Transcriptomic analysis of Manila clam collected in different Venice lagoon areas and exposed to heavy metal. <i>Aquatic Toxicology</i> , 2016, 174, 123-133.	1.9	27
4054	Cardiac concentric hypertrophy promoted by activated Met receptor is mitigated in vivo by inhibition of Erk1,2 signalling with Pimasertib. <i>Journal of Molecular and Cellular Cardiology</i> , 2016, 93, 84-97.	0.9	12
4055	Gene expression variability in mammalian embryonic stem cells using single cell RNA-seq data. <i>Computational Biology and Chemistry</i> , 2016, 63, 52-61.	1.1	28
4056	Spermatogenesis Drives Rapid Gene Creation and Masculinization of the X Chromosome in Stalk-Eyed Flies (Diptera). <i>Genome Biology and Evolution</i> , 2016, 8, 896-914.	1.1	9
4057	Identification of genomic biomarkers for anthracycline-induced cardiotoxicity in human iPSC-derived cardiomyocytes: an in vitro repeated exposure toxicity approach for safety assessment. <i>Archives of Toxicology</i> , 2016, 90, 2763-2777.	1.9	87
4058	Mitochondrial iron chelation ameliorates cigarette smoke-induced bronchitis and emphysema in mice. <i>Nature Medicine</i> , 2016, 22, 163-174.	15.2	206
4059	Genetic analysis of the clonal stability of Chinese hamster ovary cells for recombinant protein production. <i>Molecular BioSystems</i> , 2016, 12, 102-109.	2.9	23
4060	Molecular diagnosis: Implications for ophthalmology. <i>Progress in Retinal and Eye Research</i> , 2016, 50, 25-33.	7.3	7
4061	Identification of therapeutic targets for childhood severe asthmatics with DNA microarray. <i>Allergologia Et Immunopathologia</i> , 2016, 44, 76-82.	1.0	3
4062	Review: High-performance computing to detect epistasis in genome scale data sets. <i>Briefings in Bioinformatics</i> , 2016, 17, 368-379.	3.2	39
4063	Targeting downstream transcription factors and epigenetic modifications following Toll-like receptor 7/8 ligation to forestall tissue injury in anti-Ro60 associated heart block. <i>Journal of Autoimmunity</i> , 2016, 67, 36-45.	3.0	19
4064	Membrane gene ontology bias in sequencing and microarray obtained by housekeeping-gene analysis. <i>Gene</i> , 2016, 575, 559-566.	1.0	10
4065	Prognostic factors and genes associated with endometrial cancer based on gene expression profiling by bioinformatics analysis. <i>Archives of Gynecology and Obstetrics</i> , 2016, 293, 1287-1295.	0.8	21
4066	Prediction of the engendering mechanism and specific genes of primary melanoma by bioinformatics analysis. <i>Dermatologica Sinica</i> , 2016, 34, 14-19.	0.2	7
4067	Gene network analysis reveals the association of important functional partners involved in antibiotic resistance: A report on an important pathogenic bacterium <i>Staphylococcus aureus</i> . <i>Gene</i> , 2016, 575, 253-263.	1.0	55
4068	Gene expression in the mammary gland of the tammar wallaby during the lactation cycle reveals conserved mechanisms regulating mammalian lactation. <i>Reproduction, Fertility and Development</i> , 2016, 28, 1241.	0.1	6
4069	Five miRNAs considered as molecular targets for predicting neuroglioma. <i>Tumor Biology</i> , 2016, 37, 1051-1059.	0.8	21

#	ARTICLE	IF	CITATIONS
4070	Heat-shock factor 2 is a suppressor of prostate cancer invasion. <i>Oncogene</i> , 2016, 35, 1770-1784.	2.6	48
4071	Differential activation of immune/inflammatory response-related co-expression modules in the hippocampus across the major psychiatric disorders. <i>Molecular Psychiatry</i> , 2016, 21, 376-385.	4.1	60
4072	Whole-genome association analysis of treatment response in obsessive-compulsive disorder. <i>Molecular Psychiatry</i> , 2016, 21, 270-276.	4.1	49
4073	A survey of current trends in computational drug repositioning. <i>Briefings in Bioinformatics</i> , 2016, 17, 2-12.	3.2	459
4074	Integrated bioinformatics analysis of miRNA expression in osteosarcoma. <i>Artificial Cells, Nanomedicine and Biotechnology</i> , 2017, 45, 936-943.	1.9	25
4075	Role of DNA methylation at the placental <i>RTL1</i> gene locus in type 1 diabetes. <i>Pediatric Diabetes</i> , 2017, 18, 178-187.	1.2	9
4076	Lipid and sterol gene sequence variation in autism and correlates with neurodevelopmental status: A pilot study. <i>European Journal of Molecular and Clinical Medicine</i> , 2017, 2, 137.	0.5	1
4077	Analysis of genomic responses in a rat lung model treated with a humidifier sterilizer containing polyhexamethyleneguanidine phosphate. <i>Toxicology Letters</i> , 2017, 268, 36-43.	0.4	16
4078	Epigenetic silencing and activation of transcription: influence on the radiation sensitivity of glioma cell lines. <i>International Journal of Radiation Biology</i> , 2017, 93, 494-506.	1.0	10
4079	Novel interacting proteins identified by tandem affinity purification coupled to nano LC-MS/MS interact with ribosomal S6 protein kinase 4 (RSK4) and its variant protein (RSK4m). <i>International Journal of Biological Macromolecules</i> , 2017, 96, 421-428.	3.6	7
4080	Intestinal Farnesoid X Receptor Controls Transintestinal Cholesterol Excretion in Mice. <i>Gastroenterology</i> , 2017, 152, 1126-1138.e6.	0.6	109
4081	Myoblast replication is reduced in the IUGR fetus despite maintained proliferative capacity in vitro. <i>Journal of Endocrinology</i> , 2017, 232, 475-491.	1.2	32
4082	Blockade to pathological remodeling of infarcted heart tissue using a porcupine antagonist. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1649-1654.	3.3	53
4083	Identification of biomarkers of intrahepatic cholangiocarcinoma via integrated analysis of mRNA and miRNA microarray data. <i>Molecular Medicine Reports</i> , 2017, 15, 1051-1056.	1.1	7
4084	Aerosol from Tobacco Heating System 2.2 has reduced impact on mouse heart gene expression compared with cigarette smoke. <i>Food and Chemical Toxicology</i> , 2017, 101, 157-167.	1.8	14
4085	Novel blood-based microRNA biomarker panel for early diagnosis of chronic pancreatitis. <i>Scientific Reports</i> , 2017, 7, 40019.	1.6	44
4086	Construction of an miRNA-regulated drug-pathway network reveals drug repurposing candidates for myasthenia gravis. <i>International Journal of Molecular Medicine</i> , 2017, 39, 268-278.	1.8	13
4087	Identification of the molecular mechanisms underlying dilated cardiomyopathy via bioinformatic analysis of gene expression profiles. <i>Experimental and Therapeutic Medicine</i> , 2017, 13, 273-279.	0.8	10

#	ARTICLE	IF	CITATIONS
4088	Hypercalcemia induces targeted autophagic degradation of aquaporin-2 at the onset of nephrogenic diabetes insipidus. <i>Kidney International</i> , 2017, 91, 1070-1087.	2.6	53
4089	Circadian deep sequencing reveals stress-response genes that adopt robust rhythmic expression during aging. <i>Nature Communications</i> , 2017, 8, 14529.	5.8	112
4090	Distal CpG islands can serve as alternative promoters to transcribe genes with silenced proximal promoters. <i>Genome Research</i> , 2017, 27, 553-566.	2.4	32
4091	Nucleosome repositioning during differentiation of a human myeloid leukemia cell line. <i>Nucleus</i> , 2017, 8, 188-204.	0.6	21
4092	Human enterovirus 71 protein interaction network prompts antiviral drug repositioning. <i>Scientific Reports</i> , 2017, 7, 43143.	1.6	19
4093	Blood Proteomic Profiling in Inherited (ATTRm) and Acquired (ATTRwt) Forms of Transthyretin-Associated Cardiac Amyloidosis. <i>Journal of Proteome Research</i> , 2017, 16, 1659-1668.	1.8	56
4094	Effect of myeloid differentiation primary response gene 88 on expression profiles of genes during the development and progression of Helicobacter-induced gastric cancer. <i>BMC Cancer</i> , 2017, 17, 133.	1.1	20
4095	Involvement of matrix metalloproteinases in chronic Q fever. <i>Clinical Microbiology and Infection</i> , 2017, 23, 487.e7-487.e13.	2.8	10
4096	Identification and characterization of differentially expressed miRNAs in subcutaneous adipose between Wagyu and Holstein cattle. <i>Scientific Reports</i> , 2017, 7, 44026.	1.6	54
4097	Bioinformatics analysis on the differentiation of bone mesenchymal stem cells into osteoblasts and adipocytes. <i>Molecular Medicine Reports</i> , 2017, 15, 1571-1576.	1.1	26
4098	Identification of prognostic genes in kidney renal clear cell carcinoma by RNA-seq data analysis. <i>Molecular Medicine Reports</i> , 2017, 15, 1661-1667.	1.1	43
4099	Drug Response Prediction as a Link Prediction Problem. <i>Scientific Reports</i> , 2017, 7, 40321.	1.6	64
4100	Identification of novel NF- $\kappa$ B transcriptional targets in TNF $\alpha$ -treated HeLa and HepG2 cells. <i>Cell Biology International</i> , 2017, 41, 555-569.	1.4	10
4101	Proteome Analysis of Human Perilymph Using an Intraoperative Sampling Method. <i>Journal of Proteome Research</i> , 2017, 16, 1911-1923.	1.8	59
4102	Analysis of gene expression changes associated with human carcinoma-associated fibroblasts in non-small cell lung carcinoma. <i>Biological Research</i> , 2017, 50, 6.	1.5	20
4103	Identification of miRNA biomarkers of pneumonia using RNA-sequencing and bioinformatics analysis. <i>Experimental and Therapeutic Medicine</i> , 2017, 13, 1235-1244.	0.8	30
4104	TORC1-dependent sumoylation of Rpc82 promotes RNA polymerase III assembly and activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1039-1044.	3.3	38
4105	Proteomic Analyses of Changes in <i>Synechococcus</i> sp. PCC7942 Following UV Stress. <i>Photochemistry and Photobiology</i> , 2017, 93, 1073-1080.	1.3	5

#	ARTICLE	IF	CITATIONS
4106	Therapeutic properties of <i>Scutellaria baicalensis</i> in db/db mice evaluated using Connectivity Map and network pharmacology. <i>Scientific Reports</i> , 2017, 7, 41711.	1.6	19
4107	Activated Platelets Induce Endothelial Cell Activation via an Interleukin-1 $\beta$ Pathway in Systemic Lupus Erythematosus. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2017, 37, 707-716.	1.1	77
4108	Tdp-43 cryptic exons are highly variable between cell types. <i>Molecular Neurodegeneration</i> , 2017, 12, 13.	4.4	63
4109	Dense genotyping of immune-related loci implicates host responses to microbial exposure in Behçet's disease susceptibility. <i>Nature Genetics</i> , 2017, 49, 438-443.	9.4	129
4110	Expression profiling of colorectal cancer cells reveals inhibition of DNA replication licensing by extracellular calcium. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 987-996.	1.9	8
4111	Biochemical Fractionation of Time-Resolved <i>Drosophila</i> Embryos Reveals Similar Transcriptomic Alterations in Replication Checkpoint and Histone mRNA Processing Mutants. <i>Journal of Molecular Biology</i> , 2017, 429, 3264-3279.	2.0	7
4112	Systematic analysis of microarray datasets to identify Parkinson's disease-associated pathways and genes. <i>Molecular Medicine Reports</i> , 2017, 15, 1252-1262.	1.1	19
4113	Intrinsic Subtypes and Gene Expression Profiles in Primary and Metastatic Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2213-2221.	0.4	168
4114	miR-425 regulates inflammatory cytokine production in CD4+ T cells via N-Ras upregulation in primary biliary cholangitis. <i>Journal of Hepatology</i> , 2017, 66, 1223-1230.	1.8	37
4115	Identification of potential drug targets based on a computational biology algorithm for venous thromboembolism. <i>International Journal of Molecular Medicine</i> , 2017, 39, 463-471.	1.8	1
4116	Exploration of bladder cancer molecular mechanisms based on miRNA-mRNA regulatory network. <i>Oncology Reports</i> , 2017, 37, 1461-1468.	1.2	10
4117	TAZ contributes to pulmonary fibrosis by activating profibrotic functions of lung fibroblasts. <i>Scientific Reports</i> , 2017, 7, 42595.	1.6	84
4118	Proteomic Profiling Analysis Reveals a Link between Experimental Autoimmune Uveitis and Complement Activation in Rats. <i>Scandinavian Journal of Immunology</i> , 2017, 85, 331-342.	1.3	9
4119	Identification of Key Gene Modules in Human Osteosarcoma by Co-expression Analysis Weighted Gene Co-expression Network Analysis (WGCNA). <i>Journal of Cellular Biochemistry</i> , 2017, 118, 3953-3959.	1.2	99
4120	H3K4 demethylase KDM5B regulates global dynamics of transcription elongation and alternative splicing in embryonic stem cells. <i>Nucleic Acids Research</i> , 2017, 45, 6427-6441.	6.5	42
4121	Disease biomarker identification from gene network modules for metastasized breast cancer. <i>Scientific Reports</i> , 2017, 7, 1072.	1.6	13
4122	Toxicity of nano- and ionic silver to embryonic stem cells: a comparative toxicogenomic study. <i>Journal of Nanobiotechnology</i> , 2017, 15, 31.	4.2	40
4123	Impact of Neutron Exposure on Global Gene Expression in a Human Peripheral Blood Model. <i>Radiation Research</i> , 2017, 187, 443.	0.7	35

#	ARTICLE	IF	CITATIONS
4124	Global Transcriptomic Profiling of Cortex and Striatum: Cerebral Injury after Ischemia/Reperfusion in a Mouse Model. <i>Journal of Stroke and Cerebrovascular Diseases</i> , 2017, 26, 1622-1634.	0.7	7
4125	Metallothionein 1G promotes the differentiation of HT-29 human colorectal cancer cells. <i>Oncology Reports</i> , 2017, 37, 2633-2651.	1.2	27
4126	WGCNA Application to Proteomic and Metabolomic Data Analysis. <i>Methods in Enzymology</i> , 2017, 585, 135-158.	0.4	244
4127	Transcriptomic Analysis of Host Immune Response in the Skin of Chickens Infected with Marek's Disease Virus. <i>Viral Immunology</i> , 2017, 30, 377-387.	0.6	18
4128	5-methylcytosine promotes mRNA export â€” NSUN2 as the methyltransferase and ALYREF as an m5C reader. <i>Cell Research</i> , 2017, 27, 606-625.	5.7	666
4129	ORIO (Online Resource for Integrative Omics): a web-based platform for rapid integration of next generation sequencing data. <i>Nucleic Acids Research</i> , 2017, 45, 5678-5690.	6.5	11
4130	The Longitudinal Transcriptional Response to Neoadjuvant Chemotherapy with and without Bevacizumab in Breast Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 4662-4670.	3.2	31
4131	Microarray profiling of long non-coding RNAs associated with idiopathic pulmonary arterial hypertension. <i>Experimental and Therapeutic Medicine</i> , 2017, 13, 2657-2666.	0.8	13
4132	Microarray-based screening of differentially expressed genes in glucocorticoid-induced avascular necrosis. <i>Molecular Medicine Reports</i> , 2017, 15, 3583-3590.	1.1	4
4133	Identification of key genes associated with Schmid-type metaphyseal chondrodysplasia based on microarray data. <i>International Journal of Molecular Medicine</i> , 2017, 39, 1428-1436.	1.8	6
4134	Reduction of the tumorigenic potential of human retinoblastoma cell lines by <i>TFF1</i> overexpression involves p53/caspase signaling and miR-18a regulation. <i>International Journal of Cancer</i> , 2017, 141, 549-560.	2.3	38
4135	Dysregulation of MS risk genes and pathways at distinct stages of disease. <i>Neurology: Neuroimmunology and Neuroinflammation</i> , 2017, 4, e337.	3.1	34
4136	Deep sequencing reveals complex mechanisms of microRNA regulation during retinoic acid-induced neuronal differentiation of mesenchymal stem cells. <i>Genomics</i> , 2017, 109, 302-311.	1.3	9
4137	Statistical Analysis of ATM-Dependent Signaling in Quantitative Mass Spectrometry Phosphoproteomics. <i>Methods in Molecular Biology</i> , 2017, 1599, 229-244.	0.4	6
4138	Expression signatures of long non-coding RNA in the substantia nigra of pre-symptomatic mouse model of Parkinson's disease. <i>Behavioural Brain Research</i> , 2017, 331, 123-130.	1.2	24
4139	Overexpression of hsa-miR-939 follows by NGFR down-regulation and apoptosis reduction. <i>Journal of Biosciences</i> , 2017, 42, 23-30.	0.5	5
4140	Identification of Key Gene Modules of Neuropathic Pain by Co-Expression Analysis. <i>Journal of Cellular Biochemistry</i> , 2017, 118, 4436-4443.	1.2	9
4141	STRIP2 Is Indispensable for the Onset of Embryonic Stem Cell Differentiation. <i>Molecular Therapy - Methods and Clinical Development</i> , 2017, 5, 116-129.	1.8	16

#	ARTICLE	IF	CITATIONS
4142	The effect of maternal chromium status on lipid metabolism in female elderly mice offspring and involved molecular mechanism. <i>Bioscience Reports</i> , 2017, 37, .	1.1	6
4143	Integrated analysis of mRNA and miRNA expression profiles in pancreatic ductal adenocarcinoma. <i>Oncology Reports</i> , 2017, 37, 2779-2786.	1.2	11
4144	Reconstruction and analysis of the lncRNA-miRNA-mRNA network based on competitive endogenous RNA reveal functional lncRNAs in rheumatoid arthritis. <i>Molecular BioSystems</i> , 2017, 13, 1182-1192.	2.9	87
4145	Whole genome sequence association and ancestry-informed polygenic profile of EEG alpha in a Native American population. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 435-450.	1.1	5
4146	Cell diversity and network dynamics in photosensitive human brain organoids. <i>Nature</i> , 2017, 545, 48-53.	13.7	933
4147	Comparative analysis of gene expression profiles for several migrating cell types identifies cell migration regulators. <i>Mechanisms of Development</i> , 2017, 148, 40-55.	1.7	15
4148	Methods, Tools and Current Perspectives in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 959-981.	2.5	130
4149	Binge Alcohol Intake After Hypergravity Stress Sustainably Decreases AMPK and Transcription Factors Necessary for Hepatocyte Survival. <i>Alcoholism: Clinical and Experimental Research</i> , 2017, 41, 76-86.	1.4	3
4150	Theobromine Upregulates Osteogenesis by Human Mesenchymal Stem Cells In Vitro and Accelerates Bone Development in Rats. <i>Calcified Tissue International</i> , 2017, 100, 298-310.	1.5	15
4151	A PAM50-Based Chemoendocrine Score for Hormone Receptor-Positive Breast Cancer with an Intermediate Risk of Relapse. <i>Clinical Cancer Research</i> , 2017, 23, 3035-3044.	3.2	28
4152	Construction and analysis of a human testis/sperm-enriched interaction network: Unraveling the PPP1CC2 interactome. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 375-385.	1.1	9
4153	Integrated gene expression profiling and chromatin immunoprecipitation followed by sequencing: Analysis of the C-terminal binding protein in breast cancer. <i>Journal of Obstetrics and Gynaecology Research</i> , 2017, 43, 1472-1480.	0.6	2
4154	A hormonal cue promotes timely follicle cell migration by modulating transcription profiles. <i>Mechanisms of Development</i> , 2017, 148, 56-68.	1.7	19
4155	Integrative analysis of multiple genomic variables using a hierarchical Bayesian model. <i>Bioinformatics</i> , 2017, 33, 3220-3227.	1.8	5
4156	Interaction of reactive astrocytes with type I collagen induces astrocytic scar formation through the integrin-N-cadherin pathway after spinal cord injury. <i>Nature Medicine</i> , 2017, 23, 818-828.	15.2	355
4157	The effect of elevated progesterone levels before oocyte retrieval in women undergoing ovarian stimulation for IVF treatment on the genomic profile of peri-implantation endometrium. <i>Journal of Reproductive Immunology</i> , 2017, 121, 17-25.	0.8	27
4158	Differential gene expression in porcine oviduct during the oestrous cycle. <i>Reproduction, Fertility and Development</i> , 2017, 29, 2387.	0.1	19
4159	Silencing TAK1 alters gene expression signatures in bladder cancer cells. <i>Oncology Letters</i> , 2017, 13, 2975-2981.	0.8	20

#	ARTICLE	IF	CITATIONS
4160	Candidate miRNAs and pathogenesis investigation for hepatocellular carcinoma based on bioinformatics analysis. <i>Oncology Letters</i> , 2017, 13, 3409-3414.	0.8	12
4161	KrÄ1/4ppel-like factors compete for promoters and enhancers to fine-tune transcription. <i>Nucleic Acids Research</i> , 2017, 45, 6572-6588.	6.5	40
4162	Sequence analysis of chromosome 1 revealed different selection patterns between Chinese wild mice and laboratory strains. <i>Molecular Genetics and Genomics</i> , 2017, 292, 1111-1121.	1.0	2
4163	Structural evidence of quercetin multi-target bioactivity: A reverse virtual screening strategy. <i>European Journal of Pharmaceutical Sciences</i> , 2017, 106, 393-403.	1.9	33
4164	Dicer Deficiency Differentially Impacts Microglia of the Developing and Adult Brain. <i>Immunity</i> , 2017, 46, 1030-1044.e8.	6.6	68
4165	Genetics of alcohol consumption in <i>Drosophila melanogaster</i> . <i>Genes, Brain and Behavior</i> , 2017, 16, 675-685.	1.1	17
4166	Cardiac fibroblast transcriptome analyses support a role for interferogenic, profibrotic, and inflammatory genes in anti-SSA/Ro-associated congenital heart block. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2017, 313, H631-H640.	1.5	15
4167	Genome-wide gene expression profiling reveals that CD274 is up-regulated new-onset type 1 diabetes mellitus. <i>Acta Diabetologica</i> , 2017, 54, 757-767.	1.2	15
4168	Inhalation of a racemic mixture (R,S)-linalool by rats experiencing restraint stress alters neuropeptide and MHC class I gene expression in the hypothalamus. <i>Neuroscience Letters</i> , 2017, 653, 314-319.	1.0	13
4169	Precision medicine for hepatocellular carcinoma using molecular pattern diagnostics: results from a preclinical pilot study. <i>Cell Death and Disease</i> , 2017, 8, e2867-e2867.	2.7	8
4170	CONSTANS Imparts DNA Sequence Specificity to the Histone Fold NF-YB/NF-YC Dimer. <i>Plant Cell</i> , 2017, 29, 1516-1532.	3.1	108
4171	Embryonic AP1 Transcription Factor Deficiency Causes a Collodion Baby-Like Phenotype. <i>Journal of Investigative Dermatology</i> , 2017, 137, 1868-1877.	0.3	3
4172	Identifying miRNA-mRNA regulation network of chronic pancreatitis based on the significant functional expression. <i>Medicine (United States)</i> , 2017, 96, e6668.	0.4	24
4173	Downregulation of TRPM7 suppressed migration and invasion by regulating epithelialâmesenchymal transition in prostate cancer cells. <i>Medical Oncology</i> , 2017, 34, 127.	1.2	31
4174	Targeting of super-enhancers and mutant BRAF can suppress growth of BRAF -mutant colon cancer cells via repression of MAPK signaling pathway. <i>Cancer Letters</i> , 2017, 402, 100-109.	3.2	28
4175	Major hnRNP proteins act as general TDP-43 functional modifiers both in <i>Drosophila</i> and human neuronal cells. <i>Nucleic Acids Research</i> , 2017, 45, 8026-8045.	6.5	62
4176	Estrogen Receptor-Î² Modulation of the ERÎ±-p53 Loop Regulating Gene Expression, Proliferation, and Apoptosis in Breast Cancer. <i>Hormones and Cancer</i> , 2017, 8, 230-242.	4.9	39
4177	Data for the generation of RNA spatiotemporal distributions and interpretation of Chk1 and SLBP protein depletion phenotypes during <i>Drosophila</i> embryogenesis. <i>Data in Brief</i> , 2017, 13, 28-31.	0.5	3

#	ARTICLE	IF	CITATIONS
4178	Proteome dynamics during postnatal mouse corpus callosum development. <i>Scientific Reports</i> , 2017, 7, 45359.	1.6	5
4179	G9A performs important roles in the progression of breast cancer through upregulating its targets. <i>Oncology Letters</i> , 2017, 13, 4127-4132.	0.8	3
4180	Bioinformatics analysis of gene expression alterations in microRNA-122 knockout mice with hepatocellular carcinoma. <i>Molecular Medicine Reports</i> , 2017, 15, 3681-3689.	1.1	10
4181	Identification of microRNA biomarkers in the blood of breast cancer patients based on microRNA profiling. <i>Gene</i> , 2017, 619, 10-20.	1.0	80
4182	Omics Approaches to Identify Potential Biomarkers of Inflammatory Diseases in the Focal Adhesion Complex. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 101-109.	3.0	10
4183	The molecular mechanisms of androgen receptor in nephrolithiasis. <i>Gene</i> , 2017, 616, 16-21.	1.0	7
4184	In Silico Approaches Toward Combating Antibiotic Resistance. , 2017, , 577-593.		2
4185	Potentially Important MicroRNAs in Form-Deprivation Myopia Revealed by Bioinformatics Analysis of MicroRNA Profiling. <i>Ophthalmic Research</i> , 2017, 57, 186-193.	1.0	26
4186	Cecal MicroRNAome response to <i>Salmonella enterica</i> serovar Enteritidis infection in White Leghorn Layer. <i>BMC Genomics</i> , 2017, 18, 77.	1.2	31
4187	The Generation and Validation of a 20â€œGenes Model Influencing the Prognosis of Colorectal Cancer. <i>Journal of Cellular Biochemistry</i> , 2017, 118, 3675-3685.	1.2	6
4188	<sc>TFE</sc> 3 regulates wholeâ€œbody energy metabolism in cooperation with <sc>TFEB</sc>. <i>EMBO Molecular Medicine</i> , 2017, 9, 605-621.	3.3	101
4189	Genomeâ€œwide association study of cellâ€œmediated immune response in chicken. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 405-411.	0.8	15
4190	Immunoproteomic identification and characterization of Ni <sup>2+</sup> -regulated proteins implicates Ni <sup>2+</sup> in the induction of monocyte cell death. <i>Cell Death and Disease</i> , 2017, 8, e2684-e2684.	2.7	13
4191	Molecular Evidence for Differential Long-term Outcomes of Early Life Severe Acute Malnutrition. <i>EBioMedicine</i> , 2017, 18, 274-280.	2.7	15
4192	The histone demethylase KDM3A, and its downstream target MCAM, promote Ewing Sarcoma cell migration and metastasis. <i>Oncogene</i> , 2017, 36, 4150-4160.	2.6	56
4193	Recurrent rewiring and emergence of RNA regulatory networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2816-E2825.	3.3	32
4194	Global DNA methylation profiling of manganese-exposed human neuroblastoma SH-SY5Y cells reveals epigenetic alterations in Parkinsonâ€œs disease-associated genes. <i>Archives of Toxicology</i> , 2017, 91, 2629-2641.	1.9	41
4195	Comparative analysis of TCDD-induced AhR-mediated gene expression in human, mouse and rat primary B cells. <i>Toxicology and Applied Pharmacology</i> , 2017, 316, 95-106.	1.3	31



#	ARTICLE	IF	CITATIONS
4196	Effect of different early weaning regimens for calves on adipogenic gene expression in Hanwoo loin at the fattening stage. <i>Livestock Science</i> , 2017, 195, 87-98.	0.6	12
4197	The functional consequences and prognostic value of dosage sensitivity in ovarian cancer. <i>Molecular BioSystems</i> , 2017, 13, 380-391.	2.9	10
4198	Hepatic gene transcription profiles in turbot ( <i>Scophthalmus maximus</i> ) experimentally exposed to heavy fuel oil n° 6 and to styrene. <i>Marine Environmental Research</i> , 2017, 123, 14-24.	1.1	7
4199	Profiling bovine blastocyst microRNAs using deep sequencing. <i>Reproduction, Fertility and Development</i> , 2017, 29, 1545.	0.1	9
4200	Comparative analysis of hepatocellular carcinoma and cirrhosis gene expression profiles. <i>Molecular Medicine Reports</i> , 2017, 15, 380-386.	1.1	16
4201	Identification of potential therapeutic targets for gliomas by bioinformatics analysis. <i>Oncology Letters</i> , 2017, 14, 5203-5210.	0.8	3
4202	Combined analysis of ChIP-seq and gene microarray datasets identify the E2-mediated genes in ER±-dependent manner in osteosarcoma. <i>Oncology Reports</i> , 2017, 38, 2335-2342.	1.2	2
4203	Bivalent complexes of PRC1 with orthologs of BRD4 and MOZ/MORF target developmental genes in <i>Drosophila</i> . <i>Genes and Development</i> , 2017, 31, 1988-2002.	2.7	25
4204	Screening and identification of critical transcription factors involved in the protection of cardiomyocytes against hydrogen peroxide-induced damage by Yixin-shu. <i>Scientific Reports</i> , 2017, 7, 13867.	1.6	13
4205	Network-based analysis of the molecular mechanisms of multiple myeloma and monoclonal gammopathy of undetermined significance. <i>Oncology Letters</i> , 2017, 14, 4167-4175.	0.8	16
4206	Transcriptome profiling and functional analysis of sheep fed with high zinc-supplemented diet: A nutrigenomic approach. <i>Animal Feed Science and Technology</i> , 2017, 234, 195-204.	1.1	11
4207	Relevance of iPSC-derived human PGC-like cells at the surface of embryoid bodies to prechemotaxis migrating PGCs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9913-E9922.	3.3	41
4208	MCbiclust: a novel algorithm to discover large-scale functionally related gene sets from massive transcriptomics data collections. <i>Nucleic Acids Research</i> , 2017, 45, 8712-8730.	6.5	13
4209	Prognostic genes of breast cancer revealed by gene co-expression network analysis. <i>Oncology Letters</i> , 2017, 14, 4535-4542.	0.8	27
4210	Molecular-level effects of acupuncture on depression: a genome-wide transcriptome analysis of pituitary gland in rats exposed to chronic restraint stress. <i>Journal of Traditional Chinese Medicine = Chung I Tsa Chih Ying Wen Pan / Sponsored By All-China Association of Traditional Chinese Medicine, Academy of Traditional Chinese Medicine</i> , 2017, 37, 486-495.	0.4	4
4211	Differential protein-coding gene and long noncoding RNA expression in smoking-related lung squamous cell carcinoma. <i>Thoracic Cancer</i> , 2017, 8, 672-681.	0.8	27
4212	Investigating the mechanisms of papillary thyroid carcinoma using transcriptome analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 5954-5964.	1.1	3
4213	Bi-directional and shared epigenomic signatures following proton and 56Fe irradiation. <i>Scientific Reports</i> , 2017, 7, 10227.	1.6	36

#	ARTICLE	IF	CITATIONS
4214	Therapeutic potential of Bifidobacterium breve strain A1 for preventing cognitive impairment in Alzheimer's disease. Scientific Reports, 2017, 7, 13510.	1.6	270
4215	High rate of translocation-based gene birth on the <i>Drosophila</i> Y chromosome. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11721-11726.	3.3	35
4216	Dynamic and Modularized MicroRNA Regulation and Its Implication in Human Cancers. Scientific Reports, 2017, 7, 13356.	1.6	60
4217	A Problem-Driven Approach for Building a Bioinformatics GraphDB. Lecture Notes in Computer Science, 2017, , 134-144.	1.0	0
4218	Rapid Evolution of Genes Involved in Learning and Energy Metabolism for Domestication of the Laboratory Rat. Molecular Biology and Evolution, 2017, 34, 3148-3153.	3.5	14
4219	Effect of metabolic status on conceptus' maternal interactions on day 19 in dairy cattle: II. Effects on the endometrial transcriptome. Biology of Reproduction, 2017, 97, 413-425.	1.2	19
4220	Increased heme synthesis in yeast induces a metabolic switch from fermentation to respiration even under conditions of glucose repression. Journal of Biological Chemistry, 2017, 292, 16942-16954.	1.6	48
4221	Bioinformatics analysis of gene expression profiling for identification of potential key genes among ischemic stroke. Medicine (United States), 2017, 96, e7564.	0.4	10
4222	CtBP2 is associated with angiogenesis and regulates the apoptosis of prostate cancer cells. Oncology Reports, 2017, 38, 1259-1267.	1.2	7
4223	A systems biology approach to identify microRNAs contributing to cisplatin resistance in human ovarian cancer cells. Molecular BioSystems, 2017, 13, 2268-2276.	2.9	28
4224	Membrane Proteomics of Impaired Energetics and Cytoskeletal Disorganization in Elderly Diet-Induced Diabetic Mice. Journal of Proteome Research, 2017, 16, 3504-3513.	1.8	6
4225	Phosphoproteomics reveals that glycogen synthase kinase-3 phosphorylates multiple splicing factors and is associated with alternative splicing. Journal of Biological Chemistry, 2017, 292, 18240-18255.	1.6	52
4226	High-content siRNA screen of the kinome identifies kinases involved in Git2-induced mesenchymal-epithelial transition. Molecular Biology, 2017, 51, 614-620.	0.4	0
4227	RNA-seq analysis of the kidneys of broiler chickens fed diets containing different concentrations of calcium. Scientific Reports, 2017, 7, 11740.	1.6	16
4228	Postnatal diet remodels hepatic DNA methylation in metabolic pathways established by a maternal high-fat diet. Epigenomics, 2017, 9, 1387-1402.	1.0	22
4229	Screening candidate microRNA-mRNA regulatory pairs for predicting the response to chemoradiotherapy in rectal cancer by a bioinformatics approach. Scientific Reports, 2017, 7, 11312.	1.6	4
4230	Identification of hypoxia-regulated angiogenic genes in colorectal cancer. Biochemical and Biophysical Research Communications, 2017, 493, 461-467.	1.0	15
4231	The non-canonical poly(A) polymerase FAM46C acts as an onco-suppressor in multiple myeloma. Nature Communications, 2017, 8, 619.	5.8	77

#	ARTICLE	IF	CITATIONS
4232	Bioinformatics method identifies potential biomarkers of dilated cardiomyopathy in a human induced pluripotent stem cell-derived cardiomyocyte model. <i>Experimental and Therapeutic Medicine</i> , 2017, 14, 2771-2778.	0.8	10
4233	Transcriptional dysregulation of Interferome in experimental and human Multiple Sclerosis. <i>Scientific Reports</i> , 2017, 7, 8981.	1.6	22
4234	Neuroblastoma patient-derived xenograft cells cultured in stem-cell promoting medium retain tumorigenic and metastatic capacities but differentiate in serum. <i>Scientific Reports</i> , 2017, 7, 10274.	1.6	26
4235	SOCS2 exacerbates myocardial injury induced by ischemia/reperfusion in diabetic mice and H9c2 cells through inhibiting the JAK-STAT-IGF-1 pathway. <i>Life Sciences</i> , 2017, 188, 101-109.	2.0	24
4236	Differential alternative splicing coupled to nonsense-mediated decay of mRNA ensures dietary restriction-induced longevity. <i>Nature Communications</i> , 2017, 8, 306.	5.8	63
4237	Conditional deletion of ELL2 induces murine prostate intraepithelial neoplasia. <i>Journal of Endocrinology</i> , 2017, 235, 123-136.	1.2	12
4238	Global transcriptional regulatory network for <i>Escherichia coli</i> robustly connects gene expression to transcription factor activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10286-10291.	3.3	89
4239	Time-series expression profile analysis of fracture healing in young and old mice. <i>Molecular Medicine Reports</i> , 2017, 16, 4529-4536.	1.1	10
4240	NRF2 deficiency replicates transcriptomic changes in Alzheimer's patients and worsens APP and TAU pathology. <i>Redox Biology</i> , 2017, 13, 444-451.	3.9	161
4241	Transcriptome landscape of human primary monocytes at different sequencing depth. <i>Genomics</i> , 2017, 109, 463-470.	1.3	9
4242	scRNA sequencing in post-mortem human brains of neuropsychiatric disorders. <i>Psychiatry and Clinical Neurosciences</i> , 2017, 71, 663-672.	1.0	14
4243	Systematic analysis of gene expression patterns associated with postmortem interval in human tissues. <i>Scientific Reports</i> , 2017, 7, 5435.	1.6	80
4244	Integrative analysis of mRNA and miRNA expression profiles in oral lichen planus: preliminary results. <i>Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology</i> , 2017, 124, 390-402.e17.	0.2	22
4245	Prognosis genes in gastric adenocarcinoma identified by cross talk genes in disease-related pathways. <i>Molecular Medicine Reports</i> , 2017, 16, 1232-1240.	1.1	10
4246	High-depth, high-accuracy microsatellite genotyping enables precision lung cancer risk classification. <i>Oncogene</i> , 2017, 36, 6383-6390.	2.6	13
4247	ALM1 is an actin-binding protein that suppresses cell migration and micrometastatic dissemination. <i>Nature Communications</i> , 2017, 8, 142.	5.8	36
4248	Transcriptome profiling of monocytes from XLA patients revealed the innate immune function dysregulation due to the BTK gene expression deficiency. <i>Scientific Reports</i> , 2017, 7, 6836.	1.6	19
4249	Virus and dsRNA-triggered transcriptional responses reveal key components of honey bee antiviral defense. <i>Scientific Reports</i> , 2017, 7, 6448.	1.6	97

#	ARTICLE	IF	CITATIONS
4250	T2DiACoD: A Gene Atlas of Type 2 Diabetes Mellitus Associated Complex Disorders. <i>Scientific Reports</i> , 2017, 7, 6892.	1.6	38
4251	Clinical and genomic responses to ultra-short course chemotherapy in spinal tuberculosis. <i>Experimental and Therapeutic Medicine</i> , 2017, 13, 1681-1688.	0.8	3
4252	Angiotensin II regulates phosphorylation of actin-associated proteins in human podocytes. <i>FASEB Journal</i> , 2017, 31, 5019-5035.	0.2	18
4253	Role for High-Affinity IgE Receptor in Prognosis of Lung Adenocarcinoma Patients. <i>Cancer Immunology Research</i> , 2017, 5, 821-829.	1.6	14
4254	Genome-wide transcriptome analysis of hippocampus in rats indicated that TLR/NLR signaling pathway was involved in the pathogenesis of depressive disorder induced by chronic restraint stress. <i>Brain Research Bulletin</i> , 2017, 134, 195-204.	1.4	29
4255	Potential therapeutic targets and small molecular drugs for pediatric B-precursor acute lymphoblastic leukemia treatment based on microarray data. <i>Oncology Letters</i> , 2017, 14, 1543-1549.	0.8	7
4256	An integrated approach to identify critical transcription factors in the protection against hydrogen peroxide-induced oxidative stress by Danhong injection. <i>Free Radical Biology and Medicine</i> , 2017, 112, 480-493.	1.3	17
4257	Transcriptomic characterization of bovine primary cultured hepatocytes; a cross-comparison with a bovine liver and the Madin-Darby bovine kidney cells. <i>Research in Veterinary Science</i> , 2017, 113, 40-49.	0.9	8
4258	Effect of SMYD3 on the microRNA expression profile of MCF-7 breast cancer cells. <i>Oncology Letters</i> , 2017, 14, 1831-1840.	0.8	8
4259	The interplay of matrix metalloproteinase-8, transforming growth factor- $\beta$ 1 and vascular endothelial growth factor-C cooperatively contributes to the aggressiveness of oral tongue squamous cell carcinoma. <i>British Journal of Cancer</i> , 2017, 117, 1007-1016.	2.9	27
4260	Time-series analysis in imatinib-resistant chronic myeloid leukemia K562-cells under different drug treatments. <i>Journal of Huazhong University of Science and Technology [Medical Sciences]</i> , 2017, 37, 621-627.	1.0	4
4261	AP-2 $\beta$ and AP-2 $\gamma$ cooperatively orchestrate homeobox gene expression during branchial arch patterning. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	35
4262	Comparative transcriptomic analysis of endothelial progenitor cells derived from umbilical cord blood and adult peripheral blood: Implications for the generation of induced pluripotent stem cells. <i>Stem Cell Research</i> , 2017, 25, 202-212.	0.3	12
4263	Bioinformatics analysis of gene expression data for the identification of critical genes in breast invasive carcinoma. <i>Molecular Medicine Reports</i> , 2017, 16, 8657-8664.	1.1	4
4264	E2F/DP Prevents Cell-Cycle Progression in Endocycling Fat Body Cells by Suppressing dATM Expression. <i>Developmental Cell</i> , 2017, 43, 689-703.e5.	3.1	21
4265	Co-expression network analysis identified six hub genes in association with progression and prognosis in human clear cell renal cell carcinoma (ccRCC). <i>Genomics Data</i> , 2017, 14, 132-140.	1.3	83
4266	Exome array analysis identifies GPR35 as a novel susceptibility gene for anthracycline-induced cardiotoxicity in childhood cancer. <i>Pharmacogenetics and Genomics</i> , 2017, 27, 445-453.	0.7	22
4267	In silico-based screen synergistic drug combinations from herb medicines: a case using <i>Cistanche tubulosa</i> . <i>Scientific Reports</i> , 2017, 7, 16364.	1.6	17

#	ARTICLE	IF	CITATIONS
4268	Exploration of the mechanism of colorectal cancer metastasis using microarray analysis. <i>Oncology Letters</i> , 2017, 14, 6671-6677.	0.8	13
4269	Effect of Andrographolide on Gene Expression Profile and Intracellular Calcium in Primary Rat Myocardium Microvascular Endothelial Cells. <i>Journal of Cardiovascular Pharmacology</i> , 2017, 70, 369-381.	0.8	7
4270	Deep sequencing and comprehensive expression analysis identifies several molecules potentially related to human poorly differentiated hepatocellular carcinoma. <i>FEBS Open Bio</i> , 2017, 7, 1696-1706.	1.0	17
4271	sPAGM: inferring subpathway activity by integrating gene and miRNA expression-robust functional signature identification for melanoma prognoses. <i>Scientific Reports</i> , 2017, 7, 15322.	1.6	6
4272	Genomic Subtypes of Non-invasive Bladder Cancer with Distinct Metabolic Profile and Female Gender Bias in KDM6A Mutation Frequency. <i>Cancer Cell</i> , 2017, 32, 701-715.e7.	7.7	224
4273	Histone methyltransferase G9a is a key regulator of the starvation-induced behaviors in <i>Drosophila melanogaster</i> . <i>Scientific Reports</i> , 2017, 7, 14763.	1.6	9
4274	Combinatory Evaluation of Transcriptome and Metabolome Profiles of Low Temperature-induced Resistant Ascites Syndrome in Broiler Chickens. <i>Scientific Reports</i> , 2017, 7, 2389.	1.6	5
4275	Systemic analysis of different colorectal cancer cell lines and TCGA datasets identified IGF-1R/EGFR-PPAR-CASPASE axis as important indicator for radiotherapy sensitivity. <i>Gene</i> , 2017, 627, 484-490.	1.0	13
4276	Discover mouse gene coexpression landscapes using dictionary learning and sparse coding. <i>Brain Structure and Function</i> , 2017, 222, 4253-4270.	1.2	7
4277	Modeling cancer driver events in vitro using barrier bypass-clonal expansion assays and massively parallel sequencing. <i>Oncogene</i> , 2017, 36, 6041-6048.	2.6	10
4278	Maternal chromium restriction modulates miRNA profiles related to lipid metabolism disorder in mice offspring. <i>Experimental Biology and Medicine</i> , 2017, 242, 1444-1452.	1.1	10
4279	Scalable FRaC Variants: Anomaly Detection for Precision Medicine. , 2017, , .		0
4280	Oviductal transcriptional profiling of a bovine fertility model by next-generation sequencing. <i>Genomics Data</i> , 2017, 13, 27-29.	1.3	8
4281	Changes of Protein Turnover in Aging <i>Caenorhabditis elegans</i> . <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1621-1633.	2.5	46
4282	Identification and functional analysis of the risk microRNAs associated with cerebral low-grade glioma prognosis. <i>Molecular Medicine Reports</i> , 2017, 16, 1173-1179.	1.1	12
4283	Uterine responses to early pre-attachment embryos in the domestic dog and comparisons with other domestic animal species. <i>Biology of Reproduction</i> , 2017, 97, 197-216.	1.2	22
4284	Comparative proteome analysis between <i>C. briggsae</i> embryos and larvae reveals a role of chromatin modification proteins in embryonic cell division. <i>Scientific Reports</i> , 2017, 7, 4296.	1.6	2
4285	Transcriptomic responses of the liver and adipose tissues to altered carbohydrate-fat ratio in diet: an isoenergetic study in young rats. <i>Genes and Nutrition</i> , 2017, 12, 10.	1.2	9

#	ARTICLE	IF	CITATIONS
4286	NaviGO: interactive tool for visualization and functional similarity and coherence analysis with gene ontology. <i>BMC Bioinformatics</i> , 2017, 18, 177.	1.2	53
4287	Associating transcriptional modules with colon cancer survival through weighted gene co-expression network analysis. <i>BMC Genomics</i> , 2017, 18, 361.	1.2	58
4288	Biological mechanisms discriminating growth rate and adult body weight phenotypes in two Chinese indigenous chicken breeds. <i>BMC Genomics</i> , 2017, 18, 469.	1.2	12
4289	RNAi reveals proteins for metabolism and protein processing associated with Langkat virus infection in <i>Ixodes scapularis</i> (black-legged tick) ISE6 cells. <i>Parasites and Vectors</i> , 2017, 10, 24.	1.0	30
4290	SMYD5 regulates H4K20me3-marked heterochromatin to safeguard ES cell self-renewal and prevent spurious differentiation. <i>Epigenetics and Chromatin</i> , 2017, 10, 8.	1.8	45
4291	NetProt: Complex-based Feature Selection. <i>Journal of Proteome Research</i> , 2017, 16, 3102-3112.	1.8	16
4292	High motivation for exercise is associated with altered chromatin regulators of monoamine receptor gene expression in the striatum of selectively bred mice. <i>Genes, Brain and Behavior</i> , 2017, 16, 328-341.	1.1	33
4293	Correlation of B7-H3 with androgen receptor, immune pathways and poor outcome in prostate cancer: an expression-based analysis. <i>Prostate Cancer and Prostatic Diseases</i> , 2017, 20, 28-35.	2.0	120
4294	Cell Cycle M-Phase Genes Are Highly Upregulated in Anaplastic Thyroid Carcinoma. <i>Thyroid</i> , 2017, 27, 236-252.	2.4	54
4295	The molecular basis of breast cancer pathological phenotypes. <i>Journal of Pathology</i> , 2017, 241, 375-391.	2.1	86
4296	Proteomic analysis of mucopolysaccharidosis I mouse brain with two-dimensional polyacrylamide gel electrophoresis. <i>Molecular Genetics and Metabolism</i> , 2017, 120, 101-110.	0.5	12
4297	Western diet enhances intestinal tumorigenesis in Min/+ mice, associating with mucosal metabolic and inflammatory stress and loss of Apc heterozygosity. <i>Journal of Nutritional Biochemistry</i> , 2017, 39, 126-133.	1.9	12
4298	A Cell Type-Specific Expression Signature Predicts Haploinsufficient Autism-Susceptibility Genes. <i>Human Mutation</i> , 2017, 38, 204-215.	1.1	38
4299	Reciprocal Regulation between the Circadian Clock and Hypoxia Signaling at the Genome Level in Mammals. <i>Cell Metabolism</i> , 2017, 25, 73-85.	7.2	215
4300	Dynamic remodeling of endometrial extracellular matrix regulates embryo receptivity in cattle. <i>Reproduction</i> , 2017, 153, 49-61.	1.1	25
4301	Network-based expression analysis reveals key genes related to glucocorticoid resistance in infant acute lymphoblastic leukemia. <i>Cellular Oncology (Dordrecht)</i> , 2017, 40, 33-45.	2.1	21
4302	Genetic and hormonal control of hepatic steatosis in female and male mice. <i>Journal of Lipid Research</i> , 2017, 58, 178-187.	2.0	46
4303	Machine learning techniques to discover genes with potential prognosis role in Alzheimer's disease using different biological sources. <i>Information Fusion</i> , 2017, 36, 114-129.	11.7	22

#	ARTICLE	IF	CITATIONS
4304	Liver p53 is stabilized upon starvation and required for amino acid catabolism and gluconeogenesis. <i>FASEB Journal</i> , 2017, 31, 732-742.	0.2	55
4305	The Value of a Novel Panel of Cervical Cancer Biomarkers for Triage of HPV Positive Patients and for Detecting Disease Progression. <i>Pathology and Oncology Research</i> , 2017, 23, 295-305.	0.9	10
4306	Genome-wide genetic variation discovery in Chinese Taihu pig breeds using next generation sequencing. <i>Animal Genetics</i> , 2017, 48, 38-47.	0.6	27
4307	Identified key genes related to carotid atheroma plaque from gene expression chip. <i>Artificial Cells, Nanomedicine and Biotechnology</i> , 2017, 45, 1132-1137.	1.9	4
4308	Identification of genes and proteins associated with anagen wool growth. <i>Animal Genetics</i> , 2017, 48, 67-79.	0.6	10
4309	Combined Analysis of ChIP Sequencing and Gene Expression Dataset in Breast Cancer. <i>Pathology and Oncology Research</i> , 2017, 23, 361-368.	0.9	14
4310	CCAR2 Is Required for Proliferation and Tumor Maintenance in Human Squamous Cell Carcinoma. <i>Journal of Investigative Dermatology</i> , 2017, 137, 506-512.	0.3	17
4311	Downregulation of lysosomal and further gene expression characterization in lung cancer patients with bone metastasis. <i>Artificial Cells, Nanomedicine and Biotechnology</i> , 2017, 45, 758-764.	1.9	5
4312	Differentially expressed mitochondrial genes in breast cancer cells: Potential new targets for anti-cancer therapies. <i>Gene</i> , 2017, 596, 45-52.	1.0	18
4313	Rare deleterious mutations are associated with disease in bipolar disorder families. <i>Molecular Psychiatry</i> , 2017, 22, 1009-1014.	4.1	28
4314	Cardiomyogenesis of periodontal ligament-derived stem cells by dynamic tensile strain. <i>Cell and Tissue Research</i> , 2017, 367, 229-241.	1.5	20
4315	Carcinogenic effects of oil dispersants: A KEGG pathway-based RNA-seq study of human airway epithelial cells. <i>Gene</i> , 2017, 602, 16-23.	1.0	11
4316	Aberrant DNA methylation in lymphocytes of children with neurodevelopmental disorders. <i>Russian Journal of Genetics</i> , 2017, 53, 1243-1258.	0.2	1
4317	Biomarkers identification for acute myocardial infarction detection via weighted gene co-expression network analysis. <i>Medicine (United States)</i> , 2017, 96, e8375.	0.4	32
4318	A next generation sequencing based approach to identify extracellular vesicle mediated mRNA transfers between cells. <i>BMC Genomics</i> , 2017, 18, 987.	1.2	19
4319	Identification of key miRNA-gene pairs in chronic lymphocytic leukemia through integrated analysis of mRNA and miRNA microarray. <i>Oncology Letters</i> , 2017, 15, 361-367.	0.8	9
4320	Gene expression profiles and protein-protein interaction networks during tongue carcinogenesis in the tumor microenvironment. <i>Molecular Medicine Reports</i> , 2017, 17, 165-171.	1.1	8
4321	A novel correlation between ATP5A1 gene expression and progression of human clear cell renal cell carcinoma identified by co-expression analysis. <i>Oncology Reports</i> , 2018, 39, 525-536.	1.2	20

#	ARTICLE	IF	CITATIONS
4322	Twenty-four signature genes predict the prognosis of oral squamous cell carcinoma with high accuracy and repeatability. <i>Molecular Medicine Reports</i> , 2018, 17, 2982-2990.	1.1	12
4323	Nup98 recruits the Wdr82-Set1A/COMPASS complex to promoters to regulate H3K4 trimethylation in hematopoietic progenitor cells. <i>Genes and Development</i> , 2017, 31, 2222-2234.	2.7	68
4324	Cysteine-rich angiogenic inducer 61 (Cyr61): a novel soluble biomarker of acute myocardial injury improves risk stratification after acute coronary syndromes. <i>European Heart Journal</i> , 2017, 38, 3493-3502.	1.0	46
4325	SIRT7-dependent deacetylation of CDK9 activates RNA polymerase II transcription. <i>Nucleic Acids Research</i> , 2017, 45, 2675-2686.	6.5	49
4326	ciaR impacts biofilm formation by regulating an arginine biosynthesis pathway in <i>Streptococcus sanguinis</i> SK36. <i>Scientific Reports</i> , 2017, 7, 17183.	1.6	47
4327	Impact of hormonal modulation at proestrus on ovarian responses and uterine gene expression of suckled anestrous beef cows. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 79.	2.1	13
4328	Comparative transcriptomics of 5 high-altitude vertebrates and their low-altitude relatives. <i>GigaScience</i> , 2017, 6, 1-9.	3.3	50
4329	Bioinformatics identification of dysregulated microRNAs in triple negative breast cancer based on microRNA expression profiling. <i>Oncology Letters</i> , 2018, 15, 3017-3023.	0.8	9
4330	Functional enrichment of human protein complexes in malaria parasites. , 2017, , .		0
4331	Identification of common key genes in breast, lung and prostate cancer and exploration of their heterogeneous expression. <i>Oncology Letters</i> , 2017, 15, 1680-1690.	0.8	7
4332	Bioinformatical analysis of gene expression signatures of different glioma subtypes. <i>Oncology Letters</i> , 2017, 15, 2807-2814.	0.8	7
4333	Immunoglobulin superfamily genes are novel prognostic biomarkers for breast cancer. <i>Oncotarget</i> , 2017, 8, 2444-2456.	0.8	7
4334	Transcriptomic pathway analysis of urokinase receptor silenced breast cancer cells: a microarray study. <i>Oncotarget</i> , 2017, 8, 101572-101590.	0.8	13
4335	Interaction of Epstein-Barr virus genes with human gastric carcinoma transcriptome. <i>Oncotarget</i> , 2017, 8, 38399-38412.	0.8	11
4336	Silencing of <i>HJURP</i> induces dysregulation of cell cycle and ROS metabolism in bladder cancer cells via PPAR $\beta$ -SIRT1 feedback loop. <i>Journal of Cancer</i> , 2017, 8, 2282-2295.	1.2	35
4337	A Microarray Study of Carpet-Shell Clam ( <i>Ruditapes decussatus</i> ) Shows Common and Organ-Specific Growth-Related Gene Expression Differences in Gills and Digestive Gland. <i>Frontiers in Physiology</i> , 2017, 8, 943.	1.3	8
4338	Co-expression Network Approach Reveals Functional Similarities among Diseases Affecting Human Skeletal Muscle. <i>Frontiers in Physiology</i> , 2017, 8, 980.	1.3	19
4339	Associations between gene expression profiles of invasive breast cancer and Breast Imaging Reporting and Data System MRI lexicon. <i>Annals of Surgical Treatment and Research</i> , 2017, 93, 18.	0.4	7



#	ARTICLE	IF	CITATIONS
4340	Interspecies NASH disease activity whole-genome profiling identifies a fibrogenic role of PPAR1 $\pm$ -regulated dermatopontin. <i>JCI Insight</i> , 2017, 2, .	2.3	96
4341	Canonical and non-canonical JAK/STAT transcriptional targets may be involved in distinct and overlapping cellular processes. <i>BMC Genomics</i> , 2017, 18, 718.	1.2	11
4342	Exploration of the molecular mechanism of prostate cancer based on mRNA and miRNA expression profiles. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 3225-3232.	1.0	11
4343	Induced Pluripotent Stem Cells: Advances in the Quest for Genetic Stability during Reprogramming Process. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1952.	1.8	45
4344	In-Cardiome: integrated knowledgebase for coronary artery disease enabling translational research. Database: the <i>Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	3
4345	Nuclear Compartmentalization Contributes to Stage-Specific Gene Expression Control in <i>Trypanosoma cruzi</i> . <i>Frontiers in Cell and Developmental Biology</i> , 2017, 5, 8.	1.8	32
4346	Circular RNA expression profiles and features in human tissues: a study using RNA-seq data. <i>BMC Genomics</i> , 2017, 18, 680.	1.2	193
4347	Saliva as a Blood Alternative for Genome-Wide DNA Methylation Profiling by Methylated DNA Immunoprecipitation (MeDIP) Sequencing. <i>Epigenomes</i> , 2017, 1, 14.	0.8	8
4348	The Stearoyl-CoA Desaturase-1 (Desat1) in <i>Drosophila</i> cooperated with Myc to Induce Autophagy and Growth, a Potential New Link to Tumor Survival. <i>Genes</i> , 2017, 8, 131.	1.0	9
4349	Low-Grade Dysplastic Nodules Revealed as the Tipping Point during Multistep Hepatocarcinogenesis by Dynamic Network Biomarkers. <i>Genes</i> , 2017, 8, 268.	1.0	10
4350	The Emerging Role of Zfp217 in Adipogenesis. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1367.	1.8	17
4351	<i>Systems Biology: Methods and Applications</i> . , 2017, , 434-480.		0
4352	Genome-Wide Association Study of Piglet Uniformity and Farrowing Interval. <i>Frontiers in Genetics</i> , 2017, 8, 194.	1.1	37
4353	Human and Epstein-Barr Virus miRNA Profiling as Predictive Biomarkers for Endemic Burkitt Lymphoma. <i>Frontiers in Microbiology</i> , 2017, 8, 501.	1.5	19
4354	Comparative Genomics of <i>Glossina palpalis gambiensis</i> and <i>G. morsitans morsitans</i> to Reveal Gene Orthologs Involved in Infection by <i>Trypanosoma brucei gambiense</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 540.	1.5	6
4355	Quantitative Analysis of Cellular Proteome Alterations in CDV-Infected Mink Lung Epithelial Cells. <i>Frontiers in Microbiology</i> , 2017, 8, 2564.	1.5	1
4356	PI3K and Inhibitor of Apoptosis Proteins Modulate Gentamicin- Induced Hair Cell Death in the Zebrafish Lateral Line. <i>Frontiers in Cellular Neuroscience</i> , 2017, 11, 326.	1.8	20
4357	Combinatorial Ranking of Gene Sets to Predict Disease Relapse: The Retinoic Acid Pathway in Early Prostate Cancer. <i>Frontiers in Oncology</i> , 2017, 7, 30.	1.3	5

#	ARTICLE	IF	CITATIONS
4358	Antidepressant Mechanism Research of Acupuncture: Insights from a Genome-Wide Transcriptome Analysis of Frontal Cortex in Rats with Chronic Restraint Stress. Evidence-based Complementary and Alternative Medicine, 2017, 2017, 1-13.	0.5	24
4359	Circular RNA Profiling and Bioinformatic Modeling Identify Its Regulatory Role in Hepatic Steatosis. BioMed Research International, 2017, 2017, 1-13.	0.9	50
4360	Screening of Tumor Suppressor Genes in Metastatic Colorectal Cancer. BioMed Research International, 2017, 2017, 1-7.	0.9	11
4361	Effects of Radix Astragali and Its Split Components on Gene Expression Profiles Related to Water Metabolism in Rats with the Dampness Stagnancy due to Spleen Deficiency Syndrome. Evidence-based Complementary and Alternative Medicine, 2017, 2017, 1-10.	0.5	16
4362	Global transcriptome-wide analysis of the function of GDDR in acute gastric lesions. Molecular Medicine Reports, 2017, 16, 8673-8684.	1.1	3
4363	Knockdown of <i>SIRT1</i> Suppresses Bladder Cancer Cell Proliferation and Migration and Induces Cell Cycle Arrest and Antioxidant Response through FOXO3a-Mediated Pathways. BioMed Research International, 2017, 2017, 1-14.	0.9	38
4364	Diagnostic MicroRNA Biomarker Discovery for Non-Small-Cell Lung Cancer Adenocarcinoma by Integrative Bioinformatics Analysis. BioMed Research International, 2017, 2017, 1-9.	0.9	28
4365	An Integrative Developmental Genomics and Systems Biology Approach to Identify an In Vivo Sox Trio-Mediated Gene Regulatory Network in Murine Embryos. BioMed Research International, 2017, 2017, 1-16.	0.9	11
4366	Biomarker MicroRNAs for Diagnosis of Oral Squamous Cell Carcinoma Identified Based on Gene Expression Data and MicroRNA-mRNA Network Analysis. Computational and Mathematical Methods in Medicine, 2017, 2017, 1-8.	0.7	16
4367	The Identification of Key Genes and Pathways in Glioma by Bioinformatics Analysis. Journal of Immunology Research, 2017, 2017, 1-9.	0.9	39
4368	A New Network-Based Strategy for Predicting the Potential miRNA-mRNA Interactions in Tumorigenesis. International Journal of Genomics, 2017, 2017, 1-11.	0.8	5
4369	Fish Oil Feeding Modulates the Expression of Hepatic MicroRNAs in a Western-Style Diet-Induced Nonalcoholic Fatty Liver Disease Rat Model. BioMed Research International, 2017, 2017, 1-11.	0.9	16
4370	Effects of genistein supplementation on genome-wide DNA methylation and gene expression in patients with localized prostate cancer. International Journal of Oncology, 2017, 51, 223-234.	1.4	61
4371	Identification of Key Transcription Factors Associated with Lung Squamous Cell Carcinoma. Medical Science Monitor, 2017, 23, 172-206.	0.5	25
4372	Identification of lncRNAs involved in biological regulation in early age-related macular degeneration. International Journal of Nanomedicine, 2017, Volume 12, 7589-7602.	3.3	30
4373	Clinical Value and Prospective Pathway Signaling of MicroRNA-375 in Lung Adenocarcinoma: A Study Based on the Cancer Genome Atlas (TCGA), Gene Expression Omnibus (GEO) and Bioinformatics Analysis. Medical Science Monitor, 2017, 23, 2453-2464.	0.5	40
4374	Glycosylation-related gene expression in HT29-MTX-E12 cells upon infection by Helicobacter pylori. World Journal of Gastroenterology, 2017, 23, 6817-6832.	1.4	16
4375	Positioning of Tacrolimus for the Treatment of Diabetic Nephropathy Based on Computational Network Analysis. PLoS ONE, 2017, 12, e0169518.	1.1	6

#	ARTICLE	IF	CITATIONS
4376	Ancestry as a potential modifier of gene expression in breast tumors from Colombian women. PLoS ONE, 2017, 12, e0183179.	1.1	18
4377	MicroRNA-223 and microRNA-21 in peripheral blood B cells associated with progression of primary biliary cholangitis patients. PLoS ONE, 2017, 12, e0184292.	1.1	16
4378	Large-scale cross-species chemogenomic platform proposes a new drug discovery strategy of veterinary drug from herbal medicines. PLoS ONE, 2017, 12, e0184880.	1.1	7
4379	Transcriptome analysis of genes involved in defense against alkaline stress in roots of wild jujube ( <i>Ziziphus acidujuba</i> ). PLoS ONE, 2017, 12, e0185732.	1.1	29
4380	Network analysis based on TCGA reveals hub genes in colon cancer. Wspolczesna Onkologia, 2017, 2, 136-144.	0.7	11
4381	Novel linear motif filtering protocol reveals the role of the LC8 dynein light chain in the Hippo pathway. PLoS Computational Biology, 2017, 13, e1005885.	1.5	20
4382	Evidence of high-altitude adaptation in the glyptosternoid fish, <i>Creteuchiloglanis macropterus</i> from the Nujiang River obtained through transcriptome analysis. BMC Evolutionary Biology, 2017, 17, 229.	3.2	33
4383	First gene-ontology enrichment analysis based on bacterial coregenome variants: insights into adaptations of <i>Salmonella</i> serovars to mammalian- and avian-hosts. BMC Microbiology, 2017, 17, 222.	1.3	41
4384	Integrative microRNA and mRNA deep-sequencing expression profiling in endemic Burkitt lymphoma. BMC Cancer, 2017, 17, 761.	1.1	22
4385	In vitro characterization of CD133lo cancer stem cells in Retinoblastoma Y79 cell line. BMC Cancer, 2017, 17, 779.	1.1	20
4386	Aberrantly methylated-differentially expressed genes and pathways in colorectal cancer. Cancer Cell International, 2017, 17, 75.	1.8	65
4387	MHC class II expression and potential antigen-presenting cells in the retina during experimental autoimmune uveitis. Journal of Neuroinflammation, 2017, 14, 136.	3.1	46
4388	A network pharmacology-based strategy deciphers the underlying molecular mechanisms of Qixuehe Capsule in the treatment of menstrual disorders. Chinese Medicine, 2017, 12, 23.	1.6	36
4389	OCDD: an obesity and co-morbid disease database. BioData Mining, 2017, 10, 33.	2.2	10
4390	Serum microRNA array analysis identifies miR-140-3p, miR-33b-3p and miR-671-3p as potential osteoarthritis biomarkers involved in metabolic processes. Clinical Epigenetics, 2017, 9, 127.	1.8	114
4391	Deciphering Gene Sets Annotations with Ontology Based Visualization. , 2017, , .		1
4392	Maternal chromium restriction induces insulin resistance in adult mice offspring through miRNA. International Journal of Molecular Medicine, 2018, 41, 1547-1559.	1.8	15
4393	DEXseq and Cuffdiff approaches weighing differential spliced genes exons modulation in estrogen receptor (Er) breast cancer cells. African Journal of Biotechnology, 2017, 16, 1404-1427.	0.3	0

#	ARTICLE	IF	CITATIONS
4394	Long non-coding RNA associated-competing endogenous RNAs are induced by clusterin in retinal pigment epithelial cells. <i>Molecular Medicine Reports</i> , 2017, 16, 8399-8405.	1.1	10
4395	Identification of the anticancer effects of a novel proteasome inhibitor, ixazomib, on colorectal cancer using a combined method of microarray and bioinformatics analysis. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 3591-3606.	1.0	13
4396	The genomic architecture of mastitis resistance in dairy sheep. <i>BMC Genomics</i> , 2017, 18, 624.	1.2	59
4397	Identification of microRNAs in acute respiratory distress syndrome based on microRNA expression profile in rats. <i>Molecular Medicine Reports</i> , 2017, 16, 3357-3362.	1.1	7
4398	Promiscuous DNA-binding of a mutant zinc finger protein corrupts the transcriptome and diminishes cell viability. <i>Nucleic Acids Research</i> , 2017, 45, 1130-1143.	6.5	33
4399	<i>Actinidia chinensis</i> Planch root extract inhibits cholesterol metabolism in hepatocellular carcinoma through upregulation of PCSK9. <i>Oncotarget</i> , 2017, 8, 42136-42148.	0.8	25
4400	CpG methylation patterns are associated with gene expression variation in osteosarcoma. <i>Molecular Medicine Reports</i> , 2017, 16, 901-907.	1.1	12
4401	Screening of FOXD3 targets in lung cancer via bioinformatics analysis. <i>Oncology Letters</i> , 2017, 15, 3214-3220.	0.8	0
4402	Characterization of Cytosine Methylation and the DNA Methyltransferases of <i>Toxoplasma gondii</i> . <i>International Journal of Biological Sciences</i> , 2017, 13, 458-470.	2.6	13
4403	Identification of Key Genes Affecting Results of Hyperthermia in Osteosarcoma Based on Integrative ChIP-Seq/TargetScan Analysis. <i>Medical Science Monitor</i> , 2017, 23, 2042-2048.	0.5	47
4404	Identification of key mRNAs and microRNAs in the pathogenesis and progression of osteoarthritis using microarray analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 5659-5666.	1.1	6
4405	A 16-gene signature predicting prognosis of patients with oral tongue squamous cell carcinoma. <i>PeerJ</i> , 2017, 5, e4062.	0.9	23
4406	The effects of DLEU1 gene expression in Burkitt lymphoma (BL): potential mechanism of chemoimmunotherapy resistance in BL. <i>Oncotarget</i> , 2017, 8, 27839-27853.	0.8	31
4407	Identification of Key Genes and Pathways in Tongue Squamous Cell Carcinoma Using Bioinformatics Analysis. <i>Medical Science Monitor</i> , 2017, 23, 5924-5932.	0.5	40
4408	Nucleosome Positioning of Intronless Genes in the Human Genome. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1111-1121.	1.9	3
4409	Circulating miRNA Profiles Associated With Hyperglycemia in Patients With Type 1 Diabetes. <i>Diabetes</i> , 2018, 67, 1013-1023.	0.3	73
4410	STAT3 is required for proliferation and exhibits a cell type-specific binding preference in mouse female germline stem cells. <i>Molecular Omics</i> , 2018, 14, 95-102.	1.4	9
4411	Overexpression of PIK3CA in head and neck squamous cell carcinoma is associated with poor outcome and activation of the YAP pathway. <i>Oral Oncology</i> , 2018, 79, 55-63.	0.8	54

#	ARTICLE	IF	CITATIONS
4412	Genomic signatures reveal selection of characteristics within and between Meishan pig populations. <i>Animal Genetics</i> , 2018, 49, 119-126.	0.6	19
4413	Cell-type-specific brain methylomes profiled via ultralow-input microfluidics. <i>Nature Biomedical Engineering</i> , 2018, 2, 183-194.	11.6	29
4414	Hyperglycemia drives intestinal barrier dysfunction and risk for enteric infection. <i>Science</i> , 2018, 359, 1376-1383.	6.0	582
4415	Identification of Three Rheumatoid Arthritis Disease Subtypes by Machine Learning Integration of Synovial Histologic Features and <i>scRNA</i> Sequencing Data. <i>Arthritis and Rheumatology</i> , 2018, 70, 690-701.	2.9	157
4416	Thermopriming triggers splicing memory in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2018, 69, 2659-2675.	2.4	119
4417	Extracellular vesicle <i>scRNA</i> s reflect placenta dysfunction and are a biomarker source for preterm labour. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 2760-2773.	1.6	62
4418	Identification of key genes of papillary thyroid cancer using integrated bioinformatics analysis. <i>Journal of Endocrinological Investigation</i> , 2018, 41, 1237-1245.	1.8	31
4419	The Histone Variant MacroH2A Blocks Cellular Reprogramming by Inhibiting Mesenchymal-to-Epithelial Transition. <i>Molecular and Cellular Biology</i> , 2018, 38, .	1.1	13
4420	Comparative proteomic analyses of human adipose extracellular matrices decellularized using alternative procedures. <i>Journal of Biomedical Materials Research - Part A</i> , 2018, 106, 2481-2493.	2.1	37
4421	Evaluation of Animal Models by Comparison with Human Late-Onset Alzheimer's Disease. <i>Molecular Neurobiology</i> , 2018, 55, 9234-9250.	1.9	19
4422	Rationalizing Drug Response in Cancer Cell Lines. <i>Journal of Molecular Biology</i> , 2018, 430, 3016-3027.	2.0	9
4423	Sex steroids drive the remodeling of oviductal extracellular matrix in cattle. <i>Biology of Reproduction</i> , 2018, 99, 590-599.	1.2	8
4424	Identification of Prognostic Biomarkers by Combined mRNA and miRNA Expression Microarray Analysis in Pancreatic Cancer. <i>Translational Oncology</i> , 2018, 11, 700-714.	1.7	40
4425	Dengue virus causes changes of MicroRNA-genes regulatory network revealing potential targets for antiviral drugs. <i>BMC Systems Biology</i> , 2018, 12, 2.	3.0	17
4426	Identification of genes and pathways associated with MDR in MCF-7/MDR breast cancer cells by RNA-seq analysis. <i>Molecular Medicine Reports</i> , 2018, 17, 6211-6226.	1.1	27
4427	Calorie restriction is the most reasonable anti-ageing intervention: a meta-analysis of survival curves. <i>Scientific Reports</i> , 2018, 8, 5779.	1.6	75
4428	Identification of Novel Response and Predictive Biomarkers to Hsp90 Inhibitors Through Proteomic Profiling of Patient-derived Prostate Tumor Explants. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1470-1486.	2.5	26
4429	Gastric cancer biomarkers; A systems biology approach. <i>Biochemistry and Biophysics Reports</i> , 2018, 13, 141-146.	0.7	20

#	ARTICLE	IF	CITATIONS
4430	Widespread modulation of gene expression by copy number variation in skeletal muscle. <i>Scientific Reports</i> , 2018, 8, 1399.	1.6	25
4431	RNA-seq transcriptomic analysis of adult zebrafish inner ear hair cells. <i>Scientific Data</i> , 2018, 5, 180005.	2.4	51
4432	Chemical proteomic profiling of protein N-homocysteinylation with a thioester probe. <i>Chemical Science</i> , 2018, 9, 2826-2830.	3.7	23
4433	Liraglutide protects cardiac function in diabetic rats through the PPAR $\alpha$ pathway. <i>Bioscience Reports</i> , 2018, 38, .	1.1	19
4434	Immune-Related Transcriptional Responses to Parasitic Infection in a Naturally Inbred Fish: Roles of Genotype and Individual Variation. <i>Genome Biology and Evolution</i> , 2018, 10, 319-327.	1.1	10
4435	Identifying potential quality markers of Xin-Su-Ning capsules acting on arrhythmia by integrating UHPLC-LTQ-Orbitrap, ADME prediction and network target analysis. <i>Phytomedicine</i> , 2018, 44, 117-128.	2.3	39
4436	The Mechanisms of Bushen-Yizhi Formula as a Therapeutic Agent against Alzheimer's Disease. <i>Scientific Reports</i> , 2018, 8, 3104.	1.6	46
4437	Interaction of DCF1 with ATP1B1 induces impairment in astrocyte structural plasticity via the P38 signaling pathway. <i>Experimental Neurology</i> , 2018, 302, 214-229.	2.0	3
4438	Rbfox Splicing Factors Promote Neuronal Maturation and Axon Initial Segment Assembly. <i>Neuron</i> , 2018, 97, 853-868.e6.	3.8	90
4439	Cell death mechanisms of the anti-cancer drug etoposide on human cardiomyocytes isolated from pluripotent stem cells. <i>Archives of Toxicology</i> , 2018, 92, 1507-1524.	1.9	51
4440	Hepatic transcriptional profiling response to fava bean-induced oxidative stress in glucose-6-phosphate dehydrogenase-deficient mice. <i>Gene</i> , 2018, 652, 66-77.	1.0	2
4441	Revealing the action mechanisms of dexamethasone on the birth weight of infant using RNA-sequencing data of trophoblast cells. <i>Medicine (United States)</i> , 2018, 97, e9653.	0.4	2
4442	Plant Response to Metal-Containing Engineered Nanomaterials: An Omics-Based Perspective. <i>Environmental Science &amp; Technology</i> , 2018, 52, 2451-2467.	4.6	106
4443	Comprehensive circRNA expression profile and construction of circRNA-associated ceRNA network in fur skin. <i>Experimental Dermatology</i> , 2018, 27, 251-257.	1.4	45
4444	Prenatal Exposure to Bisphenol A Disrupts Naturally Occurring Bimodal DNA Methylation at Proximal Promoter of fggy, an Obesity-Relevant Gene Encoding a Carbohydrate Kinase, in Gonadal White Adipose Tissues of CD-1 Mice. <i>Endocrinology</i> , 2018, 159, 779-794.	1.4	29
4445	RNentropy: an entropy-based tool for the detection of significant variation of gene expression across multiple RNA-Seq experiments. <i>Nucleic Acids Research</i> , 2018, 46, e46-e46.	6.5	30
4446	Learning-dependent chromatin remodeling highlights noncoding regulatory regions linked to autism. <i>Science Signaling</i> , 2018, 11, .	1.6	25
4447	Gene and MicroRNA Perturbations of Cellular Response to Pemetrexed Implicate Biological Networks and Enable Imputation of Response in Lung Adenocarcinoma. <i>Scientific Reports</i> , 2018, 8, 733.	1.6	12

#	ARTICLE	IF	CITATIONS
4448	BMI1 regulates androgen receptor in prostate cancer independently of the polycomb repressive complex 1. <i>Nature Communications</i> , 2018, 9, 500.	5.8	65
4449	Alpha-1-antitrypsin: a novel predictor for long-term recovery of chronic disorder of consciousness. <i>Expert Review of Molecular Diagnostics</i> , 2018, 18, 307-313.	1.5	4
4450	Identifying Novel Signaling Pathways: An Exercise Scientists Guide to Phosphoproteomics. <i>Exercise and Sport Sciences Reviews</i> , 2018, 46, 76-85.	1.6	5
4451	T lymphocytes facilitate brain metastasis of breast cancer by inducing Guanylate-Binding Protein 1 expression. <i>Acta Neuropathologica</i> , 2018, 135, 581-599.	3.9	63
4452	Differential gene expression in trigeminal ganglia of male and female rats following chronic constriction of the infraorbital nerve. <i>European Journal of Pain</i> , 2018, 22, 875-888.	1.4	25
4453	Population-based dose-response analysis of liver transcriptional response to trichloroethylene in mouse. <i>Mammalian Genome</i> , 2018, 29, 168-181.	1.0	13
4454	A genomic map of clinal variation across the European rabbit hybrid zone. <i>Molecular Ecology</i> , 2018, 27, 1457-1478.	2.0	30
4455	Identification of differential protein-coding gene expressions in early phase lung adenocarcinoma. <i>Thoracic Cancer</i> , 2018, 9, 234-240.	0.8	4
4456	Systems pharmacology dissection of the anti-stroke mechanism for the Chinese traditional medicine Xing-Nao-Jing. <i>Journal of Pharmacological Sciences</i> , 2018, 136, 16-25.	1.1	17
4457	Hyperglycemia Alters Expression of Cerebral Metabolic Genes after Cardiac Arrest. <i>Journal of Stroke and Cerebrovascular Diseases</i> , 2018, 27, 1200-1211.	0.7	0
4458	Proteomics and Metabolomics for AKI Diagnosis. <i>Seminars in Nephrology</i> , 2018, 38, 63-87.	0.6	59
4459	Body composition, serum lipid levels, and transcriptomic characterization in the adipose tissue of male pigs in response to sex hormone deficiency. <i>Gene</i> , 2018, 646, 74-82.	1.0	7
4460	Integrated sequencing of exome and mRNA of large-sized single cells. <i>Scientific Reports</i> , 2018, 8, 384.	1.6	12
4461	Boolean network modeling in systems pharmacology. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , 2018, 45, 159-180.	0.8	60
4462	Transcriptome signature identifies distinct cervical pathways induced in lipopolysaccharide-mediated preterm birth. <i>Biology of Reproduction</i> , 2018, 98, 408-421.	1.2	30
4463	Augmentation of Myc-Dependent Mitotic Gene Expression by the Pygopus2 Chromatin Effector. <i>Cell Reports</i> , 2018, 23, 1516-1529.	2.9	7
4464	Metabolic systems analysis of LPS induced endothelial dysfunction applied to sepsis patient stratification. <i>Scientific Reports</i> , 2018, 8, 6811.	1.6	29
4465	Histone H4 acetylation regulates behavioral inter-individual variability in zebrafish. <i>Genome Biology</i> , 2018, 19, 55.	3.8	25

#	ARTICLE	IF	CITATIONS
4466	Independent prognostic genes and mechanism investigation for colon cancer. <i>Biological Research</i> , 2018, 51, 10.	1.5	25
4467	Identification of novel drug targets for diamond-blackfan anemia based on RPS19 gene mutation using protein-protein interaction network. <i>BMC Systems Biology</i> , 2018, 12, 39.	3.0	15
4468	Involvement of dysregulated coding and long non-coding RNAs in the pathogenesis of strabismus. <i>Molecular Medicine Reports</i> , 2018, 17, 7737-7745.	1.1	3
4469	Blastocyst-like structures generated solely from stem cells. <i>Nature</i> , 2018, 557, 106-111.	13.7	366
4470	Chromatin analysis in human early development reveals epigenetic transition during ZGA. <i>Nature</i> , 2018, 557, 256-260.	13.7	241
4471	Galactic Cosmic Radiation Induces Persistent Epigenome Alterations Relevant to Human Lung Cancer. <i>Scientific Reports</i> , 2018, 8, 6709.	1.6	26
4472	Saquinone controls hepatic cholesterol homeostasis by the negative regulation of PCSK9 transcriptional network. <i>Scientific Reports</i> , 2018, 8, 6737.	1.6	26
4473	Prognostic significance of microsatellite instability-associated pathways and genes in gastric cancer. <i>International Journal of Molecular Medicine</i> , 2018, 42, 149-160.	1.8	13
4474	Bayesian nonparametric discovery of isoforms and individual specific quantification. <i>Nature Communications</i> , 2018, 9, 1681.	5.8	8
4475	Presence of aggregates of smooth endoplasmic reticulum in MII oocytes affects oocyte competence: molecular-based evidence. <i>Molecular Human Reproduction</i> , 2018, 24, 310-317.	1.3	18
4476	A New Database for Drug Discovery Through Application of Data-Integration and Semantics. , 2018, , .		1
4477	Credentialing Individual Samples for Proteogenomic Analysis. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1515-1530.	2.5	5
4478	Gene expression profiles and pathway enrichment analysis of human osteosarcoma cells exposed to sorafenib. <i>FEBS Open Bio</i> , 2018, 8, 860-867.	1.0	11
4479	Genome-wide DNA methylation profiling in infants born to gestational diabetes mellitus. <i>Diabetes Research and Clinical Practice</i> , 2018, 142, 10-18.	1.1	47
4480	Identification of candidate genes for necrotizing enterocolitis based on microarray data. <i>Gene</i> , 2018, 661, 152-159.	1.0	11
4481	iSeq: Web-Based RNA-seq Data Analysis and Visualization. <i>Methods in Molecular Biology</i> , 2018, 1754, 167-181.	0.4	13
4482	Leukemia cell-derived microvesicles induce T cell exhaustion via miRNA delivery. <i>Oncolmmunology</i> , 2018, 7, e1448330.	2.1	24
4483	Impaired Mitochondrial Energetics Characterize Poor Early Recovery of Muscle Mass Following Hind Limb Unloading in Old Mice. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2018, 73, 1313-1322.	1.7	37



#	ARTICLE	IF	CITATIONS
4484	Circulating lncRNAs Analysis in Patients with Type 2 Diabetes Reveals Novel Genes Influencing Glucose Metabolism and Islet $\beta$ -Cell Function. <i>Cellular Physiology and Biochemistry</i> , 2018, 46, 335-350.	1.1	80
4485	Prognostic value of alcohol dehydrogenase mRNA expression in gastric cancer. <i>Oncology Letters</i> , 2018, 15, 5505-5516.	0.8	11
4486	Identification of key differentially expressed genes associated with non-small cell lung cancer by bioinformatics analyses. <i>Molecular Medicine Reports</i> , 2018, 17, 6379-6386.	1.1	22
4487	Neural Invasion Spreads Macrophage-Related Allodynia via Neural Root in Pancreatic Cancer. <i>Anesthesia and Analgesia</i> , 2018, 126, 1729-1738.	1.1	11
4488	Bach2 Promotes B Cell Receptor-Induced Proliferation of B Lymphocytes and Represses Cyclin-Dependent Kinase Inhibitors. <i>Journal of Immunology</i> , 2018, 200, 2882-2893.	0.4	31
4489	A standardized fold change method for microarray differential expression analysis used to reveal genes involved in acute rejection in murine allograft models. <i>FEBS Open Bio</i> , 2018, 8, 481-490.	1.0	2
4490	Gene Expression Profiling of Advanced Penile Squamous Cell Carcinoma Receiving Cisplatin-based Chemotherapy Improves Prognostication and Identifies Potential Therapeutic Targets. <i>European Urology Focus</i> , 2018, 4, 733-736.	1.6	18
4491	A Review on Methods for Detecting SNP Interactions in High-Dimensional Genomic Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 599-612.	1.9	42
4492	Genome-wide characterization of lncRNAs in acute myeloid leukemia. <i>Briefings in Bioinformatics</i> , 2018, 19, 627-635.	3.2	34
4493	IGF2 mRNA binding protein 3 (IMP3) mediated regulation of transcriptome and translome in glioma cells. <i>Cancer Biology and Therapy</i> , 2018, 19, 42-52.	1.5	14
4494	Genome-Wide DNA Methylation Patterns Analysis of Noncoding RNAs in Temporal Lobe Epilepsy Patients. <i>Molecular Neurobiology</i> , 2018, 55, 793-803.	1.9	36
4495	The benefits (and misfortunes) of SDS in top-down proteomics. <i>Journal of Proteomics</i> , 2018, 175, 75-86.	1.2	25
4496	Genomic Regions in Local Endangered Sheep Encode Potentially Favorable Genes. <i>Animal Biotechnology</i> , 2018, 29, 12-19.	0.7	1
4497	Comparison of the general co-expression landscapes between human and mouse. <i>Briefings in Bioinformatics</i> , 2018, 19, 811-820.	3.2	3
4498	Theoretical and Biological Evaluation of the Link between Low Exercise Capacity and Disease Risk. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2018, 8, a029868.	2.9	44
4499	Genome-wide gene expression profiling of tongue squamous cell carcinoma by RNA-seq. <i>Clinical Oral Investigations</i> , 2018, 22, 209-216.	1.4	34
4500	Exploring the molecular pathogenesis and biomarkers of high risk oral premalignant lesions on the basis of long noncoding RNA expression profiling by serial analysis of gene expression. <i>European Journal of Cancer Prevention</i> , 2018, 27, 370-378.	0.6	16
4501	The proto-oncogene tyrosine protein kinase Src is essential for macrophage-myofibroblast transition during renal scarring. <i>Kidney International</i> , 2018, 93, 173-187.	2.6	94

#	ARTICLE	IF	CITATIONS
4502	SCPortalen: human and mouse single-cell centric database. <i>Nucleic Acids Research</i> , 2018, 46, D781-D787.	6.5	48
4503	<i>Lactobacillus gasseri</i> attenuates allergic airway inflammation through PPAR $\gamma$ activation in dendritic cells. <i>Journal of Molecular Medicine</i> , 2018, 96, 39-51.	1.7	22
4504	Weighted Gene Co-expression Network Analysis Identifies Gender Specific Modules and Hub Genes Related to Metabolism and Inflammation in Response to an Acute Lipid Challenge. <i>Molecular Nutrition and Food Research</i> , 2018, 62, 1700388.	1.5	18
4505	Transcriptome analysis using de novo RNA-seq to compare ginseng roots cultivated in different environments. <i>Plant Growth Regulation</i> , 2018, 84, 149-157.	1.8	6
4506	Main active constituent identification in Guanxinjing capsule, a traditional Chinese medicine, for the treatment of coronary heart disease complicated with depression. <i>Acta Pharmacologica Sinica</i> , 2018, 39, 975-987.	2.8	24
4507	Genomic characterization of chromosome translocations in patients with T/myeloid mixed-phenotype acute leukemia. <i>Leukemia and Lymphoma</i> , 2018, 59, 1231-1238.	0.6	8
4508	A Comparative Proteome Profile of Female Mouse Gonads Suggests a Tight Link between the Electron Transport Chain and Meiosis Initiation. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 31-42.	2.5	7
4509	Discovery and Mechanistic Elucidation of a Class of Protein Disulfide Isomerase Inhibitors for the Treatment of Glioblastoma. <i>ChemMedChem</i> , 2018, 13, 164-177.	1.6	50
4510	Transcriptome analysis reveals novel genes involved in anthocyanin biosynthesis in the flesh of peach. <i>Plant Physiology and Biochemistry</i> , 2018, 123, 94-102.	2.8	47
4511	ZikaBase: An integrated ZIKV- Human Interactome Map database. <i>Virology</i> , 2018, 514, 203-210.	1.1	13
4512	Shotgun label-free proteomic analysis for identification of proteins in HaCaT human skin keratinocytes regulated by the administration of collagen from soft-shelled turtle. <i>Journal of Biomedical Materials Research - Part B Applied Biomaterials</i> , 2018, 106, 2403-2413.	1.6	2
4513	Computational systems biology approaches for Parkinson's disease. <i>Cell and Tissue Research</i> , 2018, 373, 91-109.	1.5	19
4514	Sperm RNA elements as markers of health. <i>Systems Biology in Reproductive Medicine</i> , 2018, 64, 25-38.	1.0	32
4515	RNA-Sequencing of <i>Drosophila melanogaster</i> Head Tissue on High-Sugar and High-Fat Diets. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 279-290.	0.8	21
4516	Comparative transcriptomic characterization of a new mib mutant allele, mib, in zebrafish. <i>Gene</i> , 2018, 642, 51-57.	1.0	0
4517	The sbv IMPROVER Systems Toxicology computational challenge: Identification of human and species-independent blood response markers as predictors of smoking exposure and cessation status. <i>Computational Toxicology</i> , 2018, 5, 38-51.	1.8	13
4518	Analysis of biological functional networks during sciatic nerve repair and regeneration. <i>Molecular and Cellular Biochemistry</i> , 2018, 439, 141-150.	1.4	2
4519	SMART Cancer Navigator: A Framework for Implementing ASCO Workshop Recommendations to Enable Precision Cancer Medicine. <i>JCO Precision Oncology</i> , 2018, 2018, 1-14.	1.5	19

#	ARTICLE	IF	CITATIONS
4520	Thyroid follicular adenomas and carcinomas: molecular profiling provides evidence for a continuous evolution. <i>Oncotarget</i> , 2018, 9, 10343-10359.	0.8	29
4521	A Proteomic Approach for Understanding the Mechanisms of Delayed Corneal Wound Healing in Diabetic Keratopathy Using Diabetic Model Rat. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3635.	1.8	19
4522	Abnormal DNA Methylation in Thoracic Spinal Cord Tissue Following Transection Injury. <i>Medical Science Monitor</i> , 2018, 24, 8878-8890.	0.5	10
4523	Predicting Small Molecule Potency to Inhibit Estrogen Receptors using Machine Learning and Deep Learning Approaches. , 2018, , .		1
4524	Coexpression modules constructed by weighted gene co-expression network analysis indicate ubiquitin-mediated proteolysis as a potential biomarker of uveal melanoma. <i>Experimental and Therapeutic Medicine</i> , 2019, 17, 237-243.	0.8	4
4525	The cellular economy of the <i>Saccharomyces cerevisiae</i> zinc proteome. <i>Metallomics</i> , 2018, 10, 1755-1776.	1.0	66
4526	Collagen peptides from soft-shelled turtle induce calpain-1 expression and regulate inflammatory cytokine expression in HaCaT human skin keratinocytes. <i>International Journal of Molecular Medicine</i> , 2018, 42, 1168-1180.	1.8	1
4527	A vascular endothelial growth factor receptor gene variant is associated with susceptibility to acute respiratory distress syndrome. <i>Intensive Care Medicine Experimental</i> , 2018, 6, 16.	0.9	9
4528	Comprehensive analysis of long noncoding RNA-associated competing endogenous RNA network in cholangiocarcinoma. <i>Biochemical and Biophysical Research Communications</i> , 2018, 506, 1004-1012.	1.0	19
4529	Integrated whole genome microarray analysis and immunohistochemical assay identifies COL11A1, GJB2 and CTRL as predictive biomarkers for pancreatic cancer. <i>Cancer Cell International</i> , 2018, 18, 174.	1.8	28
4530	ICGdb: An Integrative Cancer Genomic Database. , 2018, , .		0
4531	Transcriptomic changes with increasing algal symbiont reveal the detailed process underlying establishment of coral-algal symbiosis. <i>Scientific Reports</i> , 2018, 8, 16802.	1.6	46
4532	Identification of hub genes with diagnostic values in pancreatic cancer by bioinformatics analyses and supervised learning methods. <i>World Journal of Surgical Oncology</i> , 2018, 16, 223.	0.8	24
4533	Ensemble learning for detecting gene-gene interactions in colorectal cancer. <i>PeerJ</i> , 2018, 6, e5854.	0.9	21
4534	Diagnostic and prognostic values of the mRNA expression of excision repair cross-complementation enzymes in hepatitis B virus-related hepatocellular carcinoma. <i>Cancer Management and Research</i> , 2018, Volume 10, 5313-5328.	0.9	3
4535	Deep proteome of human nNOS/NOS1-positive versus MOCK SH-SY5Y neuroblastoma cells under full nutrition, serum free starvation and rapamycin treatment. <i>Data in Brief</i> , 2018, 21, 1309-1314.	0.5	1
4536	Prognostic Value of Excision Repair Cross-Complementing mRNA Expression in Gastric Cancer. <i>BioMed Research International</i> , 2018, 2018, 1-16.	0.9	6
4537	Widespread Enhancer Dememorization and Promoter Priming during Parental-to-Zygotic Transition. <i>Molecular Cell</i> , 2018, 72, 673-686.e6.	4.5	57

#	ARTICLE	IF	CITATIONS
4538	Short-lived AUF1 p42-binding mRNAs of RANKL and BCL6 have two distinct instability elements each. PLoS ONE, 2018, 13, e0206823.	1.1	0
4539	Extraction and biomolecular analysis of dermal interstitial fluid collected with hollow microneedles. Communications Biology, 2018, 1, 173.	2.0	148
4540	Pancreatic-cancer-cell-derived trefoil factor 2 impairs maturation and migration of human monocyte-derived dendritic cells<i>in vitro</i>. Animal Cells and Systems, 2018, 22, 368-381.	0.8	10
4541	Proteomics of Bronchoalveolar Lavage Fluid Reveals a Lung Oxidative Stress Response in Murine Herpesvirus-68 Infection. Viruses, 2018, 10, 670.	1.5	3
4542	Identification of potential genes and pathways for response prediction of neoadjuvant chemoradiotherapy in patients with rectal cancer by systemic biological analysis. Oncology Letters, 2018, 17, 492-501.	0.8	1
4543	Pancreatic Cell Fate Determination Relies on Notch Ligand Trafficking by NFIA. Cell Reports, 2018, 25, 3811-3827.e7.	2.9	13
4544	Integrating proteomic and phosphoproteomic data for pathway analysis in breast cancer. BMC Systems Biology, 2018, 12, 130.	3.0	7
4545	Data set of differentially expressed microRNAs in sanguinarine-treated Caenorhabditis elegans and its F3 progeny. Data in Brief, 2018, 21, 899-906.	0.5	0
4546	Mutant p63 Affects Epidermal Cell Identity through Rewiring the Enhancer Landscape. Cell Reports, 2018, 25, 3490-3503.e4.	2.9	41
4547	Deciphering the evolutionary signatures of pinnipeds using novel genome sequences: The first genomes of Phoca largha, Callorhinus ursinus, and Eumetopias jubatus. Scientific Reports, 2018, 8, 16877.	1.6	7
4548	Analysis of dynamic molecular networks for pancreatic ductal adenocarcinoma progression. Cancer Cell International, 2018, 18, 214.	1.8	37
4549	Cardiac function evaluation for a novel one-step detoxification product of Aconiti Lateralis Radix Praeparata. Chinese Medicine, 2018, 13, 62.	1.6	12
4550	Proteomic Analysis of Zn Depletion/Repletion in the Hormone-Secreting Thyroid Follicular Cell Line FRTL-5. Nutrients, 2018, 10, 1981.	1.7	3
4551	Atypical GATA transcription factor TRPS1 represses gene expression by recruiting CHD4/NuRD(MTA2) and suppresses cell migration and invasion by repressing TP63 expression. Oncogenesis, 2018, 7, 96.	2.1	27
4552	Identifying mouse developmental essential genes using machine learning. DMM Disease Models and Mechanisms, 2018, 11, .	1.2	18
4553	Prognostic value of sorting nexin 10 weak expression in stomach adenocarcinoma revealed by weighted gene co-expression network analysis. World Journal of Gastroenterology, 2018, 24, 4906-4919.	1.4	17
4554	Integrated analysis reveals key genes with prognostic value in lung adenocarcinoma. Cancer Management and Research, 2018, Volume 10, 6097-6108.	0.9	36
4555	Dissecting the Genomic Architecture of Resistance to Eimeria maxima Parasitism in the Chicken. Frontiers in Genetics, 2018, 9, 528.	1.1	31

#	ARTICLE	IF	CITATIONS
4556	Zygotic gene activation in the chicken occurs in two waves, the first involving only maternally derived genes. <i>ELife</i> , 2018, 7, .	2.8	20
4557	Identification of Deregulated Signaling Pathways in Jurkat Cells in Response to a Novel Acylspermidine Analogue-N4-Erucoyl Spermidine. <i>Epigenetics Insights</i> , 2018, 11, 251686571881454.	0.6	12
4558	Identification of drug repurposing candidates based on a miRNA-mediated drug and pathway network for cardiac hypertrophy and acute myocardial infarction. <i>Human Genomics</i> , 2018, 12, 52.	1.4	6
4559	The Genomic Architecture of Fowl Typhoid Resistance in Commercial Layers. <i>Frontiers in Genetics</i> , 2018, 9, 519.	1.1	17
4560	Identifying SNPs and candidate genes for three litter traits using single-step GWAS across six parities in Landrace and Large White pigs. <i>Physiological Genomics</i> , 2018, 50, 1026-1035.	1.0	12
4561	Characterization and metabolic synthetic lethal testing in a new model of SDH-loss familial pheochromocytoma and paraganglioma. <i>Oncotarget</i> , 2018, 9, 6109-6127.	0.8	13
4562	Diagnostic Issues in Treating Brain Tumors. , 2018, , 151-159.		0
4563	Fenretinide targeting of human colon cancer sphere cells through cell cycle regulation and stress-responsive activities. <i>Oncology Letters</i> , 2018, 16, 5339-5348.	0.8	3
4564	Bioinformatics analyses of significant genes, related pathways and candidate prognostic biomarkers in glioblastoma. <i>Molecular Medicine Reports</i> , 2018, 18, 4185-4196.	1.1	39
4565	Which is the Most Reasonable Anti-aging Strategy: Meta-analysis. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1086, 267-282.	0.8	14
4566	Multi-omics integrative analysis with genome-scale metabolic model simulation reveals global cellular adaptation of <i>Aspergillus niger</i> under industrial enzyme production condition. <i>Scientific Reports</i> , 2018, 8, 14404.	1.6	36
4567	Silencing of TGF $\beta$ 2 signalling in microglia results in impaired homeostasis. <i>Nature Communications</i> , 2018, 9, 4011.	5.8	125
4568	Effects of Chronic Spinal Cord Injury on Relationships among Ion Channel and Receptor mRNAs in Mouse Lumbar Spinal Cord. <i>Neuroscience</i> , 2018, 393, 42-60.	1.1	13
4569	Identification of key genes and long non-coding RNAs in celecoxib-treated lung squamous cell carcinoma cell line by RNA-sequencing. <i>Molecular Medicine Reports</i> , 2018, 17, 6456-6464.	1.1	6
4570	Regulatory sRNAs in Cyanobacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 2399.	1.5	10
4571	Transcriptome Profile in Unilateral Adrenalectomy-Induced Compensatory Adrenal Growth in the Rat. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1111.	1.8	16
4572	De novo Mutations (DNMs) in Autism Spectrum Disorder (ASD): Pathway and Network Analysis. <i>Frontiers in Genetics</i> , 2018, 9, 406.	1.1	40
4573	Gene expression differences between thyroid carcinoma, thyroid adenoma and normal thyroid tissue. <i>Oncology Reports</i> , 2018, 40, 3359-3369.	1.2	24

#	ARTICLE	IF	CITATIONS
4574	Aberrant splicing in B-cell acute lymphoblastic leukemia. <i>Nucleic Acids Research</i> , 2018, 46, 11357-11369.	6.5	39
4575	Effect of high-fat diet feeding and associated transcriptome changes in the peak lactation mammary gland in C57BL/6 dams. <i>Physiological Genomics</i> , 2018, 50, 1059-1070.	1.0	13
4576	Effects of propofol and etomidate anesthesia on cardiovascular miRNA expression: the different profiles?. <i>BMC Anesthesiology</i> , 2018, 18, 149.	0.7	5
4577	Characterization of kinase gene expression and splicing profile in prostate cancer with RNA-Seq data. <i>BMC Genomics</i> , 2018, 19, 564.	1.2	6
4578	Identification of protein complexes associated with myocardial infarction using a bioinformatics approach. <i>Molecular Medicine Reports</i> , 2018, 18, 3569-3576.	1.1	1
4579	miRNA array analysis of plasma miRNA alterations in rats exposed to a high altitude hypoxic environment. <i>Molecular Medicine Reports</i> , 2018, 18, 5502-5510.	1.1	4
4580	MicroRNA-132 directs human periodontal ligament-derived neural crest stem cell neural differentiation. <i>Journal of Tissue Engineering and Regenerative Medicine</i> , 2019, 13, 12-24.	1.3	13
4581	Overexpression of Chicken IRF7 Increased Viral Replication and Programmed Cell Death to the Avian Influenza Virus Infection Through TGF-Beta/FoxO Signaling Axis in DF-1. <i>Frontiers in Genetics</i> , 2018, 9, 415.	1.1	9
4582	Analysis of serum microRNA expression in male workers with occupational noise-induced hearing loss. <i>Brazilian Journal of Medical and Biological Research</i> , 2018, 51, e6426.	0.7	14
4583	Maternal Melatonin Therapy Attenuates Methyl-Donor Diet-Induced Programmed Hypertension in Male Adult Rat Offspring. <i>Nutrients</i> , 2018, 10, 1407.	1.7	31
4584	Exploring Pharmacological Mechanisms of Xuefu Zhuyu Decoction in the Treatment of Traumatic Brain Injury via a Network Pharmacology Approach. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-20.	0.5	24
4585	Network pharmacology-based strategy to investigate pharmacological mechanisms of Zuojinwan for treatment of gastritis. <i>BMC Complementary and Alternative Medicine</i> , 2018, 18, 292.	3.7	101
4586	Identification of COL1A1 as an invasion-related gene in malignant astrocytoma. <i>International Journal of Oncology</i> , 2018, 53, 2542-2554.	1.4	31
4587	Anticancer activity of biogenerated silver nanoparticles: an integrated proteomic investigation. <i>Oncotarget</i> , 2018, 9, 9685-9705.	0.8	147
4588	Targeting histone methyltransferase G9a inhibits growth and Wnt signaling pathway by epigenetically regulating HP1 and APC2 gene expression in non-small cell lung cancer. <i>Molecular Cancer</i> , 2018, 17, 153.	7.9	59
4589	Screening of genes associated with inflammatory responses in the endolymphatic sac reveals underlying mechanisms for autoimmune inner ear diseases. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 2460-2470.	0.8	10
4590	Andrographolide Sulfonate Attenuates Acute Lung Injury by Reducing Expression of Myeloperoxidase and Neutrophil-Derived Proteases in Mice. <i>Frontiers in Physiology</i> , 2018, 9, 939.	1.3	24
4591	Impaired Notch Signaling Leads to a Decrease in p53 Activity and Mitotic Catastrophe in Aged Muscle Stem Cells. <i>Cell Stem Cell</i> , 2018, 23, 544-556.e4.	5.2	107

#	ARTICLE	IF	CITATIONS
4592	Transcriptional response of honey bee ( <i>Apis mellifera</i> ) to differential nutritional status and <i>Nosema</i> infection. <i>BMC Genomics</i> , 2018, 19, 628.	1.2	31
4593	Computational Approaches to Understand the Genome and Protein Sequences of Fungi. , 2018, , 635-649.		0
4594	Urinary proteomics reveals association between pediatric nephrolithiasis and cardiovascular disease. <i>International Urology and Nephrology</i> , 2018, 50, 1949-1954.	0.6	12
4595	Global Long Noncoding RNA and mRNA Expression Changes between Prenatal and Neonatal Lung Tissue in Pigs. <i>Genes</i> , 2018, 9, 443.	1.0	21
4596	Transcriptome sequencing reveals key potential long non-coding RNAs related to duration of fertility trait in the uterovaginal junction of egg-laying hens. <i>Scientific Reports</i> , 2018, 8, 13185.	1.6	12
4597	Hepatitis C virus core impacts expression of miR122 and miR204 involved in carcinogenic progression via regulation of TGFBRAP1 and HOTTIP expression. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 1173-1182.	1.0	10
4598	Tetraspanin family identified as the central genes detected in gastric cancer using bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2018, 18, 3599-3610.	1.1	12
4599	Identification of six key miRNAs associated with breast cancer through screening large-scale microarray data. <i>Oncology Letters</i> , 2018, 16, 4159-4168.	0.8	7
4600	Unravelling subclonal heterogeneity and aggressive disease states in TNBC through single-cell RNA-seq. <i>Nature Communications</i> , 2018, 9, 3588.	5.8	342
4601	TAM 2.0: tool for MicroRNA set analysis. <i>Nucleic Acids Research</i> , 2018, 46, W180-W185.	6.5	141
4602	Integrated analysis of a competing endogenous RNA network reveals key lncRNAs as potential prognostic biomarkers for human bladder cancer. <i>Medicine (United States)</i> , 2018, 97, e11887.	0.4	39
4603	Potential role of LINC00996 in colorectal cancer: a study based on data mining and bioinformatics. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 4845-4855.	1.0	37
4604	Correcting the Mean-Variance Dependency for Differential Variability Testing Using Single-Cell RNA Sequencing Data. <i>Cell Systems</i> , 2018, 7, 284-294.e12.	2.9	71
4605	Circular RNAs hsa_circ_0032462, hsa_circ_0028173, hsa_circ_0005909 are predicted to promote CADM1 expression by functioning as miRNAs sponge in human osteosarcoma. <i>PLoS ONE</i> , 2018, 13, e0202896.	1.1	33
4606	ATG5 overexpression is neuroprotective and attenuates cytoskeletal and vesicle-trafficking alterations in axotomized motoneurons. <i>Cell Death and Disease</i> , 2018, 9, 626.	2.7	15
4607	KDM5B decommissions the H3K4 methylation landscape of self-renewal genes during trophoblast stem cell differentiation. <i>Biology Open</i> , 2018, 7, .	0.6	20
4608	Combined bioinformatics analysis reveals gene expression and DNA methylation patterns in osteoarthritis. <i>Molecular Medicine Reports</i> , 2018, 17, 8069-8078.	1.1	10
4609	Nomogram Integrating Genomics with Clinicopathologic Features Improves Prognosis Prediction for Colorectal Cancer. <i>Molecular Cancer Research</i> , 2018, 16, 1373-1384.	1.5	17

#	ARTICLE	IF	CITATIONS
4610	Screening of prognostic risk microRNAs for acute myeloid leukemia. <i>Hematology</i> , 2018, 23, 747-755.	0.7	8
4611	Material basis research for Huangqi Jianzhong Tang against chronic atrophic gastritis rats through integration of urinary metabonomics and SystemsDock. <i>Journal of Ethnopharmacology</i> , 2018, 223, 1-9.	2.0	21
4612	A map of the PGC-1 $\alpha$ - and NT-PGC-1 $\alpha$ -regulated transcriptional network in brown adipose tissue. <i>Scientific Reports</i> , 2018, 8, 7876.	1.6	29
4613	Genome-wide DNA methylation profiling in a rat model with vascular dementia. <i>Molecular Medicine Reports</i> , 2018, 18, 123-130.	1.1	3
4614	Identification of potential pathogenic biomarkers in clear cell renal cell carcinoma. <i>Oncology Letters</i> , 2018, 15, 8491-8499.	0.8	8
4615	Identification of key genes in rheumatoid arthritis and osteoarthritis based on bioinformatics analysis. <i>Medicine (United States)</i> , 2018, 97, e10997.	0.4	27
4616	Mitochondrial-related consequences of heat stress exposure during bovine oocyte maturation persist in early embryo development. <i>Journal of Reproduction and Development</i> , 2018, 64, 243-251.	0.5	28
4617	The novel 19q13 KRAB zinc-finger tumour suppressor ZNF382 is frequently methylated in oesophageal squamous cell carcinoma and antagonises Wnt/ $\beta$ -catenin signalling. <i>Cell Death and Disease</i> , 2018, 9, 573.	2.7	26
4618	Poly(ADP-ribosyl)ation associated changes in CTCF-chromatin binding and gene expression in breast cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018, 1861, 718-730.	0.9	17
4619	Differential Co-expression and Regulatory Network Analysis Uncover the Relapse Factor and Mechanism of T Cell Acute Leukemia. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 12, 184-194.	2.3	20
4620	Identification of a noncoding RNA-mediated gene pair-based regulatory module in Alzheimer's disease. <i>Molecular Medicine Reports</i> , 2018, 18, 2164-2170.	1.1	1
4621	Synergistic co-regulation and competition by a SOX9-GLI-FOXA phasic transcriptional network coordinate chondrocyte differentiation transitions. <i>PLoS Genetics</i> , 2018, 14, e1007346.	1.5	56
4622	Systems Pharmacology Dissection of Traditional Chinese Medicine Wen-Dan Decoction for Treatment of Cardiovascular Diseases. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-14.	0.5	9
4623	An association between differential expression and genetic divergence in the Patagonian olive mouse ( <i>Abrothrix olivacea</i> ). <i>Molecular Ecology</i> , 2018, 27, 3274-3286.	2.0	28
4624	The Potential Protective Effect of Curcumin on Amyloid- $\beta$ 42 Induced Cytotoxicity in HT-22 Cells. <i>BioMed Research International</i> , 2018, 2018, 1-8.	0.9	18
4625	A diet defined by its content of bovine milk exosomes and their RNA cargos has moderate effects on gene expression, amino acid profiles and grip strength in skeletal muscle in C57BL/6 mice. <i>Journal of Nutritional Biochemistry</i> , 2018, 59, 123-128.	1.9	47
4626	Identification of the extracellular matrix protein Fibulin-2 as a regulator of spinal nerve organization. <i>Developmental Biology</i> , 2018, 442, 101-114.	0.9	21
4627	Systemic bioinformatics analysis of skeletal muscle gene expression profiles of sepsis. <i>Experimental and Therapeutic Medicine</i> , 2018, 15, 4637-4642.	0.8	1



#	ARTICLE	IF	CITATIONS
4628	Placental H3K27me3 establishes female resilience to prenatal insults. <i>Nature Communications</i> , 2018, 9, 2555.	5.8	110
4629	Machine learning models to predict the progression from early to late stages of papillary renal cell carcinoma. <i>Computers in Biology and Medicine</i> , 2018, 100, 92-99.	3.9	31
4630	A Possible Mechanism: Vildagliptin Prevents Aortic Dysfunction through Paraoxonase and Angiotensin-Like 3. <i>BioMed Research International</i> , 2018, 2018, 1-14.	0.9	3
4631	Biochemical characterization of human tissue kallikrein 15 and examination of its potential role in cancer. <i>Clinical Biochemistry</i> , 2018, 58, 108-115.	0.8	7
4632	The Next Generation Sequencing (NGS) of Asthma Genetics. <i>Translational Bioinformatics</i> , 2018, , 11-30.	0.0	0
4633	4-HPR Is an Endoplasmic Reticulum Stress Aggravator and Sensitizes Breast Cancer Cells Resistant to TRAIL/Apo2L. <i>Anticancer Research</i> , 2018, 38, 4403-4416.	0.5	6
4634	Comparative transcriptomics reveals specific responding genes associated with atherosclerosis in rabbit and mouse models. <i>PLoS ONE</i> , 2018, 13, e0201618.	1.1	3
4635	Screening therapeutic targets of ribavirin in hepatocellular carcinoma. <i>Oncology Letters</i> , 2018, 15, 9625-9632.	0.8	9
4636	Expression and network analysis of YBX1 interactors for identification of new drug targets in lung adenocarcinoma. <i>Journal of Genomics</i> , 2018, 6, 103-112.	0.6	10
4637	Transcriptome alteration in <i>Phytophthora infestans</i> in response to phenazine-1-carboxylic acid production by <i>Pseudomonas fluorescens</i> strain LBUM223. <i>BMC Genomics</i> , 2018, 19, 474.	1.2	21
4638	Candidate genes and microRNAs for glioma pathogenesis and prognosis based on gene expression profiles. <i>Molecular Medicine Reports</i> , 2018, 18, 2715-2723.	1.1	5
4639	Iron metabolism gene expression and prognostic features of hepatocellular carcinoma. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 9178-9204.	1.2	48
4640	Alpha-linolenic acid and linoleic acid differentially regulate the skeletal muscle secretome of obese Zucker rats. <i>Physiological Genomics</i> , 2018, 50, 580-589.	1.0	8
4641	Exploring the Mechanism of Dangguiuliuang Decoction Against Hepatic Fibrosis by Network Pharmacology and Experimental Validation. <i>Frontiers in Pharmacology</i> , 2018, 9, 187.	1.6	33
4642	GSHR, a Web-Based Platform Provides Gene Set-Level Analyses of Hormone Responses in Arabidopsis. <i>Frontiers in Plant Science</i> , 2018, 9, 23.	1.7	2
4643	Genome-Wide Identification and Characterization of Long Non-Coding RNA in Wheat Roots in Response to Ca <sup>2+</sup> Channel Blocker. <i>Frontiers in Plant Science</i> , 2018, 9, 244.	1.7	36
4644	Long non-coding RNAs RP5-821D11.7, APCDD1L-AS1 and RP11-277P12.9 were associated with the prognosis of lung squamous cell carcinoma. <i>Molecular Medicine Reports</i> , 2018, 17, 7238-7248.	1.1	16
4645	Deoxynivalenol- and zearalenone-contaminated feeds alter gene expression profiles in the livers of piglets. <i>Asian-Australasian Journal of Animal Sciences</i> , 2018, 31, 595-606.	2.4	22

#	ARTICLE	IF	CITATIONS
4646	Association Analysis between Body Mass Index and Genomic DNA Methylation across 15 Major Cancer Types. <i>Journal of Cancer</i> , 2018, 9, 2532-2542.	1.2	10
4647	Distinct Diagnostic and Prognostic Values of Minichromosome Maintenance Gene Expression in Patients with Hepatocellular Carcinoma. <i>Journal of Cancer</i> , 2018, 9, 2357-2373.	1.2	59
4648	Analysis of the complex interaction of CDR1asâ€™miRNAâ€™protein and detection of its novel role in melanoma. <i>Oncology Letters</i> , 2018, 16, 1219-1225.	0.8	12
4649	Determination of system level alterations in host transcriptome due to Zika virus (ZIKV) Infection in retinal pigment epithelium. <i>Scientific Reports</i> , 2018, 8, 11209.	1.6	37
4650	Elementary screening of lymph node metastatic-related genes in gastric cancer based on the co-expression network of messenger RNA, microRNA and long non-coding RNA. <i>Brazilian Journal of Medical and Biological Research</i> , 2018, 51, e6685.	0.7	9
4651	Messenger RNA Sequencing and Pathway Analysis Provide Novel Insights Into the Susceptibility to Salmonella enteritidis Infection in Chickens. <i>Frontiers in Genetics</i> , 2018, 9, 256.	1.1	20
4652	Alternative splicing events implicated in carcinogenesis and prognosis of colorectal cancer. <i>Journal of Cancer</i> , 2018, 9, 1754-1764.	1.2	64
4653	Comprehensive analysis of a long noncoding RNA-associated competing endogenous RNA network in colorectal cancer. <i>OncoTargets and Therapy</i> , 2018, Volume 11, 2453-2466.	1.0	27
4654	Atherosclerosis is exacerbated by chitinase-3-like-1 in amyloid precursor protein transgenic mice. <i>Theranostics</i> , 2018, 8, 749-766.	4.6	30
4655	In vivo identification of Bmp2-correlation networks during fracture healing by means of a limb-specific conditional inactivation of Bmp2. <i>Bone</i> , 2018, 116, 103-110.	1.4	5
4656	Analysis of diet-induced differential methylation, expression, and interactions of lncRNA and protein-coding genes in mouse liver. <i>Scientific Reports</i> , 2018, 8, 11537.	1.6	10
4657	Cell type-specific analysis of transcriptome changes in the porcine endometrium on Day 12 of pregnancy. <i>BMC Genomics</i> , 2018, 19, 459.	1.2	38
4658	Identification of key target genes and biological pathways in multiple sclerosis brains using microarray data obtained from the Gene Expression Omnibus database. <i>Neurological Research</i> , 2018, 40, 883-891.	0.6	10
4659	A novel gene-expression-signature-based model for prediction of response to Tripterysium glycosides tablet for rheumatoid arthritis patients. <i>Journal of Translational Medicine</i> , 2018, 16, 187.	1.8	12
4660	STAT6, PBX2, and PBRM1 Emerge as Predicted Regulators of 452 Differentially Expressed Genes Associated With Puberty in Brahman Heifers. <i>Frontiers in Genetics</i> , 2018, 9, 87.	1.1	34
4661	Gene Expression Analysis Reveals Novel Shared Gene Signatures and Candidate Molecular Mechanisms between Pemphigus and Systemic Lupus Erythematosus in CD4+ T Cells. <i>Frontiers in Immunology</i> , 2017, 8, 1992.	2.2	56
4662	Integrative Analysis of Hippocampus Gene Expression Profiles Identifies Network Alterations in Aging and Alzheimerâ€™s Disease. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 153.	1.7	58
4663	Stable STIM1 Knockdown in Self-Renewing Human Neural Precursors Promotes Premature Neural Differentiation. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 178.	1.4	22

#	ARTICLE	IF	CITATIONS
4664	Key Genes and Pathways Associated With Inner Ear Malformation in SOX10 <sup>p.R109W</sup> Mutation Pigs. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 181.	1.4	20
4665	Identification of <i>Schizosaccharomyces pombe</i> in the guts of healthy individuals and patients with colorectal cancer: preliminary evidence from a gut microbiome secretome study. <i>Gut Pathogens</i> , 2018, 10, 29.	1.6	9
4666	LXT is required for spermatogenesis in mice. <i>PLoS ONE</i> , 2018, 13, e0195747.	1.1	5
4667	In silico approach in reveal traditional medicine plants pharmacological material basis. <i>Chinese Medicine</i> , 2018, 13, 33.	1.6	75
4668	Bioinformatics analysis of novel transcription factors and related differentially regulated modules in non-union skeletal fractures. <i>Journal of Back and Musculoskeletal Rehabilitation</i> , 2018, 31, 623-628.	0.4	1
4669	Identification of key genes and pathways for esophageal squamous cell carcinoma by bioinformatics analysis. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 1121-1130.	0.8	9
4670	The Coordinated Activities of nAChR and Wnt Signaling Regulate Intestinal Stem Cell Function in Mice. <i>International Journal of Molecular Sciences</i> , 2018, 19, 738.	1.8	27
4671	Hyaluronic Acid Influence on Normal and Osteoarthritic Tissue-Engineered Cartilage. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1519.	1.8	11
4672	Identification of hub genes and potential molecular mechanisms in gastric cancer by integrated bioinformatics analysis. <i>PeerJ</i> , 2018, 6, e5180.	0.9	74
4673	Comprehensive and integrative analysis identifies microRNA-106 as a novel non-invasive biomarker for detection of gastric cancer. <i>Journal of Translational Medicine</i> , 2018, 16, 127.	1.8	23
4674	Identification of hub genes with prognostic values in gastric cancer by bioinformatics analysis. <i>World Journal of Surgical Oncology</i> , 2018, 16, 114.	0.8	59
4675	Hub genes and key pathways of non-small lung cancer identified using bioinformatics. <i>Oncology Letters</i> , 2018, 16, 2344-2354.	0.8	22
4676	Detecting the Population Structure and Scanning for Signatures of Selection in Horses ( <i>Equus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 117693431877510.	0.6	15
4677	Plasma proteomic signature of age in healthy humans. <i>Aging Cell</i> , 2018, 17, e12799.	3.0	325
4678	Identification of Biomarkers Associated With Pathological Stage and Prognosis of Clear Cell Renal Cell Carcinoma by Co-expression Network Analysis. <i>Frontiers in Physiology</i> , 2018, 9, 399.	1.3	85
4679	Identification of key genes and pathways in human clear cell renal cell carcinoma (ccRCC) by co-expression analysis. <i>International Journal of Biological Sciences</i> , 2018, 14, 266-279.	2.6	60
4680	Prognostic value of ubiquitin-conjugating enzyme E2 S overexpression in hepatocellular carcinoma. <i>International Journal of Biological Macromolecules</i> , 2018, 119, 225-231.	3.6	18
4681	An eight-miRNA signature expression-based risk scoring system for prediction of survival in pancreatic adenocarcinoma. <i>Cancer Biomarkers</i> , 2018, 23, 79-93.	0.8	14

#	ARTICLE	IF	CITATIONS
4682	Effects of a wide range of dietary forage-to-concentrate ratios on nutrient utilization and hepatic transcriptional profiles in limit-fed Holstein heifers. <i>BMC Genomics</i> , 2018, 19, 148.	1.2	19
4683	Identification of four differentially methylated genes as prognostic signatures for stage I lung adenocarcinoma. <i>Cancer Cell International</i> , 2018, 18, 60.	1.8	15
4684	Comparison of Hepatic NRF2 and Aryl Hydrocarbon Receptor Binding in 2,3,7,8-Tetrachlorodibenzo- <i>p</i> -dioxin-Treated Mice Demonstrates NRF2-Independent PKM2 Induction. <i>Molecular Pharmacology</i> , 2018, 94, 876-884.	1.0	23
4685	Ouroboros resembling competitive endogenous loop (ORCEL) in circular RNAs revealed through transcriptome sequencing dataset analysis. <i>BMC Genomics</i> , 2018, 19, 171.	1.2	6
4686	Optimized Dosing Schedule Based on Circadian Dynamics of Mouse Breast Cancer Stem Cells Improves the Antitumor Effects of Aldehyde Dehydrogenase Inhibitor. <i>Cancer Research</i> , 2018, 78, 3698-3708.	0.4	46
4687	Identification of key gene modules for human osteosarcoma by co-expression analysis. <i>World Journal of Surgical Oncology</i> , 2018, 16, 89.	0.8	21
4688	Use of DAVID algorithms for clustering custom annotated gene lists in a non-model organism, rainbow trout. <i>BMC Research Notes</i> , 2018, 11, 63.	0.6	2
4689	JAK/STAT3 regulated global gene expression dynamics during late-stage reprogramming process. <i>BMC Genomics</i> , 2018, 19, 183.	1.2	22
4690	Interpretation of biological experiments changes with evolution of the Gene Ontology and its annotations. <i>Scientific Reports</i> , 2018, 8, 5115.	1.6	110
4691	Identification of potential crucial genes and construction of microRNA-mRNA negative regulatory networks in osteosarcoma. <i>Hereditas</i> , 2018, 155, 21.	0.5	32
4692	Riboflavin Depletion Promotes Tumorigenesis in HEK293T and NIH3T3 Cells by Sustaining Cell Proliferation and Regulating Cell Cycle-Related Gene Transcription. <i>Journal of Nutrition</i> , 2018, 148, 834-843.	1.3	13
4693	Diverse reprogramming codes for neuronal identity. <i>Nature</i> , 2018, 557, 375-380.	13.7	94
4694	Identification of target genes in cardiomyopathy with fibrosis and cardiac remodeling. <i>Journal of Biomedical Science</i> , 2018, 25, 63.	2.6	54
4695	Identification of H4K20me3- and H3K4me3-associated RNAs using CARIP-Seq expands the transcriptional and epigenetic networks of embryonic stem cells. <i>Journal of Biological Chemistry</i> , 2018, 293, 15120-15135.	1.6	7
4696	Analysis of differentially expressed genes among human hair follicle-derived iPSCs, induced hepatocyte-like cells, and primary hepatocytes. <i>Stem Cell Research and Therapy</i> , 2018, 9, 211.	2.4	10
4697	Sertoli cell-specific ablation of miR-17-92 cluster significantly alters whole testis transcriptome without apparent phenotypic effects. <i>PLoS ONE</i> , 2018, 13, e0197685.	1.1	11
4698	Identification of potential prognostic microRNA biomarkers for predicting survival in patients with hepatocellular carcinoma. <i>Cancer Management and Research</i> , 2018, Volume 10, 787-803.	0.9	48
4699	Comprehensive analysis of gene expression profiles provides insight into the pathogenesis of Crohn's disease. <i>Molecular Medicine Reports</i> , 2018, 18, 2643-2650.	1.1	5

#	ARTICLE	IF	CITATIONS
4700	Bioinformatics approach reveals the key role of C&#x2013;X&#x2013;C motif chemokine receptor 2 in endometriosis development. <i>Molecular Medicine Reports</i> , 2018, 18, 2841-2849.	1.1	6
4701	Candidate gene and mechanism investigations in congenital obstructive nephropathy based on bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2018, 18, 2651-2660.	1.1	1
4702	Epigenetic regulation of the circadian gene <i>Per1</i> contributes to age-related changes in hippocampal memory. <i>Nature Communications</i> , 2018, 9, 3323.	5.8	118
4703	Integrative epigenomic analysis in differentiated human primary bronchial epithelial cells exposed to cigarette smoke. <i>Scientific Reports</i> , 2018, 8, 12750.	1.6	11
4704	Mutant <i>KLF1</i> in Adult Anemic Nan Mice Leads to Profound Transcriptome Changes and Disordered Erythropoiesis. <i>Scientific Reports</i> , 2018, 8, 12793.	1.6	14
4705	Analysis of the miRNA and mRNA involved in osteogenesis of adipose&#x2013;derived mesenchymal stem cells. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 1111-1120.	0.8	22
4706	Identification of key genes and pathways using bioinformatics analysis in septic shock children. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 1163-1174.	1.1	20
4707	Co-expression Network Analysis of Biomarkers for Adrenocortical Carcinoma. <i>Frontiers in Genetics</i> , 2018, 9, 328.	1.1	52
4708	Transcriptomic analysis reveals inflammatory and metabolic pathways that are regulated by renal perfusion pressure in the outer medulla of Dahl-S rats. <i>Physiological Genomics</i> , 2018, 50, 440-447.	1.0	10
4709	Splicing Factor <i>RBM20</i> Regulates Transcriptional Network of Titin Associated and Calcium Handling Genes in The Heart. <i>International Journal of Biological Sciences</i> , 2018, 14, 369-380.	2.6	27
4710	Malignant canine mammary epithelial cells shed exosomes containing differentially expressed microRNA that regulate oncogenic networks. <i>BMC Cancer</i> , 2018, 18, 832.	1.1	37
4711	A novel gene-diet pair modulates <i>C. elegans</i> aging. <i>PLoS Genetics</i> , 2018, 14, e1007608.	1.5	21
4712	<i>RAP2</i> mediates mechanoresponses of the Hippo pathway. <i>Nature</i> , 2018, 560, 655-660.	13.7	266
4713	Comparative Secretome Analyses of Primary Murine White and Brown Adipocytes Reveal Novel Adipokines. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2358-2370.	2.5	51
4714	A gene interaction network&#x2013;based method to measure the common and heterogeneous mechanisms of gynecological cancer. <i>Molecular Medicine Reports</i> , 2018, 18, 230-242.	1.1	13
4715	Comprehending a Killer: The Akt/mTOR Signaling Pathways Are Temporally High-Jacked by the Highly Pathogenic 1918 Influenza Virus. <i>EBioMedicine</i> , 2018, 32, 142-163.	2.7	36
4716	<i>MCV-miR-M1</i> Targets the Host-Cell Immune Response Resulting in the Attenuation of Neutrophil Chemotaxis. <i>Journal of Investigative Dermatology</i> , 2018, 138, 2343-2354.	0.3	22
4717	Integrated analysis of long noncoding RNA and mRNA expression profile in children with obesity by microarray analysis. <i>Scientific Reports</i> , 2018, 8, 8750.	1.6	38

#	ARTICLE	IF	CITATIONS
4718	Deciphering the multicomponent synergy mechanism from a systems pharmacology perspective: Application to Gualou Xiebai Decoction for coronary heart disease. <i>Journal of Functional Foods</i> , 2018, 47, 143-155.	1.6	21
4719	Exploration of the molecular mechanisms of cervical cancer based on mRNA expression profiles and predicted microRNA interactions. <i>Oncology Letters</i> , 2018, 15, 8965-8972.	0.8	13
4720	FlyXCDBâ€”A Resource for Drosophila Cell Surface and Secreted Proteins and Their Extracellular Domains. <i>Journal of Molecular Biology</i> , 2018, 430, 3353-3411.	2.0	13
4721	A genome scan for selection signatures in Taihu pig breeds using next-generation sequencing. <i>Animal</i> , 2019, 13, 683-693.	1.3	15
4722	Analyzing Transcriptome-Phenotype Correlations. , 2019, , 819-824.		1
4723	Functional Genomics. , 2019, , 118-133.		5
4724	Bayesian Negative Binomial Mixture Regression Models for the Analysis of Sequence Count and Methylation Data. <i>Biometrics</i> , 2019, 75, 183-192.	0.8	10
4725	Comprehensive analysis of the whole coding and non-coding RNA transcriptome expression profiles and construction of the circRNAâ€”lncRNA co-regulated ceRNA network in laryngeal squamous cell carcinoma. <i>Functional and Integrative Genomics</i> , 2019, 19, 109-121.	1.4	46
4726	The metastatic microenvironment: Melanomaâ€”microglia cross-talk promotes the malignant phenotype of melanoma cells. <i>International Journal of Cancer</i> , 2019, 144, 802-817.	2.3	34
4727	Integral analyses of survivalâ€”related long nonâ€”coding RNA MIR210HG and its prognostic role in colon cancer. <i>Oncology Letters</i> , 2019, 18, 1107-1116.	0.8	18
4728	Comparative Analysis of the Liver and Spleen Transcriptomes between Holstein and Yunnan Humped Cattle. <i>Animals</i> , 2019, 9, 527.	1.0	3
4729	Transcriptome profiling of the liver among the prenatal and postnatal stages in chickens. <i>Poultry Science</i> , 2019, 98, 7030-7040.	1.5	24
4730	Identification of potential core genes in Kawasaki disease using bioinformatics analysis. <i>Journal of International Medical Research</i> , 2019, 47, 4051-4058.	0.4	7
4731	Maternal-to-zygotic transition as a potential target for niclosamide during early embryogenesis. <i>Toxicology and Applied Pharmacology</i> , 2019, 380, 114699.	1.3	14
4732	The anti-inflammatory function of adenine occurs through AMPK activation and its downstream transcriptional regulation in THP-1 cells. <i>Bioscience, Biotechnology and Biochemistry</i> , 2019, 83, 2220-2229.	0.6	5
4733	Mammalian Annotation Database for improved annotation and functional classification of Omics datasets from less well-annotated organisms. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	13
4734	The genomic landscape of estrogen receptor $\beta$ binding sites in mouse mammary gland. <i>PLoS ONE</i> , 2019, 14, e0220311.	1.1	25
4735	Identification of Potential Biomarkers and Survival Analysis for Head and Neck Squamous Cell Carcinoma Using Bioinformatics Strategy: A Study Based on TCGA and GEO Datasets. <i>BioMed Research International</i> , 2019, 2019, 1-14.	0.9	44

#	ARTICLE	IF	CITATIONS
4736	Application of the High-Throughput TAB-Array for the Discovery of Novel 5-Hydroxymethylcytosine Biomarkers in Pancreatic Ductal Adenocarcinoma. <i>Epigenomes</i> , 2019, 3, 16.	0.8	15
4737	Clinical value of microRNA-198-5p downregulation in lung adenocarcinoma and its potential pathways. <i>Oncology Letters</i> , 2019, 18, 2939-2954.	0.8	12
4738	An Insight Into the Molecular Mechanism of Berberine Towards Multiple Cancer Types Through Systems Pharmacology. <i>Frontiers in Pharmacology</i> , 2019, 10, 857.	1.6	34
4740	Identification of Key Genes and Pathways in Pancreatic Cancer Gene Expression Profile by Integrative Analysis. <i>Genes</i> , 2019, 10, 612.	1.0	22
4741	Computational Assessment of Bacterial Protein Structures Indicates a Selection Against Aggregation. <i>Cells</i> , 2019, 8, 856.	1.8	9
4742	Differential network analysis and protein-protein interaction study reveals active protein modules in glucocorticoid resistance for infant acute lymphoblastic leukemia. <i>Molecular Medicine</i> , 2019, 25, 36.	1.9	7
4743	Bioinformatic validation identifies candidate key genes in diffuse large-B cell lymphoma. <i>Personalized Medicine</i> , 2019, 16, 313-323.	0.8	7
4744	Pancreatic cancer biomarker detection by two support vector strategies for recursive feature elimination. <i>Biomarkers in Medicine</i> , 2019, 13, 105-121.	0.6	16
4745	Identifying miltefosine-resistant key genes in protein-protein interactions network and experimental verification in Iranian <i>Leishmania major</i> . <i>Molecular Biology Reports</i> , 2019, 46, 5371-5388.	1.0	4
4746	RNA 5-Methylcytosine Facilitates the Maternal-to-Zygotic Transition by Preventing Maternal mRNA Decay. <i>Molecular Cell</i> , 2019, 75, 1188-1202.e11.	4.5	242
4747	Bioinformatics analysis of a long non-coding RNA and mRNA regulation network in rats with middle cerebral artery occlusion based on RNA sequencing. <i>Molecular Medicine Reports</i> , 2019, 20, 417-432.	1.1	10
4748	&lt;p&gt;Detection of a novel panel of somatic mutations in plasma cell-free DNA and its diagnostic value in hepatocellular carcinoma&lt;/p&gt;. <i>Cancer Management and Research</i> , 2019, Volume 11, 5745-5756.	0.9	20
4749	Identification of Key Genes and Pathways Involved in the Heterogeneity of Intrinsic Growth Ability Between Neurons After Spinal Cord Injury in Adult Zebrafish. <i>Neurochemical Research</i> , 2019, 44, 2057-2067.	1.6	6
4750	FunDMDeep-m6A: identification and prioritization of functional differential m6A methylation genes. <i>Bioinformatics</i> , 2019, 35, i90-i98.	1.8	34
4751	Comprehensive analysis of a long non-coding RNA-mediated competitive endogenous RNA network in glioblastoma multiforme. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 1081-1090.	0.8	16
4752	Stress, novel sex genes, and epigenetic reprogramming orchestrate socially controlled sex change. <i>Science Advances</i> , 2019, 5, eaaw7006.	4.7	99
4753	Identification of microRNA-92a and the related combination biomarkers as promising substrates in predicting risk, recurrence and poor survival of colorectal cancer. <i>Journal of Cancer</i> , 2019, 10, 3154-3171.	1.2	16
4754	An immune infiltration signature to predict the overall survival of patients with colon cancer. <i>IUBMB Life</i> , 2019, 71, 1760-1770.	1.5	67

#	ARTICLE	IF	CITATIONS
4755	The Essential Oils and Eucalyptol From <i>Artemisia vulgaris</i> L. Prevent Acetaminophen-Induced Liver Injury by Activating Nrf2-Keap1 and Enhancing APAP Clearance Through Non-Toxic Metabolic Pathway. <i>Frontiers in Pharmacology</i> , 2019, 10, 782.	1.6	64
4756	Investigating the Proteomic Profile of HT-29 Colon Cancer Cells After <i>Lactobacillus kefir</i> SGL 13 Exposure Using the SWATH Method. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 1690-1699.	1.2	13
4757	Pleiotropic effects of rfa-gene mutations on <i>Escherichia coli</i> envelope properties. <i>Scientific Reports</i> , 2019, 9, 9696.	1.6	54
4758	High-content screen in human pluripotent cells identifies miRNA-regulated pathways controlling pluripotency and differentiation. <i>Stem Cell Research and Therapy</i> , 2019, 10, 202.	2.4	11
4759	Three Biomarkers Predict Gastric Cancer Patients' Susceptibility To Fluorouracil-based Chemotherapy. <i>Journal of Cancer</i> , 2019, 10, 2953-2960.	1.2	9
4760	Wx: a neural network-based feature selection algorithm for transcriptomic data. <i>Scientific Reports</i> , 2019, 9, 10500.	1.6	12
4761	Identification of gene co-expression modules and hub genes associated with lymph node metastasis of papillary thyroid cancer. <i>Endocrine</i> , 2019, 66, 573-584.	1.1	35
4762	Transcriptome Analysis of Landrace Pig Subcutaneous Preadipocytes during Adipogenic Differentiation. <i>Genes</i> , 2019, 10, 552.	1.0	14
4763	&lt;p&gt;Gene expression profiling reveals candidate biomarkers and probable molecular mechanism in diabetic peripheral neuropathy&lt;/p&gt;. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2019, Volume 12, 1213-1223.	1.1	13
4764	Single-Cell RNA-Sequencing and Metabolomics Analyses Reveal the Contribution of Perivascular Adipose Tissue Stem Cells to Vascular Remodeling. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019, 39, 2049-2066.	1.1	72
4765	Variants at potential loci associated with Sjogren's syndrome in Koreans: A genetic association study. <i>Clinical Immunology</i> , 2019, 207, 79-86.	1.4	5
4766	Redox-sensitive <i>ZIP68</i> plays a role in balancing stress tolerance with growth in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2019, 100, 768-783.	2.8	21
4767	A Study of the Association between Breastfeeding and DNA Methylation in Peripheral Blood Cells of Infants. <i>Russian Journal of Genetics</i> , 2019, 55, 749-755.	0.2	8
4768	Patterns of Geographical and Potential Adaptive Divergence in the Genome of the Common Carp ( <i>Cyprinus carpio</i> ). <i>Frontiers in Genetics</i> , 2019, 10, 660.	1.1	12
4769	&lt;p&gt;The prognostic value of LINC01296 in pan-cancers and the molecular regulatory mechanism in hepatocellular carcinoma: a comprehensive study based on data mining, bioinformatics, and in vitro validation&lt;/p&gt;. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 5861-5885.	1.0	4
4770	Bioinformatics analysis of mRNA and miRNA microarray to identify the key miRNA-gene pairs in small-cell lung cancer. <i>Molecular Medicine Reports</i> , 2019, 20, 2199-2208.	1.1	20
4771	SETD1A protects from senescence through regulation of the mitotic gene expression program. <i>Nature Communications</i> , 2019, 10, 2854.	5.8	37
4772	FXR overexpression alters adipose tissue architecture in mice and limits its storage capacity leading to metabolic derangements. <i>Journal of Lipid Research</i> , 2019, 60, 1547-1561.	2.0	19



#	ARTICLE	IF	CITATIONS
4773	Maternal and Post-weaning High-Fat Diets Produce Distinct DNA Methylation Patterns in Hepatic Metabolic Pathways within Specific Genomic Contexts. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3229.	1.8	10
4774	Identifying miRNA-mRNA Pairs and Novel miRNAs from Hepatocellular Carcinoma miRNomes and TCGA Database. <i>Journal of Cancer</i> , 2019, 10, 2552-2559.	1.2	14
4775	PPAR $\alpha$ gene is a diagnostic and prognostic biomarker in clear cell renal cell carcinoma by integrated bioinformatics analysis. <i>Journal of Cancer</i> , 2019, 10, 2319-2331.	1.2	8
4776	Considering smoking status, coexpression network analysis of non-small cell lung cancer at different cancer stages, exhibits important genes and pathways. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 19172-19185.	1.2	5
4777	Uncovering changes in proteomic signature of rat pelvic floor muscles in pregnancy. <i>American Journal of Obstetrics and Gynecology</i> , 2019, 221, 130.e1-130.e9.	0.7	6
4778	Lipid-Associated Macrophages Control Metabolic Homeostasis in a Trem2-Dependent Manner. <i>Cell</i> , 2019, 178, 686-698.e14.	13.5	718
4779	Comprehensive Analysis of Core Genes and Potential Mechanisms in Rectal Cancer. <i>Journal of Computational Biology</i> , 2019, 26, 1262-1277.	0.8	15
4780	Bioinformatics approach reveals the critical role of TGF- $\beta$ 2 signaling pathway in pre-eclampsia development. <i>European Journal of Obstetrics, Gynecology and Reproductive Biology</i> , 2019, 240, 130-138.	0.5	13
4781	Overexpression of miR-101 May Target DUSP1 to Promote the Cartilage Degradation in Rheumatoid Arthritis. <i>Journal of Computational Biology</i> , 2019, 26, 1067-1079.	0.8	4
4782	Dissecting Alzheimer's Disease Molecular Substrates by Proteomics and Discovery of Novel Post-translational Modifications. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 350-361.	1.0	12
4783	Mitochondrial 3243A>G mutation confers pro-atherogenic and pro-inflammatory properties in MELAS iPS derived endothelial cells. <i>Cell Death and Disease</i> , 2019, 10, 802.	2.7	23
4784	The Autoimmune Protocol Diet Modifies Intestinal RNA Expression in Inflammatory Bowel Disease. <i>Crohn's &amp; Colitis</i> 360, 2019, 1, otz016.	0.5	3
4785	Disruptive mutations in TANC2 define a neurodevelopmental syndrome associated with psychiatric disorders. <i>Nature Communications</i> , 2019, 10, 4679.	5.8	43
4786	Proteomic and transcriptional profiling of rat amygdala following social play. <i>Behavioural Brain Research</i> , 2019, 376, 112210.	1.2	11
4787	GWAS on Imputed Whole-Genome Resequencing From Genotyping-by-Sequencing Data for Farrowing Interval of Different Parities in Pigs. <i>Frontiers in Genetics</i> , 2019, 10, 1012.	1.1	20
4788	HOXC10 promotes migration and invasion via the WNT-EMT signaling pathway in oral squamous cell carcinoma. <i>Journal of Cancer</i> , 2019, 10, 4540-4551.	1.2	23
4789	Generation of human induced pluripotent stem cell-derived cardiomyocytes in 2D monolayer and scalable 3D suspension bioreactor cultures with reduced batch-to-batch variations. <i>Theranostics</i> , 2019, 9, 7222-7238.	4.6	52
4790	Potential protein biomarkers for systemic lupus erythematosus determined by bioinformatics analysis. <i>Computational Biology and Chemistry</i> , 2019, 83, 107135.	1.1	14

#	ARTICLE	IF	CITATIONS
4791	Mutations in KIAA1109, CACNA1C, BSN, AKAP13, CELSR2, and HELZ2 Are Associated With the Prognosis in Endometrial Cancer. <i>Frontiers in Genetics</i> , 2019, 10, 909.	1.1	24
4792	Analysis of Transcriptome, Selected Intracellular Signaling Pathways, Proliferation and Apoptosis of LNCaP Cells Exposed to High Leptin Concentrations. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5412.	1.8	15
4793	Characterization and Identification of Lysine Succinylation Sites based on Deep Learning Method. <i>Scientific Reports</i> , 2019, 9, 16175.	1.6	30
4794	Comprehensive investigation of the clinical significance and molecular mechanisms of plasmacytoma variant translocation 1 in sarcoma using genome-wide RNA sequencing data. <i>Journal of Cancer</i> , 2019, 10, 4961-4977.	1.2	11
4795	Identification of biomarker microRNA-mRNA regulatory pairs for predicting the docetaxel resistance in prostate cancer. <i>Journal of Cancer</i> , 2019, 10, 5469-5482.	1.2	7
4796	Distinct Roles for BET Family Members in Estrogen Receptor $\beta$ Enhancer Function and Gene Regulation in Breast Cancer Cells. <i>Molecular Cancer Research</i> , 2019, 17, 2356-2368.	1.5	17
4797	Promising Prognosis Marker Candidates on the Status of Epithelial-Mesenchymal Transition and Glioma Stem Cells in Glioblastoma. <i>Cells</i> , 2019, 8, 1312.	1.8	23
4798	The Impact of Moyamoya Disease and RNF213 Mutations on the Spectrum of Plasma Protein and MicroRNA. <i>Journal of Clinical Medicine</i> , 2019, 8, 1648.	1.0	7
4799	Intrarenal microRNA signature related to the fibrosis process in chronic kidney disease: identification and functional validation of key miRNAs. <i>BMC Nephrology</i> , 2019, 20, 336.	0.8	21
4800	Identification of microRNA-181 as a promising biomarker for predicting the poor survival in colorectal cancer. <i>Cancer Medicine</i> , 2019, 8, 5995-6009.	1.3	15
4801	Brain gene expression in a novel mouse model of postpartum mood disorder. <i>Translational Neuroscience</i> , 2019, 10, 168-174.	0.7	5
4802	In silico studies reveal RSc1154 and RhIE as temperature-related pathogenic proteins of <i>Ralstonia solanacearum</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	0
4803	A Coordinated Response at The Transcriptome and Interactome Level is Required to Ensure Uropathogenic <i>Escherichia coli</i> Survival during Bacteremia. <i>Microorganisms</i> , 2019, 7, 292.	1.6	5
4804	Maternal Low-Fat Diet Programs the Hepatic Epigenome despite Exposure to an Obesogenic Postnatal Diet. <i>Nutrients</i> , 2019, 11, 2075.	1.7	8
4805	Systems pharmacology dissection of action mechanisms of <i>Dipsaci Radix</i> for osteoporosis. <i>Life Sciences</i> , 2019, 235, 116820.	2.0	27
4806	ABCD: Alzheimer's disease Biomarkers Comprehensive Database. <i>3 Biotech</i> , 2019, 9, 351.	1.1	2
4807	Prim-O-glucosylcimifugin enhances the antitumour effect of PD-1 inhibition by targeting myeloid-derived suppressor cells. , 2019, 7, 231.		32
4808	<i>P4HB</i> , a Novel Hypoxia Target Gene Related to Gastric Cancer Invasion and Metastasis. <i>BioMed Research International</i> , 2019, 2019, 1-13.	0.9	35

#	ARTICLE	IF	CITATIONS
4809	Identification of serum exosomal microRNAs in acute spinal cord injured rats. <i>Experimental Biology and Medicine</i> , 2019, 244, 1149-1161.	1.1	30
4810	Identification of modules and functional analysis in CRC subtypes by integrated bioinformatics analysis. <i>PLoS ONE</i> , 2019, 14, e0221772.	1.1	6
4811	RhoC regulates radioresistance via crosstalk of ROCK2 with the DNA repair machinery in cervical cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 392.	3.5	30
4812	The Role of MicroRNAs in Early Chondrogenesis of Human Induced Pluripotent Stem Cells (hiPSCs). <i>International Journal of Molecular Sciences</i> , 2019, 20, 4371.	1.8	21
4813	Upregulation of MAPK10, TUBB2B and RASL11B may contribute to the development of neuroblastoma. <i>Molecular Medicine Reports</i> , 2019, 20, 3475-3486.	1.1	4
4814	Human Trophoblast Differentiation Is Associated With Profound Gene Regulatory and Epigenetic Changes. <i>Endocrinology</i> , 2019, 160, 2189-2203.	1.4	35
4815	Dissection of Pharmacological Mechanism of Chinese Herbal Medicine Yihuo Huatan Formula on Chronic Obstructive Pulmonary Disease: A Systems Pharmacology-Based Study. <i>Scientific Reports</i> , 2019, 9, 13431.	1.6	12
4816	Comprehensive transcriptome analysis of adipose tissue in the Bactrian camel reveals fore hump has more specific physiological functions in immune and endocrine systems. <i>Livestock Science</i> , 2019, 228, 195-200.	0.6	6
4817	Estrogen receptors promote NSCLC progression by modulating the membrane receptor signaling network: a systems biology perspective. <i>Journal of Translational Medicine</i> , 2019, 17, 308.	1.8	29
4818	Dynamic Changes in the Molecular Signature of Adverse Left Ventricular Remodeling in Patients With Compensated and Decompensated Chronic Primary Mitral Regurgitation. <i>Circulation: Heart Failure</i> , 2019, 12, e005974.	1.6	8
4819	Identification and characterization of SEC24D as a susceptibility gene for hepatitis B virus infection. <i>Scientific Reports</i> , 2019, 9, 13425.	1.6	2
4820	Integrated Analysis of Multiple Microarray Studies to Identify Novel Gene Signatures in Non-alcoholic Fatty Liver Disease. <i>Frontiers in Endocrinology</i> , 2019, 10, 599.	1.5	46
4821	Causes and Consequences of A Glutamine Induced Normoxic HIF1 Activity for the Tumor Metabolism. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4742.	1.8	19
4822	Transcriptomic analysis reveals new hippocampal gene networks induced by prolactin. <i>Scientific Reports</i> , 2019, 9, 13765.	1.6	20
4823	Identification of key genes and microRNAs involved in kidney Wilms tumor by integrated bioinformatics analysis. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 2554-2564.	0.8	3
4824	VWF, CXCL8 and IL6 might be potential druggable genes for acute coronary syndrome (ACS). <i>Computational Biology and Chemistry</i> , 2019, 83, 107125.	1.1	1
4825	Disruptive variants of <i>CSDE1</i> associate with autism and interfere with neuronal development and synaptic transmission. <i>Science Advances</i> , 2019, 5, eaax2166.	4.7	35
4826	LGP2 binds to PACT to regulate RIG-I and MDA5-mediated antiviral responses. <i>Science Signaling</i> , 2019, 12, .	1.6	51

#	ARTICLE	IF	CITATIONS
4827	Systematic Profiling of Alternative mRNA Splicing Signature for Predicting Glioblastoma Prognosis. <i>Frontiers in Oncology</i> , 2019, 9, 928.	1.3	25
4828	Microarray-based analysis of COL11A1 and TWIST1 as important differentially expressed pathogenic genes between left and right-sided colon cancer. <i>Molecular Medicine Reports</i> , 2019, 20, 4202-4214.	1.1	6
4829	Curcumin-Gene Expression Response in Hormone Dependent and Independent Metastatic Prostate Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4891.	1.8	27
4830	The Anti-Apoptotic Effect of ASC-Exosomes in an In Vitro ALS Model and Their Proteomic Analysis. <i>Cells</i> , 2019, 8, 1087.	1.8	58
4831	Computational identification of key genes that may regulate gene expression reprogramming in Alzheimer's patients. <i>PLoS ONE</i> , 2019, 14, e0222921.	1.1	22
4832	An undergraduate laboratory on RNA sequencing analysis of bacterial gene expression. <i>Biochemistry and Molecular Biology Education</i> , 2019, 47, 161-167.	0.5	1
4833	Transcriptomics analysis of host liver and meta-transcriptome analysis of rumen epimural microbial community in young calves treated with artificial dosing of rumen content from adult donor cow. <i>Scientific Reports</i> , 2019, 9, 790.	1.6	16
4834	Hypomethylation of <i>STAT1</i> and <i>HLA-DRB1</i> is associated with type-I interferon-dependent <i>HLA-DRB1</i> expression in lupus CD8+ T cells. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 519-528.	0.5	29
4835	Gene fingerprint model for literature based detection of the associations among complex diseases: a case study of COPD. <i>BMC Medical Informatics and Decision Making</i> , 2019, 19, 20.	1.5	3
4836	GOTrapper: a tool to navigate through branches of gene ontology hierarchy. <i>BMC Bioinformatics</i> , 2019, 20, 20.	1.2	11
4837	Development and validation of nomograms integrating immune-related genomic signatures with clinicopathologic features to improve prognosis and predictive value of triple-negative breast cancer: A gene expression-based retrospective study. <i>Cancer Medicine</i> , 2019, 8, 686-700.	1.3	18
4838	Alternative splicing coupled to nonsense-mediated mRNA decay contributes to the high-altitude adaptation of maca ( <i>Lepidium meyenii</i> ). <i>Gene</i> , 2019, 694, 7-18.	1.0	10
4839	Matrix metalloproteinase 9 inhibits the motility of highly aggressive HSC-3 oral squamous cell carcinoma cells. <i>Experimental Cell Research</i> , 2019, 376, 18-26.	1.2	13
4840	Identification of hub genes and therapeutic drugs in esophageal squamous cell carcinoma based on integrated bioinformatics strategy. <i>Cancer Cell International</i> , 2019, 19, 142.	1.8	21
4841	Transcriptional Regulatory Network Analysis to Reveal the Key Genes Involved in Skeletal Muscle Injury. <i>Journal of Computational Biology</i> , 2019, 26, 1090-1099.	0.8	3
4842	Robust Transcriptional Response to Heat Shock Impacting Diverse Cellular Processes despite Lack of Heat Shock Factor in Microsporidia. <i>MSphere</i> , 2019, 4, .	1.3	6
4843	Screening of differentially expressed genes and identification of NUF2 as a prognostic marker in breast cancer. <i>International Journal of Molecular Medicine</i> , 2019, 44, 390-404.	1.8	19
4844	Network analysis of hyphae forming proteins in <i>Candida albicans</i> identifies important proteins responsible for pathovirulence in the organism. <i>Heliyon</i> , 2019, 5, e01916.	1.4	11

#	ARTICLE	IF	CITATIONS
4845	Uncovering the pharmacological mechanism of <i>Carthamus tinctorius</i> L. on cardiovascular disease by a systems pharmacology approach. <i>Biomedicine and Pharmacotherapy</i> , 2019, 117, 109094.	2.5	56
4846	Exploring the protective effect of ShengMai-Yin and Ganmaidazao decoction combination against type 2 diabetes mellitus with nonalcoholic fatty liver disease by network pharmacology and validation in KKAY mice. <i>Journal of Ethnopharmacology</i> , 2019, 242, 112029.	2.0	29
4847	Secretion of fibronectin by human pancreatic stellate cells promotes chemoresistance to gemcitabine in pancreatic cancer cells. <i>BMC Cancer</i> , 2019, 19, 596.	1.1	83
4848	Astrocyte-specific transcriptome analysis using the ALDH1L1 bacTRAP mouse reveals novel biomarkers of astrogliosis in response to neurotoxicity. <i>Journal of Neurochemistry</i> , 2019, 150, 420-440.	2.1	18
4849	Metaproteomics: Sample Preparation and Methodological Considerations. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1073, 187-215.	0.8	26
4850	MicroRNA profiling of patients with sporadic atrial septal defect. <i>Biotechnology and Biotechnological Equipment</i> , 2019, 33, 510-519.	0.5	4
4851	Network pharmacology study of traditional Chinese medicines for stroke treatment and effective constituents screening. <i>Journal of Ethnopharmacology</i> , 2019, 242, 112044.	2.0	38
4852	Differentially expressed genes between systemic sclerosis and rheumatoid arthritis. <i>Hereditas</i> , 2019, 156, 17.	0.5	5
4853	Absorption of zinc ions dissolved from zinc oxide nanoparticles in the tobacco callus improves plant productivity. <i>Plant Cell, Tissue and Organ Culture</i> , 2019, 138, 377-385.	1.2	17
4854	Normoxia is not favorable for maintaining stemness of human endothelial progenitor cells. <i>Stem Cell Research</i> , 2019, 38, 101464.	0.3	7
4855	Overexpression of NCAPH is upregulated and predicts a poor prognosis in prostate cancer. <i>Oncology Letters</i> , 2019, 17, 5768-5776.	0.8	23
4856	Significance of PTEN Mutation in Cellular Process, Prognosis, and Drug Selection in Clear Cell Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2019, 9, 357.	1.3	26
4857	NAD tagSeq reveals that NAD <sup>+</sup> -capped RNAs are mostly produced from a large number of protein-coding genes in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12072-12077.	3.3	61
4858	m6A Regulates Neurogenesis and Neuronal Development by Modulating Histone Methyltransferase Ezh2. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 154-168.	3.0	135
4859	Investigation of the clinical significance and prospective molecular mechanisms of cystatin genes in patients with hepatitis B virus-related hepatocellular carcinoma. <i>Oncology Reports</i> , 2019, 42, 189-201.	1.2	8
4860	Transcriptomic changes in the prefrontal cortex of rats as a function of age and cognitive engagement. <i>Neurobiology of Learning and Memory</i> , 2019, 163, 107035.	1.0	6
4861	Macrophage centripetal migration drives spontaneous healing process after spinal cord injury. <i>Science Advances</i> , 2019, 5, eaav5086.	4.7	60
4862	Identification of the iduronate-2-sulfatase proteome in wild-type mouse brain. <i>Heliyon</i> , 2019, 5, e01667.	1.4	8

#	ARTICLE	IF	CITATIONS
4863	DNA methylome of human neonatal umbilical cord: Enrichment of differentially methylated regions compared to umbilical cord blood DNA at transcription factor genes involved in body patterning and effects of maternal folate deficiency or children's sex. PLoS ONE, 2019, 14, e0214307.	1.1	11
4864	The R2TP complex regulates paramyxovirus RNA synthesis. PLoS Pathogens, 2019, 15, e1007749.	2.1	12
4865	Expression Profile Analysis Identifies a Novel Five-Gene Signature to Improve Prognosis Prediction of Glioblastoma. Frontiers in Genetics, 2019, 10, 419.	1.1	52
4866	Sensory experience remodels genome architecture in neural circuit to drive motor learning. Nature, 2019, 569, 708-713.	13.7	66
4867	Identification of time-series differentially expressed genes and pathways associated with heart failure post-myocardial infarction using integrated bioinformatics analysis. Molecular Medicine Reports, 2019, 19, 5281-5290.	1.1	6
4868	Integrative analysis of transcriptome-wide association study data and mRNA expression profiles identified candidate genes and pathways associated with atrial fibrillation. Heart and Vessels, 2019, 34, 1882-1888.	0.5	6
4869	Identification and characterization of circular RNAs in chicken hepatocytes. Growth Hormone and IGF Research, 2019, 46-47, 16-23.	0.5	5
4870	Identification of potential biomarkers for diagnosis of pancreatic and biliary tract cancers by sequencing of serum microRNAs. BMC Medical Genomics, 2019, 12, 62.	0.7	19
4871	Proteomic Profiling of Human Prostate Cancer-associated Fibroblasts (CAF) Reveals LOXL2-dependent Regulation of the Tumor Microenvironment. Molecular and Cellular Proteomics, 2019, 18, 1410-1427.	2.5	60
4872	Unbiased Boolean analysis of public gene expression data for cell cycle gene identification. Molecular Biology of the Cell, 2019, 30, 1770-1779.	0.9	28
4873	Distinct Prognostic Values of Phospholipase C Beta Family Members for Non-Small Cell Lung Carcinoma. BioMed Research International, 2019, 2019, 1-11.	0.9	13
4874	Identification of novel biomarkers and candidate small molecule drugs in non-small-cell lung cancer by integrated microarray analysis. OncoTargets and Therapy, 2019, Volume 12, 3545-3563.	1.0	32
4875	Quantitative Proteomics Identifies DNA Repair as a Novel Biological Function for Hepatocyte Nuclear Factor 4 $\kappa$ in Colorectal Cancer Cells. Cancers, 2019, 11, 626.	1.7	13
4876	Screening candidate microRNA-mRNA network for predicting the response to chemoresistance in osteosarcoma by bioinformatics analysis. Journal of Cellular Biochemistry, 2019, 120, 16798-16810.	1.2	12
4877	Identification of novel biomarkers and small molecule drugs in human colorectal cancer by microarray and bioinformatics analysis. Molecular Genetics & Genomic Medicine, 2019, 7, e00713.	0.6	34
4878	Sphingosine-1-phosphate signalling drives an angiogenic transcriptional programme in diffuse large B cell lymphoma. Leukemia, 2019, 33, 2884-2897.	3.3	26
4879	Fatty acid-binding protein 1 increases steer fat deposition by facilitating the synthesis and secretion of triacylglycerol in liver. PLoS ONE, 2019, 14, e0214144.	1.1	15
4880	The promising novel biomarkers and candidate small molecule drugs in lower-grade glioma: Evidence from bioinformatics analysis of high-throughput data. Journal of Cellular Biochemistry, 2019, 120, 15106-15118.	1.2	22

#	ARTICLE	IF	CITATIONS
4881	A four-gene signature for prognosis in breast cancer patients with hypermethylated IL15RA. <i>Oncology Letters</i> , 2019, 17, 4245-4254.	0.8	11
4882	Comparative RNA-seq analysis of the drought-sensitive lentil ( <i>Lens culinaris</i> ) root and leaf under short- and long-term water deficits. <i>Functional and Integrative Genomics</i> , 2019, 19, 715-727.	1.4	34
4883	TAF5L and TAF6L Maintain Self-Renewal of Embryonic Stem Cells via the MYC Regulatory Network. <i>Molecular Cell</i> , 2019, 74, 1148-1163.e7.	4.5	36
4884	Integration of transcriptomic data in a genome-scale metabolic model to investigate the link between obesity and breast cancer. <i>BMC Bioinformatics</i> , 2019, 20, 162.	1.2	22
4885	FCRL5+ Memory B Cells Exhibit Robust Recall Responses. <i>Cell Reports</i> , 2019, 27, 1446-1460.e4.	2.9	87
4886	Identification of RE1-Silencing Transcription Factor as a Promoter of Metastasis in Pancreatic Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 291.	1.3	6
4887	Identification of DNA-Methylated CpG Islands Associated With Gene Silencing in the Adult Body Tissues of the Ogye Chicken Using RNA-Seq and Reduced Representation Bisulfite Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 346.	1.1	37
4888	SETD2 regulates the maternal epigenome, genomic imprinting and embryonic development. <i>Nature Genetics</i> , 2019, 51, 844-856.	9.4	207
4889	A cell type-specific transcriptomic approach to map B cell and monocyte type I interferon-linked pathogenic signatures in Multiple Sclerosis. <i>Journal of Autoimmunity</i> , 2019, 101, 1-16.	3.0	12
4890	Osseointegration effect of biomimetic intrafibrillarly mineralized collagen applied simultaneously with titanium implant: A pilot in vivo study. <i>Clinical Oral Implants Research</i> , 2019, 30, 637-648.	1.9	10
4891	Genome-wide Kdm4 histone demethylase transcriptional regulation in <i>Drosophila</i> . <i>Molecular Genetics and Genomics</i> , 2019, 294, 1107-1121.	1.0	7
4892	DNA alteration-based classification of uveal melanoma gives better prognostic stratification than immune infiltration, which has a neutral effect in high-risk group. <i>Cancer Medicine</i> , 2019, 8, 3036-3046.	1.3	13
4893	Matrix Metalloproteinase 11 Is a Potential Therapeutic Target in Lung Adenocarcinoma. <i>Molecular Therapy - Oncolytics</i> , 2019, 14, 82-93.	2.0	35
4894	Inhibition of protein disulfide isomerase in glioblastoma causes marked downregulation of DNA repair and DNA damage response genes. <i>Theranostics</i> , 2019, 9, 2282-2298.	4.6	35
4895	Comprehensive analysis of transcriptomic changes induced by low and high doses of bisphenol A in HepG2 spheroids in vitro and rat liver in vivo. <i>Environmental Research</i> , 2019, 173, 124-134.	3.7	9
4896	Development and validation of a TP53-associated immune prognostic model for hepatocellular carcinoma. <i>EBioMedicine</i> , 2019, 42, 363-374.	2.7	257
4897	Identification of Candidate Genes and MicroRNAs for Acute Myocardial Infarction by Weighted Gene Coexpression Network Analysis. <i>BioMed Research International</i> , 2019, 2019, 1-11.	0.9	23
4898	Comparative Gene Expression Profiles in Parathyroid Adenoma and Normal Parathyroid Tissue. <i>Journal of Clinical Medicine</i> , 2019, 8, 297.	1.0	14

#	ARTICLE	IF	CITATIONS
4899	Analysis of the Functional Relevance of Epigenetic Chromatin Marks in the First Intron Associated with Specific Gene Expression Patterns. <i>Genome Biology and Evolution</i> , 2019, 11, 786-797.	1.1	13
4900	Genomic Variations in Susceptibility to Intracranial Aneurysm in the Korean Population. <i>Journal of Clinical Medicine</i> , 2019, 8, 275.	1.0	24
4901	circLPAR1 is a novel biomarker of prognosis for muscle-invasive bladder cancer with invasion and metastasis by miR-762. <i>Oncology Letters</i> , 2019, 17, 3537-3547.	0.8	34
4902	Cell Wall Hydrolases in Bacteria: Insight on the Diversity of Cell Wall Amidases, Glycosidases and Peptidases Toward Peptidoglycan. <i>Frontiers in Microbiology</i> , 2019, 10, 331.	1.5	225
4903	Prediction of platinum-resistance patients of gastric cancer using bioinformatics. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 13478-13486.	1.2	6
4904	Dietary Restriction Extends Lifespan through Metabolic Regulation of Innate Immunity. <i>Cell Metabolism</i> , 2019, 29, 1192-1205.e8.	7.2	122
4905	Clinical value screening, prognostic significance and key pathway identification of miR-204-5p in endometrial carcinoma: A study based on the Cancer Genome Atlas (TCGA), and bioinformatics analysis. <i>Pathology Research and Practice</i> , 2019, 215, 1003-1011.	1.0	15
4906	Variable outcomes of human heart attack recapitulated in genetically diverse mice. <i>Npj Regenerative Medicine</i> , 2019, 4, 5.	2.5	20
4907	Combined analysis and validation for DNA methylation and gene expression profiles associated with prostate cancer. <i>Cancer Cell International</i> , 2019, 19, 50.	1.8	28
4908	Dark-colored maple syrup treatment induces S-phase cell cycle arrest via reduced proliferating cell nuclear antigen expression in colorectal cancer cells. <i>Oncology Letters</i> , 2019, 17, 2713-2720.	0.8	3
4909	A glucagon-like peptide-1 analog, liraglutide, ameliorates endothelial dysfunction through miRNAs to inhibit apoptosis in rats. <i>PeerJ</i> , 2019, 7, e6567.	0.9	13
4910	A Computational Platform and Guide for Acceleration of Novel Medicines and Personalized Medicine. <i>Methods in Molecular Biology</i> , 2019, 1939, 181-198.	0.4	1
4911	Thrombospondin-2 regulates extracellular matrix production, LOX levels, and cross-linking via downregulation of miR-29. <i>Matrix Biology</i> , 2019, 82, 71-85.	1.5	33
4912	Transcriptome profiling analysis reveals that CXCL2 is involved in anlotinib resistance in human lung cancer cells. <i>BMC Medical Genomics</i> , 2019, 12, 38.	0.7	28
4913	Genomic and epigenomic mapping of leptin-responsive neuronal populations involved in body weight regulation. <i>Nature Metabolism</i> , 2019, 1, 475-484.	5.1	17
4914	Identification of a three-miRNA signature as a novel potential prognostic biomarker in patients with clear cell renal cell carcinoma. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 13751-13764.	1.2	32
4915	Conserved motifs in nuclear genes encoding predicted mitochondrial proteins in <i>Trypanosoma cruzi</i> . <i>PLoS ONE</i> , 2019, 14, e0215160.	1.1	5
4916	Urinary miRNA-29a-3p levels are associated with metabolic parameters via regulation of IGF1 in patients with metabolic syndrome. <i>Biomedical Reports</i> , 2019, 10, 250-258.	0.9	8



#	ARTICLE	IF	CITATIONS
4917	Identification of key pathways and genes in nasopharyngeal carcinoma using bioinformatics analysis. <i>Oncology Letters</i> , 2019, 17, 4683-4694.	0.8	9
4918	Transcriptome analysis of rumen epithelium and meta-transcriptome analysis of rumen epimural microbial community in young calves with feed induced acidosis. <i>Scientific Reports</i> , 2019, 9, 4744.	1.6	25
4919	Integrated analysis of lncRNA and mRNA repertoires in Marek's disease infected spleens identifies genes relevant to resistance. <i>BMC Genomics</i> , 2019, 20, 245.	1.2	46
4920	HDAC1 and HDAC2 independently regulate common and specific intrinsic responses in murine enteroids. <i>Scientific Reports</i> , 2019, 9, 5363.	1.6	19
4921	Deciphering the Pharmacological Mechanism of the Herb Radix Ophiopogonis in the Treatment of Nasopharyngeal Carcinoma by Integrating iTRAQ-Coupled 2-D LC-MS/MS Analysis and Network Investigation. <i>Frontiers in Pharmacology</i> , 2019, 10, 253.	1.6	11
4922	Identification of the Biomarkers and Pathological Process of Osteoarthritis: Weighted Gene Co-expression Network Analysis. <i>Frontiers in Physiology</i> , 2019, 10, 275.	1.3	38
4923	Identification of lncRNA-miRNA-mRNA regulatory network associated with epithelial ovarian cancer cisplatin-resistant. <i>Journal of Cellular Physiology</i> , 2019, 234, 19886-19894.	2.0	44
4924	Co-regulatory Network of Oncosuppressor miRNAs and Transcription Factors for Pathology of Human Hepatic Cancer Stem Cells (HCSC). <i>Scientific Reports</i> , 2019, 9, 5564.	1.6	27
4925	Building the drug-GO function network to screen significant candidate drugs for myasthenia gravis. <i>PLoS ONE</i> , 2019, 14, e0214857.	1.1	5
4926	Gene expression profiles between cystic and solid vestibular schwannoma indicate susceptible molecules and pathways in the cystic formation of vestibular schwannoma. <i>Functional and Integrative Genomics</i> , 2019, 19, 673-684.	1.4	7
4927	Identification of miRNAs as biomarkers for nonalcoholic fatty liver disease. <i>Journal of Cellular Physiology</i> , 2019, 234, 17361-17369.	2.0	6
4928	Hippocampal gene expression patterns linked to late-life physical activity oppose age and AD-related transcriptional decline. <i>Neurobiology of Aging</i> , 2019, 78, 142-154.	1.5	31
4929	Competitive Endogenous RNA (ceRNA) Regulation Network of lncRNA-miRNA-mRNA in Colorectal Carcinogenesis. <i>Digestive Diseases and Sciences</i> , 2019, 64, 1868-1877.	1.1	50
4930	Activation of Autophagy, Observed in Liver Tissues From Patients With Wilson Disease and From ATP7B-Deficient Animals, Protects Hepatocytes From Copper-Induced Apoptosis. <i>Gastroenterology</i> , 2019, 156, 1173-1189.e5.	0.6	150
4931	Conserved Disease Modules Extracted From Multilayer Heterogeneous Disease and Gene Networks for Understanding Disease Mechanisms and Predicting Disease Treatments. <i>Frontiers in Genetics</i> , 2019, 9, 745.	1.1	52
4932	Repurposing of Drugs as Novel Influenza Inhibitors From Clinical Gene Expression Infection Signatures. <i>Frontiers in Immunology</i> , 2019, 10, 60.	2.2	44
4933	RCC2, a regulator of the RalA signaling pathway, is identified as a novel therapeutic target in cisplatin-resistant ovarian cancer. <i>FASEB Journal</i> , 2019, 33, 5350-5365.	0.2	16
4934	Comparison of the Transcriptomes and Proteomes of Serum Exosomes from Marek's Disease Virus-Vaccinated and Protected and Lymphoma-Bearing Chickens. <i>Genes</i> , 2019, 10, 116.	1.0	23

#	ARTICLE	IF	CITATIONS
4935	Computational prediction of the bioactivity potential of proteomes based on expert knowledge. <i>Journal of Biomedical Informatics</i> , 2019, 91, 103121.	2.5	2
4936	Low concentrations of perfluorooctane sulfonate repress osteogenic and enhance adipogenic differentiation of human mesenchymal stem cells. <i>Toxicology and Applied Pharmacology</i> , 2019, 367, 82-91.	1.3	16
4937	Identification of key pathways and hub genes in basal-like breast cancer using bioinformatics analysis. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 1319-1331.	1.0	50
4938	Integrated bioinformatics analysis reveals novel key biomarkers and potential candidate small molecule drugs in gastric cancer. <i>Pathology Research and Practice</i> , 2019, 215, 1038-1048.	1.0	16
4939	ISL1 predicts poor outcomes for patients with gastric cancer and drives tumor progression through binding to the ZEB1 promoter together with SETD7. <i>Cell Death and Disease</i> , 2019, 10, 33.	2.7	32
4940	Proteomic analysis reveals a protective role of specific macrophage subsets in liver repair. <i>Scientific Reports</i> , 2019, 9, 2953.	1.6	16
4941	The promising novel biomarkers and candidate small molecule drugs in kidney renal clear cell carcinoma: Evidence from bioinformatics analysis of high-throughput data. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e607.	0.6	44
4942	Locomotor Training Increases Synaptic Structure With High NGL-2 Expression After Spinal Cord Hemisection. <i>Neurorehabilitation and Neural Repair</i> , 2019, 33, 225-231.	1.4	7
4943	Prediction of Drug Positioning for Quan-Du-Zhong Capsules Against Hypertensive Nephropathy Based on the Robustness of Disease Network. <i>Frontiers in Pharmacology</i> , 2019, 10, 49.	1.6	15
4944	Multi-omics Analysis of Primary Cell Culture Models Reveals Genetic and Epigenetic Basis of Intratumoral Phenotypic Diversity. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 576-589.	3.0	10
4945	Vildagliptin, a dipeptidyl peptidase-4 inhibitor, attenuated endothelial dysfunction through miRNAs in diabetic rats. <i>Archives of Medical Science</i> , 2021, 17, 1378-1387.	0.4	7
4946	Identification of key protein-coding genes in lung adenocarcinomas based on bioinformatic analysis. <i>Translational Cancer Research</i> , 2019, 8, 2829-2840.	0.4	1
4947	Systematic Investigation of Berberine for Treating Hepatocellular Carcinoma Based on Network Pharmacology. <i>Digital Chinese Medicine</i> , 2019, 2, 127-135.	0.5	2
4948	Pathway Analysis for SNP microarray data. , 2019, , .		1
4949	Analysis of mRNA biomarker predicting progression of acute lymphoblastic leukaemia by big data mining. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 332, 032022.	0.2	0
4950	Study of the Gastrointestinal Heat Retention Syndrome in Children: From Diagnostic Model to Biological Basis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2019, 2019, 1-12.	0.5	3
4951	Down-regulated hsa_circ_0067934 facilitated the progression of gastric cancer by sponging hsa-mir-4705 to downgrade the expression of BMPR1B. <i>Translational Cancer Research</i> , 2019, 8, 2691-2703.	0.4	7
4952	The four-microRNA signature identified by bioinformatics analysis predicts the prognosis of nasopharyngeal carcinoma patients. <i>Oncology Reports</i> , 2019, 42, 1767-1780.	1.2	22

#	ARTICLE	IF	CITATIONS
4953	Gene Expression Profiling of Human Adipose Tissue Stem Cells during 2D versus 3D Adipogenesis. <i>Cells Tissues Organs</i> , 2019, 208, 113-133.	1.3	8
4954	Single-Cell RNA Sequencing of Plant-Associated Bacterial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 2452.	1.5	10
4955	The assessment of efficient representation of drug features using deep learning for drug repositioning. <i>BMC Bioinformatics</i> , 2019, 20, 577.	1.2	16
4956	Identification of key biomarkers associated with development and prognosis in patients with ovarian carcinoma: evidence from bioinformatic analysis. <i>Journal of Ovarian Research</i> , 2019, 12, 110.	1.3	23
4957	In silico identification of microRNAs as candidate colorectal cancer biomarkers. <i>Tumor Biology</i> , 2019, 41, 101042831988372.	0.8	11
4958	BCL2 and hsa-miR-181a-5p are potential biomarkers associated with papillary thyroid cancer based on bioinformatics analysis. <i>World Journal of Surgical Oncology</i> , 2019, 17, 221.	0.8	11
4959	MLL3 governs human haematopoietic stem-cell self-renewal and engraftment. <i>Nature</i> , 2019, 576, 281-286.	13.7	94
4960	TS-GOEA: a web tool for tissue-specific gene set enrichment analysis based on gene ontology. <i>BMC Bioinformatics</i> , 2019, 20, 572.	1.2	7
4961	Gene Expression Profiles Controlled by the Alternative Splicing Factor Nova2 in Endothelial Cells. <i>Cells</i> , 2019, 8, 1498.	1.8	10
4962	Gcn5-Mediated Histone Acetylation Governs Nucleosome Dynamics in Spermiogenesis. <i>Developmental Cell</i> , 2019, 51, 745-758.e6.	3.1	47
4963	Arabidopsis proteome and the mass spectral assay library. <i>Scientific Data</i> , 2019, 6, 278.	2.4	39
4964	Establishment of a mouse model for injury-induced scar formation and the accompanying chronic pain: Comprehensive microarray analysis of molecular expressions in fibrosis and hyperalgesia. <i>Molecular Pain</i> , 2019, 15, 174480691989238.	1.0	1
4965	Spatial organization of endometrial gene expression at the onset of embryo attachment in pigs. <i>BMC Genomics</i> , 2019, 20, 895.	1.2	26
4966	Omics-based Investigation of Diet-induced Obesity Synergized with HBx, Src, and p53 Mutation Accelerating Hepatocarcinogenesis in Zebrafish Model. <i>Cancers</i> , 2019, 11, 1899.	1.7	18
4967	Integration of protein interaction and gene co-expression information for identification of melanoma candidate genes. <i>Melanoma Research</i> , 2019, 29, 126-133.	0.6	4
4968	A Maternal High-Fat Diet Induces DNA Methylation Changes That Contribute to Glucose Intolerance in Offspring. <i>Frontiers in Endocrinology</i> , 2019, 10, 871.	1.5	50
4969	Joint Transcriptomic Analysis of Lung Cancer and Other Lung Diseases. <i>Frontiers in Genetics</i> , 2019, 10, 1260.	1.1	9
4970	CDK1 and CCNB1 as potential diagnostic markers of rhabdomyosarcoma: validation following bioinformatics analysis. <i>BMC Medical Genomics</i> , 2019, 12, 198.	0.7	24

#	ARTICLE	IF	CITATIONS
4971	The regulatory effect of microRNA-21a-3p on the promotion of telocyte angiogenesis mediated by PI3K (p110 $\alpha$ )/AKT/mTOR in LPS induced mice ARDS. <i>Journal of Translational Medicine</i> , 2019, 17, 427.	1.8	26
4972	Construction of an miRNA-mRNA regulatory network in colorectal cancer with bioinformatics methods. <i>Anti-Cancer Drugs</i> , 2019, 30, 588-595.	0.7	8
4973	DNA methylation profiles are associated with complex regional pain syndrome after traumatic injury. <i>Pain</i> , 2019, 160, 2328-2337.	2.0	19
4974	Expression Profile of the Chromosome 14 MicroRNA Cluster (C14MC) Ortholog in Equine Maternal Circulation throughout Pregnancy and Its Potential Implications. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6285.	1.8	12
4975	Bioinformatics analysis of differentially expressed genes involved in human developmental chondrogenesis. <i>Medicine (United States)</i> , 2019, 98, e16240.	0.4	6
4976	Whole genome sequencing of <i>Entamoeba nuttalli</i> reveals mammalian host-related molecular signatures and a novel octapeptide-repeat surface protein. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007923.	1.3	7
4977	Long Noncoding RNA LINC00265 Targets EGFR and Promotes Deterioration of Colorectal Cancer: A Comprehensive Study Based on Data Mining and in vitro Validation. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 10681-10692.	1.0	14
4978	Identification of Transcriptional Metabolic Dysregulation in Subtypes of Pituitary Adenoma by Integrated Bioinformatics Analysis. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2019, Volume 12, 2441-2451.	1.1	7
4979	Epigenetic reprogramming underlies efficacy of DNA demethylation therapy in osteosarcomas. <i>Scientific Reports</i> , 2019, 9, 20360.	1.6	13
4980	Shared co-expression networks in frontal cortex of the normal aged brain and schizophrenia. <i>Schizophrenia Research</i> , 2019, 204, 253-261.	1.1	6
4981	Reconstruction of mandibular bone defects using biphasic calcium phosphate bone substitutes with simultaneous implant placement in mini-pig: A pilot in vivo study. <i>Journal of Biomedical Materials Research - Part B Applied Biomaterials</i> , 2019, 107, 2071-2079.	1.6	8
4982	Smell of Infection: A Novel, Noninvasive Method for Detection of Fish Excretory-Secretory Proteins. <i>Journal of Proteome Research</i> , 2019, 18, 1371-1379.	1.8	4
4983	Unveiling Active Constituents and Potential Targets Related to the Hematinic Effect of Steamed <i>Panax notoginseng</i> Using Network Pharmacology Coupled With Multivariate Data Analyses. <i>Frontiers in Pharmacology</i> , 2018, 9, 1514.	1.6	18
4984	Six genes as potential diagnosis and prognosis biomarkers for hepatocellular carcinoma through data mining. <i>Journal of Cellular Physiology</i> , 2019, 234, 9787-9792.	2.0	14
4985	Integrated miRNA and mRNA transcriptomes of spleen profiles between Yorkshire and Queshan black pigs. <i>Gene</i> , 2019, 688, 204-214.	1.0	8
4986	Hypocrellin A-based photodynamic action induces apoptosis in A549 cells through ROS-mediated mitochondrial signaling pathway. <i>Acta Pharmaceutica Sinica B</i> , 2019, 9, 279-293.	5.7	95
4987	Epigenetic Alternations of MicroRNAs and DNA Methylation Contribute to Liver Metastasis of Colorectal Cancer. <i>Digestive Diseases and Sciences</i> , 2019, 64, 1523-1534.	1.1	31
4988	Time series analysis of gene changes and processes after burn with human gene expression profiles. <i>Burns</i> , 2019, 45, 387-397.	1.1	5

#	ARTICLE	IF	CITATIONS
4989	PPIExp: A Web-Based Platform for Integration and Visualization of Protein-Protein Interaction Data and Spatiotemporal Proteomics Data. <i>Journal of Proteome Research</i> , 2019, 18, 633-641.	1.8	8
4990	Quantitative proteomics reveals mitochondrial respiratory chain as a dominant target for carbon ion radiation: Delayed reactive oxygen species generation caused DNA damage. <i>Free Radical Biology and Medicine</i> , 2019, 130, 436-445.	1.3	23
4991	Circulating miR-143-3p inhibition protects against insulin resistance in Metabolic Syndrome via targeting of the insulin-like growth factor 2 receptor. <i>Translational Research</i> , 2019, 205, 33-43.	2.2	55
4992	Identification of hsa-miR-34a, hsa-miR-124, and hsa-miR-204 as signatures for cataract. <i>Journal of Cellular Physiology</i> , 2019, 234, 10709-10717.	2.0	14
4993	Role of $17\beta$ -Estradiol in MCF-7 Breast Cancer Cell Line Based on the Bioinformatics Analysis. <i>Gynecologic and Obstetric Investigation</i> , 2019, 84, 268-276.	0.7	3
4994	A three-gene methylation marker panel for the nodal metastatic risk assessment of muscle-invasive bladder cancer. <i>Journal of Cancer Research and Clinical Oncology</i> , 2019, 145, 811-820.	1.2	7
4995	Gene expression profiling identifies potential molecular markers of papillary thyroid carcinoma. <i>Cancer Biomarkers</i> , 2019, 24, 71-83.	0.8	24
4996	OCT4 maintains self-renewal and reverses senescence in human hair follicle mesenchymal stem cells through the downregulation of p21 by DNA methyltransferases. <i>Stem Cell Research and Therapy</i> , 2019, 10, 28.	2.4	40
4997	Network Analyses of Integrated Differentially Expressed Genes in Papillary Thyroid Carcinoma to Identify Characteristic Genes. <i>Genes</i> , 2019, 10, 45.	1.0	8
4998	Commonly Used Pancreatic Stellate Cell Cultures Differ Phenotypically and in Their Interactions with Pancreatic Cancer Cells. <i>Cells</i> , 2019, 8, 23.	1.8	25
4999	DRMY1, a Myb-Like Protein, Regulates Cell Expansion and Seed Production in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 285-302.	1.5	15
5000	Genomic and Transcriptomic Basis of <i>Hanseniaspora vineae</i> 's Impact on Flavor Diversity and Wine Quality. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	51
5001	miRNA-223 targets the GPAM gene and regulates the differentiation of intramuscular adipocytes. <i>Gene</i> , 2019, 685, 106-113.	1.0	42
5002	Systems pharmacology uncover the mechanism of anti-non-small cell lung cancer for <i>Hedyotis diffusa</i> Willd. <i>Biomedicine and Pharmacotherapy</i> , 2019, 109, 969-984.	2.5	30
5003	Identification of six miRNAs serving as predictive biomarkers in coronary artery disease. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 1932-1942.	1.2	1
5004	Absence of Mutation Enrichment for Genes Phylogenetically Conserved in the Olivocerebellar Motor Circuitry in a Cohort of Canadian Essential Tremor Cases. <i>Molecular Neurobiology</i> , 2019, 56, 4317-4321.	1.9	2
5005	Follicle populations and gene expression profiles of Nelore and Angus heifers with low and high ovarian follicle counts. <i>Molecular Reproduction and Development</i> , 2019, 86, 197-208.	1.0	6
5006	NF- $\kappa$ B p65 dimerization and DNA-binding is important for inflammatory gene expression. <i>FASEB Journal</i> , 2019, 33, 4188-4202.	0.2	30

#	ARTICLE	IF	CITATIONS
5007	A Serum-Induced Transcriptome and Serum Cytokine Signature Obtained at Diagnosis Correlates with the Development of Early Pancreatic Ductal Adenocarcinoma Metastasis. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 680-689.	1.1	2
5008	Identification of molecular signatures of cystic fibrosis disease status with plasma-based functional genomics. <i>Physiological Genomics</i> , 2019, 51, 27-41.	1.0	14
5009	Transgene-associated human growth hormone expression in pancreatic $\beta$ -cells impairs identification of sex-based gene expression differences. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2019, 316, E196-E209.	1.8	22
5010	Identification of hub genes to regulate breast cancer metastasis to brain by bioinformatics analyses. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 9522-9531.	1.2	82
5011	Practical considerations on performing and analyzing CLIP-seq experiments to identify transcriptomic-wide RNA-protein interactions. <i>Methods</i> , 2019, 155, 49-57.	1.9	12
5012	Siglec-1 Macrophages and the Contribution of IFN to the Development of Autoimmune Congenital Heart Block. <i>Journal of Immunology</i> , 2019, 202, 48-55.	0.4	39
5013	Identification of eight meta-signature miRNAs as potential biomarkers for oropharyngeal cancers. <i>Cancer Genetics</i> , 2019, 233-234, 75-83.	0.2	5
5014	Identification of key genes in prostate cancer gene expression profile by bioinformatics. <i>Andrologia</i> , 2019, 51, e13169.	1.0	12
5015	Suppression of myopathic lamin mutations by muscle-specific activation of AMPK and modulation of downstream signaling. <i>Human Molecular Genetics</i> , 2019, 28, 351-371.	1.4	16
5016	Cell type-specific endometrial transcriptome changes during initial recognition of pregnancy in the mare. <i>Reproduction, Fertility and Development</i> , 2019, 31, 496.	0.1	17
5017	Comparative analysis of spleen transcriptome detects differences in evolutionary adaptation of immune defense functions in bighead carp and silver carp. <i>Fish and Shellfish Immunology</i> , 2019, 84, 148-157.	1.6	12
5018	Pathway enrichment analysis approach based on topological structure and updated annotation of pathway. <i>Briefings in Bioinformatics</i> , 2019, 20, 168-177.	3.2	32
5019	Comparative sequence alignment reveals River Buffalo genomic structural differences compared with cattle. <i>Genomics</i> , 2019, 111, 418-425.	1.3	8
5020	It is time to apply biclustering: a comprehensive review of biclustering applications in biological and biomedical data. <i>Briefings in Bioinformatics</i> , 2019, 20, 1450-1465.	3.2	42
5021	Prioritizing complex disease risk genes by integrating multiple data. <i>Genomics</i> , 2019, 111, 590-597.	1.3	2
5022	Flexible Non-negative Matrix Factorization to Unravel Disease-related Genes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1-1.	1.9	8
5023	The Overexpression of CD80 and ISG15 Are Associated with the Progression and Metastasis of Breast Cancer by a Meta-Analysis Integrating Three Microarray Datasets. <i>Pathology and Oncology Research</i> , 2020, 26, 443-452.	0.9	19
5024	Co-expression analysis provides important module and pathways of human dilated cardiomyopathy. <i>Journal of Cellular Physiology</i> , 2020, 235, 494-503.	2.0	8

#	ARTICLE	IF	CITATIONS
5025	Perturbation of the immune cells and prenatal neurogenesis by the triplication of the <i>Erg</i> gene in mouse models of Down syndrome. <i>Brain Pathology</i> , 2020, 30, 75-91.	2.1	8
5026	Exploration of invasive mechanisms via global ncRNA-associated virus-host crosstalk. <i>Genomics</i> , 2020, 112, 1643-1650.	1.3	7
5027	Driving Neurogenesis in Neural Stem Cells with High Sensitivity Optogenetics. <i>NeuroMolecular Medicine</i> , 2020, 22, 139-149.	1.8	7
5028	Detailed Analysis of Molecular Mechanisms in Primary and Metastatic Melanoma. <i>Journal of Computational Biology</i> , 2020, 27, 9-19.	0.8	5
5029	A Novel Genes Signature Associated with the Progression of Polycystic Ovary Syndrome. <i>Pathology and Oncology Research</i> , 2020, 26, 575-582.	0.9	11
5030	Gene coexpression analysis offers important modules and pathway of human lung adenocarcinomas. <i>Journal of Cellular Physiology</i> , 2020, 235, 454-464.	2.0	14
5031	ARAP1 is an independent prognostic biomarker in older women with ovarian high-grade serous adenocarcinoma receiving first-line platinum-based antineoplastic therapy. <i>Acta Oncologica</i> , 2020, 59, 40-47.	0.8	3
5032	Key Regulatory Effect of Activated <i>HIF-1<math>\alpha</math></i> /VEGFA Signaling Pathway in Systemic Capillary Leak Syndrome Confirmed by Bioinformatics Analysis. <i>Journal of Computational Biology</i> , 2020, 27, 914-922.	0.8	5
5033	HNF1B-mediated repression of SLUG is suppressed by EZH2 in aggressive prostate cancer. <i>Oncogene</i> , 2020, 39, 1335-1346.	2.6	32
5034	A transcriptomic study of selenium against liver injury induced by beta-cypermethrin in mice by RNA-seq. <i>Functional and Integrative Genomics</i> , 2020, 20, 343-353.	1.4	3
5035	The Nuclear Matrix Protein SAFB Cooperates with Major Satellite RNAs to Stabilize Heterochromatin Architecture Partially through Phase Separation. <i>Molecular Cell</i> , 2020, 77, 368-383.e7.	4.5	104
5036	Integrating transcriptome-wide association study and mRNA expression profiling identified candidate genes and pathways associated with osteomyelitis. <i>Scandinavian Journal of Rheumatology</i> , 2020, 49, 131-136.	0.6	1
5037	Integrated Analysis of DNA Copy Number Changes and Gene Expression Identifies Key Genes in Gastric Cancer. <i>Journal of Computational Biology</i> , 2020, 27, 877-887.	0.8	11
5038	MiR-5p protects from kidney fibrosis by metabolic reprogramming. <i>FASEB Journal</i> , 2020, 34, 410-431.	0.2	50
5039	Effects of <i>Kudoa septempunctata</i> infections in a human intestinal epithelial model (Caco-2): a DNA microarray study. <i>Bioscience, Biotechnology and Biochemistry</i> , 2020, 84, 1030-1038.	0.6	3
5040	Dysfunctional epigenetic aging of the normal colon and colorectal cancer risk. <i>Clinical Epigenetics</i> , 2020, 12, 5.	1.8	47
5041	S1PR1-Associated Molecular Signature Predicts Survival in Patients with Sepsis. <i>Shock</i> , 2020, 53, 284-292.	1.0	13
5042	The diagnosis and prognosis values of WNT mRNA expression in colon adenocarcinoma. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 3145-3161.	1.2	18

#	ARTICLE	IF	CITATIONS
5043	An Integrated Mass Spectroscopy Data Processing Strategy for Fast Identification, In-Depth, and Reproducible Quantification of Protein <i>O</i> -Glycosylation in a Large Cohort of Human Urine Samples. <i>Analytical Chemistry</i> , 2020, 92, 690-698.	3.2	21
5044	A network-based predictive gene expression signature for recurrence risks in stage II colorectal cancer. <i>Cancer Medicine</i> , 2020, 9, 179-193.	1.3	16
5045	Episo: quantitative estimation of RNA 5-methylcytosine at isoform level by high-throughput sequencing of RNA treated with bisulfite. <i>Bioinformatics</i> , 2020, 36, 2033-2039.	1.8	5
5046	Epigenomic analysis of gastrulation identifies a unique chromatin state for primed pluripotency. <i>Nature Genetics</i> , 2020, 52, 95-105.	9.4	69
5047	Identification of miR-210 and combination biomarkers as useful agents in early screening non-small cell lung cancer. <i>Gene</i> , 2020, 729, 144225.	1.0	6
5048	Serum exosomal microRNA transcriptome profiling in subacute spinal cord injured rats. <i>Genomics</i> , 2020, 112, 2092-2105.	1.3	16
5049	A dual role of dLsd1 in oogenesis: regulating developmental genes and repressing transposons. <i>Nucleic Acids Research</i> , 2020, 48, 1206-1224.	6.5	5
5050	Screening prognosis-related genes in glioblastoma by microarray analysis. <i>Anti-Cancer Drugs</i> , 2020, 31, 150-157.	0.7	1
5051	Identifying the Cellular Interactome of Epstein-Barr Virus Lytic Regulator Zta Reveals Cellular Targets Contributing to Viral Replication. <i>Journal of Virology</i> , 2020, 94, .	1.5	9
5052	TFIIIC Binding to Alu Elements Controls Gene Expression via Chromatin Looping and Histone Acetylation. <i>Molecular Cell</i> , 2020, 77, 475-487.e11.	4.5	65
5053	Brassinosteroids Antagonize Jasmonate-Activated Plant Defense Responses through BRI1-EMS-SUPPRESSOR1 (BES1). <i>Plant Physiology</i> , 2020, 182, 1066-1082.	2.3	48
5054	Systematic construction and validation of an immune prognostic model for lung adenocarcinoma. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 1233-1244.	1.6	52
5055	Identification of the potential biomarkers in patients with glioma: a weighted gene co-expression network analysis. <i>Carcinogenesis</i> , 2020, 41, 743-750.	1.3	17
5056	Advancing the Role of Gamma-Tocotrienol as Proteasomes Inhibitor: A Quantitative Proteomic Analysis of MDA-MB-231 Human Breast Cancer Cells. <i>Biomolecules</i> , 2020, 10, 19.	1.8	16
5057	RNA-seq and ChIP-seq as Complementary Approaches for Comprehension of Plant Transcriptional Regulatory Mechanism. <i>International Journal of Molecular Sciences</i> , 2020, 21, 167.	1.8	24
5058	PTPN21 CDS long isoform inhibits the response of acute lymphoblastic leukemia cells to NK-mediated lysis via the KIR/HLA axis. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 3298-3312.	1.2	3
5059	Identification of a Prognostic Model Based on Immune-Related Genes of Lung Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 1588.	1.3	16
5060	Identification of RNA Transcript Makers Associated With Prognosis of Kidney Renal Clear Cell Carcinoma by a Competing Endogenous RNA Network Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 540094.	1.1	18



#	ARTICLE	IF	CITATIONS
5061	Exosome-mediated miR-9-5p promotes proliferation and migration of renal cancer cells both in vitro and in vivo by targeting SOCS4. <i>Biochemical and Biophysical Research Communications</i> , 2020, 529, 1216-1224.	1.0	16
5062	Combined blockade of polo-like kinase and pan-RAF is effective against NRAS-mutant non-small cell lung cancer cells. <i>Cancer Letters</i> , 2020, 495, 135-144.	3.2	8
5063	The critical role of BAP1 mutation in the prognosis and treatment selection of kidney renal clear cell carcinoma. <i>Translational Andrology and Urology</i> , 2020, 9, 1725-1734.	0.6	10
5064	The Perspective of Diagnostic and Prognostic Values of Lipoygenases mRNA Expression in Colon Adenocarcinoma. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 9389-9405.	1.0	11
5065	Serum exosomal microRNA transcriptome profiling in subacute spinal cord injured rats. <i>Genomics</i> , 2020, 112, 5086-5100.	1.3	8
5066	Transcriptional Expressions of CXCL9/10/12/13 as Prognosis Factors in Breast Cancer. <i>Journal of Oncology</i> , 2020, 2020, 1-15.	0.6	11
5067	Identification of potential specific biomarkers and key signaling pathways between osteogenic and adipogenic differentiation of hBMSCs for osteoporosis therapy. <i>Journal of Orthopaedic Surgery and Research</i> , 2020, 15, 437.	0.9	11
5068	Systematically Exploring the Antitumor Mechanisms of Core Chinese Herbs on Hepatocellular Carcinoma: A Computational Study. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-13.	0.5	4
5069	A Network Pharmacology Technique to Investigate the Synergistic Mechanisms of <i>Salvia miltiorrhiza</i> and <i>Radix puerariae</i> in Treatment of Cardio-Cerebral Vascular Diseases. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-18.	0.5	6
5070	Uncovering the protective mechanism of Taohong Siwu decoction against diabetic retinopathy via HIF-1 signaling pathway based on network analysis and experimental validation. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 298.	1.2	8
5071	A prognostic gene expression signature for oropharyngeal squamous cell carcinoma. <i>EBioMedicine</i> , 2020, 61, 102805.	2.7	16
5072	Development and validation of a metastasis-related Gene Signature for predicting the Overall Survival in patients with Pancreatic Ductal Adenocarcinoma. <i>Journal of Cancer</i> , 2020, 11, 6299-6318.	1.2	26
5073	Intracellular calcium current disorder and disease phenotype in OBSCN mutant iPSC-based cardiomyocytes in arrhythmogenic right ventricular cardiomyopathy. <i>Theranostics</i> , 2020, 10, 11215-11229.	4.6	17
5074	Argonaut: A Web Platform for Collaborative Multi-omic Data Visualization and Exploration. <i>Patterns</i> , 2020, 1, 100122.	3.1	18
5075	CRISPR screening of porcine sgRNA library identifies host factors associated with Japanese encephalitis virus replication. <i>Nature Communications</i> , 2020, 11, 5178.	5.8	40
5076	Biomarker exploration of miR-203 as a promising substrate for predicting poor survival outcome in colorectal cancer. <i>BMC Cancer</i> , 2020, 20, 1003.	1.1	4
5077	Uncovering the pharmacological mechanism of motherwort ( <i>Leonurus japonicus</i> Houtt.) for treating menstrual disorders: A systems pharmacology approach. <i>Computational Biology and Chemistry</i> , 2020, 89, 107384.	1.1	10
5078	Identification of biomarkers correlated with diagnosis and prognosis of endometrial cancer using bioinformatics analysis. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 4908-4921.	1.2	7

#	ARTICLE	IF	CITATIONS
5079	Injection of seminal fluid into the hemocoel of honey bee queens ( <i>Apis mellifera</i> ) can stimulate post-mating changes. <i>Scientific Reports</i> , 2020, 10, 11990.	1.6	9
5080	A Network Pharmacology Approach to Investigate the Active Compounds and Mechanisms of Musk for Ischemic Stroke. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-14.	0.5	14
5081	Significance of tumor protein p53 mutation in cellular process and drug selection in brain lower grade (WHO grades II and III) glioma. <i>Biomarkers in Medicine</i> , 2020, 14, 1139-1150.	0.6	10
5082	Identification of Target Genes in Hypertension and Left Ventricular Remodeling. <i>Medicine (United Tj ETQq1 1 0.784314 rgBT/Overlook</i>	0.4	10
5083	Identification of candidate biomarkers and pathways associated with psoriasis using bioinformatics analysis. <i>Hereditas</i> , 2020, 157, 30.	0.5	14
5084	Multi-layered proteomic analyses decode compositional and functional effects of cancer mutations on kinase complexes. <i>Nature Communications</i> , 2020, 11, 3563.	5.8	26
5085	Mesenchymal Stem Cell-Derived Extracellular Vesicles Attenuate Radiation-Induced Lung Injury via miRNA-214-3p. <i>Antioxidants and Redox Signaling</i> , 2021, 35, 849-862.	2.5	61
5086	Fatty Acid Metabolism in Immune Cells: A Bioinformatics Analysis of Genes Involved in Ulcerative Colitis. <i>DNA and Cell Biology</i> , 2020, 39, 1573-1582.	0.9	9
5087	Large-scale site-specific mapping of the O-GalNAc glycoproteome. <i>Nature Protocols</i> , 2020, 15, 2589-2610.	5.5	28
5088	The Dysregulation and Prognostic Analysis of STRIPAK Complex Across Cancers. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 625.	1.8	8
5089	Identification and validation of novel DNA methylation markers for early diagnosis of lung adenocarcinoma. <i>Molecular Oncology</i> , 2020, 14, 2744-2758.	2.1	17
5090	Natural Selection on Exonic SNPs Shapes Allelic Expression Imbalance (AEI) Adaptability in Lung Cancer Progression. <i>Frontiers in Genetics</i> , 2020, 11, 665.	1.1	1
5091	In silico and in vitro studies reveal complement system drives coagulation cascade in SARS-CoV-2 pathogenesis. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3734-3744.	1.9	22
5092	Investigation of the miRNA and mRNA Coexpression Network and Their Prognostic Value in Hepatocellular Carcinoma. <i>BioMed Research International</i> , 2020, 2020, 1-19.	0.9	7
5093	HLH-11 modulates lipid metabolism in response to nutrient availability. <i>Nature Communications</i> , 2020, 11, 5959.	5.8	20
5094	Characterization of transcriptional response of <i>Lactobacillus plantarum</i> under acidic conditions provides insight into bacterial adaptation in fermentative environments. <i>Scientific Reports</i> , 2020, 10, 19203.	1.6	8
5095	Uncovering the pharmacological mechanism of the effects of the Banxia-Xiakucuo Chinese Herb Pair on sleep disorder by a systems pharmacology approach. <i>Scientific Reports</i> , 2020, 10, 20454.	1.6	8
5096	Identifying a Potential Key Gene, TIMP1, Associated with Liver Metastases of Uveal Melanoma by Weight Gene Co-Expression Network Analysis. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 11923-11934.	1.0	2

#	ARTICLE	IF	CITATIONS
5097	Site-Specific Phosphorylation of Histone H1.4 Is Associated with Transcription Activation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8861.	1.8	8
5098	CD74, a novel predictor for bronchopulmonary dysplasia in preterm infants. <i>Medicine (United States)</i> , 2020, 99, e23477.	0.4	3
5099	Differentially Expressed mRNAs and Their Long Noncoding RNA Regulatory Network with <i>Helicobacter pylori</i> -Associated Diseases including Atrophic Gastritis and Gastric Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-16.	0.9	6
5100	DNA methylation during human adipogenesis and the impact of fructose. <i>Genes and Nutrition</i> , 2020, 15, 21.	1.2	8
5101	Reconstruction of Dementia Gene Network Using Online Bioinformatics Tools. , 2020, , .		0
5102	Ubiquitin-Like Modifier Activating Enzyme 1 as a Novel Diagnostic and Prognostic Indicator That Correlates With Ferroptosis and the Malignant Phenotypes of Liver Cancer Cells. <i>Frontiers in Oncology</i> , 2020, 10, 592413.	1.3	36
5103	Computational Prediction of Antiangiogenesis Synergistic Mechanisms of Total Saponins of <i>Panax japonicus</i> Against Rheumatoid Arthritis. <i>Frontiers in Pharmacology</i> , 2020, 11, 566129.	1.6	4
5104	Genome-Wide Analysis of Nubian Ibex Reveals Candidate Positively Selected Genes That Contribute to Its Adaptation to the Desert Environment. <i>Animals</i> , 2020, 10, 2181.	1.0	12
5105	SITC cancer immunotherapy resource document: a compass in the land of biomarker discovery. , 2020, 8, e000705.		20
5106	TTK, CDC25A, and ESPL1 as Prognostic Biomarkers for Endometrial Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	12
5107	Combining bioinformatics techniques to explore the molecular mechanisms involved in pancreatic cancer metastasis and prognosis. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 14128-14138.	1.6	19
5108	Identification of Crucial lncRNAs, miRNAs, mRNAs, and Potential Therapeutic Compounds for Polycystic Ovary Syndrome by Bioinformatics Analysis. <i>BioMed Research International</i> , 2020, 2020, 1-16.	0.9	12
5109	Interactome analysis of gene expression profiles identifies CDC6 as a potential therapeutic target modified by miR-215-5p in hepatocellular carcinoma. <i>International Journal of Medical Sciences</i> , 2020, 17, 2926-2940.	1.1	6
5110	Identification of immune-related genes as prognostic factors in bladder cancer. <i>Scientific Reports</i> , 2020, 10, 19695.	1.6	15
5111	Transcriptomics and Prognosis Analysis to Identify Critical Biomarkers in Invasive Breast Carcinoma. <i>Technology in Cancer Research and Treatment</i> , 2020, 19, 153303382095701.	0.8	2
5112	Mechanisms of Core Chinese Herbs against Colorectal Cancer: A Study Based on Data Mining and Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-15.	0.5	5
5113	Ribosome Recycling by ABCE1 Links Lysosomal Function and Iron Homeostasis to 3' UTR-Directed Regulation and Nonsense-Mediated Decay. <i>Cell Reports</i> , 2020, 32, 107895.	2.9	36
5114	Fto-modulated lipid niche regulates adult neurogenesis through modulating adenosine metabolism. <i>Human Molecular Genetics</i> , 2020, 29, 2775-2787.	1.4	15

#	ARTICLE	IF	CITATIONS
5115	Network Pharmacology Analysis and Experiments Validation of the Inhibitory Effect of JianPi Fu Recipe on Colorectal Cancer LoVo Cells Metastasis and Growth. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-15.	0.5	15
5116	Identification of a three-long noncoding RNA prognostic model involved competitive endogenous RNA in kidney renal clear cell carcinoma. Cancer Cell International, 2020, 20, 319.	1.8	25
5117	Ferroptosis-Related Gene Signature Predicts Glioma Cell Death and Glioma Patient Progression. Frontiers in Cell and Developmental Biology, 2020, 8, 538.	1.8	105
5118	Genome-Wide Profiling of Alternative Splicing Signature Reveals Prognostic Predictor for Esophageal Carcinoma. Frontiers in Genetics, 2020, 11, 796.	1.1	5
5119	Flubendazole elicits anti-cancer effects via targeting EVA1A-modulated autophagy and apoptosis in Triple-negative Breast Cancer. Theranostics, 2020, 10, 8080-8097.	4.6	48
5120	DNA Methylation Clocks and Their Predictive Capacity for Aging Phenotypes and Healthspan. Neuroscience Insights, 2020, 15, 263310552094222.	0.9	86
5121	Natural Killer cell transcriptome during primary EBV infection and EBV associated Hodgkin Lymphoma in childrenâ€”A preliminary observation. Immunobiology, 2020, 225, 151907.	0.8	2
5122	Genes associated with survival of female bovine blastocysts produced in vivo. Cell and Tissue Research, 2020, 382, 665-678.	1.5	13
5123	Discovery of Selenocysteine as a Potential Nanomedicine Promotes Cartilage Regeneration With Enhanced Immune Response by Text Mining and Biomedical Databases. Frontiers in Pharmacology, 2020, 11, 1138.	1.6	5
5124	MiR-93/miR-375: Diagnostic Potential, Aggressiveness Correlation and Common Target Genes in Prostate Cancer. International Journal of Molecular Sciences, 2020, 21, 5667.	1.8	13
5125	Novel variants in women with premature ovarian function decline identified via whole-exome sequencing. Journal of Assisted Reproduction and Genetics, 2020, 37, 2487-2502.	1.2	11
5126	Lower expression of LINC00092 in lung adenocarcinoma might mean poorer prognosis. Medicine (United States), 2020, 99, e23012.	0.4	7
5127	Integrative Analysis of Regulatory Module Reveals Associations of Microgravity with Dysfunctions of Multi-body Systems and Tumorigenesis. International Journal of Molecular Sciences, 2020, 21, 7585.	1.8	5
5128	Analysis of Gender-Specific Regulatory Mechanisms on the Oncogenesis and Prognosis of Glioblastoma Multiforme. Journal of Physics: Conference Series, 2020, 1575, 012059.	0.3	0
5129	Amino Sugars Reshape Interactions between Streptococcus mutans and Streptococcus gordonii. Applied and Environmental Microbiology, 2020, 87, .	1.4	6
5130	Transcriptome Reveals Multi Pigmentation Genes Affecting Dorsoventral Pattern in Avian Body. Frontiers in Cell and Developmental Biology, 2020, 8, 560766.	1.8	11
5131	Identification and Validation of Novel Genes in Anaplastic Thyroid Carcinoma via Bioinformatics Analysis. Cancer Management and Research, 2020, Volume 12, 9787-9799.	0.9	10
5132	The integration of transcriptome-wide association study and mRNA expression profiling data to identify candidate genes and gene sets associated with dental caries. Archives of Oral Biology, 2020, 118, 104863.	0.8	7

#	ARTICLE	IF	CITATIONS
5133	Chromatin Looping Shapes KLF5-Dependent Transcriptional Programs in Human Epithelial Cancers. <i>Cancer Research</i> , 2020, 80, 5464-5477.	0.4	24
5134	Integrated Genome-Wide Methylation and Expression Analyses Reveal Key Regulators in Osteosarcoma. <i>Computational and Mathematical Methods in Medicine</i> , 2020, 2020, 1-11.	0.7	7
5135	Analysis of circulating-microRNA expression in lactating Holstein cows under summer heat stress. <i>PLoS ONE</i> , 2020, 15, e0231125.	1.1	14
5136	Integrative genomics analysis of various omics data and networks identify risk genes and variants vulnerable to childhood-onset asthma. <i>BMC Medical Genomics</i> , 2020, 13, 123.	0.7	15
5137	Short-Term Mild Temperature-Stress-Induced Alterations in the <i>C. elegans</i> Phosphoproteome. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6409.	1.8	13
5138	Coexpression Network Analysis Identifies a Novel Nine-RNA Signature to Improve Prognostic Prediction for Prostate Cancer Patients. <i>BioMed Research International</i> , 2020, 2020, 1-17.	0.9	8
5139	Review on the Computational Genome Annotation of Sequences Obtained by Next-Generation Sequencing. <i>Biology</i> , 2020, 9, 295.	1.3	45
5140	Neferine sensitized Taxol-resistant nasopharyngeal carcinoma to Taxol by inhibiting EMT via downregulating miR-130b-5p. <i>Biochemical and Biophysical Research Communications</i> , 2020, 531, 573-580.	1.0	11
5141	Existence and possible roles of independent non-CpG methylation in the mammalian brain. <i>DNA Research</i> , 2020, 27, .	1.5	10
5142	Can Scoliotic Discs Be Controls for Molecular Studies in Intervertebral Disc Research? Insights From Proteomics. <i>Global Spine Journal</i> , 2020, , 219256822095903.	1.2	0
5143	Systems pharmacology-based approach to investigate the mechanisms of Danggui-Shaoyao-san prescription for treatment of Alzheimer's disease. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 282.	1.2	18
5144	A network pharmacology study on analgesic mechanism of Yuanhu-Baizhi herb pair. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 284.	1.2	12
5145	Transcriptome analysis reveals key signature genes involved in the oncogenesis of lung cancer. <i>Cancer Biomarkers</i> , 2020, 29, 475-482.	0.8	5
5146	Scalable module detection for attributed networks with applications to breast cancer. <i>Journal of Applied Statistics</i> , 2020, , 1-18.	0.6	1
5147	A Bioinformatics Research on Novel Mechanism of Compound Kushen Injection for Treating Breast Cancer by Network Pharmacology and Molecular Docking Verification. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-14.	0.5	8
5148	Seven immune-related genes prognostic power and correlation with tumor-infiltrating immune cells in hepatocellular carcinoma. <i>Cancer Medicine</i> , 2020, 9, 7440-7452.	1.3	24
5149	Identification of genes and pathways associated with subchondral bone in osteoarthritis via bioinformatic analysis. <i>Medicine (United States)</i> , 2020, 99, e22142.	0.4	4
5150	Construction and analysis of the protein-protein interaction network for the olfactory system of the silkworm <i>Bombyx mori</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 105, e21737.	0.6	9

#	ARTICLE	IF	CITATIONS
5151	Systemic Expression Analysis Reveals Prognostic Significance of WIPI3 in Hepatocellular Carcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 847.	1.1	5
5152	miRTissue ce: extending miRTissue web service with the analysis of ceRNA-ceRNA interactions. <i>BMC Bioinformatics</i> , 2020, 21, 199.	1.2	12
5153	Essential amino acid supplementation alters the p53 transcriptional response and cytokine gene expression following total knee arthroplasty. <i>Journal of Applied Physiology</i> , 2020, 129, 980-991.	1.2	3
5154	Circulation of gut-preactivated naïve CD8 <sup>+</sup> T cells enhances antitumor immunity in B cell-defective mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23674-23683.	3.3	22
5155	Identification of Pathways Associated with Placental Adaptation to Maternal Nutrient Restriction in Sheep. <i>Genes</i> , 2020, 11, 1031.	1.0	5
5156	Three-dimensional facial-image analysis to predict heterogeneity of the human ageing rate and the impact of lifestyle. <i>Nature Metabolism</i> , 2020, 2, 946-957.	5.1	45
5157	Construction of circRNA-Associated ceRNA Network Reveals Novel Biomarkers for Esophageal Cancer. <i>Computational and Mathematical Methods in Medicine</i> , 2020, 2020, 1-12.	0.7	13
5158	An Integrative Serum Pharmacology-Based Approach to Study the Anti-Tumor Activity of <i>B. paniculatum</i> Aqueous Bulb Extract on the Human Hepatocellular Carcinoma Cell Line BEL-7404. <i>Frontiers in Pharmacology</i> , 2020, 11, 01261.	1.6	7
5159	RNA-Seq reveals placental growth factor regulates the human retinal endothelial cell barrier integrity by transforming growth factor (TGF- $\beta$ 2) signaling. <i>Molecular and Cellular Biochemistry</i> , 2020, 475, 93-106.	1.4	5
5160	The current landscape of coronavirus-host protein-protein interactions. <i>Journal of Translational Medicine</i> , 2020, 18, 319.	1.8	66
5161	Identification of Critical Pathways and Hub Genes in LanCL1-Overexpressed Prostate Cancer Cells. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 7653-7664.	1.0	1
5162	Functional in vivo and in vitro effects of 20q11.21 genetic aberrations on hPSC differentiation. <i>Scientific Reports</i> , 2020, 10, 18582.	1.6	17
5163	Response to iron overload in cultured hepatocytes. <i>Scientific Reports</i> , 2020, 10, 21184.	1.6	11
5164	Characterization of mRNA Profiles of Exosomes from Diverse Forms of M2 Macrophages. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	4
5165	Prognostic value of Glypican family genes in early-stage pancreatic ductal adenocarcinoma after pancreaticoduodenectomy and possible mechanisms. <i>BMC Gastroenterology</i> , 2020, 20, 415.	0.8	9
5166	MiR-218 affects hypertrophic differentiation of human mesenchymal stromal cells during chondrogenesis via targeting RUNX2, MEF2C, and COL10A1. <i>Stem Cell Research and Therapy</i> , 2020, 11, 532.	2.4	11
5167	RNA-Seq Whole Transcriptome Analysis of Bovine Mammary Epithelial Cells in Response to Intracellular <i>Staphylococcus aureus</i> . <i>Frontiers in Veterinary Science</i> , 2020, 7, 642.	0.9	9
5168	Effect of Intrauterine Smoke Exposure on microRNA-15a Expression in Human Lung Development and Subsequent Asthma Risk. <i>Healthcare (Switzerland)</i> , 2020, 8, 536.	1.0	5

#	ARTICLE	IF	CITATIONS
5169	Identifying Key MicroRNAs Targeted by Narenmandula in a Rodent Nephropathy Model. Evidence-based Complementary and Alternative Medicine, 2020, 2020, 1-9.	0.5	2
5170	Transcriptome Analyses of $\beta$ -Thalassemia $\alpha^2$ (A&G) Mutation Using Isogenic Cell Models Generated by CRISPR/Cas9 and Asymmetric Single-Stranded Oligodeoxynucleotides (ssODNs). Frontiers in Genetics, 2020, 11, 577053.	1.1	5
5171	SOX2 promotes resistance of melanoma with PD-L1 high expression to T-cell-mediated cytotoxicity that can be reversed by SAHA. , 2020, 8, e001037.		27
5172	H4K20me3 methyltransferase SUV420H2 shapes the chromatin landscape of pluripotent embryonic stem cells. Development (Cambridge), 2020, 147, .	1.2	11
5173	Proteomic analysis of platelet-rich and platelet-poor plasma. Regenerative Therapy, 2020, 15, 226-235.	1.4	13
5174	Integrative Analysis of DNA Methylation Identified 12 Signature Genes Specific to Metastatic ccRCC. Frontiers in Oncology, 2020, 10, 556018.	1.3	9
5175	Bioinformatic Analysis Identifies Potential Key Genes in the Pathogenesis of Melanoma. Frontiers in Oncology, 2020, 10, 581985.	1.3	9
5176	&lt;p&gt;Identification of Pannexin 2 as a Novel Marker Correlating with Ferroptosis and Malignant Phenotypes of Prostate Cancer Cells&lt;/p&gt;. OncoTargets and Therapy, 2020, Volume 13, 4411-4421.	1.0	24
5177	Radiation Induces Autophagy <i>via</i> Histone H4 Lysine 20 Trimethylation in Non-small Cell Lung Cancer Cells. Anticancer Research, 2020, 40, 2537-2548.	0.5	9
5178	<i>MCM2</i> and <i>NUSAP1</i> Are Potential Biomarkers for the Diagnosis and Prognosis of Pancreatic Cancer. BioMed Research International, 2020, 2020, 1-20.	0.9	21
5179	Expression profiling and analysis of some miRNAs in subcutaneous white adipose tissue during development of obesity. Genes and Nutrition, 2020, 15, 8.	1.2	15
5180	Discovery of genes and proteins possibly regulating mean wool fibre diameter using cDNA microarray and proteomic approaches. Scientific Reports, 2020, 10, 7726.	1.6	6
5181	Yeast-Based Genetic Interaction Analysis of Human Kinome. Cells, 2020, 9, 1156.	1.8	5
5182	Identification of gene expression markers and development of evaluation method using cell-based and RT-PCR-based assay for skin sensitising potential of chemicals. Xenobiotica, 2020, 50, 1359-1369.	0.5	0
5183	Nine hub genes related to the prognosis of HBV-positive hepatocellular carcinoma identified by protein interaction analysis. Annals of Translational Medicine, 2020, 8, 478-478.	0.7	13
5184	Comprehensive analysis of competing endogenous RNA network in Wilms tumor based on the TARGET database. Translational Andrology and Urology, 2020, 9, 473-484.	0.6	0
5185	Integrin-Linked Kinase Mediates Therapeutic Resistance of Quiescent CML Stem Cells to Tyrosine Kinase Inhibitors. Cell Stem Cell, 2020, 27, 110-124.e9.	5.2	29
5186	Identification of a Gene-Related Risk Signature in Melanoma Patients Using Bioinformatic Profiling. Journal of Oncology, 2020, 2020, 1-13.	0.6	8

#	ARTICLE	IF	CITATIONS
5187	Prognostic implication and functional exploration for microRNA-20a as a molecular biomarker of gastrointestinal cancer. <i>BMC Cancer</i> , 2020, 20, 420.	1.1	3
5188	MyomirDB: A unified database and server platform for muscle atrophy myomiRs, coregulatory networks and regulons. <i>Scientific Reports</i> , 2020, 10, 8593.	1.6	3
5189	T Cells Produce IFN- $\gamma$ in the TREX1 D18N Model of Lupus-like Autoimmunity. <i>Journal of Immunology</i> , 2020, 204, 348-359.	0.4	13
5190	Peptide SMIM30 promotes HCC development by inducing SRC/YES1 membrane anchoring and MAPK pathway activation. <i>Journal of Hepatology</i> , 2020, 73, 1155-1169.	1.8	111
5191	Ribosomal protein S11 influences glioma response to TOP2 poisons. <i>Oncogene</i> , 2020, 39, 5068-5081.	2.6	21
5192	Proteome characteristics of liver tissue from patients with parenteral nutrition-associated liver disease. <i>Nutrition and Metabolism</i> , 2020, 17, 43.	1.3	6
5193	The Mutant p53-Driven Secretome Has Oncogenic Functions in Pancreatic Ductal Adenocarcinoma Cells. <i>Biomolecules</i> , 2020, 10, 884.	1.8	8
5194	Identification of candidate aberrantly methylated and differentially expressed genes in Esophageal squamous cell carcinoma. <i>Scientific Reports</i> , 2020, 10, 9735.	1.6	11
5195	Exploring Mechanism of Key Chinese Herbal Medicine on Breast Cancer by Data Mining and Network Pharmacology Methods. <i>Chinese Journal of Integrative Medicine</i> , 2021, 27, 919-926.	0.7	16
5196	Changes in the host transcriptome and microbial metatranscriptome of the ileum of dairy calves subjected to artificial dosing of exogenous rumen contents. <i>Physiological Genomics</i> , 2020, 52, 333-346.	1.0	1
5197	SCDb: an integrated database of stomach cancer. <i>BMC Cancer</i> , 2020, 20, 490.	1.1	7
5198	Profiling of gene expression in methicillin-resistant <i>Staphylococcus aureus</i> in response to cyclo-(L-Val-L-Pro) and chloramphenicol isolated from <i>Streptomyces</i> sp., SUK 25 reveals gene downregulation in multiple biological targets. <i>Archives of Microbiology</i> , 2020, 202, 2083-2092.	1.0	8
5199	Biomarker roles identification of miR-106 family for predicting the risk and poor survival of colorectal cancer. <i>BMC Cancer</i> , 2020, 20, 506.	1.1	16
5200	Systems Genetics for Mechanistic Discovery in Heart Diseases. <i>Circulation Research</i> , 2020, 126, 1795-1815.	2.0	8
5201	Longitudinal Analysis of Gene Expression Changes During Cervical Carcinogenesis Reveals Potential Therapeutic Targets. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432092057.	0.6	5
5202	Quantitative proteomic analysis of aqueous humor after rabbit lensectomy reveals differences in coagulation and immunomodulatory proteins. <i>Molecular Omics</i> , 2020, 16, 126-137.	1.4	5
5203	<p>A 5-Genes Stemness Score for Rapid Determination of Risk in Multiple Myeloma</p>. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 4339-4348.	1.0	9
5204	Fermentable fiber-induced hepatocellular carcinoma in mice recapitulates gene signatures found in human liver cancer. <i>PLoS ONE</i> , 2020, 15, e0234726.	1.1	4



#	ARTICLE	IF	CITATIONS
5205	Bioinformatic analysis and experimental identification of blood biomarkers for chronic nonunion. <i>Journal of Orthopaedic Surgery and Research</i> , 2020, 15, 208.	0.9	11
5206	Blood Serum Stimulates p38-Mediated Proliferation and Changes in Global Gene Expression of Adult Human Cardiac Stem Cells. <i>Cells</i> , 2020, 9, 1472.	1.8	13
5207	Retinal endothelial cell phenotypic modifications during experimental autoimmune uveitis: a transcriptomic approach. <i>BMC Ophthalmology</i> , 2020, 20, 106.	0.6	14
5208	Identification of <i>F5</i> as a Prognostic Biomarker in Patients with Gastric Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	24
5209	Novel myocardial markers GADD45G and NDUFS5 identified by RNA-sequencing predicts left ventricular reverse remodeling in advanced non-ischemic heart failure: a retrospective cohort study. <i>BMC Cardiovascular Disorders</i> , 2020, 20, 116.	0.7	6
5210	Comparative expression profiles of host circulating miRNAs in response to <i>Trichinella spiralis</i> infection. <i>Veterinary Research</i> , 2020, 51, 39.	1.1	6
5211	Identification of hub genes and pathways in adrenocortical carcinoma by integrated bioinformatic analysis. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 4428-4438.	1.6	16
5212	RNA Sequencing and Bioinformatic Analysis on Retinoblastoma Revealing that Cell Cycle Deregulation Is a Key Process in Retinoblastoma Tumorigenesis. <i>Ophthalmologica</i> , 2021, 244, 51-59.	1.0	9
5213	Identification of PTPRR and JAG1 as key genes in castration-resistant prostate cancer by integrated bioinformatics methods. <i>Journal of Zhejiang University: Science B</i> , 2020, 21, 246-255.	1.3	6
5214	A three-phase method for identifying functionally related protein groups in weighted PPI networks. <i>Computational Biology and Chemistry</i> , 2020, 86, 107246.	1.1	4
5215	heme critically regulates mitochondrial biogenesis through the transcriptional co-activator Hap4p in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 5095-5109.	1.6	10
5216	Genomic Landscape and Mutational Spectrum of ADAMTS Family Genes in Mendelian Disorders Based on Gene Evidence Review for Variant Interpretation. <i>Biomolecules</i> , 2020, 10, 449.	1.8	4
5217	Development of an autophagy-related signature in pancreatic adenocarcinoma. <i>Biomedicine and Pharmacotherapy</i> , 2020, 126, 110080.	2.5	29
5218	Integrative Analysis for the Roles of lncRNAs in the Immune Responses of Mouse PBMC Exposed to Low-Dose Ionizing Radiation. <i>Dose-Response</i> , 2020, 18, 155932582091380.	0.7	6
5219	Transcriptome profiling of buffalo endometrium reveals molecular signature distinct to early pregnancy. <i>Gene</i> , 2020, 743, 144614.	1.0	4
5220	Establishment of a Prognostic Model Using Immune-Related Genes in Patients With Hepatocellular Carcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 55.	1.1	14
5221	Epigenetic mechanisms driving lineage commitment in mesenchymal stem cells. <i>Bone</i> , 2020, 134, 115309.	1.4	7
5222	Possible SARS-coronavirus 2 inhibitor revealed by simulated molecular docking to viral main protease and host toll-like receptor. <i>Future Virology</i> , 2020, 15, 359-368.	0.9	42

#	ARTICLE	IF	CITATIONS
5223	Proteome Analysis Reveals Syndecan 1 Regulates Porcine Sapelovirus Replication. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4386.	1.8	1
5224	SuccSite: Incorporating Amino Acid Composition and Informative k-spaced Amino Acid Pairs to Identify Protein Succinylation Sites. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 208-219.	3.0	19
5225	Two Thalamic Regions Screened Using Laser Capture Microdissection with Whole Human Genome Microarray in Schizophrenia Postmortem Samples. <i>Schizophrenia Research and Treatment</i> , 2020, 2020, 1-11.	0.7	2
5226	Identification of four hub genes as promising biomarkers to evaluate the prognosis of ovarian cancer in silico. <i>Cancer Cell International</i> , 2020, 20, 270.	1.8	21
5227	Mechanistic insights on the mode of action of an antiproliferative thiosemicarbazone-nickel complex revealed by an integrated chemogenomic profiling study. <i>Scientific Reports</i> , 2020, 10, 10524.	1.6	17
5228	Identification of Key Differentially Expressed Transcription Factors in Glioblastoma. <i>Journal of Oncology</i> , 2020, 2020, 1-9.	0.6	10
5229	DL0410 attenuates oxidative stress and neuroinflammation via BDNF/TrkB/ERK/CREB and Nrf2/HO-1 activation. <i>International Immunopharmacology</i> , 2020, 86, 106729.	1.7	36
5230	Bioinformatics analysis of high-throughput data to validate potential novel biomarkers and small molecule drugs for glioblastoma multiforme. <i>Journal of International Medical Research</i> , 2020, 48, 030006052092454.	0.4	2
5231	Systematic summarization of the expression profiles and prognostic roles of the <i>dishevelled</i> gene family in hepatocellular carcinoma. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2020, 8, e1384.	0.6	9
5232	Identification of key genes for esophageal squamous cell carcinoma via integrated bioinformatics analysis and experimental confirmation. <i>Journal of Thoracic Disease</i> , 2020, 12, 3188-3199.	0.6	10
5233	Study on the mechanisms of compound Kushen injection for the treatment of gastric cancer based on network pharmacology. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 6.	1.2	14
5234	Molecular Mechanisms of Bortezomib Action: Novel Evidence for the miRNA-mRNA Interaction Involvement. <i>International Journal of Molecular Sciences</i> , 2020, 21, 350.	1.8	19
5235	Dose-Dependent Effects of GLD-2 and GLD-1 on Germline Differentiation and Dedifferentiation in the Absence of PUF-8. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 5.	1.8	5
5236	Network Pharmacology Study on the Pharmacological Mechanism of Cinobufotalin Injection against Lung Cancer. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-13.	0.5	7
5237	Maternal Inulin Supplementation Alters Hepatic DNA Methylation Profile and Improves Glucose Metabolism in Offspring Mice. <i>Frontiers in Physiology</i> , 2020, 11, 70.	1.3	5
5238	Identification of Candidate Genes and Therapeutic Agents for Light Chain Amyloidosis Based on Bioinformatics Approach. <i>Pharmacogenomics and Personalized Medicine</i> , 2019, Volume 12, 387-396.	0.4	3
5239	A network pharmacology approach to investigating the mechanism of Tanshinone IIA for the treatment of liver fibrosis. <i>Journal of Ethnopharmacology</i> , 2020, 253, 112689.	2.0	41
5240	Transcriptome analysis reveals the difference between "healthy" and "common" aging and their connection with age-related diseases. <i>Aging Cell</i> , 2020, 19, e13121.	3.0	22

#	ARTICLE	IF	CITATIONS
5241	Whole genome sequencing and comparative genomic analysis of oleaginous red yeast <i>Sporobolomyces pararoseus</i> NGR identifies candidate genes for biotechnological potential and ballistospores-shooting. <i>BMC Genomics</i> , 2020, 21, 181.	1.2	9
5242	Integrated characterization and validation of the prognostic significance of microRNA-200s in colorectal cancer. <i>Cancer Cell International</i> , 2020, 20, 56.	1.8	4
5243	Network pharmacology-based approach to investigate the mechanisms of Shenqi Fuzheng injection in the treatment of breast cancer. <i>European Journal of Integrative Medicine</i> , 2020, 34, 101064.	0.8	4
5244	Multiomics Evaluation of Human Fat-Derived Mesenchymal Stem Cells on an Osteobiologic Nanocomposite. <i>BioResearch Open Access</i> , 2020, 9, 37-50.	2.6	6
5245	Potential frameworks to support evaluation of mechanistic data for developmental neurotoxicity outcomes: A symposium report. <i>Neurotoxicology and Teratology</i> , 2020, 78, 106865.	1.2	9
5246	Hsa_circ_0011385 accelerates the progression of thyroid cancer by targeting miR-361-3p. <i>Cancer Cell International</i> , 2020, 20, 49.	1.8	40
5247	Rett Syndrome, a Neurodevelopmental Disorder, Whole-Transcriptome, and Mitochondrial Genome Multiomics Analyses Identify Novel Variations and Disease Pathways. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 160-171.	1.0	18
5248	Quantitative Comparative Proteomics Reveals Candidate Biomarkers for the Early Prediction of Gestational Diabetes Mellitus: A Preliminary Study. <i>In Vivo</i> , 2020, 34, 517-525.	0.6	20
5249	Aberrantly methylated-differentially expressed genes and pathways in Epstein-Barr virus-associated gastric cancer. <i>Future Oncology</i> , 2020, 16, 187-197.	1.1	3
5250	Aberrant Expression of a Non-muscle RBFOX2 Isoform Triggers Cardiac Conduction Defects in Myotonic Dystrophy. <i>Developmental Cell</i> , 2020, 52, 748-763.e6.	3.1	31
5251	Local and Systemic Humoral Response to Autologous Lineage-Negative Cells Intrathecal Administration in ALS Patients. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1070.	1.8	11
5252	Loss of p53 drives neuron reprogramming in head and neck cancer. <i>Nature</i> , 2020, 578, 449-454.	13.7	241
5253	PHYTOCHROME-INTERACTING FACTORS Interact with the ABA Receptors PYL8 and PYL9 to Orchestrate ABA Signaling in Darkness. <i>Molecular Plant</i> , 2020, 13, 414-430.	3.9	69
5254	Transcriptome profiling of tolerogenic dendritic cells conditioned with dual mTOR kinase inhibitor, AZD8055. <i>International Immunopharmacology</i> , 2020, 81, 106241.	1.7	4
5255	Different proteomic profiles of cinnabar upon therapeutic and toxic exposure reveal distinctive biological manifestations. <i>Journal of Ethnopharmacology</i> , 2020, 253, 112668.	2.0	6
5256	Transcriptome analyses identify hub genes and potential mechanisms in adenoid cystic carcinoma. <i>Medicine (United States)</i> , 2020, 99, e18676.	0.4	4
5257	Integrated phytochemical analysis based on UHPLC-LTQ Orbitrap and network pharmacology approaches to explore the potential mechanism of <i>Lycium ruthenicum</i> Murr. for ameliorating Alzheimer's disease. <i>Food and Function</i> , 2020, 11, 1362-1372.	2.1	15
5258	Identification of a Sixteen-gene Prognostic Biomarker for Lung Adenocarcinoma Using a Machine Learning Method. <i>Journal of Cancer</i> , 2020, 11, 1288-1298.	1.2	37

#	ARTICLE	IF	CITATIONS
5259	Expression of apoptosis and myogenesis related genes during prenatal life in two divergent breeds of pigs. <i>Theriogenology</i> , 2020, 145, 67-76.	0.9	0
5260	A genetic variant in the flanking region of miR-182 could decrease the susceptibility to the breast cancer risk in the Iranian population. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2020, 39, 806-817.	0.4	0
5261	The conserved transcriptional regulator CdnL is required for metabolic homeostasis and morphogenesis in <i>Caulobacter</i> . <i>PLoS Genetics</i> , 2020, 16, e1008591.	1.5	16
5262	Heat Shock Factor 2 Protects against Proteotoxicity by Maintaining Cell-Cell Adhesion. <i>Cell Reports</i> , 2020, 30, 583-597.e6.	2.9	33
5263	Visualization and analysis of the interaction network of proteins associated with blood-cell targeting autoimmune diseases. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2020, 1866, 165714.	1.8	3
5264	Comparative Transcriptome Analysis of Different <i>Dendrobium</i> Species Reveals Active Ingredients-Related Genes and Pathways. <i>International Journal of Molecular Sciences</i> , 2020, 21, 861.	1.8	23
5265	Chemical composition and pharmacological mechanism of Qingfei Paidu Decoction and Ma Xing Shi Gan Decoction against Coronavirus Disease 2019 (COVID-19): In silico and experimental study. <i>Pharmacological Research</i> , 2020, 157, 104820.	3.1	171
5266	Systematic Elucidation of the Potential Mechanisms of Core Chinese Materia Medicas in Treating Liver Cancer Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-13.	0.5	7
5267	RNA-Seq transcriptome profiling in three liver regeneration models in rats: comparative analysis of partial hepatectomy, ALLPS, and PVL. <i>Scientific Reports</i> , 2020, 10, 5213.	1.6	22
5268	Exploring Alzheimer's Disease Molecular Variability via Calculation of Personalized Transcriptional Signatures. <i>Biomolecules</i> , 2020, 10, 503.	1.8	5
5269	Identification of TP53 mutation associated-immunotype and prediction of survival in patients with hepatocellular carcinoma. <i>Annals of Translational Medicine</i> , 2020, 8, 321-321.	0.7	7
5270	Screening Circular RNAs Related to Acquired Gefitinib Resistance in Non-small Cell Lung Cancer Cell Lines. <i>Journal of Cancer</i> , 2020, 11, 3816-3826.	1.2	18
5271	DEEPSMP: A deep learning model for predicting the ectodomain shedding events of membrane proteins. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050017.	0.3	3
5272	Astragaloside IV acts through multi-scale mechanisms to effectively reduce diabetic nephropathy. <i>Pharmacological Research</i> , 2020, 157, 104831.	3.1	63
5273	A network pharmacology study on the <i>Tripterygium wilfordii</i> Hook for treatment of Crohn's disease. <i>BMC Complementary Medicine and Therapies</i> , 2020, 20, 95.	1.2	13
5274	Identification of key candidate genes and pathways revealing the protective effect of liraglutide on diabetic cardiac muscle by integrated bioinformatics analysis. <i>Annals of Translational Medicine</i> , 2020, 8, 181-181.	0.7	5
5275	Fifteen Years of Gene Set Analysis for High-Throughput Genomic Data: A Review of Statistical Approaches and Future Challenges. <i>Entropy</i> , 2020, 22, 427.	1.1	34
5276	Identification of Biomarkers Related to Systemic Sclerosis With or Without Pulmonary Hypertension Using Co-expression Analysis. <i>Journal of Computational Biology</i> , 2020, 27, 1519-1531.	0.8	7

#	ARTICLE	IF	CITATIONS
5277	An RB-Condensin II Complex Mediates Long-Range Chromosome Interactions and Influences Expression at Divergently Paired Genes. <i>Molecular and Cellular Biology</i> , 2020, 40, .	1.1	8
5278	Identification of hub genes in papillary thyroid carcinoma: robust rank aggregation and weighted gene co-expression network analysis. <i>Journal of Translational Medicine</i> , 2020, 18, 170.	1.8	20
5279	Automated gene data integration with Databio. <i>BMC Research Notes</i> , 2020, 13, 195.	0.6	1
5280	&lt;p&gt;Tumor-Draining Lymph Secretome En Route to the Regional Lymph Node in Breast Cancer Metastasis&lt;/p&gt;. <i>Breast Cancer: Targets and Therapy</i> , 2020, Volume 12, 57-67.	1.0	4
5281	Knockout of IRF7 Highlights its Modulator Function of Host Response Against Avian Influenza Virus and the Involvement of MAPK and TOR Signaling Pathways in Chicken. <i>Genes</i> , 2020, 11, 385.	1.0	19
5282	Overexpression of DUSP6 enhances chemotherapy-resistance of ovarian epithelial cancer by regulating the ERK signaling pathway. <i>Journal of Cancer</i> , 2020, 11, 3151-3164.	1.2	18
5283	Prevention of age-associated neuronal hyperexcitability with improved learning and attention upon knockout or antagonism of LPAR2. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 1029-1050.	2.4	15
5284	Transcriptomic and Epigenetic Preservation of Genetic Sex Identity in Estrogen-feminized Male Chicken Embryonic Gonads. <i>Endocrinology</i> , 2021, 162, .	1.4	17
5285	Sex-dependent effects of preconception exposure to arsenite on gene transcription in parental germ cells and on transcriptomic profiles and diabetic phenotype of offspring. <i>Archives of Toxicology</i> , 2021, 95, 473-488.	1.9	7
5286	Human Respiratory Syncytial Virus-Induced Immune Signature of Infection Revealed by Transcriptome Analysis of Clinical Pediatric Nasopharyngeal Swab Samples. <i>Journal of Infectious Diseases</i> , 2021, 223, 1052-1061.	1.9	6
5287	MicroRNA and protein-coding gene expression analysis in idiopathic pulmonary fibrosis yields novel biomarker signatures associated to survival. <i>Translational Research</i> , 2021, 228, 1-12.	2.2	6
5288	From classical to new generation approaches: An excursus of -omics methods for investigation of protein-protein interaction networks. <i>Journal of Proteomics</i> , 2021, 230, 103990.	1.2	31
5289	Population Genomics Reveals Incipient Speciation, Introgression, and Adaptation in the African Mona Monkey (<i>Cercopithecus mona</i>). <i>Molecular Biology and Evolution</i> , 2021, 38, 876-890.	3.5	15
5290	Loss of the psychiatric risk factor SLC6A15 is associated with increased metabolic functions in primary hippocampal neurons. <i>European Journal of Neuroscience</i> , 2021, 53, 390-401.	1.2	8
5291	Artificial intelligence based identification of the functional role of hirudin in diabetic erectile dysfunction treatment. <i>Pharmacological Research</i> , 2021, 163, 105244.	3.1	4
5292	A MicroRNA Expression Signature as Prognostic Marker for Oropharyngeal Squamous Cell Carcinoma. <i>Journal of the National Cancer Institute</i> , 2021, 113, 752-759.	3.0	10
5293	LncSEA: a platform for long non-coding RNA related sets and enrichment analysis. <i>Nucleic Acids Research</i> , 2021, 49, D969-D980.	6.5	76
5294	Global analysis of RNA-binding protein dynamics by comparative and enhanced RNA interactome capture. <i>Nature Protocols</i> , 2021, 16, 27-60.	5.5	31

#	ARTICLE	IF	CITATIONS
5295	Identification of potential <scp>circRNAs</scp> and <scp>circRNAâ€miRNAâ€mRNA</scp> regulatory network in the development of diabetic foot ulcers by integrated bioinformatics analysis. International Wound Journal, 2021, 18, 323-331.	1.3	20
5296	Direct and Indirect Regulators of Epithelialâ€Mesenchymal Transitionâ€Mediated Immunosuppression in Breast Carcinomas. Cancer Discovery, 2021, 11, 1286-1305.	7.7	76
5297	Chronic circadian shift leads to adipose tissue inflammation and fibrosis. Molecular and Cellular Endocrinology, 2021, 521, 111110.	1.6	28
5298	Comparison of tear proteomic and neuromediator profiles changes between small incision lenticule extraction (SMILE) and femtosecond laser-assisted in-situ keratomileusis (LASIK). Journal of Advanced Research, 2021, 29, 67-81.	4.4	23
5299	Integrated Microarray to Identify the Hub miRNAs and Constructed miRNAâ€mRNA Network in Neuroblastoma Via Bioinformatics Analysis. Neurochemical Research, 2021, 46, 197-212.	1.6	12
5300	Data Treatment in Food Proteomics. , 2021, , 324-338.		1
5301	Sustained Postnatal Skin Regeneration Upon Prenatal Application of Functionalized Collagen Scaffolds. Tissue Engineering - Part A, 2021, 27, 10-25.	1.6	3
5302	Proteomic Profiling of Extracellular Vesicles Separated from Plasma of Former National Football League Players at Risk for Chronic Traumatic Encephalopathy. , 2021, 12, 1363.		12
5303	Identification of six hub genes and analysis of their correlation with drug sensitivity in acute myeloid leukemia through bioinformatics. Translational Cancer Research, 2021, 10, 126-140.	0.4	4
5304	Comparing the effects of two different strains of mycobacteria, Mycobacterium vaccae NCTC 11659 and M. vaccae ATCC 15483, on stress-resilient behaviors and lipid-immune signaling in rats. Brain, Behavior, and Immunity, 2021, 91, 212-229.	2.0	12
5305	Integrative Identification of Hub Genes Associated With Immune Cells in Atrial Fibrillation Using Weighted Gene Correlation Network Analysis. Frontiers in Cardiovascular Medicine, 2020, 7, 631775.	1.1	11
5306	Identification of abnormally methylatedâ€differentially expressed genes and pathways in osteoarthritis: a comprehensive bioinformatic study. Clinical Rheumatology, 2021, 40, 3247-3256.	1.0	7
5307	In-depth Site-specific Analysis of N-glycoproteome in Human Cerebrospinal Fluid and Glycosylation Landscape Changes in Alzheimer's Disease. Molecular and Cellular Proteomics, 2021, 20, 100081.	2.5	48
5308	HDAC inhibition results in widespread alteration of the histone acetylation landscape and BRD4 targeting to gene bodies. Cell Reports, 2021, 34, 108638.	2.9	60
5309	PredTAD: A machine learning framework that models 3D chromatin organization alterations leading to oncogene dysregulation in breast cancer cell lines. Computational and Structural Biotechnology Journal, 2021, 19, 2870-2880.	1.9	2
5310	LncTx: A network-based method to repurpose drugs acting on the survival-related lncRNAs in lung cancer. Computational and Structural Biotechnology Journal, 2021, 19, 3990-4002.	1.9	5
5311	Quantitative trait loci and transcriptome signatures associated with avian heritable resistance to Campylobacter. Scientific Reports, 2021, 11, 1623.	1.6	10
5312	A Novel mRNA-miRNA Regulatory Sub-Network Associated With Prognosis of Metastatic Clear Cell Renal Cell Carcinoma. Frontiers in Oncology, 2020, 10, 593601.	1.3	5

#	ARTICLE	IF	CITATIONS
5313	Microarray Data Mining and Preliminary Bioinformatics Analysis of Hepatitis D Virus-Associated Hepatocellular Carcinoma. <i>BioMed Research International</i> , 2021, 2021, 1-18.	0.9	5
5314	Global Gene Expression of Cultured Human Dermal Fibroblasts: Focus on Cell Cycle and Proliferation Status in Improving the Condition of Face Skin. <i>International Journal of Medical Sciences</i> , 2021, 18, 1519-1531.	1.1	1
5315	Extracellular signal-regulated kinase (ERK) pathway control of CD8+ T cell differentiation. <i>Biochemical Journal</i> , 2021, 478, 79-98.	1.7	17
5316	JAK-STAT Pathway Inhibition Partially Restores Intestinal Homeostasis in Hdac1- and Hdac2-Intestinal Epithelial Cell-Deficient Mice. <i>Cells</i> , 2021, 10, 224.	1.8	11
5317	Multiplex gene and phenotype network to characterize shared genetic pathways of epilepsy and autism. <i>Scientific Reports</i> , 2021, 11, 952.	1.6	27
5318	Identification of novel biomarkers and candidate small-molecule drugs in cutaneous melanoma by comprehensive gene microarrays analysis. <i>Journal of Cancer</i> , 2021, 12, 1307-1317.	1.2	6
5319	A Systems View of the Heparan Sulfate Interactome. <i>Journal of Histochemistry and Cytochemistry</i> , 2021, 69, 105-119.	1.3	44
5320	Bioinformatic Analysis of Differential Genes in Sinusoidal Endothelial Cells of Liver Cirrhosis Rat. <i>Yangtze Medicine</i> , 2021, 05, 133-140.	0.1	0
5321	Structural similarity-based prediction of host factors associated with SARS-CoV-2 infection and pathogenesis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 5868-5879.	2.0	12
5322	Microarray expression profile of mRNAs and long noncoding RNAs and the potential role of PFK-1 in infantile hemangioma. <i>Cell Division</i> , 2021, 16, 1.	1.1	9
5323	circRNA expression pattern and ceRNA network in the pathogenesis of aseptic loosening after total hip arthroplasty. <i>International Journal of Medical Sciences</i> , 2021, 18, 768-777.	1.1	6
5324	Identification and Characterisation of Putative Enhancer Elements in Mouse Embryonic Stem Cells. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222097462.	1.0	3
5325	Identification of HCG18 and MCM3AP-AS1 That Associate With Bone Metastasis, Poor Prognosis and Increased Abundance of M2 Macrophage Infiltration in Prostate Cancer. <i>Technology in Cancer Research and Treatment</i> , 2021, 20, 153303382199006.	0.8	24
5326	<i>Anemarrhena asphodeloides</i> modulates gut microbiota and restores pancreatic function in diabetic rats. <i>Biomedicine and Pharmacotherapy</i> , 2021, 133, 110954.	2.5	19
5327	Immune-associated molecular occurrence and prognosis predictor of hepatocellular carcinoma: an integrated analysis of GEO datasets. <i>Bioengineered</i> , 2021, 12, 5253-5265.	1.4	1
5328	Exploring the treatment of COVID-19 with Yinqiao powder based on network pharmacology. <i>Phytotherapy Research</i> , 2021, 35, 2651-2664.	2.8	36
5329	Comprehensive Analysis of ceRNA Regulation Network Involved in the Development of Coronary Artery Disease. <i>BioMed Research International</i> , 2021, 2021, 1-14.	0.9	6
5330	Comprehensive evaluation of microRNA-10b in digestive system cancers reveals prognostic implication and signaling pathways associated with tumor progression. <i>Journal of Cancer</i> , 2021, 12, 4011-4024.	1.2	2

#	ARTICLE	IF	CITATIONS
5331	Introduction to Data Analysis in Omics Sciences. , 2021, , 226-240.		0
5332	Sparsely-connected autoencoder (SCA) for single cell RNAseq data mining. Npj Systems Biology and Applications, 2021, 7, 1.	1.4	53
5335	Decrease in the T-box1 gene expression in embryonic brain and adult hippocampus of down syndrome mouse models. Biochemical and Biophysical Research Communications, 2021, 535, 87-92.	1.0	2
5336	Identification of a novel snoRNA expression signature associated with overall survival in patients with lung adenocarcinoma: A comprehensive analysis based on RNA sequencing dataset. Mathematical Biosciences and Engineering, 2021, 18, 7837-7860.	1.0	5
5337	Discovery and function exploration of microRNA-155 as a molecular biomarker for early detection of breast cancer. Breast Cancer, 2021, 28, 806-821.	1.3	7
5338	<i>CXCL10</i> potentiates immune checkpoint blockade therapy in homologous recombination-deficient tumors. Theranostics, 2021, 11, 7175-7187.	4.6	34
5339	Role of Bioinformatics in Biological Sciences. , 2021, , 37-57.		5
5340	INHBA is a novel mediator regulating cellular senescence and immune evasion in colorectal cancer. Journal of Cancer, 2021, 12, 5938-5949.	1.2	10
5341	Identification And validation of transcription factor genes involved in prostate cancer metastasis. International Journal of Transgender Health, 2021, 14, 287-299.	1.1	0
5342	Integrated Genomic and Transcriptomic Analysis reveals key genes for predicting dual-phenotype Hepatocellular Carcinoma Prognosis. Journal of Cancer, 2021, 12, 2993-3010.	1.2	5
5343	Positive selection signatures in Anqing sixâ€œendâ€œwhite pig population based on reducedâ€œrepresentation genome sequencing data. Animal Genetics, 2021, 52, 143-154.	0.6	8
5344	Identification of Core Genes Related to Progression and Prognosis of Hepatocellular Carcinoma and Small-Molecule Drug Predication. Frontiers in Genetics, 2021, 12, 608017.	1.1	5
5345	Identification of glycolysis related pathways in pancreatic adenocarcinoma and liver hepatocellular carcinoma based on TCGA and GEO datasets. Cancer Cell International, 2021, 21, 128.	1.8	3
5346	Identification of four methylation-driven genes as candidate biomarkers for monitoring single-walled carbon nanotube-induced malignant transformation of the lung. Toxicology and Applied Pharmacology, 2021, 412, 115391.	1.3	11
5347	Enrichment of IGF-1R and PPARÎ³ signalling pathways in orbital inflammatory diseases: steps toward understanding pathogenesis. British Journal of Ophthalmology, 2022, 106, 1012-1017.	2.1	2
5348	Identification of four genes and biological characteristics of esophageal squamous cell carcinoma by integrated bioinformatics analysis. Cancer Cell International, 2021, 21, 123.	1.8	13
5349	Identification of UBE2C as hub gene in driving prostate cancer by integrated bioinformatics analysis. PLoS ONE, 2021, 16, e0247827.	1.1	16
5350	Single-Cell RNA Sequencing and Quantitative Proteomics Analysis Elucidate Marker Genes and Molecular Mechanisms in Hypoplastic Left Heart Patients With Heart Failure. Frontiers in Cell and Developmental Biology, 2021, 9, 617853.	1.8	2



#	ARTICLE	IF	CITATIONS
5351	eTumorMetastasis: A Network-based Algorithm Predicts Clinical Outcomes Using Whole-exome Sequencing Data of Cancer Patients. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 973-985.	3.0	6
5352	Restoration of type I interferon signaling in intrahepatically primed CD8+ T cells promotes functional differentiation. <i>JCI Insight</i> , 2021, 6, .	2.3	6
5353	3D Genome of macaque fetal brain reveals evolutionary innovations during primate corticogenesis. <i>Cell</i> , 2021, 184, 723-740.e21.	13.5	76
5354	Comparisons of MicroRNA Set Enrichment Analysis Tools on Cancer De-regulated miRNAs from TCGA Expression Datasets. <i>Current Bioinformatics</i> , 2021, 15, 1104-1112.	0.7	5
5355	Spatiotemporal dissection of the cell cycle with single-cell proteogenomics. <i>Nature</i> , 2021, 590, 649-654.	13.7	104
5356	Investigating the role of <i>dachshund b</i> in the development of the pancreatic islet in zebrafish. <i>Journal of Diabetes Investigation</i> , 2021, 12, 710-727.	1.1	2
5357	Transcriptional Profiling Uncovers Biologically Significant RNAs and Regulatory Networks in Nucleus Pulposus from Intervertebral Disc Degeneration Patients. <i>BioMed Research International</i> , 2021, 2021, 1-33.	0.9	1
5358	Characterising cancer-associated fibroblast heterogeneity in non-small cell lung cancer: a systematic review and meta-analysis. <i>Scientific Reports</i> , 2021, 11, 3727.	1.6	27
5359	Identification of key genes and pathways at the downstream of S100BP in pancreatic cancer cells by integrated bioinformatical analysis. <i>Translational Cancer Research</i> , 2021, 10, 806-816.	0.4	3
5360	Deciphering the multi-scale mechanisms of Tephrosia purpurea against polycystic ovarian syndrome (PCOS) and its major psychiatric comorbidities: Studies from network pharmacological perspective. <i>Gene</i> , 2021, 773, 145385.	1.0	12
5361	SPAAC-NAD-seq, a sensitive and accurate method to profile NAD <sup>+</sup> -capped transcripts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	26
5362	Bi-allelic variants in HOPS complex subunit VPS41 cause cerebellar ataxia and abnormal membrane trafficking. <i>Brain</i> , 2021, 144, 769-780.	3.7	33
5363	Immune microenvironment characterisation and dynamics during anti-HER2-based neoadjuvant treatment in HER2-positive breast cancer. <i>Npj Precision Oncology</i> , 2021, 5, 23.	2.3	26
5365	A plug and play microfluidic platform for standardized sensitive low-input chromatin immunoprecipitation. <i>Genome Research</i> , 2021, 31, 919-933.	2.4	4
5366	Elevated glucose represses lysosomal and mTOR-related genes in renal epithelial cells composed of progenitor CD133+ cells. <i>PLoS ONE</i> , 2021, 16, e0248241.	1.1	5
5367	Muscle Enriched Lamin Interacting Protein (Mlip) Binds Chromatin and Is Required for Myoblast Differentiation. <i>Cells</i> , 2021, 10, 615.	1.8	8
5368	XlinkCyNET: A Cytoscape Application for Visualization of Protein Interaction Networks Based on Cross-Linking Mass Spectrometry Identifications. <i>Journal of Proteome Research</i> , 2021, 20, 1943-1950.	1.8	8
5369	Integrative pan cancer analysis reveals epigenomic variation in cancer type and cell specific chromatin domains. <i>Nature Communications</i> , 2021, 12, 1419.	5.8	46

#	ARTICLE	IF	CITATIONS
5370	Development of a Prognostic Model for Ovarian Cancer Patients Based on Novel Immune Microenvironment Related Genes. <i>Frontiers in Oncology</i> , 2021, 11, 647273.	1.3	9
5371	Signaling Pathways Regulated by Silica Nanoparticles. <i>Molecules</i> , 2021, 26, 1398.	1.7	17
5372	Ogt controls neural stem/progenitor cell pool and adult neurogenesis through modulating Notch signaling. <i>Cell Reports</i> , 2021, 34, 108905.	2.9	44
5373	C3AR1 mRNA as a Potential Therapeutic Target Associates With Clinical Outcomes and Tumor Microenvironment in Osteosarcoma. <i>Frontiers in Medicine</i> , 2021, 8, 642615.	1.2	9
5374	Distribution of microRNA profiles in pre-clinical and clinical forms of murine and human prion disease. <i>Communications Biology</i> , 2021, 4, 411.	2.0	9
5376	Identification and Analysis of Potential Key Genes Associated With Hepatocellular Carcinoma Based on Integrated Bioinformatics Methods. <i>Frontiers in Genetics</i> , 2021, 12, 571231.	1.1	25
5377	Mapping specificity, cleavage entropy, allosteric changes and substrates of blood proteases in a high-throughput screen. <i>Nature Communications</i> , 2021, 12, 1693.	5.8	17
5378	An organelle-tethering mechanism couples flagellation to cell division in bacteria. <i>Developmental Cell</i> , 2021, 56, 657-670.e4.	3.1	10
5379	Comparison of metastatic castration-resistant prostate cancer in bone with other sites: clinical characteristics, molecular features and immune status. <i>PeerJ</i> , 2021, 9, e11133.	0.9	1
5381	ARRDC3 as a Diagnostic and Prognostic Biomarker for Epithelial Ovarian Cancer Based on Data Mining. <i>International Journal of General Medicine</i> , 2021, Volume 14, 967-981.	0.8	5
5384	Deep sequencing reveals the genomic characteristics of lung adenocarcinoma presenting as ground-glass nodules (GGNs). <i>Translational Lung Cancer Research</i> , 2021, 10, 1239-1255.	1.3	4
5385	Sperm-borne miR-202 targets <i>SEPT7</i> and regulates first cleavage of bovine embryos via cytoskeletal remodeling. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	14
5386	Identification of the hub genes in gastric cancer through weighted gene co-expression network analysis. <i>PeerJ</i> , 2021, 9, e10682.	0.9	9
5387	̑-3PUFA supplementation ameliorates adipose tissue inflammation and insulin-stimulated glucose disposal in subjects with obesity: a potential role for apolipoprotein E. <i>International Journal of Obesity</i> , 2021, 45, 1331-1341.	1.6	14
5388	Transcriptomic alterations in malignant pleural mesothelioma cells in response to long-term treatment with bullfrog sialic acid-binding lectin. <i>Molecular Medicine Reports</i> , 2021, 23, .	1.1	5
5389	Prediction and analysis of novel key genes ITGAX, LPTM5, SERPINE1 in clear cell renal cell carcinoma through bioinformatics analysis. <i>PeerJ</i> , 2021, 9, e11272.	0.9	18
5390	Characterisation of PALB2 tumours through whole-exome and whole-transcriptomic analyses. <i>Npj Breast Cancer</i> , 2021, 7, 46.	2.3	6
5391	Single-cell RNA sequencing of mouse islets exposed to proinflammatory cytokines. <i>Life Science Alliance</i> , 2021, 4, e202000949.	1.3	16

#	ARTICLE	IF	CITATIONS
5392	Is acupuncture effective in the treatment of COVID-19 related symptoms? Based on bioinformatics/network topology strategy. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	32
5394	Weighted gene co expression network analysis (WGCNA) with key pathways and hub genes related to micro RNAs in ischemic stroke. <i>IET Systems Biology</i> , 2021, 15, 93-100.	0.8	4
5395	BATF Regulates T Regulatory Cell Functional Specification and Fitness of Triglyceride Metabolism in Restraining Allergic Responses. <i>Journal of Immunology</i> , 2021, 206, 2088-2100.	0.4	11
5396	An Integrative Pharmacology-Based Strategy to Uncover the Mechanism of Xiong-Pi-Fang in Treating Coronary Heart Disease with Depression. <i>Frontiers in Pharmacology</i> , 2021, 12, 590602.	1.6	4
5397	Identified a disintegrin and metalloproteinase with thrombospondin motifs 6 serve as a novel gastric cancer prognostic biomarker by bioinformatics analysis. <i>Bioscience Reports</i> , 2021, 41, .	1.1	4
5398	Identification of transcriptomic signatures and crucial pathways involved in non-alcoholic steatohepatitis. <i>Endocrine</i> , 2021, 73, 52-64.	1.1	17
5399	Identification of Potential Biomarkers From Hepatocellular Carcinoma With MT1 Deletion. <i>Pathology and Oncology Research</i> , 2021, 27, 597527.	0.9	5
5400	Stress-induced transcriptional memory accelerates promoter-proximal pause release and decelerates termination over mitotic divisions. <i>Molecular Cell</i> , 2021, 81, 1715-1731.e6.	4.5	28
5401	Identification of Glioma Specific Genes as Diagnostic and Prognostic Markers for Glioma. <i>Current Bioinformatics</i> , 2021, 16, 120-129.	0.7	2
5402	H3K27ac bookmarking promotes rapid post-mitotic activation of the pluripotent stem cell program without impacting 3D chromatin reorganization. <i>Molecular Cell</i> , 2021, 81, 1732-1748.e8.	4.5	60
5403	Construction and analysis of protein-protein interaction network of non-alcoholic fatty liver disease. <i>Computers in Biology and Medicine</i> , 2021, 131, 104243.	3.9	10
5404	Developmental Transcriptomics Reveals a Gene Network Driving Mimetic Color Variation in a Bumble Bee. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
5405	Investigating the mechanism of action of aggregation-inducing antimicrobial Pept-ins. <i>Cell Chemical Biology</i> , 2021, 28, 524-536.e4.	2.5	8
5406	MicroRNA Expression Profile Distinguishes Glioblastoma Stem Cells from Differentiated Tumor Cells. <i>Journal of Personalized Medicine</i> , 2021, 11, 264.	1.1	12
5407	MFN2 interacts with nuage-associated proteins and is essential for male germ cell development by controlling mRNA fate during spermatogenesis. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	12
5408	A cell-to-patient machine learning transfer approach uncovers novel basal-like breast cancer prognostic markers amongst alternative splice variants. <i>BMC Biology</i> , 2021, 19, 70.	1.7	13
5410	Identification of the Ingredients and Mechanisms of Curcumae Radix for Depression Based on Network Pharmacology and Molecular Docking. <i>Natural Product Communications</i> , 2021, 16, 1934578X2110166.	0.2	1
5411	Immunity-longevity tradeoff neurally controlled by GABAergic transcription factor PITX1/UNC-30. <i>Cell Reports</i> , 2021, 35, 109187.	2.9	15

#	ARTICLE	IF	CITATIONS
5412	Metformin Perturbs Pancreatic Differentiation From Human Embryonic Stem Cells. <i>Diabetes</i> , 2021, 70, 1689-1702.	0.3	6
5413	Genome of the butterfly hillstream loach provides insights into adaptations to torrential mountain stream life. <i>Molecular Ecology Resources</i> , 2021, 21, 1922-1935.	2.2	1
5414	CPA: a web-based platform for consensus pathway analysis and interactive visualization. <i>Nucleic Acids Research</i> , 2021, 49, W114-W124.	6.5	20
5415	Detection of copy number variants in African goats using whole genome sequence data. <i>BMC Genomics</i> , 2021, 22, 398.	1.2	4
5416	INPP4B promotes PI3K $\beta$ -dependent late endosome formation and Wnt/ $\beta$ -catenin signaling in breast cancer. <i>Nature Communications</i> , 2021, 12, 3140.	5.8	30
5417	Network-based analysis of key regulatory genes implicated in Type 2 Diabetes Mellitus and Recurrent Miscarriages in Turner Syndrome. <i>Scientific Reports</i> , 2021, 11, 10662.	1.6	4
5418	Significance and Mechanisms Analyses of RB1 Mutation in Bladder Cancer Disease Progression and Drug Selection by Bioinformatics Analysis. <i>Bladder Cancer</i> , 2021, 7, 133-142.	0.2	2
5419	Bioinformatics Analysis of a Prognostic miRNA Signature and Potential Key Genes in Pancreatic Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 641289.	1.3	16
5420	Overcoming false-positive gene-category enrichment in the analysis of spatially resolved transcriptomic brain atlas data. <i>Nature Communications</i> , 2021, 12, 2669.	5.8	74
5422	METTL3 mediates bone marrow mesenchymal stem cell adipogenesis to promote chemoresistance in acute myeloid leukaemia. <i>FEBS Open Bio</i> , 2021, 11, 1659-1672.	1.0	23
5423	Screening and identification of LMNB1 and DLGAP5, two key biomarkers in gliomas. <i>Bioscience Reports</i> , 2021, 41, .	1.1	7
5424	Metabolomics bridging proteomics along metabolites/oncometabolites and protein modifications: Paving the way toward integrative multiomics. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 199, 114031.	1.4	8
5425	The SAM domain-containing protein 1 (SAMD1) acts as a repressive chromatin regulator at unmethylated CpG islands. <i>Science Advances</i> , 2021, 7, .	4.7	22
5426	Identification of upregulated NF- $\kappa$ B inhibitor alpha and IRAK3 targeting lncRNA following intracranial aneurysm rupture-induced subarachnoid hemorrhage. <i>BMC Neurology</i> , 2021, 21, 197.	0.8	9
5427	Quantitative proteomics reveal the protective effects of EDS against osteoarthritis via attenuating inflammation and modulating immune response. <i>Journal of Ethnopharmacology</i> , 2021, 271, 113780.	2.0	13
5428	Significance of TP53 Mutation in Cellular Process and Disease Progression in Lung Adenocarcinoma. <i>Genetic Testing and Molecular Biomarkers</i> , 2021, 25, 346-354.	0.3	3
5429	KDM4 orchestrates epigenomic remodeling of senescent cells and potentiates the senescence-associated secretory phenotype. <i>Nature Aging</i> , 2021, 1, 454-472.	5.3	31
5430	A Semiautomated Paramagnetic Bead-Based Platform for Isobaric Tag Sample Preparation. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1519-1529.	1.2	19

#	ARTICLE	IF	CITATIONS
5431	Comparative genomics analysis of two banana Fusarium wilt biocontrol endophytes <i>Bacillus subtilis</i> R31 and TR21 provides insights into their differences on phyto-beneficial trait. <i>Genomics</i> , 2021, 113, 900-909.	1.3	14
5433	Characterization of DNA Methylation and Screening of Epigenetic Markers in Polycystic Ovary Syndrome. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 664843.	1.8	15
5434	A Phase 2 Randomised Clinical Trial Assessing the Tolerability of Two Different Ratios of Medicinal Cannabis in Patients With High Grade Gliomas. <i>Frontiers in Oncology</i> , 2021, 11, 649555.	1.3	28
5435	Potential role of chimeric genes in pathway-related gene co-expression modules. <i>World Journal of Surgical Oncology</i> , 2021, 19, 149.	0.8	7
5436	CBFB cooperates with p53 to maintain TAp73 expression and suppress breast cancer. <i>PLoS Genetics</i> , 2021, 17, e1009553.	1.5	8
5437	The glycosyltransferase ST3GAL2 is regulated by miR-615-3p in the intestinal tract of <i>Campylobacter jejuni</i> infected mice. <i>Gut Pathogens</i> , 2021, 13, 42.	1.6	5
5438	Microbiota Modulates Cardiac Transcriptional Responses to Intermittent Hypoxia and Hypercapnia. <i>Frontiers in Physiology</i> , 2021, 12, 680275.	1.3	4
5439	A two-miRNA signature of upregulated miR-185-5p and miR-362-5p as a blood biomarker for breast cancer. <i>Pathology Research and Practice</i> , 2021, 222, 153458.	1.0	16
5440	Global proteomic analyses of human cytotrophoblast differentiation/invasion. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	5
5441	Genetic basis of variation in cocaine and methamphetamine consumption in outbred populations of <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12
5442	Comparative Proteomic Analysis of Polarized Human THP-1 and Mouse RAW264.7 Macrophages. <i>Frontiers in Immunology</i> , 2021, 12, 700009.	2.2	55
5444	Cytotoxic, genotoxic, and toxicogenomic effects of dihydroxyacetone in human primary keratinocytes. <i>Cutaneous and Ocular Toxicology</i> , 2021, 40, 232-240.	0.5	7
5446	Identification of immune cell infiltration pattern and related critical genes in metastatic castration-resistant prostate cancer by bioinformatics analysis. <i>Cancer Biomarkers</i> , 2021, 32, 1-15.	0.8	6
5448	Nuclear ADP-ribosylation drives IFN $\beta$ -dependent STAT1 $\beta$ enhancer formation in macrophages. <i>Nature Communications</i> , 2021, 12, 3931.	5.8	20
5449	Identification of potential pathogenic mutations in Chinese children with first branchial cleft anomalies detected by whole-exome sequencing. <i>Pediatric Investigation</i> , 2021, 5, 211-216.	0.6	1
5450	Gene expression profiles of breast cancer metastasis according to organ site. <i>Molecular Oncology</i> , 2022, 16, 69-87.	2.1	24
5451	Comparison of transcriptome between high- and low-marbling fineness in <i>longissimus thoracis</i> muscle of Korean cattle. <i>Animal Bioscience</i> , 2021, , .	0.8	2
5452	Comprehensive Bioinformatics Analysis of mRNA Expression Profiles and Identification of a miRNA-mRNA Network Associated with the Pathogenesis of Low-Grade Gliomas. <i>Cancer Management and Research</i> , 2021, Volume 13, 5135-5147.	0.9	4

#	ARTICLE	IF	CITATIONS
5453	Identification of a Seven-lncRNA-mRNA Signature for Recurrence and Prognostic Prediction in Relapsed Acute Lymphoblastic Leukemia Based on WGCNA and LASSO Analyses. <i>Analytical Cellular Pathology</i> , 2021, 2021, 1-16.	0.7	6
5454	Tandem mass tag-based proteomics for studying the effects of a biotechnologically produced oyster mushroom against hepatic steatosis in obese Zucker rats. <i>Journal of Proteomics</i> , 2021, 242, 104255.	1.2	4
5455	TCGA dataset screening for genes implicated in endometrial cancer using RNA-seq profiling. <i>Cancer Genetics</i> , 2021, 254-255, 40-47.	0.2	2
5456	Ageing- and Tumor-Mediated Increase in CD8+CD28 <sup>hi</sup> T Cells Might Impose a Strong Barrier to Success of Immunotherapy in Glioblastoma. <i>ImmunoHorizons</i> , 2021, 5, 395-409.	0.8	8
5457	Aberrant Alternative Splicing in U2af1/Tet2 Double Mutant Mice Contributes to Major Hematological Phenotypes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6963.	1.8	5
5458	Transcriptomics-based drug repositioning pipeline identifies therapeutic candidates for COVID-19. <i>Scientific Reports</i> , 2021, 11, 12310.	1.6	31
5459	LncRNA <i>HBL1</i> is required for genome-wide PRC2 occupancy and function in cardiogenesis from human pluripotent stem cells. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	12
5460	BoxCar increases the depth and reproducibility of diabetic urinary proteome analysis. <i>Proteomics - Clinical Applications</i> , 2021, 15, e2000092.	0.8	2
5461	Revealing the Modular Similarities and Differences Among Alzheimer's Disease, Vascular Dementia, and Parkinson's Disease in Genomic Networks. <i>NeuroMolecular Medicine</i> , 2022, 24, 125-138.	1.8	7
5463	BAP1/ASXL complex modulation regulates epithelial-mesenchymal transition during trophoblast differentiation and invasion. <i>ELife</i> , 2021, 10, .	2.8	27
5464	Construction of a novel mRNA-miRNA-lncRNA network and identification of potential regulatory axis associated with prognosis in colorectal cancer liver metastases. <i>Aging</i> , 2021, 13, 14968-14988.	1.4	10
5465	Comprehensive Search for Novel Circulating miRNAs and Axon Guidance Pathway Proteins Associated with Risk of ESKD in Diabetes. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 2331-2351.	3.0	20
5466	N6-Methyladenosine-Related lncRNAs in Tumor Microenvironment Are Potential Prognostic Biomarkers in Colon Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 697949.	1.3	12
5467	An Investigation of the Antigastric Cancer Effect in Tumor Microenvironment of Radix Rhei Et Rhizome: A Network Pharmacology Study. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-9.	0.5	2
5468	Transcriptome Analyses Provide Insights into the Aggressive Behavior toward Conspecific and Heterospecific in <i>Thitarodes xiaojinensis</i> (Lepidoptera: Hepialidae). <i>Insects</i> , 2021, 12, 577.	1.0	1
5469	Identification of an immune-based mRNA <sup>hi</sup> lncRNA signature for overall survival in cervical squamous cell carcinoma. <i>Future Oncology</i> , 2021, 17, 2365-2380.	1.1	1
5470	Parental methylome reprogramming in human uniparental blastocysts reveals germline memory transition. <i>Genome Research</i> , 2021, 31, 1519-1530.	2.4	4
5471	Environmental responsiveness of flowering time in cassava genotypes and associated transcriptome changes. <i>PLoS ONE</i> , 2021, 16, e0253555.	1.1	4

#	ARTICLE	IF	CITATIONS
5472	Mutation in FBXO32 causes dilated cardiomyopathy through up-regulation of ER-stress mediated apoptosis. <i>Communications Biology</i> , 2021, 4, 884.	2.0	12
5473	Muscarinic receptor M3 contributes to intestinal stem cell maintenance via EphB/ephrin-B signaling. <i>Life Science Alliance</i> , 2021, 4, e202000962.	1.3	9
5474	Ten-gene signature reveals the significance of clinical prognosis and immuno-correlation of osteosarcoma and study on novel skeleton inhibitors regarding MMP9. <i>Cancer Cell International</i> , 2021, 21, 377.	1.8	19
5475	Construction and Validation of an Immune-Based Prognostic Model for Pancreatic Adenocarcinoma Based on Public Databases. <i>Frontiers in Genetics</i> , 2021, 12, 702102.	1.1	3
5477	Novel Post-Translational Modifications and Molecular Substrates in Glioma Identified by Bioinformatics. <i>OMICS A Journal of Integrative Biology</i> , 2021, 25, 463-473.	1.0	4
5478	CDCA1/2/3/5/7/8 as novel prognostic biomarkers and CDCA4/6 as potential targets for gastric cancer. <i>Translational Cancer Research</i> , 2021, 10, 3404-3417.	0.4	4
5479	Identification of Potential Signatures and Their Functions for Acute Lymphoblastic Leukemia: A Study Based on the Cancer Genome Atlas. <i>Frontiers in Genetics</i> , 2021, 12, 656042.	1.1	12
5480	Bioinformatics Analysis and Identification of Genes and Molecular Pathways Involved in Venous Thromboembolism (VTE). <i>Annals of Vascular Surgery</i> , 2021, 74, 389-399.	0.4	2
5481	A combined GWAS approach reveals key loci for socially-affected traits in Yorkshire pigs. <i>Communications Biology</i> , 2021, 4, 891.	2.0	9
5482	Identification of the Hub Genes in Alzheimer's Disease. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-8.	0.7	14
5483	Identifying a possible new target for diagnosis and treatment of postmenopausal osteoporosis through bioinformatics and clinical sample analysis. <i>Annals of Translational Medicine</i> , 2021, 9, 1154-1154.	0.7	10
5484	Persistent proteomic changes in glutamatergic and GABAergic signaling in the amygdala of adolescent rats exposed to chlorpyrifos as juveniles. <i>NeuroToxicology</i> , 2021, 85, 234-244.	1.4	9
5485	Long noncoding RNA LMO7DN inhibits cell proliferation by regulating the cell cycle in lung adenocarcinoma. <i>Pathology Research and Practice</i> , 2021, 223, 153475.	1.0	1
5486	Plasma hsa-miR-19b is a potential LevoDopa therapy marker. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 8715-8724.	1.6	5
5487	Dynamic Observation of Autophagy and Transcriptome Profiles in a Mouse Model of Bleomycin-Induced Pulmonary Fibrosis. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 664913.	1.6	7
5488	Circulating miRNAs in Serum as Biomarkers for Early Diagnosis of Non-small Cell Lung Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 673926.	1.1	15
5489	The Potential Effect of Rhizoma coptidis on Polycystic Ovary Syndrome Based on Network Pharmacology and Molecular Docking. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-12.	0.5	5
5490	Genome-wide DNA methylation pattern in systemic sclerosis microvascular endothelial cells: Identification of epigenetically affected key genes and pathways. <i>Journal of Scleroderma and Related Disorders</i> , 2022, 7, 71-81.	1.0	4

#	ARTICLE	IF	CITATIONS
5491	Usefulness of protein-based salivary markers in the diagnosis of oral potentially malignant disorders: A systematic review and meta-analysis. <i>Cancer Biomarkers</i> , 2021, 32, 411-424.	0.8	10
5492	Single worm transcriptomics identifies a developmental core network of oscillating genes with deep conservation across nematodes. <i>Genome Research</i> , 2021, 31, 1590-1601.	2.4	18
5493	Prognostic significance and oncogene function of cathepsin A in hepatocellular carcinoma. <i>Scientific Reports</i> , 2021, 11, 14611.	1.6	13
5494	Signature of prognostic epithelial-mesenchymal transition related long noncoding RNAs (ERLs) in hepatocellular carcinoma. <i>Medicine (United States)</i> , 2021, 100, e26762.	0.4	8
5495	A ubiquitin-like protein encoded by the noncoding RNA TINCR promotes keratinocyte proliferation and wound healing. <i>PLoS Genetics</i> , 2021, 17, e1009686.	1.5	11
5496	Identification of Long Non-Coding RNAs Involved in Porcine Fat Deposition Using Two High-Throughput Sequencing Methods. <i>Genes</i> , 2021, 12, 1374.	1.0	6
5497	Microarray Analysis Revealed Inflammatory Transcriptomic Changes after LSL60101 Treatment in 5XFAD Mice Model. <i>Genes</i> , 2021, 12, 1315.	1.0	1
5498	Multilevel systems biology analysis of lung transcriptomics data identifies key miRNAs and potential miRNA target genes for SARS-CoV-2 infection. <i>Computers in Biology and Medicine</i> , 2021, 135, 104570.	3.9	31
5499	Heparanase is a novel biomarker for immune infiltration and prognosis in breast cancer. <i>Aging</i> , 2021, 13, 20836-20852.	1.4	9
5500	Comprehensive investigation of RNA-seq dataset reveals the hub genes and molecular mechanisms of coronavirus disease 2019 acute respiratory distress syndrome. <i>IET Systems Biology</i> , 2021, 15, 205-218.	0.8	4
5501	Exosomal lncRNA TCONS_00064356 derived from injured alveolar epithelial type II cells affects the biological characteristics of mesenchymal stem cells. <i>Life Sciences</i> , 2021, 278, 119568.	2.0	6
5502	The signal transducer CD24 suppresses the germ cell program and promotes an ectodermal rather than mesodermal cell fate in embryonal carcinomas. <i>Molecular Oncology</i> , 2022, 16, 982-1008.	2.1	10
5503	Mapping the genetic architecture of human traits to cell types in the kidney identifies mechanisms of disease and potential treatments. <i>Nature Genetics</i> , 2021, 53, 1322-1333.	9.4	87
5504	The Alterations and Potential Roles of MCMs in Breast Cancer. <i>Journal of Oncology</i> , 2021, 2021, 1-17.	0.6	11
5505	Excavating the pathogenic gene of breast cancer based on high throughput data of tumor and somatic reprogramming. <i>Cell Cycle</i> , 2021, 20, 1708-1722.	1.3	0
5506	Comparative transcriptome analyses reveal genes associated with SARS-CoV-2 infection of human lung epithelial cells. <i>Scientific Reports</i> , 2021, 11, 16212.	1.6	15
5507	<i>Porphyromonas gingivalis</i> (W83) Infection Induces Alzheimer's Disease-Like Pathophysiology in Obese and Diabetic Mice. <i>Journal of Alzheimer's Disease</i> , 2021, 82, 1259-1275.	1.2	9
5508	RNA Sequence Profiling Reveals Unique Immune and Metabolic Features of Breast Cancer Brain Metastases. <i>Frontiers in Oncology</i> , 2021, 11, 679262.	1.3	4



#	ARTICLE	IF	CITATIONS
5509	Screening and Identification of Key Biomarkers of Gastric Cancer: Three Genes Jointly Predict Gastric Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 591893.	1.3	4
5510	Transcriptomic Analyses of the Adenoma-Carcinoma Sequence Identify Hallmarks Associated With the Onset of Colorectal Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 704531.	1.3	12
5511	RSPH14 regulates the proliferation, cell cycle progression, and apoptosis of non-small cell lung cancer cells. <i>FEBS Open Bio</i> , 2021, 11, 2715-2726.	1.0	0
5512	Serum proteomics reveals disorder of lipoprotein metabolism in sepsis. <i>Life Science Alliance</i> , 2021, 4, e202101091.	1.3	4
5513	Application of Weighted Gene Coexpression Network Analysis to Identify Key Modules and Hub Genes in Systemic Juvenile Idiopathic Arthritis. <i>BioMed Research International</i> , 2021, 2021, 1-13.	0.9	4
5515	20th International Workshop on Data Mining in Bioinformatics (BIOKDD 2021). , 2021, , .		0
5516	Integrated multi-omics analysis of RB-loss identifies widespread cellular programming and synthetic weaknesses. <i>Communications Biology</i> , 2021, 4, 977.	2.0	1
5517	<i>In-Silico</i> Analysis of Differentially Expressed Genes and Their Regulating microRNA Involved in Lymph Node Metastasis in Invasive Breast Carcinoma. <i>Cancer Investigation</i> , 2022, 40, 55-72.	0.6	4
5518	Global analysis of lysine acetylation in soybean leaves. <i>Scientific Reports</i> , 2021, 11, 17858.	1.6	11
5519	Integrative Analysis of the Roles of lncRNAs and mRNAs in Itaconate-Mediated Protection Against Liver Ischemia-Reperfusion Injury in Mice. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 4519-4536.	1.6	5
5520	METTL3 Is Involved in the Development of Graves' Disease by Inducing SOCS mRNA m6A Modification. <i>Frontiers in Endocrinology</i> , 2021, 12, 666393.	1.5	7
5521	Genomic and functional evidence reveals convergent evolution in fishes on the Tibetan Plateau. <i>Molecular Ecology</i> , 2021, 30, 5752-5764.	2.0	10
5522	Metabolomic Investigation of Synergistic Mechanism for Fangfeng Extract Preventing LPS Induced Neuroinflammation in BV-2 Microglia Cells. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 8155.	1.3	1
5523	Prognostic value and immune infiltration of a novel stromal/immune score-related P2RY12 in lung adenocarcinoma microenvironment. <i>International Immunopharmacology</i> , 2021, 98, 107734.	1.7	5
5524	Integrative Predictive Modeling of Metastasis in Melanoma Cancer Based on MicroRNA, mRNA, and DNA Methylation Data. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 637355.	1.6	5
5525	Identification of Prognostic Genes for Colon Cancer through Gene Co-expression Network Analysis. <i>Current Medical Science</i> , 2021, 41, 1012-1022.	0.7	3
5526	Identification of Key Genes Associated With the Process of Hepatitis B Inflammation and Cancer Transformation by Integrated Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 654517.	1.1	8
5527	Identification of LINC00173 in Myasthenia Gravis by Integration Analysis of Aberrantly Methylated-Differentially Expressed Genes and ceRNA Networks. <i>Frontiers in Genetics</i> , 2021, 12, 726751.	1.1	5

#	ARTICLE	IF	CITATIONS
5528	Traditional Chinese Medicine (TCM) in the treatment of COVID-19 and other viral infections: Efficacies and mechanisms. , 2021, 225, 107843.		258
5529	Variants of candidate genes associated with the risk of obstructive sleep apnea. <i>European Journal of Clinical Investigation</i> , 2022, 52, e13673.	1.7	9
5530	Identification of Key Candidate Genes and Chemical Perturbagens in Diabetic Kidney Disease Using Integrated Bioinformatics Analysis. <i>Frontiers in Endocrinology</i> , 2021, 12, 721202.	1.5	8
5531	Decrypting the role of predicted SARS-CoV-2 miRNAs in COVID-19 pathogenesis: A bioinformatics approach. <i>Computers in Biology and Medicine</i> , 2021, 136, 104669.	3.9	16
5532	Air pollution-induced epigenetic changes: disease development and a possible link with hypersensitivity pneumonitis. <i>Environmental Science and Pollution Research</i> , 2021, 28, 55981-56002.	2.7	24
5533	Uncovering the pharmacological mechanisms of Xijiao Dihuang decoction combined with Yinqiao powder in treating influenza viral pneumonia by an integrative pharmacology strategy. <i>Biomedicine and Pharmacotherapy</i> , 2021, 141, 111676.	2.5	11
5534	Identification of a miRNA-mRNA Regulatory Networks in Placental Tissue Associated With Tibetan High Altitude Adaptation. <i>Frontiers in Genetics</i> , 2021, 12, 671119.	1.1	3
5535	Immune Mechanism, Gene Module, and Molecular Subtype Identification of Astragalus Membranaceus in the Treatment of Dilated Cardiomyopathy: An Integrated Bioinformatics Study. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-29.	0.5	1
5536	The Emerging Plasticizer Alternative DINCH and Its Metabolite MINCH Induce Oxidative Stress and Enhance Inflammatory Responses in Human THP-1 Macrophages. <i>Cells</i> , 2021, 10, 2367.	1.8	18
5537	Analysis of the Composition and Anti-Rheumatoid Arthritis Mechanism of Qintengtongbi Decoction Based on Network Pharmacology. <i>Natural Product Communications</i> , 2021, 16, 1934578X2110414.	0.2	1
5538	Identification of Gene Signature as Diagnostic and Prognostic Blood Biomarker for Early Hepatocellular Carcinoma Using Integrated Cross-Species Transcriptomic and Network Analyses. <i>Frontiers in Genetics</i> , 2021, 12, 710049.	1.1	6
5539	SRSF protein kinase 1 modulates RAN translation and suppresses CGG repeat toxicity. <i>EMBO Molecular Medicine</i> , 2021, 13, e14163.	3.3	17
5540	Integrated Profiling Identifies PLOD3 as a Potential Prognostic and Immunotherapy Relevant Biomarker in Colorectal Cancer. <i>Frontiers in Immunology</i> , 2021, 12, 722807.	2.2	14
5541	PlantGSAD: a comprehensive gene set annotation database for plant species. <i>Nucleic Acids Research</i> , 2022, 50, D1456-D1467.	6.5	20
5542	Hub Genes and Key Pathways of Intervertebral Disc Degeneration: Bioinformatics Analysis and Validation. <i>BioMed Research International</i> , 2021, 2021, 1-10.	0.9	5
5543	Blood lead levels in Peruvian adults are associated with proximity to mining and DNA methylation. <i>Environment International</i> , 2021, 155, 106587.	4.8	13
5544	Exploring the synergistic mechanism of Gegen Qinlian Decoction on the Wnt signaling pathway using an integrated strategy of network pharmacology and RNA-seq. <i>Journal of Ethnopharmacology</i> , 2021, 278, 114283.	2.0	9
5545	The role of alcohol dehydrogenase 1C in regulating inflammatory responses in ulcerative colitis. <i>Biochemical Pharmacology</i> , 2021, 192, 114691.	2.0	8

#	ARTICLE	IF	CITATIONS
5546	Network pharmacological analysis of ethanol extract of <i>Morus alba</i> linne in the treatment of type 2 diabetes mellitus. <i>Arabian Journal of Chemistry</i> , 2021, 14, 103384.	2.3	4
5547	MiR-145 regulates steroidogenesis in mouse primary granulosa cells through targeting Crkl. <i>Life Sciences</i> , 2021, 282, 119820.	2.0	5
5548	Dysfunctional activity of classical DNA end-joining renders acquired resistance to carboplatin in human ovarian cancer cells. <i>Cancer Letters</i> , 2021, 520, 267-280.	3.2	7
5549	Amyloid beta acts synergistically as a pro-inflammatory cytokine. <i>Neurobiology of Disease</i> , 2021, 159, 105493.	2.1	29
5550	The induction of a mesenchymal phenotype by platelet cloaking of cancer cells is a universal phenomenon. <i>Translational Oncology</i> , 2021, 14, 101229.	1.7	6
5551	Database for annotation, visualisation and integrated discovery. , 2022, , 177-185.		0
5552	Exploring the Active Components of Simotang Oral Liquid and Their Potential Mechanism of Action on Gastrointestinal Disorders by Integrating Ultrahigh-Pressure Liquid Chromatography Coupled with Linear Ion Trap-Orbitrap Analysis and Network Pharmacology. <i>ACS Omega</i> , 2021, 6, 2354-2366.	1.6	6
5553	Human Pumilio proteins directly bind the CCR4-NOT deadenylase complex to regulate the transcriptome. <i>Rna</i> , 2021, 27, 445-464.	1.6	32
5554	High Expression of RhoF Predicts Worse Overall Survival: A Potential Therapeutic Target for non-M3 Acute Myeloid Leukemia. <i>Journal of Cancer</i> , 2021, 12, 5530-5542.	1.2	3
5555	Construction of a TF-miRNA-gene feed-forward loop network predicts biomarkers and potential drugs for myasthenia gravis. <i>Scientific Reports</i> , 2021, 11, 2416.	1.6	15
5556	The Identification of a Novel Fucosidosis-Associated FUCA1 Mutation: A Case of a 5-Year-Old Polish Girl with Two Additional Rare Chromosomal Aberrations and Affected DNA Methylation Patterns. <i>Genes</i> , 2021, 12, 74.	1.0	3
5557	Global Lysine Acetylation and 2-Hydroxyisobutyrylation Profiling Reveals the Metabolism Conversion Mechanism in <i>Giardia lamblia</i> . <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100043.	2.5	7
5558	Identification of key genes and pathways in scleral extracellular matrix remodeling in glaucoma: Potential therapeutic agents discovered using bioinformatics analysis. <i>International Journal of Medical Sciences</i> , 2021, 18, 1554-1565.	1.1	13
5559	Smad3 deficiency promotes beta cell proliferation and function in <i>db/db</i> mice <i>via</i> restoring Pax6 expression. <i>Theranostics</i> , 2021, 11, 2845-2859.	4.6	16
5560	Screening differentially expressed genes between endometriosis and ovarian cancer to find new biomarkers for endometriosis. <i>Annals of Medicine</i> , 2021, 53, 1377-1389.	1.5	17
5561	Identification of PARP-7 substrates reveals a role for MARYlation in microtubule control in ovarian cancer cells. <i>ELife</i> , 2021, 10, .	2.8	39
5562	Genomics and molecular analysis of RPL9 and LIAS in lung cancer: Emerging implications in carcinogenesis. <i>Informatics in Medicine Unlocked</i> , 2021, 25, 100698.	1.9	1
5563	A systematic study on the chemical diversity and efficacy of the inflorescence and succulent stem of <i>Cynomorium songaricum</i> . <i>Food and Function</i> , 2021, 12, 7501-7513.	2.1	6

#	ARTICLE	IF	CITATIONS
5564	PDX1/LOW MAFALOW $\beta^2$ -cells contribute to islet function and insulin release. <i>Nature Communications</i> , 2021, 12, 674.	5.8	51
5565	Transcriptome Analysis Identifies Altered Biological Processes and Novel Markers in Human Immunodeficiency Virus-1 Long-Term Non-Progressors. <i>Infection and Chemotherapy</i> , 2021, 53, 489.	1.0	2
5568	miR-26a attenuates cardiac apoptosis and fibrosis by targeting ataxia-telangiectasia mutated in myocardial infarction. <i>Journal of Cellular Physiology</i> , 2020, 235, 6085-6102.	2.0	36
5570	Comparative Metabolic Network Flux Analysis to Identify Differences in Cellular Metabolism. <i>Methods in Molecular Biology</i> , 2020, 2088, 223-269.	0.4	4
5571	Cancer Prevention in Populations High At-Risk for the Development of Oral Cancer: Clinical Trials with Black Raspberries. , 2011, , 259-280.		2
5572	High-Throughput Translational Medicine: Challenges and Solutions. <i>Advances in Experimental Medicine and Biology</i> , 2014, 799, 39-67.	0.8	7
5573	Transcriptomics Using Axolotls. <i>Methods in Molecular Biology</i> , 2015, 1290, 309-319.	0.4	2
5574	Systems Analysis for Interpretation of Phosphoproteomics Data. <i>Methods in Molecular Biology</i> , 2016, 1355, 341-360.	0.4	15
5575	RNA Systems Biology for Cancer: From Diagnosis to Therapy. <i>Methods in Molecular Biology</i> , 2016, 1386, 305-330.	0.4	1
5576	Bioinformatics Methods to Deduce Biological Interpretation from Proteomics Data. <i>Methods in Molecular Biology</i> , 2017, 1549, 147-161.	0.4	2
5577	Microarray Data Analysis. <i>Methods in Molecular Biology</i> , 2007, 377, 1-16.	0.4	9
5578	BiblioSphere "Hypothesis Generation in Regulatory Network Analysis. , 2009, , 401-412.		2
5579	Gene Expression Mining in Type 2 Diabetes Research. <i>Methods in Molecular Biology</i> , 2009, 560, 263-271.	0.4	2
5580	Association Analysis for Large-Scale Gene Set Data. <i>Methods in Molecular Biology</i> , 2007, 408, 19-33.	0.4	9
5581	Algorithms and Methods for Correlating Experimental Results with Annotation Databases. <i>Methods in Molecular Biology</i> , 2010, 593, 315-340.	0.4	2
5582	Data Processing and Analysis for Protein Microarrays. <i>Methods in Molecular Biology</i> , 2011, 723, 337-347.	0.4	14
5583	BiNGS!SL-seq: A Bioinformatics Pipeline for the Analysis and Interpretation of Deep Sequencing Genome-Wide Synthetic Lethal Screen. <i>Methods in Molecular Biology</i> , 2012, 802, 389-398.	0.4	28
5584	What Is the Transcriptome and How it is Evaluated?. , 2014, , 3-48.		5

#	ARTICLE	IF	CITATIONS
5585	Concentration-dependent toxicogenomic changes of silver nanoparticles in hepatocyte-like cells derived from human induced pluripotent stem cells. <i>Cell Biology and Toxicology</i> , 2021, 37, 245-259.	2.4	7
5586	Targeting Mitogen-Activated Protein Kinase Signaling in Mouse Models of Cardiomyopathy Caused by Lamin A/C Gene Mutations. <i>Methods in Enzymology</i> , 2016, 568, 557-580.	0.4	16
5587	Genome-wide identification and characterization of long non-coding RNAs involved in acquired resistance to gefitinib in non-small-cell lung cancer. <i>Computational Biology and Chemistry</i> , 2020, 87, 107288.	1.1	5
5588	Identifying of miR-98-5p/IGF1 axis contributes breast cancer progression using comprehensive bioinformatic analyses methods and experiments validation. <i>Life Sciences</i> , 2020, 261, 118435.	2.0	8
5592	Transcriptomes of cochlear inner and outer hair cells from adult mice. <i>Scientific Data</i> , 2018, 5, 180199.	2.4	101
5593	Protein Quantification by MRM for Biomarker Validation. <i>New Developments in Mass Spectrometry</i> , 2014, , 277-315.	0.2	2
5594	Functional insights into the cellular response triggered by a bile-acid platinum compound conjugated to biocompatible ferric nanoparticles using quantitative proteomic approaches. <i>Nanoscale</i> , 2017, 9, 9960-9972.	2.8	11
5595	Identification and verification of three key genes associated with survival and prognosis of COAD patients via integrated bioinformatics analysis. <i>Bioscience Reports</i> , 2020, 40, .	1.1	13
5596	Sex diversity in proximal tubule and endothelial gene expression in mice with ischemic acute kidney injury. <i>Clinical Science</i> , 2020, 134, 1887-1909.	1.8	21
5597	Visual gene network analysis of aging-specific gene co-expression in human indicates overlaps with immuno-pathological regulations. <i>4open</i> , 2018, 1, 4.	0.1	2
5598	Development of an immune-related prognostic index associated with osteosarcoma. <i>Bioengineered</i> , 2021, 12, 172-182.	1.4	12
5599	Comparative Transcriptional Analysis of Embryoid Body Versus Two-Dimensional Differentiation of Murine Embryonic Stem Cells. <i>Tissue Engineering - Part A</i> , 2008, .	1.6	1
5600	Patterns and processes of human life history evolution. , 2011, , 153-168.		24
5601	Identification of crucial genes correlated with esophageal cancer by integrated high-throughput data analysis. <i>Medicine (United States)</i> , 2020, 99, e20340.	0.4	13
5626	The proteome of red cell membranes and vesicles during storage in blood bank conditions. <i>Transfusion</i> , 2008, 48, 827-835.	0.8	99
5627	A Systematic, Data-driven Approach to the Combined Analysis of Microarray and QTL Data. <i>Developments in Biologicals</i> , 2008, 132, 293-299.	0.4	3
5628	Vitreous Modulation of Gene Expression in Low-Passage Human Retinal Pigment Epithelial Cells. , 2007, 48, 1853.		15
5629	IFN regulatory factorâ€™8 expression in macrophages governs an antimetastatic program. <i>JCI Insight</i> , 2019, 4, .	2.3	30

#	ARTICLE	IF	CITATIONS
5630	Functional significance of the discordance between transcriptional profile and left ventricular structure/function during reverse remodeling. <i>JCI Insight</i> , 2016, 1, e86038.	2.3	33
5631	Super-enhancers maintain renin-expressing cell identity and memory to preserve multi-system homeostasis. <i>Journal of Clinical Investigation</i> , 2018, 128, 4787-4803.	3.9	41
5632	uPAR isoform 2 forms a dimer and induces severe kidney disease in mice. <i>Journal of Clinical Investigation</i> , 2019, 129, 1946-1959.	3.9	48
5633	Brain somatic mutations in MTOR reveal translational dysregulations underlying intractable focal epilepsy. <i>Journal of Clinical Investigation</i> , 2019, 129, 4207-4223.	3.9	45
5634	Epigenetic driver mutations in ARID1A shape cancer immune phenotype and immunotherapy. <i>Journal of Clinical Investigation</i> , 2020, 130, 2712-2726.	3.9	112
5635	Eotaxin-3 and a uniquely conserved gene-expression profile in eosinophilic esophagitis. <i>Journal of Clinical Investigation</i> , 2006, 116, 536-547.	3.9	750
5636	Calcineurin/Nfat signaling is required for perinatal lung maturation and function. <i>Journal of Clinical Investigation</i> , 2006, 116, 2597-2609.	3.9	47
5637	Activation of MAPK pathways links LMNA mutations to cardiomyopathy in Emery-Dreifuss muscular dystrophy. <i>Journal of Clinical Investigation</i> , 2007, 117, 1282-1293.	3.9	256
5638	Gene expression analysis in pregnant women and their infants identifies unique fetal biomarkers that circulate in maternal blood. <i>Journal of Clinical Investigation</i> , 2007, 117, 3007-3019.	3.9	53
5639	B cell activator PAX5 promotes lymphomagenesis through stimulation of B cell receptor signaling. <i>Journal of Clinical Investigation</i> , 2007, 117, 2602-2610.	3.9	37
5640	Increased local expression of coagulation factor X contributes to the fibrotic response in human and murine lung injury. <i>Journal of Clinical Investigation</i> , 2009, 119, 2550-63.	3.9	251
5641	Global genomic analysis reveals rapid control of a robust innate response in SIV-infected sooty mangabeys. <i>Journal of Clinical Investigation</i> , 2009, 119, 3556-72.	3.9	351
5642	Cardiac fibrosis in mice with hypertrophic cardiomyopathy is mediated by non-myocyte proliferation and requires Tgf- $\beta$ 2. <i>Journal of Clinical Investigation</i> , 2010, 120, 3520-3529.	3.9	372
5643	A metabolic prosurvival role for PML in breast cancer. <i>Journal of Clinical Investigation</i> , 2012, 122, 3088-3100.	3.9	220
5644	Zinc transporter Slc39a8 is essential for cardiac ventricular compaction. <i>Journal of Clinical Investigation</i> , 2018, 128, 826-833.	3.9	39
5646	Gene Expression Profiling of Sporadic Parkinson's Disease Substantia Nigra Pars Compacta Reveals Impairment of Ubiquitin-Proteasome Subunits, SKP1A, Aldehyde Dehydrogenase, and Chaperone HSC-70. <i>Annals of the New York Academy of Sciences</i> , 2005, 1053, 356-375.	1.8	136
5647	Identification of Transcriptional Factors and Key Genes in Primary Osteoporosis by DNA Microarray. <i>Medical Science Monitor</i> , 2015, 21, 1333-1344.	0.5	32
5648	Screening of Target Genes and Regulatory Function of miRNAs as Prognostic Indicators for Prostate Cancer. <i>Medical Science Monitor</i> , 2015, 21, 3748-3759.	0.5	29

#	ARTICLE	IF	CITATIONS
5649	Five miRNAs Considered as Molecular Targets for Predicting Esophageal Cancer. <i>Medical Science Monitor</i> , 2015, 21, 3222-3230.	0.5	21
5650	Identification of CD20, ECM, and ITGA as Biomarkers for Osteosarcoma by Integrating Transcriptome Analysis. <i>Medical Science Monitor</i> , 2016, 22, 2075-2085.	0.5	11
5651	Clinical Value of miR-101-3p and Biological Analysis of its Prospective Targets in Breast Cancer: A Study Based on The Cancer Genome Atlas (TCGA) and Bioinformatics. <i>Medical Science Monitor</i> , 2017, 23, 1857-1871.	0.5	25
5652	Identification of Key Genes in Colorectal Cancer Regulated by miR-34a. <i>Medical Science Monitor</i> , 2017, 23, 5735-5743.	0.5	17
5653	Impact of Colon-Specific DNA Methylation-Regulated Gene Modules on Colorectal Cancer Patient Survival. <i>Medical Science Monitor</i> , 2019, 25, 3549-3557.	0.5	5
5654	Differentially Expressed Gene Screening, Biological Function Enrichment, and Correlation with Prognosis in Non-Small Cell Lung Cancer. <i>Medical Science Monitor</i> , 2019, 25, 4333-4341.	0.5	5
5655	Identification of Hub Genes and Pathways in Gastric Adenocarcinoma Based on Bioinformatics Analysis. <i>Medical Science Monitor</i> , 2020, 26, e920261.	0.5	18
5656	LYN, a Key Gene From Bioinformatics Analysis, Contributes to Development and Progression of Esophageal Adenocarcinoma. <i>Medical Science Monitor Basic Research</i> , 2015, 21, 253-261.	2.6	87
5657	Constellation Map: Downstream visualization and interpretation of gene set enrichment results. <i>F1000Research</i> , 2015, 4, 167.	0.8	3
5658	GOsummaries: an R Package for Visual Functional Annotation of Experimental Data. <i>F1000Research</i> , 2015, 4, 574.	0.8	86
5659	Associations between joint effusion in the knee and gene expression levels in the circulation: a meta-analysis. <i>F1000Research</i> , 2016, 5, 109.	0.8	6
5660	Single-Cell-Based Analysis Highlights a Surge in Cell-to-Cell Molecular Variability Preceding Irreversible Commitment in a Differentiation Process. <i>PLoS Biology</i> , 2016, 14, e1002585.	2.6	220
5661	Evolutionary and Topological Properties of Genes and Community Structures in Human Gene Regulatory Networks. <i>PLoS Computational Biology</i> , 2016, 12, e1005009.	1.5	9
5662	Identification of Entry Factors Involved in Hepatitis C Virus Infection Based on Host-Mimicking Short Linear Motifs. <i>PLoS Computational Biology</i> , 2017, 13, e1005368.	1.5	8
5663	Automated deconvolution of structured mixtures from heterogeneous tumor genomic data. <i>PLoS Computational Biology</i> , 2017, 13, e1005815.	1.5	8
5664	Circadian Clock Genes Contribute to the Regulation of Hair Follicle Cycling. <i>PLoS Genetics</i> , 2009, 5, e1000573.	1.5	146
5665	Population-Based Resequencing of Experimentally Evolved Populations Reveals the Genetic Basis of Body Size Variation in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2011, 7, e1001336.	1.5	265
5666	Selection for long and short sleep duration in <i>Drosophila melanogaster</i> reveals the complex genetic network underlying natural variation in sleep. <i>PLoS Genetics</i> , 2017, 13, e1007098.	1.5	43

#	ARTICLE	IF	CITATIONS
5667	Dissecting Inflammatory Complications in Critically Injured Patients by Within-Patient Gene Expression Changes: A Longitudinal Clinical Genomics Study. <i>PLoS Medicine</i> , 2011, 8, e1001093.	3.9	51
5668	Global Identification of Myc Target Genes Reveals Its Direct Role in Mitochondrial Biogenesis and Its E-Box Usage In Vivo. <i>PLoS ONE</i> , 2008, 3, e1798.	1.1	197
5669	Identification of a Common Gene Expression Response in Different Lung Inflammatory Diseases in Rodents and Macaques. <i>PLoS ONE</i> , 2008, 3, e2596.	1.1	42
5670	Altered Metabolism of Growth Hormone Receptor Mutant Mice: A Combined NMR Metabonomics and Microarray Study. <i>PLoS ONE</i> , 2008, 3, e2764.	1.1	43
5671	Identify Alternative Splicing Events Based on Position-Specific Evolutionary Conservation. <i>PLoS ONE</i> , 2008, 3, e2806.	1.1	24
5672	Preservation of Genes Involved in Sterol Metabolism in Cholesterol Auxotrophs: Facts and Hypotheses. <i>PLoS ONE</i> , 2008, 3, e2883.	1.1	48
5673	Improved Elucidation of Biological Processes Linked to Diabetic Nephropathy by Single Probe-Based Microarray Data Analysis. <i>PLoS ONE</i> , 2008, 3, e2937.	1.1	69
5674	Transcriptome-Wide Assessment of Human Brain and Lymphocyte Senescence. <i>PLoS ONE</i> , 2008, 3, e3024.	1.1	60
5675	The Evolving Transcriptome of Head and Neck Squamous Cell Carcinoma: A Systematic Review. <i>PLoS ONE</i> , 2008, 3, e3215.	1.1	61
5676	Different Transcriptional Control of Metabolism and Extracellular Matrix in Visceral and Subcutaneous Fat of Obese and Rimonabant Treated Mice. <i>PLoS ONE</i> , 2008, 3, e3385.	1.1	20
5677	A Molecular Function Map of Ewing's Sarcoma. <i>PLoS ONE</i> , 2009, 4, e5415.	1.1	158
5678	Detection of Transgenerational Spermatogenic Inheritance of Adult Male Acquired CNS Gene Expression Characteristics Using a Drosophila Systems Model. <i>PLoS ONE</i> , 2009, 4, e5763.	1.1	26
5679	A Genome Scan for Positive Selection in Thoroughbred Horses. <i>PLoS ONE</i> , 2009, 4, e5767.	1.1	123
5680	Identification of a Putative Network of Actin-Associated Cytoskeletal Proteins in Glomerular Podocytes Defined by Co-Purified mRNAs. <i>PLoS ONE</i> , 2009, 4, e6491.	1.1	12
5681	Global Brain Gene Expression Analysis Links Glutamatergic and GABAergic Alterations to Suicide and Major Depression. <i>PLoS ONE</i> , 2009, 4, e6585.	1.1	333
5682	Correlating Global Gene Regulation to Angiogenesis in the Developing Chick Extra-Embryonic Vascular System. <i>PLoS ONE</i> , 2009, 4, e7856.	1.1	56
5683	Gene Expression Profiling during Early Acute Febrile Stage of Dengue Infection Can Predict the Disease Outcome. <i>PLoS ONE</i> , 2009, 4, e7892.	1.1	77
5684	An Epigenetic Signature in Peripheral Blood Predicts Active Ovarian Cancer. <i>PLoS ONE</i> , 2009, 4, e8274.	1.1	291



#	ARTICLE	IF	CITATIONS
5685	3â€²-End Sequencing for Expression Quantification (3SEQ) from Archival Tumor Samples. PLoS ONE, 2010, 5, e8768.	1.1	123
5686	Genome-Wide Analysis of Binding Sites and Direct Target Genes of the Orphan Nuclear Receptor NR2F1/COUP-TFI. PLoS ONE, 2010, 5, e8910.	1.1	41
5687	Lack of nAChR Activity Depresses Cochlear Maturation and Up-Regulates GABA System Components: Temporal Profiling of Gene Expression in $\hat{1}\pm 9$ Null Mice. PLoS ONE, 2010, 5, e9058.	1.1	19
5688	Gene Expression Profiling and Network Analysis Reveals Lipid and Steroid Metabolism to Be the Most Favored by TNF $\hat{1}\pm$ in HepG2 Cells. PLoS ONE, 2010, 5, e9063.	1.1	14
5689	In Vitro Fertilization and Embryo Culture Strongly Impact the Placental Transcriptome in the Mouse Model. PLoS ONE, 2010, 5, e9218.	1.1	75
5690	Cardiac Deletion of Smyd2 Is Dispensable for Mouse Heart Development. PLoS ONE, 2010, 5, e9748.	1.1	63
5691	Dissecting Interferon-Induced Transcriptional Programs in Human Peripheral Blood Cells. PLoS ONE, 2010, 5, e9753.	1.1	134
5692	Mutations in CHMP2B in Lower Motor Neuron Predominant Amyotrophic Lateral Sclerosis (ALS). PLoS ONE, 2010, 5, e9872.	1.1	204
5693	A Study of the Influence of Sex on Genome Wide Methylation. PLoS ONE, 2010, 5, e10028.	1.1	217
5694	A Data Integration Approach to Mapping OCT4 Gene Regulatory Networks Operative in Embryonic Stem Cells and Embryonal Carcinoma Cells. PLoS ONE, 2010, 5, e10709.	1.1	81
5695	Acetaminophen Modulates the Transcriptional Response to Recombinant Interferon- $\hat{1}^2$ . PLoS ONE, 2010, 5, e11031.	1.1	16
5696	A Comparative Analysis of Extra-Embryonic Endoderm Cell Lines. PLoS ONE, 2010, 5, e12016.	1.1	47
5697	Transcription Profiling of Epstein-Barr Virus Nuclear Antigen (EBNA)-1 Expressing Cells Suggests Targeting of Chromatin Remodeling Complexes. PLoS ONE, 2010, 5, e12052.	1.1	23
5698	Sex-Related Differences in Gene Expression Following Coxiella burnetii Infection in Mice: Potential Role of Circadian Rhythm. PLoS ONE, 2010, 5, e12190.	1.1	36
5699	The Proneural Molecular Signature Is Enriched in Oligodendrogliomas and Predicts Improved Survival among Diffuse Gliomas. PLoS ONE, 2010, 5, e12548.	1.1	125
5700	Identification of Novel p53 Pathway Activating Small-Molecule Compounds Reveals Unexpected Similarities with Known Therapeutic Agents. PLoS ONE, 2010, 5, e12996.	1.1	77
5701	Identification of Genetic and Epigenetic Marks Involved in Population Structure. PLoS ONE, 2010, 5, e13209.	1.1	38
5702	eXtraembryonic ENdoderm (XEN) Stem Cells Produce Factors that Activate Heart Formation. PLoS ONE, 2010, 5, e13446.	1.1	35

#	ARTICLE	IF	CITATIONS
5703	A Comparative Analysis of Gene-Expression Data of Multiple Cancer Types. PLoS ONE, 2010, 5, e13696.	1.1	31
5704	The LARGE Principle of Cellular Reprogramming: Lost, Acquired and Retained Gene Expression in Foreskin and Amniotic Fluid-Derived Human iPS Cells. PLoS ONE, 2010, 5, e13703.	1.1	61
5705	Dual DNA Methylation Patterns in the CNS Reveal Developmentally Poised Chromatin and Monoallelic Expression of Critical Genes. PLoS ONE, 2010, 5, e13843.	1.1	23
5706	Amplification of the 20q Chromosomal Arm Occurs Early in Tumorigenic Transformation and May Initiate Cancer. PLoS ONE, 2011, 6, e14632.	1.1	69
5707	Analysis of Common and Specific Mechanisms of Liver Function Affected by Nitrotoluene Compounds. PLoS ONE, 2011, 6, e14662.	1.1	33
5708	Global Expression of Cell Surface Proteins in Embryonic Stem Cells. PLoS ONE, 2010, 5, e15795.	1.1	33
5709	A Key Role for Poly(ADP-Ribose) Polymerase 3 in Ectodermal Specification and Neural Crest Development. PLoS ONE, 2011, 6, e15834.	1.1	17
5710	A Widespread Distribution of Genomic CeMyoD Binding Sites Revealed and Cross Validated by ChIP-Chip and ChIP-Seq Techniques. PLoS ONE, 2010, 5, e15898.	1.1	24
5711	Characterization of the Contradictory Chromatin Signatures at the 3' Exons of Zinc Finger Genes. PLoS ONE, 2011, 6, e17121.	1.1	64
5712	Genomic and Proteomic Analysis of the Impact of Mitotic Quiescence on the Engraftment of Human CD34+ Cells. PLoS ONE, 2011, 6, e17498.	1.1	8
5713	Do Two Machine-Learning Based Prognostic Signatures for Breast Cancer Capture the Same Biological Processes?. PLoS ONE, 2011, 6, e17795.	1.1	35
5714	Adjunctive Dexamethasone Affects the Expression of Genes Related to Inflammation, Neurogenesis and Apoptosis in Infant Rat Pneumococcal Meningitis. PLoS ONE, 2011, 6, e17840.	1.1	23
5715	Microarray Analysis Uncovers a Role for Tip60 in Nervous System Function and General Metabolism. PLoS ONE, 2011, 6, e18412.	1.1	45
5716	A Mighty Small Heart: The Cardiac Proteome of Adult Drosophila melanogaster. PLoS ONE, 2011, 6, e18497.	1.1	81
5717	Small Molecule Amiloride Modulates Oncogenic RNA Alternative Splicing to Devitalize Human Cancer Cells. PLoS ONE, 2011, 6, e18643.	1.1	53
5718	Genome-Wide DNA Methylation Analysis Reveals Phytoestrogen Modification of Promoter Methylation Patterns during Embryonic Stem Cell Differentiation. PLoS ONE, 2011, 6, e19278.	1.1	26
5719	Proteomic Analyses Reveal Common Promiscuous Patterns of Cell Surface Proteins on Human Embryonic Stem Cells and Sperms. PLoS ONE, 2011, 6, e19386.	1.1	37
5720	Methylation Profile of Single Hepatocytes Derived from Hepatitis B Virus-Related Hepatocellular Carcinoma. PLoS ONE, 2011, 6, e19862.	1.1	59

#	ARTICLE	IF	CITATIONS
5721	Gene Expression Profiling and Association with Prion-Related Lesions in the Medulla Oblongata of Symptomatic Natural Scrapie Animals. PLoS ONE, 2011, 6, e19909.	1.1	19
5722	GLI1 Confers Profound Phenotypic Changes upon LNCaP Prostate Cancer Cells That Include the Acquisition of a Hormone Independent State. PLoS ONE, 2011, 6, e20271.	1.1	11
5723	Deep Sequencing Reveals Novel MicroRNAs and Regulation of MicroRNA Expression during Cell Senescence. PLoS ONE, 2011, 6, e20509.	1.1	73
5724	Genome-Wide Analysis Reveals a Major Role in Cell Fate Maintenance and an Unexpected Role in Endoreduplication for the Drosophila FoxA Gene Fork Head. PLoS ONE, 2011, 6, e20901.	1.1	21
5725	The Cycad Genotoxin MAM Modulates Brain Cellular Pathways Involved in Neurodegenerative Disease and Cancer in a DNA Damage-Linked Manner. PLoS ONE, 2011, 6, e20911.	1.1	57
5726	Expression Profiling of FSHD-1 and FSHD-2 Cells during Myogenic Differentiation Evidences Common and Distinctive Gene Dysregulation Patterns. PLoS ONE, 2011, 6, e20966.	1.1	39
5727	E-Cadherin Acts as a Regulator of Transcripts Associated with a Wide Range of Cellular Processes in Mouse Embryonic Stem Cells. PLoS ONE, 2011, 6, e21463.	1.1	26
5728	The Use of Genome-Wide eQTL Associations in Lymphoblastoid Cell Lines to Identify Novel Genetic Pathways Involved in Complex Traits. PLoS ONE, 2011, 6, e22070.	1.1	36
5729	Association between Genetic Subgroups of Pancreatic Ductal Adenocarcinoma Defined by High Density 500 K SNP-Arrays and Tumor Histopathology. PLoS ONE, 2011, 6, e22315.	1.1	16
5730	The Collagen Chaperone HSP47 Is a New Interactor of APP that Affects the Levels of Extracellular Beta-Amyloid Peptides. PLoS ONE, 2011, 6, e22370.	1.1	11
5731	Whole Genome Expression Array Profiling Highlights Differences in Mucosal Defense Genes in Barrett's Esophagus and Esophageal Adenocarcinoma. PLoS ONE, 2011, 6, e22513.	1.1	36
5732	Transcriptome Analysis of Epithelial and Stromal Contributions to Mammogenesis in Three Week Prepartum Cows. PLoS ONE, 2011, 6, e22541.	1.1	15
5733	SEAS: A System for SEED-Based Pathway Enrichment Analysis. PLoS ONE, 2011, 6, e22556.	1.1	8
5734	Differential Effects of Prenatal Stress in 5-Htt Deficient Mice: Towards Molecular Mechanisms of Gene × Environment Interactions. PLoS ONE, 2011, 6, e22715.	1.1	75
5735	Modulation of Androgen Receptor Signaling in Hormonal Therapy-Resistant Prostate Cancer Cell Lines. PLoS ONE, 2011, 6, e23144.	1.1	46
5736	Transcriptomic Analysis Brings New Insight into the Biological Role of the Prion Protein during Mouse Embryogenesis. PLoS ONE, 2011, 6, e23253.	1.1	22
5737	Transcriptional Profiling of Human Liver Identifies Sex-Biased Genes Associated with Polygenic Dyslipidemia and Coronary Artery Disease. PLoS ONE, 2011, 6, e23506.	1.1	143
5738	Disease Gene Interaction Pathways: A Potential Framework for How Disease Genes Associate by Disease-Risk Modules. PLoS ONE, 2011, 6, e24495.	1.1	7

#	ARTICLE	IF	CITATIONS
5739	Pattern Specification and Immune Response Transcriptional Signatures of Pericardial and Subcutaneous Adipose Tissue. PLoS ONE, 2011, 6, e26092.	1.1	6
5740	The Leukemia-Specific Fusion Gene ETV6/RUNX1 Perturbs Distinct Key Biological Functions Primarily by Gene Repression. PLoS ONE, 2011, 6, e26348.	1.1	43
5741	Strain-Dependent Host Transcriptional Responses to Toxoplasma Infection Are Largely Conserved in Mammalian and Avian Hosts. PLoS ONE, 2011, 6, e26369.	1.1	20
5742	Differential Expression of Extracellular Matrix-Mediated Pathways in Single-Suture Craniosynostosis. PLoS ONE, 2011, 6, e26557.	1.1	34
5743	Deep Sequencing of MYC DNA-Binding Sites in Burkitt Lymphoma. PLoS ONE, 2011, 6, e26837.	1.1	90
5744	Replication and Virus-Induced Transcriptome of HAdV-5 in Normal Host Cells versus Cancer Cells - Differences of Relevance for Adenoviral Oncolysis. PLoS ONE, 2011, 6, e27934.	1.1	8
5745	TRAF6 and IRF7 Control HIV Replication in Macrophages. PLoS ONE, 2011, 6, e28125.	1.1	41
5746	Comparing Statistical Methods for Constructing Large Scale Gene Networks. PLoS ONE, 2012, 7, e29348.	1.1	156
5747	A Comparative Study of Gene-Expression Data of Basal Cell Carcinoma and Melanoma Reveals New Insights about the Two Cancers. PLoS ONE, 2012, 7, e30750.	1.1	21
5748	Unraveling the Global microRNAome Responses to Ionizing Radiation in Human Embryonic Stem Cells. PLoS ONE, 2012, 7, e31028.	1.1	30
5749	Functional Complexity of the Axonal Growth Cone: A Proteomic Analysis. PLoS ONE, 2012, 7, e31858.	1.1	48
5750	Cellular Phenotype-Dependent and -Independent Effects of Vitamin C on the Renewal and Gene Expression of Mouse Embryonic Fibroblasts. PLoS ONE, 2012, 7, e32957.	1.1	11
5751	Comparison of Muscle Transcriptome between Pigs with Divergent Meat Quality Phenotypes Identifies Genes Related to Muscle Metabolism and Structure. PLoS ONE, 2012, 7, e33763.	1.1	80
5752	Systematic Identification of Spontaneous Preterm Birth-Associated RNA Transcripts in Maternal Plasma. PLoS ONE, 2012, 7, e34328.	1.1	43
5753	Involvement of microRNA Lethal-7a in the Regulation of Embryo Implantation in Mice. PLoS ONE, 2012, 7, e37039.	1.1	72
5754	De-Novo Transcriptome Sequencing of a Normalized cDNA Pool from Influenza Infected Ferrets. PLoS ONE, 2012, 7, e37104.	1.1	13
5755	High Accuracy Mutation Detection in Leukemia on a Selected Panel of Cancer Genes. PLoS ONE, 2012, 7, e38463.	1.1	58
5756	$\hat{\beta}$ -H2AX Kinetics as a Novel Approach to High Content Screening for Small Molecule Radiosensitizers. PLoS ONE, 2012, 7, e38465.	1.1	24

#	ARTICLE	IF	CITATIONS
5757	Effect of Irradiation on Cell Transcriptome and Proteome of Rat Submandibular Salivary Glands. PLoS ONE, 2012, 7, e40636.	1.1	8
5758	Proteomic and Systems Biology Analysis of Monocytes Exposed to Securinine, a GABAA Receptor Antagonist and Immune Adjuvant. PLoS ONE, 2012, 7, e41278.	1.1	12
5759	Expression Changes in the Stroma of Prostate Cancer Predict Subsequent Relapse. PLoS ONE, 2012, 7, e41371.	1.1	38
5760	Mig-6 Plays a Critical Role in the Regulation of Cholesterol Homeostasis and Bile Acid Synthesis. PLoS ONE, 2012, 7, e42915.	1.1	24
5761	Identification of Thalidomide-Specific Transcriptomics and Proteomics Signatures during Differentiation of Human Embryonic Stem Cells. PLoS ONE, 2012, 7, e44228.	1.1	83
5762	Differential Gene and MicroRNA Expression between Etoposide Resistant and Etoposide Sensitive MCF7 Breast Cancer Cell Lines. PLoS ONE, 2012, 7, e45268.	1.1	27
5763	Transient Scrotal Hyperthermia Induces Lipid Droplet Accumulation and Reveals a Different ADFP Expression Pattern between the Testes and Liver in Mice. PLoS ONE, 2012, 7, e45694.	1.1	21
5764	Genome-Wide Scan for Bats and Dolphin to Detect Their Genetic Basis for New Locomotive Styles. PLoS ONE, 2012, 7, e46455.	1.1	6
5765	Integrative Analysis Reveals Relationships of Genetic and Epigenetic Alterations in Osteosarcoma. PLoS ONE, 2012, 7, e48262.	1.1	87
5766	Prediction of <i>C. elegans</i> Longevity Genes by Human and Worm Longevity Networks. PLoS ONE, 2012, 7, e48282.	1.1	49
5767	Nuclear RNA Sequencing of the Mouse Erythroid Cell Transcriptome. PLoS ONE, 2012, 7, e49274.	1.1	35
5768	The Molecular Profiles of Neural Stem Cell Niche in the Adult Subventricular Zone. PLoS ONE, 2012, 7, e50501.	1.1	63
5769	Ablation of the Cardiac-Specific Gene Leucine-Rich Repeat Containing 10 ( <i>Lrrc10</i> ) Results in Dilated Cardiomyopathy. PLoS ONE, 2012, 7, e51621.	1.1	37
5770	Pathway Correlation Profile of Gene-Gene Co-Expression for Identifying Pathway Perturbation. PLoS ONE, 2012, 7, e52127.	1.1	16
5771	Functional Comparison of Chronological and In Vitro Aging: Differential Role of the Cytoskeleton and Mitochondria in Mesenchymal Stromal Cells. PLoS ONE, 2012, 7, e52700.	1.1	150
5772	Analysis of Gene Expression Profiling in Meningioma: Deregulated Signaling Pathways Associated with Meningioma and EGFL6 Overexpression in Benign Meningioma Tissue and Serum. PLoS ONE, 2012, 7, e52707.	1.1	64
5773	Proline: The Distribution, Frequency, Positioning, and Common Functional Roles of Proline and Polyproline Sequences in the Human Proteome. PLoS ONE, 2013, 8, e53785.	1.1	203
5774	Characterization of Transcriptional Changes in ERG Rearrangement-Positive Prostate Cancer Identifies the Regulation of Metabolic Sensors Such as Neuropeptide Y. PLoS ONE, 2013, 8, e55207.	1.1	32

#	ARTICLE	IF	CITATIONS
5775	Differences in X-Chromosome Transcriptional Activity and Cholesterol Metabolism between Placentae from Swine Breeds from Asian and Western Origins. PLoS ONE, 2013, 8, e55345.	1.1	37
5776	N-Glycoproteome of E14.Tg2a Mouse Embryonic Stem Cells. PLoS ONE, 2013, 8, e55722.	1.1	18
5777	Transcriptomic Profiling of Human Peritumoral Neocortex Tissues Revealed Genes Possibly Involved in Tumor-Induced Epilepsy. PLoS ONE, 2013, 8, e56077.	1.1	20
5778	Differential Effects of Drug Interventions and Dietary Lifestyle in Developing Type 2 Diabetes and Complications: A Systems Biology Analysis in LDLr <sup>-/-</sup> Mice. PLoS ONE, 2013, 8, e56122.	1.1	18
5779	Cell-Type-Specific Predictive Network Yields Novel Insights into Mouse Embryonic Stem Cell Self-Renewal and Cell Fate. PLoS ONE, 2013, 8, e56810.	1.1	11
5780	Transcriptome Analysis of Proximal Tubular Cells (HK-2) Exposed to Urines of Type 1 Diabetes Patients at Risk of Early Progressive Renal Function Decline. PLoS ONE, 2013, 8, e57751.	1.1	5
5781	Gene Expression Profile Analysis of Type 2 Diabetic Mouse Liver. PLoS ONE, 2013, 8, e57766.	1.1	37
5782	Discovery of Cellular Proteins Required for the Early Steps of HCV Infection Using Integrative Genomics. PLoS ONE, 2013, 8, e60333.	1.1	17
5783	miRNA Biogenesis Enzyme Drosha Is Required for Vascular Smooth Muscle Cell Survival. PLoS ONE, 2013, 8, e60888.	1.1	31
5784	Textrou!: Extracting Semantic Textual Meaning from Gene Sets. PLoS ONE, 2013, 8, e62665.	1.1	23
5785	Differential Distribution of the Ca (2+) Regulator Pcp4 in the Branchial Arches Is Regulated by Hoxa2. PLoS ONE, 2013, 8, e63160.	1.1	2
5786	Comparative Transcriptome Analysis of Adipose Tissues Reveals that ECM-Receptor Interaction Is Involved in the Depot-Specific Adipogenesis in Cattle. PLoS ONE, 2013, 8, e66267.	1.1	89
5787	Gene Expression Profiles of Metabolic Aggressiveness and Tumor Recurrence in Benign Meningioma. PLoS ONE, 2013, 8, e67291.	1.1	28
5788	Transcriptomic Analysis of Insulin-Sensitive Tissues from Anti-Diabetic Drug Treated ZDF Rats, a T2DM Animal Model. PLoS ONE, 2013, 8, e69624.	1.1	4
5789	Candidate Transcriptomic Sources of Inbreeding Depression in Drosophila melanogaster. PLoS ONE, 2013, 8, e70067.	1.1	5
5790	Biphasic Functional Regulation in Hippocampus of Rat with Chronic Cerebral Hypoperfusion Induced by Permanent Occlusion of Bilateral Common Carotid Artery. PLoS ONE, 2013, 8, e70093.	1.1	34
5791	Visual Search of Neuropil-Enriched RNAs from Brain In Situ Hybridization Data through the Image Analysis Pipeline Hippo-ATESC. PLoS ONE, 2013, 8, e74481.	1.1	9
5792	AQP9 Expression in Glioblastoma Multiforme Tumors Is Limited to a Small Population of Astrocytic Cells and CD15+/CalB+ Leukocytes. PLoS ONE, 2013, 8, e75764.	1.1	29

#	ARTICLE	IF	CITATIONS
5793	Comparison of Cellular and Transcriptional Responses to 1,25-Dihydroxyvitamin D3 and Glucocorticoids in Peripheral Blood Mononuclear Cells. PLoS ONE, 2013, 8, e76643.	1.1	9
5794	Extension of Life Span by Impaired Glucose Metabolism in <i>Caenorhabditis elegans</i> Is Accompanied by Structural Rearrangements of the Transcriptomic Network. PLoS ONE, 2013, 8, e77776.	1.1	18
5795	Proteomic Changes during B Cell Maturation: 2D-DIGE Approach. PLoS ONE, 2013, 8, e77894.	1.1	7
5796	Mechanistic Phenotypes: An Aggregative Phenotyping Strategy to Identify Disease Mechanisms Using GWAS Data. PLoS ONE, 2013, 8, e81503.	1.1	15
5797	Identification of GRB2 and GAB1 Coexpression as an Unfavorable Prognostic Factor for Hepatocellular Carcinoma by a Combination of Expression Profile and Network Analysis. PLoS ONE, 2013, 8, e85170.	1.1	60
5798	The Prolyl Isomerase Pin1 Regulates mRNA Levels of Genes with Short Half-Lives by Targeting Specific RNA Binding Proteins. PLoS ONE, 2014, 9, e85427.	1.1	28
5799	Growth Factor Priming Differentially Modulates Components of the Extracellular Matrix Proteome in Chondrocytes and Synovium-Derived Stem Cells. PLoS ONE, 2014, 9, e88053.	1.1	22
5800	Regulation of <i>Drosophila</i> Eye Development by the Transcription Factor <i>Sine oculis</i> . PLoS ONE, 2014, 9, e89695.	1.1	29
5801	High-Frequency Stimulation of the Subthalamic Nucleus Counteracts Cortical Expression of Major Histocompatibility Complex Genes in a Rat Model of Parkinson's Disease. PLoS ONE, 2014, 9, e91663.	1.1	7
5802	The Andean Adaptive Toolkit to Counteract High Altitude Maladaptation: Genome-Wide and Phenotypic Analysis of the Collas. PLoS ONE, 2014, 9, e93314.	1.1	55
5803	The SLE Transcriptome Exhibits Evidence of Chronic Endotoxin Exposure and Has Widespread Dysregulation of Non-Coding and Coding RNAs. PLoS ONE, 2014, 9, e93846.	1.1	109
5804	Comparison of the Gene Expression Profiles of Human Fetal Cortical Astrocytes with Pluripotent Stem Cell Derived Neural Stem Cells Identifies Human Astrocyte Markers and Signaling Pathways and Transcription Factors Active in Human Astrocytes. PLoS ONE, 2014, 9, e96139.	1.1	31
5805	Integration of Molecular Profiling and Chemical Imaging to Elucidate Fibroblast-Microenvironment Impact on Cancer Cell Phenotype and Endocrine Resistance in Breast Cancer. PLoS ONE, 2014, 9, e96878.	1.1	36
5806	Integrated Proteomics Identified Up-Regulated Focal Adhesion-Mediated Proteins in Human Squamous Cell Carcinoma in an Orthotopic Murine Model. PLoS ONE, 2014, 9, e98208.	1.1	10
5807	Investigation of Pathogenic Genes in Peri-Implantitis from Implant Clustering Failure Patients: A Whole-Exome Sequencing Pilot Study. PLoS ONE, 2014, 9, e99360.	1.1	20
5808	biDCC: A New Method for Discovering Global Features of DNA Microarray Data via an Iterative Re-Clustering Procedure. PLoS ONE, 2014, 9, e102445.	1.1	4
5809	Whole Proteome Analysis of Mouse Lymph Nodes in Cutaneous Anthrax. PLoS ONE, 2014, 9, e110873.	1.1	10
5810	Comparative Transcriptome Analysis Reveals Early Pregnancy-Specific Genes Expressed in Peripheral Blood of Pregnant Sows. PLoS ONE, 2014, 9, e114036.	1.1	19

#	ARTICLE	IF	CITATIONS
5811	Natural Variation in Fish Transcriptomes: Comparative Analysis of the Fathead Minnow ( <i>Pimephales</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.1	14
5812	Hepatic Farnesoid X-Receptor Isoforms $\hat{1}\pm 2$ and $\hat{1}\pm 4$ Differentially Modulate Bile Salt and Lipoprotein Metabolism in Mice. PLoS ONE, 2014, 9, e115028.	1.1	30
5813	CD14 and Complement Crosstalk and Largely Mediate the Transcriptional Response to <i>Escherichia coli</i> in Human Whole Blood as Revealed by DNA Microarray. PLoS ONE, 2015, 10, e0117261.	1.1	16
5814	Stromal Transcriptional Profiles Reveal Hierarchies of Anatomical Site, Serum Response and Disease and Identify Disease Specific Pathways. PLoS ONE, 2015, 10, e0120917.	1.1	12
5815	Exploring the Genetic Signature of Body Size in Yucatan Miniature Pig. PLoS ONE, 2015, 10, e0121732.	1.1	38
5816	Effective Population Size, Extended Linkage Disequilibrium and Signatures of Selection in the Rare Dog Breed Lundehund. PLoS ONE, 2015, 10, e0122680.	1.1	21
5817	The Transcriptome Signature of the Receptive Bovine Uterus Determined at Early Gestation. PLoS ONE, 2015, 10, e0122874.	1.1	35
5818	Comprehensive Analysis of Glycolytic Enzymes as Therapeutic Targets in the Treatment of Glioblastoma. PLoS ONE, 2015, 10, e0123544.	1.1	101
5819	Adaptation of a Bioinformatics Microarray Analysis Workflow for a Toxicogenomic Study in Rainbow Trout. PLoS ONE, 2015, 10, e0128598.	1.1	5
5820	Lung Transcriptomics during Protective Ventilatory Support in Sepsis-Induced Acute Lung Injury. PLoS ONE, 2015, 10, e0132296.	1.1	20
5821	Mechanism of Cisplatin-Induced Cytotoxicity Is Correlated to Impaired Metabolism Due to Mitochondrial ROS Generation. PLoS ONE, 2015, 10, e0135083.	1.1	210
5822	Meta-Analysis of Large-Scale Toxicogenomic Data Finds Neuronal Regeneration Related Protein and Cathepsin D to Be Novel Biomarkers of Drug-Induced Toxicity. PLoS ONE, 2015, 10, e0136698.	1.1	16
5823	Kinase Identification with Supervised Laplacian Regularized Least Squares. PLoS ONE, 2015, 10, e0139676.	1.1	5
5824	Kelch Domain of Gigaxonin Interacts with Intermediate Filament Proteins Affected in Giant Axonal Neuropathy. PLoS ONE, 2015, 10, e0140157.	1.1	24
5825	Integrated Analysis Reveals together miR-182, miR-200c and miR-221 Can Help in the Diagnosis of Prostate Cancer. PLoS ONE, 2015, 10, e0140862.	1.1	7
5826	From System-Wide Differential Gene Expression to Perturbed Regulatory Factors: A Combinatorial Approach. PLoS ONE, 2015, 10, e0142147.	1.1	2
5827	CardioGenBase: A Literature Based Multi-Omics Database for Major Cardiovascular Diseases. PLoS ONE, 2015, 10, e0143188.	1.1	23
5828	Transcriptome Analysis of Honeybee ( <i>Apis Mellifera</i> ) Haploid and Diploid Embryos Reveals Early Zygotic Transcription during Cleavage. PLoS ONE, 2016, 11, e0146447.	1.1	43



#	ARTICLE	IF	CITATIONS
5829	Meta-Analysis of Transcriptional Responses to Mastitis-Causing Escherichia coli. PLoS ONE, 2016, 11, e0148562.	1.1	21
5830	Meta-Analysis of Tumor Stem-Like Breast Cancer Cells Using Gene Set and Network Analysis. PLoS ONE, 2016, 11, e0148818.	1.1	15
5831	Experimental Neuromyelitis Optica Induces a Type I Interferon Signature in the Spinal Cord. PLoS ONE, 2016, 11, e0151244.	1.1	15
5832	Efficient Record Linkage Algorithms Using Complete Linkage Clustering. PLoS ONE, 2016, 11, e0154446.	1.1	20
5833	Integrated and Functional Genomics Analysis Validates the Relevance of the Nuclear Variant ErbB380kDa in Prostate Cancer Progression. PLoS ONE, 2016, 11, e0155950.	1.1	4
5834	Genome-Wide Prediction and Analysis of 3D-Domain Swapped Proteins in the Human Genome from Sequence Information. PLoS ONE, 2016, 11, e0159627.	1.1	5
5835	IGSA: Individual Gene Sets Analysis, including Enrichment and Clustering. PLoS ONE, 2016, 11, e0164542.	1.1	3
5836	Identification and Expression Profiling of miRNAome in Goat longissimus dorsi Muscle from Prenatal Stages to a Neonatal Stage. PLoS ONE, 2016, 11, e0165764.	1.1	39
5837	Genome-Wide Detection of Selective Signatures in Chicken through High Density SNPs. PLoS ONE, 2016, 11, e0166146.	1.1	8
5838	Drosophila Genotype Influences Commensal Bacterial Levels. PLoS ONE, 2017, 12, e0170332.	1.1	42
5839	Microarray analysis of embryo-derived bovine pluripotent cells: The vulnerable state of bovine embryonic stem cells. PLoS ONE, 2017, 12, e0173278.	1.1	6
5840	Comparative analysis of genes frequently regulated by drugs based on connectivity map transcriptome data. PLoS ONE, 2017, 12, e0179037.	1.1	11
5841	Titanium biomaterials with complex surfaces induced aberrant peripheral circadian rhythms in bone marrow mesenchymal stromal cells. PLoS ONE, 2017, 12, e0183359.	1.1	18
5842	Single nucleotide polymorphisms at miR-146a/196a2 and their primary ovarian insufficiency-related target gene regulation in granulosa cells. PLoS ONE, 2017, 12, e0183479.	1.1	18
5843	TSS-Seq analysis of low pH-induced gene expression in intercalated cells in the renal collecting duct. PLoS ONE, 2017, 12, e0184185.	1.1	4
5844	Vitamin C alters the amount of specific endoplasmic reticulum associated proteins involved in lipid metabolism in the liver of mice synthesizing a nonfunctional Werner syndrome (Wrn) mutant protein. PLoS ONE, 2018, 13, e0193170.	1.1	9
5845	Reprogramming of the estrogen responsive transcriptome contributes to tamoxifen-dependent protection against tumorigenesis in the p53 null mammary epithelial cells. PLoS ONE, 2018, 13, e0194913.	1.1	9
5846	Global gene network exploration based on explainable artificial intelligence approach. PLoS ONE, 2020, 15, e0241508.	1.1	6

#	ARTICLE	IF	CITATIONS
5847	Dynamic metabolic reprogramming in dendritic cells: An early response to influenza infection that is essential for effector function. <i>PLoS Pathogens</i> , 2020, 16, e1008957.	2.1	13
5848	Meta-analysis of 12 genomic studies in bipolar disorder. <i>Journal of Molecular Neuroscience</i> , 2007, 31, 221-243.	1.1	69
5849	Gene Expression Studies for the Development of Particle Therapy. <i>International Journal of Particle Therapy</i> , 2018, 5, 49-59.	0.9	4
5850	Detecting Positive Selection of Korean Native Goat Populations Using Next-Generation Sequencing. <i>Molecules and Cells</i> , 2016, 39, 862-868.	1.0	13
5851	Key pathways in prostate cancer with SPOP mutation identified by bioinformatic analysis. <i>Open Medicine (Poland)</i> , 2020, 15, 1039-1047.	0.6	2
5852	Uterine fluid proteome changes during diapause and resumption of embryo development in roe deer ( <i>Capreolus capreolus</i> ). <i>Reproduction</i> , 2019, 158, 13-24.	1.1	15
5853	Identification of the molecular mechanisms associated with acute type A aortic dissection through bioinformatics methods. <i>Brazilian Journal of Medical and Biological Research</i> , 2019, 52, e8950.	0.7	11
5854	Identification of potential molecular mechanisms and small molecule drugs in myocardial ischemia/reperfusion injury. <i>Brazilian Journal of Medical and Biological Research</i> , 2020, 53, .	0.7	6
5855	Expressed cDNAs from Embryonic and Larval Stages of the Horn Fly (Diptera: Muscidae). <i>Journal of Medical Entomology</i> , 2008, 45, 686-692.	0.9	6
5856	Computational Biology of Genome Expression and Regulation—A Review of Microarray Bioinformatics. <i>Journal of Environmental Pathology, Toxicology and Oncology</i> , 2008, 27, 157-179.	0.6	22
5857	MicroRNA expression analysis in endometriotic serum treated mesenchymal stem cells. <i>EXCLI Journal</i> , 2017, 16, 852-867.	0.5	6
5858	PPAR $\beta$ : the dominant regulator among PPARs in dry eye lacrimal gland and diabetic lacrimal gland. <i>International Journal of Ophthalmology</i> , 2020, 13, 860-869.	0.5	8
5859	Molecular links between cellular senescence, longevity and age-related diseases “ a systems biology perspective. <i>Aging</i> , 2011, 3, 1178-1191.	1.4	119
5860	Prenatal hyperbaric normoxia treatment improves healthspan and regulates chitin metabolic genes in <i>Drosophila melanogaster</i> . <i>Aging</i> , 2016, 8, 2538-2550.	1.4	5
5861	Age-related changes in the gene expression profile of antigen-specific mouse CD8+ T cells can be partially reversed by blockade of the BTLA/CD160 pathways during vaccination. <i>Aging</i> , 2016, 8, 3272-3297.	1.4	4
5862	Sirtuin 3 attenuates amyloid- $\beta$ induced neuronal hypometabolism. <i>Aging</i> , 2018, 10, 2874-2883.	1.4	19
5863	ERK1 indicates good prognosis and inhibits breast cancer progression by suppressing YAP1 signaling. <i>Aging</i> , 2019, 11, 12295-12314.	1.4	16
5864	SLC7A2 serves as a potential biomarker and therapeutic target for ovarian cancer. <i>Aging</i> , 2020, 12, 13281-13296.	1.4	16

#	ARTICLE	IF	CITATIONS
5865	Identification and validation of an immune-related gene signature predictive of overall survival in colon cancer. <i>Aging</i> , 2020, 12, 26095-26120.	1.4	35
5866	HMGA1 promotes metastatic processes in basal-like breast cancer regulating EMT and stemness. <i>Oncotarget</i> , 2013, 4, 1293-1308.	0.8	145
5867	Blood RNA expression profiles undergo major changes during the seventh decade. <i>Oncotarget</i> , 2016, 7, 71353-71361.	0.8	1
5868	Decreased <i>TRPM7</i> inhibits activities and induces apoptosis of bladder cancer cells via ERK1/2 pathway. <i>Oncotarget</i> , 2016, 7, 72941-72960.	0.8	60
5869	Error-prone DNA polymerase and oxidative stress increase the incidences of A to G mutations in tumors. <i>Oncotarget</i> , 2017, 8, 45154-45163.	0.8	3
5870	Conditionally reprogrammed normal and primary tumor prostate epithelial cells: a novel patient-derived cell model for studies of human prostate cancer. <i>Oncotarget</i> , 2017, 8, 22741-22758.	0.8	51
5871	Systemically identifying and prioritizing risk lncRNAs through integration of pan-cancer phenotype associations. <i>Oncotarget</i> , 2017, 8, 12041-12051.	0.8	12
5872	Genome-scale analysis identifies CJB2 and ERO1LB as prognosis markers in patients with pancreatic cancer. <i>Oncotarget</i> , 2017, 8, 21281-21289.	0.8	49
5873	iTRAQ-based quantitative proteomic analysis of Yamanaka factors reprogrammed breast cancer cells. <i>Oncotarget</i> , 2017, 8, 34330-34339.	0.8	7
5874	Lymphoid enhancer binding factor-1 (LEF1) expression as a prognostic factor in adult acute promyelocytic leukemia. <i>Oncotarget</i> , 2014, 5, 649-658.	0.8	19
5875	The highly expressed COL4A1 genes contributes to the proliferation and migration of the invasive ductal carcinomas. <i>Oncotarget</i> , 2017, 8, 58172-58183.	0.8	33
5876	Autophagy-related gene expression is an independent prognostic indicator of glioma. <i>Oncotarget</i> , 2017, 8, 60987-61000.	0.8	28
5877	Integrative analysis of novel hypomethylation and gene expression signatures in glioblastomas. <i>Oncotarget</i> , 2017, 8, 89607-89619.	0.8	19
5878	Overexpression of COL3A1 confers a poor prognosis in human bladder cancer identified by co-expression analysis. <i>Oncotarget</i> , 2017, 8, 70508-70520.	0.8	77
5879	Identification of microRNA differentially expressed in three subtypes of non-small cell lung cancer and in silico functional analysis. <i>Oncotarget</i> , 2017, 8, 74554-74566.	0.8	20
5880	Somatic intronic microsatellite loci differentiate glioblastoma from lower-grade gliomas. <i>Oncotarget</i> , 2014, 5, 6003-6014.	0.8	11
5881	Identification of potential tissue-specific cancer biomarkers and development of cancer versus normal genomic classifiers. <i>Oncotarget</i> , 2017, 8, 85692-85715.	0.8	18
5882	Differential prioritization of therapies to subtypes of triple negative breast cancer using a systems medicine method. <i>Oncotarget</i> , 2017, 8, 92926-92942.	0.8	6

#	ARTICLE	IF	CITATIONS
5883	Î±-Tocopherol succinate enhances pterostilbene anti-tumor activity in human breast cancer cells <i>in vivo</i> and <i>in vitro</i> . <i>Oncotarget</i> , 2018, 9, 4593-4606.	0.8	23
5884	IsomiR expression profiles in human lymphoblastoid cell lines exhibit population and gender dependencies. <i>Oncotarget</i> , 2014, 5, 8790-8802.	0.8	103
5885	Identification of key pathways and genes in response to trastuzumab treatment in breast cancer using bioinformatics analysis. <i>Oncotarget</i> , 2018, 9, 32149-32160.	0.8	9
5886	Somatic mutations in early onset luminal breast cancer. <i>Oncotarget</i> , 2018, 9, 22460-22479.	0.8	25
5887	Molecular profiling and computational network analysis of TAZ-mediated mammary tumorigenesis identifies actionable therapeutic targets. <i>Oncotarget</i> , 2014, 5, 12166-12176.	0.8	24
5888	Targeting the non-canonical roles of PCNA modifies and increases the response to targeted anti-cancer therapy. <i>Oncotarget</i> , 2019, 10, 7185-7197.	0.8	14
5889	Epigenetic and oncogenic regulation of SLC16A7 (MCT2) results in protein over-expression, impacting on signalling and cellular phenotypes in prostate cancer. <i>Oncotarget</i> , 2015, 6, 21675-21684.	0.8	23
5890	Virus-encoded microRNA contributes to the molecular profile of EBV-positive Burkitt lymphomas. <i>Oncotarget</i> , 2016, 7, 224-240.	0.8	33
5891	Time-course gene profiling and networks in demethylated retinoblastoma cell line. <i>Oncotarget</i> , 2015, 6, 23688-23707.	0.8	6
5892	Acyl-CoA synthetase-4, a new regulator of mTOR and a potential therapeutic target for enhanced estrogen receptor function in receptor-positive and -negative breast cancer. <i>Oncotarget</i> , 2015, 6, 42632-42650.	0.8	45
5893	Genome-wide endogenous DAF-16/FOXO recruitment dynamics during lowered insulin signalling in <i>C. elegans</i> . <i>Oncotarget</i> , 2015, 6, 41418-41433.	0.8	30
5894	MicroRNA-708-5p acts as a therapeutic agent against metastatic lung cancer. <i>Oncotarget</i> , 2016, 7, 2417-2432.	0.8	50
5895	Pathway of PPAR-gamma coactivators in thermogenesis: a pivotal traditional Chinese medicine-associated target for individualized treatment of rheumatoid arthritis. <i>Oncotarget</i> , 2016, 7, 15885-15900.	0.8	32
5896	Cinacalcet inhibits neuroblastoma tumor growth and upregulates cancer-testis antigens. <i>Oncotarget</i> , 2016, 7, 16112-16129.	0.8	19
5897	Age-related changes in the transcriptome of antibody-secreting cells. <i>Oncotarget</i> , 2016, 7, 13340-13353.	0.8	20
5898	Genomic alterations of whole exome sequencing in esophageal squamous cell carcinoma before and after radiotherapy. <i>Journal of Thoracic Disease</i> , 2020, 12, 5945-5957.	0.6	3
5899	Methylation of PLIN5 is a crucial biomarker and is involved in ovarian cancer development. <i>Translational Cancer Research</i> , 2020, 9, 2919-2930.	0.4	2
5900	Differential Network Analysis in Human Cancer Research. <i>Current Pharmaceutical Design</i> , 2014, 20, 4-10.	0.9	16

#	ARTICLE	IF	CITATIONS
5901	Systematic Understanding of the Mechanisms of <i>Flos Chrysanthemi Indici</i> -mediated Effects on Hypertension via Computational Target Fishing. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 92-110.	0.6	5
5902	Identification of Three Differentially Expressed miRNAs as Potential Biomarkers for Lung Adenocarcinoma Prognosis. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2020, 23, 148-156.	0.6	2
5903	Systems Biology Approaches to a Rational Drug Discovery Paradigm. <i>Current Topics in Medicinal Chemistry</i> , 2015, 16, 1009-1025.	1.0	25
5904	Microarray Data Integration: Frameworks and a List of Underlying Issues. <i>Current Bioinformatics</i> , 2010, 5, 280-289.	0.7	7
5905	A Computational Approach to Identify Novel Potential Precursor miRNAs and their Targets from Hepatocellular Carcinoma Cells. <i>Current Bioinformatics</i> , 2018, 14, 24-32.	0.7	9
5906	Short Gel, Long Gradient Liquid Chromatography Tandem Mass Spectrometry to Investigate the Urine Proteome of Chronic Pancreatitis. <i>The Open Proteomics Journal</i> , 2013, 6, 1-13.	0.4	8
5907	Interferon $\gamma$ -Inducible Protein 27 Computational Network Construction and Comparison between the Frontal Cortex of HIV Encephalitis (HIVE) and HIVE-Control Patients. 2010-04-06-2010-08-05-2010-09-06-. <i>The Open Genomics Journal</i> , 2010, 3, 1-8.	0.5	20
5908	Genistein Modulation of Immune-Associated Genes in LNCaP Prostate Cancer Cell Line. <i>The Open Prostate Cancer Journal</i> , 2012, 5, 1-7.	0.4	8
5909	Methylated MicroRNA Genes of the Developing Murine Palate. <i>MicroRNA (Sharjah, United Arab Emirates)</i> 10 Tf 50 4	0.6	14
5910	Analysis of Hypoxia-miRNA-Gene Regulatory Network Identifies Critical miRNAs Influencing Cell-Cycle Regulation Under Hypoxic Conditions. <i>MicroRNA (Sharjah, United Arab Emirates)</i> , 2019, 8, 223-236.	0.6	8
5911	Rapid Multiplexed Reduced Representation Bisulfite Sequencing Library Prep (rRRBS). <i>Bio-protocol</i> , 2019, 9, e3171.	0.2	6
5912	Adoption of Clinical Decision Support in Multimorbidity: A Systematic Review. <i>JMIR Medical Informatics</i> , 2015, 3, e4.	1.3	85
5913	Expression profiles and prognostic roles of m6A writers, erasers and readers in gastric cancer. <i>Future Oncology</i> , 2021, 17, 2605-2620.	1.1	18
5914	A Pilot Study of Gene Expression Analysis in Workers with Hand-Arm Vibration Syndrome. <i>Industrial Health</i> , 2008, 46, 188-193.	0.4	2
5915	Integration of bioinformatics resources for functional analysis of gene expression and proteomic data. <i>Frontiers in Bioscience - Landmark</i> , 2007, 12, 5071.	3.0	30
5916	Co-expression Network Analysis Reveals Key Genes Related to Ankylosing spondylitis Arthritis Disease: Computational and Experimental Validation. <i>Iranian Journal of Biotechnology</i> , 2021, 19, e2630.	0.3	6
5917	Molecular basis of the anti-cancer effects of genistein isoflavone in LNCaP prostate cancer cells. <i>Functional Foods in Health and Disease</i> , 2011, 1, 91.	0.3	11
5918	Separating the drivers from the driven: Integrative network and pathway approaches aid identification of disease biomarkers from high-throughput data. <i>Disease Markers</i> , 2010, 28, 253-66.	0.6	14

#	ARTICLE	IF	CITATIONS
5919	Effect of Bortezomib on Global Gene Expression in PC12-Derived Nerve Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 751.	1.8	11
5920	The Effect of 3- <sup>2</sup> -Hydroxy-3,4,5,4- <sup>2</sup> -Tetramethoxy -stilbene, the Metabolite of the Resveratrol Analogue DMU-212, on the Motility and Proliferation of Ovarian Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1100.	1.8	9
5925	A Review on The Processing and Analysis of Next-generation RNA-seq Data*. <i>Progress in Biochemistry and Biophysics</i> , 2010, 37, 834-846.	0.3	8
5926	miR-133b May Regulate Mouse B Cell Development by Targeting The Transcription Factor foxO1*. <i>Progress in Biochemistry and Biophysics</i> , 2011, 38, 744-750.	0.3	2
5927	An Integrated Analysis of Lineage-specific Small Proteins Across Eight Eukaryotes Reveals Functional and Evolutionary Significance*. <i>Progress in Biochemistry and Biophysics</i> , 2012, 39, 359-367.	0.3	2
5928	Effects of ciglitazone and troglitazone on the proliferation of human stomach cancer cells. <i>World Journal of Gastroenterology</i> , 2009, 15, 310.	1.4	24
5929	Gene expression arrays as a tool to unravel mechanisms of normal tissue radiation injury and prediction of response. <i>World Journal of Gastroenterology</i> , 2007, 13, 2669.	1.4	34
5930	Construction of a risk score prognosis model based on hepatocellular carcinoma microenvironment. <i>World Journal of Gastroenterology</i> , 2020, 26, 134-153.	1.4	36
5931	MicroRNA-150 down Regulation in Acute Myeloid Leukaemia Patients and Its Prognostic Implication. <i>Open Access Macedonian Journal of Medical Sciences</i> , 2018, 6, 1993-2000.	0.1	6
5932	Identification of differentially expressed genes in the endothelial precursor cells of patients with type 2 diabetes mellitus by bioinformatics analysis. <i>Experimental and Therapeutic Medicine</i> , 2020, 19, 499-510.	0.8	7
5933	Prediction of crucial epigenetically associated, differentially expressed genes by integrated bioinformatics analysis and the identification of S100A9 as a novel biomarker in psoriasis. <i>International Journal of Molecular Medicine</i> , 2020, 45, 93-102.	1.8	16
5934	Investigation of the molecular mechanisms underlying myotonic dystrophy types 1 and 2 cataracts using microRNA-target gene networks. <i>Molecular Medicine Reports</i> , 2017, 16, 3737-3744.	1.1	4
5935	Screening of the prognostic targets for breast cancer based co-expression modules analysis. <i>Molecular Medicine Reports</i> , 2017, 16, 4038-4044.	1.1	20
5936	Global pathway view analysis of microRNA clusters in myasthenia gravis. <i>Molecular Medicine Reports</i> , 2019, 19, 2350-2360.	1.1	3
5937	Identification of potential crucial genes and molecular mechanisms in glioblastoma multiforme by bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2020, 22, 859-869.	1.1	17
5938	POPDC3 is a potential biomarker for prognosis and radioresistance in patients with head and neck squamous cell carcinoma. <i>Oncology Letters</i> , 2019, 18, 5468-5480.	0.8	8
5939	Reduced expression of microRNA-139-5p in hepatocellular carcinoma results in a poor outcome: An exploration the roles of microRNA-139-5p in tumorigenesis, advancement and prognosis at the molecular biological level using an integrated meta-analysis and bioinformatic investigation. <i>Oncology Letters</i> , 2019, 18, 6704-6724.	0.8	5
5940	Identification of potential pathogenic candidates or diagnostic biomarkers in papillary thyroid carcinoma using expression and methylation profiles. <i>Oncology Letters</i> , 2019, 18, 6670-6678.	0.8	9

#	ARTICLE	IF	CITATIONS
5941	Overexpression of miRâ€206 in osteosarcoma and its associated molecular mechanisms as assessed through TCGA and GEO databases. <i>Oncology Letters</i> , 2020, 19, 1751-1758.	0.8	7
5942	Integrated bioinformatics analysis of the association between apolipoprotein E expression and patient prognosis in papillary thyroid carcinoma. <i>Oncology Letters</i> , 2020, 19, 2295-2305.	0.8	3
5943	Identification of a long nonâ€coding RNA signature for predicting prognosis and biomarkers in lung adenocarcinoma. <i>Oncology Letters</i> , 2020, 19, 2793-2800.	0.8	9
5944	Chemoresistanceâ€associated alternative splicing signatures in serous ovarian cancer. <i>Oncology Letters</i> , 2020, 20, 420-430.	0.8	8
5945	Atonal bHLH transcription factor 1 is an important factor for maintaining the balance of cell proliferation and differentiation in tumorigenesis (Review). <i>Oncology Letters</i> , 2020, 20, 2595-2605.	0.8	8
5946	Investigation of the association between Câ€Xâ€C motif chemokine receptor subunits and tumor infiltration levels and prognosis in patients with earlyâ€stage pancreatic ductal adenocarcinoma. <i>Oncology Letters</i> , 2020, 20, 16.	0.8	5
5947	Polyphyllin VII suppresses cell proliferation, the cell cycle and cell migration in colorectal cancer. <i>Oncology Letters</i> , 2020, 21, 1-1.	0.8	7
5948	Comprehensive analysis of the lncRNAâ€associated competing endogenous RNA network in breast cancer. <i>Oncology Reports</i> , 2019, 42, 2572-2582.	1.2	27
5949	The identification of key biomarkers in patients with lung adenocarcinoma based on bioinformatics. <i>Mathematical Biosciences and Engineering</i> , 2019, 16, 7671-7687.	1.0	24
5950	Identification of metastasis-associated genes in colorectal cancer through an integrated genomic and transcriptomic analysis. <i>Chinese Journal of Cancer Research: Official Journal of China Anti-Cancer Association, Beijing Institute for Cancer Research</i> , 2013, 25, 623-36.	0.7	10
5951	Biclustering of DNA Microarray Data. , 2011, , 148-186.		8
5952	GSK3 Restrains Germinal Center B Cells to Form Plasma Cells. <i>Journal of Immunology</i> , 2021, 206, 481-493.	0.4	7
5953	Construction of a Transcriptome-Driven Network at the Early Stage of Infection with Influenza A H1N1 in Human Lung Alveolar Epithelial Cells. <i>Biomolecules and Therapeutics</i> , 2018, 26, 290-297.	1.1	7
5954	Transcriptome analysis of porcine skeletal muscle: differentially expressed genes in Italian Large White pigs with divergent values for glycolytic potential. <i>Italian Journal of Animal Science</i> , 2007, 6, 113-115.	0.8	1
5955	Expression of microRNA during bovine adipogenesis. <i>Journal of Nucleic Acids Investigation</i> , 2010, 1, 12.	0.5	2
5956	MicroRNA alterations in Barrettâ€s esophagus, esophageal adenocarcinoma, and esophageal adenocarcinoma cell lines following cranberry extract treatment: Insights for chemoprevention. <i>Journal of Carcinogenesis</i> , 2011, 10, 34.	2.5	24
5957	Identification of protein targets for the antidepressant effects of Kai-Xin-San in Chinese medicine using isobaric tags for relative and absolute quantitation. <i>Neural Regeneration Research</i> , 2020, 15, 302.	1.6	12
5958	Protein microarray analysis of cytokine expression changes in distal stumps after sciatic nerve transection. <i>Neural Regeneration Research</i> , 2020, 15, 503.	1.6	4

#	ARTICLE	IF	CITATIONS
5959	MicroRNA regulatory pattern in spinal cord ischemia-reperfusion injury. <i>Neural Regeneration Research</i> , 2020, 15, 2123.	1.6	21
5960	Autism and Obesity: Prevalence, Molecular Basis and Potential Therapies. <i>Autism Insights</i> , 0, , 1.	0.0	2
5961	Gene Expression Profiling from a Prostate Cancer PC-3 Cell Line Treated with Salinomycin Predicts Cell Cycle Arrest and Endoplasmic Reticulum Stress. <i>Journal of Cancer Science &amp; Therapy</i> , 2013, 05, .	1.7	2
5962	Global Proteomics: Pharmacodynamic Decision Making via Geometric Interpretations of Proteomic Analyses. <i>Journal of Proteomics and Bioinformatics</i> , 2008, 01, 315-328.	0.4	6
5963	Enhanced Meta-analysis Highlights Genes Involved in Metastasis from Several Microarray Datasets. <i>Journal of Proteomics and Bioinformatics</i> , 2011, 04, .	0.4	6
5964	Transcriptomics Data Integration Reveals Jak-STAT as a Common Pathway Affected by Pathogenic Intracellular Bacteria in Natural Reservoir Hosts. <i>Journal of Proteomics and Bioinformatics</i> , 2012, 05, .	0.4	12
5965	A Proteomic Study of Human Merkel Cell Carcinoma. <i>Journal of Proteomics and Bioinformatics</i> , 2013, 06, 275-282.	0.4	23
5966	Increased Cellular Invasion and Proliferation via Estrogen Receptor after 17- $\beta$ -Estradiol Treatment in Breast Cancer Cells Using Stable Isotopic Labeling with Amino Acids in Cell Culture (SILAC). <i>Advances in Breast Cancer Research</i> , 2013, 02, 32-43.	0.1	2
5967	Applicability of the P19CL6 cells as a model of cardiomyocytes – a transcriptome analysis. <i>Health</i> , 2010, 02, 24-31.	0.1	1
5968	A New Generation of Drugs: Synthetic Peptides Based on Natural Regulatory Peptides. <i>Neuroscience and Medicine</i> , 2013, 04, 223-252.	0.2	24
5969	Identification and abundance of miRNA in chicken hypothalamus tissue determined by Solexa sequencing. <i>Genetics and Molecular Research</i> , 2012, 11, 4682-4694.	0.3	13
5970	Evaluation of Toxicity and Gene Expression Changes Triggered by Quantum Dots. <i>Bulletin of the Korean Chemical Society</i> , 2010, 31, 1555-1560.	1.0	17
5971	Evaluation of Toxicity and Gene Expression Changes Triggered by Oxide Nanoparticles. <i>Bulletin of the Korean Chemical Society</i> , 2011, 32, 2051-2057.	1.0	26
5972	Analysis of copy number variation in 8,842 Korean individuals reveals 39 genes associated with hepatic biomarkers AST and ALT. <i>BMB Reports</i> , 2010, 43, 547-553.	1.1	11
5973	A replication study of genome-wide CNV association for hepatic biomarkers identifies nine genes associated with liver function. <i>BMB Reports</i> , 2011, 44, 578-583.	1.1	7
5974	A bootstrap-based non-parametric ANOVA method with applications to factorial microarray data. <i>Statistica Sinica</i> , 2011, 21, 495.	0.2	22
5975	Effects of deoxynivalenol- and zearalenone-contaminated feed on the gene expression profiles in the kidneys of piglets. <i>Asian-Australasian Journal of Animal Sciences</i> , 2018, 31, 138-148.	2.4	13
5976	Temporal expression profiling of long noncoding RNA and mRNA in the peripheral blood during porcine development. <i>Asian-Australasian Journal of Animal Sciences</i> , 2020, 33, 836-847.	2.4	1



#	ARTICLE	IF	CITATIONS
5977	Differential Expressions of Apoptosis-related Genes in Lung Cancer Cell Lines Determine the Responsiveness to Ionizing Radiation. <i>Genomics and Informatics</i> , 2008, 6, 36-43.	0.4	4
5978	Prediction of Genes Related to Positive Selection Using Whole-Genome Resequencing in Three Commercial Pig Breeds. <i>Genomics and Informatics</i> , 2015, 13, 137.	0.4	4
5979	Insights into the Signal Transduction Pathways of Mouse Lung Type II Cells Revealed by Transcription Factor Profiling in the Transcriptome. <i>Genomics and Informatics</i> , 2019, 17, e8.	0.4	10
5980	A Study Analyzing Reference Linking Service in Digital Libraries. <i>International Journal of Knowledge Content Development and Technology</i> , 2015, 5, 69-88.	0.4	5
5981	Astragalus polysaccharides induced gene expression profiling of intraepithelial lymphocytes in immune-suppressed mice. <i>Journal of Medicinal Plants Research</i> , 2012, 6, .	0.2	3
5982	Integrative analysis of the mouse embryonic transcriptome. <i>Bioinformatics</i> , 2007, 1, 406-413.	0.2	8
5983	DAVID gene ID conversion tool. <i>Bioinformatics</i> , 2008, 2, 428-430.	0.2	156
5984	Meta analysis of Chronic Fatigue Syndrome through integration of clinical, gene expression, SNP and proteomic data. <i>Bioinformatics</i> , 2011, 6, 120-124.	0.2	8
5985	Genes2GO: A web application for querying gene sets for specific GO terms. <i>Bioinformatics</i> , 2016, 12, 231-232.	0.2	4
5986	Identification of Biomarkers for Diagnosis of Gastric Cancer by Bioinformatics. <i>Asian Pacific Journal of Cancer Prevention</i> , 2015, 16, 1361-1365.	0.5	14
5987	NOVA-dependent regulation of cryptic NMD exons controls synaptic protein levels after seizure. <i>ELife</i> , 2013, 2, e00178.	2.8	92
5988	Integrative genomic analysis of the human immune response to influenza vaccination. <i>ELife</i> , 2013, 2, e00299.	2.8	126
5989	A component of the mir-17-92 polycistronic oncomir promotes oncogene-dependent apoptosis. <i>ELife</i> , 2013, 2, e00822.	2.8	75
5990	The translational landscape of the splicing factor SRSF1 and its role in mitosis. <i>ELife</i> , 2014, 3, e02028.	2.8	96
5991	Lhx1 maintains synchrony among circadian oscillator neurons of the SCN. <i>ELife</i> , 2014, 3, e03357.	2.8	68
5992	Genome-wide errant targeting by Hairy. <i>ELife</i> , 2015, 4, .	2.8	13
5993	Control of immune ligands by members of a cytomegalovirus gene expansion suppresses natural killer cell activation. <i>ELife</i> , 2017, 6, .	2.8	67
5994	Resolving stem and progenitor cells in the adult mouse incisor through gene co-expression analysis. <i>ELife</i> , 2017, 6, .	2.8	44

#	ARTICLE	IF	CITATIONS
5995	Inhibiting the integrated stress response pathway prevents aberrant chondrocyte differentiation thereby alleviating chondrodysplasia. <i>ELife</i> , 2018, 7, .	2.8	59
5996	A new experimental platform facilitates assessment of the transcriptional and chromatin landscapes of aging yeast. <i>ELife</i> , 2018, 7, .	2.8	56
5997	Epigenetic silencing of a multifunctional plant stress regulator. <i>ELife</i> , 2019, 8, .	2.8	28
5998	Functional heterogeneity of lymphocytic patterns in primary melanoma dissected through single-cell multiplexing. <i>ELife</i> , 2020, 9, .	2.8	44
5999	A cross-kingdom conserved ER-phagy receptor maintains endoplasmic reticulum homeostasis during stress. <i>ELife</i> , 2020, 9, .	2.8	139
6000	Integrated network pharmacology and molecular docking approaches to reveal the synergistic mechanism of multiple components in <i>Venenum Bufonis</i> for ameliorating heart failure. <i>PeerJ</i> , 2020, 8, e10107.	0.9	5
6001	Identifying <i>MMP14</i> and <i>COL12A1</i> as a potential combination of prognostic biomarkers in pancreatic ductal adenocarcinoma using integrated bioinformatics analysis. <i>PeerJ</i> , 2020, 8, e10419.	0.9	17
6002	miR-21 is upregulated, promoting fibrosis and blocking G2/M in irradiated rat cardiac fibroblasts. <i>PeerJ</i> , 2020, 8, e10502.	0.9	7
6003	Chromosomal rearrangements and protein globularity changes in <i>Mycobacterium tuberculosis</i> isolates from cerebrospinal fluid. <i>PeerJ</i> , 2016, 4, e2484.	0.9	5
6004	Identification of four potential predicting miRNA biomarkers for multiple myeloma from published datasets. <i>PeerJ</i> , 2017, 5, e2831.	0.9	11
6005	Genome methylation and regulatory functions for hypoxic adaptation in Tibetan chicken embryos. <i>PeerJ</i> , 2017, 5, e3891.	0.9	17
6006	Modulation of transcriptional activity in brain lower grade glioma by alternative splicing. <i>PeerJ</i> , 2018, 6, e4686.	0.9	6
6007	The expression of chondrogenesis-related and arthritis-related genes in human ONFH cartilage with different Ficat stages. <i>PeerJ</i> , 2019, 7, e6306.	0.9	12
6008	Amorphous silica nanoparticles induce tumorigenesis via regulating ATP5H/SOD1-related oxidative stress, oxidative phosphorylation and EIF4G2/PABPC1-associated translational initiation. <i>PeerJ</i> , 2019, 7, e6455.	0.9	4
6009	Identification of differentially expressed key genes between glioblastoma and low-grade glioma by bioinformatics analysis. <i>PeerJ</i> , 2019, 7, e6560.	0.9	16
6010	Characterization of bidirectional gene pairs in The Cancer Genome Atlas (TCGA) dataset. <i>PeerJ</i> , 2019, 7, e7107.	0.9	8
6011	Identification of significant gene and pathways involved in HBV-related hepatocellular carcinoma by bioinformatics analysis. <i>PeerJ</i> , 2019, 7, e7408.	0.9	64
6012	Identification of potential biomarkers and pivotal biological pathways for prostate cancer using bioinformatics analysis methods. <i>PeerJ</i> , 2019, 7, e7872.	0.9	35

#	ARTICLE	IF	CITATIONS
6013	Identification of key genes and multiple molecular pathways of metastatic process in prostate cancer. PeerJ, 2019, 7, e7899.	0.9	12
6014	Significance of TP53 mutation in bladder cancer disease progression and drug selection. PeerJ, 2019, 7, e8261.	0.9	30
6015	A transcriptional co-expression network-based approach to identify prognostic biomarkers in gastric carcinoma. PeerJ, 2020, 8, e8504.	0.9	6
6016	Weighted gene correlation network analysis reveals novel biomarkers associated with mesenchymal stromal cell differentiation in early phase. PeerJ, 2020, 8, e8907.	0.9	10
6017	miR-224, miR-147b and miR-31 associated with lymph node metastasis and prognosis for lung adenocarcinoma by regulating PRPF4B, WDR82 or NR3C2. PeerJ, 2020, 8, e9704.	0.9	12
6018	Identification of aberrantly methylated-differentially expressed genes and potential agents for Ewing sarcoma. Annals of Translational Medicine, 2021, 9, 1557-1557.	0.7	0
6019	The Evolution of Clinically Aggressive Triple-Negative Breast Cancer Shows a Large Mutational Diversity and Early Metastasis to Lymph Nodes. Cancers, 2021, 13, 5091.	1.7	4
6020	Maternal High-Fat Diet Disturbs the DNA Methylation Profile in the Brown Adipose Tissue of Offspring Mice. Frontiers in Endocrinology, 2021, 12, 705827.	1.5	9
6021	Extracellular calcium alters calcium-sensing receptor network integrating intracellular calcium-signaling and related key pathway. Scientific Reports, 2021, 11, 20576.	1.6	8
6022	Metabolic Analysis of Potential Key Genes Associated with Systemic Lupus Erythematosus Using Liquid Chromatography-Mass Spectrometry. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-17.	0.7	2
6023	An In-Silico, In-Vitro and In-Vivo Combined Approach to Identify NMNATs as Potential Protein Targets of ProEGCG for Treatment of Endometriosis. Frontiers in Pharmacology, 2021, 12, 714790.	1.6	4
6024	GNG7 and ADCY1 as diagnostic and prognostic biomarkers for pancreatic adenocarcinoma through bioinformatic-based analyses. Scientific Reports, 2021, 11, 20441.	1.6	10
6025	CD20 positive CD8 T cells are a unique and transcriptionally-distinct subset of T cells with distinct transmigration properties. Scientific Reports, 2021, 11, 20499.	1.6	11
6026	Functional heterogeneity of POMC neurons relies on mTORC1 signaling. Cell Reports, 2021, 37, 109800.	2.9	19
6027	Exploration of alcohol use disorder-associated brain miRNA-mRNA regulatory networks. Translational Psychiatry, 2021, 11, 504.	2.4	23
6028	Vitamin C Differentially Impacts the Serum Proteome Profile in Female and Male Mice. Journal of Proteome Research, 2021, 20, 5036-5053.	1.8	8
6031	Qualitative lysine crotonylome analysis in the ovarian tissue of Harmonia axyridis (Pallas). PLoS ONE, 2021, 16, e0258371.	1.1	0
6032	Unsupervised Dense Regions Discovery in DNA Microarray Data. Lecture Notes in Computer Science, 2004, , 71-77.	1.0	0

#	ARTICLE	IF	CITATIONS
6033	Bioinformatics Data Source Integration Based on Semantic Relationships Across Species. Lecture Notes in Computer Science, 2006, , 78-93.	1.0	1
6034	GENE EXPRESSION PROFILING OF BOVINE OVARIAN FOLLICULAR SELECTION. Biology of Reproduction, 2007, 77, 98-98.	1.2	0
6035	Synaptoproteomics of Existing and new Animal Models of Depression. , 2008, , 185-202.		0
6036	Pattern-Based Gene-Set Recognition for Interpreting Genome-Wide Gene Expression Profiles.. Open Bioinformatics Journal, 2008, 2, 1-10.	1.0	0
6037	Statistical Analysis on Microarray Data: Selection of Gene Prognosis Signatures. , 2009, , 55-76.		2
6038	Pattern Discovery in Gene Expression Data. , 2009, , 45-64.		0
6039	Current Efforts to Integrate Biological Pathway Information. Lecture Notes in Computer Science, 2009, , 1092-1096.	1.0	0
6042	Photoperiodism in Insects: Molecular Basis and Consequences of Diapause. , 2009, , 287-317.		1
6043	PathAgent: Multi-agent System for Updated Pathway Information Integration. Advances in Intelligent and Soft Computing, 2010, , 77-85.	0.2	0
6044	The Evolving Transcriptome of Head and Neck Squamous Cell Carcinoma. Systems Biology, 2010, , 687-702.	0.1	0
6045	Characterization of Treatment Response to Recombinant Interferon-a2b in Osteosarcoma Xenografts. Journal of Cancer Science & Therapy, 2010, 02, 016-025.	1.7	2
6046	MADNet: A Web Server for Contextual Analysis and Visualization of High-Throughput Experiments. Systems Biology, 2010, , 877-888.	0.1	0
6047	An Evaluation of Gene Module Concepts in the Interpretation of Gene Expression Data. Computational Biology, 2010, , 331-349.	0.1	1
6048	Bone-specific master transcription factor Runx2 regulates signaling and metabolism related programs in osteoprogenitors. Biopolymers and Cell, 2010, 26, 273-278.	0.1	0
6049	Bioinformatics of High-Throughput Insertional Mutagenesis. , 2011, , 167-188.		0
6051	Visual Gene Ontology Based Knowledge Discovery in Functional Genomics. , 0, ,		1
6052	Experiment Specific Expression Patterns. Lecture Notes in Computer Science, 2011, , 339-354.	1.0	0
6053	MMRF for Proteome Annotation Applied to Human Protein Disease Prediction. Lecture Notes in Computer Science, 2011, , 67-75.	1.0	0

#	ARTICLE	IF	CITATIONS
6054	Abstract 3328: Characterization of cell lines derived from breast cancers and normal mammary tissues for the study of the intrinsic molecular subtypes. , 2011, , .		1
6055	On-Chip Living-Cell Microarrays for Network Biology. , 0, , .		0
6056	Recurrent Giant Sarcoma of the Anterior Abdominal Wall. Journal of Cancer Science & Therapy, 2012, 04, .	1.7	1
6057	Transcriptional Networks â€œ Control of Lung Maturation. Translational Bioinformatics, 2012, , 309-334.	0.0	0
6059	Transcriptional Regulation in the G1-S Cell Cycle Stage in Fungi: Insights through Computational Analysis. Open Bioinformatics Journal, 2012, 6, 43-54.	1.0	0
6060	Prioritizing Disease Genes and Understanding Disease Pathways. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 31-49.	0.8	0
6061	Protein Interactions for Functional Genomics. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 15-30.	0.8	0
6064	Genome-Wide Mapping. , 2013, , 71-109.		0
6065	Modern Techniques for DNA and RNA Assessments. Success in Academic Surgery, 2014, , 107-126.	0.1	0
6066	Epigenetics of Host-Pathogen Interactions: The Road Ahead and the Road Behind. , 2013, , 25-46.		0
6067	Acknowledgments / The Authors. , 2013, , 295-295.		0
6068	Potential Driver Genes Regulated by OncomiRNA Are Associated with Druggability in Pan-Negative Melanoma. Lecture Notes in Computer Science, 2014, , 315-321.	1.0	0
6069	Potential Candidate Genes for Hypertension with Blood Stasis Syndrome by Microarray and Databases Mining. International Journal of Bioscience, Biochemistry, Bioinformatics (IJBBB), 2014, 4, 150-154.	0.2	2
6070	Semantic Modeling for SNPs Associated with Ethnic Disparities in HapMap Samples. Genomics and Informatics, 2014, 12, 35.	0.4	0
6071	Construction of a Protein-Protein Interaction Network for Chronic Myelocytic Leukemia and Pathway Prediction of Molecular Complexes. Asian Pacific Journal of Cancer Prevention, 2014, 15, 5325-5330.	0.5	2
6072	Subspace Clustering of DNA Microarray Data. International Journal of Computational Models and Algorithms in Medicine, 2014, 4, 1-52.	0.4	1
6073	Characterization of Root Transcriptome among Korean Ginseng Cultivars and American Ginseng using Next Generation Sequencing. Korean Journal of Medicinal Crop Science, 2014, 22, 339-348.	0.1	0
6075	Rapid Evolution of DNA Methylation in Primates Tend to Occur in Conserved Sequences. Cancer Genetics and Epigenetics, 0, , .	0.0	0

#	ARTICLE	IF	CITATIONS
6076	MicroRNA-21, 204 and 125b Play Potential Roles in Tumorigenesis of Melanoma. <i>Advances in Bioscience and Biotechnology (Print)</i> , 2015, 06, 677-692.	0.3	3
6077	A Microarray Analysis of Parkinson's Disease: New Clues and Evaluation. <i>Journal of Biosciences and Medicines</i> , 2015, 03, 55-60.	0.1	0
6079	Proposal of Chance Index in Co-occurrence Network. <i>IEEJ Transactions on Electronics, Information and Systems</i> , 2015, 135, 644-650.	0.1	1
6080	Phosphoproteomics-Based Network Analysis of Cancer Cell Signaling Systems. , 2015, , 3-15.		0
6081	Computational Data Integration in Toxicogenomics. <i>Methods in Pharmacology and Toxicology</i> , 2015, , 371-392.	0.1	0
6082	Proposal of Chance Index in Co-occurrence Visualized Network. <i>International Journal of Knowledge Engineering</i> , 2015, 1, 78-82.	0.2	0
6083	Identification of prognosis-specific network and prediction for estrogen receptor-negative breast cancer using microarray data and PPI data. <i>Journal of the Korea Society of Computer and Information</i> , 2015, 20, 137-147.	0.0	0
6084	Quantitative Expression Analysis of Functional Genes in Four Dog Breeds. <i>Journal of Life Science</i> , 2015, 25, 861-869.	0.2	0
6086	Systems Biology Approaches for Elucidation of the Transcriptional Regulation of Pulmonary Maturation. <i>Translational Bioinformatics</i> , 2016, , 385-419.	0.0	0
6087	iBATCGH: Integrative Bayesian Analysis of Transcriptomic and CGH Data. <i>Abel Symposia</i> , 2016, , 105-123.	0.3	2
6091	Bioinformatic Analysis for Profiling Drug-induced Chromatin Modification Landscapes in Mouse Brain Using ChIP-seq Data. <i>Bio-protocol</i> , 2017, 7, .	0.2	0
6094	Current State and Future Perspectives in Corneal Endothelium Differentiation. , 2017, , 179-208.		0
6098	Comparative Study of Transcriptomic profiling and Functional enrichment in Ovarian Cancer Cell lines. <i>Canadian Journal of Biotechnology</i> , 2017, 1, 65-65.	0.3	0
6101	Exploring the Molecular Mechanism of Thoracic Aortic Aneurysm via Bioinformatics Analysis. <i>Medical Science Monitor</i> , 2018, 24, 1533-1539.	0.5	1
6108	Biomarker identification of thyroid associated ophthalmopathy using microarray data. <i>International Journal of Ophthalmology</i> , 2018, 11, 1482-1488.	0.5	5
6112	Dental Stem Cells in Regenerative Medicine: Emerging Trends and Prospects in the Era of Bioinformatics. , 2019, , 119-150.		0
6114	Subspace Clustering of DNA Microarray Data. , 2019, , 210-264.		0
6115	Modern Techniques for DNA, RNA, and Protein Assessment. <i>Success in Academic Surgery</i> , 2019, , 65-104.	0.1	0

#	ARTICLE	IF	CITATIONS
6122	GenomicsKG: A Knowledge Graph to Visualize Poly-Omics Data. <i>Journal of Advances in Health</i> , 2019, 01, 70-84.	0.0	1
6124	RNA Sequencing of Osteosarcoma Gene Expression Profile Revealed that miR-214-3p Facilitates Osteosarcoma Cell Proliferation via Targeting Ubiquinol-Cytochrome c Reductase Core Protein 1 (UQCRC1). <i>Medical Science Monitor</i> , 2019, 25, 4982-4991.	0.5	7
6126	Identification of CD2, CCL5 and CCR5 as potential therapeutic target genes for renal interstitial fibrosis. <i>Annals of Translational Medicine</i> , 2019, 7, 454-454.	0.7	7
6129	Bioinformatics analysis of hepatic gene expression profiles in type 2 diabetes mellitus. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 4303-4312.	0.8	4
6132	Identification of key candidate tumor biomarkers in non-small cell lung cancer by in silico analysis. <i>Oncology Letters</i> , 2020, 19, 1008-1016.	0.8	4
6140	Identification of DEGs and transcription factors involved in <i>H. pylori</i> -associated inflammation and their relevance with gastric cancer. <i>PeerJ</i> , 2020, 8, e9223.	0.9	10
6143	Development of a novel prognostic signature for predicting the overall survival of bladder cancer patients. <i>Bioscience Reports</i> , 2020, 40, .	1.1	3
6144	Role of CYP4F2 as a novel biomarker regulating malignant phenotypes of liver cancer cells via the Nrf2 signaling axis. <i>Oncology Letters</i> , 2020, 20, 13.	0.8	4
6145	Comprehensive analysis of a long non-coding RNA-associated competing endogenous RNA network in glioma. <i>Oncology Letters</i> , 2020, 20, 63.	0.8	5
6146	C9a/GLP-sensitivity of H3K9me2 Demarcates Two Types of Genomic Compartments. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 359-370.	3.0	4
6148	Overexpression of novel long intergenic non-coding RNA LINC02454 is associated with a poor prognosis in papillary thyroid cancer. <i>Oncology Reports</i> , 2020, 44, 1489-1501.	1.2	9
6153	Identification and verification of the prognostic value of the glutathione S-transferase Mu genes in gastric cancer. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	4
6154	A Novel Computational Approach for Biomarker Detection for Gene Expression-Based Computer-Aided Diagnostic Systems for Breast Cancer. <i>Methods in Molecular Biology</i> , 2021, 2190, 195-208.	0.4	5
6156	AZD9291-resistant non-small cell lung cancer cell-derived exosomal lnc-MZT2A-5:1 induces the activation of fibroblasts. <i>Annals of Translational Medicine</i> , 2021, 9, 1593-1593.	0.7	2
6157	Genome-wide screening of novel RT-qPCR reference genes for study of GLRaV-3 infection in wine grapes and refinement of an RNA isolation protocol for grape berries. <i>Plant Methods</i> , 2021, 17, 110.	1.9	7
6158	Transcriptomics analysis of Daheng broilers reveals that PLIN2 regulates chicken preadipocyte proliferation, differentiation and apoptosis. <i>Molecular Biology Reports</i> , 2021, 48, 7985-7997.	1.0	8
6159	COMPUTATIONAL APPROACHES FOR DRUG DISCOVERY FROM MEDICINAL PLANTS IN THE ERA OF DATA DRIVEN RESEARCH. <i>Indian Drugs</i> , 2021, 58, 7-23.	0.1	0
6160	The Identified Hub Gene GlcN in Osteoarthritis Progression and Treatment. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-8.	0.7	2

#	ARTICLE	IF	CITATIONS
6161	Transcriptome analysis of the effect of a novel human serine protease inhibitor SPINK13 on gene expression in MHCC97-H cells. <i>Translational Cancer Research</i> , 2021, 10, 4464-4477.	0.4	0
6162	Identification of Hub Genes in Pancreatic Ductal Adenocarcinoma Using Bioinformatics Analysis. <i>Iranian Journal of Public Health</i> , 2021, 50, 2238-2245.	0.3	2
6163	Epigenetic and Transcriptional Regulation of the Reproductive Hypothalamus. <i>Masterclass in Neuroendocrinology</i> , 2020, , 207-235.	0.1	0
6164	Differential effects of RASA3 mutations on hematopoiesis are profoundly influenced by genetic background and molecular variant. <i>PLoS Genetics</i> , 2020, 16, e1008857.	1.5	3
6167	<i>Porphyromonas gingivalis</i> facilitated the foam cell formation via lysosomal integral membrane protein 2 (LIMP2). <i>Journal of Periodontal Research</i> , 2021, 56, 265-274.	1.4	9
6169	Prognostic and immunological value of LTB4R in pan-cancer. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 9336-9356.	1.0	1
6170	Research on the Effect and Mechanism of Lactic Acid on Improving Anxiety in Mice Based on Integrated Pharmacology. <i>International Journal of Psychiatry and Neurology</i> , 2021, 10, 99-107.	0.1	0
6171	An Efficient SVM-Based Feature Selection Model for Cancer Classification Using High-Dimensional Microarray Data. <i>IEEE Access</i> , 2021, 9, 155353-155369.	2.6	14
6173	Circulating MicroRNA Expression Profiles in Patients with Stable and Unstable Angina. <i>Clinics</i> , 2020, 75, e1546.	0.6	4
6176	mRNA Big Data Analysis of Hepatoma Carcinoma Between Different Genders. , 2020, , .		0
6177	Biological Big Data Analysis of Competing Endogenous RNA Network and mRNA Biomarker in Liver Cancer. , 2020, , .		0
6178	Single-Cell Analysis Revealed the Role of CD8+ Effector T Cells in Preventing Cardioprotective Macrophage Differentiation in the Early Phase of Heart Failure. <i>Frontiers in Immunology</i> , 2021, 12, 763647.	2.2	16
6179	Bioinformatics analysis identifies DYNC111 as prognosis marker in male patients with liver hepatocellular carcinoma. <i>PLoS ONE</i> , 2021, 16, e0258797.	1.1	7
6180	Analysis of Differentially Expressed Genes That Aggravate Metabolic Diseases in Depression. <i>Life</i> , 2021, 11, 1203.	1.1	1
6181	Weighted gene co-expression network analysis to define pivotal modules and genes in diabetic heart failure. <i>Bioscience Reports</i> , 2020, 40, .	1.1	5
6184	Biclustering of DNA Microarray Data. , 0, , 513-551.		3
6185	Cross-Platform Microarray Data Integration Combining Meta-Analysis and Gene Set Enrichment Analysis. , 0, , 570-585.		0
6186	Cross-Platform Microarray Data Integration Combining Meta-Analysis and Gene Set Enrichment Analysis. <i>Advances in Bioinformatics and Biomedical Engineering Book Series</i> , 0, , 12-27.	0.2	0



#	ARTICLE	IF	CITATIONS
6187	Inferring the Origin of the Genetic Code. Springer Optimization and Its Applications, 2007, , 291-320.	0.6	0
6188	Microarray-based Gene Expression Analysis of Endocrine Systems: Principles of Experimental Design and Interpretation. , 2008, , 3-22.		0
6189	Applications, Representation, and Management of Signaling Pathway Information: Introduction to the SigPath Project. , 2007, , 372-392.		0
6190	Handling and Interpreting Gene Groups. , 2007, , 69-84.		0
6199	Identification of serum exosomal miR-98â€“5p, miR-183â€“5p, miR-323â€“3p and miR-19b-3p as potential biomarkers for glioblastoma patients and investigation of their mechanisms. Current Research in Translational Medicine, 2022, 70, 103315.	1.2	6
6200	Evolutionary epigenomic analyses in mammalian early embryos reveal species-specific innovations and conserved principles of imprinting. Science Advances, 2021, 7, eabi6178.	4.7	42
6201	Expression and Prognostic Role of E2F2 in Hepatocellular Carcinoma. International Journal of General Medicine, 2021, Volume 14, 8463-8472.	0.8	5
6202	Heterogeneity analysis of the immune microenvironment in laryngeal carcinoma revealed potential prognostic biomarkers. Human Molecular Genetics, 2022, 31, 1487-1499.	1.4	5
6203	Mechanistic insights into the renoprotective role of curcumin in cisplatin-induced acute kidney injury: network pharmacology analysis and experimental validation. Bioengineered, 2021, 12, 11039-11054.	1.4	5
6204	The U1 snRNP component RBP45d regulates temperature-responsive flowering in Arabidopsis. Plant Cell, 2022, 34, 834-851.	3.1	18
6205	Homeoprotein SIX1 compromises antitumor immunity through TGF-Î²-mediated regulation of collagens. Cellular and Molecular Immunology, 2021, 18, 2660-2672.	4.8	5
6206	Glioblastoma gene network reconstruction and ontology analysis by online bioinformatics tools. Journal of Integrative Bioinformatics, 2021, 18, .	1.0	4
6207	Deepening into Intracellular Signaling Landscape through Integrative Spatial Proteomics and Transcriptomics in a Lymphoma Model. Biomolecules, 2021, 11, 1776.	1.8	8
6208	Whole Blood Expression Pattern of Inflammation and Redox Genes in Mild Alzheimerâ€™s Disease. Journal of Inflammation Research, 2021, Volume 14, 6085-6102.	1.6	9
6209	Hippocampal neuronsâ€™ cytosolic and membrane-bound ribosomal transcript profiles are differentially regulated by learning and subsequent sleep. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2108534118.	3.3	20
6210	Changes in Methylation across Structural and MicroRNA Genes Relevant for Progression and Metastasis in Colorectal Cancer. Cancers, 2021, 13, 5951.	1.7	5
6211	Potential Pathogenic Genes and Mechanism of Ankylosing Spondylitis: A Study Based on WGCNA and Bioinformatics Analysis. World Neurosurgery, 2022, 158, e543-e556.	0.7	2
6212	LIMD2 is a Prognostic and Predictive Marker in Patients With Esophageal Cancer Based on a ceRNA Network Analysis. Frontiers in Genetics, 2021, 12, 774432.	1.1	5

#	ARTICLE	IF	CITATIONS
6213	Exploring the Mechanisms of Arsenic Trioxide (Pishuang) in Hepatocellular Carcinoma Based on Network Pharmacology. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-9.	0.5	3
6214	Web-based transcriptome analysis determines a sixteen-gene signature and associated drugs on hearing loss patients: A bioinformatics approach. Journal of Clinical Laboratory Analysis, 2021, 35, e24065.	0.9	6
6215	Sodium Selenite Enhances Antibiotics Sensitivity of Pseudomonas aeruginosa and Decreases Its Pathogenicity by Inducing Oxidative Stress and Inhibiting Quorum Sensing System. Antioxidants, 2021, 10, 1873.	2.2	1
6216	Genome-wide DNA methylation analysis of pulmonary function in middle and old-aged Chinese monozygotic twins. Respiratory Research, 2021, 22, 300.	1.4	7
6217	CD153/CD30 signaling promotes age-dependent tertiary lymphoid tissue expansion and kidney injury. Journal of Clinical Investigation, 2022, 132, .	3.9	36
6218	Combined Metabolomics and Network Toxicology to Explore the Molecular Mechanism of Phytolacca acinose Roxb-Induced Hepatotoxicity in Zebrafish Larvae in Vivo. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-13.	0.5	2
6219	Integrative investigation of the TF-miRNA coregulatory network involved in the inhibition of breast cancer cell proliferation by resveratrol. FEBS Open Bio, 2021, , .	1.0	6
6220	Association of Circulating Biomarkers of Inc-IGSF3-1:1, SCOC-AS1, and SLC8A1-AS1 with Salt Sensitivity of Blood Pressure in Chinese Population. Journal of Cardiovascular Translational Research, 2021, , 1.	1.1	5
6221	Identification of LIG1 and LIG3 as prognostic biomarkers in breast cancer. Open Medicine (Poland), 2021, 16, 1705-1717.	0.6	2
6222	Key genes associated with prognosis and metastasis of clear cell renal cell carcinoma. PeerJ, 2022, 10, e12493.	0.9	5
6223	Prognostic value of immune related genes in lung adenocarcinoma. Oncology Letters, 2020, 20, 1-1.	0.8	5
6224	Identification of hub genes associated with esophageal cancer progression using bioinformatics analysis. Oncology Letters, 2020, 20, 1-1.	0.8	3
6225	Silencing <i>KIF14</i> reverses acquired resistance to sorafenib in hepatocellular carcinoma. Aging, 2020, 12, 22975-23003.	1.4	6
6226	Genetic Parameter Estimation and Genome-Wide Association Study-Based Loci Identification of Milk-Related Traits in Chinese Holstein. Frontiers in Genetics, 2021, 12, 799664.	1.1	9
6227	Supervised Machine Learning Models and Protein-Protein Interaction Network Analysis of Gene Expression Profiles Induced by Omega-3 Polyunsaturated Fatty Acids. Current Chinese Science, 2022, 2, 118-128.	0.2	1
6228	Mitochondrial incompatibility as a hidden driver behind the genome ancestry of African admixed cattle. BMC Biology, 2022, 20, 20.	1.7	3
6229	An antisense transcript transcribed from Irs2 locus contributes to the pathogenesis of hepatic steatosis in insulin resistance. Cell Chemical Biology, 2022, , .	2.5	2
6230	First Insight into the Variation of the Milk Serum Proteome within and between Individual Cows. Dairy, 2022, 3, 47-58.	0.7	0

#	ARTICLE	IF	CITATIONS
6231	Developing Biliary Atresia-like Model by Treating Human Liver Organoids with Polyinosinic:Polycytidylic Acid (Poly (I:C)). <i>Current Issues in Molecular Biology</i> , 2022, 44, 644-653.	1.0	3
6232	Transgenerational Transcriptomic and DNA Methylome Profiling of Mouse Fetal Testicular Germline and Somatic Cells after Exposure of Pregnant Mothers to Tributyltin, a Potent Obesogen. <i>Metabolites</i> , 2022, 12, 95.	1.3	6
6233	Gene Ontology Groups and Signaling Pathways Regulating the Process of Avian Satellite Cell Differentiation. <i>Genes</i> , 2022, 13, 242.	1.0	8
6234	Overexpression of chaperonin containing TCP1 subunit 7 has diagnostic and prognostic value for hepatocellular carcinoma. <i>Aging</i> , 2022, 14, 747-769.	1.4	9
6235	BRAF Inhibitors Reprogram Cancer-Associated Fibroblasts to Drive Matrix Remodeling and Therapeutic Escape in Melanoma. <i>Cancer Research</i> , 2022, 82, 419-432.	0.4	17
6236	m6Adecom: Analysis of m6A profile matrix based on graph regularized non-negative matrix factorization. <i>Methods</i> , 2022, 203, 322-327.	1.9	4
6237	Identification of four novel hub genes as monitoring biomarkers for colorectal cancer. <i>Hereditas</i> , 2022, 159, 11.	0.5	3
6238	Bioinformatic Analysis Combined With Experimental Validation Reveals Novel Hub Genes and Pathways Associated With Focal Segmental Glomerulosclerosis. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 691966.	1.6	4
6239	Molecular Mechanism of Gelsemium elegans (Gardner and Champ.) Benth. Against Neuropathic Pain Based on Network Pharmacology and Experimental Evidence. <i>Frontiers in Pharmacology</i> , 2021, 12, 792932.	1.6	11
6240	PBK/TPK Inhibitor Suppresses the Progression of Prolactinomas. <i>Frontiers in Endocrinology</i> , 2021, 12, 706909.	1.5	1
6241	Different genes may be involved in distal and local sensitization: A genome-wide gene-based association study and meta-analysis. <i>European Journal of Pain</i> , 2022, 26, 740-753.	1.4	3
6242	Computational analyses of mechanism of action (MoA): data, methods and integration. <i>RSC Chemical Biology</i> , 2022, 3, 170-200.	2.0	32
6243	Proteomic profiling of cisplatin-resistant and cisplatin-sensitive germ cell tumour cell lines using quantitative mass spectrometry. <i>World Journal of Urology</i> , 2022, 40, 373.	1.2	3
6244	Analysis of the effect of NEKs on the prognosis of patients with non-small-cell lung carcinoma based on bioinformatics. <i>Scientific Reports</i> , 2022, 12, 1705.	1.6	4
6245	Immune Activity and Response Differences of Oncolytic Viral Therapy in Recurrent Glioblastoma: Gene Expression Analyses of a Phase IB Study. <i>Clinical Cancer Research</i> , 2022, 28, 498-506.	3.2	12
6246	Chrysin, which targets PLA2, protects PC12 cells from OGD/R-stimulated damage through repressing the NF- $\kappa$ B signaling pathway. <i>Regenerative Therapy</i> , 2022, 19, 69-76.	1.4	4
6247	Time Series Ovarian Transcriptome Analyses of the Porcine Estrous Cycle Reveals Gene Expression Changes during Steroid Metabolism and Corpus Luteum Development. <i>Animals</i> , 2022, 12, 376.	1.0	5
6248	HOXB4 Mis-Regulation Induced by Microcystin-LR and Correlated With Immune Infiltration Is Unfavorable to Colorectal Cancer Prognosis. <i>Frontiers in Oncology</i> , 2022, 12, 803493.	1.3	4

#	ARTICLE	IF	CITATIONS
6249	MYC/MAX-Activated LINC00958 Promotes Lung Adenocarcinoma by Oncogenic Transcriptional Reprogramming Through HOXA1 Activation. <i>Frontiers in Oncology</i> , 2022, 12, 807507.	1.3	6
6250	Clinical Utility of a Unique Genome-Wide DNA Methylation Signature for KMT2A-Related Syndrome. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1815.	1.8	8
6251	Network Pharmacology Prediction and Molecular Docking-Based Strategy to Discover the Potential Pharmacological Mechanism of Wen-Yu-Jin against Pulmonary Fibrosis in a Mouse Model. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-16.	0.5	5
6252	Biological response of adrenal carcinoma and melanoma cells to mitotane treatment. <i>Oncology Letters</i> , 2022, 23, 120.	0.8	6
6253	As a prognostic biomarker of clear cell renal cell carcinoma RUFY4 predicts immunotherapy responsiveness in a PDL1-related manner. <i>Cancer Cell International</i> , 2022, 22, 66.	1.8	2
6256	Proteomic Analysis of Protective Effects of Epimedium Flavonoids against Ethanol-Induced Toxicity in Retinoic Acid-Treated SH-SY5Y Cells. <i>Molecules</i> , 2022, 27, 1026.	1.7	3
6257	An instructive role for Interleukin-7 receptor $\hat{I}\pm$ in the development of human B-cell precursor leukemia. <i>Nature Communications</i> , 2022, 13, 659.	5.8	12
6258	Clinical Significance of TET2 in Female Cancers. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, 790605.	2.0	6
6259	Label-Free Quantitative Proteomics to Explore the Action Mechanism of the Pharmaceutical-Grade Triticum vulgare Extract in Speeding Up Keratinocyte Healing. <i>Molecules</i> , 2022, 27, 1108.	1.7	5
6260	Dimensionality Reduction and Louvain Agglomerative Hierarchical Clustering for Cluster-Specified Frequent Biomarker Discovery in Single-Cell Sequencing Data. <i>Frontiers in Genetics</i> , 2022, 13, 828479.	1.1	10
6261	Biomarker Value of miR-221 and miR-222 as Potential Substrates in the Differential Diagnosis of Papillary Thyroid Cancer Based on Data Synthesis and Bioinformatics Approach. <i>Frontiers in Endocrinology</i> , 2021, 12, 794490.	1.5	7
6262	Identification of key genes in oral squamous cell carcinoma by integrated bioinformatics analysis. <i>Biologia (Poland)</i> , 2022, 77, 907-914.	0.8	0
6263	Single-molecule long-read sequencing reveals the potential impact of posttranscriptional regulation on gene dosage effects on the avian Z chromosome. <i>BMC Genomics</i> , 2022, 23, 122.	1.2	2
6264	Unveiling the anti-senescence effects and senescence-associated secretory phenotype (SASP) inhibitory mechanisms of <i>Scutellaria baicalensis</i> Georgi in low glucose-induced astrocytes based on boolean network. <i>Phytomedicine</i> , 2022, 99, 153990.	2.3	3
6267	A pan-cancer analysis of the oncogenic role of Holliday junction recognition protein in human tumors. <i>Open Medicine (Poland)</i> , 2022, 17, 317-328.	0.6	3
6269	Evolutionary impacts of purine metabolism genes on mammalian oxidative stress adaptation. <i>Zoological Research</i> , 2022, 43, 241-254.	0.9	21
6270	Prognostic Values and Underlying Regulatory Network of Cohesin Subunits in Esophageal Carcinoma. <i>Journal of Cancer</i> , 2022, 13, 1588-1602.	1.2	2
6272	Molecular basis of AR and STK11 genes associated pathogenesis via AMPK pathway and adipocytokine signalling pathway in the development of metabolic disorders in PCOS women. <i>Beni-Suef University Journal of Basic and Applied Sciences</i> , 2022, 11, .	0.8	2

#	ARTICLE	IF	CITATIONS
6273	Multi-omics reveals mitochondrial metabolism proteins susceptible for drug discovery in AML. <i>Leukemia</i> , 2022, . .	3.3	7
6274	Analysis of Novel Variants Associated with Three Human Ovarian Cancer Cell Lines. <i>Current Bioinformatics</i> , 2022, 17, 380-392.	0.7	1
6275	Gene expression profiling reveals candidate biomarkers and probable molecular mechanisms in chronic stress. <i>Bioengineered</i> , 2022, 13, 6048-6060.	1.4	3
6276	In Silico Studies of Phytoconstituents from <i>Piper longum</i> and <i>Ocimum sanctum</i> as ACE2 and TMRSS2 Inhibitors: Strategies to Combat COVID-19. <i>Applied Biochemistry and Biotechnology</i> , 2023, 195, 2618-2635.	1.4	7
6277	A Pancancer Analysis of the Oncogenic Role of S100 Calcium Binding Protein A7 (S100A7) in Human Tumors. <i>Biology</i> , 2022, 11, 284.	1.3	0
6278	A hemimetabolous wing development suggests the wing origin from lateral tergum of a wingless ancestor. <i>Nature Communications</i> , 2022, 13, 979.	5.8	13
6279	Dishevelled-Associated Activator of Morphogenesis 2 (DAAM2) Predicts the Immuno-Hot Phenotype in Pancreatic Adenocarcinoma. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 750083.	1.6	1
6280	Human APOE $\epsilon$ 3 and APOE $\epsilon$ 4 Alleles Have Differential Effects on Mouse Olfactory Epithelium. <i>Journal of Alzheimer's Disease</i> , 2022, 85, 1481-1494.	1.2	3
6281	Comprehensive Analysis of LncRNA AC010789.1 Delays Androgenic Alopecia Progression by Targeting MicroRNA-21 and the Wnt/ $\beta$ -Catenin Signaling Pathway in Hair Follicle Stem Cells. <i>Frontiers in Genetics</i> , 2022, 13, 782750.	1.1	4
6283	Identification of Candidate lncRNA and Pseudogene Biomarkers Associated with Carbon-Nanotube-Induced Malignant Transformation of Lung Cells and Prediction of Potential Preventive Drugs. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 2936.	1.2	5
6285	Lichen Secondary Metabolites Inhibit the Wnt/ $\beta$ -Catenin Pathway in Glioblastoma Cells and Improve the Anticancer Effects of Temozolomide. <i>Cells</i> , 2022, 11, 1084.	1.8	17
6286	Liver X receptor-agonist treatment rescues degeneration in a <i>Drosophila</i> model of hereditary spastic paraplegia. <i>Acta Neuropathologica Communications</i> , 2022, 10, 40.	2.4	3
6287	The implication of holocytochrome c synthase mutation in Korean familial hypoplastic amelogenesis imperfecta. <i>Clinical Oral Investigations</i> , 2022, 26, 4487-4498.	1.4	1
6288	Bioinformatics Analysis and Identification of Potential Genes Associated with Pathogenesis and Prognosis of Gastric Cancer. <i>Current Medical Science</i> , 2022, 42, 357-372.	0.7	1
6289	SCAPE: a mixture model revealing single-cell polyadenylation diversity and cellular dynamics during cell differentiation and reprogramming. <i>Nucleic Acids Research</i> , 2022, 50, e66-e66.	6.5	13
6290	The transcription factor HLH-26 controls probiotic-mediated protection against intestinal infection through up-regulation of the Wnt/BAR-1 pathway. <i>PLoS Biology</i> , 2022, 20, e3001581.	2.6	7
6291	Transcriptional atlas analysis from multiple tissues reveals the expression specificity patterns in beef cattle. <i>BMC Biology</i> , 2022, 20, 79.	1.7	12
6294	Proteomic Alterations in Follicular Fluid of Human Small Antral Follicles Collected from Polycystic Ovariesâ€”A Pilot Study. <i>Life</i> , 2022, 12, 391.	1.1	0

#	ARTICLE	IF	CITATIONS
6295	Identification of the Immune Signatures for Ovarian Cancer Based on the Tumor Immune Microenvironment Genes. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 772701.	1.8	6
6296	Divergent regulatory roles of NuRD chromatin remodeling complex subunits GATAD2 and CHD4 in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2022, 221, .	1.2	2
6297	Construction of MicroRNA-mRNA Regulatory Network in the Molecular Mechanisms of Bleomycin-Induced Pulmonary Fibrosis. <i>BioMed Research International</i> , 2022, 2022, 1-12.	0.9	0
6298	Global Quantitative Proteomics Analysis Reveals the Downstream Signaling Networks of Msx1 and Msx2 in Myoblast Differentiation. <i>Phenomics</i> , 0, , 1.	0.9	0
6299	Transcriptional Profiling and Deriving a Seven-Gene Signature That Discriminates Active and Latent Tuberculosis: An Integrative Bioinformatics Approach. <i>Genes</i> , 2022, 13, 616.	1.0	12
6300	Uncovering the Pharmacological Mechanisms of Gexia-Zhuyu Formula (GXZY) in Treating Liver Cirrhosis by an Integrative Pharmacology Strategy. <i>Frontiers in Pharmacology</i> , 2022, 13, 793888.	1.6	4
6301	Anticancer Activity of Erianin: Cancer-Specific Target Prediction Based on Network Pharmacology. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 862932.	1.6	13
6302	Identification of autophagy related genes in predicting the prognosis and aiding 5- fluorouracil therapy of colorectal cancer. <i>Heliyon</i> , 2022, 8, e09033.	1.4	3
6304	Identifying Active Substances and the Pharmacological Mechanism of <i>Houttuynia cordata</i> Thunb. in Treating Radiation-Induced Lung Injury Based on Network Pharmacology and Molecular Docking Verification. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-13.	0.5	5
6305	Biotargets for mediation of arsenic-induced coronary heart disease by calycosin. <i>Food and Agricultural Immunology</i> , 2022, 33, 207-219.	0.7	0
6307	Circ_0001174 facilitates osteosarcoma cell proliferation, migration, and invasion by targeting the miR-186-5p/MACC1 axis. <i>Journal of Orthopaedic Surgery and Research</i> , 2022, 17, 159.	0.9	5
6308	Transcriptomic and fatty acid analyses of <i>Neochloris aquatica</i> grown under different nitrogen concentration. <i>Functional and Integrative Genomics</i> , 2022, 22, 407-421.	1.4	3
6309	<i>Eucommia ulmoides</i> Oliver-Tribulus terrestris L. Drug Pair Regulates Ferroptosis by Mediating the Neurovascular-Related Ligand-Receptor Interaction Pathway- A Potential Drug Pair for Treatment Hypertension and Prevention Ischemic Stroke. <i>Frontiers in Neurology</i> , 2022, 13, 833922.	1.1	16
6310	Integrated Analysis of Transcriptomic and Genomic Data Reveals Blood Biomarkers With Diagnostic and Prognostic Potential in Non-small Cell Lung Cancer. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 774738.	1.6	3
6311	Temporal and spatial cellular and molecular pathological alterations with single-cell resolution in the adult spinal cord after injury. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 65.	7.1	49
6312	Establishment of a Combined Diagnostic Model of Abdominal Aortic Aneurysm with Random Forest and Artificial Neural Network. <i>BioMed Research International</i> , 2022, 2022, 1-15.	0.9	8
6313	Identification and verification of potential core genes in pediatric septic shock. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, .	0.6	2
6314	Survival analysis of pathway activity as a prognostic determinant in breast cancer. <i>PLoS Computational Biology</i> , 2022, 18, e1010020.	1.5	4

#	ARTICLE	IF	CITATIONS
6315	Clinical significance of mitogen-activated protein kinase kinases in hepatitis B virus -related hepatocellular carcinoma and underlying mechanism exploration. <i>Bioengineered</i> , 2022, 13, 6819-6838.	1.4	0
6316	DAVID; a web server for functional enrichment analysis and functional annotation of gene lists (2021Åupdate). <i>Nucleic Acids Research</i> , 2022, 50, W216-W221.	6.5	1,694
6317	Gene Expression over Time during Cell Transformation Due to Non-Genotoxic Carcinogen Treatment of Bhas 42 Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3216.	1.8	9
6318	Adult mouse fibroblasts retain organ-specific transcriptomic identity. <i>ELife</i> , 2022, 11, .	2.8	14
6319	Centrosomal protein 290 is a novel prognostic indicator that modulates liver cancer cell ferroptosis via the Nrf2 pathway. <i>Aging</i> , 2022, 14, 2367-2382.	1.4	4
6320	Multi-Omics Characterization of Early- and Adult-Onset Major Depressive Disorder. <i>Journal of Personalized Medicine</i> , 2022, 12, 412.	1.1	7
6321	In Silico Analysis of the Correlation of KIF2C with Prognosis and Immune Infiltration in Glioma. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-22.	0.7	4
6322	Loss-of-function of KMT5B leads to neurodevelopmental disorder and impairs neuronal development and neurogenesis. <i>Journal of Genetics and Genomics</i> , 2022, 49, 881-890.	1.7	7
6323	Comprehensive proteomic profiling of plasma and serum phosphatidylserine-positive extracellular vesicles reveals tissue-specific proteins. <i>IScience</i> , 2022, 25, 104012.	1.9	24
6324	Genetic Modeling and Genomic Analyses of Yearling Temperament in American Angus Cattle and Its Relationship With Productive Efficiency and Resilience Traits. <i>Frontiers in Genetics</i> , 2022, 13, 794625.	1.1	2
6325	Identification of key candidate genes and biological pathways in the synovial tissue of patients with rheumatoid arthritis. <i>Experimental and Therapeutic Medicine</i> , 2022, 23, 368.	0.8	5
6326	Validation and Characterization of FGFR2 Rearrangements in Cholangiocarcinoma with Comprehensive Genomic Profiling. <i>Journal of Molecular Diagnostics</i> , 2022, 24, 351-364.	1.2	5
6327	Structure-based design of CDC42 effector interaction inhibitors for the treatment of cancer. <i>Cell Reports</i> , 2022, 39, 110641.	2.9	5
6328	Bioinformatics Screening of Potential Biomarkers from mRNA Expression Profiles to Discover Drug Targets and Agents for Cervical Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3968.	1.8	13
6329	Subunits of C1Q Are Associated With the Progression of Intermittent Claudication to Chronic Limb-Threatening Ischemia. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 864461.	1.1	1
6330	ADAM19 and TUBB1 correlates with tumor infiltrating immune cells and predicts prognosis in osteosarcoma. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, .	0.6	1
6331	Developing a Genetic Biomarker-based Diagnostic Model for Major Depressive Disorder using Random Forests and Artificial Neural Networks. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2022, 25, .	0.6	1
6332	Doublecortin mutation leads to persistent defects in the Golgi apparatus and mitochondria in adult hippocampal pyramidal cells. <i>Neurobiology of Disease</i> , 2022, 168, 105702.	2.1	0

#	ARTICLE	IF	CITATIONS
6333	An integrative computational approach to predict stress-specific candidate and shared genes in multiple plant stresses. <i>Plant Gene</i> , 2022, 30, 100356.	1.4	1
6334	STAT4 and COL1A2 are potential diagnostic biomarkers and therapeutic targets for heart failure comorbid with depression. <i>Brain Research Bulletin</i> , 2022, 184, 68-75.	1.4	12
6335	In silico studies reveal the anti-osteosarcoma targets and action mechanisms of resveratrol. <i>Process Biochemistry</i> , 2022, 117, 191-197.	1.8	0
6336	Cytokine and Nitric Oxide-Dependent Gene Regulation in Islet Endocrine and Nonendocrine Cells. <i>Function</i> , 2021, 3, zqab063.	1.1	5
6338	Methylome inheritance and enhancer dememorization reset an epigenetic gate safeguarding embryonic programs. <i>Science Advances</i> , 2021, 7, eabl3858.	4.7	12
6339	Potential Novel Modules and Hub Genes as Prognostic Candidates of Thyroid Cancer by Weighted Gene Co-Expression Network Analysis. <i>International Journal of General Medicine</i> , 2021, Volume 14, 9433-9444.	0.8	4
6340	Bulk and Single-Cell Profiling of Breast Tumors Identifies TREM-1 as a Dominant Immune Suppressive Marker Associated With Poor Outcomes. <i>Frontiers in Oncology</i> , 2021, 11, 734959.	1.3	8
6341	Comparative analysis of genome-wide copy number variations between Tibetan sheep and White Suffolk sheep. <i>Animal Biotechnology</i> , 2023, 34, 986-993.	0.7	3
6342	Smell Detection Agent Optimisation Framework and Systems Biology Approach to Detect Dys-Regulated Subnetwork in Cancer Data. <i>Biomolecules</i> , 2022, 12, 37.	1.8	0
6343	Combination of Wnt/ $\beta$ -Catenin Targets S100A4 and DKK1 Improves Prognosis of Human Colorectal Cancer. <i>Cancers</i> , 2022, 14, 37.	1.7	7
6344	Loss of USP28 and SPINT2 expression promotes cancer cell survival after whole genome doubling. <i>Cellular Oncology (Dordrecht)</i> , 2022, 45, 103-119.	2.1	8
6345	Rahim AÄyZÄ± Kanser Alt-Tiplerine Ä–zgÄ¼ MolekÄ¼ler Hedef, BiyoiÄYaretÄSi Adaylar ve Yeniden KonumlandÄ±rÄ¼lan Ä°laÄŞlarÄ±n Belirlenmesi. <i>International Journal of Advances in Engineering and Pure Sciences</i> , 0, , .	0.2	0
6346	Genome-wide chromosomal association of Upf1 is linked to Pol II transcription in <i>Schizosaccharomyces pombe</i> . <i>Nucleic Acids Research</i> , 2022, 50, 350-367.	6.5	4
6347	Exploring the Potential Targets and Mechanisms of Huang Lian Jie Du Decoction in the Treatment of Coronavirus Disease 2019 Based on Network Pharmacology. <i>International Journal of General Medicine</i> , 2021, Volume 14, 9873-9885.	0.8	7
6348	Lipopolysaccharide-Induced Transcriptional Changes in LBP-Deficient Rat and Its Possible Implications for Liver Dysregulation during Sepsis. <i>Journal of Immunology Research</i> , 2021, 2021, 1-14.	0.9	3
6350	Somatic DNA demethylation generates tissue-specific methylation states and impacts flowering time. <i>Plant Cell</i> , 2022, 34, 1189-1206.	3.1	24
6351	Identification of hub mRNA, miRNAs and LncRNAs of uveal melanoma with weighted gene correlation network analysis. , 2021, , .		0
6352	The <i>Chlamydomonas</i> bZIP transcription factor BLZ8 confers oxidative stress tolerance by inducing the carbon-concentrating mechanism. <i>Plant Cell</i> , 2022, 34, 910-926.	3.1	20



#	ARTICLE	IF	CITATIONS
6353	Modular characteristics and the mechanism of Chinese medicine's treatment of gastric cancer: a data mining and pharmacology-based identification. <i>Annals of Translational Medicine</i> , 2021, 9, 1777-1777.	0.7	6
6354	Proteomic Analysis of Subchronic Furan Exposure in the Liver of Male Fischer F344 Rats. <i>Toxicologic Pathology</i> , 2022, 50, 47-59.	0.9	3
6355	Identification of potential druggable targets of cell cycle with small-molecule inhibitors in oral squamous cell carcinoma. <i>Pharmacogenetics and Genomics</i> , 2021, Publish Ahead of Print, .	0.7	3
6356	Manganese transport by <i>Streptococcus sanguinis</i> in acidic conditions and its impact on growth in vitro and in vivo. <i>Molecular Microbiology</i> , 2022, 117, 375-393.	1.2	7
6357	oxLDL-Induced Trained Immunity Is Dependent on Mitochondrial Metabolic Reprogramming. <i>Immunometabolism</i> , 2021, 3, e210025.	0.7	20
6358	Phenotypical, functional and transcriptomic comparison of two modified methods of hepatocyte differentiation from human induced pluripotent stem cells. <i>Biomedical Reports</i> , 2022, 16, 43.	0.9	1
6359	Transcriptome alterations in spermatogonial stem cells exposed to bisphenol A. <i>Animal Cells and Systems</i> , 2022, 26, 70-83.	0.8	5
6360	Activation of Complement Pathways in Kidney Tissue May Mediate Tubulointerstitial Injury in Diabetic Nephropathy. <i>Frontiers in Medicine</i> , 2022, 9, 845679.	1.2	3
6361	Identification and characterization of circular RNAs in Longissimus dorsi muscle tissue from two goat breeds using RNA-Seq. <i>Molecular Genetics and Genomics</i> , 2022, 297, 817-831.	1.0	7
6362	Macrophage inflammation resolution requires CPEB4-directed offsetting of mRNA degradation. <i>ELife</i> , 2022, 11, .	2.8	13
6363	Lyophilized plasma resuscitation downregulates inflammatory gene expression in a mouse model of sepsis. <i>Journal of Trauma and Acute Care Surgery</i> , 2022, 93, S119-S127.	1.1	0
6364	Long-term artificial selection of Hanwoo (Korean) cattle left genetic signatures for the breeding traits and has altered the genomic structure. <i>Scientific Reports</i> , 2022, 12, 6438.	1.6	6
6365	PAGER Web APP: An Interactive, Online Gene Set and Network Interpretation Tool for Functional Genomics. <i>Frontiers in Genetics</i> , 2022, 13, 820361.	1.1	2
6366	The Mechanism of <i>Dendrobium officinale</i> as a Treatment for Hyperlipidemia Based on Network Pharmacology and Experimental Validation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-23.	0.5	2
6367	Unraveling the Molecular Mechanism of Xuebijing Injection in the Treatment of Chronic Obstructive Pulmonary Disease by Combining Network Pharmacology and Affymetrix Array. <i>Natural Product Communications</i> , 2022, 17, 1934578X2210927.	0.2	0
6368	High-Throughput Sequencing Reveals CXCR4 and IGF1 Behave Different Roles in Weightlessness Osteoporosis. <i>Stem Cells International</i> , 2022, 2022, 1-16.	1.2	1
6369	Identity of MMP1 and its effects on tumor progression in head and neck squamous cell carcinoma. <i>Cancer Medicine</i> , 2022, 11, 2516-2530.	1.3	10
6370	H3K4 demethylase KDM5B regulates cancer cell identity and epigenetic plasticity. <i>Oncogene</i> , 2022, 41, 2958-2972.	2.6	8

#	ARTICLE	IF	CITATIONS
6371	SLC35B2 Acts in a Dual Role in the Host Sulfation Required for EV71 Infection. <i>Journal of Virology</i> , 2022, 96, e0204221.	1.5	8
6372	Identification of novel prognostic targets in glioblastoma using bioinformatics analysis. <i>BioMedical Engineering OnLine</i> , 2022, 21, 26.	1.3	19
6373	Statistics and network-based approaches to identify molecular mechanisms that drive the progression of breast cancer. <i>Computers in Biology and Medicine</i> , 2022, 145, 105508.	3.9	24
6448	Comprehensive bioinformatics analysis reveals the hub genes and pathways associated with multiple myeloma. <i>Hematology</i> , 2022, 27, 280-292.	0.7	6
6449	Bioinformatics: Novel Insights from Genomic Information. <i>Nestle Nutrition Institute Workshop Series</i> , 2016, 84, 35-46.	1.5	1
6450	Screening the components of <i>Saussurea involucrata</i> for novel targets for the treatment of NSCLC using network pharmacology. <i>BMC Complementary Medicine and Therapies</i> , 2022, 22, 53.	1.2	6
6452	PathJam: a new service for integrating biological pathway information. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	4
6453	Gene expression data analysis using multiobjective clustering improved with SVM based ensemble. In <i>Silico Biology</i> , 2011, 11, 19-27.	0.4	1
6454	Complete Genome Sequence Analysis of <i>Ralstonia solanacearum</i> Strain PeaFJ1 Provides Insights Into Its Strong Virulence in Peanut Plants. <i>Frontiers in Microbiology</i> , 2022, 13, 830900.	1.5	10
6456	Glomerular Expression of S100A8 in Lupus Nephritis: An Integrated Bioinformatics Analysis. <i>Frontiers in Immunology</i> , 2022, 13, 843576.	2.2	3
6457	Exosomal RNA Expression Profiles and Their Prediction Performance in Patients With Gestational Diabetes Mellitus and Macrosomia. <i>Frontiers in Endocrinology</i> , 2022, 13, 864971.	1.5	8
6458	Dominant transcript expression profiles of human protein-coding genes interrogated with GTEx dataset. <i>Scientific Reports</i> , 2022, 12, 6969.	1.6	2
6459	Role of spt23 in <i>Saccharomyces cerevisiae</i> thermal tolerance. <i>Applied Microbiology and Biotechnology</i> , 2022, , 1.	1.7	2
6460	Exploring the possible molecular targeting mechanism of <i>Saussurea involucrata</i> in the treatment of COVID-19 based on bioinformatics and network pharmacology. <i>Computers in Biology and Medicine</i> , 2022, 146, 105549.	3.9	7
6461	Gene Expression Profiling of Glioblastoma to Recognize Potential Biomarker Candidates. <i>Frontiers in Genetics</i> , 2022, 13, 832742.	1.1	3
6462	Towards an Improved Understanding of the Effects of Elevated Progesterone Levels on Human Endometrial Receptivity and Oocyte/Embryo Quality during Assisted Reproductive Technologies. <i>Cells</i> , 2022, 11, 1405.	1.8	9
6463	Silencing of YAP attenuates pericyteâ€œmyofibroblast transition and subretinal fibrosis in experimental model of choroidal neovascularization. <i>Cell Biology International</i> , 2022, 46, 1249-1263.	1.4	4
6464	Butyrate Inhibits Colorectal Cancer Cell Proliferation through Autophagy Degradation of $\beta$ -Catenin Regardless of APC and $\beta$ -Catenin Mutational Status. <i>Biomedicines</i> , 2022, 10, 1131.	1.4	17

#	ARTICLE	IF	CITATIONS
6465	LINC00922 promotes deterioration of gastric cancer. PLoS ONE, 2022, 17, e0267798.	1.1	1
6466	In-silico, interactomic based screening and identification of differentially expressed miRNAs in oral submucous fibrosis and oral squamous cell carcinoma. , 2022, 33, 201041.		1
6467	An Integrated Systematic Analysis and the Clinical Significance of Hepcidin in Common Malignancies of the Male Genitourinary System. Frontiers in Genetics, 2022, 13, .	1.1	3
6468	Combinatorial Treatment with PARP-1 Inhibitors and Cisplatin Attenuates Cervical Cancer Growth through Fos-Driven Changes in Gene Expression. Molecular Cancer Research, 2022, 20, 1183-1192.	1.5	7
6469	Proteomic Analysis Revealed Metabolic Inhibition and Elongation Factor Tu Deamidation by p-Coumaric Acid in Cronobacter sakazakii. Frontiers in Microbiology, 2022, 13, .	1.5	3
6470	Identification of functionally important miRNA targeted genes associated with child obesity trait in genome-wide association studies. BMC Genomics, 2022, 23, 360.	1.2	4
6471	A time-dependently regulated gene network reveals that Aspergillus protease affects mitochondrial metabolism and airway epithelial cell barrier function via mitochondrial oxidants. Free Radical Biology and Medicine, 2022, 185, 76-89.	1.3	1
6472	Bioinformatic approach for the discovery of cis-eQTL signals during fruit ripening of a woody species as grape ( <i>Vitis vinifera</i> L.). Scientific Reports, 2022, 12, 7481.	1.6	0
6473	Single-Cell Transcriptomics Uncovers Cellular Heterogeneity, Mechanisms, and Therapeutic Targets for Parkinson's Disease. Frontiers in Genetics, 2022, 13, .	1.1	3
6474	Translocon-associated Protein Subunit SSR3 Determines and Predicts Susceptibility to Paclitaxel in Breast Cancer and Glioblastoma. Clinical Cancer Research, 2022, 28, 3156-3169.	3.2	4
6475	Genetic Basis of Left Ventricular Noncompaction. Circulation Genomic and Precision Medicine, 2022, 15, 101161CIRCGEN121003517.	1.6	23
6476	Differentially expressed <i>EREG</i> and <i>SPP1</i> are independent prognostic markers in cervical squamous cell carcinoma. Journal of Obstetrics and Gynaecology Research, 2022, 48, 1848-1858.	0.6	4
6477	Profiling the Human Phosphoproteome to Estimate the True Extent of Protein Phosphorylation. Journal of Proteome Research, 2022, 21, 1510-1524.	1.8	15
6478	Antagonistic action of a synthetic androgen ligand mediated by chromatin remodeling in a human prostate cancer cell line. Biochemical and Biophysical Research Communications, 2022, 612, 110-118.	1.0	4
6479	A ceRNA regulatory network in systemic lupus erythematosus and its molecular interplay with cancer. Annals of Translational Medicine, 2022, 10, 563-563.	0.7	2
6480	A Comparative Genome-Wide Transcriptome Analysis of Glucocorticoid Responder and Non-Responder Primary Human Trabecular Meshwork Cells. Genes, 2022, 13, 882.	1.0	5
6481	A novel hypoxia-driven gene signature that can predict the prognosis of hepatocellular carcinoma. Bioengineered, 2022, 13, 12193-12210.	1.4	6
6482	Breast Cancer-Stromal Interactions: Adipose-Derived Stromal/Stem Cell Age and Cancer Subtype Mediated Remodeling. Stem Cells and Development, 2022, 31, 604-620.	1.1	3

#	ARTICLE	IF	CITATIONS
6483	Regulator <scp>CDCA8</scp> as a potential biomarker for the prognosis of human cutaneous melanoma. <i>Journal of Cosmetic Dermatology</i> , 2022, , .	0.8	1
6484	ERBB3 methylation and immune infiltration in tumor microenvironment of cervical cancer. <i>Scientific Reports</i> , 2022, 12, 8112.	1.6	5
6485	Multi-omics approaches for comprehensive analysis and understanding of the immune response in the miniature pig breed. <i>PLoS ONE</i> , 2022, 17, e0263035.	1.1	1
6486	Proteomic characterization of four subtypes of M2 macrophages derived from human THP-1 cells. <i>Journal of Zhejiang University: Science B</i> , 2022, 23, 407-422.	1.3	19
6487	Exploring the Genetic Associations Between the Use of Statins and Alzheimer's Disease. <i>Journal of Lipid and Atherosclerosis</i> , 2022, 11, 133.	1.1	4
6488	Dysadherin awakens mechanical forces and promotes colorectal cancer progression. <i>Theranostics</i> , 2022, 12, 4399-4414.	4.6	1
6490	Constraint-Based, Score-Based and Hybrid Algorithms to Construct Bayesian Gene Networks in the Bovine Transcriptome. <i>Animals</i> , 2022, 12, 1305.	1.0	0
6491	Downregulation of ASF1B inhibits tumor progression and enhances efficacy of cisplatin in pancreatic cancer. <i>Cancer Biomarkers</i> , 2022, 34, 647-659.	0.8	7
6492	Identification of the Transcriptional Biomarkers Panel Linked to Pathological Remodelling of the Eye Tissues in Various HD Mouse Models. <i>Cells</i> , 2022, 11, 1675.	1.8	2
6493	Schwann cells in the subcutaneous adipose tissue have neurogenic potential and can be used for regenerative therapies. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	17
6494	Gamma Irradiation Triggers Immune Escape in Glioma-Propagating Cells. <i>Cancers</i> , 2022, 14, 2728.	1.7	1
6495	Hitchhiking Mapping of Candidate Regions Associated with Fat Deposition in Iranian Thin and Fat Tail Sheep Breeds Suggests New Insights into Molecular Aspects of Fat Tail Selection. <i>Animals</i> , 2022, 12, 1423.	1.0	6
6496	Bioinformatics Analysis for Identifying Differentially Expressed MicroRNAs Derived from Plasma Exosomes Associated with Radiotherapy Resistance in Non-Small-Cell Lung Cancer. <i>Applied Bionics and Biomechanics</i> , 2022, 2022, 1-8.	0.5	6
6497	LIMK1: A promising prognostic and immune infiltration indicator in colorectal cancer. <i>Oncology Letters</i> , 2022, 24, .	0.8	2
6498	Editorial: Advancement in Gene Set Analysis: Gaining Insight From High-Throughput Data. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
6499	Tissue Sampling and Homogenization with NIRL Enables Spatially Resolved Cell Layer Specific Proteomic Analysis of the Murine Intestine. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6132.	1.8	3
6500	Analysis of Age-Dependent Transcriptomic Changes in Response to Intracerebral Hemorrhage in Mice. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, .	1.4	0
6501	Dynamic DNA 5-Hydroxymethylcytosine and RNA 5-Methylcytosine Reprogramming During Early Human Development. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 805-822.	3.0	1

#	ARTICLE	IF	CITATIONS
6502	Based on network pharmacology and molecular docking to predict the mechanism of Huangqi in the treatment of castration-resistant prostate cancer. <i>PLoS ONE</i> , 2022, 17, e0263291.	1.1	4
6503	Integrated bioinformatics and statistical approaches to explore molecular biomarkers for breast cancer diagnosis, prognosis and therapies. <i>PLoS ONE</i> , 2022, 17, e0268967.	1.1	16
6504	Comprehensive Analysis of Potential ceRNA Network and Different Degrees of Immune Cell Infiltration in Acute Respiratory Distress Syndrome. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
6505	PLXDC2 enhances invadopodium formation to promote invasion and metastasis of gastric cancer cells via interacting with PTP1B. <i>Clinical and Experimental Metastasis</i> , 2022, 39, 691-710.	1.7	2
6506	A Network Pharmacology Study on the Similarities and Differences in the Mechanisms of Zuo Gui Wan/You Gui Wan for the Treatment of Premature Ovarian Failure. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2023, 26, 1167-1179.	0.6	1
6507	Network pharmacology-based prediction of active ingredient and Mechanisms of Astragalus membranaceus and Panax notoginseng coupled-herbs against Diabetic neuropathic pain. <i>Letters in Drug Design and Discovery</i> , 2022, 19, .	0.4	0
6508	m6A Modification Involves in Enriched Environment-Induced Neurogenesis and Cognition Enhancement. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	1
6509	Integrated proteomics and transcriptomics analyses identify novel cell surface markers of HIV latency. <i>Virology</i> , 2022, 573, 50-58.	1.1	2
6510	UBE2S promotes the development of ovarian cancer by promoting PI3K/AKT/mTOR signaling pathway to regulate cell cycle and apoptosis. <i>Molecular Medicine</i> , 2022, 28, .	1.9	12
6511	Beyond GWAS—Could Genetic Differentiation within the Allograft Rejection Pathway Shape Natural Immunity to COVID-19?. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6272.	1.8	3
6519	Analysis of dapagliflozin-induced expression profile of long noncoding RNAs in proximal tubular epithelial cells of diabetic kidney disease. <i>Diabetic Nephropathy</i> , 2021, 1, 77-89.	0.1	0
6520	Integrative ontology and pathway-based approach identifies distinct molecular signatures in transcriptomes of esophageal squamous cell carcinoma. <i>Advances in Protein Chemistry and Structural Biology</i> , 2022, , 177-206.	1.0	6
6521	Methodology-Centered Review of Molecular Modeling, Simulation, and Prediction of SARS-CoV-2. <i>Chemical Reviews</i> , 2022, 122, 11287-11368.	23.0	38
6522	Shotgun proteomic investigation of methyltransferase and methylation profiles in lipopolysaccharide stimulated RAW264.7 murine macrophages. <i>Biomedical Research</i> , 2022, 43, 73-80.	0.3	1
6523	Identification of Candidate Genes Regulating Drought Tolerance in Pearl Millet. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6907.	1.8	8
6524	Histone Deacetylase 6 Inhibitor JS28 Prevents Pathological Gene Expression in Cardiac Myocytes. <i>Journal of the American Heart Association</i> , 2022, 11, .	1.6	3
6525	Neutrophil Infiltration Characterized by Upregulation of S100A8, S100A9, S100A12 and CXCR2 Is Associated With the Co-Occurrence of Crohn's Disease and Peripheral Artery Disease. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	13
6526	RNA Sequencing of the Pituitary Gland and Association Analyses Reveal PRKG2 as a Candidate Gene for Growth and Carcass Traits in Chinese Ningdu Yellow Chickens. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2

#	ARTICLE	IF	CITATIONS
6527	A LytM-Domain Factor, ActS, Functions in Two Distinctive Peptidoglycan Hydrolytic Pathways in <i>E. coli</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
6528	Expression Profile of Genes Related to the Th17 Pathway in Macrophages Infected by <i>Leishmania major</i> and <i>Leishmania amazonensis</i> : The Use of Gene Regulatory Networks in Modeling This Pathway. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	2
6529	Proteomic and functional analyses of the periodic membrane skeleton in neurons. <i>Nature Communications</i> , 2022, 13, .	5.8	15
6530	Weighted Gene Co-expression Network Analysis Identifies Specific Modules and Hub Genes Related to Subacute Ruminant Acidosis. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	1
6531	Gene Expression Signatures Reveal Common Virus Infection Pathways in Target Tissues of Type 1 Diabetes, Hashimoto's Thyroiditis, and Celiac Disease. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
6532	Identification of Small-Molecule Inhibitors for Osteosarcoma Targeted Therapy: Synchronizing In Silico, In Vitro, and In Vivo Analyses. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	0
6533	Variation in glucose metabolism under acidified sodium nitrite mediated nitrosative stress in <i>Saccharomyces cerevisiae</i> . <i>Journal of Applied Microbiology</i> , 0, , .	1.4	0
6534	Identification of novel biomarkers in prostate cancer diagnosis and prognosis. <i>Journal of Biochemical and Molecular Toxicology</i> , 2022, 36, .	1.4	7
6535	Ultrasensitive Ribo-seq reveals translational landscapes during mammalian oocyte-to-embryo transition and pre-implantation development. <i>Nature Cell Biology</i> , 2022, 24, 968-980.	4.6	57
6536	Expression and Regulatory Network Analysis of BICC1 for Aged Sca-1-Positive Bone Marrow Mesenchymal Stem Cells. <i>Disease Markers</i> , 2022, 2022, 1-16.	0.6	1
6537	The splicing factor 9G8 regulates the expression of NADPH-producing enzyme genes in <i>Drosophila</i> . <i>Biochemical and Biophysical Research Communications</i> , 2022, 620, 92-97.	1.0	1
6538	SNHG5/miR-299-5p/ATF2 Axis as a Biomarker in Immune Microenvironment of Intervertebral Disc Degeneration. <i>Mediators of Inflammation</i> , 2022, 2022, 1-14.	1.4	1
6539	A rat study model of depression-driven chronic prostatitis by modulating the PI3K/Akt/mTOR network. <i>Andrologia</i> , 2022, 54, .	1.0	2
6540	Posterior cingulate cortex reveals an expression profile of resilience in cognitively intact elders. <i>Brain Communications</i> , 2022, 4, .	1.5	10
6541	Antimicrobial peptide S100A12 (calgranulin C) inhibits growth, biofilm formation, pyoverdine secretion and suppresses type VI secretion system in <i>Pseudomonas aeruginosa</i> . <i>Microbial Pathogenesis</i> , 2022, 169, 105654.	1.3	9
6542	Reconstruction of gene innovation associated with major evolutionary transitions in the kingdom Fungi. <i>BMC Biology</i> , 2022, 20, .	1.7	6
6543	Monocytic-Myeloid Derived Suppressor Cells Suppress T-Cell Responses in Recovered SARS-CoV2-Infected Individuals. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	7
6544	The association between aging-related monocyte transcriptional networks and comorbidity burden: the Multi-Ethnic Study of Atherosclerosis (MESA). <i>GeroScience</i> , 0, , .	2.1	3

#	ARTICLE	IF	CITATIONS
6545	E2F2 promotes lung adenocarcinoma progression through B-Myb- and FOXM1-facilitated core transcription regulatory circuitry. <i>International Journal of Biological Sciences</i> , 2022, 18, 4151-4170.	2.6	4
6546	DCLK1 promotes colorectal cancer stemness and aggressiveness via the XRCC5/COX2 axis. <i>Theranostics</i> , 2022, 12, 5258-5271.	4.6	16
6547	Ferroptosis-related long non-coding RNA signature predicts the prognosis of bladder cancer. <i>BMC Cancer</i> , 2022, 22, .	1.1	10
6548	Exploring Quercetin Anti-Osteoporosis Pharmacological Mechanisms with In Silico and In Vivo Models. <i>Life</i> , 2022, 12, 980.	1.1	10
6549	EGFAFS: A Novel Feature Selection Algorithm Based on Explosion Gravitation Field Algorithm. <i>Entropy</i> , 2022, 24, 873.	1.1	1
6550	A TP53 Related Immune Prognostic Model for the Prediction of Clinical Outcomes and Therapeutic Responses in Lung Adenocarcinoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	1
6551	Inferring functional communities from partially observed biological networks exploiting geometric topology and side information. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
6552	Protective Effect of <i>Hedyotis diffusa</i> Willd. Ethanol Extract on Isoniazid-Induced Liver Injury in the Zebrafish Model. <i>Drug Design, Development and Therapy</i> , 0, Volume 16, 1995-2015.	2.0	4
6553	Identification of hub genes predicting the development of prostate cancer from benign prostate hyperplasia and analyzing their clinical value in prostate cancer by bioinformatic analysis. <i>Discover Oncology</i> , 2022, 13, .	0.8	5
6554	SR5AL serves as a key regulatory gene in lycopene biosynthesis by <i>Blakeslea trispora</i> . <i>Microbial Cell Factories</i> , 2022, 21, .	1.9	2
6555	Exploring the Anti-inflammatory Effects of Protopine Total Alkaloids of <i>Macleaya Cordata</i> (Willd.) R. Br.. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	4
6556	Reduction of LPAR1 Expression in Neuroblastoma Promotes Tumor Cell Migration. <i>Cancers</i> , 2022, 14, 3346.	1.7	2
6557	In Prostate Cancer Cells Cytokines Are Early Responders to Gravitational Changes Occurring in Parabolic Flights. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7876.	1.8	3
6558	Transcriptome profile of spleen tissues from locally-adapted Kenyan pigs ( <i>Sus scrofa</i> ) experimentally infected with three varying doses of a highly virulent African swine fever virus genotype IX isolate: Ken12/busia.1 (ken-1033). <i>BMC Genomics</i> , 2022, 23, .	1.2	4
6559	Functional analysis of the <i>Vsx2</i> super-enhancer uncovers distinct <i>cis</i> -regulatory circuits controlling <i>Vsx2</i> expression during retinogenesis. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	2
6560	Profiling the <i>3D</i> interaction between germ cell tumors and microenvironmental cells at the transcriptome and secretome level. <i>Molecular Oncology</i> , 2022, 16, 3107-3127.	2.1	6
6561	Urinary extracellular vesicle as a potential biomarker of exercise-induced fatigue in young adult males. <i>European Journal of Applied Physiology</i> , 2022, 122, 2175-2188.	1.2	3
6562	Impact of bisphenol-A on the spliceosome and meiosis of sperm in the testis of adolescent mice. <i>BMC Veterinary Research</i> , 2022, 18, .	0.7	8

#	ARTICLE	IF	CITATIONS
6563	Comprehensive Analysis of circRNA-miRNA-mRNA Regulatory Network and Novel Potential Biomarkers in Acute Myocardial Infarction. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	2
6564	HLA class II molecule HLA-DRA identifies immuno-hot tumors and predicts the therapeutic response to anti-PD-1 immunotherapy in NSCLC. <i>BMC Cancer</i> , 2022, 22, .	1.1	7
6565	Miltirone Attenuates Reactive Oxygen Species-Dependent Neuronal Apoptosis in MPP+-Induced Cell Model of Parkinson's Disease Through Regulating the PI3K/Akt Pathway. <i>Neurochemical Research</i> , 2022, 47, 3137-3149.	1.6	4
6566	Downregulation of PGM5 expression correlates with tumor progression and poor prognosis in human prostate cancer. <i>Discover Oncology</i> , 2022, 13, .	0.8	1
6567	MiR-487b suppressed inflammation and neuronal apoptosis in spinal cord injury by targeted Ifitm3. <i>Metabolic Brain Disease</i> , 2022, 37, 2405-2415.	1.4	7
6568	Study on the Anti-demyelination Mechanism of Bu-Shen-Yi-Sui Capsule in the Central Nervous System Based on Network Pharmacology and Experimental Verification. <i>Mediators of Inflammation</i> , 2022, 2022, 1-23.	1.4	1
6569	Identification of molecular mechanisms underlying the therapeutic effects of Xintong granule in coronary artery disease by a network pharmacology and molecular docking approach. <i>Medicine (United States)</i> , 2022, 101, e29829.	0.4	2
6570	Integrative Analyses Identify Potential Key Genes and Calcium-Signaling Pathway in Familial Atrioventricular Nodal Reentrant Tachycardia Using Whole-Exome Sequencing. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	2
6571	Histologically resolved multiomics enables precise molecular profiling of human intratumor heterogeneity. <i>PLoS Biology</i> , 2022, 20, e3001699.	2.6	6
6572	Impact of RNA degradation on next-generation sequencing transcriptome data. <i>Genomics</i> , 2022, 114, 110429.	1.3	8
6573	Ras Inhibition in Glioblastoma Down-regulates Hypoxia-Inducible Factor-1 $\alpha$ , Causing Glycolysis Shutdown and Cell Death. <i>Cancer Research</i> , 2005, 65, 999-1006.	0.4	142
6575	Inactivation of Sirt6 ameliorates muscular dystrophy in mdx mice by releasing suppression of utrophin expression. <i>Nature Communications</i> , 2022, 13, .	5.8	6
6577	ESM1 Is a Promising Therapeutic Target and Prognostic Indicator for Esophageal Carcinogenesis/Esophageal Squamous Cell Carcinoma. <i>BioMed Research International</i> , 2022, 2022, 1-15.	0.9	2
6578	A Diagnostic Gene Expression Signature for Bladder Cancer Can Stratify Cases into Prescribed Molecular Subtypes and Predict Outcome. <i>Diagnostics</i> , 2022, 12, 1801.	1.3	2
6579	Identifying General Tumor and Specific Lung Cancer Biomarkers by Transcriptomic Analysis. <i>Biology</i> , 2022, 11, 1082.	1.3	6
6581	Lymphatic filarial serum proteome profiling for identification and characterization of diagnostic biomarkers. <i>PLoS ONE</i> , 2022, 17, e0270635.	1.1	2
6582	Uncovering temporospatial sensitive TBI targeting strategies via in vivo phage display. <i>Science Advances</i> , 2022, 8, .	4.7	3
6583	Mechanism of action of Bu Zhong Yi Qi Decoction in the treatment of chronic fatigue syndrome based on network pharmacology and molecular docking. <i>Pharmacological Research Modern Chinese Medicine</i> , 2022, 4, 100139.	0.5	0



#	ARTICLE	IF	CITATIONS
6586	Identification of Novel Genes and Associated Drugs in Advanced Clear Cell Renal Cell Carcinoma by Bioinformatic Methods. <i>Tohoku Journal of Experimental Medicine</i> , 2022, 258, 79-90.	0.5	3
6588	Î²-Glucocerebrosidase Deficiency Activates an Aberrant Lysosome-Plasma Membrane Axis Responsible for the Onset of Neurodegeneration. <i>Cells</i> , 2022, 11, 2343.	1.8	8
6589	Signature pattern of gene expression and signaling pathway in premature diabetic patients uncover their correlation to early age coronary heart disease. <i>Diabetology and Metabolic Syndrome</i> , 2022, 14, .	1.2	0
6590	Tenogenic induction of human adipose-derived stem cells by soluble tendon extracellular matrix: composition and transcriptomic analyses. <i>Stem Cell Research and Therapy</i> , 2022, 13, .	2.4	6
6591	Pan-Cancer Analysis of Voltage-Dependent Anion Channel (VDAC1) as a Cancer Therapeutic Target or Diagnostic Biomarker. <i>Disease Markers</i> , 2022, 2022, 1-19.	0.6	4
6592	Comprehensive analysis of the glutathione S-transferase Mu (GSTM) gene family in ovarian cancer identifies prognostic and expression significance. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	6
6593	Pten and p53 Loss in the Mouse Lung Causes Adenocarcinoma and Sarcomatoid Carcinoma. <i>Cancers</i> , 2022, 14, 3671.	1.7	5
6594	Distinct GmASMTs are involved in regulating transcription factors and signalling cross-talk across embryo development, biotic, and abiotic stress in soybean. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
6595	IGF-binding proteins secreted by cancer-associated fibroblasts induce context-dependent drug sensitization of lung cancer cells. <i>Science Signaling</i> , 2022, 15, .	1.6	18
6596	Metadata analysis to explore hub of the hub-genes highlighting their functions, pathways and regulators for cervical cancer diagnosis and therapies. <i>Discover Oncology</i> , 2022, 13, .	0.8	4
6597	Qingfei Jiedu decoction inhibits PD-L1 expression in lung adenocarcinoma based on network pharmacology analysis, molecular docking and experimental verification. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	9
6599	Functional Pathway and Process Enrichment Analysis of Genes Associated With Morphological Abnormalities of the Outer Ear. <i>Journal of Craniofacial Surgery</i> , 0, Publish Ahead of Print, .	0.3	1
6600	Integrative analysis of circulating microRNAs and the placental transcriptome in recurrent pregnancy loss. <i>Frontiers in Physiology</i> , 0, 13, .	1.3	3
6601	An improved Fuzzy based GWO algorithm for predicting the potential host receptor of COVID-19 infection. <i>Computers in Biology and Medicine</i> , 2022, 151, 106050.	3.9	8
6602	Upregulation of key genes Eln and Tgfb3 were associated with the severity of cardiac hypertrophy. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
6604	IQGAP1 and RNA Splicing in the Context of Head and Neck via Phosphoproteomics. <i>Journal of Proteome Research</i> , 2022, 21, 2211-2223.	1.8	4
6605	Connecting omics signatures and revealing biological mechanisms with iLINCS. <i>Nature Communications</i> , 2022, 13, .	5.8	24
6606	Yuan-Zhi decoction in the treatment of Alzheimer's disease: An integrated approach based on chemical profiling, network pharmacology, molecular docking and experimental evaluation. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	6

#	ARTICLE	IF	CITATIONS
6607	Over-Expression of Two Different Isoforms of Cattle TUSC5 Showed Opposite Effects on Adipogenesis. <i>Genes</i> , 2022, 13, 1444.	1.0	1
6608	Functional Characterization of <i>lncRNA152</i> as an Angiogenesis-Inhibiting Tumor Suppressor in Triple-Negative Breast Cancers. <i>Molecular Cancer Research</i> , 2022, 20, 1623-1635.	1.5	6
6609	Identification of differentially expressed microRNAs as potential biomarkers for carcinoma ex pleomorphic adenoma. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
6610	The peroxisomal matrix shuttling receptor Pex5 plays a role of FB1 production and virulence in <i>Fusarium verticillioides</i> . <i>Journal of Integrative Agriculture</i> , 2022, , .	1.7	1
6611	Influence of sire fertility status on conceptus-induced transcriptomic response of the bovine endometrium. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	1
6612	Potential Mechanisms of Biejiajian Pill in the Treatment of Diabetic Atherosclerosis Based on Network Pharmacology, Molecular Docking, and Molecular Dynamics Simulation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-14.	0.5	5
6614	Integrated strategy of network pharmacology, molecular docking, HPLC-DAD and mice model for exploring active ingredients and pharmacological mechanisms of <i>Penthorum chinense Pursh</i> against alcoholic liver injury. <i>Journal of Ethnopharmacology</i> , 2022, 298, 115589.	2.0	9
6616	Identification of the key immune-related genes in aneurysmal subarachnoid hemorrhage. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	5
6617	Inhibition of $\alpha$ -synuclein aggregation by MT101-5 is neuroprotective in mouse models of Parkinson's disease. <i>Biomedicine and Pharmacotherapy</i> , 2022, 154, 113637.	2.5	0
6618	Vitamin C modulates the levels of several proteins of the mitochondrial complex III and its activity in the mouse liver. <i>Redox Biology</i> , 2022, 57, 102491.	3.9	0
6619	Cellular and molecular profiles of larval and adult <i>Xenopus</i> corneal epithelia resolved at the single-cell level. <i>Developmental Biology</i> , 2022, 491, 13-30.	0.9	4
6620	Identification of immune-related genes in atopic dermatitis, contact dermatitis, and psoriasis: A bioinformatics analysis. <i>Dermatologica Sinica</i> , 2022, 40, 162.	0.2	1
6621	TEx-MST: tissue expression profiles of MANE select transcripts. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	0
6622	TCM Analysis Data Resources, Web Services and Visualizations. <i>Translational Bioinformatics</i> , 2022, , 99-110.	0.0	0
6623	Identification of hub genes related to CD4+ memory T cell infiltration with gene co-expression network predicts prognosis and immunotherapy effect in colon adenocarcinoma. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
6624	Huayu Jiedu Fang Protects Ovarian Function in Mouse with Endometriosis Iron Overload by Inhibiting Ferroptosis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-18.	0.5	4
6625	Identification of candidate biomarkers associated with gastric cancer prognosis based on an integrated bioinformatics analysis. <i>Journal of Gastrointestinal Oncology</i> , 2022, 13, 1690-1700.	0.6	2
6626	Life at the periphery: what makes CHO cells survival talents. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 6157-6167.	1.7	2

#	ARTICLE	IF	CITATIONS
6627	Screening of sphingolipid metabolism-related genes associated with immune cells in myocardial infarction: a bioinformatics analysis. <i>Journal of Thoracic Disease</i> , 2022, 14, 2987-2996.	0.6	0
6628	Integrated Microarray Analysis to Identify Genes and Small-Molecule Drugs Associated with Stroke Progression. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-11.	0.5	2
6629	Hypoxia induces an early primitive streak signature, enhancing spontaneous elongation and lineage representation in gastruloids. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	14
6630	Potential Biomarkers and Signaling Pathways Associated with the Pathogenesis of Primary Ameloblastoma: A Systems Biology Approach. <i>International Journal of Dentistry</i> , 2022, 2022, 1-14.	0.5	5
6632	Genomic Effect of DNA Methylation on Gene Expression in Colorectal Cancer. <i>Biology</i> , 2022, 11, 1388.	1.3	5
6633	Identification of the hub and prognostic genes in liver hepatocellular carcinoma via bioinformatics analysis. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	4
6634	SLC7A1 Overexpression Is Involved in Energy Metabolism Reprogramming to Induce Tumor Progression in Epithelial Ovarian Cancer and Is Associated with Immune-Infiltrating Cells. <i>Journal of Oncology</i> , 2022, 2022, 1-21.	0.6	5
6635	Novel Cinnamaldehyde Derivatives Inhibit Peripheral Nerve Degeneration by Targeting Schwann Cells. <i>Antioxidants</i> , 2022, 11, 1846.	2.2	2
6636	Dynamic regulation of the transcriptome and proteome of the equine embryo during maternal recognition of pregnancy. <i>FASEB BioAdvances</i> , 2022, 4, 775-797.	1.3	1
6637	Integrated proteomics and metabolomics analysis of rice leaves in response to rice straw return. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
6639	Atheroprone fluid shear stress-regulated ALK1-Endoglin-SMAD signaling originates from early endosomes. <i>BMC Biology</i> , 2022, 20, .	1.7	9
6640	Identifying Toxicity Mechanisms Associated with Early Lanthanide Exposure through Multidimensional Genome-Wide Screening. <i>ACS Omega</i> , 2022, 7, 34412-34419.	1.6	5
6641	DIO3 protects against thyrotoxicosis-derived cranio-encephalic and cardiac congenital abnormalities. <i>JCI Insight</i> , 2022, 7, .	2.3	5
6642	Identification and verification of CCNB1 as a potential prognostic biomarker by comprehensive analysis. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
6643	Transcriptome analysis of the response to thyroid hormone in <i>Xenopus</i> neural stem and progenitor cells. <i>Developmental Dynamics</i> , 2023, 252, 294-304.	0.8	2
6644	Integrative Bioinformatics Analysis Reveals That miR-524-5p/MEF2C Regulates Bone Metastasis in Prostate Cancer and Breast Cancer. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-13.	0.7	2
6645	Bioinformatic identification of differentially expressed genes associated with hepatocellular carcinoma prognosis. <i>Medicine (United States)</i> , 2022, 101, e30678.	0.4	0
6646	Integrated Bioinformatics and Validation of lncRNA-Mediated ceRNA Network in Myocardial Ischemia/Reperfusion Injury. <i>Journal of Immunology Research</i> , 2022, 2022, 1-13.	0.9	7

#	ARTICLE	IF	CITATIONS
6647	An Integrated Proteomic Strategy to Identify SHP2 Substrates. <i>Journal of Proteome Research</i> , 2022, 21, 2515-2525.	1.8	4
6649	Pregestational diabetes alters cardiac structure and function of neonatal rats through developmental plasticity. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	6
6650	Systematic evaluation of tumor microenvironment and construction of a machine learning model to predict prognosis and immunotherapy efficacy in triple-negative breast cancer based on data mining and sequencing validation. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	3
6651	Comprehensive analysis of PTPN gene family revealing PTPN7 as a novel biomarker for immuno-hot tumors in breast cancer. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	6
6653	Network pharmacology and in vitro experiments-based strategy to investigate the mechanisms of KangXianYiAi formula for hepatitis B virus-related hepatocellular carcinoma. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	3
6654	Fetal Programming of the Endocrine Pancreas: Impact of a Maternal Low-Protein Diet on Gene Expression in the Perinatal Rat Pancreas. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11057.	1.8	0
6655	Research into the mechanism of intervention of SanQi in endometriosis based on network pharmacology and molecular docking technology. <i>Medicine (United States)</i> , 2022, 101, e30021.	0.4	5
6656	Bioinformatics-based identification of key genes and pathways associated with colorectal cancer diagnosis, treatment, and prognosis. <i>Medicine (United States)</i> , 2022, 101, e30619.	0.4	0
6658	Structural insights into molecular mechanism for N6-adenosine methylation by MT-A70 family methyltransferase METTL4. <i>Nature Communications</i> , 2022, 13, .	5.8	18
6659	The cytotoxicity of karanjin toward breast cancer cells is involved in the PI3K/Akt signaling pathway. <i>Drug Development Research</i> , 2022, 83, 1673-1682.	1.4	3
6660	A Potential Anticancer Mechanism of Finger Root ( <i>Boesenbergia rotunda</i> ) Extracts against a Breast Cancer Cell Line. <i>Scientifica</i> , 2022, 2022, 1-17.	0.6	5
6661	Conditional Covalent Lethality Driven by Oncometabolite Accumulation. <i>ACS Chemical Biology</i> , 2022, 17, 2789-2800.	1.6	1
6662	Inhibition of <i>Staphylococcus aureus</i> biofilm formation by gurmarin, a plant-derived cyclic peptide. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	4
6663	Identification of bromodomain-containing proteins prognostic value and expression significance based on a genomic landscape analysis of ovarian serous cystadenocarcinoma. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3
6664	Single-cell RNA-seq reveals early heterogeneity during aging in yeast. <i>Aging Cell</i> , 2022, 21, .	3.0	6
6665	SIRT3 deficiency decreases oxidative metabolism capacity but increases lifespan in male mice under caloric restriction. <i>Aging Cell</i> , 2022, 21, .	3.0	8
6666	Elucidation of active ingredients and mechanism of action of hawthorn in the prevention and treatment of atherosclerosis. <i>Journal of Food Biochemistry</i> , 2022, 46, .	1.2	5
6667	Discovery and Biological Characterization of PRMT5:MEP50 Protein-Protein Interaction Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 13793-13812.	2.9	8

#	ARTICLE	IF	CITATIONS
6668	Lnc-SELPLG-2:1 enhanced osteosarcoma oncogenesis via hsa-miR-10a-5p and the BTRC cascade. <i>BMC Cancer</i> , 2022, 22, .	1.1	0
6669	Single-cell epigenome analysis reveals age-associated decay of heterochromatin domains in excitatory neurons in the mouse brain. <i>Cell Research</i> , 2022, 32, 1008-1021.	5.7	16
6670	Prognostic Significance of ANGPTL4 in Lung Adenocarcinoma: A Meta-Analysis Based on Integrated TCGA and GEO Databases. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-16.	0.5	2
6671	Identification of an 11 immune-related gene signature as the novel biomarker for acute myocardial infarction diagnosis. <i>Genes and Immunity</i> , 2022, 23, 209-217.	2.2	3
6672	Apelin as a new therapeutic target for COVID-19 treatment. <i>QJM - Monthly Journal of the Association of Physicians</i> , 2023, 116, 197-204.	0.2	5
6673	Reprogramming landscape highlighted by dynamic transcriptomes in therapy-induced neuroendocrine differentiation. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5873-5885.	1.9	1
6674	Acute Effects of Intratumor DNA Electrotransfer. <i>Pharmaceutics</i> , 2022, 14, 2097.	2.0	4
6675	Agathis robusta Bark Extract Protects from Renal Ischemia-Reperfusion Injury: Phytochemical, In Silico and In Vivo Studies. <i>Pharmaceutics</i> , 2022, 15, 1270.	1.7	8
6676	CTpathway: a CrossTalk-based pathway enrichment analysis method for cancer research. <i>Genome Medicine</i> , 2022, 14, .	3.6	10
6677	Nuclear Proteomics of Induced Leukemia Cell Differentiation. <i>Cells</i> , 2022, 11, 3221.	1.8	4
6678	Bioinformatics Analysis Identifies TNFRSF1A as a Biomarker of Liver Injury in Sepsis TNFRSF1A is a Biomarker for Septic Liver Injury. <i>Genetical Research</i> , 2022, 2022, 1-10.	0.3	0
6679	Genome-wide identification and expression analysis of BrAGC genes in Brassica rapa reveal their potential roles in sexual reproduction and abiotic stress tolerance. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
6680	Investigation of molecular mechanisms underlying JAK/STAT signaling pathway in HPV-induced cervical carcinogenesis using "omics" approach. , 2022, 39, .		1
6681	Genomic Signatures Reveal Breeding Effects of Lulai Pigs. <i>Genes</i> , 2022, 13, 1969.	1.0	4
6682	Gene expression profile suggests different mechanisms underlying sporadic and familial mesial temporal lobe epilepsy. <i>Experimental Biology and Medicine</i> , 2022, 247, 2233-2250.	1.1	2
6683	Identification of castration-dependent and -independent driver genes and pathways in castration-resistant prostate cancer (CRPC). <i>BMC Urology</i> , 2022, 22, .	0.6	0
6685	Trichostatin A-Mediated Epigenetic Modulation Predominantly Triggers Transcriptomic Alterations in the Ex Vivo Expanded Equine Chondrocytes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13168.	1.8	0
6686	Molecular Mechanisms Underlying the Effects of Bimin Kang Mixture on Allergic Rhinitis: Network Pharmacology and RNA Sequencing Analysis. <i>BioMed Research International</i> , 2022, 2022, 1-23.	0.9	1

#	ARTICLE	IF	CITATIONS
6687	SGLT-2 as a potential target in pancreatic cancer: the preliminary clue from The Cancer Genome Atlas data. <i>Journal of Gastrointestinal Oncology</i> , 2022, 13, 2539-2552.	0.6	1
6689	Network Pharmacology and Molecular Docking of Shiwei Qingwen Decoction Reveal TNF as a Potential Target for Alleviating Mild COVID-19 Symptoms. <i>Natural Product Communications</i> , 2022, 17, 1934578X2211250.	0.2	1
6690	A Pan-Cancer Analysis of the Role of PBRM1 in Human Tumors. <i>Stem Cells International</i> , 2022, 2022, 1-13.	1.2	2
6692	Novel Insights into Redox-Based Mechanisms for Auranofin-Induced Rapid Cancer Cell Death. <i>Cancers</i> , 2022, 14, 4864.	1.7	6
6693	Yiqi Huayu decoction alleviates bleomycin-induced pulmonary fibrosis in rats by inhibiting senescence. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	5
6694	Stem cell-derived extracellular vesicles reduce the expression of molecules involved in cardiac hypertrophy in a model of human-induced pluripotent stem cell-derived cardiomyocytes. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	11
6695	Variation of miRNA Content in Cow Raw Milk Depending on the Dairy Production System. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11681.	1.8	3
6697	Network analysis for the identification of hub genes and related molecules as potential biomarkers associated with the differentiation of bone marrow-derived stem cells into hepatocytes. <i>Aging</i> , 0, .	1.4	0
6698	BRANEnet: embedding multilayer networks for omics data integration. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
6699	Comprehensive analysis and validation reveal potential MYCN regulatory biomarkers associated with neuroblastoma prognosis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 8902-8917.	2.0	1
6700	AUTS2 Controls Neuronal Lineage Choice Through a Novel PRC1-Independent Complex and BMP Inhibition. <i>Stem Cell Reviews and Reports</i> , 2023, 19, 531-549.	1.7	4
6701	Expression of NMU, PPBP and GNG4 in colon cancer and their influences on prognosis. <i>Translational Cancer Research</i> , 2022, 11, 3572-3583.	0.4	3
6702	A new machine learning method for cancer mutation analysis. <i>PLoS Computational Biology</i> , 2022, 18, e1010332.	1.5	6
6703	Exploring Molecular Targets and Mechanisms of Apigenin in the Treatment of Papillary Thyroid Carcinoma Based on Network Pharmacology and Molecular Docking Analysis. <i>Natural Product Communications</i> , 2022, 17, 1934578X2211354.	0.2	1
6704	Profiling ATM regulated genes in <i>Drosophila</i> at physiological condition and after ionizing radiation. <i>Hereditas</i> , 2022, 159, .	0.5	0
6705	Comparative transcriptome and proteome analyses of the longissimus dorsi muscle for explaining the difference between donkey meat and other meats. <i>Animal Biotechnology</i> , 2023, 34, 3085-3098.	0.7	1
6706	RT-qPCR Expression Profiles of Selected Oncogenic and Oncosuppressor miRNAs in Formalin-Fixed, Paraffin-Embedded Canine Mammary Tumors. <i>Animals</i> , 2022, 12, 2898.	1.0	2
6707	Whole Transcriptome Sequencing Reveals Cancer-Related, Prognostically Significant Transcripts and Tumor-Infiltrating Immunocytes in Mantle Cell Lymphoma. <i>Cells</i> , 2022, 11, 3394.	1.8	1

#	ARTICLE	IF	CITATIONS
6708	Exploring the active ingredients and pharmacological mechanisms of the oral intake formula Huoxiang Suling Shuanghua Decoction on influenza virus type A based on network pharmacology and experimental exploration. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
6709	Parkinson's disease gene prioritising using an efficient and biologically appropriate network-based consensus strategy. <i>Journal of Computational Science</i> , 2022, 65, 101879.	1.5	0
6710	Pathway-based integration of multi-omics data reveals lipidomics alterations validated in an Alzheimer's disease mouse model and risk loci carriers. <i>Journal of Neurochemistry</i> , 2023, 164, 57-76.	2.1	8
6711	Screening and identification of CNH4 gene associated with cell proliferation in gastric cancer based on a large-scale CRISPR-Cas9 screening database DepMap. <i>Gene</i> , 2023, 850, 146961.	1.0	7
6712	Circulating MicroRNAs as Cancer Biomarkers in Liquid Biopsies. <i>Advances in Experimental Medicine and Biology</i> , 2022, , 23-73.	0.8	10
6713	Drug repurposing in psoriasis, performed by reversal of disease-associated gene expression profiles. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 6097-6107.	1.9	16
6714	From plasma membrane to mitochondria: Time-dependent photodynamic antibacterial and anticancer therapy with a near-infrared AIE-active photosensitizer. <i>Chemical Engineering Journal</i> , 2023, 454, 140189.	6.6	5
6715	Identification of Dihydropyridone Dehydrogenase as Potential Target of Vemurafenib-Resistant Melanoma Cells. <i>Molecules</i> , 2022, 27, 7800.	1.7	3
6717	Computer-Aided Screening and Revealing Action Mechanism of Food-Derived Tripeptides Intervention in Acute Colitis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13471.	1.8	2
6718	Deciphering the impact and mechanism of Trikatu, a spices-based formulation on alcoholic liver disease employing network pharmacology analysis and in vivo validation. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	15
6719	Circadian rhythm-related factors of PER and CRY family genes function as novel therapeutic targets and prognostic biomarkers in lung adenocarcinoma. <i>Aging</i> , 2022, 14, 9056-9089.	1.4	1
6721	Identification of potential key genes related to idiopathic male infertility using RNA-sequencing data: an <i>in-silico</i> approach. <i>Human Fertility</i> , 2023, 26, 1149-1163.	0.7	2
6722	Integrative analysis of multiomics data identifies selenium-related gene ALAD associating with keshan disease. <i>Free Radical Biology and Medicine</i> , 2022, 193, 702-719.	1.3	3
6724	Identifying hub genes of calcific aortic valve disease and revealing the immune infiltration landscape based on multiple WGCNA and single-cell sequence analysis. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
6725	Transcriptomic analysis of isolated and pooled human postmortem cerebellar Purkinje cells in autism spectrum disorders. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
6726	Identification of fatty acid metabolism-related molecular subtype biomarkers and their correlation with immune checkpoints in cutaneous melanoma. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
6727	Neoadjuvant chemotherapy is associated with an altered metabolic profile and increased cancer stemness in patients with pancreatic ductal adenocarcinoma. <i>Molecular Oncology</i> , 0, , .	2.1	4
6730	Mice kidney biometabolic process analysis after cantharidin exposure using widely-targeted metabolomics combined with network pharmacology. <i>Food and Chemical Toxicology</i> , 2023, 171, 113541.	1.8	4

#	ARTICLE	IF	CITATIONS
6731	In silico analysis of genomic landscape of SARS-CoV-2 and its variant of concerns (Delta and Omicron) reveals changes in the coding potential of miRNAs and their target genes. <i>Gene</i> , 2023, 853, 147097.	1.0	1
6732	Molecular mechanism of <i>Ferula asafoetida</i> for the treatment of asthma: Network pharmacology and molecular docking approach. <i>Saudi Journal of Biological Sciences</i> , 2023, 30, 103527.	1.8	10
6733	Olanzapine-induced decreases of FGF21 in brown adipose tissue via histone modulations drive UCP1-dependent thermogenetic impairment. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2023, 122, 110692.	2.5	2
6734	HSPA1A ameliorated spinal cord injury in rats by inhibiting apoptosis to exert neuroprotective effects. <i>Experimental Neurology</i> , 2023, 361, 114301.	2.0	1
6735	Slate – A Tool for Creating and Maintaining Annotated Corpora. , 2011, 26, 91-103.		8
6736	In Silico Analysis of CatSper Family Genes and APOB Gene Regulation in Male Infertility. <i>Advances in Experimental Medicine and Biology</i> , 2022, , 323-332.	0.8	0
6737	Integrative methylome and transcriptome analysis of porcine abdominal fat indicates changes in fat metabolism and immune responses during different development. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	1
6738	Intrinsic Disorder as a Natural Preservative: High Levels of Intrinsic Disorder in Proteins Found in the 2600-Year-Old Human Brain. <i>Biology</i> , 2022, 11, 1704.	1.3	3
6739	Prediction of network pharmacology and molecular docking-based strategy to determine potential pharmacological mechanism of Liuwei Dihuang pill against tinnitus. <i>Medicine (United States)</i> , 2022, 101, e31711.	0.4	2
6740	Systematic Analysis Strategy Based on Network Pharmacology to Investigate the Potential Mechanism of <i>Fritillaria thunbergii</i> Miq. against Idiopathic Pulmonary Fibrosis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-18.	0.5	1
6741	Global Transcriptional Profiling of Granulosa Cells from Polycystic Ovary Syndrome Patients: Comparative Analyses of Patients with or without History of Ovarian Hyperstimulation Syndrome Reveals Distinct Biomarkers and Pathways. <i>Journal of Clinical Medicine</i> , 2022, 11, 6941.	1.0	3
6743	Bcl-2 Family Members Bcl-xL and Bax Cooperatively Contribute to Bortezomib Resistance in Mantle Cell Lymphoma. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14474.	1.8	3
6744	GC-MS and Network Pharmacology Analysis of the Ayurvedic Fermented Medicine, Chandanasava, Against Chronic Kidney and Cardiovascular Diseases. <i>Applied Biochemistry and Biotechnology</i> , 0, .	1.4	2
6745	The integrated transcriptome bioinformatics analysis identifies key genes and cellular components for proliferative diabetic retinopathy. <i>PLoS ONE</i> , 2022, 17, e0277952.	1.1	0
6746	Detection of potential functional variants based on systems-biology: the case of feed efficiency in beef cattle. <i>BMC Genomics</i> , 2022, 23, .	1.2	0
6747	Preliminary verification of the anti-hypoxia mechanism of <i>Gentiana straminea maxim</i> based on UPLC-triple TOF MS/MS and network pharmacology. <i>BMC Complementary Medicine and Therapies</i> , 2022, 22, .	1.2	0
6748	Data analysis guidelines for single-cell RNA-seq in biomedical studies and clinical applications. <i>Military Medical Research</i> , 2022, 9, .	1.9	4
6749	Robust and rigorous identification of tissue-specific genes by statistically extending tau score. <i>BioData Mining</i> , 2022, 15, .	2.2	2



#	ARTICLE	IF	CITATIONS
6750	A Tea Plant ( <i>Camellia sinensis</i> ) FLOWERING LOCUS C-like Gene, CsFLC1, Is Correlated to Bud Dormancy and Triggers Early Flowering in Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15711.	1.8	2
6751	Transient Polycomb activity represses developmental genes in growing oocytes. <i>Clinical Epigenetics</i> , 2022, 14, .	1.8	1
6752	Systematic evaluation of genome-wide metabolic landscapes in lactic acid bacteria reveals diet- and strain-specific probiotic idiosyncrasies. <i>Cell Reports</i> , 2022, 41, 111735.	2.9	8
6753	Role of aerobic exercise in ameliorating NASH: Insights into the hepatic thyroid hormone signaling and circulating thyroid hormones. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	1
6754	Hypoxia-associated prognostic markers and competing endogenous RNA coexpression networks in lung adenocarcinoma. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
6755	Comprehensive analysis of immune cell infiltration and role of <sc>MSR1</sc> expression in aneurysmal subarachnoid haemorrhage. <i>Cell Proliferation</i> , 2023, 56, .	2.4	2
6756	Chitin contributes to the formation of a feeding structure in a predatory nematode. <i>Current Biology</i> , 2023, 33, 15-27.e6.	1.8	8
6757	Identification of Potential Treatments for Acute Lymphoblastic Leukemia through Integrated Genomic Network Analysis. <i>Pharmaceuticals</i> , 2022, 15, 1562.	1.7	2
6758	A Novel PiRNA Enhances CA19-9 Sensitivity for Pancreatic Cancer Identification by Liquid Biopsy. <i>Journal of Clinical Medicine</i> , 2022, 11, 7310.	1.0	4
6759	Identification of the Genetic Association Between Type-2-Diabetes and Pancreatic Cancer. <i>Biochemical Genetics</i> , 2023, 61, 1143-1162.	0.8	0
6760	Development of dynamical network biomarkers for regulation in Epstein-Barr virus positive peripheral T cell lymphoma unspecified type. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
6761	Excessive proteostasis contributes to pathology in fragile X syndrome. <i>Neuron</i> , 2023, 111, 508-525.e7.	3.8	6
6762	Potential diagnostic of lymph node metastasis and prognostic values of TM4SFs in papillary thyroid carcinoma patients. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	1
6763	Genome-wide unraveling SNP pairwise epistatic effects associated with sheep body weight. <i>Animal Biotechnology</i> , 0, , 1-12.	0.7	0
6764	Zika virus alters osteogenic lineage progression of human mesenchymal stromal cells. <i>Journal of Cellular Physiology</i> , 0, , .	2.0	0
6765	The Critical Biomarkers Identification of Insulin Signaling Involved in Initiating cAMP Signaling Mediated Salivary Secretion in Sjogren Syndrome: Transcriptome Sequencing in NOD Mice Model. <i>Biological Procedures Online</i> , 2022, 24, .	1.4	1
6766	Genome-wide association study for vascular aging highlights pathways shared with cardiovascular traits in Koreans. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	0
6767	Characterizing Macrophages Diversity in COVID-19 Patients Using Deep Learning. <i>Genes</i> , 2022, 13, 2264.	1.0	0

#	ARTICLE	IF	CITATIONS
6768	RNA-Sequencing Muscle Plasticity to Resistance Exercise Training and Disuse in Youth and Older Age. <i>Physiologia</i> , 2022, 2, 164-179.	0.6	0
6769	SNARE protein USE1 is involved in the glycosylation and the expression of mumps virus fusion protein and important for viral propagation. <i>PLoS Pathogens</i> , 2022, 18, e1010949.	2.1	1
6770	MALAT1 modulates alternative splicing by cooperating with the splicing factors PTBP1 and PSF. <i>Science Advances</i> , 2022, 8, .	4.7	6
6772	Bioinformatics Analysis of miRNAs Targeting TRAF5 in DLBCL Involving in NF- $\kappa$ B Signaling Pathway and Affecting the Apoptosis and Signal Transduction. <i>Genetical Research</i> , 2022, 2022, 1-14.	0.3	0
6773	Comprehensive Analysis of the lncRNA-miRNA-mRNA Regulatory Network for Intramuscular Fat in Pigs. <i>Genes</i> , 2023, 14, 168.	1.0	4
6774	Competing endogenous <i>RNA</i> network construction based on long non-coding <i>RNAs</i> , <i>microRNAs</i> , and <i>mRNAs</i> related to fat deposition in Songliao black swine. <i>Animal Genetics</i> , 0, , .	0.6	0
6775	Network Analysis of Anti-inflammatory Phytochemicals and Omics Data for Rheumatoid Arthritis. <i>Current Computer-Aided Drug Design</i> , 2023, 19, 356-366.	0.8	0
6776	Comparative proteomic analysis of seminal plasma exosomes in buffalo with high and low sperm motility. <i>BMC Genomics</i> , 2023, 24, .	1.2	2
6777	Arabidopsis DXO1 activates RNMT1 to methylate the mRNA guanosine cap. <i>Nature Communications</i> , 2023, 14, .	5.8	3
6778	Integrated bioinformatical and in vitro study on drug targets for liver cirrhosis based on unsupervised consensus clustering and immune cell infiltration. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	0
6779	Osteocyte EglN1/Phd2 links oxygen sensing and biomineralization via FGF23. <i>Bone Research</i> , 2023, 11, .	5.4	6
6780	One-day thermal regime extends the lifespan in <i>Caenorhabditis elegans</i> . <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 495-505.	1.9	1
6781	Autophagy and senescence of rat retinal precursor cells under high glucose. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	1
6782	Molecular docking, network pharmacology and experimental verification to explore the mechanism of Wulongzhiyangwan in the treatment of pruritus. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
6783	A genome-wide <i>CRISPR</i> screen identifies the <i>CCT</i> chaperonin as a critical regulator of vesicle trafficking. <i>FASEB Journal</i> , 2023, 37, .	0.2	3
6785	The metabolite alpha-ketobutyrate extends lifespan by promoting peroxisomal function in <i>C. elegans</i> . <i>Nature Communications</i> , 2023, 14, .	5.8	10
6786	Identification of Novel Pathways Regulated by APE1/Ref-1 in Human Retinal Endothelial Cells. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1101.	1.8	6
6787	Proteomic analysis of protein lysine 2-hydroxyisobutyrylation (Khib) in soybean leaves. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	1

#	ARTICLE	IF	CITATIONS
6789	Taurine, Coenzyme Q10, and Hydrogen Water Prevents Germanium Dioxide-Induced Mitochondrial Dysfunction and Associated Sensorineural Hearing Loss in mouse. <i>Hearing Research</i> , 2023, 428, 108678.	0.9	0
6790	An evaluation of gastric adenocarcinoma-associated CircRNAs based on microarray meta-analysis and ceRNA networks. <i>Translational Oncology</i> , 2023, 28, 101611.	1.7	4
6792	Chromobox Family Proteins as Putative Biomarkers for Breast Cancer Management: A Preliminary Study Based on Bioinformatics Analysis and qRT-PCR Validation. <i>Breast Cancer: Targets and Therapy</i> , 0, Volume 14, 515-535.	1.0	0
6793	A pathway analysis-based algorithm for calculating the participation degree of ncRNA in transcriptome. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
6794	Uncovering the molecular mechanism of <i>Gynostemma pentaphyllum</i> (Thunb.) Makino against breast cancer using network pharmacology and molecular docking. <i>Medicine (United States)</i> , 2022, 101, e32165.	0.4	0
6795	Single-nucleus scRNA and scATAC sequencing uncovers the molecular and cellular characteristics in the musk gland of Chinese forest musk deer ( <i>Moschus berezovskii</i> ). <i>FASEB Journal</i> , 2023, 37, .	0.2	0
6796	Genome-wide association study of the response of patients with diabetic macular edema to intravitreal Anti-VEGF injection. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
6797	Establishment of a prognostic prediction system based on tumor microenvironment of pancreatic cancer. <i>Medicine (United States)</i> , 2022, 101, e32364.	0.4	0
6798	Screening for diagnostic targets in tuberculosis and study on its pathogenic mechanism based on mRNA sequencing technology and miRNA-mRNA-pathway regulatory network. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	0
6799	Recent advances in the area of plant-based anti-cancer drug discovery using computational approaches. <i>Molecular Diversity</i> , 0, , .	2.1	7
6800	Single cell cortical bone transcriptomics define novel osteolineage gene sets altered in chronic kidney disease. <i>Frontiers in Endocrinology</i> , 0, 14, .	1.5	9
6801	Systematic Analysis of the Mechanism of <i>Polygoni Multiflori Caulis</i> in Improving Depressive Disorder in Mice via Network Pharmacology Combined with Ultra-High Performance Liquid Chromatography Coupled with Quadrupole Exactive Orbitrap Mass Spectrometer. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2023, 26, .	0.6	0
6802	TRIM28 secures skeletal stem cell fate during skeletogenesis by silencing neural gene expression and repressing GREM1/AKT/mTOR signaling axis. <i>Cell Reports</i> , 2023, 42, 112012.	2.9	1
6803	Identifying colon cancer stage related genes and their cellular pathways. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
6804	Unraveling the phenotypic and genomic background of behavioral plasticity and temperament in North American Angus cattle. <i>Genetics Selection Evolution</i> , 2023, 55, .	1.2	2
6805	The function of guanylate binding protein 3 (GBP3) in human cancers by pan-cancer bioinformatics. <i>Mathematical Biosciences and Engineering</i> , 2023, 20, 9511-9529.	1.0	0
6806	Identification of feature genes and key biological pathways in immune-mediated necrotizing myopathy: High-throughput sequencing and bioinformatics analysis. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 2228-2240.	1.9	4
6807	In-depth quantitative proteomics analysis revealed C1GALT1 depletion in ECC-1 cells mimics an aggressive endometrial cancer phenotype observed in cancer patients with low C1GALT1 expression. <i>Cellular Oncology (Dordrecht)</i> , 2023, 46, 697-715.	2.1	7

#	ARTICLE	IF	CITATIONS
6808	Single-cell analysis reveals changes in BCG vaccine-injected mice modeling tuberculous meningitis brain infection. <i>Cell Reports</i> , 2023, 42, 112177.	2.9	4
6809	Exploring the Mechanism of Bergamot Essential Oil against Asthma Based on Network Pharmacology and Experimental Verification. <i>ACS Omega</i> , 2023, 8, 10202-10213.	1.6	1
6810	The <i>Caenorhabditis elegans</i> anchor cell transcriptome: ribosome biogenesis drives cell invasion through basement membrane. <i>Development (Cambridge)</i> , 2023, 150, .	1.2	9
6811	Investigating the role of FADS family members in breast cancer based on bioinformatic analysis and experimental validation. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
6813	Pterosin sesquiterpenoids from <i>Pteris laeta</i> Wall. ex Ettingsh. protect cells from glutamate excitotoxicity by modulating mitochondrial signals. <i>Journal of Ethnopharmacology</i> , 2023, 308, 116308.	2.0	2
6814	Btg1 and Btg2 regulate neonatal cardiomyocyte cell cycle arrest. <i>Journal of Molecular and Cellular Cardiology</i> , 2023, 179, 30-41.	0.9	0
6815	The transcriptional mechanism responding to air particulate matter in <i>Laurus nobilis</i> (L.). <i>Environmental and Experimental Botany</i> , 2023, 210, 105304.	2.0	2
6816	Green tea extract enhances retinal ganglion cell survival and axonal regeneration in rats with optic nerve injury. <i>Journal of Nutritional Biochemistry</i> , 2023, 117, 109333.	1.9	2
6818	An inclusive study of deleterious missense PAX9 variants using user-friendly tools reveals structural, functional alterations, as well as potential therapeutic targets.. <i>International Journal of Biological Macromolecules</i> , 2023, 233, 123375.	3.6	2
6819	MAPKAPK2-centric transcriptome profiling reveals its major role in governing molecular crosstalk of IGFBP2, MUC4, and PRKAR2B during HNSCC pathogenesis. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 1292-1311.	1.9	1
6820	A program of successive gene expression in mouse one-cell embryos. <i>Cell Reports</i> , 2023, 42, 112023.	2.9	6
6821	Computational models for prediction of protein-protein interaction in rice and <i>Magnaporthe grisea</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
6822	SKA2-mediated transcriptional downregulation of the key enzyme of CoQ <sub>10</sub> biosynthesis PDSS2 in lung cancer cells. <i>Journal of Cancer</i> , 2023, 14, 379-392.	1.2	0
6823	Potential clinical use of azacitidine and MEK inhibitor combination therapy in PTPN11-mutated juvenile myelomonocytic leukemia. <i>Molecular Therapy</i> , 2023, 31, 986-1001.	3.7	3
6824	Antibacterial and Antibiofilm Activities of Sertindole and Its Antibacterial Mechanism against <i>Staphylococcus aureus</i> . <i>ACS Omega</i> , 2023, 8, 5415-5425.	1.6	1
6825	Hsa_circ_0072309 is a prognostic biomarker and is correlated with immune infiltration in gastric cancer. <i>Heliyon</i> , 2023, 9, e13191.	1.4	0
6826	FUS Alters circRNA Metabolism in Human Motor Neurons Carrying the ALS-Linked P525L Mutation. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3181.	1.8	6
6827	Network Pharmacological Analysis of a New Herbal Combination Targeting Hyperlipidemia and Efficacy Validation In Vitro. <i>Current Issues in Molecular Biology</i> , 2023, 45, 1314-1332.	1.0	3

#	ARTICLE	IF	CITATIONS
6828	RNA-Seq-based transcriptomics analysis during the photodynamic therapy of primary cells in secondary hyperparathyroidism. <i>Photochemical and Photobiological Sciences</i> , 0, , .	1.6	1
6831	Bioinformatics analyses of combined databases identify shared differentially expressed genes in cancer and autoimmune disease. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	4
6832	Bioinformatics-based analysis of the roles of sex hormone receptors in endometriosis development. <i>International Journal of Medical Sciences</i> , 2023, 20, 415-428.	1.1	1
6833	Exploration of the heterogeneity and interaction of epithelial cells and NK/T-cells in Laryngeal Squamous Cell Carcinoma based on single-cell RNA sequencing data. <i>Brazilian Journal of Otorhinolaryngology</i> , 2023, 89, 393-400.	0.4	1
6834	Quantitative proteomics reveals the therapeutic effects of RFAP against depression via pathway regulation of long-term depression and potentiation. <i>Heliyon</i> , 2023, 9, e13429.	1.4	1
6836	The prognostic value of DAAM2 in lower grade glioma, liver cancer, and breast cancer. <i>Clinical and Translational Oncology</i> , 0, , .	1.2	0
6838	Potential diagnostic markers and therapeutic targets for rheumatoid arthritis with comorbid depression based on bioinformatics analysis. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
6839	AURKA Identified as Potential Lung Cancer Marker through Comprehensive Bioinformatic Analysis and Experimental Verification. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2023, 33, 39-59.	0.4	1
6840	PriPath: identifying dysregulated pathways from differential gene expression via grouping, scoring, and modeling with an embedded feature selection approach. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	8
6841	Tumor-derived insulin-like growth factor-binding protein-1 contributes to resistance of hepatocellular carcinoma to tyrosine kinase inhibitors. <i>Cancer Communications</i> , 2023, 43, 415-434.	3.7	2
6842	Multitrait genome-wide analyses identify new susceptibility loci and candidate drugs to primary sclerosing cholangitis. <i>Nature Communications</i> , 2023, 14, .	5.8	10
6843	Revealing the History and Mystery of RNA-Seq. <i>Current Issues in Molecular Biology</i> , 2023, 45, 1860-1874.	1.0	5
6844	Identification of a novel eighteen-gene signature of recurrent metastasis neuroblastoma. <i>Journal of Molecular Medicine</i> , 2023, 101, 403-417.	1.7	0
6846	The Important Role of m6A-Modified circRNAs in the Differentiation of Intramuscular Adipocytes in Goats Based on MeRIP Sequencing Analysis. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4817.	1.8	0
6847	RTP4 silencing provokes tumor-intrinsic resistance to immune checkpoint blockade in colorectal cancer. <i>Journal of Gastroenterology</i> , 2023, 58, 540-553.	2.3	1
6848	Identification of Prognostic Biomarkers for Suppressing Tumorigenesis and Metastasis of Hepatocellular Carcinoma through Transcriptome Analysis. <i>Diagnostics</i> , 2023, 13, 965.	1.3	1
6849	Clinical and genomic features of non-small cell lung cancer occurring in families. <i>Thoracic Cancer</i> , 2023, 14, 940-952.	0.8	1
6850	A mechanistic analysis of spontaneous cancer remission phenomenon: identification of genomic basis and effector biomolecules for therapeutic applicability. <i>3 Biotech</i> , 2023, 13, .	1.1	0

#	ARTICLE	IF	CITATIONS
6852	CTCF controls three-dimensional enhancer network underlying the inflammatory response of bone marrow-derived dendritic cells. <i>Nature Communications</i> , 2023, 14, .	5.8	3
6853	Identification of key genes involved in secondary metabolite biosynthesis in <i>Digitalis purpurea</i> . <i>PLoS ONE</i> , 2023, 18, e0277293.	1.1	4
6854	Development and validation of an RBP gene signature for prognosis prediction in colorectal cancer based on WGCNA. <i>Hereditas</i> , 2023, 160, .	0.5	2
6855	Bioinformatics-Based Analysis of Key Genes in Steroid-Induced Osteonecrosis of the Femoral Head That Are Associated with Copper Metabolism. <i>Biomedicines</i> , 2023, 11, 873.	1.4	0
6856	The potential bioactive ingredients and hub genes of five TCM prescriptions against lung adenocarcinoma were explored based on bioinformatics. <i>Naunyn-Schmiedeberg's Archives of Pharmacology</i> , 0, .	1.4	0
6857	Tonic repression of collagen I by the bradykinin receptor 2 in skin fibroblasts. <i>Matrix Biology</i> , 2023, 118, 110-128.	1.5	0
6858	Asparagine starvation suppresses histone demethylation through iron depletion. <i>IScience</i> , 2023, 26, 106425.	1.9	1
6859	RNA-Seq reveals that overexpression of TcUBP1 switches the gene expression pattern toward that of the infective form of <i>Trypanosoma cruzi</i> . <i>Journal of Biological Chemistry</i> , 2023, 299, 104623.	1.6	4
6860	Demystifying the Role of Prognostic Biomarkers in Breast Cancer through Integrated Transcriptome and Pathway Enrichment Analyses. <i>Diagnostics</i> , 2023, 13, 1142.	1.3	1
6861	Identification of new potential downstream transcriptional targets of the strigolactone pathway including glucosinolate biosynthesis. <i>Plant Direct</i> , 2023, 7, .	0.8	6
6862	Exploring molecular signatures related to the mechanism of aging in different brain regions by integrated bioinformatics. <i>Frontiers in Molecular Neuroscience</i> , 0, 16, .	1.4	0
6864	Tregs dysfunction aggravates postoperative cognitive impairment in aged mice. <i>Journal of Neuroinflammation</i> , 2023, 20, .	3.1	5
6865	Nuclear speckleopathies: developmental disorders caused by variants in genes encoding nuclear speckle proteins. <i>Human Genetics</i> , 0, .	1.8	4
6866	Antagonistic Interactions in Mitochondria ROS Signaling Responses to Manganese. <i>Antioxidants</i> , 2023, 12, 804.	2.2	7
6867	RNA-Seq Profiling between Commercial and Indigenous Iranian Chickens Highlights Differences in Innate Immune Gene Expression. <i>Genes</i> , 2023, 14, 793.	1.0	0
6869	Anticancer Effect of Active Component of <i>Astragalus Membranaceus</i> Combined with Olaparib on Ovarian Cancer Predicted by Network-Based Pharmacology. <i>Applied Biochemistry and Biotechnology</i> , 0, .	1.4	1
6870	The Zinc-BED Transcription Factor Bedwarfed Promotes Proportional Dendritic Growth and Branching through Transcriptional and Translational Regulation in <i>Drosophila</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 6344.	1.8	0
6871	Targeting CLDN6 in germ cell tumors by an antibody-drug-conjugate and studying therapy resistance of yolk-sac tumors to identify and screen specific therapeutic options. <i>Molecular Medicine</i> , 2023, 29, .	1.9	3

#	ARTICLE	IF	CITATIONS
6872	Interleukin-10 as Covid-19 biomarker targeting KSK and its analogues: Integrated network pharmacology. <i>PLoS ONE</i> , 2023, 18, e0282263.	1.1	0
6873	Accurate Prediction of Cancer Prognosis by Exploiting Patient-Specific Cancer Driver Genes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6445.	1.8	0
6874	Differences in gene expression in field populations of Wolbachia-infected <i>Aedes aegypti</i> mosquitoes with varying release histories in northern Australia. <i>PLoS Neglected Tropical Diseases</i> , 2023, 17, e0011222.	1.3	3
6875	Identification of cancer-related genes FGFR2 and CEBPB in choledochal cyst via RNA sequencing of patient-derived liver organoids. <i>PLoS ONE</i> , 2023, 18, e0283737.	1.1	0
6876	Exploring Potential Biomarkers and Molecular Mechanisms of Ischemic Cardiomyopathy and COVID-19 Comorbidity Based on Bioinformatics and Systems Biology. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6511.	1.8	3
6877	Comprehensive proteome, phosphoproteome and kinome characterization of luminal A breast cancer. <i>Frontiers in Oncology</i> , 0, 13, .	1.3	0
6878	Exploring the association of addiction-related genetic factors with non-suicidal self-injury in adolescents. <i>Frontiers in Psychiatry</i> , 0, 14, .	1.3	0
6880	Identifying TNF and IL6 as potential hub genes and targeted drugs associated with scleritis: A bio-informative report. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
6881	Expression Signature of Immune-Related MicroRNAs in Autoimmune Skin Disease: Psoriasis and Vitiligo Insights. <i>Molecular Diagnosis and Therapy</i> , 2023, 27, 405-423.	1.6	2
6882	Persistent Lipid Accumulation Leads to Persistent Exacerbation of Endoplasmic Reticulum Stress and Inflammation in Progressive NASH via the IRE1 $\alpha$ /TRAF2 Complex. <i>Molecules</i> , 2023, 28, 3185.	1.7	1
6883	Systematic pan-cancer analysis identifies SLC31A1 as a biomarker in multiple tumor types. <i>BMC Medical Genomics</i> , 2023, 16, .	0.7	7
6885	The long non-coding RNA colon cancer-associated transcript 1-Vimentin axis promoting the migration and invasion of HeLa cells. <i>Chinese Medical Journal</i> , 0, Publish Ahead of Print, .	0.9	0
6886	Bioinformatics and network pharmacology-based study to elucidate the multi-target pharmacological mechanism of the indigenous plants of Medina valley in treating HCV-related hepatocellular carcinoma. <i>Saudi Pharmaceutical Journal</i> , 2023, , .	1.2	3
6888	Novel differential calcium regulation of hematopoietic stem and progenitor cells under physiological low oxygen conditions. <i>Journal of Cellular Physiology</i> , 2023, 238, 1492-1506.	2.0	0
6890	An integrated bioinformatics analysis of the S100 in head and neck squamous cell carcinoma. <i>Translational Cancer Research</i> , 2023, 12, 717-731.	0.4	1
6891	Serum metabolic alterations in peritoneal dialysis patients with excessive daytime sleepiness. <i>Renal Failure</i> , 2023, 45, .	0.8	0
6892	Targeted Modulation of Chicken Genes In Vitro Using CRISPRa and CRISPRi Toolkit. <i>Genes</i> , 2023, 14, 906.	1.0	1
6893	Drug Discovery in Canine Pyometra Disease Identified by Text Mining and Microarray Data Analysis. <i>BioMed Research International</i> , 2023, 2023, 1-11.	0.9	0

#	ARTICLE	IF	CITATIONS
6895	Insulin secretion deficits in a Prader-Willi syndrome $\beta$ -cell model are associated with a concerted downregulation of multiple endoplasmic reticulum chaperones. <i>PLoS Genetics</i> , 2023, 19, e1010710.	1.5	1
6896	<i>miR-145</i> regulates steroidogenesis in mouse primary granulosa cells by targeting <i>Arpc5</i> and subsequent cytoskeleton remodeling. <i>Journal of Reproduction and Development</i> , 2023, , .	0.5	0
6897	Proanthocyanidins Inhibit Osteoblast Apoptosis via the PI3K/AKT/Bcl-xL Pathway in the Treatment of Steroid-Induced Osteonecrosis of the Femoral Head in Rats. <i>Nutrients</i> , 2023, 15, 1936.	1.7	0
6899	Generation and Functional Analysis of Defective Viral Genomes during SARS-CoV-2 Infection. <i>MBio</i> , 2023, 14, .	1.8	5
6900	Differential protease content of mast cells and the processing of IL-33 in <i>Alternaria alternata</i> induced allergic airway inflammation in mice. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	1
6901	Monitoring Cultured Rat Hepatocytes Using RNA-Seq In Vitro. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7534.	1.8	2
6902	The Enhanced Expression of ZWILCH Predicts Poor Survival of Adrenocortical Carcinoma Patients. <i>Biomedicines</i> , 2023, 11, 1233.	1.4	2
7027	Analysis of Differentially Expressed circRNAs and mRNAs and Their Correlation Network in Peripheral Blood of COVID-19 Patients. , 2023, , .		0
7074	Computational Tools for Functional Analysis of Circular RNAs. <i>RNA Technologies</i> , 2023, , 327-342.	0.2	0
7125	Machine learning applications in cancer genomics. , 2024, , 41-72.		0