

DAVID: Database for Annotation, Visualization, and Int

Genome Biology

4, P3

Citation Report

#	ARTICLE	IF	CITATIONS
1	POCUS: mining genomic sequence annotation to predict disease genes. <i>Genome Biology</i> , 2003, 4, R75.	13.9	199
2	Identifying biological themes within lists of genes with EASE. <i>Genome Biology</i> , 2003, 4, R70.	3.8	1,664
3	Gender-Specific Gene Expression in Post-Mortem Human Brain: Localization to Sex Chromosomes. <i>Neuropsychopharmacology</i> , 2004, 29, 373-384.	2.8	206
4	GFINDER: Genome Function INtegrated Discoverer through dynamic annotation, statistical analysis, and mining. <i>Nucleic Acids Research</i> , 2004, 32, W293-W300.	6.5	72
5	From Mice to Humans. <i>Cancer Research</i> , 2004, 64, 7748-7755.	0.4	77
6	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
7	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
8	Lineage-Specific Gene Duplication and Loss in Human and Great Ape Evolution. <i>PLoS Biology</i> , 2004, 2, e207.	2.6	263
9	Handling multiple testing while interpreting microarrays with the Gene Ontology Database. <i>BMC Bioinformatics</i> , 2004, 5, 124.	1.2	28
10	Consensus clustering and functional interpretation of gene-expression data. <i>Genome Biology</i> , 2004, 5, R94.	13.9	122
11	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
12	Transcription profiling of C/EBP targets identifies Per2 as a gene implicated in myeloid leukemia. <i>Blood</i> , 2005, 106, 2827-2836.	0.6	145
13	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
14	PAGE: parametric analysis of gene set enrichment. <i>BMC Bioinformatics</i> , 2005, 6, 144.	1.2	649
15	FACT--a framework for the functional interpretation of high-throughput experiments. <i>BMC Bioinformatics</i> , 2005, 6, 161.	1.2	6
16	Storing, linking, and mining microarray databases using SRS. <i>BMC Bioinformatics</i> , 2005, 6, 192.	1.2	12
17	A TNF-induced gene expression program under oscillatory NF- κ B control. <i>BMC Genomics</i> , 2005, 6, 137.	1.2	159
18	cGMP-independent nitric oxide signaling and regulation of the cell cycle. <i>BMC Genomics</i> , 2005, 6, 151.	1.2	45

#	ARTICLE	IF	CITATIONS
19	Gene expression signature of estrogen receptor $\hat{\pm}$ status in breast cancer. BMC Genomics, 2005, 6, 37.	1.2	126
20	PathwayVoyager: pathway mapping using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database. BMC Genomics, 2005, 6, 60.	1.2	286
21	Gene expression profile of cervical tissue compared to exfoliated cells: Impact on biomarker discovery. BMC Genomics, 2005, 6, 64.	1.2	18
22	Identification and validation of novel ERBB2 (HER2, NEU) targets including genes involved in angiogenesis. International Journal of Cancer, 2005, 114, 590-597.	2.3	53
23	Wound Site Neutrophil Transcriptome in Response to Psychological Stress in Young Men. Gene Expression, 2005, 12, 273-287.	0.5	30
24	Effects of ADMA upon Gene Expression: An Insight into the Pathophysiological Significance of Raised Plasma ADMA. PLoS Medicine, 2005, 2, e264.	3.9	52
25	Molecular Dissection of Mesenchymal-Epithelial Interactions in the Hair Follicle. PLoS Biology, 2005, 3, e331.	2.6	405
26	Recent additions and improvements to the Onto-Tools. Nucleic Acids Research, 2005, 33, W762-W765.	6.5	106
27	PBK/TOPK, a Proliferating Neural Progenitor-Specific Mitogen-Activated Protein Kinase Kinase. Journal of Neuroscience, 2005, 25, 10773-10785.	1.7	90
28	Global gene expression profiles reveal significant nuclear reprogramming by the blastocyst stage after cloning. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17582-17587.	3.3	184
29	The promoters of human cell cycle genes integrate signals from two tumor suppressive pathways during cellular transformation. Molecular Systems Biology, 2005, 1, 2005.0022.	3.2	64
30	Inactivation of Myc in Murine Two-Hit B lymphomas Causes Dormancy with Elevated Levels of Interleukin 10 Receptor and CD20: Implications for Adjuvant Therapies. Cancer Research, 2005, 65, 5454-5461.	0.4	29
31	ArrayXPath II: mapping and visualizing microarray gene-expression data with biomedical ontologies and integrated biological pathway resources using Scalable Vector Graphics. Nucleic Acids Research, 2005, 33, W621-W626.	6.5	52
32	GFINDER: genetic disease and phenotype location statistical analysis and mining of dynamically annotated gene lists. Nucleic Acids Research, 2005, 33, W717-W723.	6.5	61
33	RACE: Remote Analysis Computation for gene Expression data. Nucleic Acids Research, 2005, 33, W638-W643.	6.5	53
34	Isolation of mRNA from specific tissues of Drosophila by mRNA tagging. Nucleic Acids Research, 2005, 33, e148-e148.	6.5	71
35	WebGestalt: an integrated system for exploring gene sets in various biological contexts. Nucleic Acids Research, 2005, 33, W741-W748.	6.5	1,630
36	Genomic analysis of metabolic pathway gene expression in mice. Genome Biology, 2005, 6, R59.	13.9	70

#	ARTICLE	IF	CITATIONS
37	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
38	Promoter features related to tissue specificity as measured by Shannon entropy. <i>Genome Biology</i> , 2005, 6, R33.	3.8	377
39	Breast cancer prognosis by combinatorial analysis of gene expression data. <i>Breast Cancer Research</i> , 2006, 8, R41.	2.2	53
40	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
41	Shuffling of cis-regulatory elements is a pervasive feature of the vertebrate lineage. <i>Genome Biology</i> , 2006, 7, R56.	13.9	41
42	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
43	Deciphering cellular states of innate tumor drug responses. <i>Genome Biology</i> , 2006, 7, R19.	13.9	110
44	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
45	Cellular, Molecular Consequences of Peroxisome Proliferator- Activated Receptor- γ Activation in Ovarian Cancer Cells. <i>Neoplasia</i> , 2006, 8, 851-1N12.	2.3	48
46	Methamphetamine Modulates Gene Expression Patterns in Monocyte Derived Mature Dendritic Cells. <i>Molecular Diagnosis and Therapy</i> , 2006, 10, 257-269.	1.6	45
47	A Genomic Approach to Identify Regulatory Nodes in the Transcriptional Network of Systemic Acquired Resistance in Plants. <i>PLoS Pathogens</i> , 2006, 2, e123.	2.1	651
48	Hepatic Gene Expression Response to Acute Indomethacin Exposure. <i>Molecular Diagnosis and Therapy</i> , 2006, 10, 187-196.	1.6	6
49	Involvement of HTLV-I Tax and CREB in aneuploidy: a bioinformatics approach. <i>Retrovirology</i> , 2006, 3, 43.	0.9	14
50	BMI1 is a target gene of E2F-1 and is strongly expressed in primary neuroblastomas. <i>Nucleic Acids Research</i> , 2006, 34, 1745-1754.	6.5	127
51	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
52	Gene expression profiles in developing nephrons using Lim1 metanephric mesenchyme-specific conditional mutant mice. <i>BMC Nephrology</i> , 2006, 7, 1.	0.8	23
53	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
54	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

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	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
58	A multiplexed proteomics approach to differentiate neurite outgrowth patterns. <i>Journal of Neuroscience Methods</i> , 2006, 158, 22-29.	1.3	18
59	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
60	K-SPMM: a database of murine spermatogenic promoters modules & motifs. <i>BMC Bioinformatics</i> , 2006, 7, 238.	1.2	6
61	Integrated functional visualization of eukaryotic genomes. <i>BMC Bioinformatics</i> , 2006, 7, 348.	1.2	3
62	CROPPER: a metagene creator resource for cross-platform and cross-species compendium studies. <i>BMC Bioinformatics</i> , 2006, 7, 418.	1.2	3
63	Analysis with respect to instrumental variables for the exploration of microarray data structures. <i>BMC Bioinformatics</i> , 2006, 7, 422.	1.2	55
64	Mining expressed sequence tags identifies cancer markers of clinical interest. <i>BMC Bioinformatics</i> , 2006, 7, 481.	1.2	23
65	Transcriptomic response to differentiation induction. <i>BMC Bioinformatics</i> , 2006, 7, 81.	1.2	1
66	Gene expression alterations in brains of mice infected with three strains of scrapie. <i>BMC Genomics</i> , 2006, 7, 114.	1.2	80
67	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
68	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
69	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
70	Defining the gene expression signature of rhabdomyosarcoma by meta-analysis. <i>BMC Genomics</i> , 2006, 7, 287.	1.2	37
71	Comparison of gene coverage of mouse oligonucleotide microarray platforms. <i>BMC Genomics</i> , 2006, 7, 58.	1.2	24
72	An online database for brain disease research. <i>BMC Genomics</i> , 2006, 7, 70.	1.2	101

#	ARTICLE	IF	CITATIONS
73	Absolute enrichment: gene set enrichment analysis for homeostatic systems. <i>Nucleic Acids Research</i> , 2006, 34, e151-e151.	6.5	55
74	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
75	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
76	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
77	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
78	Integrating Genetic and Network Analysis to Characterize Genes Related to Mouse Weight. <i>PLoS Genetics</i> , 2006, 2, e130.	1.5	419
79	A multivariate approach for integrating genome-wide expression data and biological knowledge. <i>Bioinformatics</i> , 2006, 22, 2373-2380.	1.8	122
80	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
81	Filaria-Induced Monocyte Dysfunction and Its Reversal following Treatment. <i>Infection and Immunity</i> , 2006, 74, 4409-4417.	1.0	55
82	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
83	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
84	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
85	Identification of an NF- κ B-Dependent Gene Network in Cells Infected by Mammalian Reovirus. <i>Journal of Virology</i> , 2006, 80, 1077-1086.	1.5	54
86	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
87	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
88	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
89	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
90	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

#	ARTICLE	IF	CITATIONS
91	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
92	Global Transcriptome Analysis of Genetically Identified Neurons in the Adult Cortex. <i>Journal of Neuroscience</i> , 2006, 26, 9956-9966.	1.7	88
93	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
94	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
95	A molecular-properties-based approach to understanding PDZ domain proteins and PDZ ligands. <i>Genome Research</i> , 2006, 16, 1056-1072.	2.4	45
96	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
97	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
98	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
99	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
100	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
101	The (In)dependence of Alternative Splicing and Gene Duplication. <i>PLoS Computational Biology</i> , 2007, 3, e33.	1.5	66
102	A genome-wide approach identifies distinct but overlapping subsets of cellular mRNAs associated with Stauf1- and Stauf2-containing ribonucleoprotein complexes. <i>Rna</i> , 2008, 14, 324-335.	1.6	104
103	Regulatory Pathway Analysis by High-Throughput In Situ Hybridization. <i>PLoS Genetics</i> , 2007, 3, e178.	1.5	55
104	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
105	Challenges and Solutions in Proteomics. <i>Current Genomics</i> , 2007, 8, 21-28.	0.7	12
106	A High-Resolution Map of Segmental DNA Copy Number Variation in the Mouse Genome. <i>PLoS Genetics</i> , 2007, 3, e3.	1.5	196
107	Unbiased Gene Expression Analysis Implicates the huntingtin Polyglutamine Tract in Extra-mitochondrial Energy Metabolism. <i>PLoS Genetics</i> , 2007, 3, e135.	1.5	72
108	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

#	ARTICLE	IF	CITATIONS
109	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
110	Investigating the Genetic Circuitry of Mastermind in <i>Drosophila</i> , a Notch Signal Effector. <i>Genetics</i> , 2007, 177, 2493-2505.	1.2	57
111	GO PaD: the Gene Ontology Partition Database. <i>Nucleic Acids Research</i> , 2007, 35, D322-D327.	6.5	113
112	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
113	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
114	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
115	The Proteome of the Mouse Photoreceptor Sensory Cilium Complex. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1299-1317.	2.5	310
116	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
117	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
118	AgBase: a unified resource for functional analysis in agriculture. <i>Nucleic Acids Research</i> , 2007, 35, D599-D603.	6.5	94
119	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
120	Gene Expression Profiles Differentiate Between Sterile SIRS and Early Sepsis. <i>Annals of Surgery</i> , 2007, 245, 611-621.	2.1	100
121	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
122	Identification of mRNAs that continue to associate with polysomes during hypoxia. <i>Rna</i> , 2007, 13, 1116-1131.	1.6	83
123	Amplified Expression Profiling of Platelet Transcriptome Reveals Changes in Arginine Metabolic Pathways in Patients With Sickle Cell Disease. <i>Circulation</i> , 2007, 115, 1551-1562.	1.6	126
124	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
125	Noninfectious papilloma virus-like particles inhibit HIV-1 replication: implications for immune control of HIV-1 infection by IL-27. <i>Blood</i> , 2007, 109, 1841-1849.	0.6	94
126	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

#	ARTICLE	IF	CITATIONS
127	Co-factors of LIM domains (Clm1/Ldb/Nli) regulate corneal homeostasis and maintenance of hair follicle stem cells. <i>Developmental Biology</i> , 2007, 312, 484-500.	0.9	25
128	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
129	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
130	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
131	Repetitive sequence environment distinguishes housekeeping genes. <i>Gene</i> , 2007, 390, 153-165.	1.0	47
132	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
133	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
134	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
135	MYC2 Differentially Modulates Diverse Jasmonate-Dependent Functions in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2007, 19, 2225-2245.	3.1	947
136	Aging impacts transcriptomes but not genomes of hormone-dependent breast cancers. <i>Breast Cancer Research</i> , 2007, 9, R59.	2.2	64
137	Prediction of synergistic transcription factors by function conservation. <i>Genome Biology</i> , 2007, 8, R257.	13.9	24
138	Broad network-based predictability of <i>Saccharomyces cerevisiae</i> gene loss-of-function phenotypes. <i>Genome Biology</i> , 2007, 8, R258.	13.9	87
139	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
140	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
141	Gene expression profiling of Hfe ^{-/-} 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
142	Simplified ontologies allowing comparison of developmental mammalian gene expression. <i>Genome Biology</i> , 2007, 8, R229.	13.9	12
143	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
144	Regional differences in dosage compensation on the chicken Z chromosome. <i>Genome Biology</i> , 2007, 8, R202.	13.9	98

#	ARTICLE	IF	CITATIONS
145	Transcriptomic and phenotypic analysis of murine embryonic stem cell derived BMP2+ lineage cells: an insight into mesodermal patterning. <i>Genome Biology</i> , 2007, 8, R184.	13.9	22
146	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
147	A functional map of NF κ B signaling identifies novel modulators and multiple system controls. <i>Genome Biology</i> , 2007, 8, R104.	13.9	20
148	Morphine effects on striatal transcriptome in mice. <i>Genome Biology</i> , 2007, 8, R128.	13.9	74
149	Revealing signaling pathway deregulation by using gene expression signatures and regulatory motif analysis. <i>Genome Biology</i> , 2007, 8, R77.	13.9	18
150	Global transcriptome analysis of murine embryonic stem cell-derived cardiomyocytes. <i>Genome Biology</i> , 2007, 8, R56.	13.9	54
151	microRNA expression in the prefrontal cortex of individuals with schizophrenia and schizoaffective disorder. <i>Genome Biology</i> , 2007, 8, R27.	13.9	489
152	DiscoverySpace: an interactive data analysis application. <i>Genome Biology</i> , 2007, 8, R6.	13.9	41
153	GENECODIS: a web-based tool for finding significant concurrent annotations in gene lists. <i>Genome Biology</i> , 2007, 8, R3.	13.9	554
154	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
155	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
156	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
157	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
158	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
159	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
160	Differential Cerebral Cortex Transcriptomes of Baboon Neonates Consuming Moderate and High Docosahexaenoic Acid Formulas. <i>PLoS ONE</i> , 2007, 2, e370.	1.1	49
161	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
162	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
163	Dysregulation of X-linked gene expression in Klinefelter's syndrome and association with verbal cognition. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2007, 144B, 728-734.	1.1	68
164	Silencing of core transcription factors in human EC cells highlights the importance of autocrine FGF signaling for self-renewal. <i>BMC Developmental Biology</i> , 2007, 7, 46.	2.1	62
165	Characterization of the effect of sample quality on high density oligonucleotide microarray data using progressively degraded rat liver RNA. <i>BMC Biotechnology</i> , 2007, 7, 57.	1.7	72
166	Common molecular pathways involved in human CD133+/CD34+ progenitor cell expansion and cancer. <i>Cancer Cell International</i> , 2007, 7, 11.	1.8	15
167	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. <i>Cancer Cell International</i> , 2007, 7, 14.	1.8	48
168	OCPAT: an online codon-preserved alignment tool for evolutionary genomic analysis of protein coding sequences. <i>Source Code for Biology and Medicine</i> , 2007, 2, 5.	1.7	11
169	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
170	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
171	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
172	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
173	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
174	Understanding network concepts in modules. <i>BMC Systems Biology</i> , 2007, 1, 24.	3.0	385
175	Eigengene networks for studying the relationships between co-expression modules. <i>BMC Systems Biology</i> , 2007, 1, 54.	3.0	813
176	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
177	Joint mapping of genes and conditions via multidimensional unfolding analysis. <i>BMC Bioinformatics</i> , 2007, 8, 181.	1.2	10
178	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
179	Portraits of breast cancer progression. <i>BMC Bioinformatics</i> , 2007, 8, 291.	1.2	32
180	EDISA: extracting biclusters from multiple time-series of gene expression profiles. <i>BMC Bioinformatics</i> , 2007, 8, 334.	1.2	52

#	ARTICLE	IF	CITATIONS
181	Linking microarray reporters with protein functions. <i>BMC Bioinformatics</i> , 2007, 8, 360.	1.2	12
182	Improved human disease candidate gene prioritization using mouse phenotype. <i>BMC Bioinformatics</i> , 2007, 8, 392.	1.2	232
183	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
184	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
185	Including probe-level uncertainty in model-based gene expression clustering. <i>BMC Bioinformatics</i> , 2007, 8, 98.	1.2	16
186	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
187	EasyGO: Gene Ontology-based annotation and functional enrichment analysis tool for agronomical species. <i>BMC Genomics</i> , 2007, 8, 246.	1.2	137
188	Genomic expression during human myelopoiesis. <i>BMC Genomics</i> , 2007, 8, 264.	1.2	31
189	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
190	Characterization of oligopeptide patterns in large protein sets. <i>BMC Genomics</i> , 2007, 8, 346.	1.2	11
191	Proteomics reveals multiple routes to the osteogenic phenotype in mesenchymal stem cells. <i>BMC Genomics</i> , 2007, 8, 380.	1.2	24
192	BMDEExpress: a software tool for the benchmark dose analyses of genomic data. <i>BMC Genomics</i> , 2007, 8, 387.	1.2	171
193	Computational selection and prioritization of candidate genes for Fetal Alcohol Syndrome. <i>BMC Genomics</i> , 2007, 8, 389.	1.2	36
194	Large-scale analysis by SAGE reveals new mechanisms of v-erbA oncogene action. <i>BMC Genomics</i> , 2007, 8, 390.	1.2	15
195	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
196	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
197	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
198	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

#	ARTICLE	IF	CITATIONS
199	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
200	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
201	The <i>C. elegans</i> TGF- β Dauer Pathway Regulates Longevity via Insulin Signaling. <i>Current Biology</i> , 2007, 17, 1635-1645.	1.8	242
202	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
203	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
204	Time course investigation of PPAR α - 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
205	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
206	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
207	Lung response to <i>Bordetella pertussis</i> infection in mice identified by gene-expression profiling. <i>Immunogenetics</i> , 2007, 59, 555-564.	1.2	19
208	Weighted gene coexpression network analysis strategies applied to mouse weight. <i>Mammalian Genome</i> , 2007, 18, 463-472.	1.0	337
209	Analysis of breast cancer progression using principal component analysis and clustering. <i>Journal of Biosciences</i> , 2007, 32, 1027-1039.	0.5	39
210	Sexually dimorphic gene expression in the heart of mice and men. <i>Journal of Molecular Medicine</i> , 2008, 86, 61-74.	1.7	135
211	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
212	¹⁸ O Labeling for a Quantitative Proteomic Analysis of Glycoproteins in Hepatocellular Carcinoma. <i>Clinical Proteomics</i> , 2008, 4, 137-155.	1.1	18
213	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
214	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
215	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
216	Association between PPAR α C1A polymorphisms and the occurrence of nonalcoholic fatty liver disease (NAFLD). <i>BMC Gastroenterology</i> , 2008, 8, 27.	0.8	59

#	ARTICLE	IF	CITATIONS
217	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
218	Putative psychosis genes in the prefrontal cortex: combined analysis of gene expression microarrays. <i>BMC Psychiatry</i> , 2008, 8, 87.	1.1	48
219	'Systems toxicology' approach identifies coordinated metabolic responses to copper in a terrestrial non-model invertebrate, the earthworm <i>Lumbricus rubellus</i> . <i>BMC Biology</i> , 2008, 6, 25.	1.7	168
220	Transcriptomic signature of Bexarotene (Rexinoid LGD1069) on mammary gland from three transgenic mouse mammary cancer models. <i>BMC Medical Genomics</i> , 2008, 1, 40.	0.7	12
221	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
222	Monocytes of patients with familial hypercholesterolemia show alterations in cholesterol metabolism. <i>BMC Medical Genomics</i> , 2008, 1, 60.	0.7	52
223	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
224	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
225	Exploration of the normal human bronchoalveolar lavage fluid proteome. <i>Proteomics - Clinical Applications</i> , 2008, 2, 585-595.	0.8	51
226	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
227	Two-dimensional strong cation exchange/porous layer open tubular/mass spectrometry for ultratrace proteomic analysis using a 10 μ m id poly(styrene- <i>co</i> -divinylbenzene) porous layer open tubular column with an online triphasic trapping column. <i>Electrophoresis</i> , 2008, 29, 1604-1611.	1.3	40
228	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
229	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
230	Differential placental gene expression in preeclampsia. <i>American Journal of Obstetrics and Gynecology</i> , 2008, 199, 566.e1-566.e11.	0.7	131
231	The fibromatosis signature defines a robust stromal response in breast carcinoma. <i>Laboratory Investigation</i> , 2008, 88, 591-601.	1.7	100
232	The MYCN oncogene is a direct target of miR-34a. <i>Oncogene</i> , 2008, 27, 5204-5213.	2.6	273
233	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
234	Haploinsufficiency of <i>RPS14</i> in 5q ⁺ syndrome is associated with deregulation of ribosomal- and translation-related genes. <i>British Journal of Haematology</i> , 2008, 142, 57-64.	1.2	91

#	ARTICLE	IF	CITATIONS
235	Simple integrative preprocessing preserves what is shared in data sources. BMC Bioinformatics, 2008, 9, 111.	1.2	12
236	Merging microarray data from separate breast cancer studies provides a robust prognostic test. BMC Bioinformatics, 2008, 9, 125.	1.2	82
237	Stability of gene contributions and identification of outliers in multivariate analysis of microarray data. BMC Bioinformatics, 2008, 9, 289.	1.2	15
238	Literature-aided meta-analysis of microarray data: a compendium study on muscle development and disease. BMC Bioinformatics, 2008, 9, 291.	1.2	21
239	Combining Shapley value and statistics to the analysis of gene expression data in children exposed to air pollution. BMC Bioinformatics, 2008, 9, 361.	1.2	29
240	SQUAT: A web tool to mine human, murine and avian SAGE data. BMC Bioinformatics, 2008, 9, 378.	1.2	7
241	Presenting and exploring biological pathways with PathVisio. BMC Bioinformatics, 2008, 9, 399.	1.2	305
242	Meta-analysis of breast cancer microarray studies in conjunction with conserved cis-elements suggest patterns for coordinate regulation. BMC Bioinformatics, 2008, 9, 63.	1.2	41
243	Improving the power for detecting overlapping genes from multiple DNA microarray-derived gene lists. BMC Bioinformatics, 2008, 9, S14.	1.2	14
244	From microarray to biology: an integrated experimental, statistical and in silico analysis of how the extracellular matrix modulates the phenotype of cancer cells. BMC Bioinformatics, 2008, 9, S4.	1.2	15
245	Coordinated evolution of co-expressed gene clusters in the Drosophila transcriptome. BMC Evolutionary Biology, 2008, 8, 2.	3.2	30
246	MADIBA: A web server toolkit for biological interpretation of Plasmodium and plant gene clusters. BMC Genomics, 2008, 9, 105.	1.2	21
247	Transcriptome analysis identifies pathways associated with enhanced maternal performance in QSi5 mice. BMC Genomics, 2008, 9, 197.	1.2	18
248	In vivo gene expression profiling of human intestinal epithelial cells: analysis by laser microdissection of formalin fixed tissues. BMC Genomics, 2008, 9, 209.	1.2	45
249	Genomic analysis of post-mating changes in the honey bee queen (<i>Apis mellifera</i>). BMC Genomics, 2008, 9, 232.	1.2	116
250	Transcriptome profiling of developmental and xenobiotic responses in a keystone soil animal, the oligochaete annelid <i>Lumbricus rubellus</i> . BMC Genomics, 2008, 9, 266.	1.2	93
251	Functional characterization of endogenous siRNA target genes in <i>Caenorhabditis elegans</i> . BMC Genomics, 2008, 9, 270.	1.2	19
252	Sources of variation in baseline gene expression levels from toxicogenomics study control animals across multiple laboratories. BMC Genomics, 2008, 9, 285.	1.2	76

#	ARTICLE	IF	CITATIONS
253	Meta-analysis of nasopharyngeal carcinoma microarray data explores mechanism of EBV-regulated neoplastic transformation. <i>BMC Genomics</i> , 2008, 9, 322.	1.2	17
254	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
255	Trait correlated expression combined with expression QTL analysis reveals biological pathways and candidate genes affecting water holding capacity of muscle. <i>BMC Genomics</i> , 2008, 9, 367.	1.2	80
256	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
257	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
258	Transcriptional response of Mexican axolotls to <i>Ambystoma tigrinum</i> virus (ATV) infection. <i>BMC Genomics</i> , 2008, 9, 493.	1.2	40
259	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
260	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
261	Characterization of a newly developed chicken 44K Agilent microarray. <i>BMC Genomics</i> , 2008, 9, 60.	1.2	68
262	Activation of counter-regulatory mechanisms in a rat renal acute rejection model. <i>BMC Genomics</i> , 2008, 9, 71.	1.2	24
263	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
264	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
265	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
266	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
267	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
268	Differential gene expression associated with postnatal equine articular cartilage maturation. <i>BMC Musculoskeletal Disorders</i> , 2008, 9, 149.	0.8	38
269	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
270	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

#	ARTICLE	IF	CITATIONS
271	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
272	Temporal Profiling of the Chromatin Proteome Reveals System-wide Responses to Replication Inhibition. <i>Current Biology</i> , 2008, 18, 838-843.	1.8	36
273	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
274	Diabetic neuropathy: Mechanisms to management. , 2008, 120, 1-34.		588
275	Transcriptional dysregulation in a transgenic model of Parkinson disease. <i>Neurobiology of Disease</i> , 2008, 29, 515-528.	2.1	62
276	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
277	WGCNA: an R package for weighted correlation network analysis. <i>BMC Bioinformatics</i> , 2008, 9, 559.	1.2	17,294
278	Comprehensive analysis of the mouse renal cortex using two-dimensional HPLC tandem mass spectrometry. <i>Proteome Science</i> , 2008, 6, 15.	0.7	21
279	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
280	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
281	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
282	In silico regulatory analysis for exploring human disease progression. <i>Biology Direct</i> , 2008, 3, 24.	1.9	6
283	Genome-wide transcriptional response of primary alveolar macrophages following infection with porcine reproductive and respiratory syndrome virus. <i>Journal of General Virology</i> , 2008, 89, 2550-2564.	1.3	100
284	Network-based global inference of human disease genes. <i>Molecular Systems Biology</i> , 2008, 4, 189.	3.2	583
285	Genes responsive to both oxidant stress and loss of estrogen receptor function identify a poor prognosis group of estrogen receptor positive primary breast cancers. <i>Breast Cancer Research</i> , 2008, 10, R61.	2.2	40
286	Boolean implication networks derived from large scale, whole genome microarray datasets. <i>Genome Biology</i> , 2008, 9, R157.	13.9	108
287	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
288	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

#	ARTICLE	IF	CITATIONS
289	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
290	A sequence-based survey of the complex structural organization of tumor genomes. <i>Genome Biology</i> , 2008, 9, R59.	13.9	31
291	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
292	Genomic chart guiding embryonic stem cell cardiopoiesis. <i>Genome Biology</i> , 2008, 9, R6.	13.9	66
293	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
294	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
295	A Role for Mammalian Sin3 in Permanent Gene Silencing. <i>Molecular Cell</i> , 2008, 32, 359-370.	4.5	112
296	The role of mtDNA mutations in the pathogenesis of age-related hearing loss in mice carrying a mutator DNA polymerase β . <i>Neurobiology of Aging</i> , 2008, 29, 1080-1092.	1.5	83
297	Sequential and concerted gene expression changes in a chronic in vitro model of parkinsonism. <i>Neuroscience</i> , 2008, 152, 198-207.	1.1	10
298	Misexpression of MIA disrupts lung morphogenesis and causes neonatal death. <i>Developmental Biology</i> , 2008, 316, 441-455.	0.9	13
299	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
300	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
301	Heterogeneity of Human Macrophages in Culture and in Atherosclerotic Plaques. <i>American Journal of Pathology</i> , 2008, 172, 1112-1126.	1.9	213
302	Cross-Species Comparison of Human and Mouse Intestinal Polyps Reveals Conserved Mechanisms in Adenomatous Polyposis Coli (APC)-Driven Tumorigenesis. <i>American Journal of Pathology</i> , 2008, 172, 1363-1380.	1.9	71
303	Effect of Dietary Calcium and Dairy Proteins on the Adipose Tissue Gene Expression Profile in Diet-Induced Obesity. <i>Journal of Nutrigenetics and Nutrigenomics</i> , 2008, 1, 240-251.	1.8	24
304	Network integration and graph analysis in mammalian molecular systems biology. <i>IET Systems Biology</i> , 2008, 2, 206-221.	0.8	42
305	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. <i>Neoplasia</i> , 2008, 10, 1222-IN26.	2.3	37
306	Age-Dependent Signature of Metallothionein Expression in Primary CD4 T Cell Responses Is Due to Sustained Zinc Signaling. <i>Rejuvenation Research</i> , 2008, 11, 1001-1011.	0.9	39

#	ARTICLE	IF	CITATIONS
307	Gene network dynamics controlling keratinocyte migration. <i>Molecular Systems Biology</i> , 2008, 4, 199.	3.2	52
308	Significance Analysis of Spectral Count Data in Label-free Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2373-2385.	2.5	344
309	E2F in vivo binding specificity: Comparison of consensus versus nonconsensus binding sites. <i>Genome Research</i> , 2008, 18, 1763-1777.	2.4	121
310	Effect of starvation on transcriptomes of brain and liver in adult female zebrafish (<i>Danio</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.0	111
311	Genomic evolution of the placenta using co-option and duplication and divergence. <i>Genome Research</i> , 2008, 18, 695-705.	2.4	108
312	Using ChIP-chip technology to reveal common principles of transcriptional repression in normal and cancer cells. <i>Genome Research</i> , 2008, 18, 521-532.	2.4	44
313	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
314	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
315	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
316	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
317	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
318	Genomic Analysis of <i>Drosophila</i> 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
319	Metabolomic Signatures of Inbreeding at Benign and Stressful Temperatures in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2008, 180, 1233-1243.	1.2	71
320	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
321	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
322	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
323	MassNet: a functional annotation service for protein mass spectrometry data. <i>Nucleic Acids Research</i> , 2008, 36, W491-W495.	6.5	9
324	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

#	ARTICLE	IF	CITATIONS
325	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
326	Defining the regulatory network of the tissue-specific splicing factors Fox-1 and Fox-2. <i>Genes and Development</i> , 2008, 22, 2550-2563.	2.7	264
327	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
328	PPAR β 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
329	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
330	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
331	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
332	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
333	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
334	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
335	Pleiotropic Effects of <i>Drosophila</i> neuralized on Complex Behaviors and Brain Structure. <i>Genetics</i> , 2008, 179, 1327-1336.	1.2	32
336	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
337	Exon-Level Expression Profiling: A Comprehensive Transcriptome Analysis of Oral Fluids. <i>Clinical Chemistry</i> , 2008, 54, 824-832.	1.5	66
338	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
339	Kruppel-like factor 5 is required for perinatal lung morphogenesis and function. <i>Development (Cambridge)</i> , 2008, 135, 2563-2572.	1.2	113
340	Supervised principal component analysis for gene set enrichment of microarray data with continuous or survival outcomes. <i>Bioinformatics</i> , 2008, 24, 2474-2481.	1.8	73
341	An Integrated Approach for the Analysis of Biological Pathways using Mixed Models. <i>PLoS Genetics</i> , 2008, 4, e1000115.	1.5	59
342	Integrating Global Gene Expression Analysis and Genetics. <i>Advances in Genetics</i> , 2008, 60, 571-601.	0.8	48

#	ARTICLE	IF	CITATIONS
343	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
344	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
345	Validating the genomic signature of pediatric septic shock. <i>Physiological Genomics</i> , 2008, 34, 127-134.	1.0	94
346	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
347	The Mediator Subunit MDT-15 Confers Metabolic Adaptation to Ingested Material. <i>PLoS Genetics</i> , 2008, 4, e1000021.	1.5	100
348	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
349	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
350	Effect of destrin mutations on the gene expression profile in vivo. <i>Physiological Genomics</i> , 2008, 34, 9-21.	1.0	32
351	An Evolutionarily Conserved Sexual Signature in the Primate Brain. <i>PLoS Genetics</i> , 2008, 4, e1000100.	1.5	81
352	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
353	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
354	Human neural crest cells display molecular and phenotypic hallmarks of stem cells. <i>Human Molecular Genetics</i> , 2008, 17, 3411-3425.	1.4	87
355	Babelomics: advanced functional profiling of transcriptomics, proteomics and genomics experiments. <i>Nucleic Acids Research</i> , 2008, 36, W341-W346.	6.5	73
356	Ascorbate Peroxidase 1 Plays a Key Role in the Response of <i>Arabidopsis thaliana</i> to Stress Combination. <i>Journal of Biological Chemistry</i> , 2008, 283, 34197-34203.	1.6	357
357	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
358	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
359	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
360	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

#	ARTICLE	IF	CITATIONS
361	MADNet: microarray database network web server. <i>Nucleic Acids Research</i> , 2008, 36, W332-W335.	6.5	8
362	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
363	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
364	Antagonism of microRNA-122 in mice by systemically administered LNA-antimiR 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
365	Early vertebrate whole genome duplications were predated by a period of intense genome rearrangement. <i>Genome Research</i> , 2008, 18, 1582-1591.	2.4	80
366	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
367	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
368	GOEAST: a web-based software toolkit for Gene Ontology enrichment analysis. <i>Nucleic Acids Research</i> , 2008, 36, W358-W363.	6.5	569
369	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
370	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
371	Liver-Specific Hepatocyte Nuclear Factor-4 μ B Deficiency: Greater Impact on Gene Expression in Male than in Female Mouse Liver. <i>Molecular Endocrinology</i> , 2008, 22, 1274-1286.	3.7	87
372	Sex-Specific Early Growth Hormone Response Genes in Rat Liver. <i>Molecular Endocrinology</i> , 2008, 22, 1962-1974.	3.7	69
373	Rosiglitazone Treatment Reduces Diabetic Neuropathy in Streptozotocin-Treated DBA/2J Mice. <i>Endocrinology</i> , 2008, 149, 4928-4937.	1.4	53
374	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
375	Effects of Prenatal Tobacco Exposure on Gene Expression Profiling in Umbilical Cord Tissue. <i>Pediatric Research</i> , 2008, 64, 147-153.	1.1	11
376	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
377	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
378	SH2B1 β (SH2-B β) Enhances Expression of a Subset of Nerve Growth Factor-Regulated Genes Important for Neuronal Differentiation Including Genes Encoding Urokinase Plasminogen Activator Receptor and Matrix Metalloproteinase 3/10. <i>Molecular Endocrinology</i> , 2008, 22, 454-476.	3.7	33

#	ARTICLE	IF	CITATIONS
379	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
380	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
381	CD4 ⁺ 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
382	Genome-wide profiling of PPAR α :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
383	The MHC class I peptide repertoire is molded by the transcriptome. <i>Journal of Experimental Medicine</i> , 2008, 205, 595-610.	4.2	174
384	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
385	Microarray Analysis of Distinct Gene Transcription Profiles in Non-eosinophilic Chronic Sinusitis with Nasal Polyps. <i>American Journal of Rhinology & Allergy</i> , 2008, 22, 568-581.	2.3	35
386	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
387	Genetic associations with thalidomide mediated venous thrombotic events in myeloma identified using targeted genotyping. <i>Blood</i> , 2008, 112, 4924-4934.	0.6	65
388	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
389	Topological Properties of Co-Occurrence Networks in Published Gene Expression Signatures. <i>Bioinformatics and Biology Insights</i> , 2008, 2, BBI.S518.	1.0	3
390	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
391	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
392	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
393	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
394	Genome-Wide Analysis of Natural Selection on Human Cis-Elements. <i>PLoS ONE</i> , 2008, 3, e3137.	1.1	24
395	Identification and Analysis of Co-Occurrence Networks with NetCutter. <i>PLoS ONE</i> , 2008, 3, e3178.	1.1	20
396	STOX1 Overexpression in Choriocarcinoma Cells Mimics Transcriptional Alterations Observed in Preeclamptic Placentas. <i>PLoS ONE</i> , 2008, 3, e3905.	1.1	60

#	ARTICLE	IF	CITATIONS
397	Genome-Wide Co-Expression Analysis in Multiple Tissues. PLoS ONE, 2008, 3, e4033.	1.1	21
398	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
399	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
400	Hedgehog signaling regulates epithelial-mesenchymal transition during biliary fibrosis in rodents and humans. Journal of Clinical Investigation, 2008, 118, 3331-42.	3.9	284
401	Î±- and Î³-Tocopherol Prevent Age-Related Transcriptional Alterations in the Heart and Brain of Mice ³ . Journal of Nutrition, 2008, 138, 1010-1018.	1.3	45
402	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
403	Gene Expression Profiling of Lymphoblasts from Autistic and Nonaffected Sib Pairs: Altered Pathways in Neuronal Development and Steroid Biosynthesis. PLoS ONE, 2009, 4, e5775.	1.1	134
404	Modulated Modularity Clustering as an Exploratory Tool for Functional Genomic Inference. PLoS Genetics, 2009, 5, e1000479.	1.5	118
405	Overexpression of Myocilin in the Drosophila Eye Activates the Unfolded Protein Response: Implications for Glaucoma. PLoS ONE, 2009, 4, e4216.	1.1	41
406	Comparison of Proteomic and Transcriptomic Profiles in the Bronchial Airway Epithelium of Current and Never Smokers. PLoS ONE, 2009, 4, e5043.	1.1	66
407	Transcriptome-Wide Prediction of miRNA Targets in Human and Mouse Using FASTH. PLoS ONE, 2009, 4, e5745.	1.1	27
408	Impact of the TCR Signal on Regulatory T Cell Homeostasis, Function, and Trafficking. PLoS ONE, 2009, 4, e6580.	1.1	52
409	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
410	Induction of Epithelial Mesenchymal Transition and Vasculogenesis in the Lenses of Dbl Oncogene Transgenic Mice. PLoS ONE, 2009, 4, e7058.	1.1	3
411	Global Transcriptional Response to Hfe Deficiency and Dietary Iron Overload in Mouse Liver and Duodenum. PLoS ONE, 2009, 4, e7212.	1.1	10
412	Transcriptional Profiling of Rats Subjected to Gestational Undernutrition: Implications for the Developmental Variations in Metabolic Traits. PLoS ONE, 2009, 4, e7271.	1.1	33
413	Effect of DLK1 and RTL1 but Not MEG3 or MEG8 on Muscle Gene Expression in Callipyge Lambs. PLoS ONE, 2009, 4, e7399.	1.1	52
414	Alternative Splicing and Transcriptome Profiling of Experimental Autoimmune Encephalomyelitis Using Genome-Wide Exon Arrays. PLoS ONE, 2009, 4, e7773.	1.1	20

#	ARTICLE	IF	CITATIONS
415	Gender Differences in a <i>Drosophila</i> Transcriptomic Model of Chronic Pentylentetrazole Induced Behavioral Deficit. <i>PLoS ONE</i> , 2009, 4, e8136.	1.1	7
416	Global MYCN Transcription Factor Binding Analysis in Neuroblastoma Reveals Association with Distinct E-Box Motifs and Regions of DNA Hypermethylation. <i>PLoS ONE</i> , 2009, 4, e8154.	1.1	72
417	Immunological Profiles of <i>Bos taurus</i> and <i>Bos indicus</i> Cattle Infested with the Cattle Tick, <i>Rhipicephalus</i> (<i>Boophilus</i>) <i>microplus</i> . <i>Vaccine Journal</i> , 2009, 16, 1074-1086.	3.2	86
418	Earthworm genomes, genes and proteins: the (re)discovery of Darwin's worms. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 789-797.	1.2	38
419	Selenoprotein T deficiency alters cell adhesion and elevates selenoprotein W expression in murine fibroblast cells. <i>Biochemistry and Cell Biology</i> , 2009, 87, 953-961.	0.9	53
420	Genome-wide strategies for discovering genetic influences on cognition and cognitive disorders: Methodological considerations. <i>Cognitive Neuropsychiatry</i> , 2009, 14, 391-418.	0.7	93
421	From disease ontology to disease-ontology lite: statistical methods to adapt a general-purpose ontology for the test of gene-ontology associations. <i>Bioinformatics</i> , 2009, 25, i63-i68.	1.8	99
422	Co-inhibition of <i>Plasmodium falciparum</i> S-Adenosylmethionine Decarboxylase/Ornithine Decarboxylase Reveals Perturbation-specific Compensatory Mechanisms by Transcriptome, Proteome, and Metabolome Analyses. <i>Journal of Biological Chemistry</i> , 2009, 284, 4635-4646.	1.6	73
423	Characterization of a Naturally Occurring Breast Cancer Subset Enriched in Epithelial-to-Mesenchymal Transition and Stem Cell Characteristics. <i>Cancer Research</i> , 2009, 69, 4116-4124.	0.4	768
424	Dysregulated gene expression networks in human acute myelogenous leukemia stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3396-3401.	3.3	253
425	DNA methylation is widespread and associated with differential gene expression in castes of the honeybee, <i>Apis mellifera</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11206-11211.	3.3	303
426	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
427	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
428	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
429	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
430	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
431	Immune dysregulation in severe influenza. <i>Journal of Leukocyte Biology</i> , 2009, 85, 1036-1043.	1.5	106
432	Testing significance relative to a fold-change threshold is a TREAT. <i>Bioinformatics</i> , 2009, 25, 765-771.	1.8	570

#	ARTICLE	IF	CITATIONS
433	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
434	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
435	The deacetylase HDAC4 controls myocyte enhancing factor α -dependent structural gene expression in response to neural activity. <i>FASEB Journal</i> , 2009, 23, 99-106.	0.2	75
436	Overexpressed vs mutated Kras in murine fibroblasts: a molecular phenotyping study. <i>British Journal of Cancer</i> , 2009, 100, 656-662.	2.9	28
437	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
438	COFECO: composite function annotation enriched by protein complex data. <i>Nucleic Acids Research</i> , 2009, 37, W350-W355.	6.5	19
439	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
440	Coexpression network based on natural variation in human gene expression reveals gene interactions and functions. <i>Genome Research</i> , 2009, 19, 1953-1962.	2.4	112
441	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
442	Blocking the Metabolism of Starch Breakdown Products in Arabidopsis Leaves Triggers Chloroplast Degradation. <i>Molecular Plant</i> , 2009, 2, 1233-1246.	3.9	127
443	Thymic OX40 Expression Discriminates Cells Undergoing Strong Responses to Selection Ligands. <i>Journal of Immunology</i> , 2009, 182, 4581-4589.	0.4	60
444	Mouse models of human AML accurately predict chemotherapy response. <i>Genes and Development</i> , 2009, 23, 877-889.	2.7	235
445	The presence of RNA polymerase II, active or stalled, predicts epigenetic fate of promoter CpG islands. <i>Genome Research</i> , 2009, 19, 1974-1982.	2.4	121
446	Global Gene Expression in the Human Fetal Testis and Ovary1. <i>Biology of Reproduction</i> , 2009, 81, 438-443.	1.2	100
447	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
448	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
449	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
450	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

#	ARTICLE	IF	CITATIONS
451	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
452	Genome-wide Association of Hypoxia-inducible Factor (HIF)-1 β and HIF-2 β DNA Binding with Expression Profiling of Hypoxia-inducible Transcripts. <i>Journal of Biological Chemistry</i> , 2009, 284, 16767-16775.	1.6	516
453	The organization of the transcriptional network in specific neuronal classes. <i>Molecular Systems Biology</i> , 2009, 5, 291.	3.2	114
454	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
455	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
456	Enrichment constrained time-dependent clustering analysis for finding meaningful temporal transcription modules. <i>Bioinformatics</i> , 2009, 25, 1521-1527.	1.8	18
457	Time-Warped Comparison of Gene Expression in Adaptive and Maladaptive Cardiac Hypertrophy. <i>Circulation: Cardiovascular Genetics</i> , 2009, 2, 116-124.	5.1	28
458	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
459	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
460	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
461	Transcriptional Regulation of Metabolism Associated With the Increased Desiccation Resistance of the Cactophilic <i>Drosophila mojavensis</i> . <i>Genetics</i> , 2009, 182, 1279-1288.	1.2	38
462	Alcohol Sensitivity in <i>Drosophila</i> : Translational Potential of Systems Genetics. <i>Genetics</i> , 2009, 183, 733-745.	1.2	45
463	Gene Profiling of Human Adipose Tissue During Evoked Inflammation In Vivo. <i>Diabetes</i> , 2009, 58, 2211-2219.	0.3	57
464	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
465	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
466	Modulated expression of WFDC1 during carcinogenesis and cellular senescence. <i>Carcinogenesis</i> , 2009, 30, 20-27.	1.3	76
467	Comparative prion disease gene expression profiling using the prion disease mimetic, cuprizone. <i>Prion</i> , 2009, 3, 99-109.	0.9	17
468	The epithelial splicing factors ESRP1 and ESRP2 positively and negatively regulate diverse types of alternative splicing events. <i>RNA Biology</i> , 2009, 6, 546-562.	1.5	201

#	ARTICLE	IF	CITATIONS
469	<i>Rac1</i> Is a Critical Mediator of Endothelium-Derived Neurotrophic Activity. <i>Science Signaling</i> , 2009, 2, ra10.	1.6	26
470	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
471	The Constitutive Active/Androstane Receptor Facilitates Unique Phenobarbital-Induced Expression Changes of Genes Involved in Key Pathways in Precancerous Liver and Liver Tumors. <i>Toxicological Sciences</i> , 2009, 110, 319-333.	1.4	28
472	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
473	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
474	DNA Replication Licensing and Progenitor Numbers Are Increased by Progesterone in Normal Human Breast. <i>Endocrinology</i> , 2009, 150, 3318-3326.	1.4	122
475	The Role of miR-206 in the Epidermal Growth Factor (EGF) Induced Repression of Estrogen Receptor- β (ER β) Signaling and a Luminal Phenotype in MCF-7 Breast Cancer Cells. <i>Molecular Endocrinology</i> , 2009, 23, 1215-1230.	3.7	98
476	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
477	Influence of fatty acid diets on gene expression in rat mammary epithelial cells. <i>Physiological Genomics</i> , 2009, 38, 80-88.	1.0	15
478	Influence of hyperthyroid conditions on gene expression in extraocular muscles of rats. <i>Physiological Genomics</i> , 2009, 37, 231-238.	1.0	6
479	<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
480	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
481	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
482	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
483	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
484	Elucidating the Role of Gonadal Hormones in Sexually Dimorphic Gene Coexpression Networks. <i>Endocrinology</i> , 2009, 150, 1235-1249.	1.4	224
485	Estrogen Receptor β Is Required for Optimal cAMP Production in Mouse Granulosa Cells. <i>Molecular Endocrinology</i> , 2009, 23, 955-965.	3.7	48
486	Retinoblastoma Protein Plays Multiple Essential Roles in the Terminal Differentiation of Sertoli Cells. <i>Molecular Endocrinology</i> , 2009, 23, 1900-1913.	3.7	39

#	ARTICLE	IF	CITATIONS
487	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
488	Genome-Wide Innate Immune Responses in HIV-1-Infected Macrophages Are Preserved Despite Attenuation of the NF- κ B Activation Pathway. <i>Journal of Immunology</i> , 2009, 182, 319-328.	0.4	28
489	Perturbation of Defense Pathways by Low-Dose Arsenic Exposure in Zebrafish Embryos. <i>Environmental Health Perspectives</i> , 2009, 117, 981-987.	2.8	49
490	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
491	Discovery and Annotation of Functional Chromatin Signatures in the Human Genome. <i>PLoS Computational Biology</i> , 2009, 5, e1000566.	1.5	143
492	Host Cell Factors in HIV Replication: Meta-Analysis of Genome-Wide Studies. <i>PLoS Pathogens</i> , 2009, 5, e1000437.	2.1	396
493	Conserved Expression Patterns Predict microRNA Targets. <i>PLoS Computational Biology</i> , 2009, 5, e1000513.	1.5	49
494	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
495	An Abundance of Ubiquitously Expressed Genes Revealed by Tissue Transcriptome Sequence Data. <i>PLoS Computational Biology</i> , 2009, 5, e1000598.	1.5	777
496	Expression Quantitative Trait Loci Are Highly Sensitive to Cellular Differentiation State. <i>PLoS Genetics</i> , 2009, 5, e1000692.	1.5	85
497	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
498	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
499	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
500	Diffuse-Type Gastric Carcinoma: Progression, Angiogenesis, and Transforming Growth Factor β Signaling. <i>Journal of the National Cancer Institute</i> , 2009, 101, 592-604.	3.0	66
501	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
502	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
503	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
504	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

#	ARTICLE	IF	CITATIONS
505	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
506	LRpath: a logistic regression approach for identifying enriched biological groups in gene expression data. <i>Bioinformatics</i> , 2009, 25, 211-217.	1.8	163
507	SimCT: a generic tool to visualize ontology-based relationships for biological objects. <i>Bioinformatics</i> , 2009, 25, 3197-3198.	1.8	11
508	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
509	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
510	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
511	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
512	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
513	Aging Mice Show a Decreasing Correlation of Gene Expression within Genetic Modules. <i>PLoS Genetics</i> , 2009, 5, e1000776.	1.5	157
514	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
515	Widespread cleavage of A-to-I hyperediting substrates. <i>Rna</i> , 2009, 15, 1632-1639.	1.6	41
516	Large-scale analysis of DNA methylation in chronic lymphocytic leukemia. <i>Epigenomics</i> , 2009, 1, 39-61.	1.0	57
517	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
518	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
519	Effect of Leptin on Mouse Trophoblast Giant Cells1. <i>Biology of Reproduction</i> , 2009, 80, 415-424.	1.2	23
520	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
521	The Macrophage Colony-Stimulating Factor 1 Response Signature in Breast Carcinoma. <i>Clinical Cancer Research</i> , 2009, 15, 778-787.	3.2	177
522	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

#	ARTICLE	IF	CITATIONS
523	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
524	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
525	MMP-9 Sheds the β 2 Integrin Subunit (CD18) from Macrophages. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1044-1060.	2.5	76
526	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
527	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
528	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
529	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
530	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
531	Age-related gene expression in Tourette syndrome. <i>Journal of Psychiatric Research</i> , 2009, 43, 319-330.	1.5	25
532	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
533	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
534	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
535	A joint finite mixture model for clustering genes from independent Gaussian and beta distributed data. <i>BMC Bioinformatics</i> , 2009, 10, 165.	1.2	11
536	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
537	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
538	Genephony: a knowledge management tool for genome-wide research. <i>BMC Bioinformatics</i> , 2009, 10, 278.	1.2	8
539	ArraylDer: automated structural re-annotation pipeline for DNA microarrays. <i>BMC Bioinformatics</i> , 2009, 10, 30.	1.2	11
540	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

#	ARTICLE	IF	CITATIONS
541	ArrayMining: a modular web-application for microarray analysis combining ensemble and consensus methods with cross-study normalization. BMC Bioinformatics, 2009, 10, 358.	1.2	85
542	Illumina WG-6 BeadChip strips should be normalized separately. BMC Bioinformatics, 2009, 10, 372.	1.2	19
543	GORilla: a tool for discovery and visualization of enriched GO terms in ranked gene lists. BMC Bioinformatics, 2009, 10, 48.	1.2	3,032
544	ContDist: a tool for the analysis of quantitative gene and promoter properties. BMC Bioinformatics, 2009, 10, 7.	1.2	8
545	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. BMC Bioinformatics, 2009, 10, S11.	1.2	33
546	Comparing gene annotation enrichment tools for functional modeling of agricultural microarray data. BMC Bioinformatics, 2009, 10, S9.	1.2	21
547	Human microRNA target analysis and gene ontology clustering by GOMir, a novel stand-alone application. BMC Bioinformatics, 2009, 10, S20.	1.2	34
548	Natural genetic variation in transcriptome reflects network structure inferred with major effect mutations: insulin/TOR and associated phenotypes in <i>Drosophila melanogaster</i> . BMC Genomics, 2009, 10, 124.	1.2	19
549	Transcription and splicing regulation in human umbilical vein endothelial cells under hypoxic stress conditions by exon array. BMC Genomics, 2009, 10, 126.	1.2	47
550	Reconstruction and functional analysis of altered molecular pathways in human atherosclerotic arteries. BMC Genomics, 2009, 10, 13.	1.2	80
551	Functional annotation of the human retinal pigment epithelium transcriptome. BMC Genomics, 2009, 10, 164.	1.2	52
552	Distinct patterns of gene and protein expression elicited by organophosphorus pesticides in <i>Caenorhabditis elegans</i> . BMC Genomics, 2009, 10, 202.	1.2	40
553	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
554	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
555	Discernment of possible mechanisms of hepatotoxicity via biological processes over-represented by co-expressed genes. BMC Genomics, 2009, 10, 272.	1.2	9
556	Impact of animal strain on gene expression in a rat model of acute cardiac rejection. BMC Genomics, 2009, 10, 280.	1.2	3
557	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
558	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

#	ARTICLE	IF	CITATIONS
559	Signed weighted gene co-expression network analysis of transcriptional regulation in murine embryonic stem cells. BMC Genomics, 2009, 10, 327.	1.2	209
560	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
561	The steady-state transcriptome of the four major life-cycle stages of Trypanosoma cruzi. BMC Genomics, 2009, 10, 370.	1.2	125
562	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
563	Weighted gene co-expression network analysis of the peripheral blood from Amyotrophic Lateral Sclerosis patients. BMC Genomics, 2009, 10, 405.	1.2	156
564	Expulsion of Trichuris muris 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
565	Transcriptome analysis of differentiating trypanosomes reveals the existence of multiple post-transcriptional regulons. BMC Genomics, 2009, 10, 495.	1.2	127
566	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
567	RNA profiles of rat olfactory epithelia: individual and age related variations. BMC Genomics, 2009, 10, 572.	1.2	25
568	Deciphering the transcriptional circuitry of microRNA genes expressed during human monocytic differentiation. BMC Genomics, 2009, 10, 595.	1.2	65
569	Increased epithelial stem cell traits in advanced endometrial endometrioid carcinoma. BMC Genomics, 2009, 10, 613.	1.2	18
570	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
571	Understanding Haemophilus parasuis infection in porcine spleen through a transcriptomics approach. BMC Genomics, 2009, 10, 64.	1.2	59
572	Identification of genes differentially expressed as result of adenovirus type 5- and adenovirus type 12-transformation. BMC Genomics, 2009, 10, 67.	1.2	6
573	Somatic, germline and sex hierarchy regulated gene expression during Drosophila metamorphosis. BMC Genomics, 2009, 10, 80.	1.2	49
574	Rapid evolution of mammalian X-linked testis microRNAs. BMC Genomics, 2009, 10, 97.	1.2	98
575	Annotating the human genome with Disease Ontology. BMC Genomics, 2009, 10, S6.	1.2	204
576	A Candida albicans early stage biofilm detachment event in rich medium. BMC Microbiology, 2009, 9, 25.	1.3	43

#	ARTICLE	IF	CITATIONS
577	Integrating microRNA and mRNA expression profiles of neuronal progenitors to identify regulatory networks underlying the onset of cortical neurogenesis. <i>BMC Neuroscience</i> , 2009, 10, 98.	0.8	65
578	DDEC: Dragon database of genes implicated in esophageal cancer. <i>BMC Cancer</i> , 2009, 9, 219.	1.1	24
579	Gene expression down-regulation in CD90+prostate tumor-associated stromal cells involves potential organ-specific genes. <i>BMC Cancer</i> , 2009, 9, 317.	1.1	39
580	Identification of pediatric septic shock subclasses based on genome-wide expression profiling. <i>BMC Medicine</i> , 2009, 7, 34.	2.3	216
581	A <i>Drosophila</i> systems model of pentylenetetrazole induced locomotor plasticity responsive to antiepileptic drugs. <i>BMC Systems Biology</i> , 2009, 3, 11.	3.0	25
582	A pro-inflammatory signature mediates FGF2-induced angiogenesis. <i>Journal of Cellular and Molecular Medicine</i> , 2009, 13, 2083-2108.	1.6	66
583	A Gene Expression Signature Associated with K-Ras Addiction Reveals Regulators of EMT and Tumor Cell Survival. <i>Cancer Cell</i> , 2009, 15, 489-500.	7.7	735
584	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
585	Age-related decrease in proteasome expression contributes to defective nuclear factor- κ B activation during hepatic ischemia/reperfusion. <i>Hepatology</i> , 2009, 49, 1718-1728.	3.6	38
586	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
587	Housekeeping genes in prostate tumorigenesis. <i>International Journal of Cancer</i> , 2009, 125, 2603-2608.	2.3	14
588	Cellular expression of <i>Midkine</i> and <i>Midkine</i> during retinal development and photoreceptor regeneration in zebrafish. <i>Journal of Comparative Neurology</i> , 2009, 514, 1-10.	0.9	42
589	Analysis of Rex1 (<i>zfp42</i>) function in embryonic stem cell differentiation. <i>Developmental Dynamics</i> , 2009, 238, 1863-1877.	0.8	61
590	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
591	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
592	Retinoid-responsive transcriptional changes in epidermal keratinocytes. <i>Journal of Cellular Physiology</i> , 2009, 220, 427-439.	2.0	96
593	Genomic landscape of developing male germ cells. <i>Birth Defects Research Part C: Embryo Today Reviews</i> , 2009, 87, 43-63.	3.6	40
594	Detection of low-abundant novel transcripts in mouse hematopoietic stem cells. <i>Molecular Genetics and Genomics</i> , 2009, 282, 363-370.	1.0	0

#	ARTICLE	IF	CITATIONS
595	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
596	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
597	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
598	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
599	Meiotic behavior of aneuploid chromatin in mouse models of Down syndrome. <i>Chromosoma</i> , 2009, 118, 723-736.	1.0	20
600	Spatial Mapping of Thymic Stromal Microenvironments Reveals Unique Features Influencing T Lymphoid Differentiation. <i>Immunity</i> , 2009, 31, 999-1009.	6.6	76
601	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
602	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
603	Gene expression microarray analysis of early oxygen-induced retinopathy in the rat. <i>Journal of Ocular Biology, Diseases, and Informatics</i> , 2009, 2, 190-201.	0.2	23
604	Identification of human sperm transcripts as candidate markers of male fertility. <i>Journal of Molecular Medicine</i> , 2009, 87, 735-748.	1.7	76
605	Genome-wide analysis and proteomic studies reveal APE1/Ref1 multifunctional role in mammalian cells. <i>Proteomics</i> , 2009, 9, 1058-1074.	1.3	90
606	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
607	Proteins that underlie neoplastic progression of ulcerative colitis. <i>Proteomics - Clinical Applications</i> , 2009, 3, 1326-1337.	0.8	47
608	Unique patterns of molecular profiling between human prostate cancer LNCaP and PC3 cells. <i>Prostate</i> , 2009, 69, 1077-1090.	1.2	82
609	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
610	Global transcriptional response after exposure of fission yeast cells to ultraviolet light. <i>BMC Cell Biology</i> , 2009, 10, 87.	3.0	5
611	Gene expression profiling of human alveolar macrophages infected by B. anthracis spores demonstrates TNF- α and NF- κ B are key components of the innate immune response to the pathogen. <i>BMC Infectious Diseases</i> , 2009, 9, 152.	1.3	27
612	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

#	ARTICLE	IF	CITATIONS
613	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
614	Microarray and cDNA sequence analysis of transcription during nerve-dependent limb regeneration. <i>BMC Biology</i> , 2009, 7, 1.	1.7	203
615	Mutations in many genes affect aggressive behavior in <i>Drosophila melanogaster</i> . <i>BMC Biology</i> , 2009, 7, 29.	1.7	85
616	Effect of hydroxyurea on the promoter occupancy profiles of tumor suppressor p53 and p73. <i>BMC Biology</i> , 2009, 7, 35.	1.7	2
617	Environmentally-acquired bacteria influence microbial diversity and natural innate immune responses at gut surfaces. <i>BMC Biology</i> , 2009, 7, 79.	1.7	228
618	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
619	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
620	Identification of gene co-regulatory modules and associated cis-elements involved in degenerative heart disease. <i>BMC Medical Genomics</i> , 2009, 2, 31.	0.7	7
621	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
622	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
623	Transcriptional profiling differences for articular cartilage and repair tissue in equine joint surface lesions. <i>BMC Medical Genomics</i> , 2009, 2, 60.	0.7	33
624	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
625	A taxonomy of epithelial human cancer and their metastases. <i>BMC Medical Genomics</i> , 2009, 2, 69.	0.7	19
626	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
627	Autism genome-wide copy number variation reveals ubiquitin and neuronal genes. <i>Nature</i> , 2009, 459, 569-573.	13.7	1,270
628	Targeted bisulfite sequencing reveals changes in DNA methylation associated with nuclear reprogramming. <i>Nature Biotechnology</i> , 2009, 27, 353-360.	9.4	458
629	The proteomic analysis of human neonatal umbilical cord serum by mass spectrometry. <i>Acta Pharmacologica Sinica</i> , 2009, 30, 1550-1558.	2.8	17
630	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

#	ARTICLE	IF	CITATIONS
631	Co-regulated transcriptional networks contribute to natural genetic variation in <i>Drosophila</i> sleep. <i>Nature Genetics</i> , 2009, 41, 371-375.	9.4	91
632	Systems genetics of complex traits in <i>Drosophila melanogaster</i> . <i>Nature Genetics</i> , 2009, 41, 299-307.	9.4	490
633	Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. <i>Nature Protocols</i> , 2009, 4, 44-57.	5.5	31,831
634	Network visualization and analysis of gene expression data using BioLayout Express3D. <i>Nature Protocols</i> , 2009, 4, 1535-1550.	5.5	443
635	Detecting shared pathogenesis from the shared genetics of immune-related diseases. <i>Nature Reviews Genetics</i> , 2009, 10, 43-55.	7.7	475
636	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
637	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
638	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
639	The role of <i>lfn3</i> in alterations in liver gene expression in a mouse model of fulminant autoimmune hepatitis. <i>Liver International</i> , 2009, 29, 1307-1315.	1.9	13
640	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
641	Conditionally 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
642	<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
643	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
644	Meta-analysis of age-related gene expression profiles identifies common signatures of aging. <i>Bioinformatics</i> , 2009, 25, 875-881.	1.8	651
645	Evaluation of 3 Clinical Dendritic Cell Maturation Protocols Containing Lipopolysaccharide and Interferon- β . <i>Journal of Immunotherapy</i> , 2009, 32, 399-407.	1.2	58
646	Identification of Astrocyte Secreted Proteins with a Combination of Shotgun Proteomics and Bioinformatics. <i>Journal of Proteome Research</i> , 2009, 8, 4135-4143.	1.8	96
647	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
648	Genetic Control of Human Brain Transcript Expression in Alzheimer Disease. <i>American Journal of Human Genetics</i> , 2009, 84, 445-458.	2.6	290

#	ARTICLE	IF	CITATIONS
649	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
650	Next-generation tag sequencing for cancer gene expression profiling. <i>Genome Research</i> , 2009, 19, 1825-1835.	2.4	306
651	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
652	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
653	Establishment of Intestinal Identity and Epithelial-Mesenchymal Signaling by Cdx2. <i>Developmental Cell</i> , 2009, 16, 588-599.	3.1	332
654	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
655	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
656	A Genome-wide RNAi Screen for Modifiers of the Circadian Clock in Human Cells. <i>Cell</i> , 2009, 139, 199-210.	13.5	437
657	Induction of Intestinal Th17 Cells by Segmented Filamentous Bacteria. <i>Cell</i> , 2009, 139, 485-498.	13.5	3,818
658	Jumonji Modulates Polycomb Activity and Self-Renewal versus Differentiation of Stem Cells. <i>Cell</i> , 2009, 139, 1303-1314.	13.5	398
659	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
660	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
661	Tissue specific differentially methylated regions (TDMR): Changes in DNA methylation during development. <i>Genomics</i> , 2009, 93, 130-139.	1.3	116
662	Candidate Agtr2 influenced genes and pathways identified by expression profiling in the developing brain of Agtr2 ^{fl/y} mice. <i>Genomics</i> , 2009, 94, 188-195.	1.3	14
663	Technical considerations in using DNA microarrays to define regulons. <i>Methods</i> , 2009, 47, 63-72.	1.9	12
664	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
665	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
666	Identification of neuronal target genes for CCAAT/Enhancer Binding Proteins. <i>Molecular and Cellular Neurosciences</i> , 2009, 40, 313-327.	1.0	40

#	ARTICLE	IF	CITATIONS
667	Primary biliary cirrhosis is associated with altered hepatic microRNA expression. <i>Journal of Autoimmunity</i> , 2009, 32, 246-253.	3.0	191
668	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
669	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
670	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
671	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
672	Transcriptome Profiling Reveals TGF- β Signaling Involvement in Epileptogenesis. <i>Journal of Neuroscience</i> , 2009, 29, 8927-8935.	1.7	317
673	Differential Testicular Gene Expression in Seasonal Fertility. <i>Journal of Biological Rhythms</i> , 2009, 24, 114-125.	1.4	10
674	Chromatin Immunoprecipitation on Microarray Analysis of Smad2/3 Binding Sites Reveals Roles of ETS1 and TFAP2A in Transforming Growth Factor β Signaling. <i>Molecular and Cellular Biology</i> , 2009, 29, 172-186.	1.1	179
675	Downregulation of oligodendrocyte transcripts is associated with impaired prefrontal cortex function in rats. <i>Schizophrenia Research</i> , 2009, 113, 277-287.	1.1	54
676	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
677	Disruption of Dicer1 Induces Dysregulated Fetal Gene Expression and Promotes Hepatocarcinogenesis. <i>Gastroenterology</i> , 2009, 136, 2304-2315.e4.	0.6	167
678	Expression profiling identifies genes involved in emphysema severity. <i>Respiratory Research</i> , 2009, 10, 81.	1.4	35
679	Comprehensive proteomic analysis of human cervical-vaginal fluid using colposcopy samples. <i>Proteome Science</i> , 2009, 7, 17.	0.7	84
680	Proteins recruited by SH3 domains of Ruk/CIN85 adaptor identified by LC-MS/MS. <i>Proteome Science</i> , 2009, 7, 21.	0.7	41
681	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
682	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
683	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
684	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

#	ARTICLE	IF	CITATIONS
685	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
686	Transcriptional effects of CRP* expression in <i>Escherichia coli</i> . <i>Journal of Biological Engineering</i> , 2009, 3, 13.	2.0	75
687	CTCF binding site classes exhibit distinct evolutionary, genomic, epigenomic and transcriptomic features. <i>Genome Biology</i> , 2009, 10, R131.	13.9	72
688	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
689	Studying alternative splicing regulatory networks through partial correlation analysis. <i>Genome Biology</i> , 2009, 10, R3.	13.9	49
690	Interactions among type I and type II interferon, tumor necrosis factor, and β -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
691	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
692	Mining gene functional networks to improve mass-spectrometry-based protein identification. <i>Bioinformatics</i> , 2009, 25, 2955-2961.	1.8	34
693	Generation of Gene Ontology benchmark datasets with various types of positive signal. <i>BMC Bioinformatics</i> , 2009, 10, 319.	1.2	5
694	Dissecting the dynamics of dysregulation of cellular processes in mouse mammary gland tumor. <i>BMC Genomics</i> , 2009, 10, 601.	1.2	28
695	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
696	Gene Expression Profiling of Human Neural Progenitor Cells Following the Serum-Induced Astrocyte Differentiation. <i>Cellular and Molecular Neurobiology</i> , 2009, 29, 423-438.	1.7	53
697	HIV-1 infection of macrophages is dependent on evasion of innate immune cellular activation. <i>Aids</i> , 2009, 23, 2255-2263.	1.0	91
698	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
699	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
700	HIV-1 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
701	MicroRNA 29b functions in acute myeloid leukemia. <i>Blood</i> , 2009, 114, 5331-5341.	0.6	412
702	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

#	ARTICLE	IF	CITATIONS
703	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
704	Orientation, distance, regulation and function of neighbouring genes. <i>Human Genomics</i> , 2009, 3, 143-56.	1.4	22
705	Exploring the relationship between polymorphic (TG/CA) n repeats in intron 1 regions and gene expression. <i>Human Genomics</i> , 2009, 3, 236-45.	1.4	10
706	Molecular Signature of HPV-Induced Carcinogenesis: pRb, p53 and Gene Expression Profiling. <i>Current Genomics</i> , 2009, 10, 26-34.	0.7	81
707	Validation of Rearrangement Break Points Identified by Paired-End Sequencing in Natural Populations of <i>Drosophila melanogaster</i> . <i>Genome Biology and Evolution</i> , 2010, 2, 83-101.	1.1	46
708	Functional Annotation of Genes Overlapping Copy Number Variants in Autistic Patients: Focus on Axon Pathfinding. <i>Current Genomics</i> , 2010, 11, 136-145.	0.7	29
709	An introduction to effective use of enrichment analysis software. <i>Human Genomics</i> , 2010, 4, 202.	1.4	60
710	TNFRSF11B computational development network construction and analysis between frontal cortex of HIV encephalitis (HIVE) and HIVE-control patients. <i>Journal of Inflammation</i> , 2010, 7, 50.	1.5	24
711	Integrated biochemical and computational approach identifies BCL6 direct target genes controlling multiple pathways in normal germinal center B cells. <i>Blood</i> , 2010, 115, 975-984.	0.6	216
712	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. <i>Blood</i> , 2010, 115, 3930-3938.	0.6	0
713	Novel early response genes in osteoblasts exposed to dynamic fluid flow. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2010, 368, 605-616.	1.6	14
714	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
715	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
716	Transcriptomic analysis of patients with tetralogy of Fallot reveals the effect of chronic hypoxia on myocardial gene expression. <i>Journal of Thoracic and Cardiovascular Surgery</i> , 2010, 140, 337-345.e26.	0.4	47
717	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
718	Shotgun Proteomics Analysis of Hibernating Arctic Ground Squirrels. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 313-326.	2.5	81
719	Defining TNF- α - 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
720	Mitochondrial abnormalities in the putamen in Parkinson's disease dyskinesia. <i>Acta Neuropathologica</i> , 2010, 120, 623-631.	3.9	30

#	ARTICLE	IF	CITATIONS
721	Genetics of keloid scarring. Archives of Dermatological Research, 2010, 302, 319-339.	1.1	210
722	Gene expression profiling for the investigation of soft tissue sarcoma pathogenesis and the identification of diagnostic, prognostic, and predictive biomarkers. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2010, 456, 141-151.	1.4	43
723	Effect of mood stabilizers on gene expression in lymphoblastoid cells. Journal of Neural Transmission, 2010, 117, 155-164.	1.4	30
724	Modulation of gene expression in endothelial cells by hyperlipaemic postprandial serum from healthy volunteers. Genes and Nutrition, 2010, 5, 263-274.	1.2	10
725	Expression Profile of Rat Hippocampal Neurons Treated with the Neuroprotective Compound 2,4-Dinitrophenol: Up-Regulation of cAMP Signaling Genes. Neurotoxicity Research, 2010, 18, 112-123.	1.3	17
726	Gene Expression Profiling Reveals Differentially Expressed Genes in Ovarian Cancer of the Hen: Support for Oviductal Origin?. Hormones and Cancer, 2010, 1, 177-186.	4.9	38
727	Quantitative proteomic analysis of S-nitrosated proteins in diabetic mouse liver with ICAT switch method. Protein and Cell, 2010, 1, 675-687.	4.8	22
728	AFP computational secreted network construction and analysis between human hepatocellular carcinoma (HCC) and no-tumor hepatitis/cirrhotic liver tissues. Tumor Biology, 2010, 31, 417-425.	0.8	37
729	A Common Neuronal Response to Alpha herpesvirus Infection. Journal of NeuroImmune Pharmacology, 2010, 5, 418-427.	2.1	32
730	Identification of novel epithelial ovarian cancer biomarkers by cross-laboratory microarray analysis. Journal of Huazhong University of Science and Technology [Medical Sciences], 2010, 30, 354-359.	1.0	4
731	Characterization of the Human Cervical Mucous Proteome. Clinical Proteomics, 2010, 6, 18-28.	1.1	32
732	A Functional Role of RB-Dependent Pathway in the Control of Quiescence in Adult Epidermal Stem Cells Revealed by Genomic Profiling. Stem Cell Reviews and Reports, 2010, 6, 162-177.	5.6	18
733	Gene expression profiles in the PC-3 human prostate cancer cells induced by NKX3.1. Molecular Biology Reports, 2010, 37, 1505-1512.	1.0	12
734	Stem cell associated gene expression in glioblastoma multiforme: relationship to survival and the subventricular zone. Journal of Neuro-Oncology, 2010, 96, 359-367.	1.4	86
735	PCB153-elicited hepatic responses in the immature, ovariectomized C57BL/6 mice: Comparative toxicogenomic effects of dioxin and non-dioxin-like ligands. Toxicology and Applied Pharmacology, 2010, 243, 359-371.	1.3	47
736	AutoSOME: a clustering method for identifying gene expression modules without prior knowledge of cluster number. BMC Bioinformatics, 2010, 11, 117.	1.2	92
737	GOAL: A software tool for assessing biological significance of genes groups. BMC Bioinformatics, 2010, 11, 229.	1.2	27
738	PhenoFam-gene set enrichment analysis through protein structural information. BMC Bioinformatics, 2010, 11, 254.	1.2	6

#	ARTICLE	IF	CITATIONS
739	Bayesian integrated modeling of expression data: a case study on RhoG. BMC Bioinformatics, 2010, 11, 295.	1.2	2
740	UFFizi: a generic platform for ranking informative features. BMC Bioinformatics, 2010, 11, 300.	1.2	2
741	PCA2GO: a new multivariate statistics based method to identify highly expressed GO-Terms. BMC Bioinformatics, 2010, 11, 336.	1.2	4
742	Integration and visualization of systems biology data in context of the genome. BMC Bioinformatics, 2010, 11, 382.	1.2	31
743	Uncovering packaging features of co-regulated modules based on human protein interaction and transcriptional regulatory networks. BMC Bioinformatics, 2010, 11, 392.	1.2	10
744	TAM: A method for enrichment and depletion analysis of a microRNA category in a list of microRNAs. BMC Bioinformatics, 2010, 11, 419.	1.2	121
745	Asymmetric microarray data produces gene lists highly predictive of research literature on multiple cancer types. BMC Bioinformatics, 2010, 11, 483.	1.2	13
746	Trimming of mammalian transcriptional networks using network component analysis. BMC Bioinformatics, 2010, 11, 511.	1.2	14
747	PathEx: a novel multi factors based datasets selector web tool. BMC Bioinformatics, 2010, 11, 528.	1.2	4
748	Epigenetic domains found in mouse embryonic stem cells via a hidden Markov model. BMC Bioinformatics, 2010, 11, 557.	1.2	16
749	Extending pathways and processes using molecular interaction networks to analyse cancer genome data. BMC Bioinformatics, 2010, 11, 597.	1.2	40
750	Lists2Networks: Integrated analysis of gene/protein lists. BMC Bioinformatics, 2010, 11, 87.	1.2	38
751	A statistical framework for differential network analysis from microarray data. BMC Bioinformatics, 2010, 11, 95.	1.2	134
752	Microarray analysis of a salamander hopeful monster reveals transcriptional signatures of paedomorphic brain development. BMC Evolutionary Biology, 2010, 10, 199.	3.2	24
753	Schizophrenia and vitamin D related genes could have been subject to latitude-driven adaptation. BMC Evolutionary Biology, 2010, 10, 351.	3.2	32
754	Expression profiling of mouse embryonic fibroblasts with a deletion in the helicase domain of the Werner Syndrome gene homologue treated with hydrogen peroxide. BMC Genomics, 2010, 11, 127.	1.2	12
755	Pediatric primary central nervous system germ cell tumors of different prognosis groups show characteristic miRNome traits and chromosome copy number variations. BMC Genomics, 2010, 11, 132.	1.2	45
756	Distribution of candidate genes for experimentally induced arthritis in rats. BMC Genomics, 2010, 11, 146.	1.2	2

#	ARTICLE	IF	CITATIONS
757	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
758	Reciprocal regulation of metabolic and signaling pathways. BMC Genomics, 2010, 11, 197.	1.2	10
759	Downregulation of genes with a function in axon outgrowth and synapse formation in motor neurones of the VEGF β mouse model of amyotrophic lateral sclerosis. BMC Genomics, 2010, 11, 203.	1.2	38
760	Whole transcriptome analysis of the hippocampus: toward a molecular portrait of epileptogenesis. BMC Genomics, 2010, 11, 230.	1.2	92
761	Identification of copy number variations and common deletion polymorphisms in cattle. BMC Genomics, 2010, 11, 232.	1.2	126
762	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
763	Systems genetics analysis of body weight and energy metabolism traits in <i>Drosophila melanogaster</i> . BMC Genomics, 2010, 11, 297.	1.2	84
764	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
765	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
766	Bioinformatic identification and characterization of human endothelial cell-restricted genes. BMC Genomics, 2010, 11, 342.	1.2	54
767	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
768	Transcriptional regulation of gene expression clusters in motor neurons following spinal cord injury. BMC Genomics, 2010, 11, 365.	1.2	36
769	Transcription profiling provides insights into gene pathways involved in horn and scurs development in cattle. BMC Genomics, 2010, 11, 370.	1.2	32
770	A gene network switch enhances the oxidative capacity of ovine skeletal muscle during late fetal development. BMC Genomics, 2010, 11, 378.	1.2	27
771	Global transcriptional response to carbonic anhydrase IX deficiency in the mouse stomach. BMC Genomics, 2010, 11, 397.	1.2	11
772	Characterization of the equine skeletal muscle transcriptome identifies novel functional responses to exercise training. BMC Genomics, 2010, 11, 398.	1.2	81
773	A systems approach to mapping transcriptional networks controlling surfactant homeostasis. BMC Genomics, 2010, 11, 451.	1.2	28
774	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
775	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
776	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
777	Dynamic transcriptomic profiles of zebrafish gills in response to zinc depletion. <i>BMC Genomics</i> , 2010, 11, 548.	1.2	26
778	Dynamic transcriptomic profiles of zebrafish gills in response to zinc supplementation. <i>BMC Genomics</i> , 2010, 11, 553.	1.2	44
779	Gene duplications in prokaryotes can be associated with environmental adaptation. <i>BMC Genomics</i> , 2010, 11, 588.	1.2	102
780	Differential alterations in gene expression profiles contribute to time-dependent effects of nandrolone to prevent denervation atrophy. <i>BMC Genomics</i> , 2010, 11, 596.	1.2	20
781	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
782	Insights into metazoan evolution from <i>alvinella pompejana</i> cDNAs. <i>BMC Genomics</i> , 2010, 11, 634.	1.2	46
783	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
784	Analysis of transcript and protein overlap in a human osteosarcoma cell line. <i>BMC Genomics</i> , 2010, 11, 684.	1.2	13
785	Relationship between operon preference and functional properties of persistent genes in bacterial genomes. <i>BMC Genomics</i> , 2010, 11, 71.	1.2	24
786	Investigation gene and microRNA expression in glioblastoma. <i>BMC Genomics</i> , 2010, 11, S16.	1.2	36
787	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
788	Gram-positive pathogenic bacteria induce a common early response in human monocytes. <i>BMC Microbiology</i> , 2010, 10, 275.	1.3	17
789	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
790	Analysis of gene expression in prostate cancer epithelial and interstitial stromal cells using laser capture microdissection. <i>BMC Cancer</i> , 2010, 10, 165.	1.1	57
791	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
792	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

#	ARTICLE	IF	CITATIONS
793	Expression profiling in canine osteosarcoma: identification of biomarkers and pathways associated with outcome. <i>BMC Cancer</i> , 2010, 10, 506.	1.1	47
794	Prioritizing genes associated with prostate cancer development. <i>BMC Cancer</i> , 2010, 10, 599.	1.1	28
795	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
796	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
797	Impact of methoxyacetic acid on mouse Leydig cell gene expression. <i>Reproductive Biology and Endocrinology</i> , 2010, 8, 65.	1.4	14
798	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
799	Molecular mechanistic associations of human diseases. <i>BMC Systems Biology</i> , 2010, 4, 124.	3.0	11
800	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
801	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
802	Dissecting the Unique Role of the Retinoblastoma Tumor Suppressor during Cellular Senescence. <i>Cancer Cell</i> , 2010, 17, 376-387.	7.7	323
803	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
804	Significant Downregulation of Platelet Gene Expression in Metastatic Lung Cancer. <i>Clinical and Translational Science</i> , 2010, 3, 227-232.	1.5	101
805	A systems biology approach to understanding atherosclerosis. <i>EMBO Molecular Medicine</i> , 2010, 2, 79-89.	3.3	69
806	Integrated approach for the identification of human hepatocyte nuclear factor 4 β target genes using protein binding microarrays. <i>Hepatology</i> , 2010, 51, 642-653.	3.6	151
807	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
808	Genome-wide tissue-specific farnesoid X receptor binding in mouse liver and intestine. <i>Hepatology</i> , 2010, 51, 1410-1419.	3.6	173
809	Selective control of gene expression by CDK9 in human cells. <i>Journal of Cellular Physiology</i> , 2010, 222, 200-208.	2.0	45
810	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

#	ARTICLE	IF	CITATIONS
811	Analysis of whole genome biomarker expression in blood and brain. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 919-936.	1.1	149
812	Network Analysis of EtOH-Related Candidate Genes. Chemistry and Biodiversity, 2010, 7, 1142-1152.	1.0	3
813	Developmental microRNA expression profiling of murine embryonic orofacial tissue. Birth Defects Research Part A: Clinical and Molecular Teratology, 2010, 88, 511-534.	1.6	44
814	A systems-based approach to investigate dose- and time-dependent methylmercury-induced gene expression response in C57BL/6 mouse embryos undergoing neurulation. Birth Defects Research Part B: Developmental and Reproductive Toxicology, 2010, 89, 188-200.	1.4	13
815	Microarray analysis of cutaneous squamous cell carcinomas reveals enhanced expression of epidermal differentiation complex genes. Molecular Carcinogenesis, 2010, 49, 619-629.	1.3	36
816	Identification of JAK-STAT pathways as important for the anti-inflammatory activity of a Hypericum perforatum fraction and bioactive constituents in RAW 264.7 mouse macrophages. Phytochemistry, 2010, 71, 716-725.	1.4	24
817	Assembling Ligands In Situ Using Bioorthogonal Boronate Ester Synthesis. Chemistry and Biology, 2010, 17, 1171-1176.	6.2	34
818	Akt regulates the expression of MafK, synaptotagmin I, and syntenin-1, which play roles in neuronal function. Journal of Biomedical Science, 2010, 17, 18.	2.6	12
819	A maternal low protein diet has pronounced effects on mitochondrial gene expression in offspring liver and skeletal muscle; protective effect of taurine. Journal of Biomedical Science, 2010, 17, S38.	2.6	43
820	Octamer-binding factor 6 (Oct-6/Pou3f1) is induced by interferon and contributes to dsRNA-mediated transcriptional responses. BMC Cell Biology, 2010, 11, 61.	3.0	12
821	Global transcriptional profiles of beating clusters derived from human induced pluripotent stem cells and embryonic stem cells are highly similar. BMC Developmental Biology, 2010, 10, 98.	2.1	76
822	Modeling complex genetic and environmental influences on comorbid bipolar disorder with tobacco use disorder. BMC Medical Genetics, 2010, 11, 14.	2.1	26
823	Protective effects and potential mechanisms of Pien Tze Huang on cerebral chronic ischemia and hypertensive stroke. Chinese Medicine, 2010, 5, 35.	1.6	14
824	GTC: A web server for integrating systems biology data with web tools and desktop applications. Source Code for Biology and Medicine, 2010, 5, 7.	1.7	2
825	Mural granulosa cell gene expression associated with oocyte developmental competence. Journal of Ovarian Research, 2010, 3, 6.	1.3	40
826	Global analysis of the rat and human platelet proteome - the molecular blueprint for illustrating multi-functional platelets and cross-species function evolution. Proteomics, 2010, 10, 2444-2457.	1.3	33
827	Pathway analysis of dilated cardiomyopathy using global proteomic profiling and enrichment maps. Proteomics, 2010, 10, 1316-1327.	1.3	55
828	Identification of osteocyte-selective proteins. Proteomics, 2010, 10, 3688-3698.	1.3	49

#	ARTICLE	IF	CITATIONS
829	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
830	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
831	The effects of mating and instrumental insemination on queen honey bee flight behaviour and gene expression. <i>Insect Molecular Biology</i> , 2010, 19, 153-162.	1.0	37
832	An ESRP-regulated splicing programme is abrogated during the epithelial-mesenchymal transition. <i>EMBO Journal</i> , 2010, 29, 3286-3300.	3.5	346
833	Global H4 acetylation analysis by ChIP-chip in systemic lupus erythematosus monocytes. <i>Genes and Immunity</i> , 2010, 11, 124-133.	2.2	113
834	Schizophrenia is associated with an increase in cortical microRNA biogenesis. <i>Molecular Psychiatry</i> , 2010, 15, 1176-1189.	4.1	396
835	Chromatin signature of embryonic pluripotency is established during genome activation. <i>Nature</i> , 2010, 464, 922-926.	13.7	340
836	Genome-wide analysis of a long-term evolution experiment with <i>Drosophila</i> . <i>Nature</i> , 2010, 467, 587-590.	13.7	410
837	Chronic high-fat diet in fathers programs β -cell dysfunction in female rat offspring. <i>Nature</i> , 2010, 467, 963-966.	13.7	1,214
838	Global analysis of lysine ubiquitination by ubiquitin remnant immunoaffinity profiling. <i>Nature Biotechnology</i> , 2010, 28, 868-873.	9.4	460
839	Ontology engineering. <i>Nature Biotechnology</i> , 2010, 28, 128-130.	9.4	113
840	A map of open chromatin in human pancreatic islets. <i>Nature Genetics</i> , 2010, 42, 255-259.	9.4	515
841	Trans-SILAC: sorting out the non-cell-autonomous proteome. <i>Nature Methods</i> , 2010, 7, 923-927.	9.0	30
842	Next-generation genomics: an integrative approach. <i>Nature Reviews Genetics</i> , 2010, 11, 476-486.	7.7	554
843	Statistical analysis strategies for association studies involving rare variants. <i>Nature Reviews Genetics</i> , 2010, 11, 773-785.	7.7	426
844	Transient Peripheral Immune Response and Central Nervous System Leaky Compartmentalization in a Viral Model for Multiple Sclerosis. <i>Brain Pathology</i> , 2010, 20, 890-901.	2.1	20
845	Differential Expression of Lipid and Carbohydrate Metabolism Genes in Upper Airway versus Diaphragm Muscle. <i>Sleep</i> , 2010, 33, 363-370.	0.6	6
846	DNA Methylation and Genome Evolution in Honeybee: Gene Length, Expression, Functional Enrichment Covary with the Evolutionary Signature of DNA Methylation. <i>Genome Biology and Evolution</i> , 2010, 2, 770-780.	1.1	45

#	ARTICLE	IF	CITATIONS
847	Automated Network Analysis Identifies Core Pathways in Glioblastoma. PLoS ONE, 2010, 5, e8918.	1.1	318
848	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
849	A New Strategy to Identify and Annotate Human RPE-Specific Gene Expression. PLoS ONE, 2010, 5, e9341.	1.1	72
850	Phenotypic Covariance of Longevity, Immunity and Stress Resistance in the Caenorhabditis Nematodes. PLoS ONE, 2010, 5, e9978.	1.1	36
851	Systematic Analysis of a Novel Human Renal Glomerulus-Enriched Gene Expression Dataset. PLoS ONE, 2010, 5, e11545.	1.1	71
852	Gene Network Disruptions and Neurogenesis Defects in the Adult Ts1Cje Mouse Model of Down Syndrome. PLoS ONE, 2010, 5, e11561.	1.1	44
853	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
854	NK Cell Terminal Differentiation: Correlated Stepwise Decrease of NKG2A and Acquisition of KIRs. PLoS ONE, 2010, 5, e11966.	1.1	179
855	Profiling and Functional Analyses of MicroRNAs and Their Target Gene Products in Human Uterine Leiomyomas. PLoS ONE, 2010, 5, e12362.	1.1	64
856	MicroRNA-218 Is Deleted and Downregulated in Lung Squamous Cell Carcinoma. PLoS ONE, 2010, 5, e12560.	1.1	100
857	Self-Contained Gene-Set Analysis of Expression Data: An Evaluation of Existing and Novel Methods. PLoS ONE, 2010, 5, e12693.	1.1	52
858	QKI-7 Regulates Expression of Interferon-Related Genes in Human Astrocyte Glioma Cells. PLoS ONE, 2010, 5, e13079.	1.1	8
859	Transcript Profiling of Elf5+ Mammary Glands during Pregnancy Identifies Novel Targets of Elf5. PLoS ONE, 2010, 5, e13150.	1.1	8
860	A Network of Cancer Genes with Co-Occurring and Anti-Co-Occurring Mutations. PLoS ONE, 2010, 5, e13180.	1.1	31
861	Gene Expression Profiling of U12-Type Spliceosome Mutant Drosophila Reveals Widespread Changes in Metabolic Pathways. PLoS ONE, 2010, 5, e13215.	1.1	26
862	Study on Differences in the Pathology, T Cell Subsets and Gene Expression in Susceptible and Non-Susceptible Hosts Infected with Schistosoma japonicum. PLoS ONE, 2010, 5, e13494.	1.1	42
863	Bypass Mechanisms of the Androgen Receptor Pathway in Therapy-Resistant Prostate Cancer Cell Models. PLoS ONE, 2010, 5, e13500.	1.1	88
864	Enrichment Map: A Network-Based Method for Gene-Set Enrichment Visualization and Interpretation. PLoS ONE, 2010, 5, e13984.	1.1	1,883

#	ARTICLE	IF	CITATIONS
865	Phosphoproteomics Profiling of Human Skin Fibroblast Cells Reveals Pathways and Proteins Affected by Low Doses of Ionizing Radiation. <i>PLoS ONE</i> , 2010, 5, e14152.	1.1	21
866	The Reverse Transcription Inhibitor Abacavir Shows Anticancer Activity in Prostate Cancer Cell Lines. <i>PLoS ONE</i> , 2010, 5, e14221.	1.1	48
867	Chromatin Remodeling Pathways in Smooth Muscle Cell Differentiation, and Evidence for an Integral Role for p300. <i>PLoS ONE</i> , 2010, 5, e14301.	1.1	26
868	ZNF274 Recruits the Histone Methyltransferase SETDB1 to the 3' Ends of ZNF Genes. <i>PLoS ONE</i> , 2010, 5, e15082.	1.1	147
869	RNAi Screen of DAF-16/FOXO Target Genes in <i>C. elegans</i> Links Pathogenesis and Dauer Formation. <i>PLoS ONE</i> , 2010, 5, e15902.	1.1	27
870	Alterations in gene expression profiles correlated with cisplatin cytotoxicity in the glioma U343 cell line. <i>Genetics and Molecular Biology</i> , 2010, 33, 159-168.	0.6	17
871	Association Rule Based Similarity Measures for the Clustering of Gene Expression Data. <i>Open Medical Informatics Journal</i> , 2010, 4, 63-73.	1.0	15
872	Gene targeting and Calcium handling efficiencies in mouse embryonic stem cell lines. <i>World Journal of Stem Cells</i> , 2010, 2, 127.	1.3	6
873	A Two-tiered compensatory response to loss of DNA repair modulates aging and stress response pathways. <i>Aging</i> , 2010, 2, 133-159.	1.4	23
874	Reversal of preexisting hyperglycemia in diabetic mice by acute deletion of the <i>Men1</i> gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20358-20363.	3.3	44
875	Novel multi-nucleotide polymorphisms in the human genome characterized by whole genome and exome sequencing. <i>Nucleic Acids Research</i> , 2010, 38, 6102-6111.	6.5	44
876	SAFB1 Mediates Repression of Immune Regulators and Apoptotic Genes in Breast Cancer Cells. <i>Journal of Biological Chemistry</i> , 2010, 285, 3608-3616.	1.6	30
877	Cell Sorting-Assisted Microarray Profiling of Host Cell Response to <i>Cryptosporidium parvum</i> Infection. <i>Infection and Immunity</i> , 2010, 78, 1040-1048.	1.0	17
878	MGMT modulates glioblastoma angiogenesis and response to the tyrosine kinase inhibitor sunitinib. <i>Neuro-Oncology</i> , 2010, 12, 822-833.	0.6	74
879	Gene Expression Profiles in a Rabbit Model of Systemic Lupus Erythematosus Autoantibody Production. <i>Journal of Immunology</i> , 2010, 185, 4446-4456.	0.4	8
880	Genome-wide assessment of differential roles for p300 and CBP in transcription regulation. <i>Nucleic Acids Research</i> , 2010, 38, 5396-5408.	6.5	133
881	A Critical Role for Ceramide Synthase 2 in Liver Homeostasis. <i>Journal of Biological Chemistry</i> , 2010, 285, 10911-10923.	1.6	200
882	Genomewide Association Analysis of Respiratory Syncytial Virus Infection in Mice. <i>Journal of Virology</i> , 2010, 84, 2257-2269.	1.5	15

#	ARTICLE	IF	CITATIONS
883	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
884	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
885	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
886	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
887	Integrated Pathways for Neutrophil Recruitment and Inflammation in Leprosy. <i>Journal of Infectious Diseases</i> , 2010, 201, 558-569.	1.9	65
888	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
889	Regulation of Fibroblast Growth Factor-2 by an Endogenous Antisense RNA and by Argonaute-2. <i>Molecular Endocrinology</i> , 2010, 24, 800-812.	3.7	18
890	Characterization of Macaque Pulmonary Fluid Proteome during Monkeypox Infection. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2760-2771.	2.5	16
891	Distinct roles for miR-1 and miR-133a in the proliferation and differentiation of rhabdomyosarcoma cells. <i>FASEB Journal</i> , 2010, 24, 3427-3437.	0.2	118
892	Identification of Methylmercury Tolerance Gene Candidates in <i>Drosophila</i> . <i>Toxicological Sciences</i> , 2010, 116, 225-238.	1.4	34
893	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
894	Nuclear Translocation of β -Actin Is Involved in Transcriptional Regulation during Macrophage Differentiation of HL-60 Cells. <i>Molecular Biology of the Cell</i> , 2010, 21, 811-820.	0.9	67
895	Neuronal MicroRNA Deregulation in Response to Alzheimer's Disease Amyloid- β . <i>PLoS ONE</i> , 2010, 5, e11070.	1.1	183
896	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
897	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
898	ConceptGen: a gene set enrichment and gene set relation mapping tool. <i>Bioinformatics</i> , 2010, 26, 456-463.	1.8	134
899	Differential Roles of Sall4 Isoforms in Embryonic Stem Cell Pluripotency. <i>Molecular and Cellular Biology</i> , 2010, 30, 5364-5380.	1.1	157
900	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

#	ARTICLE	IF	CITATIONS
901	Quantitative Proteomic Analyses of Influenza Virus-Infected Cultured Human Lung Cells. <i>Journal of Virology</i> , 2010, 84, 10888-10906.	1.5	151
902	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
903	Upstream transcription factor 1 influences plasma lipid and metabolic traits in mice. <i>Human Molecular Genetics</i> , 2010, 19, 597-608.	1.4	30
904	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
905	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
906	Atoh1 Inhibits Neuronal Differentiation and Collaborates with Gli1 to Generate Medulloblastoma-Initiating Cells. <i>Cancer Research</i> , 2010, 70, 5618-5627.	0.4	87
907	Genetic Dependence of Central Corneal Thickness among Inbred Strains of Mice. , 2010, 51, 160.		47
908	PHF8 Targets Histone Methylation and RNA Polymerase II To Activate Transcription. <i>Molecular and Cellular Biology</i> , 2010, 30, 3286-3298.	1.1	98
909	Distinct gene expression profiles characterize cellular responses to palmitate and oleate. <i>Journal of Lipid Research</i> , 2010, 51, 2121-2131.	2.0	29
910	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
911	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
912	Estrogen-related Receptor β Is a Key Regulator of Muscle Mitochondrial Activity and Oxidative Capacity. <i>Journal of Biological Chemistry</i> , 2010, 285, 22619-22629.	1.6	153
913	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
914	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
915	Cyclic Stretch Magnitude and Duration Affect Rat Alveolar Epithelial Gene Expression. <i>Cellular Physiology and Biochemistry</i> , 2010, 25, 113-122.	1.1	28
916	Maternal Hyperglycemia Modifies Extracellular Matrix Signaling Pathways in Neonatal Rat Lung. <i>Neonatology</i> , 2010, 98, 387-396.	0.9	7
917	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
918	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

#	ARTICLE	IF	CITATIONS
919	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
920	Evolution of alternative splicing in primate brain transcriptomes. <i>Human Molecular Genetics</i> , 2010, 19, 2958-2973.	1.4	47
921	Rank hypergeometric overlap: identification of statistically significant overlap between gene-expression signatures. <i>Nucleic Acids Research</i> , 2010, 38, e169-e169.	6.5	357
922	<i>ATF3</i> , an adaptive-response gene, enhances TGF β ² signaling and cancer-initiating cell features in breast cancer cells. <i>Journal of Cell Science</i> , 2010, 123, 3558-3565.	1.2	152
923	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
924	Exon-Level Microarray Analyses Identify Alternative Splicing Programs in Breast Cancer. <i>Molecular Cancer Research</i> , 2010, 8, 961-974.	1.5	121
925	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
926	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
927	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
928	Of mice and men: comparative proteomics of bronchoalveolar fluid. <i>European Respiratory Journal</i> , 2010, 35, 1388-1395.	3.1	43
929	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
930	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
931	Genetic Associations of Variants in Genes Encoding HIV-1 Dependency Factors Required for HIV-1 Infection. <i>Journal of Infectious Diseases</i> , 2010, 202, 1836-1845.	1.9	29
932	Immunobiological Characterization of Cancer Stem Cells Isolated from Glioblastoma Patients. <i>Clinical Cancer Research</i> , 2010, 16, 800-813.	3.2	295
933	In Situ Proteomic Analysis of Human Breast Cancer Epithelial Cells Using Laser Capture Microdissection: Annotation by Protein Set Enrichment Analysis and Gene Ontology. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2529-2544.	2.5	72
934	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
935	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
936	Foxa1 and Foxa2 Maintain the Metabolic and Secretory Features of the Mature β -Cell. <i>Molecular Endocrinology</i> , 2010, 24, 1594-1604.	3.7	105

#	ARTICLE	IF	CITATIONS
937	Deciphering the Mesodermal Potency of Porcine Skin-Derived Progenitors (SKP) by Microarray Analysis. <i>Cellular Reprogramming</i> , 2010, 12, 161-173.	0.5	8
938	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
939	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
940	Trinucleotide repeats in human genome and exome. <i>Nucleic Acids Research</i> , 2010, 38, 4027-4039.	6.5	124
941	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
942	Integrative epigenomic and genomic analysis of malignant pheochromocytoma. <i>Experimental and Molecular Medicine</i> , 2010, 42, 484.	3.2	32
943	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
944	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
945	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
946	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
947	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
948	Enhanced Function of Prefrontal Serotonin 5-HT ₂ Receptors in a Rat Model of Psychiatric Vulnerability. <i>Journal of Neuroscience</i> , 2010, 30, 12138-12150.	1.7	78
949	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
950	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
951	Cdx2 regulates endo-lysosomal function and epithelial cell polarity. <i>Genes and Development</i> , 2010, 24, 1295-1305.	2.7	75
952	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
953	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
954	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

#	ARTICLE	IF	CITATIONS
955	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
956	NF- κ B-related factor 2 regulates the stress response to UVA-induced oxidized phospholipids in skin cells. <i>FASEB Journal</i> , 2010, 24, 39-48.	0.2	71
957	miR-451 protects against erythroid oxidant stress by repressing 14-3-3 η . <i>Genes and Development</i> , 2010, 24, 1620-1633.	2.7	192
958	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
959	Targets of the Tal1 Transcription Factor in Erythrocytes. <i>Journal of Biological Chemistry</i> , 2010, 285, 5338-5346.	1.6	16
960	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
961	Strong synaptic transmission impact by copy number variations in schizophrenia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10584-10589.	3.3	212
962	The G protein-coupled receptor T-cell death-associated gene 8 (TDAG8) facilitates tumor development by serving as an extracellular pH sensor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17309-17314.	3.3	80
963	Interactome analysis of longitudinal pharyngeal infection of cynomolgus macaques by group A <i>Streptococcus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4693-4698.	3.3	30
964	G _{Lay} : community structure analysis of biological networks. <i>Bioinformatics</i> , 2010, 26, 3135-3137.	1.8	241
965	Identification of differential protein interactors of lamin A and progerin. <i>Nucleus</i> , 2010, 1, 513-525.	0.6	81
966	Cytokine-Induced Monocyte Characteristics in SLE. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-13.	3.0	21
967	Deep SAGE analysis of the <i>Caenorhabditis elegans</i> transcriptome. <i>Nucleic Acids Research</i> , 2010, 38, 3252-3262.	6.5	16
968	Pathogen Specific, IRF3-Dependent Signaling and Innate Resistance to Human Kidney Infection. <i>PLoS Pathogens</i> , 2010, 6, e1001109.	2.1	68
969	Genomic Analysis Highlights the Role of the JAK-STAT Signaling in the Anti-Proliferative Effects of Dietary Flavonoid "Ashwagandha"™ in Prostate Cancer Cells. <i>Evidence-based Complementary and Alternative Medicine</i> , 2010, 7, 177-187.	0.5	51
970	Conditional deletion of <i>Abca3</i> in alveolar type II cells alters surfactant homeostasis in newborn and adult mice. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2010, 298, L646-L659.	1.3	58
971	Altered Gene Expression and DNA Damage in Peripheral Blood Cells from Friedreich's Ataxia Patients: Cellular Model of Pathology. <i>PLoS Genetics</i> , 2010, 6, e1000812.	1.5	93
972	Gene Expression Variability within and between Human Populations and Implications toward Disease Susceptibility. <i>PLoS Computational Biology</i> , 2010, 6, e1000910.	1.5	85

#	ARTICLE	IF	CITATIONS
973	Deciphering Normal Blood Gene Expression Variation—The NOWAC Postgenome Study. <i>PLoS Genetics</i> , 2010, 6, e1000873.	1.5	76
974	Proteomic analysis of brush-border membrane vesicles isolated from purified proximal convoluted tubules. <i>American Journal of Physiology - Renal Physiology</i> , 2010, 298, F1323-F1331.	1.3	32
975	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
976	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
977	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
978	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
979	Finding the “Dark Matter” in Human and Yeast Protein Network Prediction and Modelling. <i>PLoS Computational Biology</i> , 2010, 6, e1000945.	1.5	21
980	Transcriptional Regulation by CHIP/LDB Complexes. <i>PLoS Genetics</i> , 2010, 6, e1001063.	1.5	28
981	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
982	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
983	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
984	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. <i>Genome Research</i> , 2010, 20, 791-803.	2.4	84
985	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
986	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
987	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
988	EPS8 upregulates FOXM1 expression, enhancing cell growth and motility. <i>Carcinogenesis</i> , 2010, 31, 1132-1141.	1.3	47
989	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
990	RB-pathway disruption in breast cancer. <i>Cell Cycle</i> , 2010, 9, 4153-4163.	1.3	163

#	ARTICLE	IF	CITATIONS
991	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
992	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
993	Accelerated Ovarian Aging in the Absence of the Transcription Regulator TAF4B in Mice. <i>Biology of Reproduction</i> , 2010, 82, 23-34.	1.2	34
994	Constitutive Activation of Smoothed Leads to Female Infertility and Altered Uterine Differentiation in the Mouse. <i>Biology of Reproduction</i> , 2010, 82, 991-999.	1.2	47
995	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
996	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
997	Using Expression Genetics to Study the Neurobiology of Ethanol and Alcoholism. <i>International Review of Neurobiology</i> , 2010, 91, 95-128.	0.9	41
998	Scalp fibroblasts have a shared expression profile in monogenic craniosynostosis. <i>Journal of Medical Genetics</i> , 2010, 47, 803-808.	1.5	15
999	Functional Conservation of DNA Methylation in the Pea Aphid and the Honeybee. <i>Genome Biology and Evolution</i> , 2010, 2, 719-728.	1.1	109
1000	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
1001	REDD1 Is a Major Target of Testosterone Action in Preventing Dexamethasone-Induced Muscle Loss. <i>Endocrinology</i> , 2010, 151, 1050-1059.	1.4	58
1002	Defective erythroid differentiation in miR-451 mutant mice mediated by 14-3-3Î¶. <i>Genes and Development</i> , 2010, 24, 1614-1619.	2.7	156
1003	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
1004	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
1005	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
1006	Transcriptomic Analysis of Human Lung Development. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2010, 181, 54-63.	2.5	107
1007	Transcriptome analysis and molecular signature of human retinal pigment epithelium. <i>Human Molecular Genetics</i> , 2010, 19, 2468-2486.	1.4	249
1008	Direct Transfer of Î±-Synuclein from Neuron to Astroglia Causes Inflammatory Responses in Synucleinopathies. <i>Journal of Biological Chemistry</i> , 2010, 285, 9262-9272.	1.6	704

#	ARTICLE	IF	CITATIONS
1009	Integrative Systems Biology for Data-Driven Knowledge Discovery. <i>Seminars in Nephrology</i> , 2010, 30, 443-454.	0.6	20
1010	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
1011	An in silico analysis of microRNAs: Mining the miRNAome. <i>Molecular BioSystems</i> , 2010, 6, 1853.	2.9	42
1012	Widespread Protein Aggregation as an Inherent Part of Aging in <i>C. elegans</i> . <i>PLoS Biology</i> , 2010, 8, e1000450.	2.6	551
1013	Involvement of mast cells in eosinophilic esophagitis. <i>Journal of Allergy and Clinical Immunology</i> , 2010, 126, 140-149.	1.5	261
1014	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
1015	From RNA-seq reads to differential expression results. <i>Genome Biology</i> , 2010, 11, 220.	13.9	603
1016	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
1017	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
1018	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
1019	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
1020	A Genome-wide screen identifies frequently methylated genes in haematological and epithelial cancers. <i>Molecular Cancer</i> , 2010, 9, 44.	7.9	92
1021	Identification of 5 novel genes methylated in breast and other epithelial cancers. <i>Molecular Cancer</i> , 2010, 9, 51.	7.9	83
1022	MFSD2A is a novel lung tumor suppressor gene modulating cell cycle and matrix attachment. <i>Molecular Cancer</i> , 2010, 9, 62.	7.9	32
1023	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
1024	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
1025	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
1026	Structural similarity-based predictions of protein interactions between HIV-1 and <i>Homo sapiens</i> . <i>Virology Journal</i> , 2010, 7, 82.	1.4	70

#	ARTICLE	IF	CITATIONS
1027	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
1028	Activation of Aortic Endothelial Cells by Oxidized Phospholipids: A Phosphoproteomic Analysis. <i>Journal of Proteome Research</i> , 2010, 9, 2812-2824.	1.8	38
1029	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
1030	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
1031	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
1032	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
1033	Phospholipid Transfer Protein in Human Plasma Associates with Proteins Linked to Immunity and Inflammation. <i>Biochemistry</i> , 2010, 49, 7314-7322.	1.2	47
1034	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
1035	Expectations, validity, and reality in gene expression profiling. <i>Journal of Clinical Epidemiology</i> , 2010, 63, 950-959.	2.4	55
1036	Prediction of regulatory networks in mouse abdominal wall. <i>Gene</i> , 2010, 469, 1-8.	1.0	5
1037	Hopx and Hdac2 Interact to Modulate Gata4 Acetylation and Embryonic Cardiac Myocyte Proliferation. <i>Developmental Cell</i> , 2010, 19, 450-459.	3.1	125
1038	The use of neuroproteomics in drug abuse research. <i>Drug and Alcohol Dependence</i> , 2010, 107, 11-22.	1.6	17
1039	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
1040	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
1041	Comparative Epigenomic Analysis of Murine and Human Adipogenesis. <i>Cell</i> , 2010, 143, 156-169.	13.5	460
1042	A Myc Network Accounts for Similarities between Embryonic Stem and Cancer Cell Transcription Programs. <i>Cell</i> , 2010, 143, 313-324.	13.5	606
1043	TGF- β 2 and Insulin Signaling Regulate Reproductive Aging via Oocyte and Germline Quality Maintenance. <i>Cell</i> , 2010, 143, 299-312.	13.5	238
1044	A Tissue-Specific Atlas of Mouse Protein Phosphorylation and Expression. <i>Cell</i> , 2010, 143, 1174-1189.	13.5	1,564

#	ARTICLE	IF	CITATIONS
1045	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
1047	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
1048	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. <i>Cell Stem Cell</i> , 2010, 6, 479-491.	5.2	747
1049	Friedreich's Ataxia Induced Pluripotent Stem Cells Model Intergenerational GAA...TTC Triplet Repeat Instability. <i>Cell Stem Cell</i> , 2010, 7, 631-637.	5.2	191
1050	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
1051	NF- κ 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
1052	Restriction of Receptor Movement Alters Cellular Response: Physical Force Sensing by EphA2. <i>Science</i> , 2010, 327, 1380-1385.	6.0	301
1053	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
1054	<i>Porphyrromonas gingivalis</i> infection-induced tissue and bone transcriptional profiles. <i>Molecular Oral Microbiology</i> , 2010, 25, 61-74.	1.3	48
1055	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
1056	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
1057	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
1058	Estrogen Receptor \pm 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
1059	Differential Gene Regulation by the Human and Mouse Aryl Hydrocarbon Receptor. <i>Toxicological Sciences</i> , 2010, 114, 217-225.	1.4	90
1060	U87MG Decoded: The Genomic Sequence of a Cytogenetically Aberrant Human Cancer Cell Line. <i>PLoS Genetics</i> , 2010, 6, e1000832.	1.5	229
1061	agriGO: a GO analysis toolkit for the agricultural community. <i>Nucleic Acids Research</i> , 2010, 38, W64-W70.	6.5	2,289
1062	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
1063	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

#	ARTICLE	IF	CITATIONS
1064	Vitreous Proteomics and Diabetic Retinopathy. <i>Seminars in Ophthalmology</i> , 2010, 25, 289-294.	0.8	27
1065	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
1066	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
1067	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
1068	Gene expression profiling of peripheral blood cells for early detection of breast cancer. <i>Breast Cancer Research</i> , 2010, 12, R7.	2.2	95
1069	Quantifying the mechanisms of domain gain in animal proteins. <i>Genome Biology</i> , 2010, 11, R74.	13.9	93
1070	A mouse embryonic stem cell bank for inducible overexpression of human chromosome 21 genes. <i>Genome Biology</i> , 2010, 11, R64.	13.9	16
1071	Identification of functional modules that correlate with phenotypic difference: the influence of network topology. <i>Genome Biology</i> , 2010, 11, R23.	13.9	67
1072	Matrix metalloproteinase-8 deficiency increases joint inflammation and bone erosion in the K/BxN serum-transfer arthritis model. <i>Arthritis Research and Therapy</i> , 2010, 12, R224.	1.6	48
1073	Three-Dimensional Culture Alters Primary Cardiac Cell Phenotype. <i>Tissue Engineering - Part A</i> , 2010, 16, 629-641.	1.6	40
1074	Translation efficiency in humans: tissue specificity, global optimization and differences between developmental stages. <i>Nucleic Acids Research</i> , 2010, 38, 2964-2974.	6.5	69
1075	Heat Shock Transcription Factor 1 Localizes to Sex Chromatin during Meiotic Repression. <i>Journal of Biological Chemistry</i> , 2010, 285, 34469-34476.	1.6	62
1076	Transcriptional control of the proliferation cluster by the tumor suppressor p53. <i>Molecular BioSystems</i> , 2010, 6, 17-29.	2.9	28
1077	Protein phosphorylation analysis in archival clinical cancer samples by shotgun and targeted proteomics approaches. <i>Molecular BioSystems</i> , 2011, 7, 2368.	2.9	35
1078	Investigating Neoplastic Progression of Ulcerative Colitis with Label-Free Comparative Proteomics. <i>Journal of Proteome Research</i> , 2011, 10, 200-209.	1.8	41
1079	Early gene response of human brain microvascular endothelial cells to <i>Listeria monocytogenes</i> infection. <i>Canadian Journal of Microbiology</i> , 2011, 57, 441-446.	0.8	5
1080	Histone deacetylase 3 is an epigenomic brake in macrophage alternative activation. <i>Genes and Development</i> , 2011, 25, 2480-2488.	2.7	254
1081	Alternative translation start sites are conserved in eukaryotic genomes. <i>Nucleic Acids Research</i> , 2011, 39, 567-577.	6.5	133

#	ARTICLE	IF	CITATIONS
1082	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
1083	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
1084	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
1085	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
1086	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
1087	Polycomb preferentially targets stalled promoters of coding and noncoding transcripts. <i>Genome Research</i> , 2011, 21, 216-226.	2.4	146
1088	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
1089	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
1090	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
1091	Aberrant Overexpression of Satellite Repeats in Pancreatic and Other Epithelial Cancers. <i>Science</i> , 2011, 331, 593-596.	6.0	452
1092	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
1093	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
1094	Deconstructing the molecular portraits of breast cancer. <i>Molecular Oncology</i> , 2011, 5, 5-23.	2.1	1,059
1095	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
1096	GO Trimming: Systematically reducing redundancy in large Gene Ontology datasets. <i>BMC Research Notes</i> , 2011, 4, 267.	0.6	86
1097	Transcriptome signature of the adult mouse choroid plexus. <i>Fluids and Barriers of the CNS</i> , 2011, 8, 10.	2.4	88
1098	Intrinsic disorder of the extracellular matrix. <i>Molecular BioSystems</i> , 2011, 7, 3353.	2.9	54
1099	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

#	ARTICLE	IF	CITATIONS
1100	Systematic Approaches towards the Development of Host-Directed Antiviral Therapeutics. <i>International Journal of Molecular Sciences</i> , 2011, 12, 4027-4052.	1.8	79
1101	Genome-wide dFOXO targets and topology of the transcriptomic response to stress and insulin signalling. <i>Molecular Systems Biology</i> , 2011, 7, 502.	3.2	112
1102	The autism disconnect. <i>Nature</i> , 2011, 474, 294-295.	13.7	6
1103	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
1104	Ageing 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
1105	Cistrome: an integrative platform for transcriptional regulation studies. <i>Genome Biology</i> , 2011, 12, R83.	13.9	598
1106	Modeling the cumulative genetic risk for multiple sclerosis from genome-wide association data. <i>Genome Medicine</i> , 2011, 3, 3.	3.6	63
1107	Mechanisms of stable lipid loss in a social insect. <i>Journal of Experimental Biology</i> , 2011, 214, 3808-3821.	0.8	88
1108	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
1109	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
1110	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
1111	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
1112	Mbd3/NURD Complex Regulates Expression of 5-Hydroxymethylcytosine Marked Genes in Embryonic Stem Cells. <i>Cell</i> , 2011, 147, 1498-1510.	13.5	424
1113	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
1114	ATXN1 Protein Family and CIC Regulate Extracellular Matrix Remodeling and Lung Alveolarization. <i>Developmental Cell</i> , 2011, 21, 746-757.	3.1	89
1115	Chronic alcohol exposure induced gene expression changes in the zebrafish brain. <i>Behavioural Brain Research</i> , 2011, 216, 66-76.	1.2	64
1116	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
1117	Transcriptional profiling of intrinsic PNS factors in the postnatal mouse. <i>Molecular and Cellular Neurosciences</i> , 2011, 46, 32-44.	1.0	53

#	ARTICLE	IF	CITATIONS
1118	Oxidative stress induced carbonylation in human plasma. <i>Journal of Proteomics</i> , 2011, 74, 2395-2416.	1.2	37
1119	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
1120	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
1121	The transcriptional coactivator TAZ regulates mesenchymal differentiation in malignant glioma. <i>Genes and Development</i> , 2011, 25, 2594-2609.	2.7	326
1122	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
1123	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
1124	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
1125	MicroRNA dysregulation following spinal cord contusion: implications for neural plasticity and repair. <i>Neuroscience</i> , 2011, 186, 146-160.	1.1	128
1126	Polymicrobial periodontal pathogen transcriptomes in calvarial bone and soft tissue. <i>Molecular Oral Microbiology</i> , 2011, 26, 303-320.	1.3	11
1127	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
1128	Transcriptome analysis of embryonic mammary cells reveals insights into mammary lineage establishment. <i>Breast Cancer Research</i> , 2011, 13, R79.	2.2	46
1129	System Level Changes in Gene Expression in Maturing Bladder Mucosa. <i>Journal of Urology</i> , 2011, 185, 1952-1958.	0.2	5
1130	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
1131	Microarray Analysis of Iris Gene Expression in Mice with Mutations Influencing Pigmentation. , 2011, 52, 237.		14
1132	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
1133	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
1134	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
1135	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

#	ARTICLE	IF	CITATIONS
1136	On Acute Gene Expression Changes after Ventral Root Replantation. <i>Frontiers in Neurology</i> , 2011, 1, 159.	1.1	13
1137	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
1138	Transcriptomic Analysis in a <i>Drosophila</i> 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
1139	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
1140	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
1141	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
1142	A Network-Based Approach to Prioritize Results from Genome-Wide Association Studies. <i>PLoS ONE</i> , 2011, 6, e24220.	1.1	64
1143	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
1144	Genome-Wide Polymorphism and Comparative Analyses in the White-Tailed Deer (<i>Odocoileus</i>) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 42	1.1	41
1145	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
1146	Autism and Increased Paternal Age Related Changes in Global Levels of Gene Expression Regulation. <i>PLoS ONE</i> , 2011, 6, e16715.	1.1	91
1147	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
1148	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
1149	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
1150	Identification of ER Proteins Involved in the Functional Organisation of the Early Secretory Pathway in <i>Drosophila</i> Cells by a Targeted RNAi Screen. <i>PLoS ONE</i> , 2011, 6, e17173.	1.1	34
1151	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
1152	A New FACS Approach Isolates hESC Derived Endoderm Using Transcription Factors. <i>PLoS ONE</i> , 2011, 6, e17536.	1.1	23
1153	Identification and Replication of Loci Involved in Camptothecin-Induced Cytotoxicity Using CEPH Pedigrees. <i>PLoS ONE</i> , 2011, 6, e17561.	1.1	14

#	ARTICLE	IF	CITATIONS
1154	GOBO: Gene Expression-Based Outcome for Breast Cancer Online. PLoS ONE, 2011, 6, e17911.	1.1	361
1155	Identification of a Gene Regulatory Network Necessary for the Initiation of Oligodendrocyte Differentiation. PLoS ONE, 2011, 6, e18088.	1.1	88
1156	Relationship between Gene Body DNA Methylation and Intragenic H3K9me3 and H3K36me3 Chromatin Marks. PLoS ONE, 2011, 6, e18844.	1.1	131
1157	Dose-Dependent Onset of Regenerative Program in Neutron Irradiated Mouse Skin. PLoS ONE, 2011, 6, e19242.	1.1	13
1158	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
1159	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
1160	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
1161	A High-Throughput Platform for Lentiviral Overexpression Screening of the Human ORFeome. PLoS ONE, 2011, 6, e20057.	1.1	43
1162	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
1163	A Systems Level, Functional Genomics Analysis of Chronic Epilepsy. PLoS ONE, 2011, 6, e20763.	1.1	67
1164	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
1165	Interplay between SIN3A and STAT3 Mediates Chromatin Conformational Changes and GFAP Expression during Cellular Differentiation. PLoS ONE, 2011, 6, e22018.	1.1	48
1166	Quantitative Proteomics Identify Novel miR-155 Target Proteins. PLoS ONE, 2011, 6, e22146.	1.1	28
1167	Voluntary Wheel Running Reverses Age-Induced Changes in Hippocampal Gene Expression. PLoS ONE, 2011, 6, e22654.	1.1	61
1168	Genomic Analysis of Parent-of-Origin Allelic Expression in Arabidopsis thaliana Seeds. PLoS ONE, 2011, 6, e23687.	1.1	178
1169	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
1170	Proteomic Interrogation of Human Chromatin. PLoS ONE, 2011, 6, e24747.	1.1	35
1171	Necdin, a Negative Growth Regulator, Is a Novel STAT3 Target Gene Down-Regulated in Human Cancer. PLoS ONE, 2011, 6, e24923.	1.1	16

#	ARTICLE	IF	CITATIONS
1172	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
1173	attract: A Method for Identifying Core Pathways That Define Cellular Phenotypes. PLoS ONE, 2011, 6, e25445.	1.1	37
1174	HIF-1 and SKN-1 Coordinate the Transcriptional Response to Hydrogen Sulfide in Caenorhabditis elegans. PLoS ONE, 2011, 6, e25476.	1.1	55
1175	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
1176	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
1177	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
1178	Identification of Prognostic Genes for Recurrent Risk Prediction in Triple Negative Breast Cancer Patients in Taiwan. PLoS ONE, 2011, 6, e28222.	1.1	25
1179	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
1180	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
1181	Microarray Analysis for <i>Saccharomyces cerevisiae</i> . Journal of Visualized Experiments, 2011, , .	0.2	3
1182	Analysis of the Human Pancreatic Stellate Cell Secreted Proteome. Pancreas, 2011, 40, 557-566.	0.5	83
1183	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
1184	Aberrant DNA hypermethylation signature in acute myeloid leukemia directed by EVI1. Blood, 2011, 117, 234-241.	0.6	94
1185	Classical Hodgkin's lymphoma shows epigenetic features of abortive plasma cell differentiation. Haematologica, 2011, 96, 863-870.	1.7	20
1186	A meta-analysis of single base-pair substitutions in translational termination codons ('nonstop') Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18	1.4	34
1187	Gene expression profiling in male genital lichen sclerosis. International Journal of Experimental Pathology, 2011, 92, 320-325.	0.6	37
1188	The effects of mitochondrial genotype on hypoxic survival and gene expression in a hybrid population of the killifish, Fundulus heteroclitus. Molecular Ecology, 2011, 20, 4503-4520.	2.0	27
1189	Crx broadly modulates the pineal transcriptome. Journal of Neurochemistry, 2011, 119, 262-274.	2.1	25

#	ARTICLE	IF	CITATIONS
1190	Microarray analysis of nemorosoneâ€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
1191	Cytosine arabinoside induces ectoderm and inhibits mesoderm expression in human embryonic stem cells during multilineage differentiation. <i>British Journal of Pharmacology</i> , 2011, 162, 1743-1756.	2.7	44
1192	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
1193	Up-Regulation of MicroRNAs in Brain of Human Alcoholics. <i>Alcoholism: Clinical and Experimental Research</i> , 2011, 35, 1928-1937.	1.4	174
1194	Prdm14 initiates lymphoblastic leukemia after expanding a population of cells resembling common lymphoid progenitors. <i>Oncogene</i> , 2011, 30, 2859-2873.	2.6	52
1195	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
1196	The unfolded protein response transducer IRE1Î± prevents ER stress-induced hepatic steatosis. <i>EMBO Journal</i> , 2011, 30, 1357-1375.	3.5	302
1197	Extensive chromatin remodelling and establishment of transcription factor â€˜hotspotsâ€™ during early adipogenesis. <i>EMBO Journal</i> , 2011, 30, 1459-1472.	3.5	300
1198	KDM5B regulates embryonic stem cell self-renewal and represses cryptic intragenic transcription. <i>EMBO Journal</i> , 2011, 30, 1473-1484.	3.5	144
1199	Characterization of the macrophage transcriptome in glomerulonephritis-susceptible and -resistant rat strains. <i>Genes and Immunity</i> , 2011, 12, 78-89.	2.2	11
1200	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
1201	Somatic coding mutations in human induced pluripotent stem cells. <i>Nature</i> , 2011, 471, 63-67.	13.7	1,147
1202	Recapitulation of premature ageing with iPSCs from Hutchinsonâ€™s Gilford progeria syndrome. <i>Nature</i> , 2011, 472, 221-225.	13.7	510
1203	Î³Np63 is an ectodermal gatekeeper of epidermal morphogenesis. <i>Cell Death and Differentiation</i> , 2011, 18, 887-896.	5.0	119
1204	Mutant p53R175H upregulates Twist1 expression and promotes epithelialâ€™mesenchymal transition in immortalized prostate cells. <i>Cell Death and Differentiation</i> , 2011, 18, 271-281.	5.0	136
1205	Arsenic- and cadmium-induced toxicogenomic response in mouse embryos undergoing neurulation. <i>Toxicology and Applied Pharmacology</i> , 2011, 250, 117-129.	1.3	45
1206	Non-additive hepatic gene expression elicited by 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD) and 2,2â€™,4,4â€™,5,5â€™-hexachlorobiphenyl (PCB153) co-treatment in C57BL/6 mice. <i>Toxicology and Applied Pharmacology</i> , 2011, 256, 154-167.	1.3	23
1207	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

#	ARTICLE	IF	CITATIONS
1208	TGF β 2-1 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
1209	Comprehensive analysis of host gene expression in <i>Autographa californica</i> nucleopolyhedrovirus-infected <i>Spodoptera frugiperda</i> cells. <i>Virology</i> , 2011, 412, 167-178.	1.1	59
1210	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
1211	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
1212	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
1213	Trachealess (<i>Trh</i>) regulates all tracheal genes during <i>Drosophila</i> embryogenesis. <i>Developmental Biology</i> , 2011, 360, 160-172.	0.9	44
1214	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
1215	Effects of genome-wide copy number variation on expression in mammalian cells. <i>BMC Genomics</i> , 2011, 12, 562.	1.2	19
1216	Limited redundancy in genes regulated by Cyclin T2 and Cyclin T1. <i>BMC Research Notes</i> , 2011, 4, 260.	0.6	16
1217	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
1218	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
1219	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
1220	Microproteomic analysis of 10,000 laser captured microdissected breast tumor cells using short-range sodium dodecyl sulfate-polyacrylamide gel electrophoresis and porous layer open tubular liquid chromatography tandem mass spectrometry. <i>Journal of Chromatography A</i> , 2011, 1218, 8168-8174.	1.8	57
1221	Large-Scale Discovery of ERK2 Substrates Identifies ERK-Mediated Transcriptional Regulation by ETV3. <i>Science Signaling</i> , 2011, 4, rs11.	1.6	125
1222	Breast Cancer Methylomes Establish an Epigenomic Foundation for Metastasis. <i>Science Translational Medicine</i> , 2011, 3, 75ra25.	5.8	242
1223	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
1224	A systems biological view of intracellular pathogens. <i>Immunological Reviews</i> , 2011, 240, 117-128.	2.8	23
1225	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
1226	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
1227	Recent Admixture in an Indian Population of African Ancestry. <i>American Journal of Human Genetics</i> , 2011, 89, 111-120.	2.6	32
1228	<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
1229	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
1230	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
1231	A systems view of epithelial-mesenchymal transition signaling states. <i>Clinical and Experimental Metastasis</i> , 2011, 28, 137-155.	1.7	190
1232	OLIG2 is differentially expressed in pediatric astrocytic and in ependymal neoplasms. <i>Journal of Neuro-Oncology</i> , 2011, 104, 423-438.	1.4	63
1233	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
1234	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
1235	Genetic analysis of Down syndrome-associated heart defects in mice. <i>Human Genetics</i> , 2011, 130, 623-632.	1.8	47
1236	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
1237	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
1238	Rat neonatal beta cells lack the specialised metabolic phenotype of mature beta cells. <i>Diabetologia</i> , 2011, 54, 594-604.	2.9	111
1239	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
1240	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
1241	Genetic control of chicken heterophil function in advanced intercross lines: associations with novel and with known <i>Salmonella</i> resistance loci and a likely mechanism for cell death in extracellular trap production. <i>Immunogenetics</i> , 2011, 63, 449-458.	1.2	42
1242	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
1243	Effects of Cryopreservation on the Transcriptome of Human Embryonic Stem Cells After Thawing and Culturing. <i>Stem Cell Reviews and Reports</i> , 2011, 7, 506-517.	5.6	45

#	ARTICLE	IF	CITATIONS
1244	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
1245	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
1246	Flies selected for longevity retain a young gene expression profile. <i>Age</i> , 2011, 33, 69-80.	3.0	43
1247	TEAD1-dependent expression of the FoxO3a gene in mouse skeletal muscle. <i>BMC Molecular Biology</i> , 2011, 12, 1.	3.0	39
1248	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
1249	Parental ages and levels of DNA methylation in the newborn are correlated. <i>BMC Medical Genetics</i> , 2011, 12, 47.	2.1	86
1250	Expression patterns of microRNAs associated with CML phases and their disease related targets. <i>Molecular Cancer</i> , 2011, 10, 41.	7.9	124
1251	Analysis of EGFR signaling pathway in nasopharyngeal carcinoma cells by quantitative phosphoproteomics. <i>Proteome Science</i> , 2011, 9, 35.	0.7	30
1252	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
1253	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
1254	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
1255	Role of adhesion molecules and inflammation in Venezuelan equine encephalitis virus infected mouse brain. <i>Virology Journal</i> , 2011, 8, 197.	1.4	31
1256	The biology of lysine acetylation integrates transcriptional programming and metabolism. <i>Nutrition and Metabolism</i> , 2011, 8, 12.	1.3	59
1257	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
1258	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
1259	In Silico discovery of transcription factors as potential diagnostic biomarkers of ovarian cancer. <i>BMC Systems Biology</i> , 2011, 5, 144.	3.0	12
1260	Identifying cancer biomarkers by network-constrained support vector machines. <i>BMC Systems Biology</i> , 2011, 5, 161.	3.0	76
1261	Regulatory coordination of clustered microRNAs based on microRNA-transcription factor regulatory network. <i>BMC Systems Biology</i> , 2011, 5, 199.	3.0	57

#	ARTICLE	IF	CITATIONS
1262	Exploring molecular links between lymph node invasion and cancer prognosis in human breast cancer. <i>BMC Systems Biology</i> , 2011, 5, S4.	3.0	8
1263	Jejunal gene expression patterns correlate with severity of systemic infection in chicken. <i>BMC Proceedings</i> , 2011, 5, S4.	1.8	4
1264	Time course analysis of gene expression identifies multiple genes with differential expression in patients with in-stent restenosis. <i>BMC Medical Genomics</i> , 2011, 4, 20.	0.7	6
1265	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. <i>BMC Medical Genomics</i> , 2011, 4, 71.	0.7	20
1266	Alignment of gene expression profiles from test samples against a reference database: New method for context-specific interpretation of microarray data. <i>BioData Mining</i> , 2011, 4, 5.	2.2	5
1267	Genome-wide mapping of imprinted differentially methylated regions by DNA methylation profiling of human placentas from triploidies. <i>Epigenetics and Chromatin</i> , 2011, 4, 10.	1.8	84
1268	Extensive epigenetic reprogramming in human somatic tissues between fetus and adult. <i>Epigenetics and Chromatin</i> , 2011, 4, 7.	1.8	57
1269	A noise-reduction CWAS analysis implicates altered regulation of neurite outgrowth and guidance in autism. <i>Molecular Autism</i> , 2011, 2, 1.	2.6	191
1270	Transcriptional landscape of bone marrow-derived very small embryonic-like stem cells during hypoxia. <i>Respiratory Research</i> , 2011, 12, 63.	1.4	12
1271	Expression analysis of asthma candidate genes during human and murine lung development. <i>Respiratory Research</i> , 2011, 12, 86.	1.4	55
1272	Pathway-based analysis using reduced gene subsets in genome-wide association studies. <i>BMC Bioinformatics</i> , 2011, 12, 17.	1.2	30
1273	TAFFEL: Independent Enrichment Analysis of gene sets. <i>BMC Bioinformatics</i> , 2011, 12, 171.	1.2	1
1274	Identifier mapping performance for integrating transcriptomics and proteomics experimental results. <i>BMC Bioinformatics</i> , 2011, 12, 213.	1.2	73
1275	Discovering biological connections between experimental conditions based on common patterns of differential gene expression. <i>BMC Bioinformatics</i> , 2011, 12, 381.	1.2	21
1276	Network based transcription factor analysis of regenerating axolotl limbs. <i>BMC Bioinformatics</i> , 2011, 12, 80.	1.2	25
1277	Integrated metabolome and transcriptome analysis of the NCI60 dataset. <i>BMC Bioinformatics</i> , 2011, 12, S36.	1.2	38
1278	Construction and analysis of the protein-protein interaction networks for schizophrenia, bipolar disorder, and major depression. <i>BMC Bioinformatics</i> , 2011, 12, S20.	1.2	46
1279	Genome-wide mapping of Sox6 binding sites in skeletal muscle reveals both direct and indirect regulation of muscle terminal differentiation by Sox6. <i>BMC Developmental Biology</i> , 2011, 11, 59.	2.1	46

#	ARTICLE	IF	CITATIONS
1280	Identification of common and cell type specific LXXLL motif EcR cofactors using a bioinformatics refined candidate RNAi screen in <i>Drosophila melanogaster</i> cell lines. <i>BMC Developmental Biology</i> , 2011, 11, 66.	2.1	9
1281	Genome-wide analysis of gene expression during <i>Xenopus tropicalis</i> tadpole tail regeneration. <i>BMC Developmental Biology</i> , 2011, 11, 70.	2.1	74
1282	Identification of microRNA-mRNA modules using microarray data. <i>BMC Genomics</i> , 2011, 12, 138.	1.2	57
1283	Sequential analysis of global gene expression profiles in immature and in vitro matured bovine oocytes: potential molecular markers of oocyte maturation. <i>BMC Genomics</i> , 2011, 12, 151.	1.2	70
1284	Comparative transcriptome profiling of amyloid precursor protein family members in the adult cortex. <i>BMC Genomics</i> , 2011, 12, 160.	1.2	39
1285	Differences in TCDD-elicited gene expression profiles in human HepG2, mouse Hepa1c1c7 and rat H4IIE hepatoma cells. <i>BMC Genomics</i> , 2011, 12, 193.	1.2	48
1286	Gene expression patterns in four brain areas associate with quantitative measure of estrous behavior in dairy cows. <i>BMC Genomics</i> , 2011, 12, 200.	1.2	16
1287	Genome-wide survey reveals dynamic widespread tissue-specific changes in DNA methylation during development. <i>BMC Genomics</i> , 2011, 12, 231.	1.2	121
1288	Integration of Genome-Wide Computation DRE Search, AhR ChIP-chip and Gene Expression Analyses of TCDD-Elicited Responses in the Mouse Liver. <i>BMC Genomics</i> , 2011, 12, 365.	1.2	112
1289	Histological and transcriptome-wide level characteristics of fetal myofiber hyperplasia during the second half of gestation in Texel and Ujumqin sheep. <i>BMC Genomics</i> , 2011, 12, 411.	1.2	27
1290	Differential gene expression profiling of human bone marrow-derived mesenchymal stem cells during adipogenic development. <i>BMC Genomics</i> , 2011, 12, 461.	1.2	92
1291	Genome-wide examination of the transcriptional response to ecdysteroids 20-hydroxyecdysone and ponasterone A in <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2011, 12, 475.	1.2	17
1292	Deciphering c-MYC-regulated genes in two distinct tissues. <i>BMC Genomics</i> , 2011, 12, 476.	1.2	16
1293	Meta-analysis and genome-wide interpretation of genetic susceptibility to drug addiction. <i>BMC Genomics</i> , 2011, 12, 508.	1.2	34
1294	Searching ChIP-seq genomic islands for combinatorial regulatory codes in mouse embryonic stem cells. <i>BMC Genomics</i> , 2011, 12, 515.	1.2	6
1295	Sex-dimorphism in Cardiac Nutrigenomics: effect of Trans fat and/or Monosodium Glutamate consumption. <i>BMC Genomics</i> , 2011, 12, 555.	1.2	14
1296	Global assessment of genomic variation in cattle by genome resequencing and high-throughput genotyping. <i>BMC Genomics</i> , 2011, 12, 557.	1.2	74
1297	Genetic architecture of gene expression in ovine skeletal muscle. <i>BMC Genomics</i> , 2011, 12, 607.	1.2	18

#	ARTICLE	IF	CITATIONS
1298	Proteomic analysis of endothelial cold-adaptation. <i>BMC Genomics</i> , 2011, 12, 630.	1.2	19
1299	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
1300	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
1301	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
1302	Protease-associated cellular networks in malaria parasite <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2011, 12, S9.	1.2	22
1303	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
1304	<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
1305	A comparison of the <i>Giardia lamblia</i> trophozoite and cyst transcriptome using microarrays. <i>BMC Microbiology</i> , 2011, 11, 91.	1.3	24
1306	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
1307	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
1308	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
1309	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
1310	Quantitative temporal proteomic analysis of human embryonic stem cell differentiation into oligodendrocyte progenitor cells. <i>Proteomics</i> , 2011, 11, 4007-4020.	1.3	39
1311	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
1312	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
1313	Activation of interferon signaling pathways in spinal cord astrocytes from an ALS mouse model. <i>Glia</i> , 2011, 59, 946-958.	2.5	82
1314	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
1315	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

#	ARTICLE	IF	CITATIONS
1316	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
1317	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
1318	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
1319	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
1320	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
1321	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
1322	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
1323	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
1324	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
1325	Crosstalk between c-Jun and TAp73 β contributes to the apoptosis-survival balance. <i>Nucleic Acids Research</i> , 2011, 39, 6069-6085.	6.5	49
1326	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
1327	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
1328	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
1329	Waves of early transcriptional activation and pluripotency program initiation during human preimplantation development. <i>Development (Cambridge)</i> , 2011, 138, 3699-3709.	1.2	237
1330	FoxO3A promotes metabolic adaptation to hypoxia by antagonizing Myc function. <i>EMBO Journal</i> , 2011, 30, 4554-4570.	3.5	103
1331	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
1332	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
1333	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

#	ARTICLE	IF	CITATIONS
1334	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
1335	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
1336	Phosphoinositide 3-Kinase (PI3K(p110 β)) Directly Regulates Key Components of the Z-disc and Cardiac Structure*. <i>Journal of Biological Chemistry</i> , 2011, 286, 30837-30846.	1.6	32
1337	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
1338	microRNA-Seq reveals cocaine-regulated expression of striatal microRNAs. <i>Rna</i> , 2011, 17, 1529-1543.	1.6	113
1339	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
1340	Transcriptional Profiling of Diabetic Neuropathy in the BKS <i>db/db</i> Mouse. <i>Diabetes</i> , 2011, 60, 1981-1989.	0.3	107
1341	seqMINER: an integrated ChIP-seq data interpretation platform. <i>Nucleic Acids Research</i> , 2011, 39, e35-e35.	6.5	377
1342	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
1343	Mechanisms of Urokinase Plasminogen Activator (uPA)-mediated Atherosclerosis. <i>Journal of Biological Chemistry</i> , 2011, 286, 22665-22677.	1.6	51
1344	SigReannot-mart: a query environment for expression microarray probe re-annotations. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar025-bar025.	1.4	6
1345	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
1346	Conservation of Salmonella Infection Mechanisms in Plants and Animals. <i>PLoS ONE</i> , 2011, 6, e24112.	1.1	114
1347	A Comprehensive Expression Profile of MicroRNAs in Porcine Pituitary. <i>PLoS ONE</i> , 2011, 6, e24883.	1.1	22
1348	A Physical Interaction Network of Dengue Virus and Human Proteins. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.012187.	2.5	153
1349	P-Selectin Glycoprotein Ligand-1 Deficiency Is Protective Against Obesity-Related Insulin Resistance. <i>Diabetes</i> , 2011, 60, 189-199.	0.3	33
1350	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
1351	A Drosophila 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
1352	A CHOP-regulated microRNA controls rhodopsin expression. <i>Journal of Cell Biology</i> , 2011, 192, 919-927.	2.3	108
1353	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
1354	ChIP-seq analysis reveals distinct H3K27me3 profiles that correlate with transcriptional activity. <i>Nucleic Acids Research</i> , 2011, 39, 7415-7427.	6.5	250
1355	Mindbomb 1, an E3 ubiquitin ligase, forms a complex with RYK to activate Wnt/ β -catenin signaling. <i>Journal of Cell Biology</i> , 2011, 194, 737-750.	2.3	90
1356	Foxl1-Cre-marked adult hepatic progenitors have clonogenic and bilineage differentiation potential. <i>Genes and Development</i> , 2011, 25, 1185-1192.	2.7	138
1357	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
1358	Redox Proteomics of Protein-bound Methionine Oxidation. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006866.	2.5	117
1359	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
1360	Time-resolved Quantitative Proteome Analysis of In Vivo Intestinal Development. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.005231.	2.5	25
1361	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
1362	Prospective isolation of a bipotential clonogenic liver progenitor cell in adult mice. <i>Genes and Development</i> , 2011, 25, 1193-1203.	2.7	209
1363	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
1364	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
1365	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
1366	Nuclear and cytoplasmic localization of neural stem cell microRNAs. <i>Rna</i> , 2011, 17, 675-686.	1.6	105
1367	Characterization of the Core Elements of the NF- κ B Signaling Pathway of the Sea Anemone <i>Nematostella vectensis</i> . <i>Molecular and Cellular Biology</i> , 2011, 31, 1076-1087.	1.1	56
1368	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
1369	Human Papillomavirus 16 E5 Modulates the Expression of Host MicroRNAs. <i>PLoS ONE</i> , 2011, 6, e21646.	1.1	82

#	ARTICLE	IF	CITATIONS
1370	An integrative functional genomics approach for discovering biomarkers in schizophrenia. <i>Briefings in Functional Genomics</i> , 2011, 10, 387-399.	1.3	19
1371	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
1372	MicroRNAs Regulate the Timing of Embryo Maturation in Arabidopsis. <i>Plant Physiology</i> , 2011, 155, 1871-1884.	2.3	147
1373	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
1374	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
1375	An integrated transcriptomic and computational analysis for biomarker identification in gastric cancer. <i>Nucleic Acids Research</i> , 2011, 39, 1197-1207.	6.5	188
1376	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
1377	Suppression of Stra8 Expression in the Mouse Gonad by WIN 18,4461. <i>Biology of Reproduction</i> , 2011, 84, 957-965.	1.2	57
1378	Patterns of Gene Expression in Drosophila 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
1379	Genome-wide RNA-seq analysis of human and mouse platelet transcriptomes. <i>Blood</i> , 2011, 118, e101-e111.	0.6	484
1380	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
1381	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
1382	Gene Coexpression Network Topology of Cardiac Development, Hypertrophy, and Failure. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 26-35.	5.1	88
1383	Connectedness of PPI network neighborhoods identifies regulatory hub proteins. <i>Bioinformatics</i> , 2011, 27, 1135-1142.	1.8	28
1384	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
1385	Conjunctival Transcriptome in Scarring Trachoma. <i>Infection and Immunity</i> , 2011, 79, 499-511.	1.0	59
1386	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
1387	Sequentially acting Sox transcription factors in neural lineage development. <i>Genes and Development</i> , 2011, 25, 2453-2464.	2.7	263

#	ARTICLE	IF	CITATIONS
1388	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
1389	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
1390	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
1391	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
1392	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
1393	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
1394	Functional MicroRNA Involved in Endometriosis. <i>Molecular Endocrinology</i> , 2011, 25, 821-832.	3.7	220
1395	Diagnosis of Prostate Cancer Using Differentially Expressed Genes in Stroma. <i>Cancer Research</i> , 2011, 71, 2476-2487.	0.4	84
1396	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
1397	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
1398	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
1399	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
1400	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
1401	Overlapping and distinct pRb pathways in the mammalian auditory and vestibular organs. <i>Cell Cycle</i> , 2011, 10, 337-351.	1.3	29
1402	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
1403	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
1404	Functional Relevance of CpG Island Length for Regulation of Gene Expression. <i>Genetics</i> , 2011, 187, 1077-1083.	1.2	53
1405	Organelles Contribute Differentially to Reactive Oxygen Species-Related Events during Extended Darkness. <i>Plant Physiology</i> , 2011, 156, 185-201.	2.3	102

#	ARTICLE	IF	CITATIONS
1406	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
1407	Large-scale methylation domains mark a functional subset of neuronally expressed genes. <i>Genome Research</i> , 2011, 21, 1583-1591.	2.4	86
1408	Specific and Shared Targets of Ephrin A Signaling in Epidermal Keratinocytes. <i>Journal of Biological Chemistry</i> , 2011, 286, 9419-9428.	1.6	37
1409	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
1410	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
1411	Genomic Analysis Reveals a Novel Nuclear Factor- κ B (NF- κ B)-binding Site in Alu-repetitive Elements. <i>Journal of Biological Chemistry</i> , 2011, 286, 38768-38782.	1.6	55
1412	Combined transcriptome analysis of fetal human and mouse cerebral cortex exposed to alcohol. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4212-4217.	3.3	66
1413	Cardiac pressure overload hypertrophy is differentially regulated by β -adrenergic receptor subtypes. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2011, 301, H1461-H1470.	1.5	32
1414	piRNA profiling during specific stages of mouse spermatogenesis. <i>Rna</i> , 2011, 17, 1191-1203.	1.6	94
1415	Modulation of chromatin position and gene expression by HDAC4 interaction with nucleoporins. <i>Journal of Cell Biology</i> , 2011, 193, 21-29.	2.3	83
1416	Identification and Expression of Potential Regulators of the Mammalian Mitotic-to-Meiotic Transition1. <i>Biology of Reproduction</i> , 2011, 84, 34-42.	1.2	38
1417	Genetic and expression analysis of cattle identifies candidate genes in pathways responding to <i>Trypanosoma congolense</i> infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9304-9309.	3.3	92
1418	Functional Analysis of KAP1 Genomic Recruitment. <i>Molecular and Cellular Biology</i> , 2011, 31, 1833-1847.	1.1	99
1419	The Virulence of 1997 H5N1 Influenza Viruses in the Mouse Model Is Increased by Correcting a Defect in Their NS1 Proteins. <i>Journal of Virology</i> , 2011, 85, 7048-7058.	1.5	71
1420	NOA: a novel Network Ontology Analysis method. <i>Nucleic Acids Research</i> , 2011, 39, e87-e87.	6.5	101
1421	Fibroblast growth factor 9 delivery during angiogenesis produces durable, vasoresponsive microvessels wrapped by smooth muscle cells. <i>Nature Biotechnology</i> , 2011, 29, 421-427.	9.4	107
1422	CD140a identifies a population of highly myelinogenic, migration-competent and efficiently engrafting human oligodendrocyte progenitor cells. <i>Nature Biotechnology</i> , 2011, 29, 934-941.	9.4	185
1423	Genetic regulation of Nrx1 expression: an integrative cross-species analysis of schizophrenia candidate genes. <i>Translational Psychiatry</i> , 2011, 1, e25-e25.	2.4	26

#	ARTICLE	IF	CITATIONS
1424	Resolution of infection promotes a state of dormancy and long survival of CD4 memory T cells. <i>Immunology and Cell Biology</i> , 2011, 89, 870-881.	1.0	22
1425	Identification of maternally regulated fetal gene networks in the placenta with a novel embryo transfer system in mice. <i>Physiological Genomics</i> , 2011, 43, 317-324.	1.0	3
1426	An integrative clustering and modeling algorithm for dynamical gene expression data. <i>Bioinformatics</i> , 2011, 27, i392-i400.	1.8	26
1427	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
1428	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
1429	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
1430	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
1431	Mapping Protein Interactions between Dengue Virus and Its Human and Insect Hosts. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e954.	1.3	93
1432	Proteomic Analysis of Sera from Common Variable Immunodeficiency Patients Undergoing Replacement Intravenous Immunoglobulin Therapy. <i>Journal of Biomedicine and Biotechnology</i> , 2011, 2011, 1-10.	3.0	4
1433	Identifying Causal Genes and Dysregulated Pathways in Complex Diseases. <i>PLoS Computational Biology</i> , 2011, 7, e1001095.	1.5	163
1434	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
1435	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
1436	Biologicals and Fetal Cell Therapy for Wound and Scar Management. <i>ISRN Dermatology</i> , 2011, 2011, 1-16.	1.9	21
1437	COSINE: COndition-Specific sub-NEtwork identification using a global optimization method. <i>Bioinformatics</i> , 2011, 27, 1290-1298.	1.8	101
1438	Gene Expression in the Rodent Brain is Associated with Its Regional Connectivity. <i>PLoS Computational Biology</i> , 2011, 7, e1002040.	1.5	54
1439	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
1440	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
1441	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

#	ARTICLE	IF	CITATIONS
1442	Interactions between Glucocorticoid Treatment and Cis-Regulatory Polymorphisms Contribute to Cellular Response Phenotypes. <i>PLoS Genetics</i> , 2011, 7, e1002162.	1.5	103
1443	Over-Expression of DSCAM and COL6A2 Cooperatively Generates Congenital Heart Defects. <i>PLoS Genetics</i> , 2011, 7, e1002344.	1.5	79
1444	<i>Candida albicans</i> Infection of <i>Caenorhabditis elegans</i> Induces Antifungal Immune Defenses. <i>PLoS Pathogens</i> , 2011, 7, e1002074.	2.1	131
1445	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
1446	Prolyl Endopeptidase Is Involved in Cellular Signalling in Human Neuroblastoma SH-SY5Y Cells. <i>NeuroSignals</i> , 2011, 19, 97-109.	0.5	25
1447	RNA-Seq analysis in MeV. <i>Bioinformatics</i> , 2011, 27, 3209-3210.	1.8	461
1448	<i>GO-Module</i>: functional synthesis and improved interpretation of Gene Ontology patterns. <i>Bioinformatics</i> , 2011, 27, 1444-1446.	1.8	97
1449	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
1450	Fenfluramine-Induced Gene Dysregulation in Human Pulmonary Artery Smooth Muscle and Endothelial Cells. <i>Pulmonary Circulation</i> , 2011, 1, 405-418.	0.8	7
1451	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
1452	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
1453	Nuclear localization of β -tubulin affects E2F transcriptional activity and S-phase progression. <i>FASEB Journal</i> , 2011, 25, 3815-3827.	0.2	46
1454	Gene Expression Profiling in Human High-Grade Astrocytomas. <i>Comparative and Functional Genomics</i> , 2011, 2011, 1-10.	2.0	25
1455	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
1456	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
1457	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
1458	Temporal Coordination of Gene Networks by Zelda in the Early <i>Drosophila</i> Embryo. <i>PLoS Genetics</i> , 2011, 7, e1002339.	1.5	222
1459	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
1460	Retinoic acid inhibits endometrial cancer cell growth via multiple genomic mechanisms. <i>Journal of Molecular Endocrinology</i> , 2011, 46, 139-153.	1.1	34
1461	Biological assessment of robust noise models in microarray data analysis. <i>Bioinformatics</i> , 2011, 27, 807-814.	1.8	27
1462	RuleGO: a logical rules-based tool for description of gene groups by means of Gene Ontology. <i>Nucleic Acids Research</i> , 2011, 39, W293-W301.	6.5	12
1463	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
1464	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
1465	ELK1 Uses Different DNA Binding Modes to Regulate Functionally Distinct Classes of Target Genes. <i>PLoS Genetics</i> , 2012, 8, e1002694.	1.5	66
1466	Rapid Turnover of Long Noncoding RNAs and the Evolution of Gene Expression. <i>PLoS Genetics</i> , 2012, 8, e1002841.	1.5	284
1467	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
1468	Quantifying the white blood cell transcriptome as an accessible window to the multiorgan transcriptome. <i>Bioinformatics</i> , 2012, 28, 538-545.	1.8	52
1469	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
1470	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
1471	Enhancing the Prioritization of Disease-Causing Genes through Tissue Specific Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2012, 8, e1002690.	1.5	145
1472	Transcriptional Profiling of the Bladder in Urogenital Schistosomiasis Reveals Pathways of Inflammatory Fibrosis and Urothelial Compromise. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1912.	1.3	44
1473	An Integrated Regulatory Network Reveals Pervasive Cross-Regulation among Transcription and Splicing Factors. <i>PLoS Computational Biology</i> , 2012, 8, e1002603.	1.5	14
1474	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
1475	Overactivation of Hedgehog Signaling Alters Development of the Ovarian Vasculature in Mice1. <i>Biology of Reproduction</i> , 2012, 86, 174.	1.2	34
1476	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
1477	The human phosphotyrosine signaling network: Evolution and hotspots of hijacking in cancer. <i>Genome Research</i> , 2012, 22, 1222-1230.	2.4	72

#	ARTICLE	IF	CITATIONS
1478	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
1479	Interleukin-1 β modulates smooth muscle cell phenotype to a distinct inflammatory state relative to PDGF-DD via NF- κ B-dependent mechanisms. <i>Physiological Genomics</i> , 2012, 44, 417-429.	1.0	106
1480	Transcriptomic Characterization of Temperature Stress Responses in Larval Zebrafish. <i>PLoS ONE</i> , 2012, 7, e37209.	1.1	171
1481	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
1482	A promoter DNA demethylation landscape of human hematopoietic differentiation. <i>Nucleic Acids Research</i> , 2012, 40, 116-131.	6.5	97
1483	GenomeRunner: automating genome exploration. <i>Bioinformatics</i> , 2012, 28, 419-420.	1.8	41
1484	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
1485	A microRNA network regulates expression and biosynthesis of wild-type and Δ 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
1486	Abnormal p38 α 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
1487	A Quantitative Spatial Proteomics Analysis of Proteome Turnover in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011429.	2.5	332
1488	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
1489	Gene-Expression Changes Caused by Inbreeding Protect Against Inbreeding Depression in <i>Drosophila</i> . <i>Genetics</i> , 2012, 192, 161-172.	1.2	18
1490	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
1491	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
1492	GeneWeaver: a web-based system for integrative functional genomics. <i>Nucleic Acids Research</i> , 2012, 40, D1067-D1076.	6.5	112
1493	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
1494	Protein Kinase C (PKC) δ -mediated G_{i2} Stimulation of ERK5 Protein Pathway in Cardiomyocytes and Cardiac Fibroblasts. <i>Journal of Biological Chemistry</i> , 2012, 287, 7792-7802.	1.6	27
1495	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

#	ARTICLE	IF	CITATIONS
1496	FoxO6 regulates memory consolidation and synaptic function. <i>Genes and Development</i> , 2012, 26, 2780-2801.	2.7	116
1497	Gene Expression Analysis of the Embryonic Subplate. <i>Cerebral Cortex</i> , 2012, 22, 1343-1359.	1.6	83
1498	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
1499	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
1500	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
1501	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
1502	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
1503	Notch1 mediates uterine stromal differentiation and is critical for complete decidualization in the mouse. <i>FASEB Journal</i> , 2012, 26, 282-294.	0.2	94
1504	DAVID-WS: a stateful web service to facilitate gene/protein list analysis. <i>Bioinformatics</i> , 2012, 28, 1805-1806.	1.8	955
1505	Genome-wide mapping of Myc binding and gene regulation in serum-stimulated fibroblasts. <i>Oncogene</i> , 2012, 31, 1695-1709.	2.6	90
1506	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
1507	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
1508	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
1509	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
1510	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
1511	Association between SNPs and gene expression in multiple regions of the human brain. <i>Translational Psychiatry</i> , 2012, 2, e113-e113.	2.4	40
1512	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
1513	Advanced Bone Formation in Mice with a Dominant-negative Mutation in the Thyroid Hormone Receptor β^2 Gene due to Activation of Wnt/ β^2 -Catenin Protein Signaling. <i>Journal of Biological Chemistry</i> , 2012, 287, 17812-17822.	1.6	37

#	ARTICLE	IF	CITATIONS
1514	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
1515	Human Adipose Tissue Macrophages Display Activation of Cancer-related Pathways. <i>Journal of Biological Chemistry</i> , 2012, 287, 21904-21913.	1.6	60
1516	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
1517	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
1518	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
1519	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
1520	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
1521	Global Transcriptomic and Proteomic Responses of <i>Dehalococcoides ethenogenes</i> Strain 195 to Fixed Nitrogen Limitation. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1424-1436.	1.4	24
1522	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
1523	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
1524	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
1525	A program for annotating and predicting the effects of single nucleotide polymorphisms, SnpEff. <i>Fly</i> , 2012, 6, 80-92.	0.9	8,643
1526	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
1527	Tissue-Selective Regulation of Androgen-Responsive Genes. <i>Endocrine Research</i> , 2012, 37, 203-215.	0.6	14
1528	ReLiance: a machine learning and literature-based prioritization of receptor-ligand pairings. <i>Bioinformatics</i> , 2012, 28, i569-i574.	1.8	5
1529	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
1530	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
1531	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

#	ARTICLE	IF	CITATIONS
1532	Progesterone Inhibits Uterine Gland Development in the Neonatal Mouse Uterus1. <i>Biology of Reproduction</i> , 2012, 86, 146, 1-9.	1.2	66
1533	A New Approach for the Joint Analysis of Multiple Chip-Seq Libraries with Application to Histone Modification. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, Article 1.	0.2	15
1534	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
1535	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
1536	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
1537	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
1538	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
1539	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
1540	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
1541	Down-regulation of NF- κ B Transcriptional Activity in HIV-associated Kidney Disease by BRD4 Inhibition. <i>Journal of Biological Chemistry</i> , 2012, 287, 28840-28851.	1.6	172
1542	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
1543	Single-cell analysis of population context advances RNAi screening at multiple levels. <i>Molecular Systems Biology</i> , 2012, 8, 579.	3.2	153
1544	Microtubule stability, Golgi organization, and transport flux require dystonin-a2-MAP1B interaction. <i>Journal of Cell Biology</i> , 2012, 196, 727-742.	2.3	60
1545	Elephant Transcriptome Provides Insights into the Evolution of Eutherian Placentation. <i>Genome Biology and Evolution</i> , 2012, 4, 713-725.	1.1	27
1546	Mice Lacking the β 2 Adrenergic Receptor Have a Unique Genetic Profile before and after Focal Brain Ischaemia. <i>ASN Neuro</i> , 2012, 4, AN20110020.	1.5	20
1547	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
1548	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
1549	CUGBP1 and MBNL1 preferentially bind to 3' UTRs and facilitate mRNA decay. <i>Scientific Reports</i> , 2012, 2, 209.	1.6	150

#	ARTICLE	IF	CITATIONS
1550	A Novel Tumor suppressor network in squamous malignancies. <i>Scientific Reports</i> , 2012, 2, 828.	1.6	11
1551	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
1552	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
1553	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
1554	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
1555	KAP1 regulates gene networks controlling mouse B-lymphoid cell differentiation and function. <i>Blood</i> , 2012, 119, 4675-4685.	0.6	39
1556	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
1557	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
1558	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
1559	EnrichNet: network-based gene set enrichment analysis. <i>Bioinformatics</i> , 2012, 28, i451-i457.	1.8	269
1560	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
1561	Host Response Signature to Staphylococcus aureus Alpha-Hemolysin Implicates Pulmonary Th17 Response. <i>Infection and Immunity</i> , 2012, 80, 3161-3169.	1.0	44
1562	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
1563	The Cytokines Interleukin 27 and Interferon- γ Promote Distinct Treg Cell Populations Required to Limit Infection-Induced Pathology. <i>Immunity</i> , 2012, 37, 511-523.	6.6	340
1564	Alkylation Sensitivity Screens Reveal a Conserved Cross-species Functionome. <i>Molecular Cancer Research</i> , 2012, 10, 1580-1596.	1.5	35
1565	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
1566	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
1567	Implications for health and disease in the genetic signature of the Ashkenazi Jewish population. <i>Genome Biology</i> , 2012, 13, R2.	13.9	48

#	ARTICLE	IF	CITATIONS
1568	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
1569	Muscle Gene Expression Is a Marker of Amyotrophic Lateral Sclerosis Severity. <i>Neurodegenerative Diseases</i> , 2012, 9, 38-52.	0.8	41
1570	miR-10b*, a master inhibitor of the cell cycle, is downregulated in human breast tumours. <i>EMBO Molecular Medicine</i> , 2012, 4, 1214-1229.	3.3	85
1571	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
1572	Three Distinct Patterns of Histone H3Y41 Phosphorylation Mark Active Genes. <i>Cell Reports</i> , 2012, 2, 470-477.	2.9	54
1573	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
1574	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
1575	Genomic analysis of sleep deprivation reveals translational regulation in the hippocampus. <i>Physiological Genomics</i> , 2012, 44, 981-991.	1.0	123
1576	Transcriptional responses to loss of RNase H2 in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2012, 11, 933-941.	1.3	20
1577	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
1578	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
1579	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
1580	ANAP: An Integrated Knowledge Base for Arabidopsis Protein Interaction Network Analysis. <i>Plant Physiology</i> , 2012, 158, 1523-1533.	2.3	31
1581	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
1582	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
1583	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
1584	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
1585	Proteomic analysis of extracellular matrix from the hepatic stellate cell line LX-2 identifies CYR61 and Wnt-5a as novel constituents of fibrotic liver. <i>Journal of Proteome Research</i> , 2012, 11, 4052-4064.	1.8	66

#	ARTICLE	IF	CITATIONS
1586	Evolution and function of CAG/polyglutamine repeats in protein-protein interaction networks. <i>Nucleic Acids Research</i> , 2012, 40, 4273-4287.	6.5	166
1587	Clinical and molecular characteristics of congenital glioblastoma. <i>Neuro-Oncology</i> , 2012, 14, 931-941.	0.6	45
1588	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
1589	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
1590	Using Rule-Based Machine Learning for Candidate Disease Gene Prioritization and Sample Classification of Cancer Gene Expression Data. <i>PLoS ONE</i> , 2012, 7, e39932.	1.1	95
1591	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
1592	Wnt5a Potentiates TGF- β 2 Signaling to Promote Colonic Crypt Regeneration After Tissue Injury. <i>Science</i> , 2012, 338, 108-113.	6.0	402
1593	SIRT7 links H3K18 deacetylation to maintenance of oncogenic transformation. <i>Nature</i> , 2012, 487, 114-118.	13.7	503
1594	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
1595	Transcriptome-wide Analysis of Exosome Targets. <i>Molecular Cell</i> , 2012, 48, 422-433.	4.5	184
1596	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
1597	KAP1 regulates gene networks controlling T-cell development and responsiveness. <i>FASEB Journal</i> , 2012, 26, 4561-4575.	0.2	45
1598	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
1599	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
1600	Sources of variance in baseline gene expression in the rodent liver. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2012, 746, 104-112.	0.9	16
1601	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
1602	Cell-Surface Proteomics Identifies Lineage-Specific Markers of Embryo-Derived Stem Cells. <i>Developmental Cell</i> , 2012, 22, 887-901.	3.1	134
1603	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

#	ARTICLE	IF	CITATIONS
1604	TAK1 Inhibition Promotes Apoptosis in KRAS-Dependent Colon Cancers. <i>Cell</i> , 2012, 148, 639-650.	13.5	245
1605	Quantitative proteomic analysis of mitochondrial proteins reveals prosurvival mechanisms in the perpetuation of radiation-induced genomic instability. <i>Free Radical Biology and Medicine</i> , 2012, 53, 618-628.	1.3	13
1606	Quantitative Proteomic Profiling Identifies Protein Correlates to EGFR Kinase Inhibition. <i>Molecular Cancer Therapeutics</i> , 2012, 11, 1071-1081.	1.9	6
1607	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
1608	AbsIDconvert: An absolute approach for converting genetic identifiers at different granularities. <i>BMC Bioinformatics</i> , 2012, 13, 229.	1.2	8
1609	Augmented annotation and orthologue analysis for <i>Oryctolagus cuniculus</i> : Better Bunny. <i>BMC Bioinformatics</i> , 2012, 13, 84.	1.2	23
1610	Transcriptome landscape of the human placenta. <i>BMC Genomics</i> , 2012, 13, 115.	1.2	83
1611	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
1612	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
1613	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
1614	Postmortem cardiac tissue maintains gene expression profile even after late harvesting. <i>BMC Genomics</i> , 2012, 13, 26.	1.2	39
1615	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
1616	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
1617	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
1618	Brain transcriptome variation among behaviorally distinct strains of zebrafish (<i>Danio rerio</i>). <i>BMC Genomics</i> , 2012, 13, 323.	1.2	53
1619	<i>Burkholderia pseudomallei</i> transcriptional adaptation in macrophages. <i>BMC Genomics</i> , 2012, 13, 328.	1.2	52
1620	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
1621	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

#	ARTICLE	IF	CITATIONS
1622	Genome-wide analysis of hepatic LXR-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
1623	LRpath analysis reveals common pathways dysregulated via DNA methylation across cancer types. <i>BMC Genomics</i> , 2012, 13, 526.	1.2	65
1624	Conservation and divergence of chemical defense system in the tunicate <i>Oikopleura dioica</i> revealed by genome wide response to two xenobiotics. <i>BMC Genomics</i> , 2012, 13, 55.	1.2	24
1625	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
1626	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
1627	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
1628	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
1629	Systems analysis of inflammatory bowel disease based on comprehensive gene information. <i>BMC Medical Genetics</i> , 2012, 13, 25.	2.1	8
1630	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
1631	NF- κ 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
1632	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
1633	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
1634	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
1635	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
1636	An antibody microarray analysis of serum cytokines in neurodegenerative Parkinsonian syndromes. <i>Proteome Science</i> , 2012, 10, 71.	0.7	22
1637	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
1638	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
1639	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

#	ARTICLE	IF	CITATIONS
1640	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
1641	Recurrent mutations in the U2AF1 splicing factor in myelodysplastic syndromes. <i>Nature Genetics</i> , 2012, 44, 53-57.	9.4	513
1642	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
1643	Noncanonical MicroRNAs and Endogenous siRNAs in Lytic Infection of Murine Gammaherpesvirus. <i>PLoS ONE</i> , 2012, 7, e47863.	1.1	20
1644	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
1645	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
1646	A Noncoding, Regulatory Mutation Implicates HCFC1 in Nonsyndromic Intellectual Disability. <i>American Journal of Human Genetics</i> , 2012, 91, 694-702.	2.6	89
1647	Prediction of gene network models in limb muscle precursors. <i>Gene</i> , 2012, 509, 16-23.	1.0	8
1648	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
1649	Clonal Architecture of Secondary Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2012, 366, 1090-1098.	13.9	688
1650	Systems-pharmacology dissection of a drug synergy in imatinib-resistant CML. <i>Nature Chemical Biology</i> , 2012, 8, 905-912.	3.9	96
1651	Dysregulation of Uterine Signaling Pathways in Progesterone Receptor-Cre Knockout of Dicer. <i>Molecular Endocrinology</i> , 2012, 26, 1552-1566.	3.7	28
1652	Hypothesis-driven candidate genes for schizophrenia compared to genome-wide association results. <i>Psychological Medicine</i> , 2012, 42, 607-616.	2.7	83
1653	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
1654	Application of a systems approach to study developmental gene regulation. <i>Biophysical Reviews</i> , 2012, 4, 245-253.	1.5	2
1655	Identification of Cell Surface Targets through Meta-analysis of Microarray Data. <i>Neoplasia</i> , 2012, 14, 666-669.	2.3	17
1656	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
1657	Mapping of lamin A- and progerin-interacting genome regions. <i>Chromosoma</i> , 2012, 121, 447-464.	1.0	86

#	ARTICLE	IF	CITATIONS
1658	Position-dependent FUS-RNA interactions regulate alternative splicing events and transcriptions. <i>Scientific Reports</i> , 2012, 2, 529.	1.6	180
1659	Proteomic Analysis (GeLC-MS/MS) of ePFT-Collected Pancreatic Fluid in Chronic Pancreatitis. <i>Journal of Proteome Research</i> , 2012, 11, 1897-1912.	1.8	25
1660	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
1661	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
1662	Quantitative biomedical annotation using medical subject heading over-representation profiles (MeSHOPs). <i>BMC Bioinformatics</i> , 2012, 13, 249.	1.2	24
1663	Probing the <i>Xenopus laevis</i> inner ear transcriptome for biological function. <i>BMC Genomics</i> , 2012, 13, 225.	1.2	11
1664	Cliques for the identification of gene signatures for colorectal cancer across population. <i>BMC Systems Biology</i> , 2012, 6, S17.	3.0	44
1665	Computational gene network analysis reveals TNF-induced angiogenesis. <i>BMC Systems Biology</i> , 2012, 6, S12.	3.0	16
1666	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
1667	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
1668	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
1669	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
1670	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
1671	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
1672	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
1673	Mixing of Honeybees with Different Genotypes Affects Individual Worker Behavior and Transcription of Genes in the Neuronal Substrate. <i>PLoS ONE</i> , 2012, 7, e31653.	1.1	17
1674	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
1675	Knockdown of SF-1 and RNF31 Affects Components of Steroidogenesis, TGF β 2, and Wnt/ β -catenin Signaling in Adrenocortical Carcinoma Cells. <i>PLoS ONE</i> , 2012, 7, e32080.	1.1	24

#	ARTICLE	IF	CITATIONS
1676	PTRF/Cavin-1 and MIF Proteins Are Identified as Non-Small Cell Lung Cancer Biomarkers by Label-Free Proteomics. PLoS ONE, 2012, 7, e33752.	1.1	60
1677	HDL Proteome in Hemodialysis Patients: A Quantitative Nanoflow Liquid Chromatography-Tandem Mass Spectrometry Approach. PLoS ONE, 2012, 7, e34107.	1.1	67
1678	Gene Regulation of Intestinal Porcine Epithelial Cells IPEC-J2 Is Dependent on the Site of Deoxyvalenol Toxicological Action. PLoS ONE, 2012, 7, e34136.	1.1	28
1679	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
1680	A Systems Biology Approach to Characterize the Regulatory Networks Leading to Trabectedin Resistance in an In Vitro Model of Myxoid Liposarcoma. PLoS ONE, 2012, 7, e35423.	1.1	19
1681	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
1682	Linking Proteins to Signaling Pathways for Experiment Design and Evaluation. PLoS ONE, 2012, 7, e36202.	1.1	28
1683	Transcriptional Programs Controlling Perinatal Lung Maturation. PLoS ONE, 2012, 7, e37046.	1.1	67
1684	Expression Profiling Reveals Novel Hypoxic Biomarkers in Peripheral Blood of Adult Mice Exposed to Chronic Hypoxia. PLoS ONE, 2012, 7, e37497.	1.1	16
1685	Oligonucleotide Microarray Analysis of Dietary-Induced Hyperlipidemia Gene Expression Profiles in Miniature Pigs. PLoS ONE, 2012, 7, e37581.	1.1	16
1686	Circadian Rhythm-Dependent Alterations of Gene Expression in Drosophila Brain Lacking Fragile X Mental Retardation Protein. PLoS ONE, 2012, 7, e37937.	1.1	19
1687	Role of MXD3 in Proliferation of DAOY Human Medulloblastoma Cells. PLoS ONE, 2012, 7, e38508.	1.1	24
1688	Intra- and Inter-Individual Variance of Gene Expression in Clinical Studies. PLoS ONE, 2012, 7, e38650.	1.1	35
1689	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
1690	CD28 Costimulation Regulates Genome-Wide Effects on Alternative Splicing. PLoS ONE, 2012, 7, e40032.	1.1	51
1691	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
1692	Twist1 Transcriptional Targets in the Developing Atrio-Ventricular Canal of the Mouse. PLoS ONE, 2012, 7, e40815.	1.1	10
1693	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

#	ARTICLE	IF	CITATIONS
1694	Cre-Mediated Stress Affects Sirtuin Expression Levels, Peroxisome Biogenesis and Metabolism, Antioxidant and Proinflammatory Signaling Pathways. PLoS ONE, 2012, 7, e41097.	1.1	26
1695	Measuring the Maturity of the Fast-Spiking Interneuron Transcriptional Program in Autism, Schizophrenia, and Bipolar Disorder. PLoS ONE, 2012, 7, e41215.	1.1	64
1696	Prion Protein and Shadoo Are Involved in Overlapping Embryonic Pathways and Trophoblastic Development. PLoS ONE, 2012, 7, e41959.	1.1	22
1697	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
1698	Phosphoproteome of Human Glioblastoma Initiating Cells Reveals Novel Signaling Regulators Encoded by the Transcriptome. PLoS ONE, 2012, 7, e43398.	1.1	34
1699	miRNA Regulation of Gene Expression: A Predictive Bioinformatics Analysis in the Postnatally Developing Monkey Hippocampus. PLoS ONE, 2012, 7, e43435.	1.1	13
1700	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
1701	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
1702	Peripheral Blood Gene Expression as a Novel Genomic Biomarker in Complicated Sarcoidosis. PLoS ONE, 2012, 7, e44818.	1.1	73
1703	Multi-Edge Gene Set Networks Reveal Novel Insights into Global Relationships between Biological Themes. PLoS ONE, 2012, 7, e45211.	1.1	10
1704	Inhibition of AKT with the Orally Active Allosteric AKT Inhibitor, MK-2206, Sensitizes Endometrial Cancer Cells to Progesterone. PLoS ONE, 2012, 7, e41593.	1.1	45
1705	Exploring the Transcriptome of Ciliated Cells Using In Silico Dissection of Human Tissues. PLoS ONE, 2012, 7, e35618.	1.1	73
1706	Elongation Factor 1 alpha1 and Genes Associated with Usher Syndromes Are Downstream Targets of GBX2. PLoS ONE, 2012, 7, e47366.	1.1	13
1707	DNA Hypomethylation Affects Cancer-Related Biological Functions and Genes Relevant in Neuroblastoma Pathogenesis. PLoS ONE, 2012, 7, e48401.	1.1	31
1708	Novel SNP Discovery in African Buffalo, <i>Syncerus caffer</i> , Using High-Throughput Sequencing. PLoS ONE, 2012, 7, e48792.	1.1	15
1709	Structural, Genetic, and Functional Signatures of Disordered Neuro-Immunological Development in Autism Spectrum Disorder. PLoS ONE, 2012, 7, e48835.	1.1	15
1710	Building a Statistical Model for Predicting Cancer Genes. PLoS ONE, 2012, 7, e49175.	1.1	2
1711	Characteristics and Predictive Value of Blood Transcriptome Signature in Males with Autism Spectrum Disorders. PLoS ONE, 2012, 7, e49475.	1.1	151

#	ARTICLE	IF	CITATIONS
1712	Micro-Scale Genomic DNA Copy Number Aberrations as Another Means of Mutagenesis in Breast Cancer. <i>PLoS ONE</i> , 2012, 7, e51719.	1.1	13
1713	Application of an Integrative Computational Framework in Transcriptomic Data of Atherosclerotic Mice Suggests Numerous Molecular Players. <i>Advances in Bioinformatics</i> , 2012, 2012, 1-9.	5.7	5
1714	Genome-Wide Identification and Quantification of cis- and trans-Regulated Genes Responding to Marek's Disease Virus Infection via Analysis of Allele-Specific Expression. <i>Frontiers in Genetics</i> , 2012, 2, 113.	1.1	20
1715	Systems Biology Approach to Identify Gene Network Signatures for Colorectal Cancer. <i>Frontiers in Genetics</i> , 2012, 3, 80.	1.1	16
1716	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
1717	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
1718	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
1719	Sex-Specific Modulation of Gene Expression Networks in Murine Hypothalamus. <i>Frontiers in Neuroscience</i> , 2012, 6, 63.	1.4	49
1720	In Vivo Topoisomerase I Inhibition Attenuates the Expression of Hypoxia-Inducible Factor 1 α Target Genes and Decreases Tumor Angiogenesis. <i>Molecular Medicine</i> , 2012, 18, 83-94.	1.9	36
1721	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
1722	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
1723	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
1724	Mass spectrometry-based proteomics: qualitative identification to activity-based protein profiling. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2012, 4, 141-162.	6.6	12
1725	Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. <i>Genome Research</i> , 2012, 22, 246-258.	2.4	476
1726	A decade of 3C technologies: insights into nuclear organization. <i>Genes and Development</i> , 2012, 26, 11-24.	2.7	631
1727	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
1728	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
1729	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

#	ARTICLE	IF	CITATIONS
1730	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
1731	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
1732	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
1733	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
1734	RNA Profiling and Chromatin Immunoprecipitation-Sequencing Reveal that PTF1a Stabilizes Pancreas Progenitor Identity via the Control of MNX1/HLXB9 and a Network of Other Transcription Factors. <i>Molecular and Cellular Biology</i> , 2012, 32, 1189-1199.	1.1	51
1735	Intermittent hypoxia activates temporally coordinated transcriptional programs in visceral adipose tissue. <i>Journal of Molecular Medicine</i> , 2012, 90, 435-445.	1.7	33
1736	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
1737	Genome-wide identification of palmitate-regulated immediate early genes and target genes in pancreatic beta-cells reveals a central role of NF- κ B. <i>Molecular Biology Reports</i> , 2012, 39, 6781-6789.	1.0	20
1738	Functional Characterization and Gene Expression Profiling of β -Smooth Muscle Actin Expressing Cardiomyocytes Derived from Murine Induced Pluripotent Stem Cells. <i>Stem Cell Reviews and Reports</i> , 2012, 8, 229-242.	5.6	8
1739	Effects of Oestrogen on MicroRNA Expression in Hormone-Responsive Breast Cancer Cells. <i>Hormones and Cancer</i> , 2012, 3, 65-78.	4.9	51
1740	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
1741	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
1742	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
1743	GENOMIC BASIS OF AGING AND LIFE-HISTORY EVOLUTION IN <i>DROSOPHILA MELANOGASTER</i> . Evolution; <i>International Journal of Organic Evolution</i> , 2012, 66, 3390-3403.	1.1	134
1744	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
1745	Transcriptional insights on the regenerative mechanics of axotomized neurons <i>in vitro</i> . <i>Journal of Cellular and Molecular Medicine</i> , 2012, 16, 789-811.	1.6	8
1746	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
1747	Gene expression profiling of the brain: Pondering facts and fiction. <i>Neurobiology of Disease</i> , 2012, 45, 3-7.	2.1	13

#	ARTICLE	IF	CITATIONS
1748	Post-fasting olfactory, transcriptional, and feeding responses in <i>Drosophila</i> . <i>Physiology and Behavior</i> , 2012, 105, 544-553.	1.0	60
1749	Genome-wide association analysis for feed efficiency in Angus cattle. <i>Animal Genetics</i> , 2012, 43, 367-374.	0.6	110
1750	Ex vivo 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
1751	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
1752	A systematic comparison of genome-scale clustering algorithms. <i>BMC Bioinformatics</i> , 2012, 13, S7.	1.2	55
1753	Downregulation of HuR as a new mechanism of doxorubicin resistance in breast cancer cells. <i>Molecular Cancer</i> , 2012, 11, 13.	7.9	63
1754	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
1755	Transcriptional response to foraging experience in the honey bee mushroom bodies. <i>Developmental Neurobiology</i> , 2012, 72, 153-166.	1.5	36
1756	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
1757	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
1758	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
1759	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
1760	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
1761	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
1762	Transcriptome profiling of mice testes following low dose irradiation. <i>Reproductive Biology and Endocrinology</i> , 2013, 11, 50.	1.4	11
1763	Genetic variability in the rat Aplec C-type lectin gene cluster regulates lymphocyte trafficking and motor neuron survival after traumatic nerve root injury. <i>Journal of Neuroinflammation</i> , 2013, 10, 60.	3.1	9
1764	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
1765	Embryonic mammary signature subsets are activated in Brca1 -/- and basal-like breast cancers. <i>Breast Cancer Research</i> , 2013, 15, R25.	2.2	52

#	ARTICLE	IF	CITATIONS
1766	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
1767	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
1768	Genome-wide analysis reveals downregulation of miR-379/miR-656 cluster in human cancers. <i>Biology Direct</i> , 2013, 8, 10.	1.9	69
1769	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
1770	DNA methylation and transcriptional noise. <i>Epigenetics and Chromatin</i> , 2013, 6, 9.	1.8	115
1771	MeCP2 modulates gene expression pathways in astrocytes. <i>Molecular Autism</i> , 2013, 4, 3.	2.6	74
1772	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
1773	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
1774	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
1775	Genome-wide association study of antibody response to Newcastle disease virus in chicken. <i>BMC Genetics</i> , 2013, 14, 42.	2.7	32
1776	Deep brain stimulation modulates nonsense-mediated RNA decay in Parkinson's patients leukocytes. <i>BMC Genomics</i> , 2013, 14, 478.	1.2	14
1777	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
1778	Transcriptome analysis of porcine <i>M. semimembranosus</i> divergent in intramuscular fat as a consequence of dietary protein restriction. <i>BMC Genomics</i> , 2013, 14, 453.	1.2	58
1779	Detection of selective sweeps in cattle using genome-wide SNP data. <i>BMC Genomics</i> , 2013, 14, 382.	1.2	102
1780	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
1781	Genome-wide association study of sleep in <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2013, 14, 281.	1.2	131
1782	Extensive circadian and light regulation of the transcriptome in the malaria mosquito <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , 2013, 14, 218.	1.2	69
1783	Dynamic regulation of epigenomic landscapes during hematopoiesis. <i>BMC Genomics</i> , 2013, 14, 193.	1.2	41

#	ARTICLE	IF	CITATIONS
1784	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
1785	Profiling and metaanalysis of epidermal keratinocytes responses to epidermal growth factor. <i>BMC Genomics</i> , 2013, 14, 85.	1.2	29
1786	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
1787	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
1788	Microarray gene expression profiling of neural tissues in bovine spastic paresis. <i>BMC Veterinary Research</i> , 2013, 9, 122.	0.7	8
1789	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
1790	Integrative analysis of congenital muscular torticollis: from gene expression to clinical significance. <i>BMC Medical Genomics</i> , 2013, 6, S10.	0.7	17
1791	Validation of microarray data in human lymphoblasts shows a role of the ubiquitin-proteasome system and NF- κ B in the pathogenesis of Down syndrome. <i>BMC Medical Genomics</i> , 2013, 6, 24.	0.7	22
1792	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
1793	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
1794	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
1795	Personal genomes, quantitative dynamic omics and personalized medicine. <i>Quantitative Biology</i> , 2013, 1, 71-90.	0.3	29
1796	An EST dataset for <i>Metasequoia glyptostroboides</i> buds: the first EST resource for molecular genomics studies in <i>Metasequoia</i> . <i>Planta</i> , 2013, 237, 755-770.	1.6	10
1797	Identification of circulating microRNAs in HNF1A-MODY carriers. <i>Diabetologia</i> , 2013, 56, 1743-1751.	2.9	26
1798	Research Resource: Progesterone Receptor Targetome Underlying Mammary Gland Branching Morphogenesis. <i>Molecular Endocrinology</i> , 2013, 27, 1743-1761.	3.7	37
1799	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
1800	A decision theory paradigm for evaluating identifier mapping and filtering methods using data integration. <i>BMC Bioinformatics</i> , 2013, 14, 223.	1.2	18
1801	Early Growth Response 3 (Egr-3) Is Induced by Transforming Growth Factor- β 2 and Regulates Fibrogenic Responses. <i>American Journal of Pathology</i> , 2013, 183, 1197-1208.	1.9	48

#	ARTICLE	IF	CITATIONS
1802	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
1803	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
1804	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
1805	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
1806	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
1807	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
1808	Differential L1 regulation in pluripotent stem cells of humans and apes. <i>Nature</i> , 2013, 503, 525-529.	13.7	220
1809	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
1810	Extended Self-Renewal and Accelerated Reprogramming in the Absence of Kdm5b. <i>Molecular and Cellular Biology</i> , 2013, 33, 4793-4810.	1.1	58
1811	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
1812	Thymic Stromal Lymphopoietin-Mediated Extramedullary Hematopoiesis Promotes Allergic Inflammation. <i>Immunity</i> , 2013, 39, 1158-1170.	6.6	64
1813	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
1814	The molecular diversity of Luminal A breast tumors. <i>Breast Cancer Research and Treatment</i> , 2013, 141, 409-420.	1.1	120
1815	Cytoplasmic polyadenylation is a major mRNA regulator during oogenesis and egg activation in <i>Drosophila</i> . <i>Developmental Biology</i> , 2013, 383, 121-131.	0.9	59
1816	Specification of Functional Cranial Placode Derivatives from Human Pluripotent Stem Cells. <i>Cell Reports</i> , 2013, 5, 1387-1402.	2.9	99
1817	SHANK3 overexpression causes manic-like behaviour with unique pharmacogenetic properties. <i>Nature</i> , 2013, 503, 72-77.	13.7	323
1818	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
1819	Gene expression analysis of induced pluripotent stem cells from aneuploid chromosomal syndromes. <i>BMC Genomics</i> , 2013, 14, S8.	1.2	30

#	ARTICLE	IF	CITATIONS
1820	Gene expression of sternohyoid and diaphragm muscles in type 2 diabetic rats. <i>BMC Endocrine Disorders</i> , 2013, 13, 43.	0.9	2
1821	Intronic Non-CG DNA hydroxymethylation and alternative mRNA splicing in honey bees. <i>BMC Genomics</i> , 2013, 14, 666.	1.2	62
1822	MultiFacTV: module detection from higher-order time series biological data. <i>BMC Genomics</i> , 2013, 14, S2.	1.2	5
1823	HeLa cell response proteome alterations induced by mammalian reovirus T3D infection. <i>Virology Journal</i> , 2013, 10, 202.	1.4	5
1824	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
1826	PKIS: computational identification of protein kinases for experimentally discovered protein phosphorylation sites. <i>BMC Bioinformatics</i> , 2013, 14, 247.	1.2	43
1827	MicroRNAs implicated in dysregulation of gene expression following human lung transplantation. <i>Translational Respiratory Medicine</i> , 2013, 1, .	3.8	22
1828	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
1829	Mining differential top-k co-expression patterns from time course comparative gene expression datasets. <i>BMC Bioinformatics</i> , 2013, 14, 230.	1.2	27
1830	Microarray characterization of gene expression changes in blood during acute ethanol exposure. <i>BMC Medical Genomics</i> , 2013, 6, 26.	0.7	15
1831	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
1832	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
1833	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
1834	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
1835	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
1836	Integrating human omics data to prioritize candidate genes. <i>BMC Medical Genomics</i> , 2013, 6, 57.	0.7	36
1837	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
1838	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

#	ARTICLE	IF	CITATIONS
1839	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
1840	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
1841	Stress susceptibility-specific phenotype associated with different hippocampal transcriptomic responses to chronic tricyclic antidepressant treatment in mice. <i>BMC Neuroscience</i> , 2013, 14, 144.	0.8	27
1842	Characterization of cell lines derived from breast cancers and normal mammary tissues for the study of the intrinsic molecular subtypes. <i>Breast Cancer Research and Treatment</i> , 2013, 142, 237-255.	1.1	169
1843	Mesenchymal Differentiation Mediated by NF- κ B Promotes Radiation Resistance in Glioblastoma. <i>Cancer Cell</i> , 2013, 24, 331-346.	7.7	856
1844	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
1845	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
1846	CDK-mediated activation of the SCF ^{FBXO} 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
1847	Integrative genomics of gene and metabolic regulation by estrogen receptors $\text{ER}\alpha$ and $\text{ER}\beta$, and their coregulators. <i>Molecular Systems Biology</i> , 2013, 9, 676.	3.2	81
1848	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
1849	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
1850	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
1851	Th-MYC ^N Mice with Caspase-8 Deficiency Develop Advanced Neuroblastoma with Bone Marrow Metastasis. <i>Cancer Research</i> , 2013, 73, 4086-4097.	0.4	57
1852	Ontogeny of erythroid gene expression. <i>Blood</i> , 2013, 121, e5-e13.	0.6	150
1853	Proteomics-Based Methods for Discovery, Quantification, and Validation of Protein-Protein Interactions. <i>Analytical Chemistry</i> , 2013, 85, 749-768.	3.2	85
1854	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
1855	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
1856	Glycoproteomics enabled by tagging sialic acid- or galactose-terminated glycans. <i>Glycobiology</i> , 2013, 23, 211-221.	1.3	81

#	ARTICLE	IF	CITATIONS
1857	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
1858	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
1859	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
1860	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
1861	Proteomic snapshot of breast cancer cell cycle: G1/S transition point. <i>Proteomics</i> , 2013, 13, 48-60.	1.3	19
1862	Comparative proteomic analysis of the ATP-sensitive K ⁺ channel complex in different tissue types. <i>Proteomics</i> , 2013, 13, 368-378.	1.3	16
1863	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
1864	Insulin/IGF-1 Controls Epidermal Morphogenesis via Regulation of FoxO-Mediated p63 Inhibition. <i>Developmental Cell</i> , 2013, 26, 176-187.	3.1	41
1865	Obesity and airway responsiveness: Role of TNFR2. <i>Pulmonary Pharmacology and Therapeutics</i> , 2013, 26, 444-454.	1.1	44
1866	Sost and its paralog Sostdc1 coordinate digit number in a Gli3-dependent manner. <i>Developmental Biology</i> , 2013, 383, 90-105.	0.9	47
1867	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
1868	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
1869	Basal Splicing Factors Regulate the Stability of Mature mRNAs in Trypanosomes. <i>Journal of Biological Chemistry</i> , 2013, 288, 4991-5006.	1.6	33
1870	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
1871	Dual Pten/Tp53 Suppression Promotes Sarcoma Progression by Activating Notch Signaling. <i>American Journal of Pathology</i> , 2013, 182, 2015-2027.	1.9	21
1872	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
1873	Family-wide Investigation of PDZ Domain-Mediated Protein-Protein Interactions Implicates β -Catenin in Maintaining the Integrity of Tight Junctions. <i>Chemistry and Biology</i> , 2013, 20, 816-827.	6.2	33
1874	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

#	ARTICLE	IF	CITATIONS
1875	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
1876	Evolutionary conservation of the polyproline II conformation surrounding intrinsically disordered phosphorylation sites. <i>Protein Science</i> , 2013, 22, 405-417.	3.1	50
1877	Network-Based Analysis of Multivariate Gene Expression Data. <i>Methods in Molecular Biology</i> , 2013, 972, 121-139.	0.4	7
1878	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
1879	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
1880	Cumulus and granulosa cell markers of oocyte and embryo quality. <i>Fertility and Sterility</i> , 2013, 99, 979-997.	0.5	224
1881	Accelerated gene evolution through replication-transcription conflicts. <i>Nature</i> , 2013, 495, 512-515.	13.7	120
1882	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
1883	The \pm Crystallin Domain of Small Heat Shock Protein β 8 (Hspb8) Acts as Survival and Differentiation Factor in Adult Hippocampal Neurogenesis. <i>Journal of Neuroscience</i> , 2013, 33, 5785-5796.	1.7	27
1884	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
1885	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013, 9, 652.	3.2	61
1886	Mapping the Human miRNA Interactome by CLASH Reveals Frequent Noncanonical Binding. <i>Cell</i> , 2013, 153, 654-665.	13.5	1,164
1887	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
1888	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
1889	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
1890	Regulation of IRS1/Akt insulin signaling by microRNA-128a during myogenesis. <i>Journal of Cell Science</i> , 2013, 126, 2678-91.	1.2	105
1891	TFEB controls cellular lipid metabolism through a starvation-induced autoregulatory loop. <i>Nature Cell Biology</i> , 2013, 15, 647-658.	4.6	796
1892	Glucocorticoid-Dependent Hippocampal Transcriptome in Male Rats: Pathway-Specific Alterations With Aging. <i>Endocrinology</i> , 2013, 154, 2807-2820.	1.4	30

#	ARTICLE	IF	CITATIONS
1893	Escherichia coli- and Staphylococcus aureus-induced mastitis differentially modulate transcriptional responses in neighbouring uninfected bovine mammary gland quarters. BMC Genomics, 2013, 14, 36.	1.2	125
1894	HDAC inhibitors induce tumor-cell-selective pro-apoptotic transcriptional responses. Cell Death and Disease, 2013, 4, e519-e519.	2.7	150
1895	Network-Based Multiple Sclerosis Pathway Analysis with GWAS Data from 15,000 Cases and 30,000 Controls. American Journal of Human Genetics, 2013, 92, 854-865.	2.6	164
1896	Methylomics of gene expression in human monocytes. Human Molecular Genetics, 2013, 22, 5065-5074.	1.4	95
1897	A NETWORK VIEW ON PARKINSON'S DISEASE. Computational and Structural Biotechnology Journal, 2013, 7, e201304004.	1.9	48
1898	Wood chemistry analysis and expression profiling of a poplar clone expressing a tyrosine-rich peptide. Plant Cell Reports, 2013, 32, 1827-1841.	2.8	5
1899	Transcriptional profiling identifies genes induced by hepatocyte-derived extracellular matrix in metastatic human colorectal cancer cell lines. Clinical and Experimental Metastasis, 2013, 30, 189-200.	1.7	19
1900	Cancer-related marketing centrality motifs acting as pivot units in the human signaling network and mediating cross-talk between biological pathways. Molecular BioSystems, 2013, 9, 3026.	2.9	13
1901	Tracking recent adaptive evolution in microbial species using TimeZone. Nature Protocols, 2013, 8, 652-665.	5.5	23
1902	Loss of Phosphatase and Tensin Homolog (PTEN) Induces Leptin-mediated Leptin Gene Expression. Journal of Biological Chemistry, 2013, 288, 29821-29835.	1.6	32
1903	Brain-Derived Neurotrophic Factor Signaling Rewrites the Glucocorticoid Transcriptome via Glucocorticoid Receptor Phosphorylation. Molecular and Cellular Biology, 2013, 33, 3700-3714.	1.1	93
1904	Changes in Eutopic Endometrial Gene Expression During the Progression of Experimental Endometriosis in the Baboon, Papio Anubis1. Biology of Reproduction, 2013, 88, 44.	1.2	62
1905	Prioritising risk pathways of complex human diseases based on functional profiling. European Journal of Human Genetics, 2013, 21, 666-672.	1.4	1
1906	Hepatic Differentiation and Maturation of Human Embryonic Stem Cells Cultured in a Perfused Three-Dimensional Bioreactor. Stem Cells and Development, 2013, 22, 581-594.	1.1	56
1907	Transcriptome Profiling Following Neuronal and Glial Expression of ALS-Linked SOD1 in <i>Drosophila</i> . G3: Genes, Genomes, Genetics, 2013, 3, 695-708.	0.8	23
1908	Systems-level approaches reveal conservation of trans-regulated genes in the rat and genetic determinants of blood pressure in humans. Cardiovascular Research, 2013, 97, 653-665.	1.8	31
1909	Systems biology of Ewing sarcoma: a network model of EWS-FLI1 effect on proliferation and apoptosis. Nucleic Acids Research, 2013, 41, 8853-8871.	6.5	45
1910	Analysis of the cartilage proteome from three different mouse models of genetic skeletal diseases reveals common and discrete disease signatures. Biology Open, 2013, 2, 802-811.	0.6	12

#	ARTICLE	IF	CITATIONS
1911	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
1912	Rat retinal transcriptome: Effects of aging and AMD-like retinopathy. <i>Cell Cycle</i> , 2013, 12, 1745-1761.	1.3	62
1913	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
1914	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
1915	Oncogenic ETS fusions deregulate E2F3 target genes in Ewing sarcoma and prostate cancer. <i>Genome Research</i> , 2013, 23, 1797-1809.	2.4	99
1916	Characterization of the rat developmental liver transcriptome. <i>Physiological Genomics</i> , 2013, 45, 301-311.	1.0	21
1917	iBAG: integrative Bayesian analysis of high-dimensional multiplatform genomics data. <i>Bioinformatics</i> , 2013, 29, 149-159.	1.8	115
1918	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
1919	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
1920	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
1921	Mechanisms Underlying the Antiproliferative and Prodifferentiative Effects of Psoralen on Adult Neural Stem Cells via DNA Microarray. <i>Evidence-based Complementary and Alternative Medicine</i> , 2013, 2013, 1-15.	0.5	6
1922	Gene Expression Profile of the A549 Human Non-Small Cell Lung Carcinoma Cell Line following Treatment with the Seeds of <i>Descurainia sophia</i> , a Potential Anticancer Drug. <i>Evidence-based Complementary and Alternative Medicine</i> , 2013, 2013, 1-13.	0.5	15
1923	Nanoporous silica coatings on implant surfaces: characterization, stability, biocompatibility and drug release properties. <i>BioNanoMaterials</i> , 2013, 14, 89-100.	1.4	3
1924	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
1925	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
1926	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
1927	Post-transcriptional regulation of myotube elongation and myogenesis by Hoi Polloi. <i>Development (Cambridge)</i> , 2013, 140, 3645-3656.	1.2	41
1928	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

#	ARTICLE	IF	CITATIONS
1929	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
1930	Prediction of clustered RNA-binding protein motif sites in the mammalian genome. <i>Nucleic Acids Research</i> , 2013, 41, 6793-6807.	6.5	64
1931	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
1932	Gene Set Signature of Reversal Reaction Type I in Leprosy Patients. <i>PLoS Genetics</i> , 2013, 9, e1003624.	1.5	32
1933	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
1934	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
1935	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
1936	Network-Based Inference Framework for Identifying Cancer Genes from Gene Expression Data. <i>BioMed Research International</i> , 2013, 2013, 1-12.	0.9	10
1937	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
1938	Transcriptional Profiling of Swine Lung Tissue after Experimental Infection with <i>Actinobacillus pleuropneumoniae</i> . <i>International Journal of Molecular Sciences</i> , 2013, 14, 10626-10660.	1.8	18
1939	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
1940	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
1941	Genome-wide Analysis of Immune System Genes by Expressed Sequence Tag Profiling. <i>Journal of Immunology</i> , 2013, 190, 5578-5587.	0.4	14
1942	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
1943	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
1944	Highly conserved elements discovered in vertebrates are present in non-syntenic loci of tunicates, act as enhancers and can be transcribed during development. <i>Nucleic Acids Research</i> , 2013, 41, 3600-3618.	6.5	24
1945	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
1946	Lipids as Tumoricidal Components of Human α -Lactalbumin Made Lethal to Tumor Cells (HAMLET). <i>Journal of Biological Chemistry</i> , 2013, 288, 17460-17471.	1.6	19

#	ARTICLE	IF	CITATIONS
1947	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
1948	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
1949	The WASH complex, an endosomal Arp2/3 activator, interacts with the Hermansky-Pudlak syndrome complex BLOC-1 and its cargo phosphatidylinositol-4-kinase type III β . <i>Molecular Biology of the Cell</i> , 2013, 24, 2269-2284.	0.9	101
1950	NF-E2 p45 Is Important for Establishing Normal Function of Platelets. <i>Molecular and Cellular Biology</i> , 2013, 33, 2659-2670.	1.1	35
1951	Influenza-Induced Inflammation Drives Pneumococcal Otitis Media. <i>Infection and Immunity</i> , 2013, 81, 645-652.	1.0	58
1952	Translational profiling of hypocretin neurons identifies candidate molecules for sleep regulation. <i>Genes and Development</i> , 2013, 27, 565-578.	2.7	87
1953	Graphite Web: web tool for gene set analysis exploiting pathway topology. <i>Nucleic Acids Research</i> , 2013, 41, W89-W97.	6.5	49
1954	Depletion of FOXP3+ regulatory T cells promotes hypercholesterolemia and atherosclerosis. <i>Journal of Clinical Investigation</i> , 2013, 123, 1323-1334.	3.9	304
1955	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
1956	CDKN2B expression in adipose tissue of familial combined hyperlipidemia patients. <i>Journal of Lipid Research</i> , 2013, 54, 3491-3505.	2.0	23
1957	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
1958	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
1959	Analysis of disease-associated objects at the Rat Genome Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat046.	1.4	11
1960	Autophagy and Cellular Senescence Mediated by Sox2 Suppress Malignancy of Cancer Cells. <i>PLoS ONE</i> , 2013, 8, e57172.	1.1	42
1961	Peeling Back the Evolutionary Layers of Molecular Mechanisms Responsive to Exercise-Stress in the Skeletal Muscle of the Racing Horse. <i>DNA Research</i> , 2013, 20, 287-298.	1.5	20
1962	Germinal centre protein HGAL promotes lymphoid hyperplasia and amyloidosis via BCR-mediated Syk activation. <i>Nature Communications</i> , 2013, 4, 1338.	5.8	37
1963	Reduced Insulin/Insulin-like Growth Factor-1 Signaling and Dietary Restriction Inhibit Translation but Preserve Muscle Mass in <i>Caenorhabditis elegans</i> . <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3624-3639.	2.5	79
1964	Molecular Characterization of Basal-Like and Non-Basal-Like Triple-Negative Breast Cancer. <i>Oncologist</i> , 2013, 18, 123-133.	1.9	454

#	ARTICLE	IF	CITATIONS
1965	Enriching the gene set analysis of genome-wide data by incorporating directionality of gene expression and combining statistical hypotheses and methods. <i>Nucleic Acids Research</i> , 2013, 41, 4378-4391.	6.5	684
1966	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. <i>Human Molecular Genetics</i> , 2013, 22, 3283-3295.	1.4	15
1967	STAT3 promotes motor neuron differentiation by collaborating with motor neuron-specific LIM complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11445-11450.	3.3	35
1968	A strategy to capture and characterize the synaptic transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7464-7469.	3.3	49
1969	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. <i>Journal of Biological Chemistry</i> , 2013, 288, 13936-13949.	1.6	73
1970	Collaborative Regulation of Development but Independent Control of Metabolism by Two Epidermis-specific Transcription Factors in <i>Caenorhabditis elegans</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 33411-33426.	1.6	29
1971	Activin A Suppresses Osteoblast Mineralization Capacity by Altering Extracellular Matrix (ECM) Composition and Impairing Matrix Vesicle (MV) Production. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2890-2900.	2.5	57
1972	Release of Severe Acute Respiratory Syndrome Coronavirus Nuclear Import Block Enhances Host Transcription in Human Lung Cells. <i>Journal of Virology</i> , 2013, 87, 3885-3902.	1.5	140
1973	Metabolomic Dynamic Analysis of Hypoxia in MDA-MB-231 and the Comparison with Inferred Metabolites from Transcriptomics Data. <i>Cancers</i> , 2013, 5, 491-510.	1.7	14
1974	Evaluation of Different Normalization and Analysis Procedures for Illumina Gene Expression Microarray Data Involving Small Changes. <i>Microarrays (Basel, Switzerland)</i> , 2013, 2, 131-152.	1.4	12
1975	Bioinformatics and Gene Network Analyses of the Swine Mammary Gland Transcriptome during Late Gestation. <i>Bioinformatics and Biology Insights</i> , 2013, 7, BBI.S12205.	1.0	13
1976	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
1977	E2F2 and CREB cooperatively regulate transcriptional activity of cell cycle genes. <i>Nucleic Acids Research</i> , 2013, 41, 10185-10198.	6.5	45
1978	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
1979	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
1980	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
1981	Comparing the Gene Expression Profile of Stromal Cells from Human Cord Blood and Bone Marrow: Lack of the Typical â€Boneâ€Signature in Cord Blood Cells. <i>Stem Cells International</i> , 2013, 2013, 1-13.	1.2	77
1982	Systems-Level Analysis of Genome-Wide Association Data. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 119-129.	0.8	55

#	ARTICLE	IF	CITATIONS
1983	Tissue Inhibitor of Metalloproteinases ³ Moderates the Proinflammatory Status of Macrophages. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2013, 49, 768-777.	1.4	41
1984	Review of Biological Network Data and Its Applications. <i>Genomics and Informatics</i> , 2013, 11, 200.	0.4	79
1985	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
1986	Noncanonical microRNAs and endogenous siRNAs in normal and psoriatic human skin. <i>Human Molecular Genetics</i> , 2013, 22, 737-748.	1.4	43
1987	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
1988	Draft genome sequence of the Tibetan antelope. <i>Nature Communications</i> , 2013, 4, 1858.	5.8	229
1989	Nontrisomic 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
1990	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
1991	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
1992	The Trithorax Group Protein Ash2l 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
1993	Coordinate Changes in Histone Modifications, mRNA Levels, and Metabolite Profiles in Clonal INS-1 832/13 β^2 -Cells Accompany Functional Adaptations to Lipotoxicity. <i>Journal of Biological Chemistry</i> , 2013, 288, 11973-11987.	1.6	66
1994	MicroRNAs miR-30b, miR-30d, and miR-494 Regulate Human Endometrial Receptivity. <i>Reproductive Sciences</i> , 2013, 20, 308-317.	1.1	169
1995	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
1996	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
1997	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
1998	Adaptive Changes in the Neuronal Proteome: Mitochondrial Energy Production, Endoplasmic Reticulum Stress, and Ribosomal Dysfunction in the Cellular Response to Metabolic Stress. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2013, 33, 673-683.	2.4	38
1999	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
2000	Inter-ethnic differences in lymphocyte sensitivity to glucocorticoids reflect variation in transcriptional response. <i>Pharmacogenomics Journal</i> , 2013, 13, 121-129.	0.9	26

#	ARTICLE	IF	CITATIONS
2001	ER stress-mediated apoptosis induced by celastrol in cancer cells and important role of glycogen synthase kinase-3 β in the signal network. <i>Cell Death and Disease</i> , 2013, 4, e715-e715.	2.7	48
2002	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
2003	Surface functionalities of gold nanoparticles impact embryonic gene expression responses. <i>Nanotoxicology</i> , 2013, 7, 192-201.	1.6	64
2004	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
2005	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
2006	Genomics of a Metamorphic Timing QTL: met1 Maps to a Unique Genomic Position and Regulates Morph and Species-Specific Patterns of Brain Transcription. <i>Genome Biology and Evolution</i> , 2013, 5, 1716-1730.	1.1	19
2007	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
2008	Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. <i>Genome Research</i> , 2013, 23, 1422-1433.	2.4	457
2009	Genomic Analyses across Six Cancer Types Identify Basal-like Breast Cancer as a Unique Molecular Entity. <i>Scientific Reports</i> , 2013, 3, 3544.	1.6	45
2010	Gene-expression signatures differ between different clinical forms of familial hemophagocytic lymphohistiocytosis. <i>Blood</i> , 2013, 121, e14-e24.	0.6	20
2011	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
2012	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
2013	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
2014	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
2015	Global Gene Expression Analysis of Term Amniotic Fluid Cell-Free Fetal RNA. <i>Obstetrics and Gynecology</i> , 2013, 121, 1248-1254.	1.2	28
2016	FGFR2 signaling underlies p63 oncogenic function in squamous cell carcinoma. <i>Journal of Clinical Investigation</i> , 2013, 123, 3525-3538.	3.9	111
2017	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
2018	An analysis and validation pipeline for large-scale RNAi-based screens. <i>Scientific Reports</i> , 2013, 3, 1076.	1.6	5

#	ARTICLE	IF	CITATIONS
2019	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
2020	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		
2021	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
2022	Pathogen Induced Changes in the Protein Profile of Human Tears from Fusarium Keratitis Patients. <i>PLoS ONE</i> , 2013, 8, e53018.	1.1	48
2023	Copy Number Variations in Alternative Splicing Gene Networks Impact Lifespan. <i>PLoS ONE</i> , 2013, 8, e53846.	1.1	13
2024	DNA Methylation Dynamics in Blood after Hematopoietic Cell Transplant. <i>PLoS ONE</i> , 2013, 8, e56931.	1.1	24
2025	Comparative GO: A Web Application for Comparative Gene Ontology and Gene Ontology-Based Gene Selection in Bacteria. <i>PLoS ONE</i> , 2013, 8, e58759.	1.1	97
2026	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
2027	Striatal Molecular Signature of Subchronic Subthalamic Nucleus High Frequency Stimulation in Parkinsonian Rat. <i>PLoS ONE</i> , 2013, 8, e60447.	1.1	18
2028	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
2029	Proteomic Characterization of Inbreeding-Related Cold Sensitivity in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2013, 8, e62680.	1.1	5
2030	Age-Specific Signatures of Glioblastoma at the Genomic, Genetic, and Epigenetic Levels. <i>PLoS ONE</i> , 2013, 8, e62982.	1.1	49
2031	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
2032	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
2033	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
2034	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
2035	Effects of Fertility on Gene Expression and Function of the Bovine Endometrium. <i>PLoS ONE</i> , 2013, 8, e69444.	1.1	58
2036	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

#	ARTICLE	IF	CITATIONS
2037	Reverse Differentiation as a Gene Filtering Tool in Genome Expression Profiling of Adipogenesis for Fat Marker Gene Selection and Their Analysis. PLoS ONE, 2013, 8, e69754.	1.1	23
2038	Partial Restoration of Macrophage Alteration from Diet-Induced Obesity in Response to Porphyromonas gingivalis Infection. PLoS ONE, 2013, 8, e70320.	1.1	5
2039	Bovine Mammary Gene Expression Profiling during the Onset of Lactation. PLoS ONE, 2013, 8, e70393.	1.1	60
2040	Prioritizing Disease Candidate Proteins in Cardiomyopathy-Specific Protein-Protein Interaction Networks Based on α -Guilt by Association Analysis. PLoS ONE, 2013, 8, e71191.	1.1	14
2041	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
2042	HDAC1 and HDAC2 Restrain the Intestinal Inflammatory Response by Regulating Intestinal Epithelial Cell Differentiation. PLoS ONE, 2013, 8, e73785.	1.1	84
2043	Transcriptional Profiling of Human Monocytes Identifies the Inhibitory Receptor CD300a as Regulator of Transendothelial Migration. PLoS ONE, 2013, 8, e73981.	1.1	7
2044	The Genome-Wide Early Temporal Response of Saccharomyces cerevisiae to Oxidative Stress Induced by Cumene Hydroperoxide. PLoS ONE, 2013, 8, e74939.	1.1	29
2045	Genome-Wide Promoter Methylation of Small Renal Masses. PLoS ONE, 2013, 8, e77309.	1.1	13
2046	The Human Placental Sexome Differs between Trophoblast Epithelium and Villous Vessel Endothelium. PLoS ONE, 2013, 8, e79233.	1.1	96
2047	Computational Prediction of Human Salivary Proteins from Blood Circulation and Application to Diagnostic Biomarker Identification. PLoS ONE, 2013, 8, e80211.	1.1	29
2048	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
2049	Comprehensive Analysis of Gene Expression Profiles of the Beet Armyworm Spodoptera exigua Larvae Challenged with Bacillus thuringiensis Vip3Aa Toxin. PLoS ONE, 2013, 8, e81927.	1.1	50
2050	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
2051	Infection with a Virulent Strain of Wolbachia Disrupts Genome Wide-Patterns of Cytosine Methylation in the Mosquito Aedes aegypti. PLoS ONE, 2013, 8, e66482.	1.1	57
2052	Machine-Based Morphologic Analysis of Glioblastoma Using Whole-Slide Pathology Images Uncover Clinically Relevant Molecular Correlates. PLoS ONE, 2013, 8, e81049.	1.1	91
2053	Anticancer Agent Shikonin Is an Incompetent Inducer of Cancer Drug Resistance. PLoS ONE, 2013, 8, e52706.	1.1	51
2054	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

#	ARTICLE	IF	CITATIONS
2055	Maximal information component analysis: a novel non-linear network analysis method. <i>Frontiers in Genetics</i> , 2013, 4, 28.	1.1	22
2056	Construction and Analysis of the Cell Surface ^{â€™} s Protein Network for Human Sperm-Egg Interaction. , 2013, 2013, 1-8.		8
2057	Impact of Intramammary Treatment on Gene Expression Profiles in Bovine <i>Escherichia coli</i> Mastitis. <i>PLoS ONE</i> , 2014, 9, e85579.	1.1	28
2058	Protection Genes in Nucleus Accumbens Shell Affect Vulnerability to Nicotine Self-Administration across Isogenic Strains of Adolescent Rat. <i>PLoS ONE</i> , 2014, 9, e86214.	1.1	10
2059	Investigating the Different Mechanisms of Genotoxic and Non-Genotoxic Carcinogens by a Gene Set Analysis. <i>PLoS ONE</i> , 2014, 9, e86700.	1.1	11
2060	Model Steatogenic Compounds (Amiodarone, Valproic Acid, and Tetracycline) Alter Lipid Metabolism by Different Mechanisms in Mouse Liver Slices. <i>PLoS ONE</i> , 2014, 9, e86795.	1.1	47
2061	Differential Induction of TLR3-Dependent Innate Immune Signaling by Closely Related Parasite Species. <i>PLoS ONE</i> , 2014, 9, e88398.	1.1	57
2062	Meta-Analysis of Pathway Enrichment: Combining Independent and Dependent Omics Data Sets. <i>PLoS ONE</i> , 2014, 9, e89297.	1.1	44
2063	A Method for Predicting Protein-Protein Interaction Types. <i>PLoS ONE</i> , 2014, 9, e90904.	1.1	18
2064	Integrated Analysis of DNA Methylation and RNA Transcriptome during In Vitro Differentiation of Human Pluripotent Stem Cells into Retinal Pigment Epithelial Cells. <i>PLoS ONE</i> , 2014, 9, e91416.	1.1	19
2065	Studying the System-Level Involvement of MicroRNAs in Parkinson's Disease. <i>PLoS ONE</i> , 2014, 9, e93751.	1.1	21
2066	Genes Influenced by the Non-Muscle Isoform of Myosin Light Chain Kinase Impact Human Cancer Prognosis. <i>PLoS ONE</i> , 2014, 9, e94325.	1.1	17
2067	Systemic Inflammatory Response to Smoking in Chronic Obstructive Pulmonary Disease: Evidence of a Gender Effect. <i>PLoS ONE</i> , 2014, 9, e97491.	1.1	40
2068	Human Endogenous Retrovirus-K(II) Envelope Induction Protects Neurons during HIV/AIDS. <i>PLoS ONE</i> , 2014, 9, e97984.	1.1	41
2069	Intracellular Bacteria Interfere with Dendritic Cell Functions: Role of the Type I Interferon Pathway. <i>PLoS ONE</i> , 2014, 9, e99420.	1.1	64
2070	Differential Transcriptional Effects of EGFR Inhibitors. <i>PLoS ONE</i> , 2014, 9, e102466.	1.1	12
2071	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. <i>PLoS ONE</i> , 2014, 9, e104563.	1.1	11
2072	Dynamic Modularity of Host Protein Interaction Networks in <i>Salmonella Typhi</i> Infection. <i>PLoS ONE</i> , 2014, 9, e104911.	1.1	6

#	ARTICLE	IF	CITATIONS
2073	Genetic and Epigenetic Changes in Chromosomally Stable and Unstable Progeny of Irradiated Cells. PLoS ONE, 2014, 9, e107722.	1.1	19
2074	Transcriptomic Characterization of C57BL/6 Mouse Embryonic Stem Cell Differentiation and Its Modulation by Developmental Toxicants. PLoS ONE, 2014, 9, e108510.	1.1	14
2075	Computational Surprisal Analysis Speeds-Up Genomic Characterization of Cancer Processes. PLoS ONE, 2014, 9, e108549.	1.1	3
2076	Genome-Wide Microarray Expression and Genomic Alterations by Array-CGH Analysis in Neuroblastoma Stem-Like Cells. PLoS ONE, 2014, 9, e113105.	1.1	5
2077	Kismet Positively Regulates Glutamate Receptor Localization and Synaptic Transmission at the Drosophila Neuromuscular Junction. PLoS ONE, 2014, 9, e113494.	1.1	18
2078	Transcriptome Analysis of Enterococcus faecalis during Mammalian Infection Shows Cells Undergo Adaptation and Exist in a Stringent Response State. PLoS ONE, 2014, 9, e115839.	1.1	35
2079	Differential Network Analyses of Alzheimer's Disease Identify Early Events in Alzheimer's Disease Pathology. International Journal of Alzheimer's Disease, 2014, 2014, 1-18.	1.1	12
2080	Cell Surface Proteomics Analysis Indicates a Neural Lineage Bias of Rat Bone Marrow Mesenchymal Stromal Cells. BioMed Research International, 2014, 2014, 1-13.	0.9	4
2081	Cyclin D activates the Rb tumor suppressor by mono-phosphorylation. ELife, 2014, 3, .	2.8	332
2082	Network Analysis of Neurodegenerative Disease Highlights a Role of Toll-Like Receptor Signaling. BioMed Research International, 2014, 2014, 1-16.	0.9	19
2083	Docetaxel-loaded solid lipid nanoparticles suppress breast cancer cells growth with reduced myelosuppression toxicity. International Journal of Nanomedicine, 2014, 9, 4829.	3.3	38
2084	Myeloid decidual dendritic cells and immunoregulation of pregnancy: defective responsiveness to Coxiella burnetii and Brucella abortus. Frontiers in Cellular and Infection Microbiology, 2014, 4, 179.	1.8	17
2085	Transduction motif analysis of gastric cancer based on a human signaling network. Brazilian Journal of Medical and Biological Research, 2014, 47, 369-375.	0.7	2
2086	Proteomics-Based Identification of Differentially Abundant Proteins from Human Keratinocytes Exposed to Arsenic Trioxide. Journal of Proteomics and Bioinformatics, 2014, 07, 166-178.	0.4	17
2087	CGG repeats in RNA modulate expression of TDP-43 in mouse and fly models of fragile X tremor ataxia syndrome. Human Molecular Genetics, 2014, 23, 5906-5915.	1.4	21
2088	A genome-wide scan for selection signatures in Yorkshire and Landrace pigs based on sequencing data. Animal Genetics, 2014, 45, 808-816.	0.6	19
2089	Lipid Droplet Protein LID-1 Mediates ATGL-1-Dependent Lipolysis during Fasting in Caenorhabditis elegans. Molecular and Cellular Biology, 2014, 34, 4165-4176.	1.1	82
2090	Epigenome-wide analysis of piRNAs in gene-specific DNA methylation. RNA Biology, 2014, 11, 1301-1312.	1.5	55

#	ARTICLE	IF	CITATIONS
2091	Proteomic alteration of PK-15 cells after infection by porcine circovirus type 2. <i>Virus Genes</i> , 2014, 49, 400-416.	0.7	10
2092	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
2093	Network-based analysis identifies epigenetic biomarkers of esophageal squamous cell carcinoma progression. <i>Bioinformatics</i> , 2014, 30, 3054-3061.	1.8	15
2094	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
2095	Identifying candidate genes for discrimination of ulcerative colitis and Crohn's disease. <i>Molecular Biology Reports</i> , 2014, 41, 6349-6355.	1.0	7
2096	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
2097	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
2098	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
2099	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
2101	Liver transcriptome analysis in gilthead sea bream upon exposure to low temperature. <i>BMC Genomics</i> , 2014, 15, 765.	1.2	96
2102	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
2103	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
2105	Understanding disease mechanisms with models of signaling pathway activities. <i>BMC Systems Biology</i> , 2014, 8, 121.	3.0	42
2106	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
2107	ChIP-Enrich: gene set enrichment testing for ChIP-seq data. <i>Nucleic Acids Research</i> , 2014, 42, e105-e105.	6.5	136
2108	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
2109	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
2110	Integrative genomics and transcriptomics analysis of human embryonic and induced pluripotent stem cells. <i>BioData Mining</i> , 2014, 7, 32.	2.2	2

#	ARTICLE	IF	CITATIONS
2111	Patterns of gene expression associated with recovery and injury in heat-stressed rats. <i>BMC Genomics</i> , 2014, 15, 1058.	1.2	34
2112	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
2113	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
2114	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
2115	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
2116	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
2117	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
2118	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
2119	Finding Novel Molecular Connections between Developmental Processes and Disease. <i>PLoS Computational Biology</i> , 2014, 10, e1003578.	1.5	10
2120	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
2121	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
2122	Essential Functional Modules for Pathogenic and Defensive Mechanisms in <i>Candida albicans</i> Infections. <i>BioMed Research International</i> , 2014, 2014, 1-15.	0.9	7
2123	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
2124	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
2125	Immunology of Bats and Their Viruses: Challenges and Opportunities. <i>Viruses</i> , 2014, 6, 4880-4901.	1.5	87
2126	Urinary Prognostic Biomarkers in Patients With Focal Segmental Glomerulosclerosis. <i>Nephro-Urology Monthly</i> , 2014, 6, e16806.	0.0	24
2127	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
2128	The Genomic Architecture of Population Divergence between Subspecies of the European Rabbit. <i>PLoS Genetics</i> , 2014, 10, e1003519.	1.5	82

#	ARTICLE	IF	CITATIONS
2129	Pathogenesis analysis of pituitary adenoma based on gene expression profiling. <i>Oncology Letters</i> , 2014, 8, 2423-2430.	0.8	10
2130	Learning Dysregulated Pathways in Cancers from Differential Variability Analysis. <i>Cancer Informatics</i> , 2014, 13s5, CIN.S14066.	0.9	37
2131	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
2132	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
2133	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
2134	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
2135	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
2136	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
2137	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
2138	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
2139	Integrated Omic Analysis of Oropharyngeal Carcinomas Reveals Human Papillomavirus (HPV)-dependent Regulation of the Activator Protein 1 (AP-1) Pathway. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3572-3584.	2.5	19
2140	Biological pathway selection through Bayesian integrative modeling. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 435-57.	0.2	1
2141	Cell-type specific transcriptomic profiling to dissect mechanisms of differential dendritogenesis. <i>Genomics Data</i> , 2014, 2, 378-381.	1.3	5
2142	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
2143	Fam40b is required for lineage commitment of murine embryonic stem cells. <i>Cell Death and Disease</i> , 2014, 5, e1320-e1320.	2.7	19
2144	Dexmedetomidine preconditioning ameliorates kidney ischemia-reperfusion injury. <i>Pharmacology Research and Perspectives</i> , 2014, 2, e00045.	1.1	61
2145	A systematic review of microRNA expression profiling studies in human gastric cancer. <i>Cancer Medicine</i> , 2014, 3, 878-888.	1.3	125
2146	Molecular Aspects of Adipoepithelial Transdifferentiation in Mouse Mammary Gland. <i>Stem Cells</i> , 2014, 32, 2756-2766.	1.4	47

#	ARTICLE	IF	CITATIONS
2147	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
2148	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
2149	Identifying progression related disease risk modules based on the human subcellular signaling networks. <i>Molecular BioSystems</i> , 2014, 10, 3298-3309.	2.9	2
2150	A system-level model for the microbial regulatory genome. <i>Molecular Systems Biology</i> , 2014, 10, 740.	3.2	64
2151	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
2152	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
2153	Extensive Differences in Gene Expression Between Symbiotic and Aposymbiotic Cnidarians. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 277-295.	0.8	150
2154	The ETS family member GABP± modulates androgen receptor signalling and mediates an aggressive phenotype in prostate cancer. <i>Nucleic Acids Research</i> , 2014, 42, 6256-6269.	6.5	33
2155	Architecture for interoperable software in biology. <i>Briefings in Bioinformatics</i> , 2014, 15, 626-636.	3.2	4
2156	Transcriptomic signatures of peroxisome proliferator-activated receptor ± (PPAR±) in different mouse liver models identify novel aspects of its biology. <i>BMC Genomics</i> , 2014, 15, 1106.	1.2	33
2157	Systematic transcriptome analysis of the zebrafish model of diamond-blackfan anemia induced by RPS24 deficiency. <i>BMC Genomics</i> , 2014, 15, 759.	1.2	18
2158	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
2159	Transcriptomic portrait of human Mesenchymal Stromal/Stem cells isolated from bone marrow and placenta. <i>BMC Genomics</i> , 2014, 15, 910.	1.2	59
2160	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
2161	Alterations in lung gene expression in streptozotocin-induced diabetic rats. <i>BMC Endocrine Disorders</i> , 2014, 14, 5.	0.9	11
2162	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
2163	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
2164	Differential microRNA expression following infection with a mouse-adapted, highly virulent avian H5N2 virus. <i>BMC Microbiology</i> , 2014, 14, 252.	1.3	42

#	ARTICLE	IF	CITATIONS
2165	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
2166	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
2167	<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
2168	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
2169	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
2170	Noise exposure immediately activates cochlear mitogen-activated protein kinase signaling. <i>Noise and Health</i> , 2014, 16, 400.	0.4	25
2171	<i>Nox1</i> is a master regulator of alternative splicing in pancreatic beta cells. <i>Nucleic Acids Research</i> , 2014, 42, 11818-11830.	6.5	71
2172	Pharmacogenomic predictors of citalopram treatment outcome in major depressive disorder. <i>World Journal of Biological Psychiatry</i> , 2014, 15, 135-144.	1.3	23
2173	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
2174	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
2175	The Novel Diagnostic Biomarkers for Focal Segmental Glomerulosclerosis. <i>International Journal of Nephrology</i> , 2014, 2014, 1-10.	0.7	23
2176	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
2177	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
2178	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
2179	Stress-induced changes in gene interactions in human cells. <i>Nucleic Acids Research</i> , 2014, 42, 1757-1771.	6.5	20
2180	Cell cycle-dependent regulation of the RNA-binding protein Staufen1. <i>Nucleic Acids Research</i> , 2014, 42, 7867-7883.	6.5	35
2181	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
2182	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

#	ARTICLE	IF	CITATIONS
2183	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
2184	Mutations in USP9X 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
2185	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
2186	Pathway-based Analysis of the Hidden Genetic Heterogeneities in Cancers. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 31-38.	3.0	6
2187	Early life perfluorooctanesulphonic acid (PFOS) exposure impairs zebrafish organogenesis. <i>Aquatic Toxicology</i> , 2014, 150, 124-132.	1.9	53
2188	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
2189	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
2190	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
2191	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
2192	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
2193	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
2194	Unique features of the transcriptional response to model aneuploidy in human cells. <i>BMC Genomics</i> , 2014, 15, 139.	1.2	87
2195	Protein signatures of oxidative stress response in a patient specific cell line model for autism. <i>Molecular Autism</i> , 2014, 5, 10.	2.6	22
2196	DFLAT: functional annotation for human development. <i>BMC Bioinformatics</i> , 2014, 15, 45.	1.2	27
2197	Induction of polyploidy by nuclear fusion mechanism upon decreased expression of the nuclear envelope protein LAP2 ² in the human osteosarcoma cell line U2OS. <i>Molecular Cytogenetics</i> , 2014, 7, 9.	0.4	9
2198	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
2199	Gene expression profiling of mesenteric lymph nodes from sheep with natural scrapie. <i>BMC Genomics</i> , 2014, 15, 59.	1.2	27
2200	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
2201	ISAAC - InterSpecies Analysing Application using Containers. BMC Bioinformatics, 2014, 15, 18.	1.2	5
2202	Molecular sub-group-specific immunophenotypic changes are associated with outcome in recurrent posterior fossa ependymoma. Acta Neuropathologica, 2014, 127, 731-745.	3.9	73
2203	Comprehensive analysis of gene expression in human retina and supporting tissues. Human Molecular Genetics, 2014, 23, 4001-4014.	1.4	109
2204	Novel Insights into Embryonic Stem Cell Self-Renewal Revealed Through Comparative Human and Mouse Systems Biology Networks. Stem Cells, 2014, 32, 1161-1172.	1.4	15
2205	Principles and methods of integrative genomic analyses in cancer. Nature Reviews Cancer, 2014, 14, 299-313.	12.8	337
2206	c-Myc-dependent transcriptional regulation of cell cycle and nucleosomal histones during oligodendrocyte differentiation. Neuroscience, 2014, 276, 72-86.	1.1	35
2207	Expression analysis of genes and pathways associated with liver metastases of the uveal melanoma. BMC Medical Genetics, 2014, 15, 29.	2.1	35
2208	The Transcription Factor Gata6 Links Tissue Macrophage Phenotype and Proliferative Renewal. Science, 2014, 344, 645-648.	6.0	317
2209	Comparison of Reprogramming Genes in Induced Pluripotent Stem Cells and Nuclear Transfer Cloned Embryos. Stem Cell Reviews and Reports, 2014, 10, 548-560.	5.6	4
2210	A genome-wide association study identifies major loci affecting the immune response against infectious bronchitis virus in chicken. Infection, Genetics and Evolution, 2014, 21, 351-358.	1.0	16
2211	Genomic changes under rapid evolution: selection for parasitoid resistance. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20132303.	1.2	41
2212	The ALS/FTLD-related RNA-binding proteins TDP43 and FUS have common downstream RNA targets in cortical neurons. FEBS Open Bio, 2014, 4, 1-10.	1.0	50
2214	PIWI proteins and PIWI-interacting RNAs function in <i>Hydra</i> somatic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 337-342.	3.3	140
2215	Resources for Functional Genomics Studies in <i>Drosophila melanogaster</i> . Genetics, 2014, 197, 1-18.	1.2	61
2216	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. Development (Cambridge), 2014, 141, 4580-4589.	1.2	50
2217	Age-related variations in the methylome associated with gene expression in human monocytes and T cells. Nature Communications, 2014, 5, 5366.	5.8	168
2218	Endometrial gene expression reveals compromised progesterone signaling in women refractory to embryo implantation. Reproductive Biology and Endocrinology, 2014, 12, 92.	1.4	34
2219	Mating system variation drives rapid evolution of the female transcriptome in <i>Drosophila pseudoobscura</i> . Ecology and Evolution, 2014, 4, 2186-2201.	0.8	38

#	ARTICLE	IF	CITATIONS
2220	Shotgun <scp>MS</scp> proteomic analysis of bronchoalveolar lavage fluid in normal subjects. <i>Proteomics - Clinical Applications</i> , 2014, 8, 737-747.	0.8	17
2221	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
2222	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
2223	p21 suppresses inflammation and tumorigenesis on pRB-deficient stratified epithelia. <i>Oncogene</i> , 2014, 33, 4599-4612.	2.6	13
2224	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
2225	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
2226	A System-Level Pathway-Phenotype Association Analysis Using Synthetic Feature Random Forest. <i>Genetic Epidemiology</i> , 2014, 38, 209-219.	0.6	13
2228	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
2229	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. <i>Nature Communications</i> , 2014, 5, 3365.	5.8	123
2230	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
2231	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
2232	Predicting response and survival in chemotherapy-treated triple-negative breast cancer. <i>British Journal of Cancer</i> , 2014, 111, 1532-1541.	2.9	100
2234	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
2235	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
2236	MiningABs: mining associated biomarkers across multi-connected gene expression datasets. <i>BMC Bioinformatics</i> , 2014, 15, 173.	1.2	1
2237	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
2238	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
2239	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

#	ARTICLE	IF	CITATIONS
2240	A network-based approach to dissect the cilia/centrosome complex interactome. <i>BMC Genomics</i> , 2014, 15, 658.	1.2	19
2241	Human immunodeficiency virus Tat associates with a specific set of cellular RNAs. <i>Retrovirology</i> , 2014, 11, 53.	0.9	9
2242	Selecting biologically informative genes in co-expression networks with a centrality score. <i>Biology Direct</i> , 2014, 9, 12.	1.9	49
2243	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
2244	Transcriptional profiling of Arabidopsis root hairs and pollen defines an apical cell growth signature. <i>BMC Plant Biology</i> , 2014, 14, 197.	1.6	49
2245	A Smad3 and TTF-1/NKX2-1 complex regulates Smad4-independent gene expression. <i>Cell Research</i> , 2014, 24, 994-1008.	5.7	45
2246	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
2247	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
2248	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
2249	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
2250	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
2251	Differential expression of genes and proteins associated with wool follicle cycling. <i>Molecular Biology Reports</i> , 2014, 41, 5343-5349.	1.0	25
2252	Interactions among mitochondrial proteins altered in glioblastoma. <i>Journal of Neuro-Oncology</i> , 2014, 118, 247-256.	1.4	57
2253	Hippocampal HDAC4 Contributes to Postnatal Fluoxetine-Evoked Depression-Like Behavior. <i>Neuropsychopharmacology</i> , 2014, 39, 2221-2232.	2.8	65
2254	Synovial phenotypes in rheumatoid arthritis correlate with response to biologic therapeutics. <i>Arthritis Research and Therapy</i> , 2014, 16, R90.	1.6	292
2255	DNA methylome profiling of human tissues identifies global and tissue-specific methylation patterns. <i>Genome Biology</i> , 2014, 15, r54.	3.8	325
2256	Quantitative Proteomic Profiling Reveals Differentially Regulated Proteins in Cystic Fibrosis Cells. <i>Journal of Proteome Research</i> , 2014, 13, 4668-4675.	1.8	25
2257	A Comprehensive Analysis of MicroProteins Reveals Their Potentially Widespread Mechanism of Transcriptional Regulation. <i>Plant Physiology</i> , 2014, 165, 149-159.	2.3	21

#	ARTICLE	IF	CITATIONS
2258	Developmental transcriptome analysis of human erythropoiesis. <i>Human Molecular Genetics</i> , 2014, 23, 4528-4542.	1.4	45
2259	Peripheral nerve morphogenesis induced by scaffold micropatterning. <i>Biomaterials</i> , 2014, 35, 4035-4045.	5.7	39
2260	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
2261	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
2262	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
2263	GO2MSIG, an automated GO based multi-species gene set generator for gene set enrichment analysis. <i>BMC Bioinformatics</i> , 2014, 15, 146.	1.2	49
2264	DNA methylation subgroups and the CpG island methylator phenotype in gastric cancer: a comprehensive profiling approach. <i>BMC Gastroenterology</i> , 2014, 14, 55.	0.8	34
2265	Berberine moderates glucose metabolism through the GnRH-GLP-1 and MAPK pathways in the intestine. <i>BMC Complementary and Alternative Medicine</i> , 2014, 14, 188.	3.7	44
2266	Stringent homology-based prediction of H. sapiens-M. tuberculosis H37Rv protein-protein interactions. <i>Biology Direct</i> , 2014, 9, 5.	1.9	74
2267	Optic nerve crush induces spatial and temporal gene expression patterns in retina and optic nerve of BALB/c mice. <i>Molecular Neurodegeneration</i> , 2014, 9, 14.	4.4	26
2268	Gene signatures related to cell proliferation predict influenza vaccine-induced antibody response. <i>European Journal of Immunology</i> , 2014, 44, 285-295.	1.6	57
2269	Integrative analysis of independent transcriptome data for rare diseases. <i>Methods</i> , 2014, 69, 315-325.	1.9	6
2270	Genome-Wide DNA Methylation Patterns in Naive CD4+ T Cells From Patients With Primary Sjögren's Syndrome. <i>Arthritis and Rheumatology</i> , 2014, 66, 731-739.	2.9	147
2271	A Phase I Study of the First-in-Class Antimitochondrial Metabolism Agent, CPI-613, in Patients with Advanced Hematologic Malignancies. <i>Clinical Cancer Research</i> , 2014, 20, 5255-5264.	3.2	82
2272	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
2273	Mouse SCNT ESCs Have Lower Somatic Mutation Load Than Syngeneic iPSCs. <i>Stem Cell Reports</i> , 2014, 2, 399-405.	2.3	20
2274	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
2275	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

#	ARTICLE	IF	CITATIONS
2276	Integrated microRNA-mRNA analysis of coronary artery disease. <i>Molecular Biology Reports</i> , 2014, 41, 5505-5511.	1.0	19
2277	A bi-Poisson model for clustering gene expression profiles by RNA-seq. <i>Briefings in Bioinformatics</i> , 2014, 15, 534-541.	3.2	6
2278	Pathway and network analysis in proteomics. <i>Journal of Theoretical Biology</i> , 2014, 362, 44-52.	0.8	98
2279	Genome-Wide Analysis of Long Noncoding RNA (lncRNA) Expression in Hepatoblastoma Tissues. <i>PLoS ONE</i> , 2014, 9, e85599.	1.1	78
2280	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
2281	DNA methylation temporal profiling following peripheral versus central nervous system axotomy. <i>Scientific Data</i> , 2014, 1, 140038.	2.4	16
2282	A Bayesian Integrative Model for Genetical Genomics with Spatially Informed Variable Selection. <i>Cancer Informatics</i> , 2014, 13s2, CIN.S13784.	0.9	3
2283	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
2284	Complex-based analysis of dysregulated cellular processes in cancer. <i>BMC Systems Biology</i> , 2014, 8, S1.	3.0	19
2285	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
2286	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
2287	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
2288	Multiple sources of bias confound functional enrichment analysis of global -omics data. <i>Genome Biology</i> , 2015, 16, 186.	3.8	131
2289	Gene expression profiling of brakeless mutant <i>Drosophila</i> embryos. <i>Data in Brief</i> , 2015, 5, 134-137.	0.5	2
2290	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
2291	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
2292	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
2293	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

#	ARTICLE	IF	CITATIONS
2294	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
2295	Vaccinia Virus Infection Requires Maturation of Macropinosomes. <i>Traffic</i> , 2015, 16, 814-831.	1.3	44
2296	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
2297	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
2298	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
2299	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
2300	miR-34a screened by miRNA profiling negatively regulates Wnt/ β -catenin signaling pathway in Aflatoxin B1 induced hepatotoxicity. <i>Scientific Reports</i> , 2015, 5, 16732.	1.6	65
2301	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
2302	MicroRNA profiling of CD3+CD56+ cytokine-induced killer cells. <i>Scientific Reports</i> , 2015, 5, 9571.	1.6	8
2303	Identifying miRNA/mRNA negative regulation pairs in colorectal cancer. <i>Scientific Reports</i> , 2015, 5, 12995.	1.6	43
2304	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
2305	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
2306	Aberrant expression of long noncoding RNAs in chronic thromboembolic pulmonary hypertension. <i>Molecular Medicine Reports</i> , 2015, 11, 2631-2643.	1.1	33
2307	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
2308	Deficiency of Capicua disrupts bile acid homeostasis. <i>Scientific Reports</i> , 2015, 5, 8272.	1.6	28
2309	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
2310	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
2311	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

#	ARTICLE	IF	CITATIONS
2312	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
2313	Transcription factor p63 bookmarks and regulates dynamic enhancers during epidermal differentiation. <i>EMBO Reports</i> , 2015, 16, 863-878.	2.0	134
2314	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
2315	Network-assisted analysis of primary Sjögren's syndrome GWAS data in Han Chinese. <i>Scientific Reports</i> , 2015, 5, 18855.	1.6	13
2316	Unique Toll-Like Receptor 4 Activation by NAMPT/PBEF Induces NF- κ B Signaling and Inflammatory Lung Injury. <i>Scientific Reports</i> , 2015, 5, 13135.	1.6	126
2317	Discrete domains of gene expression in germinal layers distinguish the development of gyrencephaly. <i>EMBO Journal</i> , 2015, 34, 1859-1874.	3.5	146
2318	miR-9a-5p suppresses pro-fibrogenic transformation of fibroblasts and prevents organ fibrosis by targeting <sc>NOX</sc> 4 and <sc>TGFBR</sc> 2. <i>EMBO Reports</i> , 2015, 16, 1358-1377.	2.0	87
2319	Expression analysis of the estrogen receptor target genes in renal cell carcinoma. <i>Molecular Medicine Reports</i> , 2015, 11, 75-82.	1.1	6
2320	Advanced Applications of RNA Sequencing and Challenges. <i>Bioinformatics and Biology Insights</i> , 2015, 9s1, BBI.S28991.	1.0	178
2321	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
2322	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
2323	Copy number variations in the genome of the Qatari population. <i>BMC Genomics</i> , 2015, 16, 834.	1.2	9
2324	Blood transcriptomics of drug-naïve sporadic Parkinson's disease patients. <i>BMC Genomics</i> , 2015, 16, 876.	1.2	64
2325	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
2326	A survey of computational tools for downstream analysis of proteomic and other omic datasets. <i>Human Genomics</i> , 2015, 9, 28.	1.4	16
2327	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
2328	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
2329	Fibrinogen production is enhanced in an in-vitro model of non-alcoholic fatty liver disease: an isolated risk factor for cardiovascular events?. <i>Lipids in Health and Disease</i> , 2015, 14, 86.	1.2	16

#	ARTICLE	IF	CITATIONS
2330	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
2331	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
2332	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
2333	Integrative network-based approach identifies key genetic elements in breast invasive carcinoma. <i>BMC Genomics</i> , 2015, 16, S2.	1.2	30
2334	Memory acquisition and retrieval impact different epigenetic processes that regulate gene expression. <i>BMC Genomics</i> , 2015, 16, S5.	1.2	50
2335	Reconstruction of novel transcription factor regulons through inference of their binding sites. <i>BMC Bioinformatics</i> , 2015, 16, 299.	1.2	3
2336	Identification of candidate gonadal sex differentiation genes in the chicken embryo using RNA-seq. <i>BMC Genomics</i> , 2015, 16, 704.	1.2	54
2337	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. <i>BMC Genomics</i> , 2015, 16, 713.	1.2	16
2338	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. <i>BMC Genomics</i> , 2015, 16, 822.	1.2	6
2339	Genome-wide DNA methylome variation in two genetically distinct chicken lines using MethylC-seq. <i>BMC Genomics</i> , 2015, 16, 851.	1.2	39
2340	Reconstruction of temporal activity of microRNAs from gene expression data in breast cancer cell line. <i>BMC Genomics</i> , 2015, 16, 1077.	1.2	5
2341	Transfection of Sertoli cells with androgen receptor alters gene expression without androgen stimulation. <i>BMC Molecular Biology</i> , 2015, 16, 23.	3.0	4
2342	Association between in vivo bone formation and ex vivo migratory capacity of human bone marrow stromal cells. <i>Stem Cell Research and Therapy</i> , 2015, 6, 196.	2.4	17
2343	Transcriptional profiling of differentially vulnerable motor neurons at pre-symptomatic stage in the <i>Smn 2b</i> ⁻ mouse model of spinal muscular atrophy. <i>Acta Neuropathologica Communications</i> , 2015, 3, 55.	2.4	61
2344	Discovering All Transcriptome Single-Nucleotide Polymorphisms and Scanning for Selection Signatures in Ducks (<i>Anas platyrhynchos</i>). <i>Evolutionary Bioinformatics</i> , 2015, 11s1, EBO.S21545.	0.6	5
2345	Regulation of monocyte/macrophage polarisation by extracellular RNA. <i>Thrombosis and Haemostasis</i> , 2015, 113, 473-481.	1.8	36
2346	Identification of a mitochondrial defect gene signature reveals NUPR1 as a key regulator of liver cancer progression. <i>Hepatology</i> , 2015, 62, 1174-1189.	3.6	50
2347	Gene expression profiles and protein-protein interaction network analysis in AIDS patients with HIV-associated encephalitis and dementia. <i>HIV/AIDS - Research and Palliative Care</i> , 2015, 7, 265.	0.4	12

#	ARTICLE	IF	CITATIONS
2348	Novel prognostic genes of diffuse large B-cell lymphoma revealed by survival analysis of gene expression data. <i>OncoTargets and Therapy</i> , 2015, 8, 3407.	1.0	10
2349	NOB1 is essential for the survival of RKO colorectal cancer cells. <i>World Journal of Gastroenterology</i> , 2015, 21, 868.	1.4	17
2350	ATF4 licenses C/EBP β activity in human mesenchymal stem cells primed for adipogenesis. <i>ELife</i> , 2015, 4, e06821.	2.8	45
2351	Lipid-mediated regulation of SKN-1/Nrf in response to germ cell absence. <i>ELife</i> , 2015, 4, .	2.8	171
2352	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
2353	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
2354	Nitric oxide as a regulator of <i>B. anthracis</i> pathogenicity. <i>Frontiers in Microbiology</i> , 2015, 6, 921.	1.5	12
2355	Noncoding RNA in the transcriptional landscape of human neural progenitor cell differentiation. <i>Frontiers in Neuroscience</i> , 2015, 9, 392.	1.4	11
2356	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
2357	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
2358	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
2359	Characterization of the Kidney Transcriptome of the Long-Haired Mouse <i>Abrothrix hirta</i> (Rodentia). <i>Tj ETQq1 1 0.784314 rgBJ /Overlock</i>	1.1	7
2360	Identification of MicroRNAs and their Targets Associated with Embryo Abortion during <i>Chrysanthemum</i> Cross Breeding via High-Throughput Sequencing. <i>PLoS ONE</i> , 2015, 10, e0124371.	1.1	19
2361	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
2362	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
2363	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
2364	Disruption of Mitochondrion-To-Nucleus Interaction in Deceased Cloned Piglets. <i>PLoS ONE</i> , 2015, 10, e0129378.	1.1	7
2365	Immunological Response to Single Pathogen Challenge with Agents of the Bovine Respiratory Disease Complex: An RNA-Sequence Analysis of the Bronchial Lymph Node Transcriptome. <i>PLoS ONE</i> , 2015, 10, e0131459.	1.1	51

#	ARTICLE	IF	CITATIONS
2366	Comparing Two Intestinal Porcine Epithelial Cell Lines (IPECs): Morphological Differentiation, Function and Metabolism. PLoS ONE, 2015, 10, e0132323.	1.1	48
2367	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
2368	Meta-Analysis of Microarray Data of Rainbow Trout Fry Gonad Differentiation Modulated by Ethynylestradiol. PLoS ONE, 2015, 10, e0135799.	1.1	10
2369	Social Regulation of Gene Expression in Threespine Sticklebacks. PLoS ONE, 2015, 10, e0137726.	1.1	32
2370	Recurrent Glioblastomas Reveal Molecular Subtypes Associated with Mechanistic Implications of Drug-Resistance. PLoS ONE, 2015, 10, e0140528.	1.1	38
2371	Analysis of Stage-Specific Gene Expression Profiles in the Uterine Endometrium during Pregnancy in Pigs. PLoS ONE, 2015, 10, e0143436.	1.1	20
2372	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
2373	Expression Profiling after Prolonged Experimental Febrile Seizures in Mice Suggests Structural Remodeling in the Hippocampus. PLoS ONE, 2015, 10, e0145247.	1.1	13
2374	Size of the Ovulatory Follicle Dictates Spatial Differences in the Oviductal Transcriptome in Cattle. PLoS ONE, 2015, 10, e0145321.	1.1	29
2375	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
2376	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
2377	Detecting Key Genes Regulated by miRNAs in Dysfunctional Crosstalk Pathway of Myasthenia Gravis. BioMed Research International, 2015, 2015, 1-10.	0.9	12
2378	Embryonic attenuated Wnt/ β -catenin signaling defines niche location and long-term stem cell fate in hair follicle. ELife, 2015, 4, e10567.	2.8	57
2379	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
2380	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
2381	Discover the Molecular Biomarker Associated with Cell Death and Extracellular Matrix Module in Ovarian Cancer. BioMed Research International, 2015, 2015, 1-6.	0.9	1
2382	Whole-transcriptome analysis of flow-sorted cervical cancer samples reveals that B cell expressed TCL1A is correlated with improved survival. Oncotarget, 2015, 6, 38681-38694.	0.8	15
2383	Network-based approach to identify prognostic biomarkers for estrogen receptor ⁺ positive breast cancer treatment with tamoxifen. Cancer Biology and Therapy, 2015, 16, 317-324.	1.5	72

#	ARTICLE	IF	CITATIONS
2384	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
2385	Evidence that MHC I-E dampens thyroid autoantibodies and prevents spreading to a second thyroid autoantigen in I-A ^k NOD mice. <i>Genes and Immunity</i> , 2015, 16, 268-274.	2.2	25
2386	Prmt5 is a regulator of muscle stem cell expansion in adult mice. <i>Nature Communications</i> , 2015, 6, 7140.	5.8	98
2387	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
2388	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
2389	Position-specific binding of FUS to nascent RNA regulates mRNA length. <i>Genes and Development</i> , 2015, 29, 1045-1057.	2.7	98
2390	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
2391	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
2392	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
2393	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
2394	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
2395	Bioinformatics Analysis of Potential Candidates for Therapy of TDRD7 Deficiency-Induced Congenital Cataract. <i>Ophthalmic Research</i> , 2015, 54, 10-17.	1.0	5
2396	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
2397	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
2398	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
2399	Transcriptomic profiles of aging in purified human immune cells. <i>BMC Genomics</i> , 2015, 16, 333.	1.2	58
2400	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
2401	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

#	ARTICLE	IF	CITATIONS
2402	Dysregulated mechanisms underlying Duchenne muscular dystrophy from co-expression network preservation analysis. <i>BMC Research Notes</i> , 2015, 8, 182.	0.6	24
2403	Ascorbic Acid-Induced Cardiac Differentiation of Murine Pluripotent Stem Cells: Transcriptional Profiling and Effect of a Small Molecule Synergist of Wnt/ β -Catenin Signaling Pathway. <i>Cellular Physiology and Biochemistry</i> , 2015, 36, 810-830.	1.1	23
2404	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
2405	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
2406	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
2407	Profiling of promoter occupancy by the SND1 transcriptional coactivator identifies downstream glycerolipid metabolic genes involved in TNF α response in human hepatoma cells. <i>Nucleic Acids Research</i> , 2015, 43, 10673-10688.	6.5	27
2408	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
2409	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
2410	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
2411	MVDA: a multi-view genomic data integration methodology. <i>BMC Bioinformatics</i> , 2015, 16, 261.	1.2	62
2412	A simplicial complex-based approach to unmixing tumor progression data. <i>BMC Bioinformatics</i> , 2015, 16, 254.	1.2	11
2413	Selective Coregulator Function and Restriction of Steroid Receptor Chromatin Occupancy by Hic-5. <i>Molecular Endocrinology</i> , 2015, 29, 716-729.	3.7	19
2414	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
2415	PAGER: constructing PAGs and new PAG-PAG relationships for network biology. <i>Bioinformatics</i> , 2015, 31, i250-i257.	1.8	21
2416	Genome-wide gene expression analysis for target genes to differentiate patients with intestinal tuberculosis and Crohn's disease and discriminative value of FOXP3 mRNA expression. <i>Gastroenterology Report</i> , 2016, 4, gov015.	0.6	11
2417	EvoTol: a protein-sequence based evolutionary intolerance framework for disease-gene prioritization. <i>Nucleic Acids Research</i> , 2015, 43, e33-e33.	6.5	33
2418	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
2419	Acute Cellular Rejection Elicits Distinct MicroRNA Signatures in Airway Epithelium of Lung Transplant Patients. <i>Transplantation Direct</i> , 2015, 1, e44.	0.8	8

#	ARTICLE	IF	CITATIONS
2420	Response and survival of breast cancer intrinsic subtypes following multi-agent neoadjuvant chemotherapy. <i>BMC Medicine</i> , 2015, 13, 303.	2.3	113
2421	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
2422	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
2423	Understanding the molecular aspects of oriental obesity pattern differentiation using DNA microarray. <i>Journal of Translational Medicine</i> , 2015, 13, 331.	1.8	1
2424	The homeobox gene <i>DLX4</i> regulates erythro-megakaryocytic differentiation by stimulating IL-1/NF- κ B signaling. <i>Journal of Cell Science</i> , 2015, 128, 3055-67.	1.2	12
2425	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
2426	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
2427	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
2428	Zic2 Is an Enhancer-Binding Factor Required for Embryonic Stem Cell Specification. <i>Molecular Cell</i> , 2015, 57, 685-694.	4.5	92
2429	mRNA expression profiles in circulating tumor cells of metastatic colorectal cancer patients. <i>Molecular Oncology</i> , 2015, 9, 920-932.	2.1	37
2430	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
2431	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
2432	Gene expression-based classifications of fibroadenomas and phyllodes tumours of the breast. <i>Molecular Oncology</i> , 2015, 9, 1081-1090.	2.1	39
2433	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
2434	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
2435	Resistin-Like Molecule \pm in Allergen-Induced Pulmonary Vascular Remodeling. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2015, 53, 303-313.	1.4	18
2436	Multiple comparison procedures for neuroimaging genomewide association studies. <i>Biostatistics</i> , 2015, 16, 17-30.	0.9	9
2437	The clinicopathological and gene expression patterns associated with ulceration of primary melanoma. <i>Pigment Cell and Melanoma Research</i> , 2015, 28, 94-104.	1.5	26

#	ARTICLE	IF	CITATIONS
2438	The Novel Small Leucine-rich Protein Chondroadherin-like (CHADL) Is Expressed in Cartilage and Modulates Chondrocyte Differentiation. <i>Journal of Biological Chemistry</i> , 2015, 290, 918-925.	1.6	30
2439	Identification of copy number variations in Qinchuan cattle using BovineHD Genotyping Beadchip array. <i>Molecular Genetics and Genomics</i> , 2015, 290, 319-327.	1.0	48
2440	A search for protein biomarkers links olfactory signal transduction to social immunity. <i>BMC Genomics</i> , 2015, 16, 63.	1.2	45
2441	Integrative analysis of lung developmentâ€“cancer expression associations reveals the roles of signatures with inverse expression patterns. <i>Molecular BioSystems</i> , 2015, 11, 1271-1284.	2.9	9
2442	Mutations in early follicular lymphoma progenitors are associated with suppressed antigen presentation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1116-25.	3.3	307
2443	Time-restricted feeding attenuates age-related cardiac decline in <i>Drosophila</i> . <i>Science</i> , 2015, 347, 1265-1269.	6.0	223
2444	Effects of an 11-nm DMSA-coated iron nanoparticle on the gene expression profile of two human cell lines, THP-1 and HepG2. <i>Journal of Nanobiotechnology</i> , 2015, 13, 3.	4.2	16
2445	Identification of potential genomic biomarkers for Sjögren's syndrome using data pooling of gene expression microarrays. <i>Rheumatology International</i> , 2015, 35, 829-836.	1.5	55
2446	Identification of targets for rational pharmacological therapy in childhood craniopharyngioma. <i>Acta Neuropathologica Communications</i> , 2015, 3, 30.	2.4	85
2447	Epigenetic and in vivo comparison of diverse MSC sources reveals an endochondral signature for human hematopoietic niche formation. <i>Blood</i> , 2015, 125, 249-260.	0.6	201
2448	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
2449	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
2450	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
2451	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
2452	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
2453	ABCG2 Localizes to the Nucleus and Modulates CDH1 Expression in Lung Cancer Cells. <i>Neoplasia</i> , 2015, 17, 265-278.	2.3	45
2454	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
2455	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

#	ARTICLE	IF	CITATIONS
2456	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
2457	Genome-wide burden of deleterious coding variants increased in schizophrenia. <i>Nature Communications</i> , 2015, 6, 7501.	5.8	22
2458	Vitamin B ₁₂ modulates the transcriptome of the skin microbiota in acne pathogenesis. <i>Science Translational Medicine</i> , 2015, 7, 293ra103.	5.8	138
2459	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
2460	Parallel Gene Expression Changes in Sarcoidosis Involving the Lacrimal Gland, Orbital Tissue, or Blood. <i>JAMA Ophthalmology</i> , 2015, 133, 770.	1.4	31
2461	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
2462	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
2463	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
2464	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015, 6, 7866.	5.8	676
2465	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
2466	FOXG1-Dependent Dysregulation of GABA/Glutamate Neuron Differentiation in Autism Spectrum Disorders. <i>Cell</i> , 2015, 162, 375-390.	13.5	894
2467	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
2468	Highly Constrained Intergenic Drosophila Ultraconserved Elements Are Candidate ncRNAs. <i>Genome Biology and Evolution</i> , 2015, 7, 689-698.	1.1	16
2469	Genomic characteristics of miscarriage copy number variants. <i>Molecular Human Reproduction</i> , 2015, 21, 655-661.	1.3	28
2470	Ataxin-2 Regulates RGS8 Translation in a New BAC-SCA2 Transgenic Mouse Model. <i>PLoS Genetics</i> , 2015, 11, e1005182.	1.5	70
2471	Destabilization of pluripotency in the absence of Mad2l2. <i>Cell Cycle</i> , 2015, 14, 1596-1610.	1.3	13
2472	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
2473	MPTP's Pathway of Toxicity Indicates Central Role of Transcription Factor SP1. <i>Archives of Toxicology</i> , 2015, 89, 743-755.	1.9	33

#	ARTICLE	IF	CITATIONS
2474	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
2475	BACA: bubble chArt to compare annotations. <i>BMC Bioinformatics</i> , 2015, 16, 37.	1.2	16
2476	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
2477	Global liver gene expression differences in Nelore steers with divergent residual feed intake phenotypes. <i>BMC Genomics</i> , 2015, 16, 242.	1.2	109
2478	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
2479	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
2480	DNA methylation changes in the placenta are associated with fetal manganese exposure. <i>Reproductive Toxicology</i> , 2015, 57, 43-49.	1.3	43
2481	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
2482	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
2483	Cigarette smoking hinders human periodontal ligament-derived stem cell proliferation, migration and differentiation potentials. <i>Scientific Reports</i> , 2015, 5, 7828.	1.6	73
2484	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
2485	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
2486	Interactions between horizontally acquired genes create a fitness cost in <i>Pseudomonas aeruginosa</i> . <i>Nature Communications</i> , 2015, 6, 6845.	5.8	147
2487	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
2488	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
2489	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
2490	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
2491	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

#	ARTICLE	IF	CITATIONS
2492	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
2493	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
2494	Graph-based unsupervised feature selection and multiview clustering for microarray data. <i>Journal of Biosciences</i> , 2015, 40, 755-767.	0.5	11
2495	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
2496	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. <i>Neuron</i> , 2015, 87, 1215-1233.	3.8	1,219
2497	The DNA damage response induces inflammation and senescence by inhibiting autophagy of GATA4. <i>Science</i> , 2015, 349, aaa5612.	6.0	693
2498	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
2499	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
2500	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
2501	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
2502	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
2503	A mutation profile for top- <i>k</i> patient search exploiting Gene-Ontology and orthogonal non-negative matrix factorization. <i>Bioinformatics</i> , 2015, 31, 3653-3659.	1.8	12
2504	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
2505	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
2506	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
2507	Genome-wide identification of microRNAs regulating cholesterol and triglyceride homeostasis. <i>Nature Medicine</i> , 2015, 21, 1290-1297.	15.2	214
2508	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
2509	Monocyte enhancers are highly altered in systemic lupus erythematosus. <i>Epigenomics</i> , 2015, 7, 921-935.	1.0	27

#	ARTICLE	IF	CITATIONS
2510	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
2511	KnowEnG: a knowledge engine for genomics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1115-1119.	2.2	13
2512	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
2513	Molecular insight into thiopurine resistance: transcriptomic signature in lymphoblastoid cell lines. <i>Genome Medicine</i> , 2015, 7, 37.	3.6	19
2514	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
2515	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
2516	Microarray profiling of long non-coding RNA (lncRNA) associated with hypertrophic cardiomyopathy. <i>BMC Cardiovascular Disorders</i> , 2015, 15, 62.	0.7	49
2517	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
2518	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
2519	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
2520	Defining the phospho-adesome through the phosphoproteomic analysis of integrin signalling. <i>Nature Communications</i> , 2015, 6, 6265.	5.8	150
2521	New Perspectives for the Rescue of Cognitive Disability in Down Syndrome. <i>Journal of Neuroscience</i> , 2015, 35, 13843-13852.	1.7	28
2522	Potential anti-cancer effect of curcumin in human lung squamous cell carcinoma. <i>Thoracic Cancer</i> , 2015, 6, 508-516.	0.8	25
2523	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
2524	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
2525	Gene expression profiling of ovarian carcinomas and prognostic analysis of outcome. <i>Journal of Ovarian Research</i> , 2015, 8, 50.	1.3	10
2526	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
2527	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

#	ARTICLE	IF	CITATIONS
2528	Ageing-Dependent Demethylation of Regulatory Elements Correlates with Chromatin State and Improved \hat{I}^2 Cell Function. <i>Cell Metabolism</i> , 2015, 22, 619-632.	7.2	172
2529	SPINK1 promotes colorectal cancer progression by downregulating Metallothioneins expression. <i>Oncogenesis</i> , 2015, 4, e162-e162.	2.1	50
2530	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
2531	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
2532	Isolated Rat Epididymal Basal Cells Share Common Properties with Adult Stem Cells1. <i>Biology of Reproduction</i> , 2015, 93, 115.	1.2	39
2533	Recurrent internal tandem duplications of BCOR in clear cell sarcoma of the kidney. <i>Nature Communications</i> , 2015, 6, 8891.	5.8	126
2534	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
2535	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
2536	Expression profiling of circulating tumor cells in metastatic breast cancer. <i>Breast Cancer Research and Treatment</i> , 2015, 149, 121-131.	1.1	48
2537	Transcriptome organization for chronic alcohol abuse in human brain. <i>Molecular Psychiatry</i> , 2015, 20, 1438-1447.	4.1	111
2538	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
2539	TRIM24 links glucose metabolism with transformation of human mammary epithelial cells. <i>Oncogene</i> , 2015, 34, 2836-2845.	2.6	50
2540	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
2541	Dauer-independent insulin/IGF-1-signalling implicates collagen remodelling in longevity. <i>Nature</i> , 2015, 519, 97-101.	13.7	251
2542	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
2544	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
2545	Proteins associated with pancreatic cancer survival in patients with resectable pancreatic ductal adenocarcinoma. <i>Laboratory Investigation</i> , 2015, 95, 43-55.	1.7	44
2546	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

#	ARTICLE	IF	CITATIONS
2547	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
2548	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
2549	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
2550	Argonaute CLIP-Seq reveals miRNA targetome diversity across tissue types. <i>Scientific Reports</i> , 2014, 4, 5947.	1.6	88
2551	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
2552	H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells. <i>Genome Research</i> , 2015, 25, 27-40.	2.4	119
2553	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
2554	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
2555	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
2556	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
2557	Inferring the progression of multifocal liver cancer from spatial and temporal genomic heterogeneity. <i>Oncotarget</i> , 2016, 7, 2867-2877.	0.8	38
2558	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
2559	Bioinformatics analysis of differentially expressed proteins in prostate cancer based on proteomics data. <i>OncoTargets and Therapy</i> , 2016, 9, 1545.	1.0	21
2560	Molecular crosstalk between tumour and brain parenchyma instructs histopathological features in glioblastoma. <i>Oncotarget</i> , 2016, 7, 31955-31971.	0.8	69
2561	Practical aspects of NGS-based pathways analysis for personalized cancer science and medicine. <i>Oncotarget</i> , 2016, 7, 52493-52516.	0.8	15
2562	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
2563	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
2564	Identification of Molecular Targets for Predicting Colon Adenocarcinoma. <i>Medical Science Monitor</i> , 2016, 22, 460-468.	0.5	13

#	ARTICLE	IF	CITATIONS
2565	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
2566	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
2567	A Transcriptomic Signature of Mouse Liver Progenitor Cells. <i>Stem Cells International</i> , 2016, 2016, 1-15.	1.2	5
2568	Human Epithelial Cells Discriminate between Commensal and Pathogenic Interactions with <i>Candida albicans</i> . <i>PLoS ONE</i> , 2016, 11, e0153165.	1.1	16
2569	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
2570	<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
2571	Immunosenescence-Related Transcriptomic and Immunologic Changes in Older Individuals Following Influenza Vaccination. <i>Frontiers in Immunology</i> , 2016, 7, 450.	2.2	40
2572	Ageing Shapes the Population-Mean and -Dispersion of Gene Expression in Human Brains. <i>Frontiers in Aging Neuroscience</i> , 2016, 8, 183.	1.7	31
2573	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
2574	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
2575	Systematic Analysis of Protein Interaction Network Associated with Azoospermia. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1857.	1.8	14
2576	The Pleiotropic Antibacterial Mechanisms of Ursolic Acid against Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA). <i>Molecules</i> , 2016, 21, 884.	1.7	26
2577	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
2578	Differential effect of mild and severe pulmonary embolism on the rat lung transcriptome. <i>Respiratory Research</i> , 2016, 17, 86.	1.4	9
2579	Behavioral and molecular studies of quantitative differences in hygienic behavior in honeybees. <i>BMC Research Notes</i> , 2016, 9, 474.	0.6	11
2580	Low expression levels of putative HPV encoded microRNAs in cervical samples. <i>SpringerPlus</i> , 2016, 5, 1856.	1.2	17
2581	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
2582	Context Specific and Differential Gene Co-expression Networks via Bayesian Biclustering. <i>PLoS Computational Biology</i> , 2016, 12, e1004791.	1.5	46

#	ARTICLE	IF	CITATIONS
2583	Comparative Transcriptomic and Epigenomic Analyses Reveal New Regulators of Murine Brown Adipogenesis. <i>PLoS Genetics</i> , 2016, 12, e1006474.	1.5	44
2584	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
2585	Association of MicroRNA-196a2 Variant with Response to Short-Acting β_2 -Agonist in COPD: An Egyptian Pilot Study. <i>PLoS ONE</i> , 2016, 11, e0152834.	1.1	31
2586	WDR76 Co-Localizes with Heterochromatin Related Proteins and Rapidly Responds to DNA Damage. <i>PLoS ONE</i> , 2016, 11, e0155492.	1.1	27
2587	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
2588	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
2589	Transcriptional Profiling of Cultured, Embryonic Epicardial Cells Identifies Novel Genes and Signaling Pathways Regulated by TGF β 3 In Vitro. <i>PLoS ONE</i> , 2016, 11, e0159710.	1.1	19
2590	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
2591	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
2592	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
2593	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
2594	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
2595	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
2596	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
2597	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
2598	Functional Genomic Analyses Identify Pathways Dysregulated in Animal Model of Autism. <i>CNS Neuroscience and Therapeutics</i> , 2016, 22, 845-853.	1.9	22
2599	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
2600	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

#	ARTICLE	IF	CITATIONS
2601	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
2602	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
2603	Feature Subset Selection for Cancer Classification Using Weight Local Modularity. <i>Scientific Reports</i> , 2016, 6, 34759.	1.6	17
2604	Tocotrienols induce endoplasmic reticulum stress and apoptosis in cervical cancer cells. <i>Genes and Nutrition</i> , 2016, 11, 32.	1.2	23
2605	hTERT promotes cell adhesion and migration independent of telomerase activity. <i>Scientific Reports</i> , 2016, 6, 22886.	1.6	45
2606	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
2607	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
2608	Transcriptome sequencing of the choroid plexus in schizophrenia. <i>Translational Psychiatry</i> , 2016, 6, e964-e964.	2.4	50
2609	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
2610	Comprehensive genomic characterization of five canine lymphoid tumor cell lines. <i>BMC Veterinary Research</i> , 2016, 12, 207.	0.7	5
2611	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
2612	Var2GO: a web-based tool for gene variants selection. <i>BMC Bioinformatics</i> , 2016, 17, 376.	1.2	7
2613	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
2614	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
2615	Cross-tissue Analysis of Gene and Protein Expression in Normal and Cancer Tissues. <i>Scientific Reports</i> , 2016, 6, 24799.	1.6	155
2616	Lrrc75b is a novel negative regulator of C2C12 myogenic differentiation. <i>International Journal of Molecular Medicine</i> , 2016, 38, 1411-1418.	1.8	4
2617	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
2618	An Atlas of annotations of <i>Hydra vulgaris</i> transcriptome. <i>BMC Bioinformatics</i> , 2016, 17, 360.	1.2	1

#	ARTICLE	IF	CITATIONS
2619	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
2620	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
2621	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
2622	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
2623	Systematic analysis of the regulatory functions of microRNAs in chicken hepatic lipid metabolism. <i>Scientific Reports</i> , 2016, 6, 31766.	1.6	36
2624	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
2625	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
2626	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
2627	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
2628	Genome-wide analysis of DNA methylation in hepatoblastoma tissues. <i>Oncology Letters</i> , 2016, 12, 1529-1534.	0.8	23
2629	A SILAC-Based Method for Quantitative Proteomic Analysis of Intestinal Organoids. <i>Scientific Reports</i> , 2016, 6, 38195.	1.6	24
2630	Identification of novel noncoding transcripts in telomerase-negative yeast using RNA-seq. <i>Scientific Reports</i> , 2016, 6, 19376.	1.6	8
2631	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
2632	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
2633	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
2634	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
2635	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
2636	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

#	ARTICLE	IF	CITATIONS
2637	Common integration sites of published datasets identified using a graph-based framework. Computational and Structural Biotechnology Journal, 2016, 14, 87-90.	1.9	2
2638	An examination of the regulatory mechanism of Pxdn mutation-induced eye disorders using microarray analysis. International Journal of Molecular Medicine, 2016, 37, 1449-1456.	1.8	5
2639	Genomic Landscape of Colorectal Mucosa and Adenomas. Cancer Prevention Research, 2016, 9, 417-427.	0.7	65
2640	Altered gene expression in the lower respiratory tract of Car6 ^{+/+} mice. Transgenic Research, 2016, 25, 649-664.	1.3	7
2641	Endometrial transcriptional profiling of a bovine fertility model by Next-Generation Sequencing. Genomics Data, 2016, 7, 26-28.	1.3	4
2642	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. Journal of Biological Chemistry, 2016, 291, 7831-7843.	1.6	21
2643	Evolution of a transcriptional regulator from a transmembrane nucleoporin. Genes and Development, 2016, 30, 1155-1171.	2.7	34
2644	Skeletal muscle transcriptional profiles in two Italian beef breeds, Chianina and Maremmana, reveal breed specific variation. Molecular Biology Reports, 2016, 43, 253-268.	1.0	16
2645	The tumor microenvironment underlies acquired resistance to CSF-1R inhibition in gliomas. Science, 2016, 352, aad3018.	6.0	477
2646	Evidence for embryonic stem-like signature and epithelial-mesenchymal transition features in the spheroid cells derived from lung adenocarcinoma. Tumor Biology, 2016, 37, 11843-11859.	0.8	19
2647	Adipose tissue RNASeq reveals novel gene-nutrient interactions following n-3 PUFA supplementation and evoked inflammation in humans. Journal of Nutritional Biochemistry, 2016, 30, 126-132.	1.9	30
2648	Sevoflurane exerts a more marked influence compared with propofol on gene expression in patients undergoing coronary artery bypass graft surgery. Experimental and Therapeutic Medicine, 2016, 11, 448-454.	0.8	1
2649	Using biological networks to integrate, visualize and analyze genomics data. Genetics Selection Evolution, 2016, 48, 27.	1.2	86
2650	Oncomirs miRNA-221/222 and Tumor Suppressors miRNA-199a/195 Are Crucial miRNAs in Liver Cancer: A Systematic Analysis. Digestive Diseases and Sciences, 2016, 61, 2315-2327.	1.1	33
2651	Identification of microRNA and target gene associated with marbling score in Korean cattle (Hanwoo). Genes and Genomics, 2016, 38, 529-538.	0.5	20
2652	Immunogenic Subtypes of Breast Cancer Delineated by Gene Classifiers of Immune Responsiveness. Cancer Immunology Research, 2016, 4, 600-610.	1.6	86
2653	ISL1 and JMJD3 synergistically control cardiac differentiation of embryonic stem cells. Nucleic Acids Research, 2016, 44, 6741-6755.	6.5	40
2654	Calcineurin Orchestrates Lateral Transfer of <i>Aspergillus fumigatus</i> during Macrophage Cell Death. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 1127-1139.	2.5	54

#	ARTICLE	IF	CITATIONS
2655	Identification of potential therapeutic targets for papillary thyroid carcinoma by bioinformatics analysis. <i>Oncology Letters</i> , 2016, 11, 51-58.	0.8	15
2656	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
2657	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
2658	Identification of key pathways and genes in colorectal cancer using bioinformatics analysis. <i>Medical Oncology</i> , 2016, 33, 111.	1.2	112
2659	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
2660	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
2661	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
2662	Identification of genes involved in Epstein-Barr virus-associated nasopharyngeal carcinoma. <i>Oncology Letters</i> , 2016, 12, 2375-2380.	0.8	8
2663	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
2664	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
2665	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
2666	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
2667	A chromatin modifier integrates insulin/IGF1 signalling and dietary restriction to regulate longevity. <i>Aging Cell</i> , 2016, 15, 694-705.	3.0	15
2668	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
2669	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
2670	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
2671	A small molecule inhibitor of mutant IDH2 rescues cardiomyopathy in a D-2-hydroxyglutaric aciduria type II mouse model. <i>Journal of Inherited Metabolic Disease</i> , 2016, 39, 807-820.	1.7	11
2672	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

#	ARTICLE	IF	CITATIONS
2673	Carbonic anhydrase enzymes regulate mast cell-mediated inflammation. <i>Journal of Experimental Medicine</i> , 2016, 213, 1663-1673.	4.2	26
2674	Insights into the human mesenchymal stromal/stem cell identity through integrative transcriptomic profiling. <i>BMC Genomics</i> , 2016, 17, 944.	1.2	55
2675	Differentially expressed circulating lncRNAs and mRNA identified by microarray analysis in obese patients. <i>Scientific Reports</i> , 2016, 6, 35421.	1.6	42
2676	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
2677	Macrophage Ontogeny Underlies Differences in Tumor-Specific Education in Brain Malignancies. <i>Cell Reports</i> , 2016, 17, 2445-2459.	2.9	450
2678	Diet-Microbiota Interactions Mediate Global Epigenetic Programming in Multiple Host Tissues. <i>Molecular Cell</i> , 2016, 64, 982-992.	4.5	405
2679	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
2680	v-Src Oncogene Induces Trop2 Proteolytic Activation via Cyclin D1. <i>Cancer Research</i> , 2016, 76, 6723-6734.	0.4	22
2681	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
2682	FOXO/DAF-16 Activation Slows Down Turnover of the Majority of Proteins in <i>C.Âlegans</i> . <i>Cell Reports</i> , 2016, 16, 3028-3040.	2.9	44
2683	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
2684	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, dww313.	1.4	25
2685	Reactive Oxygen Species-Associated Molecular Signature Predicts Survival in Patients with Sepsis. <i>Pulmonary Circulation</i> , 2016, 6, 196-201.	0.8	25
2686	Expression Profiling Elucidates a Molecular Gene Signature for Pulmonary Hypertension in Sarcoidosis. <i>Pulmonary Circulation</i> , 2016, 6, 465-471.	0.8	10
2687	Identification of potential therapeutic targets for lung cancer by bioinformatics analysis. <i>Molecular Medicine Reports</i> , 2016, 13, 1975-1982.	1.1	15
2688	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
2689	Chromatin remodeling inactivates activity genes and regulates neural coding. <i>Science</i> , 2016, 353, 300-305.	6.0	96
2690	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

#	ARTICLE	IF	CITATIONS
2691	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
2692	Differential expression of TGF- β 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
2693	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
2694	Identification of potential therapeutic targets for colorectal cancer by bioinformatics analysis. <i>Oncology Letters</i> , 2016, 12, 5092-5098.	0.8	23
2695	SOX7 co-regulates Wnt/ β -catenin signaling with Axin-2: both expressed at low levels in breast cancer. <i>Scientific Reports</i> , 2016, 6, 26136.	1.6	25
2696	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
2697	Analysis of the molecular mechanism of osteosarcoma using a bioinformatics approach. <i>Oncology Letters</i> , 2016, 12, 3075-3080.	0.8	13
2698	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
2699	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
2700	A YY1-dependent increase in aerobic metabolism is indispensable for intestinal organogenesis. <i>Development (Cambridge)</i> , 2016, 143, 3711-3722.	1.2	22
2701	Mechanistic evaluation and transcriptional signature of a glutathione S-transferase omega 1 inhibitor. <i>Nature Communications</i> , 2016, 7, 13084.	5.8	53
2702	Pathogenic landscape of idiopathic male infertility: new insight towards its regulatory networks. <i>Npj Genomic Medicine</i> , 2016, 1, 16023.	1.7	35
2703	RYR2, PTDSS1 and AREG genes are implicated in a Lebanese population-based study of copy number variation in autism. <i>Scientific Reports</i> , 2016, 6, 19088.	1.6	27
2704	SYVN1, NEDD8, and FBXO2 Proteins Regulate β 508 Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) Ubiquitin-mediated Proteasomal Degradation. <i>Journal of Biological Chemistry</i> , 2016, 291, 25489-25504.	1.6	27
2705	Transcriptome Analysis on Monocytes from Patients with Neovascular Age-Related Macular Degeneration. <i>Scientific Reports</i> , 2016, 6, 29046.	1.6	32
2706	A restricted period for formation of outer subventricular zone defined by <i>Cdh1</i> and <i>Trnp1</i> levels. <i>Nature Communications</i> , 2016, 7, 11812.	5.8	108
2707	Identification of Changes in Gene expression of rats after Sensory and Motor Nerves Injury. <i>Scientific Reports</i> , 2016, 6, 26579.	1.6	6
2708	Long noncoding RNA linc00598 regulates CCND2 transcription and modulates the G1 checkpoint. <i>Scientific Reports</i> , 2016, 6, 32172.	1.6	13

#	ARTICLE	IF	CITATIONS
2709	Injury-induced <i>ctgfa</i> directs glial bridging and spinal cord regeneration in zebrafish. <i>Science</i> , 2016, 354, 630-634.	6.0	196
2710	iTRAQ-based quantitative proteomic analysis reveals potential early diagnostic markers of clear-cell Renal cell carcinoma. <i>BioScience Trends</i> , 2016, 10, 210-219.	1.1	21
2711	A new strategy for exploring the hierarchical structure of cancers by adaptively partitioning functional modules from gene expression network. <i>Scientific Reports</i> , 2016, 6, 28720.	1.6	13
2712	Mammalian Brain Development is Accompanied by a Dramatic Increase in Bipolar DNA Methylation. <i>Scientific Reports</i> , 2016, 6, 32298.	1.6	13
2713	Genome-wide association studies of immune, disease and production traits in indigenous chicken ecotypes. <i>Genetics Selection Evolution</i> , 2016, 48, 74.	1.2	36
2714	Most of the tight positional conservation of transcription factor binding sites near the transcription start site reflects their co-localization within regulatory modules. <i>BMC Bioinformatics</i> , 2016, 17, 479.	1.2	1
2715	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
2716	Prediction of scaffold proteins based on protein interaction and domain architectures. <i>BMC Bioinformatics</i> , 2016, 17, 220.	1.2	6
2717	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
2718	Potential molecular characteristics in situ in response to repetitive UVB irradiation. <i>Diagnostic Pathology</i> , 2016, 11, 129.	0.9	8
2719	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
2720	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
2721	SOHSite: incorporating evolutionary information and physicochemical properties to identify protein S-sulfenylation sites. <i>BMC Genomics</i> , 2016, 17, 9.	1.2	45
2722	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
2723	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
2724	Identification of genes associated with renal cell carcinoma using gene expression profiling analysis. <i>Oncology Letters</i> , 2016, 12, 73-78.	0.8	18
2725	Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, W90-W97.	6.5	7,240
2726	Identification of key genes in glioblastoma-associated stromal cells using bioinformatics analysis. <i>Oncology Letters</i> , 2016, 11, 3999-4007.	0.8	11

#	ARTICLE	IF	CITATIONS
2727	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
2728	Microarray data on altered transcriptional program of Phgdh-deficient mouse embryonic fibroblasts caused by 5-HT-serine depletion. <i>Data in Brief</i> , 2016, 7, 1598-1601.	0.5	4
2729	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
2730	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
2731	Identification of novel gene and pathway targets for human epilepsy treatment. <i>Biological Research</i> , 2016, 49, 3.	1.5	10
2732	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
2733	Medoidshift clustering applied to genomic bulk tumor data. <i>BMC Genomics</i> , 2016, 17, 6.	1.2	4
2734	MiR-210 promotes sensory hair cell formation in the organ of corti. <i>BMC Genomics</i> , 2016, 17, 309.	1.2	25
2735	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
2736	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
2737	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
2738	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
2739	KeyPathwayMinerWeb: online multi-omics network enrichment. <i>Nucleic Acids Research</i> , 2016, 44, W98-W104.	6.5	45
2740	SPATIAL: A System-level PATHway Impact Analysis approach. <i>Nucleic Acids Research</i> , 2016, 44, 5034-5044.	6.5	18
2741	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
2742	miR-143 mediates prostate cancer cell death induced by combinatorial targeting of the androgen receptor. <i>BMC Cancer</i> , 2016, 16, 141.	1.1	10
2743	The landscape of accessible chromatin in mammalian preimplantation embryos. <i>Nature</i> , 2016, 534, 652-657.	13.7	550
2744	PCBP1/HNRNP E1 Protects Chromosomal Integrity by Translational Regulation of CDC27. <i>Molecular Cancer Research</i> , 2016, 14, 634-646.	1.5	22

#	ARTICLE	IF	CITATIONS
2745	Network motif-based method for identifying coronary artery disease. <i>Experimental and Therapeutic Medicine</i> , 2016, 12, 257-261.	0.8	1
2746	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
2747	An essential role for UTX in resolution and activation of bivalent promoters. <i>Nucleic Acids Research</i> , 2016, 44, 3659-3674.	6.5	63
2748	Genome-wide methylation profiling identifies novel methylated genes in neuroblastoma tumors. <i>Epigenetics</i> , 2016, 11, 74-84.	1.3	63
2749	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
2750	Mapping the O-Mannose Glycoproteome in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1323-1337.	2.5	61
2751	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
2752	<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
2753	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
2754	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
2755	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
2756	Circulating microRNAs as Potential Biomarkers of Endothelial Dysfunction in Obese Children. <i>Chest</i> , 2016, 149, 786-800.	0.4	66
2757	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
2758	Ancestral vinclozolin exposure alters the epigenetic transgenerational inheritance of sperm small noncoding RNAs. <i>Environmental Epigenetics</i> , 2016, 2, dvw001.	0.9	90
2759	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
2760	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
2761	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
2762	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

#	ARTICLE	IF	CITATIONS
2763	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
2764	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
2765	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
2766	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
2767	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
2768	Spermatogenesis Drives Rapid Gene Creation and Masculinization of the X Chromosome in Stalk-Eyed Flies (Diopsidae). <i>Genome Biology and Evolution</i> , 2016, 8, 896-914.	1.1	9
2769	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
2770	Mitochondrial iron chelation ameliorates cigarette smoke-induced bronchitis and emphysema in mice. <i>Nature Medicine</i> , 2016, 22, 163-174.	15.2	206
2771	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
2772	Molecular diagnosis: Implications for ophthalmology. <i>Progress in Retinal and Eye Research</i> , 2016, 50, 25-33.	7.3	7
2773	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
2774	Five miRNAs considered as molecular targets for predicting neuroglioma. <i>Tumor Biology</i> , 2016, 37, 1051-1059.	0.8	21
2775	Heat-shock factor 2 is a suppressor of prostate cancer invasion. <i>Oncogene</i> , 2016, 35, 1770-1784.	2.6	48
2776	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
2777	Whole-genome association analysis of treatment response in obsessive-compulsive disorder. <i>Molecular Psychiatry</i> , 2016, 21, 270-276.	4.1	49
2778	A survey of current trends in computational drug repositioning. <i>Briefings in Bioinformatics</i> , 2016, 17, 2-12.	3.2	459
2779	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
2780	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

#	ARTICLE	IF	CITATIONS
2781	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
2782	Novel blood-based microRNA biomarker panel for early diagnosis of chronic pancreatitis. <i>Scientific Reports</i> , 2017, 7, 40019.	1.6	44
2783	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
2784	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
2785	Circadian deep sequencing reveals stress-response genes that adopt robust rhythmic expression during aging. <i>Nature Communications</i> , 2017, 8, 14529.	5.8	112
2786	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
2787	Nucleosome repositioning during differentiation of a human myeloid leukemia cell line. <i>Nucleus</i> , 2017, 8, 188-204.	0.6	21
2788	Human enterovirus 71 protein interaction network prompts antiviral drug repositioning. <i>Scientific Reports</i> , 2017, 7, 43143.	1.6	19
2789	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
2790	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
2791	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
2792	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
2793	Drug Response Prediction as a Link Prediction Problem. <i>Scientific Reports</i> , 2017, 7, 40321.	1.6	64
2794	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
2795	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
2796	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
2797	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
2798	Activated Platelets Induce Endothelial Cell Activation via an Interleukin-1 β Pathway in Systemic Lupus Erythematosus. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2017, 37, 707-716.	1.1	77

#	ARTICLE	IF	CITATIONS
2799	Tdp-43 cryptic exons are highly variable between cell types. <i>Molecular Neurodegeneration</i> , 2017, 12, 13.	4.4	63
2800	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
2801	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
2802	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
2803	Intrinsic Subtypes and Gene Expression Profiles in Primary and Metastatic Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2213-2221.	0.4	168
2804	TAZ contributes to pulmonary fibrosis by activating profibrotic functions of lung fibroblasts. <i>Scientific Reports</i> , 2017, 7, 42595.	1.6	84
2805	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
2806	Disease biomarker identification from gene network modules for metastasized breast cancer. <i>Scientific Reports</i> , 2017, 7, 1072.	1.6	13
2807	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
2808	Impact of Neutron Exposure on Global Gene Expression in a Human Peripheral Blood Model. <i>Radiation Research</i> , 2017, 187, 443.	0.7	35
2809	Metallothionein 1G promotes the differentiation of HT-29 human colorectal cancer cells. <i>Oncology Reports</i> , 2017, 37, 2633-2651.	1.2	27
2810	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
2811	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
2812	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
2813	Microarray-based screening of differentially expressed genes in glucocorticoid-induced avascular necrosis. <i>Molecular Medicine Reports</i> , 2017, 15, 3583-3590.	1.1	4
2814	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
2815	Dysregulation of MS risk genes and pathways at distinct stages of disease. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2017, 4, e337.	3.1	34
2816	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

#	ARTICLE	IF	CITATIONS
2817	Hyper-phosphorylation of Sequestosome-1 Distinguishes Resistance to Cisplatin in Patient Derived High Grade Serous Ovarian Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1377-1392.	2.5	17
2818	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
2819	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
2820	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
2821	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
2822	Cell diversity and network dynamics in photosensitive human brain organoids. <i>Nature</i> , 2017, 545, 48-53.	13.7	933
2823	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
2824	Methods, Tools and Current Perspectives in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 959-981.	2.5	130
2825	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
2826	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
2827	A hormonal cue promotes timely follicle cell migration by modulating transcription profiles. <i>Mechanisms of Development</i> , 2017, 148, 56-68.	1.7	19
2828	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
2829	Silencing TAK1 alters gene expression signatures in bladder cancer cells. <i>Oncology Letters</i> , 2017, 13, 2975-2981.	0.8	20
2830	Candidate miRNAs and pathogenesis investigation for hepatocellular carcinoma based on bioinformatics analysis. <i>Oncology Letters</i> , 2017, 13, 3409-3414.	0.8	12
2831	Krüppel-like factors compete for promoters and enhancers to fine-tune transcription. <i>Nucleic Acids Research</i> , 2017, 45, 6572-6588.	6.5	40
2832	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
2833	Genetics of alcohol consumption in <i>Drosophila melanogaster</i> . <i>Genes, Brain and Behavior</i> , 2017, 16, 675-685.	1.1	17
2834	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

#	ARTICLE	IF	CITATIONS
2835	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
2836	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
2837	Embryonic AP1 Transcription Factor Deficiency Causes a Collodion Baby-Like Phenotype. <i>Journal of Investigative Dermatology</i> , 2017, 137, 1868-1877.	0.3	3
2838	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
2839	Downregulation of TRPM7 suppressed migration and invasion by regulating epithelial-mesenchymal transition in prostate cancer cells. <i>Medical Oncology</i> , 2017, 34, 127.	1.2	31
2840	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
2841	Estrogen Receptor- β Modulation of the ER β -p53 Loop Regulating Gene Expression, Proliferation, and Apoptosis in Breast Cancer. <i>Hormones and Cancer</i> , 2017, 8, 230-242.	4.9	39
2842	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
2843	Proteome dynamics during postnatal mouse corpus callosum development. <i>Scientific Reports</i> , 2017, 7, 45359.	1.6	5
2844	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
2845	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
2846	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
2847	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
2848	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
2849	<scp>TFE</scp> 3 regulates whole-body energy metabolism in cooperation with <scp>TFEB</scp>. <i>EMBO Molecular Medicine</i> , 2017, 9, 605-621.	3.3	101
2850	Immunoproteomic identification and characterization of Ni ²⁺ -regulated proteins implicates Ni ²⁺ in the induction of monocyte cell death. <i>Cell Death and Disease</i> , 2017, 8, e2684-e2684.	2.7	13
2851	Molecular Evidence for Differential Long-term Outcomes of Early Life Severe Acute Malnutrition. <i>EBioMedicine</i> , 2017, 18, 274-280.	2.7	15
2852	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

#	ARTICLE	IF	CITATIONS
2853	Recurrent rewiring and emergence of RNA regulatory networks. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2816-E2825.	3.3	32
2854	Comparative analysis of TCDD-induced AhR-mediated gene expression in human, mouse and rat primary B cells. Toxicology and Applied Pharmacology, 2017, 316, 95-106.	1.3	31
2855	The functional consequences and prognostic value of dosage sensitivity in ovarian cancer. Molecular BioSystems, 2017, 13, 380-391.	2.9	10
2856	Comparative analysis of hepatocellular carcinoma and cirrhosis gene expression profiles. Molecular Medicine Reports, 2017, 15, 380-386.	1.1	16
2857	Identification of potential therapeutic targets for gliomas by bioinformatics analysis. Oncology Letters, 2017, 14, 5203-5210.	0.8	3
2858	Bivalent complexes of PRC1 with orthologs of BRD4 and MOZ/MORF target developmental genes in <i>Drosophila</i> . Genes and Development, 2017, 31, 1988-2002.	2.7	25
2859	Screening and identification of critical transcription factors involved in the protection of cardiomyocytes against hydrogen peroxide-induced damage by Yixin-shu. Scientific Reports, 2017, 7, 13867.	1.6	13
2860	Network-based analysis of the molecular mechanisms of multiple myeloma and monoclonal gammopathy of undetermined significance. Oncology Letters, 2017, 14, 4167-4175.	0.8	16
2861	Relevance of iPSC-derived human PGC-like cells at the surface of embryoid bodies to prechemotaxis migrating PGCs. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9913-E9922.	3.3	41
2862	MCbiclust: a novel algorithm to discover large-scale functionally related gene sets from massive transcriptomics data collections. Nucleic Acids Research, 2017, 45, 8712-8730.	6.5	13
2863	Prognostic genes of breast cancer revealed by gene co-expression network analysis. Oncology Letters, 2017, 14, 4535-4542.	0.8	27
2864	Differential protein-coding gene and long noncoding RNA expression in smoking-related lung squamous cell carcinoma. Thoracic Cancer, 2017, 8, 672-681.	0.8	27
2865	Investigating the mechanisms of papillary thyroid carcinoma using transcriptome analysis. Molecular Medicine Reports, 2017, 16, 5954-5964.	1.1	3
2866	Transcription profiling analysis of genes and pathomechanisms underlying the defense response against Tobacco Etch Virus infection in <i>Arabidopsis thaliana</i> . Russian Journal of Plant Physiology, 2017, 64, 930-938.	0.5	1
2867	Bi-directional and shared epigenomic signatures following proton and ⁵⁶ Fe irradiation. Scientific Reports, 2017, 7, 10227.	1.6	36
2868	Therapeutic potential of <i>Bifidobacterium breve</i> strain A1 for preventing cognitive impairment in Alzheimer's disease. Scientific Reports, 2017, 7, 13510.	1.6	270
2869	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
2870	Dynamic and Modularized MicroRNA Regulation and Its Implication in Human Cancers. Scientific Reports, 2017, 7, 13356.	1.6	60

#	ARTICLE	IF	CITATIONS
2871	Bioinformatics analysis of gene expression profiling for identification of potential key genes among ischemic stroke. <i>Medicine (United States)</i> , 2017, 96, e7564.	0.4	10
2872	A systems biology approach to identify microRNAs contributing to cisplatin resistance in human ovarian cancer cells. <i>Molecular BioSystems</i> , 2017, 13, 2268-2276.	2.9	28
2873	Phosphoproteomics reveals that glycogen synthase kinase-3 phosphorylates multiple splicing factors and is associated with alternative splicing. <i>Journal of Biological Chemistry</i> , 2017, 292, 18240-18255.	1.6	52
2874	RNA-seq analysis of the kidneys of broiler chickens fed diets containing different concentrations of calcium. <i>Scientific Reports</i> , 2017, 7, 11740.	1.6	16
2875	Screening candidate microRNA-mRNA regulatory pairs for predicting the response to chemoradiotherapy in rectal cancer by a bioinformatics approach. <i>Scientific Reports</i> , 2017, 7, 11312.	1.6	4
2876	The non-canonical poly(A) polymerase FAM46C acts as an onco-suppressor in multiple myeloma. <i>Nature Communications</i> , 2017, 8, 619.	5.8	77
2877	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
2878	Transcriptional dysregulation of Interferome in experimental and human Multiple Sclerosis. <i>Scientific Reports</i> , 2017, 7, 8981.	1.6	22
2879	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
2880	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
2881	Conditional deletion of ELL2 induces murine prostate intraepithelial neoplasia. <i>Journal of Endocrinology</i> , 2017, 235, 123-136.	1.2	12
2882	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
2883	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
2884	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
2885	Systematic analysis of gene expression patterns associated with postmortem interval in human tissues. <i>Scientific Reports</i> , 2017, 7, 5435.	1.6	80
2886	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
2887	High-depth, high-accuracy microsatellite genotyping enables precision lung cancer risk classification. <i>Oncogene</i> , 2017, 36, 6383-6390.	2.6	13
2888	ALM1 is an actin-binding protein that suppresses cell migration and micrometastatic dissemination. <i>Nature Communications</i> , 2017, 8, 142.	5.8	36

#	ARTICLE	IF	CITATIONS
2889	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
2890	Virus and dsRNA-triggered transcriptional responses reveal key components of honey bee antiviral defense. <i>Scientific Reports</i> , 2017, 7, 6448.	1.6	97
2891	T2DiACoD: A Gene Atlas of Type 2 Diabetes Mellitus Associated Complex Disorders. <i>Scientific Reports</i> , 2017, 7, 6892.	1.6	38
2892	Protein microarray analysis identifies key cytokines associated with malignant middle cerebral artery infarction. <i>Brain and Behavior</i> , 2017, 7, e00746.	1.0	12
2893	Transcriptome predictors of coral survival and growth in a highly variable environment. <i>Ecology and Evolution</i> , 2017, 7, 4794-4803.	0.8	55
2894	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
2895	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
2896	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
2897	The interplay of matrix metalloproteinase-8, transforming growth factor- β 21 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
2898	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
2899	AP-2 β and AP-2 γ cooperatively orchestrate homeobox gene expression during branchial arch patterning. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	35
2900	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
2901	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
2902	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
2903	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
2904	Exploration of the mechanism of colorectal cancer metastasis using microarray analysis. <i>Oncology Letters</i> , 2017, 14, 6671-6677.	0.8	13
2905	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
2906	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

#	ARTICLE	IF	CITATIONS
2907	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
2908	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
2909	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
2910	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
2911	EWS-FLI1 perturbs MRTFB/YAP-1/TEAD target gene regulation inhibiting cytoskeletal autoregulatory feedback in Ewing sarcoma. <i>Oncogene</i> , 2017, 36, 5995-6005.	2.6	46
2912	Oviductal transcriptional profiling of a bovine fertility model by next-generation sequencing. <i>Genomics Data</i> , 2017, 13, 27-29.	1.3	8
2913	Changes of Protein Turnover in Aging <i>Caenorhabditis elegans</i> . <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1621-1633.	2.5	46
2914	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
2915	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
2916	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
2917	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
2918	NaviGO: interactive tool for visualization and functional similarity and coherence analysis with gene ontology. <i>BMC Bioinformatics</i> , 2017, 18, 177.	1.2	53
2919	Associating transcriptional modules with colon cancer survival through weighted gene co-expression network analysis. <i>BMC Genomics</i> , 2017, 18, 361.	1.2	58
2920	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
2921	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
2922	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
2923	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
2924	Cell Cycle M-Phase Genes Are Highly Upregulated in Anaplastic Thyroid Carcinoma. <i>Thyroid</i> , 2017, 27, 236-252.	2.4	54

#	ARTICLE	IF	CITATIONS
2925	The molecular basis of breast cancer pathological phenotypes. <i>Journal of Pathology</i> , 2017, 241, 375-391.	2.1	86
2926	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
2927	A Cell Type-Specific Expression Signature Predicts Haploinsufficient Autism-Susceptibility Genes. <i>Human Mutation</i> , 2017, 38, 204-215.	1.1	38
2928	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
2929	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
2930	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
2931	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
2932	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
2933	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
2934	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
2935	Rare deleterious mutations are associated with disease in bipolar disorder families. <i>Molecular Psychiatry</i> , 2017, 22, 1009-1014.	4.1	28
2936	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
2937	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
2938	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
2939	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
2940	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
2941	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
2942	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

#	ARTICLE	IF	CITATIONS
2943	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
2944	SIRT7-dependent deacetylation of CDK9 activates RNA polymerase II transcription. <i>Nucleic Acids Research</i> , 2017, 45, 2675-2686.	6.5	49
2945	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
2946	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
2947	Comparative transcriptomics of 5 high-altitude vertebrates and their low-altitude relatives. <i>GigaScience</i> , 2017, 6, 1-9.	3.3	50
2948	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
2949	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
2950	Bioinformatical analysis of gene expression signatures of different glioma subtypes. <i>Oncology Letters</i> , 2017, 15, 2807-2814.	0.8	7
2951	Immunoglobulin superfamily genes are novel prognostic biomarkers for breast cancer. <i>Oncotarget</i> , 2017, 8, 2444-2456.	0.8	7
2952	Transcriptomic pathway analysis of urokinase receptor silenced breast cancer cells: a microarray study. <i>Oncotarget</i> , 2017, 8, 101572-101590.	0.8	13
2953	Interaction of Epstein-Barr virus genes with human gastric carcinoma transcriptome. <i>Oncotarget</i> , 2017, 8, 38399-38412.	0.8	11
2954	Silencing of <i>HJURP</i> induces dysregulation of cell cycle and ROS metabolism in bladder cancer cells via PPARI ³ -SIRT1 feedback loop. <i>Journal of Cancer</i> , 2017, 8, 2282-2295.	1.2	35
2955	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
2956	Co-expression Network Approach Reveals Functional Similarities among Diseases Affecting Human Skeletal Muscle. <i>Frontiers in Physiology</i> , 2017, 8, 980.	1.3	19
2957	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
2958	Interspecies NASH disease activity whole-genome profiling identifies a fibrogenic role of PPARI [±] -regulated dermatopontin. <i>JCI Insight</i> , 2017, 2, .	2.3	96
2959	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
2960	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

#	ARTICLE	IF	CITATIONS
2961	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
2962	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
2963	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
2964	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
2965	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
2966	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
2967	The Emerging Role of Zfp217 in Adipogenesis. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1367.	1.8	17
2968	Genome-Wide Association Study of Piglet Uniformity and Farrowing Interval. <i>Frontiers in Genetics</i> , 2017, 8, 194.	1.1	37
2969	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
2970	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
2971	Quantitative Analysis of Cellular Proteome Alterations in CDV-Infected Mink Lung Epithelial Cells. <i>Frontiers in Microbiology</i> , 2017, 8, 2564.	1.5	1
2972	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
2973	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
2974	Antidepressant Mechanism Research of Acupuncture: Insights from a Genome-Wide Transcriptome Analysis of Frontal Cortex in Rats with Chronic Restraint Stress. <i>Evidence-based Complementary and Alternative Medicine</i> , 2017, 2017, 1-13.	0.5	24
2975	Circular RNA Profiling and Bioinformatic Modeling Identify Its Regulatory Role in Hepatic Steatosis. <i>BioMed Research International</i> , 2017, 2017, 1-13.	0.9	50
2976	Screening of Tumor Suppressor Genes in Metastatic Colorectal Cancer. <i>BioMed Research International</i> , 2017, 2017, 1-7.	0.9	11
2977	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. <i>Evidence-based Complementary and Alternative Medicine</i> , 2017, 2017, 1-10.	0.5	16
2978	Global transcriptome-wide analysis of the function of GDDR in acute gastric lesions. <i>Molecular Medicine Reports</i> , 2017, 16, 8673-8684.	1.1	3

#	ARTICLE	IF	CITATIONS
2979	Knockdown of <i>SIRT1</i> Suppresses Bladder Cancer Cell Proliferation and Migration and Induces Cell Cycle Arrest and Antioxidant Response through FOXO3a-Mediated Pathways. <i>BioMed Research International</i> , 2017, 2017, 1-14.	0.9	38
2980	Diagnostic MicroRNA Biomarker Discovery for Non-Small-Cell Lung Cancer Adenocarcinoma by Integrative Bioinformatics Analysis. <i>BioMed Research International</i> , 2017, 2017, 1-9.	0.9	28
2981	An Integrative Developmental Genomics and Systems Biology Approach to Identify an In Vivo Sox Trio-Mediated Gene Regulatory Network in Murine Embryos. <i>BioMed Research International</i> , 2017, 2017, 1-16.	0.9	11
2982	Biomarker MicroRNAs for Diagnosis of Oral Squamous Cell Carcinoma Identified Based on Gene Expression Data and MicroRNA-mRNA Network Analysis. <i>Computational and Mathematical Methods in Medicine</i> , 2017, 2017, 1-8.	0.7	16
2983	The Identification of Key Genes and Pathways in Glioma by Bioinformatics Analysis. <i>Journal of Immunology Research</i> , 2017, 2017, 1-9.	0.9	39
2984	A New Network-Based Strategy for Predicting the Potential miRNA-mRNA Interactions in Tumorigenesis. <i>International Journal of Genomics</i> , 2017, 2017, 1-11.	0.8	5
2985	Fish Oil Feeding Modulates the Expression of Hepatic MicroRNAs in a Western-Style Diet-Induced Nonalcoholic Fatty Liver Disease Rat Model. <i>BioMed Research International</i> , 2017, 2017, 1-11.	0.9	16
2986	Effects of genistein supplementation on genome-wide DNA methylation and gene expression in patients with localized prostate cancer. <i>International Journal of Oncology</i> , 2017, 51, 223-234.	1.4	61
2987	Identification of Key Transcription Factors Associated with Lung Squamous Cell Carcinoma. <i>Medical Science Monitor</i> , 2017, 23, 172-206.	0.5	25
2988	Identification of lncRNAs involved in biological regulation in early age-related macular degeneration. <i>International Journal of Nanomedicine</i> , 2017, Volume 12, 7589-7602.	3.3	30
2989	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. <i>Medical Science Monitor</i> , 2017, 23, 2453-2464.	0.5	40
2990	Glycosylation-related gene expression in HT29-MTX-E12 cells upon infection by <i>Helicobacter pylori</i> . <i>World Journal of Gastroenterology</i> , 2017, 23, 6817-6832.	1.4	16
2991	Positioning of Tacrolimus for the Treatment of Diabetic Nephropathy Based on Computational Network Analysis. <i>PLoS ONE</i> , 2017, 12, e0169518.	1.1	6
2992	Ancestry as a potential modifier of gene expression in breast tumors from Colombian women. <i>PLoS ONE</i> , 2017, 12, e0183179.	1.1	18
2993	MicroRNA-223 and microRNA-21 in peripheral blood B cells associated with progression of primary biliary cholangitis patients. <i>PLoS ONE</i> , 2017, 12, e0184292.	1.1	16
2994	Large-scale cross-species chemogenomic platform proposes a new drug discovery strategy of veterinary drug from herbal medicines. <i>PLoS ONE</i> , 2017, 12, e0184880.	1.1	7
2995	Transcriptome analysis of genes involved in defense against alkaline stress in roots of wild jujube (<i>Ziziphus acidojujuba</i>). <i>PLoS ONE</i> , 2017, 12, e0185732.	1.1	29
2996	Network analysis based on TCGA reveals hub genes in colon cancer. <i>Wspolczesna Onkologia</i> , 2017, 2, 136-144.	0.7	11

#	ARTICLE	IF	CITATIONS
2997	Novel linear motif filtering protocol reveals the role of the LC8 dynein light chain in the Hippo pathway. <i>PLoS Computational Biology</i> , 2017, 13, e1005885.	1.5	20
2998	Evidence of high-altitude adaptation in the glyptosternoid fish, <i>Creteuchiloglanis macropterus</i> from the Nujiang River obtained through transcriptome analysis. <i>BMC Evolutionary Biology</i> , 2017, 17, 229.	3.2	33
2999	First gene-ontology enrichment analysis based on bacterial coregenome variants: insights into adaptations of <i>Salmonella</i> serovars to mammalian- and avian-hosts. <i>BMC Microbiology</i> , 2017, 17, 222.	1.3	41
3000	Integrative microRNA and mRNA deep-sequencing expression profiling in endemic Burkitt lymphoma. <i>BMC Cancer</i> , 2017, 17, 761.	1.1	22
3001	In vitro characterization of CD133 ^{lo} cancer stem cells in Retinoblastoma Y79 cell line. <i>BMC Cancer</i> , 2017, 17, 779.	1.1	20
3002	Aberrantly methylated-differentially expressed genes and pathways in colorectal cancer. <i>Cancer Cell International</i> , 2017, 17, 75.	1.8	65
3003	MHC class II expression and potential antigen-presenting cells in the retina during experimental autoimmune uveitis. <i>Journal of Neuroinflammation</i> , 2017, 14, 136.	3.1	46
3004	A network pharmacology-based strategy deciphers the underlying molecular mechanisms of Qixuehe Capsule in the treatment of menstrual disorders. <i>Chinese Medicine</i> , 2017, 12, 23.	1.6	36
3005	OCDD: an obesity and co-morbid disease database. <i>BioData Mining</i> , 2017, 10, 33.	2.2	10
3006	Serum microRNA array analysis identifies miR-140-3p, miR-33b-3p and miR-671-3p as potential osteoarthritis biomarkers involved in metabolic processes. <i>Clinical Epigenetics</i> , 2017, 9, 127.	1.8	114
3007	Maternal chromium restriction induces insulin resistance in adult mice offspring through miRNA. <i>International Journal of Molecular Medicine</i> , 2018, 41, 1547-1559.	1.8	15
3008	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
3009	The genomic architecture of mastitis resistance in dairy sheep. <i>BMC Genomics</i> , 2017, 18, 624.	1.2	59
3010	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
3011	<i>Actinidia chinensis</i> Planch root extract inhibits cholesterol metabolism in hepatocellular carcinoma through upregulation of <i>PCSK9</i> . <i>Oncotarget</i> , 2017, 8, 42136-42148.	0.8	25
3012	Screening of FOXD3 targets in lung cancer via bioinformatics analysis. <i>Oncology Letters</i> , 2017, 15, 3214-3220.	0.8	0
3013	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
3014	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

#	ARTICLE	IF	CITATIONS
3015	A 16-gene signature predicting prognosis of patients with oral tongue squamous cell carcinoma. PeerJ, 2017, 5, e4062.	0.9	23
3016	The effects of DLEU1 gene expression in Burkitt lymphoma (BL): potential mechanism of chemoimmunotherapy resistance in BL. Oncotarget, 2017, 8, 27839-27853.	0.8	31
3017	Identification of Key Genes and Pathways in Tongue Squamous Cell Carcinoma Using Bioinformatics Analysis. Medical Science Monitor, 2017, 23, 5924-5932.	0.5	40
3018	Circulating miRNA Profiles Associated With Hyperglycemia in Patients With Type 1 Diabetes. Diabetes, 2018, 67, 1013-1023.	0.3	73
3019	STAT3 is required for proliferation and exhibits a cell type-specific binding preference in mouse female germline stem cells. Molecular Omics, 2018, 14, 95-102.	1.4	9
3020	Identification of Three Rheumatoid Arthritis Disease Subtypes by Machine Learning Integration of Synovial Histologic Features and <i>scRNA</i> Sequencing Data. Arthritis and Rheumatology, 2018, 70, 690-701.	2.9	157
3021	Thermopriming triggers splicing memory in Arabidopsis. Journal of Experimental Botany, 2018, 69, 2659-2675.	2.4	119
3022	Extracellular vesicle <i>scRNA</i> s reflect placenta dysfunction and are a biomarker source for preterm labour. Journal of Cellular and Molecular Medicine, 2018, 22, 2760-2773.	1.6	62
3023	Identification of key genes of papillary thyroid cancer using integrated bioinformatics analysis. Journal of Endocrinological Investigation, 2018, 41, 1237-1245.	1.8	31
3024	The Histone Variant MacroH2A Blocks Cellular Reprogramming by Inhibiting Mesenchymal-to-Epithelial Transition. Molecular and Cellular Biology, 2018, 38, .	1.1	13
3025	Comparative proteomic analyses of human adipose extracellular matrices decellularized using alternative procedures. Journal of Biomedical Materials Research - Part A, 2018, 106, 2481-2493.	2.1	37
3026	Evaluation of Animal Models by Comparison with Human Late-Onset Alzheimer's Disease. Molecular Neurobiology, 2018, 55, 9234-9250.	1.9	19
3027	Identification of Prognostic Biomarkers by Combined mRNA and miRNA Expression Microarray Analysis in Pancreatic Cancer. Translational Oncology, 2018, 11, 700-714.	1.7	40
3028	Dengue virus causes changes of MicroRNA-genes regulatory network revealing potential targets for antiviral drugs. BMC Systems Biology, 2018, 12, 2.	3.0	17
3029	Identification of genes and pathways associated with MDR in MCF-7/MDR breast cancer cells by RNA-seq analysis. Molecular Medicine Reports, 2018, 17, 6211-6226.	1.1	27
3030	Calorie restriction is the most reasonable anti-ageing intervention: a meta-analysis of survival curves. Scientific Reports, 2018, 8, 5779.	1.6	75
3031	Identification of Novel Response and Predictive Biomarkers to Hsp90 Inhibitors Through Proteomic Profiling of Patient-derived Prostate Tumor Explants. Molecular and Cellular Proteomics, 2018, 17, 1470-1486.	2.5	26
3032	Gastric cancer biomarkers; A systems biology approach. Biochemistry and Biophysics Reports, 2018, 13, 141-146.	0.7	20

#	ARTICLE	IF	CITATIONS
3033	Widespread modulation of gene expression by copy number variation in skeletal muscle. <i>Scientific Reports</i> , 2018, 8, 1399.	1.6	25
3034	RNA-seq transcriptomic analysis of adult zebrafish inner ear hair cells. <i>Scientific Data</i> , 2018, 5, 180005.	2.4	51
3035	Chemical proteomic profiling of protein N-homocysteinylation with a thioester probe. <i>Chemical Science</i> , 2018, 9, 2826-2830.	3.7	23
3036	Liraglutide protects cardiac function in diabetic rats through the PPAR α pathway. <i>Bioscience Reports</i> , 2018, 38, .	1.1	19
3037	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
3038	The Mechanisms of Bushen-Yizhi Formula as a Therapeutic Agent against Alzheimer's Disease. <i>Scientific Reports</i> , 2018, 8, 3104.	1.6	46
3039	Rbfox Splicing Factors Promote Neuronal Maturation and Axon Initial Segment Assembly. <i>Neuron</i> , 2018, 97, 853-868.e6.	3.8	90
3040	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
3041	Investigation into the underlying molecular mechanisms of hypertensive nephrosclerosis using bioinformatics analyses. <i>Molecular Medicine Reports</i> , 2018, 17, 4440-4448.	1.1	5
3042	N-glycome of the Lysosomal Glycocalyx is Altered in Niemann-Pick Type C Disease (NPC) Model Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 631-642.	2.5	26
3043	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
3044	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
3045	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
3046	Learning-dependent chromatin remodeling highlights noncoding regulatory regions linked to autism. <i>Science Signaling</i> , 2018, 11, .	1.6	25
3047	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
3048	BMI1 regulates androgen receptor in prostate cancer independently of the polycomb repressive complex 1. <i>Nature Communications</i> , 2018, 9, 500.	5.8	65
3049	Identifying Novel Signaling Pathways: An Exercise Scientists Guide to Phosphoproteomics. <i>Exercise and Sport Sciences Reviews</i> , 2018, 46, 76-85.	1.6	5
3050	The GPR120 agonist TUG-891 promotes metabolic health by stimulating mitochondrial respiration in brown fat. <i>EMBO Molecular Medicine</i> , 2018, 10, .	3.3	91

#	ARTICLE	IF	CITATIONS
3051	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
3052	Population-based doseâ€‘response analysis of liver transcriptional response to trichloroethylene in mouse. <i>Mammalian Genome</i> , 2018, 29, 168-181.	1.0	13
3053	Identification of differential proteinâ€‘coding gene expressions in early phase lung adenocarcinoma. <i>Thoracic Cancer</i> , 2018, 9, 234-240.	0.8	4
3054	Integrated sequencing of exome and mRNA of large-sized single cells. <i>Scientific Reports</i> , 2018, 8, 384.	1.6	12
3055	Boolean network modeling in systems pharmacology. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , 2018, 45, 159-180.	0.8	60
3056	Transcriptome signature identifies distinct cervical pathways induced in lipopolysaccharide-mediated preterm birthâ€‘â€‘. <i>Biology of Reproduction</i> , 2018, 98, 408-421.	1.2	30
3057	Metabolic systems analysis of LPS induced endothelial dysfunction applied to sepsis patient stratification. <i>Scientific Reports</i> , 2018, 8, 6811.	1.6	29
3058	Histone H4 acetylation regulates behavioral inter-individual variability in zebrafish. <i>Genome Biology</i> , 2018, 19, 55.	3.8	25
3059	Independent prognostic genes and mechanism investigation for colon cancer. <i>Biological Research</i> , 2018, 51, 10.	1.5	25
3060	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
3061	Involvement of dysregulated coding and long nonâ€‘coding RNAs in the pathogenesis of strabismus. <i>Molecular Medicine Reports</i> , 2018, 17, 7737-7745.	1.1	3
3062	Galactic Cosmic Radiation Induces Persistent Epigenome Alterations Relevant to Human Lung Cancer. <i>Scientific Reports</i> , 2018, 8, 6709.	1.6	26
3063	Sauchinone controls hepatic cholesterol homeostasis by the negative regulation of PCSK9 transcriptional network. <i>Scientific Reports</i> , 2018, 8, 6737.	1.6	26
3064	Prognostic significance of microsatellite instabilityâ€‘associated pathways and genes in gastric cancer. <i>International Journal of Molecular Medicine</i> , 2018, 42, 149-160.	1.8	13
3065	Bayesian nonparametric discovery of isoforms and individual specific quantification. <i>Nature Communications</i> , 2018, 9, 1681.	5.8	8
3066	Credentialing Individual Samples for Proteogenomic Analysis. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1515-1530.	2.5	5
3067	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
3068	Leukemia cell-derived microvesicles induce T cell exhaustion via miRNA delivery. <i>OncotImmunology</i> , 2018, 7, e1448330.	2.1	24

#	ARTICLE	IF	CITATIONS
3069	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
3070	Circulating lncRNAs Analysis in Patients with Type 2 Diabetes Reveals Novel Genes Influencing Glucose Metabolism and Islet β -Cell Function. <i>Cellular Physiology and Biochemistry</i> , 2018, 46, 335-350.	1.1	80
3071	Prognostic value of alcohol dehydrogenase mRNA expression in gastric cancer. <i>Oncology Letters</i> , 2018, 15, 5505-5516.	0.8	11
3072	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
3073	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
3074	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
3075	Genome-wide characterization of lncRNAs in acute myeloid leukemia. <i>Briefings in Bioinformatics</i> , 2018, 19, 627-635.	3.2	34
3076	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
3077	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
3078	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
3079	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
3080	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
3081	SCPortalen: human and mouse single-cell centric database. <i>Nucleic Acids Research</i> , 2018, 46, D781-D787.	6.5	48
3082	<i>Lactobacillus gasseri</i> attenuates allergic airway inflammation through PPAR γ activation in dendritic cells. <i>Journal of Molecular Medicine</i> , 2018, 96, 39-51.	1.7	22
3083	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
3084	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
3085	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
3086	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

#	ARTICLE	IF	CITATIONS
3087	Orthogonality and Burdens of Heterologous AND Gate Gene Circuits in <i>E. coli</i> . ACS Synthetic Biology, 2018, 7, 553-564.	1.9	49
3088	Shotgun label-free proteomic analysis for identification of proteins in HaCaT human skin keratinocytes regulated by the administration of collagen from soft-shelled turtle. Journal of Biomedical Materials Research - Part B Applied Biomaterials, 2018, 106, 2403-2413.	1.6	2
3089	Computational systems biology approaches for Parkinson's disease. Cell and Tissue Research, 2018, 373, 91-109.	1.5	19
3090	RNA-Sequencing of <i>Drosophila melanogaster</i> Head Tissue on High-Sugar and High-Fat Diets. G3: Genes, Genomes, Genetics, 2018, 8, 279-290.	0.8	21
3091	The sbv IMPROVER Systems Toxicology computational challenge: Identification of human and species-independent blood response markers as predictors of smoking exposure and cessation status. Computational Toxicology, 2018, 5, 38-51.	1.8	13
3092	Analysis of biological functional networks during sciatic nerve repair and regeneration. Molecular and Cellular Biochemistry, 2018, 439, 141-150.	1.4	2
3093	SMART Cancer Navigator: A Framework for Implementing ASCO Workshop Recommendations to Enable Precision Cancer Medicine. JCO Precision Oncology, 2018, 2018, 1-14.	1.5	19
3094	Thyroid follicular adenomas and carcinomas: molecular profiling provides evidence for a continuous evolution. Oncotarget, 2018, 9, 10343-10359.	0.8	29
3095	A Proteomic Approach for Understanding the Mechanisms of Delayed Corneal Wound Healing in Diabetic Keratopathy Using Diabetic Model Rat. International Journal of Molecular Sciences, 2018, 19, 3635.	1.8	19
3096	Abnormal DNA Methylation in Thoracic Spinal Cord Tissue Following Transection Injury. Medical Science Monitor, 2018, 24, 8878-8890.	0.5	10
3097	Coexpression modules constructed by weighted gene co-expression network analysis indicate ubiquitin-mediated proteolysis as a potential biomarker of uveal melanoma. Experimental and Therapeutic Medicine, 2019, 17, 237-243.	0.8	4
3098	The cellular economy of the <i>Saccharomyces cerevisiae</i> zinc proteome. Metallomics, 2018, 10, 1755-1776.	1.0	66
3099	A vascular endothelial growth factor receptor gene variant is associated with susceptibility to acute respiratory distress syndrome. Intensive Care Medicine Experimental, 2018, 6, 16.	0.9	9
3100	Integrated whole genome microarray analysis and immunohistochemical assay identifies COL11A1, GJB2 and CTRL as predictive biomarkers for pancreatic cancer. Cancer Cell International, 2018, 18, 174.	1.8	28
3101	Transcriptomic changes with increasing algal symbiont reveal the detailed process underlying establishment of coral-algal symbiosis. Scientific Reports, 2018, 8, 16802.	1.6	46
3102	Identification of hub genes with diagnostic values in pancreatic cancer by bioinformatics analyses and supervised learning methods. World Journal of Surgical Oncology, 2018, 16, 223.	0.8	24
3103	Ensemble learning for detecting gene-gene interactions in colorectal cancer. PeerJ, 2018, 6, e5854.	0.9	21
3104	Diagnostic and prognostic values of the mRNA expression of excision repair cross-complementation enzymes in hepatitis B virus-related hepatocellular carcinoma. Cancer Management and Research, 2018, Volume 10, 5313-5328.	0.9	3

#	ARTICLE	IF	CITATIONS
3105	Deep proteome of human nNOS/NOS1-positive versus MOCK SH-SY5Y neuroblastoma cells under full nutrition, serum free starvation and rapamycin treatment. Data in Brief, 2018, 21, 1309-1314.	0.5	1
3106	Prognostic Value of Excision Repair Cross-Complementing mRNA Expression in Gastric Cancer. BioMed Research International, 2018, 2018, 1-16.	0.9	6
3107	Short-lived AUF1 p42-binding mRNAs of RANKL and BCL6 have two distinct instability elements each. PLoS ONE, 2018, 13, e0206823.	1.1	0
3108	Extraction and biomolecular analysis of dermal interstitial fluid collected with hollow microneedles. Communications Biology, 2018, 1, 173.	2.0	148
3109	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
3110	Proteomics of Bronchoalveolar Lavage Fluid Reveals a Lung Oxidative Stress Response in Murine Herpesvirus-68 Infection. Viruses, 2018, 10, 670.	1.5	3
3111	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
3112	Integrating proteomic and phosphoproteomic data for pathway analysis in breast cancer. BMC Systems Biology, 2018, 12, 130.	3.0	7
3113	Data set of differentially expressed microRNAs in sanguinarine-treated <i>Caenorhabditis elegans</i> and its F3 progeny. Data in Brief, 2018, 21, 899-906.	0.5	0
3114	Deciphering the evolutionary signatures of pinnipeds using novel genome sequences: The first genomes of <i>Phoca largha</i> , <i>Callorhinus ursinus</i> , and <i>Eumetopias jubatus</i> . Scientific Reports, 2018, 8, 16877.	1.6	7
3115	Analysis of dynamic molecular networks for pancreatic ductal adenocarcinoma progression. Cancer Cell International, 2018, 18, 214.	1.8	37
3116	Cardiac function evaluation for a novel one-step detoxification product of <i>Aconiti Lateralis Radix Praeparata</i> . Chinese Medicine, 2018, 13, 62.	1.6	12
3117	Proteomic Analysis of Zn Depletion/Repletion in the Hormone-Secreting Thyroid Follicular Cell Line FRTL-5. Nutrients, 2018, 10, 1981.	1.7	3
3118	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
3119	Identifying mouse developmental essential genes using machine learning. DMM Disease Models and Mechanisms, 2018, 11, .	1.2	18
3120	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
3121	Integrated analysis reveals key genes with prognostic value in lung adenocarcinoma. Cancer Management and Research, 2018, Volume 10, 6097-6108.	0.9	36
3122	Dissecting the Genomic Architecture of Resistance to <i>Eimeria maxima</i> Parasitism in the Chicken. Frontiers in Genetics, 2018, 9, 528.	1.1	31

#	ARTICLE	IF	CITATIONS
3123	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
3124	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
3125	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
3126	The Genomic Architecture of Fowl Typhoid Resistance in Commercial Layers. <i>Frontiers in Genetics</i> , 2018, 9, 519.	1.1	17
3127	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
3128	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
3129	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
3130	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
3131	Silencing of TGF β 2 signalling in microglia results in impaired homeostasis. <i>Nature Communications</i> , 2018, 9, 4011.	5.8	125
3132	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
3133	Regulatory sRNAs in Cyanobacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 2399.	1.5	10
3134	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
3135	De novo Mutations (DNMs) in Autism Spectrum Disorder (ASD): Pathway and Network Analysis. <i>Frontiers in Genetics</i> , 2018, 9, 406.	1.1	40
3136	Gene expression differences between thyroid carcinoma, thyroid adenoma and normal thyroid tissue. <i>Oncology Reports</i> , 2018, 40, 3359-3369.	1.2	24
3137	Aberrant splicing in B-cell acute lymphoblastic leukemia. <i>Nucleic Acids Research</i> , 2018, 46, 11357-11369.	6.5	39
3138	Effects of propofol and etomidate anesthesia on cardiovascular miRNA expression: the different profiles?. <i>BMC Anesthesiology</i> , 2018, 18, 149.	0.7	5
3139	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
3140	Impact of <i>Escherichia coli</i> K12 and O18:K1 on human platelets: Differential effects on platelet activation, RNAs and proteins. <i>Scientific Reports</i> , 2018, 8, 16145.	1.6	9

#	ARTICLE	IF	CITATIONS
3141	Identification of protein complexes associated with myocardial infarction using a bioinformatics approach. <i>Molecular Medicine Reports</i> , 2018, 18, 3569-3576.	1.1	1
3142	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
3143	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
3144	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
3145	Maternal Melatonin Therapy Attenuates Methyl-Donor Diet-Induced Programmed Hypertension in Male Adult Rat Offspring. <i>Nutrients</i> , 2018, 10, 1407.	1.7	31
3146	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
3147	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
3148	Identification of COL1A1 as an invasion-related gene in malignant astrocytoma. <i>International Journal of Oncology</i> , 2018, 53, 2542-2554.	1.4	31
3149	Anticancer activity of biogenerated silver nanoparticles: an integrated proteomic investigation. <i>Oncotarget</i> , 2018, 9, 9685-9705.	0.8	147
3150	Targeting histone methyltransferase G9a inhibits growth and Wnt signaling pathway by epigenetically regulating HP1 α and APC2 gene expression in non-small cell lung cancer. <i>Molecular Cancer</i> , 2018, 17, 153.	7.9	59
3151	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
3152	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
3153	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
3154	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
3155	Urinary proteomics reveals association between pediatric nephrolithiasis and cardiovascular disease. <i>International Urology and Nephrology</i> , 2018, 50, 1949-1954.	0.6	12
3156	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
3157	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
3158	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

#	ARTICLE	IF	CITATIONS
3159	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
3160	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
3161	Unravelling subclonal heterogeneity and aggressive disease states in TNBC through single-cell RNA-seq. <i>Nature Communications</i> , 2018, 9, 3588.	5.8	342
3162	TAM 2.0: tool for MicroRNA set analysis. <i>Nucleic Acids Research</i> , 2018, 46, W180-W185.	6.5	141
3163	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
3164	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
3165	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
3166	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
3167	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
3168	Integrated Analysis of MiRNA and Genes Associated with Meat Quality Reveals that Gga-MiR-140-5p Affects Intramuscular Fat Deposition in Chickens. <i>Cellular Physiology and Biochemistry</i> , 2018, 46, 2421-2433.	1.1	46
3169	KDM5B decommissions the H3K4 methylation landscape of self-renewal genes during trophoblast stem cell differentiation. <i>Biology Open</i> , 2018, 7, .	0.6	20
3170	Combined bioinformatics analysis reveals gene expression and DNA methylation patterns in osteoarthritis. <i>Molecular Medicine Reports</i> , 2018, 17, 8069-8078.	1.1	10
3171	Reconstruction of the diapsid ancestral genome permits chromosome evolution tracing in avian and non-avian dinosaurs. <i>Nature Communications</i> , 2018, 9, 1883.	5.8	60
3172	A map of the PGC-1 β - and NT-PGC-1 β -regulated transcriptional network in brown adipose tissue. <i>Scientific Reports</i> , 2018, 8, 7876.	1.6	29
3173	Genome-wide DNA methylation profiling in a rat model with vascular dementia. <i>Molecular Medicine Reports</i> , 2018, 18, 123-130.	1.1	3
3174	Identification of potential pathogenic biomarkers in clear cell renal cell carcinoma. <i>Oncology Letters</i> , 2018, 15, 8491-8499.	0.8	8
3175	Identification of key genes in rheumatoid arthritis and osteoarthritis based on bioinformatics analysis. <i>Medicine (United States)</i> , 2018, 97, e10997.	0.4	27
3176	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

#	ARTICLE	IF	CITATIONS
3177	The novel 19q13 KRAB zinc-finger tumour suppressor ZNF382 is frequently methylated in oesophageal squamous cell carcinoma and antagonises Wnt/ β -catenin signalling. <i>Cell Death and Disease</i> , 2018, 9, 573.	2.7	26
3178	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
3179	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
3180	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
3181	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
3182	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
3183	The Potential Protective Effect of Curcumin on Amyloid- β 42 Induced Cytotoxicity in HT-22 Cells. <i>BioMed Research International</i> , 2018, 2018, 1-8.	0.9	18
3184	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
3185	Systemic bioinformatics analysis of skeletal muscle gene expression profiles of sepsis. <i>Experimental and Therapeutic Medicine</i> , 2018, 15, 4637-4642.	0.8	1
3186	Placental H3K27me3 establishes female resilience to prenatal insults. <i>Nature Communications</i> , 2018, 9, 2555.	5.8	110
3187	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
3188	Comparative transcriptomics reveals specific responding genes associated with atherosclerosis in rabbit and mouse models. <i>PLoS ONE</i> , 2018, 13, e0201618.	1.1	3
3189	Screening therapeutic targets of ribavirin in hepatocellular carcinoma. <i>Oncology Letters</i> , 2018, 15, 9625-9632.	0.8	9
3190	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
3191	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
3192	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
3193	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
3194	Exploring the Mechanism of Dangguihuang Decoction Against Hepatic Fibrosis by Network Pharmacology and Experimental Validation. <i>Frontiers in Pharmacology</i> , 2018, 9, 187.	1.6	33

#	ARTICLE	IF	CITATIONS
3195	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
3196	Genome-Wide Identification and Characterization of Long Non-Coding RNA in Wheat Roots in Response to Ca ²⁺ Channel Blocker. <i>Frontiers in Plant Science</i> , 2018, 9, 244.	1.7	36
3197	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
3198	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
3199	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
3200	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
3201	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
3202	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
3203	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
3204	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
3205	Alternative splicing events implicated in carcinogenesis and prognosis of colorectal cancer. <i>Journal of Cancer</i> , 2018, 9, 1754-1764.	1.2	64
3206	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
3207	Atherosclerosis is exacerbated by chitinase-3-like-1 in amyloid precursor protein transgenic mice. <i>Theranostics</i> , 2018, 8, 749-766.	4.6	30
3208	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
3209	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
3210	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
3211	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
3212	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

#	ARTICLE	IF	CITATIONS
3213	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
3214	Integrative Analysis of Hippocampus Gene Expression Profiles Identifies Network Alterations in Aging and Alzheimer's Disease. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 153.	1.7	58
3215	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
3216	Key Genes and Pathways Associated With Inner Ear Malformation in SOX10 p.R109W Mutation Pigs. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 181.	1.4	20
3217	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
3218	UXT is required for spermatogenesis in mice. <i>PLoS ONE</i> , 2018, 13, e0195747.	1.1	5
3219	In silico approach in reveal traditional medicine plants pharmacological material basis. <i>Chinese Medicine</i> , 2018, 13, 33.	1.6	75
3220	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
3221	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
3222	Hyaluronic Acid Influence on Normal and Osteoarthritic Tissue-Engineered Cartilage. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1519.	1.8	11
3223	Identification of hub genes and potential molecular mechanisms in gastric cancer by integrated bioinformatics analysis. <i>PeerJ</i> , 2018, 6, e5180.	0.9	74
3224	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
3225	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
3226	Hub genes and key pathways of non-small lung cancer identified using bioinformatics. <i>Oncology Letters</i> , 2018, 16, 2344-2354.	0.8	22
3227	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
3228	Plasma proteomic signature of age in healthy humans. <i>Aging Cell</i> , 2018, 17, e12799.	3.0	325
3229	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
3230	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

#	ARTICLE	IF	CITATIONS
3231	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
3232	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
3233	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
3234	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
3235	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
3236	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
3237	JAK/STAT3 regulated global gene expression dynamics during late-stage reprogramming process. <i>BMC Genomics</i> , 2018, 19, 183.	1.2	22
3238	Interpretation of biological experiments changes with evolution of the Gene Ontology and its annotations. <i>Scientific Reports</i> , 2018, 8, 5115.	1.6	110
3239	Identification of potential crucial genes and construction of microRNA-mRNA negative regulatory networks in osteosarcoma. <i>Hereditas</i> , 2018, 155, 21.	0.5	32
3240	Diverse reprogramming codes for neuronal identity. <i>Nature</i> , 2018, 557, 375-380.	13.7	94
3241	Identification of target genes in cardiomyopathy with fibrosis and cardiac remodeling. <i>Journal of Biomedical Science</i> , 2018, 25, 63.	2.6	54
3242	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
3243	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
3244	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
3245	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
3246	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
3247	Bioinformatics approach reveals the key role of C motif chemokine receptor 2 in endometriosis development. <i>Molecular Medicine Reports</i> , 2018, 18, 2841-2849.	1.1	6
3248	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

#	ARTICLE	IF	CITATIONS
3249	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
3250	Integrative epigenomic analysis in differentiated human primary bronchial epithelial cells exposed to cigarette smoke. <i>Scientific Reports</i> , 2018, 8, 12750.	1.6	11
3251	Mutant KLF1 in Adult Anemic Nan Mice Leads to Profound Transcriptome Changes and Disordered Erythropoiesis. <i>Scientific Reports</i> , 2018, 8, 12793.	1.6	14
3252	Analysis of the miRNA and mRNA involved in osteogenesis of adipose-derived mesenchymal stem cells. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 1111-1120.	0.8	22
3253	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
3254	Co-expression Network Analysis of Biomarkers for Adrenocortical Carcinoma. <i>Frontiers in Genetics</i> , 2018, 9, 328.	1.1	52
3255	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
3256	Identification of Potential Prognostic Long Non-Coding RNA Biomarkers for Predicting Survival in Patients with Hepatocellular Carcinoma. <i>Cellular Physiology and Biochemistry</i> , 2018, 48, 1854-1869.	1.1	37
3257	Splicing Factor RBM20 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
3258	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
3259	A novel gene-diet pair modulates <i>C. elegans</i> aging. <i>PLoS Genetics</i> , 2018, 14, e1007608.	1.5	21
3260	RAP2 mediates mechanoresponses of the Hippo pathway. <i>Nature</i> , 2018, 560, 655-660.	13.7	266
3261	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
3262	A gene interaction network-based method to measure the common and heterogeneous mechanisms of gynecological cancer. <i>Molecular Medicine Reports</i> , 2018, 18, 230-242.	1.1	13
3263	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
3264	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
3265	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
3266	Comprehensive analysis of the whole coding and non-coding RNA transcriptome expression profiles and construction of the circRNA-lncRNA co-regulated ceRNA network in laryngeal squamous cell carcinoma. <i>Functional and Integrative Genomics</i> , 2019, 19, 109-121.	1.4	46

#	ARTICLE	IF	CITATIONS
3267	Integral analyses of survival-related long non-coding RNA MIR210HG and its prognostic role in colon cancer. <i>Oncology Letters</i> , 2019, 18, 1107-1116.	0.8	18
3268	Uncovering missed indels by leveraging unmapped reads. <i>Scientific Reports</i> , 2019, 9, 11093.	1.6	8
3269	Comparative Analysis of the Liver and Spleen Transcriptomes between Holstein and Yunnan Humped Cattle. <i>Animals</i> , 2019, 9, 527.	1.0	3
3270	Transcriptome profiling of the liver among the prenatal and postnatal stages in chickens. <i>Poultry Science</i> , 2019, 98, 7030-7040.	1.5	24
3271	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
3272	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
3273	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
3274	The genomic landscape of estrogen receptor β binding sites in mouse mammary gland. <i>PLoS ONE</i> , 2019, 14, e0220311.	1.1	25
3275	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
3276	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
3277	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
3278	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
3279	Characterization of cellular transcriptomic signatures induced by different respiratory viruses in human reconstituted airway epithelia. <i>Scientific Reports</i> , 2019, 9, 11493.	1.6	33
3280	Neurotoxic potential of reactive astrocytes in canine distemper demyelinating leukoencephalitis. <i>Scientific Reports</i> , 2019, 9, 11689.	1.6	13
3281	Identification of Key Genes and Pathways in Pancreatic Cancer Gene Expression Profile by Integrative Analysis. <i>Genes</i> , 2019, 10, 612.	1.0	22
3282	Computational Assessment of Bacterial Protein Structures Indicates a Selection Against Aggregation. <i>Cells</i> , 2019, 8, 856.	1.8	9
3283	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
3284	Differential gene expression analysis reveals novel genes and pathways in pediatric septic shock patients. <i>Scientific Reports</i> , 2019, 9, 11270.	1.6	24

#	ARTICLE	IF	CITATIONS
3285	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
3286	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
3287	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
3288	Detection of a novel panel of somatic mutations in plasma cell-free DNA and its diagnostic value in hepatocellular carcinoma. <i>Cancer Management and Research</i> , 2019, Volume 11, 5745-5756.	0.9	20
3289	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
3290	FunDMDep-m6A: identification and prioritization of functional differential m6A methylation genes. <i>Bioinformatics</i> , 2019, 35, i90-i98.	1.8	34
3291	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
3292	Stress, novel sex genes, and epigenetic reprogramming orchestrate socially controlled sex change. <i>Science Advances</i> , 2019, 5, eaaw7006.	4.7	99
3293	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
3294	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
3295	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
3296	Pleiotropic effects of rfa-gene mutations on <i>Escherichia coli</i> envelope properties. <i>Scientific Reports</i> , 2019, 9, 9696.	1.6	54
3297	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
3298	Three Biomarkers Predict Gastric Cancer Patients' Susceptibility To Fluorouracil-based Chemotherapy. <i>Journal of Cancer</i> , 2019, 10, 2953-2960.	1.2	9
3299	Wx: a neural network-based feature selection algorithm for transcriptomic data. <i>Scientific Reports</i> , 2019, 9, 10500.	1.6	12
3300	Insights about multi-targeting and synergistic neuromodulators in Ayurvedic herbs against epilepsy: integrated computational studies on drug-target and protein-protein interaction networks. <i>Scientific Reports</i> , 2019, 9, 10565.	1.6	31
3301	Systems biology and network pharmacology of frailty reveal novel epigenetic targets and mechanisms. <i>Scientific Reports</i> , 2019, 9, 10593.	1.6	6
3302	Transcriptome Analysis of Landrace Pig Subcutaneous Preadipocytes during Adipogenic Differentiation. <i>Genes</i> , 2019, 10, 552.	1.0	14

#	ARTICLE	IF	CITATIONS
3303	<p><p>Gene expression profiling reveals candidate biomarkers and probable molecular mechanism in diabetic peripheral neuropathy</p>. Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy, 2019, Volume 12, 1213-1223.	1.1	13
3304	Single-Cell RNA-Sequencing and Metabolomics Analyses Reveal the Contribution of Perivascular Adipose Tissue Stem Cells to Vascular Remodeling. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 2049-2066.	1.1	72
3305	Patterns of Geographical and Potential Adaptive Divergence in the Genome of the Common Carp (Cyprinus carpio). Frontiers in Genetics, 2019, 10, 660.	1.1	12
3306	<p><p>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</p>. OncoTargets and Therapy, 2019, Volume 12, 5861-5885.	1.0	4
3307	Bioinformatics analysis of mRNA and miRNA microarray to identify the key miRNAâgene pairs in smallâcell lung cancer. Molecular Medicine Reports, 2019, 20, 2199-2208.	1.1	20
3308	SETD1A protects from senescence through regulation of the mitotic gene expression program. Nature Communications, 2019, 10, 2854.	5.8	37
3309	FXR overexpression alters adipose tissue architecture in mice and limits its storage capacity leading to metabolic derangements. Journal of Lipid Research, 2019, 60, 1547-1561.	2.0	19
3310	Maternal and Post-weaning High-Fat Diets Produce Distinct DNA Methylation Patterns in Hepatic Metabolic Pathways within Specific Genomic Contexts. International Journal of Molecular Sciences, 2019, 20, 3229.	1.8	10
3311	Identifying miRNA-mRNA Pairs and Novel miRNAs from Hepatocellular Carcinoma miRNomes and TCGA Database. Journal of Cancer, 2019, 10, 2552-2559.	1.2	14
3312	PPARâ gene is a diagnostic and prognostic biomarker in clear cell renal cell carcinoma by integrated bioinformatics analysis. Journal of Cancer, 2019, 10, 2319-2331.	1.2	8
3313	Uncovering changes in proteomic signature of rat pelvic floor muscles in pregnancy. American Journal of Obstetrics and Gynecology, 2019, 221, 130.e1-130.e9.	0.7	6
3314	Lipid-Associated Macrophages Control Metabolic Homeostasis in a Trem2-Dependent Manner. Cell, 2019, 178, 686-698.e14.	13.5	718
3315	Mitochondrial 3243AââG mutation confers pro-atherogenic and pro-inflammatory properties in MELAS iPS derived endothelial cells. Cell Death and Disease, 2019, 10, 802.	2.7	23
3316	The Autoimmune Protocol Diet Modifies Intestinal RNA Expression in Inflammatory Bowel Disease. Crohn's & Colitis 360, 2019, 1, otz016.	0.5	3
3317	Disruptive mutations in TANC2 define a neurodevelopmental syndrome associated with psychiatric disorders. Nature Communications, 2019, 10, 4679.	5.8	43
3318	Low Dose Carbon Monoxide Exposure in Idiopathic Pulmonary Fibrosis Produces a CO Signature Comprised of Oxidative Phosphorylation Genes. Scientific Reports, 2019, 9, 14802.	1.6	12
3319	Proteomic and transcriptional profiling of rat amygdala following social play. Behavioural Brain Research, 2019, 376, 112210.	1.2	11
3320	Co-expression network modeling identifies key long non-coding RNA and mRNA modules in altering molecular phenotype to develop stress-induced depression in rats. Translational Psychiatry, 2019, 9, 125.	2.4	30

#	ARTICLE	IF	CITATIONS
3321	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
3322	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
3323	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
3324	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
3325	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
3326	Characterization and Identification of Lysine Succinylation Sites based on Deep Learning Method. <i>Scientific Reports</i> , 2019, 9, 16175.	1.6	30
3327	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
3328	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
3329	Distinct Roles for BET Family Members in Estrogen Receptor β Enhancer Function and Gene Regulation in Breast Cancer Cells. <i>Molecular Cancer Research</i> , 2019, 17, 2356-2368.	1.5	17
3330	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
3331	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
3332	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
3333	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
3334	Brain gene expression in a novel mouse model of postpartum mood disorder. <i>Translational Neuroscience</i> , 2019, 10, 168-174.	0.7	5
3335	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
3336	Maternal Low-Fat Diet Programs the Hepatic Epigenome despite Exposure to an Obesogenic Postnatal Diet. <i>Nutrients</i> , 2019, 11, 2075.	1.7	8
3337	ABCD: Alzheimer's disease Biomarkers Comprehensive Database. <i>3 Biotech</i> , 2019, 9, 351.	1.1	2
3338	Prim-O-glucosylcymifugin enhances the antitumour effect of PD-1 inhibition by targeting myeloid-derived suppressor cells. , 2019, 7, 231.		32

#	ARTICLE	IF	CITATIONS
3339	<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
3340	Identification of serum exosomal microRNAs in acute spinal cord injured rats. <i>Experimental Biology and Medicine</i> , 2019, 244, 1149-1161.	1.1	30
3341	Identification of modules and functional analysis in CRC subtypes by integrated bioinformatics analysis. <i>PLoS ONE</i> , 2019, 14, e0221772.	1.1	6
3342	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
3343	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
3344	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
3345	Human Trophoblast Differentiation Is Associated With Profound Gene Regulatory and Epigenetic Changes. <i>Endocrinology</i> , 2019, 160, 2189-2203.	1.4	35
3346	Comparative adipose transcriptome analysis digs out genes related to fat deposition in two pig breeds. <i>Scientific Reports</i> , 2019, 9, 12925.	1.6	41
3347	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
3348	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
3349	Identification and characterization of SEC24D as a susceptibility gene for hepatitis B virus infection. <i>Scientific Reports</i> , 2019, 9, 13425.	1.6	2
3350	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
3351	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
3352	Transcriptomic analysis reveals new hippocampal gene networks induced by prolactin. <i>Scientific Reports</i> , 2019, 9, 13765.	1.6	20
3353	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
3354	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
3355	Systematic Profiling of Alternative mRNA Splicing Signature for Predicting Glioblastoma Prognosis. <i>Frontiers in Oncology</i> , 2019, 9, 928.	1.3	25
3356	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

#	ARTICLE	IF	CITATIONS
3357	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
3358	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
3359	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
3360	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
3361	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
3362	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
3363	GOTrapper: a tool to navigate through branches of gene ontology hierarchy. <i>BMC Bioinformatics</i> , 2019, 20, 20.	1.2	11
3364	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
3365	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
3366	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
3367	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
3368	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
3369	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
3370	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
3371	Discovery and characterization of functional modules associated with body weight in broilers. <i>Scientific Reports</i> , 2019, 9, 9125.	1.6	18
3372	Differentially expressed genes between systemic sclerosis and rheumatoid arthritis. <i>Hereditas</i> , 2019, 156, 17.	0.5	5
3373	Overexpression of NCAPH is upregulated and predicts a poor prognosis in prostate cancer. <i>Oncology Letters</i> , 2019, 17, 5768-5776.	0.8	23
3374	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

#	ARTICLE	IF	CITATIONS
3375	NAD tagSeq reveals that NAD ⁺ -capped RNAs are mostly produced from a large number of protein-coding genes in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12072-12077.	3.3	61
3376	Runx2 stimulates neoangiogenesis through the Runt domain in melanoma. Scientific Reports, 2019, 9, 8052.	1.6	19
3377	m6A Regulates Neurogenesis and Neuronal Development by Modulating Histone Methyltransferase Ezh2. Genomics, Proteomics and Bioinformatics, 2019, 17, 154-168.	3.0	135
3378	Investigation of the clinical significance and prospective molecular mechanisms of cystatin genes in patients with hepatitis B virus-related hepatocellular carcinoma. Oncology Reports, 2019, 42, 189-201.	1.2	8
3379	Transcriptomic changes in the prefrontal cortex of rats as a function of age and cognitive engagement. Neurobiology of Learning and Memory, 2019, 163, 107035.	1.0	6
3380	Macrophage centripetal migration drives spontaneous healing process after spinal cord injury. Science Advances, 2019, 5, eaav5086.	4.7	60
3381	Identification of the iduronate-2-sulfatase proteome in wild-type mouse brain. Heliyon, 2019, 5, e01667.	1.4	8
3382	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
3383	The R2TP complex regulates paramyxovirus RNA synthesis. PLoS Pathogens, 2019, 15, e1007749.	2.1	12
3384	Expression Profile Analysis Identifies a Novel Five-Gene Signature to Improve Prognosis Prediction of Glioblastoma. Frontiers in Genetics, 2019, 10, 419.	1.1	52
3385	Sensory experience remodels genome architecture in neural circuit to drive motor learning. Nature, 2019, 569, 708-713.	13.7	66
3386	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
3387	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
3388	Tobacco-Related Alterations in Airway Gene Expression are Rapidly Reversed Within Weeks Following Smoking-Cessation. Scientific Reports, 2019, 9, 6978.	1.6	16
3389	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
3390	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
3391	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
3392	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

#	ARTICLE	IF	CITATIONS
3393	<p>Identification of novel biomarkers and candidate small molecule drugs in non-small-cell lung cancer by integrated microarray analysis</p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 3545-3563.	1.0	32
3394	Quantitative Proteomics Identifies DNA Repair as a Novel Biological Function for Hepatocyte Nuclear Factor 4l± in Colorectal Cancer Cells. <i>Cancers</i> , 2019, 11, 626.	1.7	13
3395	Identification of novel biomarkers and small molecule drugs in human colorectal cancer by microarray and bioinformatics analysis. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e00713.	0.6	34
3396	Sphingosine-1-phosphate signalling drives an angiogenic transcriptional programme in diffuse large B cell lymphoma. <i>Leukemia</i> , 2019, 33, 2884-2897.	3.3	26
3397	Fatty acid-binding protein 1 increases steer fat deposition by facilitating the synthesis and secretion of triacylglycerol in liver. <i>PLoS ONE</i> , 2019, 14, e0214144.	1.1	15
3398	A fourâ€ gene signature for prognosis in breast cancer patients with hypermethylated IL15RA. <i>Oncology Letters</i> , 2019, 17, 4245-4254.	0.8	11
3399	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
3400	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
3401	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
3402	FCRL5+ Memory B Cells Exhibit Robust Recall Responses. <i>Cell Reports</i> , 2019, 27, 1446-1460.e4.	2.9	87
3403	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
3404	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
3405	Histone acetylation promotes long-lasting defense responses and longevity following early life heat stress. <i>PLoS Genetics</i> , 2019, 15, e1008122.	1.5	39
3406	Genome-wide Kdm4 histone demethylase transcriptional regulation in <i>Drosophila</i> . <i>Molecular Genetics and Genomics</i> , 2019, 294, 1107-1121.	1.0	7
3407	DNA alterationâ€based classification of uveal melanoma gives better prognostic stratification than immune infiltration, which has a neutral effect in highâ€risk group. <i>Cancer Medicine</i> , 2019, 8, 3036-3046.	1.3	13
3408	Matrix Metalloproteinase 11 Is a Potential Therapeutic Target in Lung Adenocarcinoma. <i>Molecular Therapy - Oncolytics</i> , 2019, 14, 82-93.	2.0	35
3409	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
3410	Development and validation of a TP53-associated immune prognostic model for hepatocellular carcinoma. <i>EBioMedicine</i> , 2019, 42, 363-374.	2.7	257

#	ARTICLE	IF	CITATIONS
3411	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
3412	Comparative Gene Expression Profiles in Parathyroid Adenoma and Normal Parathyroid Tissue. <i>Journal of Clinical Medicine</i> , 2019, 8, 297.	1.0	14
3413	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
3414	Genomic Variations in Susceptibility to Intracranial Aneurysm in the Korean Population. <i>Journal of Clinical Medicine</i> , 2019, 8, 275.	1.0	24
3415	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
3416	Dietary Restriction Extends Lifespan through Metabolic Regulation of Innate Immunity. <i>Cell Metabolism</i> , 2019, 29, 1192-1205.e8.	7.2	122
3417	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , 2019, 10, 1383.	5.8	37
3418	Variable outcomes of human heart attack recapitulated in genetically diverse mice. <i>Npj Regenerative Medicine</i> , 2019, 4, 5.	2.5	20
3419	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
3420	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
3421	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
3422	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
3423	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
3424	Conserved motifs in nuclear genes encoding predicted mitochondrial proteins in <i>Trypanosoma cruzi</i> . <i>PLoS ONE</i> , 2019, 14, e0215160.	1.1	5
3425	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
3426	Identification of key pathways and genes in nasopharyngeal carcinoma using bioinformatics analysis. <i>Oncology Letters</i> , 2019, 17, 4683-4694.	0.8	9
3427	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
3428	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

#	ARTICLE	IF	CITATIONS
3429	HDAC1 and HDAC2 independently regulate common and specific intrinsic responses in murine enteroids. <i>Scientific Reports</i> , 2019, 9, 5363.	1.6	19
3430	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
3431	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
3432	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
3433	Building the drug-GO function network to screen significant candidate drugs for myasthenia gravis. <i>PLoS ONE</i> , 2019, 14, e0214857.	1.1	5
3434	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
3435	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
3436	Effects of CPAP on the transcriptional signatures in patients with obstructive sleep apnea via coexpression network analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 9277-9290.	1.2	6
3437	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
3438	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
3439	Repurposing of Drugs as Novel Influenza Inhibitors From Clinical Gene Expression Infection Signatures. <i>Frontiers in Immunology</i> , 2019, 10, 60.	2.2	44
3440	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
3441	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
3442	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
3443	Proteomic analysis reveals a protective role of specific macrophage subsets in liver repair. <i>Scientific Reports</i> , 2019, 9, 2953.	1.6	16
3444	Induction of desiccation tolerance in desiccation sensitive <i>Citrus limon</i> seeds. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 624-638.	4.1	20
3445	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 & Genomic Medicine</i> , 2019, 7, e607.	0.6	44
3446	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

#	ARTICLE	IF	CITATIONS
3447	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
3448	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
3449	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
3450	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
3451	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
3452	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
3453	Single-Cell RNA Sequencing of Plant-Associated Bacterial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 2452.	1.5	10
3454	The assessment of efficient representation of drug features using deep learning for drug repositioning. <i>BMC Bioinformatics</i> , 2019, 20, 577.	1.2	16
3455	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
3456	Transcriptome analysis of miRNA and mRNA in the livers of pigs with highly diverged backfat thickness. <i>Scientific Reports</i> , 2019, 9, 16740.	1.6	18
3457	Integrative analysis of DNA methylation and gene expression identified cervical cancer-specific diagnostic biomarkers. <i>Signal Transduction and Targeted Therapy</i> , 2019, 4, 55.	7.1	86
3458	Characterization of a five-microRNA signature as a prognostic biomarker for esophageal squamous cell carcinoma. <i>Scientific Reports</i> , 2019, 9, 19847.	1.6	14
3459	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
3460	MLL3 governs human haematopoietic stem-cell self-renewal and engraftment. <i>Nature</i> , 2019, 576, 281-286.	13.7	94
3461	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
3462	Gene Expression Profiles Controlled by the Alternative Splicing Factor Nova2 in Endothelial Cells. <i>Cells</i> , 2019, 8, 1498.	1.8	10
3463	Suppression of FOXM1 activities and breast cancer growth in vitro and in vivo by a new class of compounds. <i>Npj Breast Cancer</i> , 2019, 5, 45.	2.3	54
3464	Gcn5-Mediated Histone Acetylation Governs Nucleosome Dynamics in Spermiogenesis. <i>Developmental Cell</i> , 2019, 51, 745-758.e6.	3.1	47

#	ARTICLE	IF	CITATIONS
3465	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
3466	Spatial organization of endometrial gene expression at the onset of embryo attachment in pigs. <i>BMC Genomics</i> , 2019, 20, 895.	1.2	26
3467	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
3468	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
3469	Joint Transcriptomic Analysis of Lung Cancer and Other Lung Diseases. <i>Frontiers in Genetics</i> , 2019, 10, 1260.	1.1	9
3470	CDK1 and CCNB1 as potential diagnostic markers of rhabdomyosarcoma: validation following bioinformatics analysis. <i>BMC Medical Genomics</i> , 2019, 12, 198.	0.7	24
3471	The regulatory effect of microRNA-21a-3p on the promotion of telocyte angiogenesis mediated by PI3K (p110 α)/AKT/mTOR in LPS induced mice ARDS. <i>Journal of Translational Medicine</i> , 2019, 17, 427.	1.8	26
3472	Changes in meta-transcriptome of rumen epimural microbial community and liver transcriptome in young calves with feed induced acidosis. <i>Scientific Reports</i> , 2019, 9, 18967.	1.6	8
3473	DNA methylation profiles are associated with complex regional pain syndrome after traumatic injury. <i>Pain</i> , 2019, 160, 2328-2337.	2.0	19
3474	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
3475	Bioinformatics analysis of differentially expressed genes involved in human developmental chondrogenesis. <i>Medicine (United States)</i> , 2019, 98, e16240.	0.4	6
3476	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
3477	<p>Long Noncoding RNA LINC00265 Targets EGFR and Promotes Deterioration of Colorectal Cancer: A Comprehensive Study Based on Data Mining and in vitro Validation</p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 10681-10692.	1.0	14
3478	<p>Identification of Transcriptional Metabolic Dysregulation in Subtypes of Pituitary Adenoma by Integrated Bioinformatics Analysis</p>. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2019, Volume 12, 2441-2451.	1.1	7
3479	Epigenetic reprogramming underlies efficacy of DNA demethylation therapy in osteosarcomas. <i>Scientific Reports</i> , 2019, 9, 20360.	1.6	13
3480	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
3481	Unveiling Active Constituents and Potential Targets Related to the Hematinic Effect of Steamed Panax notoginseng Using Network Pharmacology Coupled With Multivariate Data Analyses. <i>Frontiers in Pharmacology</i> , 2018, 9, 1514.	1.6	18
3482	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

#	ARTICLE	IF	CITATIONS
3483	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
3484	Role of $\hat{1}^2$ -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
3485	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
3486	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
3487	Network Analyses of Integrated Differentially Expressed Genes in Papillary Thyroid Carcinoma to Identify Characteristic Genes. <i>Genes</i> , 2019, 10, 45.	1.0	8
3488	Identifying Molecular Markers of Cervical Cancer Based on Competing Endogenous RNA Network Analysis. <i>Gynecologic and Obstetric Investigation</i> , 2019, 84, 350-359.	0.7	7
3489	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
3490	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
3491	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
3492	NF $\hat{1}^B$ p65 dimerization and DNA $\hat{1}^B$ binding is important for inflammatory gene expression. <i>FASEB Journal</i> , 2019, 33, 4188-4202.	0.2	30
3493	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
3494	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
3495	Transgene-associated human growth hormone expression in pancreatic $\hat{1}^2$ -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
3496	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
3497	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
3498	Suppression of myopathic lamin mutations by muscle-specific activation of <i>AMPK</i> and modulation of downstream signaling. <i>Human Molecular Genetics</i> , 2019, 28, 351-371.	1.4	16
3499	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
3500	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

#	ARTICLE	IF	CITATIONS
3501	Thyroid hormone influences brain gene expression programs and behaviors in later generations by altering germ line epigenetic information. <i>Molecular Psychiatry</i> , 2020, 25, 939-950.	4.1	35
3502	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
3503	Driving Neurogenesis in Neural Stem Cells with High Sensitivity Optogenetics. <i>NeuroMolecular Medicine</i> , 2020, 22, 139-149.	1.8	7
3504	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
3505	Statistical genomics in rare cancer. <i>Seminars in Cancer Biology</i> , 2020, 61, 1-10.	4.3	15
3506	<i>Arabidopsis</i> DXO1 possesses deNADding and exonuclease activities and its mutation affects defense-related and photosynthetic gene expression. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 967-983.	4.1	29
3507	HNF1B-mediated repression of SLUG is suppressed by EZH2 in aggressive prostate cancer. <i>Oncogene</i> , 2020, 39, 1335-1346.	2.6	32
3508	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
3509	Dysfunctional epigenetic aging of the normal colon and colorectal cancer risk. <i>Clinical Epigenetics</i> , 2020, 12, 5.	1.8	47
3510	S1PR1-Associated Molecular Signature Predicts Survival in Patients with Sepsis. <i>Shock</i> , 2020, 53, 284-292.	1.0	13
3511	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
3512	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
3513	Epigenomic analysis of gastrulation identifies a unique chromatin state for primed pluripotency. <i>Nature Genetics</i> , 2020, 52, 95-105.	9.4	69
3514	Systematic expression analysis of WEE family kinases reveals the importance of PKMYT1 in breast carcinogenesis. <i>Cell Proliferation</i> , 2020, 53, e12741.	2.4	27
3515	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
3516	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
3517	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
3518	Brassinosteroids Antagonize Jasmonate-Activated Plant Defense Responses through BRI1-EMS-SUPPRESSOR1 (BES1). <i>Plant Physiology</i> , 2020, 182, 1066-1082.	2.3	48

#	ARTICLE	IF	CITATIONS
3519	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
3520	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
3521	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
3522	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
3523	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
3524	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
3525	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
3526	<p>The Perspective of Diagnostic and Prognostic Values of Lipoxygenases mRNA Expression in Colon Adenocarcinoma</p>. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 9389-9405.	1.0	11
3527	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
3528	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
3529	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
3530	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
3531	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
3532	A prognostic gene expression signature for oropharyngeal squamous cell carcinoma. <i>EBioMedicine</i> , 2020, 61, 102805.	2.7	16
3533	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
3534	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
3535	Argonaut: A Web Platform for Collaborative Multi-omic Data Visualization and Exploration. <i>Patterns</i> , 2020, 1, 100122.	3.1	18
3536	Machine learning techniques for sequence-based prediction of viral-host interactions between SARS-CoV-2 and human proteins. <i>Biomedical Journal</i> , 2020, 43, 438-450.	1.4	73

#	ARTICLE	IF	CITATIONS
3537	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
3538	Biomarker exploration of miRNA-203 as a promising substrate for predicting poor survival outcome in colorectal cancer. <i>BMC Cancer</i> , 2020, 20, 1003.	1.1	4
3539	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
3540	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
3541	Identification of Target Genes in Hypertension and Left Ventricular Remodeling. <i>Medicine (United States)</i> , 2020, 99, 10.	0.4	10
3542	Identification of candidate biomarkers and pathways associated with psoriasis using bioinformatics analysis. <i>Hereditas</i> , 2020, 157, 30.	0.5	14
3543	AMPK Enhances Transcription of Selected Nrf2 Target Genes via Negative Regulation of Bach1. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 628.	1.8	8
3544	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
3545	Large-scale site-specific mapping of the O-GalNAc glycoproteome. <i>Nature Protocols</i> , 2020, 15, 2589-2610.	5.5	28
3546	The Dysregulation and Prognostic Analysis of STRIPAK Complex Across Cancers. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 625.	1.8	8
3547	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
3548	A bioinformatics investigation into molecular mechanism of Yinzhihuang granules for treating hepatitis B by network pharmacology and molecular docking verification. <i>Scientific Reports</i> , 2020, 10, 11448.	1.6	27
3549	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
3550	ID1 As a Prognostic Biomarker and Promising Drug Target Plays a Pivotal Role in Deterioration of Clear Cell Renal Cell Carcinoma. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	1
3551	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
3552	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
3553	HLH-11 modulates lipid metabolism in response to nutrient availability. <i>Nature Communications</i> , 2020, 11, 5959.	5.8	20
3554	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

#	ARTICLE	IF	CITATIONS
3555	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
3556	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
3557	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
3558	CD74, a novel predictor for bronchopulmonary dysplasia in preterm infants. <i>Medicine (United States)</i> , 2020, 99, e23477.	0.4	3
3559	Differentially Expressed mRNAs and Their Long Noncoding RNA Regulatory Network with Helicobacter pylori-Associated Diseases including Atrophic Gastritis and Gastric Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-16.	0.9	6
3560	DNA methylation during human adipogenesis and the impact of fructose. <i>Genes and Nutrition</i> , 2020, 15, 21.	1.2	8
3561	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
3562	Computational Prediction of Antiangiogenesis Synergistic Mechanisms of Total Saponins of Panax japonicus Against Rheumatoid Arthritis. <i>Frontiers in Pharmacology</i> , 2020, 11, 566129.	1.6	4
3563	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
3564	Tumor-promoting macrophages prevail in malignant ascites of advanced gastric cancer. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1976-1988.	3.2	53
3565	m5C RNA Methylation Primarily Affects the ErbB and PI3K/Akt Signaling Pathways in Gastrointestinal Cancer. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 599340.	1.6	17
3566	SITC cancer immunotherapy resource document: a compass in the land of biomarker discovery. , 2020, 8, e000705.		20
3567	TTK, CDC25A, and ESPL1 as Prognostic Biomarkers for Endometrial Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	12
3568	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
3569	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
3570	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
3571	Identification of immune-related genes as prognostic factors in bladder cancer. <i>Scientific Reports</i> , 2020, 10, 19695.	1.6	15
3572	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

#	ARTICLE	IF	CITATIONS
3573	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
3574	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
3575	Network Pharmacology Analysis and Experiments Validation of the Inhibitory Effect of JianPi Fu Recipe on Colorectal Cancer LoVo Cells Metastasis and Growth. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-15.	0.5	15
3576	Deciphering the mode of action and position of genetic variants impacting on egg number in broiler breeders. <i>BMC Genomics</i> , 2020, 21, 512.	1.2	9
3577	Identification of a three-long noncoding RNA prognostic model involved competitive endogenous RNA in kidney renal clear cell carcinoma. <i>Cancer Cell International</i> , 2020, 20, 319.	1.8	25
3578	Kinase Interaction Network Expands Functional and Disease Roles of Human Kinases. <i>Molecular Cell</i> , 2020, 79, 504-520.e9.	4.5	74
3579	Ferroptosis-Related Gene Signature Predicts Glioma Cell Death and Glioma Patient Progression. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 538.	1.8	105
3580	Genome-Wide Profiling of Alternative Splicing Signature Reveals Prognostic Predictor for Esophageal Carcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 796.	1.1	5
3581	Flubendazole elicits anti-cancer effects via targeting EVA1A-modulated autophagy and apoptosis in Triple-negative Breast Cancer. <i>Theranostics</i> , 2020, 10, 8080-8097.	4.6	48
3582	DNA Methylation Clocks and Their Predictive Capacity for Aging Phenotypes and Healthspan. <i>Neuroscience Insights</i> , 2020, 15, 263310552094222.	0.9	86
3583	Interactome of miRNAs and transcriptome of human umbilical cord endothelial cells exposed to short-term simulated microgravity. <i>Npj Microgravity</i> , 2020, 6, 18.	1.9	14
3584	Genes associated with survival of female bovine blastocysts produced in vivo. <i>Cell and Tissue Research</i> , 2020, 382, 665-678.	1.5	13
3585	A review of computational drug repositioning: strategies, approaches, opportunities, challenges, and directions. <i>Journal of Cheminformatics</i> , 2020, 12, 46.	2.8	194
3586	Discovery of Selenocysteine as a Potential Nanomedicine Promotes Cartilage Regeneration With Enhanced Immune Response by Text Mining and Biomedical Databases. <i>Frontiers in Pharmacology</i> , 2020, 11, 1138.	1.6	5
3587	MiR-93/miR-375: Diagnostic Potential, Aggressiveness Correlation and Common Target Genes in Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5667.	1.8	13
3588	Novel variants in women with premature ovarian function decline identified via whole-exome sequencing. <i>Journal of Assisted Reproduction and Genetics</i> , 2020, 37, 2487-2502.	1.2	11
3589	Lower expression of LINC00092 in lung adenocarcinoma might mean poorer prognosis. <i>Medicine (United States)</i> , 2020, 99, e23012.	0.4	7
3590	Integrative Analysis of Regulatory Module Reveals Associations of Microgravity with Dysfunctions of Multi-body Systems and Tumorigenesis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7585.	1.8	5

#	ARTICLE	IF	CITATIONS
3591	Amino Sugars Reshape Interactions between <i>Streptococcus mutans</i> and <i>Streptococcus gordonii</i> . <i>Applied and Environmental Microbiology</i> , 2020, 87, .	1.4	6
3592	Transcriptome Reveals Multi Pigmentation Genes Affecting Dorsoventral Pattern in Avian Body. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 560766.	1.8	11
3593	Identification and Validation of Novel Genes in Anaplastic Thyroid Carcinoma via Bioinformatics Analysis. <i>Cancer Management and Research</i> , 2020, Volume 12, 9787-9799.	0.9	10
3594	Chromatin Looping Shapes KLF5-Dependent Transcriptional Programs in Human Epithelial Cancers. <i>Cancer Research</i> , 2020, 80, 5464-5477.	0.4	24
3595	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
3596	Tumor Suppressor Role of hsa-miR-193a-3p and -5p in Cutaneous Melanoma. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6183.	1.8	16
3597	Analysis of circulating-microRNA expression in lactating Holstein cows under summer heat stress. <i>PLoS ONE</i> , 2020, 15, e0231125.	1.1	14
3598	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
3599	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
3600	miR-16 integrates signal pathways in myofibroblasts: determinant of cell fate necessary for fibrosis resolution. <i>Cell Death and Disease</i> , 2020, 11, 639.	2.7	7
3601	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
3602	Review on the Computational Genome Annotation of Sequences Obtained by Next-Generation Sequencing. <i>Biology</i> , 2020, 9, 295.	1.3	45
3603	Existence and possible roles of independent non-CpG methylation in the mammalian brain. <i>DNA Research</i> , 2020, 27, .	1.5	10
3604	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
3605	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
3606	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
3607	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
3608	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

#	ARTICLE	IF	CITATIONS
3609	Proteomic Profiling of Extracellular Vesicles Derived from Cerebrospinal Fluid of Alzheimer's Disease Patients: A Pilot Study. <i>Cells</i> , 2020, 9, 1959.	1.8	75
3610	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
3611	Brain Transcriptomics of Wild and Domestic Rabbits Suggests That Changes in Dopamine Signaling and Ciliary Function Contributed to Evolution of Tameness. <i>Genome Biology and Evolution</i> , 2020, 12, 1918-1928.	1.1	17
3612	Systemic Expression Analysis Reveals Prognostic Significance of WIPI3 in Hepatocellular Carcinoma. <i>Frontiers in Genetics</i> , 2020, 11, 847.	1.1	5
3613	miRTissue ce: extending miRTissue web service with the analysis of ceRNA-ceRNA interactions. <i>BMC Bioinformatics</i> , 2020, 21, 199.	1.2	12
3614	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
3615	Circulation of gut-preactivated naïve CD8 ⁺ 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
3616	Identification of Pathways Associated with Placental Adaptation to Maternal Nutrient Restriction in Sheep. <i>Genes</i> , 2020, 11, 1031.	1.0	5
3617	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
3618	Improving Model Performance on the Stratification of Breast Cancer Patients by Integrating Multiscale Genomic Features. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	1
3619	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
3620	An Integrative Serum Pharmacology-Based Approach to Study the Anti-Tumor Activity of B. paniculatum Aqueous Bulb Extract on the Human Hepatocellular Carcinoma Cell Line BEL-7404. <i>Frontiers in Pharmacology</i> , 2020, 11, 01261.	1.6	7
3621	Identification and Validation of an Energy Metabolism-Related lncRNA-mRNA Signature for Lower-Grade Glioma. <i>BioMed Research International</i> , 2020, 2020, 1-14.	0.9	5
3622	RNA-Seq reveals placental growth factor regulates the human retinal endothelial cell barrier integrity by transforming growth factor (TGF- β^2) signaling. <i>Molecular and Cellular Biochemistry</i> , 2020, 475, 93-106.	1.4	5
3623	Transcript Profiles of Stria Vascularis in Models of Waardenburg Syndrome. <i>Neural Plasticity</i> , 2020, 2020, 1-9.	1.0	3
3624	The current landscape of coronavirus-host protein-protein interactions. <i>Journal of Translational Medicine</i> , 2020, 18, 319.	1.8	66
3625	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
3626	Integrated Phytochemical Analysis Based on UPLC-MS and Network Pharmacology Approaches to Explore the Quality Control Markers for the Quality Assessment of <i>Trifolium pratense</i> L.. <i>Molecules</i> , 2020, 25, 3787.	1.7	13

#	ARTICLE	IF	CITATIONS
3627	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
3628	Co-expression network analysis of protein phosphatase 2A (PP2A) genes with stress-responsive genes in <i>Arabidopsis thaliana</i> reveals 13 key regulators. <i>Scientific Reports</i> , 2020, 10, 21480.	1.6	8
3629	Response to iron overload in cultured hepatocytes. <i>Scientific Reports</i> , 2020, 10, 21184.	1.6	11
3630	Key Modules and Hub Genes Identified by Coexpression Network Analysis for Revealing Novel Biomarkers for Spina Bifida. <i>Frontiers in Genetics</i> , 2020, 11, 583316.	1.1	6
3631	Phosphatase and Tensin Homolog Mutation in Immune Cell Infiltration and Clinicopathological Features of Low-Grade Gliomas. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 562416.	1.6	2
3632	Metabolomic and Transcriptomic Analysis of MCF-7 Cells Exposed to 23 Chemicals at Human-Relevant Levels: Estimation of Individual Chemical Contribution to Effects. <i>Environmental Health Perspectives</i> , 2020, 128, 127008.	2.8	33
3633	Characterization of mRNA Profiles of Exosomes from Diverse Forms of M2 Macrophages. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	4
3634	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
3635	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
3636	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
3637	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
3638	Identifying Key MicroRNAs Targeted by Narenmandula in a Rodent Nephropathy Model. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-9.	0.5	2
3639	Transcriptome Analyses of β -Thalassemia α^0 Mutation Using Isogenic Cell Models Generated by CRISPR/Cas9 and Asymmetric Single-Stranded Oligodeoxynucleotides (ssODNs). <i>Frontiers in Genetics</i> , 2020, 11, 577053.	1.1	5
3640	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
3641	H4K20me3 methyltransferase SUV420H2 shapes the chromatin landscape of pluripotent embryonic stem cells. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	11
3642	Proteomic analysis of platelet-rich and platelet-poor plasma. <i>Regenerative Therapy</i> , 2020, 15, 226-235.	1.4	13
3643	Integrative Analysis of DNA Methylation Identified 12 Signature Genes Specific to Metastatic ccRCC. <i>Frontiers in Oncology</i> , 2020, 10, 556018.	1.3	9
3644	Bioinformatic Analysis Identifies Potential Key Genes in the Pathogenesis of Melanoma. <i>Frontiers in Oncology</i> , 2020, 10, 581985.	1.3	9

#	ARTICLE	IF	CITATIONS
3645	Cholesterol Regulates Innate Immunity via Nuclear Hormone Receptor NHR-8. <i>IScience</i> , 2020, 23, 101068.	1.9	30
3646	Epigenome-Wide Tobacco-Related Methylation Signature Identification and Their Multilevel Regulatory Network Inference for Lung Adenocarcinoma. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	5
3647	Identification of Pannexin 2 as a Novel Marker Correlating with Ferroptosis and Malignant Phenotypes of Prostate Cancer Cells. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 4411-4421.	1.0	24
3648	MCM2 and NUSAP1 Are Potential Biomarkers for the Diagnosis and Prognosis of Pancreatic Cancer. <i>BioMed Research International</i> , 2020, 2020, 1-20.	0.9	21
3649	Expression profiling and analysis of some miRNAs in subcutaneous white adipose tissue during development of obesity. <i>Genes and Nutrition</i> , 2020, 15, 8.	1.2	15
3650	Discovery of genes and proteins possibly regulating mean wool fibre diameter using cDNA microarray and proteomic approaches. <i>Scientific Reports</i> , 2020, 10, 7726.	1.6	6
3651	Yeast-Based Genetic Interaction Analysis of Human Kinome. <i>Cells</i> , 2020, 9, 1156.	1.8	5
3652	Nine hub genes related to the prognosis of HBV-positive hepatocellular carcinoma identified by protein interaction analysis. <i>Annals of Translational Medicine</i> , 2020, 8, 478-478.	0.7	13
3653	Comprehensive analysis of competing endogenous RNA network in Wilms tumor based on the TARGET database. <i>Translational Andrology and Urology</i> , 2020, 9, 473-484.	0.6	0
3654	Identification of a Gene-Related Risk Signature in Melanoma Patients Using Bioinformatic Profiling. <i>Journal of Oncology</i> , 2020, 2020, 1-13.	0.6	8
3655	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
3656	T Cells Produce IFN- γ in the TREX1 D18N Model of Lupus-like Autoimmunity. <i>Journal of Immunology</i> , 2020, 204, 348-359.	0.4	13
3657	N-glycosylation Site Analysis Reveals Sex-related Differences in Protein N-glycosylation in the Rice Brown Planthopper (<i>Nilaparvata lugens</i>). <i>Molecular and Cellular Proteomics</i> , 2020, 19, 529-539.	2.5	10
3658	Ribosomal protein S11 influences glioma response to TOP2 poisons. <i>Oncogene</i> , 2020, 39, 5068-5081.	2.6	21
3659	Proteome characteristics of liver tissue from patients with parenteral nutrition-associated liver disease. <i>Nutrition and Metabolism</i> , 2020, 17, 43.	1.3	6
3660	The Mutant p53-Driven Secretome Has Oncogenic Functions in Pancreatic Ductal Adenocarcinoma Cells. <i>Biomolecules</i> , 2020, 10, 884.	1.8	8
3661	Identification of candidate aberrantly methylated and differentially expressed genes in Esophageal squamous cell carcinoma. <i>Scientific Reports</i> , 2020, 10, 9735.	1.6	11
3662	SCDb: an integrated database of stomach cancer. <i>BMC Cancer</i> , 2020, 20, 490.	1.1	7

#	ARTICLE	IF	CITATIONS
3663	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
3664	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
3665	Systems Genetics for Mechanistic Discovery in Heart Diseases. <i>Circulation Research</i> , 2020, 126, 1795-1815.	2.0	8
3666	Longitudinal Analysis of Gene Expression Changes During Cervical Carcinogenesis Reveals Potential Therapeutic Targets. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432092057.	0.6	5
3667	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
3668	<p>A 5-Gene Stemness Score for Rapid Determination of Risk in Multiple Myeloma</p>. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 4339-4348.	1.0	9
3669	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
3670	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
3671	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
3672	Retinal endothelial cell phenotypic modifications during experimental autoimmune uveitis: a transcriptomic approach. <i>BMC Ophthalmology</i> , 2020, 20, 106.	0.6	14
3673	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
3674	Novel myocardial markers GADD45G and NDUF55 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
3675	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
3676	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
3677	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
3678	Deregulation of miR-27a may contribute to canine fibroblast activation after coculture with a mast cell tumour cell line. <i>FEBS Open Bio</i> , 2020, 10, 802-816.	1.0	4
3679	Understanding of Zaire ebolavirus-human protein interaction for drug repurposing. <i>VirusDisease</i> , 2020, 31, 28-37.	1.0	5
3680	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

#	ARTICLE	IF	CITATIONS
3681	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
3682	Phenotypic Screening of Chemical Libraries Enriched by Molecular Docking to Multiple Targets Selected from Glioblastoma Genomic Data. <i>ACS Chemical Biology</i> , 2020, 15, 1424-1444.	1.6	4
3683	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
3684	Proteome Analysis Reveals Syndecan 1 Regulates Porcine Sapelovirus Replication. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4386.	1.8	1
3685	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
3686	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
3687	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
3688	Identification of Immune-Related Genes Contributing to the Development of Glioblastoma Using Weighted Gene Co-expression Network Analysis. <i>Frontiers in Immunology</i> , 2020, 11, 1281.	2.2	40
3689	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
3690	Identification of Key Differentially Expressed Transcription Factors in Glioblastoma. <i>Journal of Oncology</i> , 2020, 2020, 1-9.	0.6	10
3691	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
3692	Systematic summarization of the expression profiles and prognostic roles of the <i>dishevelled</i> gene family in hepatocellular carcinoma. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1384.	0.6	9
3693	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
3694	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
3695	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
3696	Statin-induced myopathic changes in primary human muscle cells and reversal by a prostaglandin F2 alpha analogue. <i>Scientific Reports</i> , 2020, 10, 2158.	1.6	18
3697	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
3698	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

#	ARTICLE	IF	CITATIONS
3699	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
3700	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
3701	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
3702	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
3703	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
3704	Multimiomics Evaluation of Human Fat-Derived Mesenchymal Stem Cells on an Osteobiologic Nanocomposite. <i>BioResearch Open Access</i> , 2020, 9, 37-50.	2.6	6
3705	19q13 KRAB zinc-finger protein ZNF471 activates MAPK10/JNK3 signaling but is frequently silenced by promoter CpG methylation in esophageal cancer. <i>Theranostics</i> , 2020, 10, 2243-2259.	4.6	31
3706	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
3707	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
3708	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
3709	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
3710	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
3711	Loss of p53 drives neuron reprogramming in head and neck cancer. <i>Nature</i> , 2020, 578, 449-454.	13.7	241
3712	Transcriptome analyses identify hub genes and potential mechanisms in adenoid cystic carcinoma. <i>Medicine (United States)</i> , 2020, 99, e18676.	0.4	4
3713	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
3714	Establishment and Characterization of Paired Primary Cultures of Human Pancreatic Cancer Cells and Stellate Cells Derived from the Same Tumor. <i>Cells</i> , 2020, 9, 227.	1.8	6
3715	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
3716	White matter structure and myelin-related gene expression alterations with experience in adult rats. <i>Progress in Neurobiology</i> , 2020, 187, 101770.	2.8	30

#	ARTICLE	IF	CITATIONS
3717	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
3718	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
3719	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
3720	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
3721	Exploring Alzheimer's Disease Molecular Variability via Calculation of Personalized Transcriptional Signatures. <i>Biomolecules</i> , 2020, 10, 503.	1.8	5
3722	Bioinformatics Methods for Mass Spectrometry-Based Proteomics Data Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2873.	1.8	134
3723	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
3724	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
3725	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
3726	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
3727	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
3728	Old Mice Have Less Transcriptional Activation But Similar Periosteal Cell Proliferation Compared to Young Adult Mice in Response to in vivo Mechanical Loading. <i>Journal of Bone and Mineral Research</i> , 2020, 35, 1751-1764.	3.1	26
3729	Discovery of novel biomarkers for atherosclerotic aortic aneurysm through proteomics-based assessment of disease progression. <i>Scientific Reports</i> , 2020, 10, 6429.	1.6	10
3730	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
3731	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
3732	Gene expression responses to anti-tuberculous drugs in a whole blood model. <i>BMC Microbiology</i> , 2020, 20, 81.	1.3	5
3733	Automated gene data integration with Databio. <i>BMC Research Notes</i> , 2020, 13, 195.	0.6	1
3734	Tumor-Draining Lymph Secretome En Route to the Regional Lymph Node in Breast Cancer Metastasis. <i>Breast Cancer: Targets and Therapy</i> , 2020, Volume 12, 57-67.	1.0	4

#	ARTICLE	IF	CITATIONS
3735	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
3736	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
3737	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
3738	Analysis of Thyroid Hormone Receptor \pm -Knockout Tadpoles Reveals That the Activation of Cell Cycle Program Is Involved in Thyroid Hormone-Induced Larval Epithelial Cell Death and Adult Intestinal Stem Cell Development During <i>Xenopus tropicalis</i> Metamorphosis. <i>Thyroid</i> , 2021, 31, 128-142.	2.4	21
3739	Transcriptomic and Epigenetic Preservation of Genetic Sex Identity in Estrogen-feminized Male Chicken Embryonic Gonads. <i>Endocrinology</i> , 2021, 162, .	1.4	17
3740	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
3741	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
3742	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
3743	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
3744	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
3745	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
3746	Identification of potential <i>circRNAs</i> and <i>circRNA-miRNA-mRNA</i> regulatory network in the development of diabetic foot ulcers by integrated bioinformatics analysis. <i>International Wound Journal</i> , 2021, 18, 323-331.	1.3	20
3747	Direct and Indirect Regulators of Epithelial-Mesenchymal Transition-Mediated Immunosuppression in Breast Carcinomas. <i>Cancer Discovery</i> , 2021, 11, 1286-1305.	7.7	76
3748	Chronic circadian shift leads to adipose tissue inflammation and fibrosis. <i>Molecular and Cellular Endocrinology</i> , 2021, 521, 111110.	1.6	28
3749	Comparison of tear proteomic and neuromediator profiles changes between small incision lenticule extraction (SMILE) and femtosecond laser-assisted in-situ keratomileusis (LASIK). <i>Journal of Advanced Research</i> , 2021, 29, 67-81.	4.4	23
3750	Proteomic Profiling of Extracellular Vesicles Separated from Plasma of Former National Football League Players at Risk for Chronic Traumatic Encephalopathy. , 2021, 12, 1363.		12
3751	Identification of six hub genes and analysis of their correlation with drug sensitivity in acute myeloid leukemia through bioinformatics. <i>Translational Cancer Research</i> , 2021, 10, 126-140.	0.4	4
3752	Age and Tumor Differentiation-Associated Gene Expression Based Analysis of Non-Familial Prostate Cancers. <i>Frontiers in Oncology</i> , 2020, 10, 584280.	1.3	4

#	ARTICLE	IF	CITATIONS
3753	Comparing the effects of two different strains of mycobacteria, <i>Mycobacterium vaccae</i> NCTC 11659 and <i>M. vaccae</i> ATCC 15483, on stress-resilient behaviors and lipid-immune signaling in rats. <i>Brain, Behavior, and Immunity</i> , 2021, 91, 212-229.	2.0	12
3754	Integrative Identification of Hub Genes Associated With Immune Cells in Atrial Fibrillation Using Weighted Gene Correlation Network Analysis. <i>Frontiers in Cardiovascular Medicine</i> , 2020, 7, 631775.	1.1	11
3755	In-depth Site-specific Analysis of N-glycoproteome in Human Cerebrospinal Fluid and Glycosylation Landscape Changes in Alzheimer's Disease. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100081.	2.5	48
3756	HDAC inhibition results in widespread alteration of the histone acetylation landscape and BRD4 targeting to gene bodies. <i>Cell Reports</i> , 2021, 34, 108638.	2.9	60
3757	PredTAD: A machine learning framework that models 3D chromatin organization alterations leading to oncogene dysregulation in breast cancer cell lines. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2870-2880.	1.9	2
3758	LncTx: A network-based method to repurpose drugs acting on the survival-related lncRNAs in lung cancer. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3990-4002.	1.9	5
3759	Enrichment of Phosphorylated Tau (Thr181) and Functionally Interacting Molecules in Chronic Traumatic Encephalopathy Brain-derived Extracellular Vesicles. , 2021, 12, 1376.		3
3760	Quantitative trait loci and transcriptome signatures associated with avian heritable resistance to <i>Campylobacter</i> . <i>Scientific Reports</i> , 2021, 11, 1623.	1.6	10
3761	A Novel mRNA-miRNA Regulatory Sub-Network Associated With Prognosis of Metastatic Clear Cell Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 593601.	1.3	5
3762	A novel similarity score based on gene ranks to reveal genetic relationships among diseases. <i>PeerJ</i> , 2021, 9, e10576.	0.9	3
3763	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
3764	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
3765	Extracellular signal-regulated kinase (ERK) pathway control of CD8+ T cell differentiation. <i>Biochemical Journal</i> , 2021, 478, 79-98.	1.7	17
3766	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
3767	Multiplex gene and phenotype network to characterize shared genetic pathways of epilepsy and autism. <i>Scientific Reports</i> , 2021, 11, 952.	1.6	27
3768	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
3769	A Systems View of the Heparan Sulfate Interactome. <i>Journal of Histochemistry and Cytochemistry</i> , 2021, 69, 105-119.	1.3	44
3770	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

#	ARTICLE	IF	CITATIONS
3771	Genome-Wide Association Study of Maize Aboveground Dry Matter Accumulation at Seedling Stage. <i>Frontiers in Genetics</i> , 2020, 11, 571236.	1.1	9
3772	Deciphering the miRNA transcriptome of breast muscle from the embryonic to post-hatching periods in chickens. <i>BMC Genomics</i> , 2021, 22, 64.	1.2	11
3773	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
3774	Identification and Characterisation of Putative Enhancer Elements in Mouse Embryonic Stem Cells. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222097462.	1.0	3
3775	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
3776	Comparison of Growth Performance and Meat Quality Traits of Commercial Cross-Bred Pigs versus the Large Black Pig Breed. <i>Animals</i> , 2021, 11, 200.	1.0	22
3777	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
3778	Exploring the treatment of COVID-19 with Yinqiao powder based on network pharmacology. <i>Phytotherapy Research</i> , 2021, 35, 2651-2664.	2.8	36
3779	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
3780	GATA3 somatic mutations are associated with clinicopathological features and expression profile in TCGA breast cancer patients. <i>Scientific Reports</i> , 2021, 11, 1679.	1.6	15
3781	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
3782	Sparsely-connected autoencoder (SCA) for single cell RNAseq data mining. <i>Npj Systems Biology and Applications</i> , 2021, 7, 1.	1.4	53
3783	Discovery and function exploration of microRNA-155 as a molecular biomarker for early detection of breast cancer. <i>Breast Cancer</i> , 2021, 28, 806-821.	1.3	7
3784	CXCL10 potentiates immune checkpoint blockade therapy in homologous recombination-deficient tumors. <i>Theranostics</i> , 2021, 11, 7175-7187.	4.6	34
3785	INHBA is a novel mediator regulating cellular senescence and immune evasion in colorectal cancer. <i>Journal of Cancer</i> , 2021, 12, 5938-5949.	1.2	10
3786	Prognostic gene expression signatures of breast cancer are lacking a sensible biological meaning. <i>Scientific Reports</i> , 2021, 11, 156.	1.6	26
3787	Integrated Genomic and Transcriptomic Analysis reveals key genes for predicting dual-phenotype Hepatocellular Carcinoma Prognosis. <i>Journal of Cancer</i> , 2021, 12, 2993-3010.	1.2	5
3788	Identification of Core Genes Related to Progression and Prognosis of Hepatocellular Carcinoma and Small-Molecule Drug Prediction. <i>Frontiers in Genetics</i> , 2021, 12, 608017.	1.1	5

#	ARTICLE	IF	CITATIONS
3789	Identification of glycolysis related pathways in pancreatic adenocarcinoma and liver hepatocellular carcinoma based on TCGA and GEO datasets. <i>Cancer Cell International</i> , 2021, 21, 128.	1.8	3
3790	Enrichment of Neurodegenerative Microglia Signature in Brain-Derived Extracellular Vesicles Isolated from Alzheimer's Disease Mouse Models. <i>Journal of Proteome Research</i> , 2021, 20, 1733-1743.	1.8	34
3791	Identification of four genes and biological characteristics of esophageal squamous cell carcinoma by integrated bioinformatics analysis. <i>Cancer Cell International</i> , 2021, 21, 123.	1.8	13
3792	Calcium-binding and coiled-coil domain 2 promotes the proliferation and suppresses apoptosis of prostate cancer cells. <i>Experimental and Therapeutic Medicine</i> , 2021, 21, 405.	0.8	3
3793	Integrated Bioinformatics Analysis Exhibits Pivotal Exercise-Induced Genes and Corresponding Pathways in Malignant Melanoma. <i>Frontiers in Genetics</i> , 2020, 11, 637320.	1.1	5
3794	Identification of UBE2C as hub gene in driving prostate cancer by integrated bioinformatics analysis. <i>PLoS ONE</i> , 2021, 16, e0247827.	1.1	16
3795	Single-Cell RNA Sequencing and Quantitative Proteomics Analysis Elucidate Marker Genes and Molecular Mechanisms in Hypoplastic Left Heart Patients With Heart Failure. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 617853.	1.8	2
3796	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
3797	Restoration of type I interferon signaling in intrahepatically primed CD8+ T cells promotes functional differentiation. <i>JCI Insight</i> , 2021, 6, .	2.3	6
3798	Global Transcriptomic Analyses Reveal Genes Involved in Conceptus Development During the Implantation Stages in Pigs. <i>Frontiers in Genetics</i> , 2021, 12, 584995.	1.1	10
3799	Recursive ensemble feature selection provides a robust mRNA expression signature for myalgic encephalomyelitis/chronic fatigue syndrome. <i>Scientific Reports</i> , 2021, 11, 4541.	1.6	14
3800	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
3801	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
3802	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
3803	A Systematic Review of Genomic Regions and Candidate Genes Underlying Behavioral Traits in Farmed Mammals and Their Link with Human Disorders. <i>Animals</i> , 2021, 11, 715.	1.0	13
3805	SPAAC-NAD-seq, a sensitive and accurate method to profile NAD ⁺ -capped transcripts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	26
3806	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
3807	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

#	ARTICLE	IF	CITATIONS
3808	Identification and Validation of a Tumor Microenvironment-Related Gene Signature for Prognostic Prediction in Advanced-Stage Non-Small-Cell Lung Cancer. <i>BioMed Research International</i> , 2021, 2021, 1-18.	0.9	9
3809	Disruption of Circadian Transcriptome in Lung by Acute Sleep Deprivation. <i>Frontiers in Genetics</i> , 2021, 12, 664334.	1.1	7
3810	A plug and play microfluidic platform for standardized sensitive low-input chromatin immunoprecipitation. <i>Genome Research</i> , 2021, 31, 919-933.	2.4	4
3811	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
3812	Changes in protein expression due to metformin treatment and hyperinsulinemia in a human endometrial cancer cell line. <i>PLoS ONE</i> , 2021, 16, e0248103.	1.1	9
3813	Muscle Enriched Lamin Interacting Protein (Mlip) Binds Chromatin and Is Required for Myoblast Differentiation. <i>Cells</i> , 2021, 10, 615.	1.8	8
3814	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
3815	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
3816	Signaling Pathways Regulated by Silica Nanoparticles. <i>Molecules</i> , 2021, 26, 1398.	1.7	17
3817	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
3818	A Streamlined Approach to Pathway Analysis from RNA-Sequencing Data. <i>Methods and Protocols</i> , 2021, 4, 21.	0.9	0
3819	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
3820	Quantitative proteome profiling stratifies fibroepithelial lesions of the breast. <i>Oncotarget</i> , 2021, 12, 507-518.	0.8	7
3821	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
3822	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
3823	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
3824	A network pharmacology-based investigation on the bioactive ingredients and molecular mechanisms of Gelsemium elegans Benth against colorectal cancer. <i>BMC Complementary Medicine and Therapies</i> , 2021, 21, 99.	1.2	9
3825	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

#	ARTICLE	IF	CITATIONS
3826	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
3827	Identification of the hub genes in gastric cancer through weighted gene co-expression network analysis. <i>PeerJ</i> , 2021, 9, e10682.	0.9	9
3828	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
3829	Network Pharmacology-Based Strategy for Elucidating the Molecular Basis For the Pharmacologic Effects of Licorice (<i>Glycyrrhiza</i> spp.). <i>Frontiers in Pharmacology</i> , 2021, 12, 590477.	1.6	10
3830	Epithelial Splicing Regulatory Protein 1 Is Overexpressed in Breast Cancer and Predicts Poor Prognosis for Breast Cancer Patients. <i>Medical Science Monitor</i> , 2021, 27, e931102.	0.5	10
3831	Prediction of single-cell mechanisms for disease progression in hypertrophic remodelling by a trans-omics approach. <i>Scientific Reports</i> , 2021, 11, 8112.	1.6	4
3832	Prediction and analysis of novel key genes ITGAX, LAPTM5, SERPINE1 in clear cell renal cell carcinoma through bioinformatics analysis. <i>PeerJ</i> , 2021, 9, e11272.	0.9	18
3833	Characterisation of PALB2 tumours through whole-exome and whole-transcriptomic analyses. <i>Npj Breast Cancer</i> , 2021, 7, 46.	2.3	6
3834	Single-cell RNA sequencing of mouse islets exposed to proinflammatory cytokines. <i>Life Science Alliance</i> , 2021, 4, e202000949.	1.3	16
3835	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
3836	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
3837	CXCL1 Clone Evolution Induced by the HDAC Inhibitor Belinostat Might Be a Favorable Prognostic Indicator in Triple-Negative Breast Cancer. <i>BioMed Research International</i> , 2021, 2021, 1-12.	0.9	4
3838	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
3839	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
3840	EVA1B to Evaluate the Tumor Immune Microenvironment and Clinical Prognosis in Glioma. <i>Frontiers in Immunology</i> , 2021, 12, 648416.	2.2	20
3841	Identification of Potential Biomarkers From Hepatocellular Carcinoma With MT1 Deletion. <i>Pathology and Oncology Research</i> , 2021, 27, 597527.	0.9	5
3842	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
3843	STAM Prolongs Clear Cell Renal Cell Carcinoma Patients' Survival via Inhibiting Cell Growth and Invasion. <i>Frontiers in Oncology</i> , 2021, 11, 611081.	1.3	2

#	ARTICLE	IF	CITATIONS
3844	Genome-wide association and transcriptome studies identify candidate genes and pathways for feed conversion ratio in pigs. <i>BMC Genomics</i> , 2021, 22, 294.	1.2	11
3845	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
3846	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
3847	Genetic diversity in global chicken breeds in relation to their genetic distances to wild populations. <i>Genetics Selection Evolution</i> , 2021, 53, 36.	1.2	9
3848	Multi-omics integration strategies for animal epigenetic studies. <i>Animal Bioscience</i> , 2021, 34, 1271-1282.	0.8	15
3849	Bacterial Quality, Prevalence of Pathogens, and Molecular Characterization of Biofilm-Producing <i>Staphylococcus aureus</i> from Korean Dairy Farm Environments. <i>Animals</i> , 2021, 11, 1306.	1.0	4
3850	MicroRNA Expression Profile Distinguishes Glioblastoma Stem Cells from Differentiated Tumor Cells. <i>Journal of Personalized Medicine</i> , 2021, 11, 264.	1.1	12
3851	Investigation and verification of the clinical significance and perspective of natural killer group 2 member D ligands in colon adenocarcinoma. <i>Aging</i> , 2021, 13, 12565-12586.	1.4	4
3852	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
3854	Flower Development in Cassava Is Feminized by Cytokinin, While Proliferation Is Stimulated by Anti-Ethylene and Pruning: Transcriptome Responses. <i>Frontiers in Plant Science</i> , 2021, 12, 666266.	1.7	12
3855	Phosphatidylcholine mediates the crosstalk between LET-607 and DAF-16 stress response pathways. <i>PLoS Genetics</i> , 2021, 17, e1009573.	1.5	7
3856	Immunity-longevity tradeoff neurally controlled by GABAergic transcription factor PITX1/UNC-30. <i>Cell Reports</i> , 2021, 35, 109187.	2.9	15
3857	CPA: a web-based platform for consensus pathway analysis and interactive visualization. <i>Nucleic Acids Research</i> , 2021, 49, W114-W124.	6.5	20
3858	Detection of copy number variants in African goats using whole genome sequence data. <i>BMC Genomics</i> , 2021, 22, 398.	1.2	4
3859	INPP4B promotes PI3K β -dependent late endosome formation and Wnt/ β -catenin signaling in breast cancer. <i>Nature Communications</i> , 2021, 12, 3140.	5.8	30
3860	Genome-Wide Identification of Candidate Genes for Milk Production Traits in Korean Holstein Cattle. <i>Animals</i> , 2021, 11, 1392.	1.0	12
3861	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
3862	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

#	ARTICLE	IF	CITATIONS
3863	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
3864	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
3865	Screening and identification of LMNB1 and DLGAP5, two key biomarkers in gliomas. <i>Bioscience Reports</i> , 2021, 41, .	1.1	7
3866	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
3867	Identification of upregulated NF- κ B inhibitor alpha and IRAK3 targeting lncRNA following intracranial aneurysm rupture-induced subarachnoid hemorrhage. <i>BMC Neurology</i> , 2021, 21, 197.	0.8	9
3868	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
3869	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
3870	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
3871	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
3872	Extracellular microRNAs: key players to explore the outcomes of in vitro fertilization. <i>Reproductive Biology and Endocrinology</i> , 2021, 19, 72.	1.4	12
3873	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
3874	CBFB cooperates with p53 to maintain TAp73 expression and suppress breast cancer. <i>PLoS Genetics</i> , 2021, 17, e1009553.	1.5	8
3875	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
3876	Microbiota Modulates Cardiac Transcriptional Responses to Intermittent Hypoxia and Hypercapnia. <i>Frontiers in Physiology</i> , 2021, 12, 680275.	1.3	4
3877	Global proteomic analyses of human cytotrophoblast differentiation/invasion. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	5
3878	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
3879	Comparative Proteomic Analysis of Polarized Human THP-1 and Mouse RAW264.7 Macrophages. <i>Frontiers in Immunology</i> , 2021, 12, 700009.	2.2	55
3880	Genome Scan for Variable Genes Involved in Environmental Adaptations of Nubian Ibex. <i>Journal of Molecular Evolution</i> , 2021, 89, 448-457.	0.8	0

#	ARTICLE	IF	CITATIONS
3881	The Role of Early Growth Response Family Members 1â€“4 in Prognostic Value of Breast Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 680132.	1.1	4
3882	Nuclear ADP-ribosylation drives IFN β -dependent STAT1 \pm enhancer formation in macrophages. <i>Nature Communications</i> , 2021, 12, 3931.	5.8	20
3883	Identification of potential pathogenic mutations in Chinese children with first branchial cleft anomalies detected by wholeâ€“exome sequencing. <i>Pediatric Investigation</i> , 2021, 5, 211-216.	0.6	1
3884	Gene expression profiles of breast cancer metastasis according to organ site. <i>Molecular Oncology</i> , 2022, 16, 69-87.	2.1	24
3885	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
3886	Global Screening of LUBAC and OTULIN Interacting Proteins by Human Proteome Microarray. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 686395.	1.8	0
3887	Comprehensive Bioinformatics Analysis of mRNA Expression Profiles and Identification of a miRNAâ€“mRNA Network Associated with the Pathogenesis of Low-Grade Gliomas. <i>Cancer Management and Research</i> , 2021, Volume 13, 5135-5147.	0.9	4
3888	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
3889	Aging- and Tumor-Mediated Increase in CD8+CD28 $^{\text{low}}$ T Cells Might Impose a Strong Barrier to Success of Immunotherapy in Glioblastoma. <i>ImmunoHorizons</i> , 2021, 5, 395-409.	0.8	8
3890	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
3891	Transcriptomics-based drug repositioning pipeline identifies therapeutic candidates for COVID-19. <i>Scientific Reports</i> , 2021, 11, 12310.	1.6	31
3892	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
3893	Transcriptomic analysis of caecal tissue in inbred chicken lines that exhibit heritable differences in resistance to <i>Campylobacter jejuni</i> . <i>BMC Genomics</i> , 2021, 22, 411.	1.2	7
3895	Identification and Comparative Analysis of Long Non-coding RNAs in High- and Low-Fecundity Goat Ovaries During Estrus. <i>Frontiers in Genetics</i> , 2021, 12, 648158.	1.1	4
3896	BAP1/ASXL complex modulation regulates epithelial-mesenchymal transition during trophoblast differentiation and invasion. <i>ELife</i> , 2021, 10, .	2.8	27
3897	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
3898	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
3899	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

#	ARTICLE	IF	CITATIONS
3900	A Comprehensive Analysis of the Downregulation of miRNA-1827 and Its Prognostic Significance by Targeting SPTBN2 and BCL2L1 in Ovarian Cancer. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 687576.	1.6	6
3901	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
3902	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
3903	Parental methylome reprogramming in human uniparental blastocysts reveals germline memory transition. <i>Genome Research</i> , 2021, 31, 1519-1530.	2.4	4
3904	Environmental responsiveness of flowering time in cassava genotypes and associated transcriptome changes. <i>PLoS ONE</i> , 2021, 16, e0253555.	1.1	4
3905	Mutation in FBXO32 causes dilated cardiomyopathy through up-regulation of ER-stress mediated apoptosis. <i>Communications Biology</i> , 2021, 4, 884.	2.0	12
3906	Action potential-coupled Rho GTPase signaling drives presynaptic plasticity. <i>ELife</i> , 2021, 10, .	2.8	18
3907	Identification of Potential Prognostic Biomarkers Associated With Cancerometastasis in Skin Cutaneous Melanoma. <i>Frontiers in Genetics</i> , 2021, 12, 687979.	1.1	5
3908	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
3909	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
3910	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
3911	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
3912	Predicting Agents That Can Overcome 5-FU Resistance in Colorectal Cancers via Pharmacogenomic Analysis. <i>Biomedicines</i> , 2021, 9, 882.	1.4	5
3913	Text mining of gene-phenotype associations reveals new phenotypic profiles of autism-associated genes. <i>Scientific Reports</i> , 2021, 11, 15269.	1.6	3
3914	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
3915	Aberrantly methylated-differentially genes and pathways among Iranian patients with colorectal cancer. <i>Cancer Cell International</i> , 2021, 21, 346.	1.8	2
3916	A combined GWAS approach reveals key loci for socially-affected traits in Yorkshire pigs. <i>Communications Biology</i> , 2021, 4, 891.	2.0	9
3917	Identification of the Hub Genes in Alzheimer's Disease. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-8.	0.7	14

#	ARTICLE	IF	CITATIONS
3918	The Compressed Vocabulary of Microbial Life. <i>Frontiers in Microbiology</i> , 2021, 12, 655990.	1.5	8
3919	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
3920	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
3921	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
3922	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
3923	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
3924	The Potential Effect of <i>Rhizoma coptidis</i> 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
3925	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
3926	Castration delays epigenetic aging and feminizes DNA methylation at androgen-regulated loci. <i>ELife</i> , 2021, 10, .	2.8	45
3927	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
3928	Prognostic significance and oncogene function of cathepsin A in hepatocellular carcinoma. <i>Scientific Reports</i> , 2021, 11, 14611.	1.6	13
3929	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
3930	Haplotype-resolved de novo assembly of the Vero cell line genome. <i>Npj Vaccines</i> , 2021, 6, 106.	2.9	14
3931	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
3932	Genome-Wide Association Study of Growth Performance and Immune Response to Newcastle Disease Virus of Indigenous Chicken in Rwanda. <i>Frontiers in Genetics</i> , 2021, 12, 723980.	1.1	5
3933	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
3934	Altered chromatin states drive cryptic transcription in aging mammalian stem cells. <i>Nature Aging</i> , 2021, 1, 684-697.	5.3	26
3935	Microarray Analysis Revealed Inflammatory Transcriptomic Changes after LSL60101 Treatment in 5XFAD Mice Model. <i>Genes</i> , 2021, 12, 1315.	1.0	1

#	ARTICLE	IF	CITATIONS
3936	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
3937	Prognostic role of DFNA5 in head and neck squamous cell carcinoma revealed by systematic expression analysis. <i>BMC Cancer</i> , 2021, 21, 951.	1.1	10
3938	Heparanase is a novel biomarker for immune infiltration and prognosis in breast cancer. <i>Aging</i> , 2021, 13, 20836-20852.	1.4	9
3939	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
3940	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
3941	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
3942	Bioinformatics analysis of the transcriptional expression of minichromosome maintenance proteins as potential indicators of survival in patients with cervical cancer. <i>BMC Cancer</i> , 2021, 21, 928.	1.1	14
3943	The Alterations and Potential Roles of MCMs in Breast Cancer. <i>Journal of Oncology</i> , 2021, 2021, 1-17.	0.6	11
3944	Attenuation of PIP3 Signaling Cascade Can Inhibit Breast Cancer Progression. <i>Biomolecules</i> , 2021, 11, 1265.	1.8	1
3945	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
3946	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
3947	Potential genes and pathways associated with heterotopic ossification derived from analyses of gene expression profiles. <i>Journal of Orthopaedic Surgery and Research</i> , 2021, 16, 499.	0.9	6
3948	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
3949	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
3950	Modulation of Cellular MicroRNA by HIV-1 in Burkitt Lymphoma Cells—A Pathway to Promoting Oncogenesis. <i>Genes</i> , 2021, 12, 1302.	1.0	5
3951	Integrative Analysis of Gene Expression Data by RNA Sequencing for Differential Diagnosis of Acute Leukemia: Potential Application of Machine Learning. <i>Frontiers in Oncology</i> , 2021, 11, 717616.	1.3	6
3952	Interactome analysis of Bag-1 isoforms reveals novel interaction partners in endoplasmic reticulum-associated degradation. <i>PLoS ONE</i> , 2021, 16, e0256640.	1.1	3
3953	An Integrative Systems Biology Approach Identifies Molecular Signatures Associated with Gallbladder Cancer Pathogenesis. <i>Journal of Clinical Medicine</i> , 2021, 10, 3520.	1.0	3

#	ARTICLE	IF	CITATIONS
3954	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
3955	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
3956	Serum proteomics reveals disorder of lipoprotein metabolism in sepsis. <i>Life Science Alliance</i> , 2021, 4, e202101091.	1.3	4
3957	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
3958	MTF1 Is Essential for the Expression of MT1B, MT1F, MT1G, and MT1H Induced by PHMG, but Not CMIT, in the Human Pulmonary Alveolar Epithelial Cells. <i>Toxics</i> , 2021, 9, 203.	1.6	7
3959	Identification of differentially expressed genes using microarray analysis and COL6A1 induction of bone metastasis in non-small cell lung cancer. <i>Oncology Letters</i> , 2021, 22, 693.	0.8	6
3960	Integrated multi-omics analysis of RB-loss identifies widespread cellular programming and synthetic weaknesses. <i>Communications Biology</i> , 2021, 4, 977.	2.0	1
3961	Global analysis of lysine acetylation in soybean leaves. <i>Scientific Reports</i> , 2021, 11, 17858.	1.6	11
3962	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
3963	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
3964	Integration and gene co-expression network analysis of scRNA-seq transcriptomes reveal heterogeneity and key functional genes in human spermatogenesis. <i>Scientific Reports</i> , 2021, 11, 19089.	1.6	12
3965	Pan-Cancer Analysis of Atrial-Fibrillation-Related Innate Immunity Gene ANXA4. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 713983.	1.1	6
3966	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
3967	Enhanced Directed Random Walk for the Identification of Breast Cancer Prognostic Markers from Multiclass Expression Data. <i>Entropy</i> , 2021, 23, 1232.	1.1	3
3968	Identification of Immune Function-Related Subtypes in Cutaneous Melanoma. <i>Life</i> , 2021, 11, 925.	1.1	2
3969	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
3970	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
3971	Traditional Chinese Medicine (TCM) in the treatment of COVID-19 and other viral infections: Efficacies and mechanisms. , 2021, 225, 107843.		258

#	ARTICLE	IF	CITATIONS
3972	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
3973	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
3974	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
3975	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
3976	Immune Mechanism, Gene Module, and Molecular Subtype Identification of <i>Astragalus Membranaceus</i> 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
3977	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
3978	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
3979	SRSF protein kinase 1 modulates RAN translation and suppresses CGG repeat toxicity. <i>EMBO Molecular Medicine</i> , 2021, 13, e14163.	3.3	17
3980	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
3981	PlantGSAD: a comprehensive gene set annotation database for plant species. <i>Nucleic Acids Research</i> , 2022, 50, D1456-D1467.	6.5	20
3982	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
3983	RNA Profiles of the Korat Chicken Breast Muscle with Increased Carnosine Content Produced through Dietary Supplementation with ^l -Alanine or L-Histidine. <i>Animals</i> , 2021, 11, 2596.	1.0	4
3984	Hepatocyte-Specific Phgdh-Deficient Mice Culminate in Mild Obesity, Insulin Resistance, and Enhanced Vulnerability to Protein Starvation. <i>Nutrients</i> , 2021, 13, 3468.	1.7	6
3985	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
3986	Amyloid beta acts synergistically as a pro-inflammatory cytokine. <i>Neurobiology of Disease</i> , 2021, 159, 105493.	2.1	29
3987	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
3988	Human Pumilio proteins directly bind the CCR4-NOT deadenylase complex to regulate the transcriptome. <i>Rna</i> , 2021, 27, 445-464.	1.6	32
3989	The role of striated muscle Pik3r1 in glucose and protein metabolism following chronic glucocorticoid exposure. <i>Journal of Biological Chemistry</i> , 2021, 296, 100395.	1.6	7

#	ARTICLE	IF	CITATIONS
3990	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
3991	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
3992	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
3993	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
3994	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
3995	Smad3 deficiency promotes beta cell proliferation and function in <i>db/db</i> mice via restoring Pax6 expression. <i>Theranostics</i> , 2021, 11, 2845-2859.	4.6	16
3996	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
3997	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
3998	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
3999	PDX1LOW MAFALOW ⁺ cells contribute to islet function and insulin release. <i>Nature Communications</i> , 2021, 12, 674.	5.8	51
4000	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
4001	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
4002	Transcriptomes of cochlear inner and outer hair cells from adult mice. <i>Scientific Data</i> , 2018, 5, 180199.	2.4	101
4003	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
4004	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
4005	Development of an immune-related prognostic index associated with osteosarcoma. <i>Bioengineered</i> , 2021, 12, 172-182.	1.4	12
4006	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
4013	MINING FUNCTIONALLY RELEVANT GENE SETS FOR ANALYZING PHYSIOLOGICALLY NOVEL CLINICAL EXPRESSION DATA. , 2010, , 50-61.		3

#	ARTICLE	IF	CITATIONS
4014	IFN regulatory factor α 8 expression in macrophages governs an antimetastatic program. JCI Insight, 2019, 4, .	2.3	30
4015	Functional significance of the discordance between transcriptional profile and left ventricular structure/function during reverse remodeling. JCI Insight, 2016, 1, e86038.	2.3	33
4016	Super-enhancers maintain renin-expressing cell identity and memory to preserve multi-system homeostasis. Journal of Clinical Investigation, 2018, 128, 4787-4803.	3.9	41
4017	uPAR isoform 2 forms a dimer and induces severe kidney disease in mice. Journal of Clinical Investigation, 2019, 129, 1946-1959.	3.9	48
4018	Brain somatic mutations in MTOR reveal translational dysregulations underlying intractable focal epilepsy. Journal of Clinical Investigation, 2019, 129, 4207-4223.	3.9	45
4019	Epigenetic driver mutations in ARID1A shape cancer immune phenotype and immunotherapy. Journal of Clinical Investigation, 2020, 130, 2712-2726.	3.9	112
4020	Eotaxin-3 and a uniquely conserved gene-expression profile in eosinophilic esophagitis. Journal of Clinical Investigation, 2006, 116, 536-547.	3.9	750
4021	Calcineurin/Nfat signaling is required for perinatal lung maturation and function. Journal of Clinical Investigation, 2006, 116, 2597-2609.	3.9	43
4022	Activation of MAPK pathways links LMNA mutations to cardiomyopathy in Emery-Dreifuss muscular dystrophy. Journal of Clinical Investigation, 2007, 117, 1282-1293.	3.9	256
4023	Gene expression analysis in pregnant women and their infants identifies unique fetal biomarkers that circulate in maternal blood. Journal of Clinical Investigation, 2007, 117, 3007-3019.	3.9	53
4024	B cell activator PAX5 promotes lymphomagenesis through stimulation of B cell receptor signaling. Journal of Clinical Investigation, 2007, 117, 2602-2610.	3.9	37
4025	Increased local expression of coagulation factor X contributes to the fibrotic response in human and murine lung injury. Journal of Clinical Investigation, 2009, 119, 2550-63.	3.9	251
4026	Global genomic analysis reveals rapid control of a robust innate response in SIV-infected sooty mangabeys. Journal of Clinical Investigation, 2009, 119, 3556-72.	3.9	351
4027	Cardiac fibrosis in mice with hypertrophic cardiomyopathy is mediated by non-myocyte proliferation and requires Tgf- β 2. Journal of Clinical Investigation, 2010, 120, 3520-3529.	3.9	372
4028	A metabolic prosurvival role for PML in breast cancer. Journal of Clinical Investigation, 2012, 122, 3088-3100.	3.9	220
4029	Zinc transporter Slc39a8 is essential for cardiac ventricular compaction. Journal of Clinical Investigation, 2018, 128, 826-833.	3.9	39
4030	Identification of Transcriptional Factors and Key Genes in Primary Osteoporosis by DNA Microarray. Medical Science Monitor, 2015, 21, 1333-1344.	0.5	32
4031	Screening of Target Genes and Regulatory Function of miRNAs as Prognostic Indicators for Prostate Cancer. Medical Science Monitor, 2015, 21, 3748-3759.	0.5	29

#	ARTICLE	IF	CITATIONS
4032	Five miRNAs Considered as Molecular Targets for Predicting Esophageal Cancer. <i>Medical Science Monitor</i> , 2015, 21, 3222-3230.	0.5	21
4033	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
4034	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
4035	Identification of Key Genes in Colorectal Cancer Regulated by miR-34a. <i>Medical Science Monitor</i> , 2017, 23, 5735-5743.	0.5	17
4036	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
4037	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
4038	Identification of Hub Genes and Pathways in Gastric Adenocarcinoma Based on Bioinformatics Analysis. <i>Medical Science Monitor</i> , 2020, 26, e920261.	0.5	18
4039	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
4040	Constellation Map: Downstream visualization and interpretation of gene set enrichment results. <i>F1000Research</i> , 2015, 4, 167.	0.8	3
4041	GOsummaries: an R Package for Visual Functional Annotation of Experimental Data. <i>F1000Research</i> , 2015, 4, 574.	0.8	86
4042	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
4043	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
4044	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
4045	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
4046	Automated deconvolution of structured mixtures from heterogeneous tumor genomic data. <i>PLoS Computational Biology</i> , 2017, 13, e1005815.	1.5	8
4047	Integrating Genetic and Network Analysis to Characterize Genes Related to Mouse Weight. <i>PLoS Genetics</i> , 2005, preprint, e130.	1.5	1
4048	Circadian Clock Genes Contribute to the Regulation of Hair Follicle Cycling. <i>PLoS Genetics</i> , 2009, 5, e1000573.	1.5	146
4049	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

#	ARTICLE	IF	CITATIONS
4050	Robust stratification of breast cancer subtypes using differential patterns of transcript isoform expression. <i>PLoS Genetics</i> , 2017, 13, e1006589.	1.5	53
4051	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
4052	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
4053	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
4054	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
4055	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
4056	Identify Alternative Splicing Events Based on Position-Specific Evolutionary Conservation. <i>PLoS ONE</i> , 2008, 3, e2806.	1.1	24
4057	Preservation of Genes Involved in Sterol Metabolism in Cholesterol Auxotrophs: Facts and Hypotheses. <i>PLoS ONE</i> , 2008, 3, e2883.	1.1	48
4058	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
4059	Transcriptome-Wide Assessment of Human Brain and Lymphocyte Senescence. <i>PLoS ONE</i> , 2008, 3, e3024.	1.1	60
4060	The Evolving Transcriptome of Head and Neck Squamous Cell Carcinoma: A Systematic Review. <i>PLoS ONE</i> , 2008, 3, e3215.	1.1	61
4061	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
4062	Meta-Analysis and Gene Set Enrichment Relative to ER Status Reveal Elevated Activity of MYC and E2F in the "Basal" Breast Cancer Subgroup. <i>PLoS ONE</i> , 2009, 4, e4710.	1.1	88
4063	A Molecular Function Map of Ewing's Sarcoma. <i>PLoS ONE</i> , 2009, 4, e5415.	1.1	158
4064	Detection of Transgenerational Spermatogenic Inheritance of Adult Male Acquired CNS Gene Expression Characteristics Using a <i>Drosophila</i> Systems Model. <i>PLoS ONE</i> , 2009, 4, e5763.	1.1	26
4065	A Genome Scan for Positive Selection in Thoroughbred Horses. <i>PLoS ONE</i> , 2009, 4, e5767.	1.1	123
4066	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
4067	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

#	ARTICLE	IF	CITATIONS
4068	Correlating Global Gene Regulation to Angiogenesis in the Developing Chick Extra-Embryonic Vascular System. PLoS ONE, 2009, 4, e7856.	1.1	56
4069	Gene Expression Profiling during Early Acute Febrile Stage of Dengue Infection Can Predict the Disease Outcome. PLoS ONE, 2009, 4, e7892.	1.1	77
4070	An Epigenetic Signature in Peripheral Blood Predicts Active Ovarian Cancer. PLoS ONE, 2009, 4, e8274.	1.1	291
4071	3â€²-End Sequencing for Expression Quantification (3SEQ) from Archival Tumor Samples. PLoS ONE, 2010, 5, e8768.	1.1	123
4072	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
4073	Lack of nAChR Activity Depresses Cochlear Maturation and Up-Regulates GABA System Components: Temporal Profiling of Gene Expression in $\alpha 9$ Null Mice. PLoS ONE, 2010, 5, e9058.	1.1	19
4074	Gene Expression Profiling and Network Analysis Reveals Lipid and Steroid Metabolism to Be the Most Favored by TNF α in HepG2 Cells. PLoS ONE, 2010, 5, e9063.	1.1	14
4075	In Vitro Fertilization and Embryo Culture Strongly Impact the Placental Transcriptome in the Mouse Model. PLoS ONE, 2010, 5, e9218.	1.1	75
4076	Cardiac Deletion of Smyd2 Is Dispensable for Mouse Heart Development. PLoS ONE, 2010, 5, e9748.	1.1	63
4077	Dissecting Interferon-Induced Transcriptional Programs in Human Peripheral Blood Cells. PLoS ONE, 2010, 5, e9753.	1.1	134
4078	Mutations in CHMP2B in Lower Motor Neuron Predominant Amyotrophic Lateral Sclerosis (ALS). PLoS ONE, 2010, 5, e9872.	1.1	204
4079	A Study of the Influence of Sex on Genome Wide Methylation. PLoS ONE, 2010, 5, e10028.	1.1	217
4080	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
4081	Acetaminophen Modulates the Transcriptional Response to Recombinant Interferon- β . PLoS ONE, 2010, 5, e11031.	1.1	16
4082	A Comparative Analysis of Extra-Embryonic Endoderm Cell Lines. PLoS ONE, 2010, 5, e12016.	1.1	47
4083	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
4084	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
4085	The Proneural Molecular Signature Is Enriched in Oligodendrogliomas and Predicts Improved Survival among Diffuse Gliomas. PLoS ONE, 2010, 5, e12548.	1.1	125

#	ARTICLE	IF	CITATIONS
4086	Identification of Novel p53 Pathway Activating Small-Molecule Compounds Reveals Unexpected Similarities with Known Therapeutic Agents. PLoS ONE, 2010, 5, e12996.	1.1	77
4087	Identification of Genetic and Epigenetic Marks Involved in Population Structure. PLoS ONE, 2010, 5, e13209.	1.1	38
4088	eXtraembryonic ENdoderm (XEN) Stem Cells Produce Factors that Activate Heart Formation. PLoS ONE, 2010, 5, e13446.	1.1	35
4089	A Comparative Analysis of Gene-Expression Data of Multiple Cancer Types. PLoS ONE, 2010, 5, e13696.	1.1	31
4090	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
4091	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
4092	Amplification of the 20q Chromosomal Arm Occurs Early in Tumorigenic Transformation and May Initiate Cancer. PLoS ONE, 2011, 6, e14632.	1.1	69
4093	Analysis of Common and Specific Mechanisms of Liver Function Affected by Nitrotoluene Compounds. PLoS ONE, 2011, 6, e14662.	1.1	33
4094	Global Expression of Cell Surface Proteins in Embryonic Stem Cells. PLoS ONE, 2010, 5, e15795.	1.1	33
4095	A Key Role for Poly(ADP-Ribose) Polymerase 3 in Ectodermal Specification and Neural Crest Development. PLoS ONE, 2011, 6, e15834.	1.1	17
4096	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
4097	A PXR-Mediated Negative Feedback Loop Attenuates the Expression of CYP3A in Response to the PXR Agonist Pregnenalone-16 β -Carbonitrile. PLoS ONE, 2011, 6, e16703.	1.1	24
4098	Characterization of the Contradictory Chromatin Signatures at the 3 α Exons of Zinc Finger Genes. PLoS ONE, 2011, 6, e17121.	1.1	64
4099	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
4100	Do Two Machine-Learning Based Prognostic Signatures for Breast Cancer Capture the Same Biological Processes?. PLoS ONE, 2011, 6, e17795.	1.1	35
4101	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
4102	Microarray Analysis Uncovers a Role for Tip60 in Nervous System Function and General Metabolism. PLoS ONE, 2011, 6, e18412.	1.1	45
4103	A Mighty Small Heart: The Cardiac Proteome of Adult Drosophila melanogaster. PLoS ONE, 2011, 6, e18497.	1.1	81

#	ARTICLE	IF	CITATIONS
4104	Small Molecule Amiloride Modulates Oncogenic RNA Alternative Splicing to Devitalize Human Cancer Cells. PLoS ONE, 2011, 6, e18643.	1.1	53
4105	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
4106	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
4107	Real-Time Monitoring of Cisplatin-Induced Cell Death. PLoS ONE, 2011, 6, e19714.	1.1	88
4108	Methylation Profile of Single Hepatocytes Derived from Hepatitis B Virus-Related Hepatocellular Carcinoma. PLoS ONE, 2011, 6, e19862.	1.1	59
4109	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
4110	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
4111	Deep Sequencing Reveals Novel MicroRNAs and Regulation of MicroRNA Expression during Cell Senescence. PLoS ONE, 2011, 6, e20509.	1.1	73
4112	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
4113	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
4114	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
4115	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
4116	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
4117	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
4118	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
4119	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
4120	Transcriptome Analysis of Epithelial and Stromal Contributions to Mammary Gland Development in Three Week Parturient Cows. PLoS ONE, 2011, 6, e22541.	1.1	15
4121	SEAS: A System for SEED-Based Pathway Enrichment Analysis. PLoS ONE, 2011, 6, e22556.	1.1	8

#	ARTICLE	IF	CITATIONS
4122	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
4123	Modulation of Androgen Receptor Signaling in Hormonal Therapy-Resistant Prostate Cancer Cell Lines. PLoS ONE, 2011, 6, e23144.	1.1	46
4124	Transcriptomic Analysis Brings New Insight into the Biological Role of the Prion Protein during Mouse Embryogenesis. PLoS ONE, 2011, 6, e23253.	1.1	22
4125	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
4126	Disease Gene Interaction Pathways: A Potential Framework for How Disease Genes Associate by Disease-Risk Modules. PLoS ONE, 2011, 6, e24495.	1.1	7
4127	Pattern Specification and Immune Response Transcriptional Signatures of Pericardial and Subcutaneous Adipose Tissue. PLoS ONE, 2011, 6, e26092.	1.1	6
4128	The Leukemia-Specific Fusion Gene ETV6/RUNX1 Perturbs Distinct Key Biological Functions Primarily by Gene Repression. PLoS ONE, 2011, 6, e26348.	1.1	43
4129	Strain-Dependent Host Transcriptional Responses to Toxoplasma Infection Are Largely Conserved in Mammalian and Avian Hosts. PLoS ONE, 2011, 6, e26369.	1.1	20
4130	Differential Expression of Extracellular Matrix-Mediated Pathways in Single-Suture Craniosynostosis. PLoS ONE, 2011, 6, e26557.	1.1	34
4131	Deep Sequencing of MYC DNA-Binding Sites in Burkitt Lymphoma. PLoS ONE, 2011, 6, e26837.	1.1	90
4132	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
4133	TRAF6 and IRF7 Control HIV Replication in Macrophages. PLoS ONE, 2011, 6, e28125.	1.1	41
4134	Comparing Statistical Methods for Constructing Large Scale Gene Networks. PLoS ONE, 2012, 7, e29348.	1.1	156
4135	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
4136	Unraveling the Global microRNAome Responses to Ionizing Radiation in Human Embryonic Stem Cells. PLoS ONE, 2012, 7, e31028.	1.1	30
4137	Functional Complexity of the Axonal Growth Cone: A Proteomic Analysis. PLoS ONE, 2012, 7, e31858.	1.1	48
4138	A Role for Nonsense-Mediated mRNA Decay in Plants: Pathogen Responses Are Induced in Arabidopsis thaliana NMD Mutants. PLoS ONE, 2012, 7, e31917.	1.1	114
4139	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

#	ARTICLE	IF	CITATIONS
4140	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
4141	Systematic Identification of Spontaneous Preterm Birth-Associated RNA Transcripts in Maternal Plasma. PLoS ONE, 2012, 7, e34328.	1.1	43
4142	Involvement of microRNA Lethal-7a in the Regulation of Embryo Implantation in Mice. PLoS ONE, 2012, 7, e37039.	1.1	72
4143	De-Novo Transcriptome Sequencing of a Normalized cDNA Pool from Influenza Infected Ferrets. PLoS ONE, 2012, 7, e37104.	1.1	13
4144	mRNA Expression in Papillary and Anaplastic Thyroid Carcinoma: Molecular Anatomy of a Killing Switch. PLoS ONE, 2012, 7, e37807.	1.1	62
4145	An Interferon-Related Signature in the Transcriptional Core Response of Human Macrophages to Mycobacterium tuberculosis Infection. PLoS ONE, 2012, 7, e38367.	1.1	29
4146	High Accuracy Mutation Detection in Leukemia on a Selected Panel of Cancer Genes. PLoS ONE, 2012, 7, e38463.	1.1	58
4147	γ -H2AX Kinetics as a Novel Approach to High Content Screening for Small Molecule Radiosensitizers. PLoS ONE, 2012, 7, e38465.	1.1	24
4148	Effect of Irradiation on Cell Transcriptome and Proteome of Rat Submandibular Salivary Glands. PLoS ONE, 2012, 7, e40636.	1.1	8
4149	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
4150	Expression Changes in the Stroma of Prostate Cancer Predict Subsequent Relapse. PLoS ONE, 2012, 7, e41371.	1.1	38
4151	Mig-6 Plays a Critical Role in the Regulation of Cholesterol Homeostasis and Bile Acid Synthesis. PLoS ONE, 2012, 7, e42915.	1.1	24
4152	Identification of Thalidomide-Specific Transcriptomics and Proteomics Signatures during Differentiation of Human Embryonic Stem Cells. PLoS ONE, 2012, 7, e44228.	1.1	83
4153	Differential Gene and MicroRNA Expression between Etoposide Resistant and Etoposide Sensitive MCF7 Breast Cancer Cell Lines. PLoS ONE, 2012, 7, e45268.	1.1	27
4154	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
4155	Genome-Wide Scan for Bats and Dolphin to Detect Their Genetic Basis for New Locomotive Styles. PLoS ONE, 2012, 7, e46455.	1.1	6
4156	Integrative Analysis Reveals Relationships of Genetic and Epigenetic Alterations in Osteosarcoma. PLoS ONE, 2012, 7, e48262.	1.1	87
4157	Prediction of C. elegans Longevity Genes by Human and Worm Longevity Networks. PLoS ONE, 2012, 7, e48282.	1.1	49

#	ARTICLE	IF	CITATIONS
4158	Nuclear RNA Sequencing of the Mouse Erythroid Cell Transcriptome. PLoS ONE, 2012, 7, e49274.	1.1	35
4159	The Molecular Profiles of Neural Stem Cell Niche in the Adult Subventricular Zone. PLoS ONE, 2012, 7, e50501.	1.1	63
4160	Ablation of the Cardiac-Specific Gene Leucine-Rich Repeat Containing 10 (Lrrc10) Results in Dilated Cardiomyopathy. PLoS ONE, 2012, 7, e51621.	1.1	37
4161	Pathway Correlation Profile of Gene-Gene Co-Expression for Identifying Pathway Perturbation. PLoS ONE, 2012, 7, e52127.	1.1	16
4162	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
4163	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
4164	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
4165	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
4166	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
4167	N-Glycoproteome of E14.Tg2a Mouse Embryonic Stem Cells. PLoS ONE, 2013, 8, e55722.	1.1	18
4168	Transcriptomic Profiling of Human Peritumoral Neocortex Tissues Revealed Genes Possibly Involved in Tumor-Induced Epilepsy. PLoS ONE, 2013, 8, e56077.	1.1	20
4169	Differential Effects of Drug Interventions and Dietary Lifestyle in Developing Type 2 Diabetes and Complications: A Systems Biology Analysis in LDLR ^{-/-} Mice. PLoS ONE, 2013, 8, e56122.	1.1	18
4170	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
4171	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
4172	Gene Expression Profile Analysis of Type 2 Diabetic Mouse Liver. PLoS ONE, 2013, 8, e57766.	1.1	37
4173	Discovery of Cellular Proteins Required for the Early Steps of HCV Infection Using Integrative Genomics. PLoS ONE, 2013, 8, e60333.	1.1	17
4174	miRNA Biogenesis Enzyme Drosha Is Required for Vascular Smooth Muscle Cell Survival. PLoS ONE, 2013, 8, e60888.	1.1	31
4175	A Multi-Platform Draft de novo Genome Assembly and Comparative Analysis for the Scarlet Macaw (<i>Ara macao</i>). PLoS ONE, 2013, 8, e62415.	1.1	51

#	ARTICLE	IF	CITATIONS
4176	Textrousl!: Extracting Semantic Textual Meaning from Gene Sets. PLoS ONE, 2013, 8, e62665.	1.1	23
4177	Differential Distribution of the Ca (2+) Regulator Pcp4 in the Branchial Arches Is Regulated by Hoxa2. PLoS ONE, 2013, 8, e63160.	1.1	2
4178	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
4179	Gene Expression Profiles of Metabolic Aggressiveness and Tumor Recurrence in Benign Meningioma. PLoS ONE, 2013, 8, e67291.	1.1	28
4180	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
4181	Candidate Transcriptomic Sources of Inbreeding Depression in Drosophila melanogaster. PLoS ONE, 2013, 8, e70067.	1.1	5
4182	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
4183	Functional Genomic Analyses of Two Morphologically Distinct Classes of Drosophila Sensory Neurons: Post-Mitotic Roles of Transcription Factors in Dendritic Patterning. PLoS ONE, 2013, 8, e72434.	1.1	69
4184	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
4185	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
4186	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
4187	Extension of Life Span by Impaired Glucose Metabolism in Caenorhabditis elegans Is Accompanied by Structural Rearrangements of the Transcriptomic Network. PLoS ONE, 2013, 8, e77776.	1.1	18
4188	Proteomic Changes during B Cell Maturation: 2D-DIGE Approach. PLoS ONE, 2013, 8, e77894.	1.1	7
4189	Mechanistic Phenotypes: An Aggregative Phenotyping Strategy to Identify Disease Mechanisms Using CWAS Data. PLoS ONE, 2013, 8, e81503.	1.1	15
4190	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
4191	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
4192	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
4193	Regulation of Drosophila Eye Development by the Transcription Factor Sine oculis. PLoS ONE, 2014, 9, e89695.	1.1	29

#	ARTICLE	IF	CITATIONS
4194	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
4195	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
4196	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
4197	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
4198	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
4199	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
4200	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
4201	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
4202	Whole Proteome Analysis of Mouse Lymph Nodes in Cutaneous Anthrax. PLoS ONE, 2014, 9, e110873.	1.1	10
4203	Comparative Transcriptome Analysis Reveals Early Pregnancy-Specific Genes Expressed in Peripheral Blood of Pregnant Sows. PLoS ONE, 2014, 9, e114036.	1.1	19
4204	Natural Variation in Fish Transcriptomes: Comparative Analysis of the Fathead Minnow (Pimephales) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.1	14
4205	Hepatic Farnesoid X-Receptor Isoforms $\hat{\pm}2$ and $\hat{\pm}4$ Differentially Modulate Bile Salt and Lipoprotein Metabolism in Mice. PLoS ONE, 2014, 9, e115028.	1.1	30
4206	Synergistic and Antagonistic Interplay between Myostatin Gene Expression and Physical Activity Levels on Gene Expression Patterns in Triceps Brachii Muscles of C57/BL6 Mice. PLoS ONE, 2015, 10, e0116828.	1.1	10
4207	CD14 and Complement Crosstalk and Largely Mediate the Transcriptional Response to Escherichia coli in Human Whole Blood as Revealed by DNA Microarray. PLoS ONE, 2015, 10, e0117261.	1.1	16
4208	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
4209	Exploring the Genetic Signature of Body Size in Yucatan Miniature Pig. PLoS ONE, 2015, 10, e0121732.	1.1	38
4210	Effective Population Size, Extended Linkage Disequilibrium and Signatures of Selection in the Rare Dog Breed Lundehund. PLoS ONE, 2015, 10, e0122680.	1.1	21
4211	The Transcriptome Signature of the Receptive Bovine Uterus Determined at Early Gestation. PLoS ONE, 2015, 10, e0122874.	1.1	35

#	ARTICLE	IF	CITATIONS
4212	Comprehensive Analysis of Glycolytic Enzymes as Therapeutic Targets in the Treatment of Glioblastoma. PLoS ONE, 2015, 10, e0123544.	1.1	101
4213	Adaptation of a Bioinformatics Microarray Analysis Workflow for a Toxicogenomic Study in Rainbow Trout. PLoS ONE, 2015, 10, e0128598.	1.1	5
4214	Lung Transcriptomics during Protective Ventilatory Support in Sepsis-Induced Acute Lung Injury. PLoS ONE, 2015, 10, e0132296.	1.1	20
4215	Mechanism of Cisplatin-Induced Cytotoxicity Is Correlated to Impaired Metabolism Due to Mitochondrial ROS Generation. PLoS ONE, 2015, 10, e0135083.	1.1	210
4216	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
4217	Kinase Identification with Supervised Laplacian Regularized Least Squares. PLoS ONE, 2015, 10, e0139676.	1.1	5
4218	Kelch Domain of Gigaxonin Interacts with Intermediate Filament Proteins Affected in Giant Axonal Neuropathy. PLoS ONE, 2015, 10, e0140157.	1.1	24
4219	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
4220	From System-Wide Differential Gene Expression to Perturbed Regulatory Factors: A Combinatorial Approach. PLoS ONE, 2015, 10, e0142147.	1.1	2
4221	CardioGenBase: A Literature Based Multi-Omics Database for Major Cardiovascular Diseases. PLoS ONE, 2015, 10, e0143188.	1.1	23
4222	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
4223	Meta-Analysis of Transcriptional Responses to Mastitis-Causing <i>Escherichia coli</i> . PLoS ONE, 2016, 11, e0148562.	1.1	21
4224	Meta-Analysis of Tumor Stem-Like Breast Cancer Cells Using Gene Set and Network Analysis. PLoS ONE, 2016, 11, e0148818.	1.1	15
4225	Experimental Neuromyelitis Optica Induces a Type I Interferon Signature in the Spinal Cord. PLoS ONE, 2016, 11, e0151244.	1.1	15
4226	Efficient Record Linkage Algorithms Using Complete Linkage Clustering. PLoS ONE, 2016, 11, e0154446.	1.1	20
4227	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
4228	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
4229	IGSA: Individual Gene Sets Analysis, including Enrichment and Clustering. PLoS ONE, 2016, 11, e0164542.	1.1	3

#	ARTICLE	IF	CITATIONS
4230	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
4231	Genome-Wide Detection of Selective Signatures in Chicken through High Density SNPs. PLoS ONE, 2016, 11, e0166146.	1.1	8
4232	Drosophila Genotype Influences Commensal Bacterial Levels. PLoS ONE, 2017, 12, e0170332.	1.1	42
4233	Microarray analysis of embryo-derived bovine pluripotent cells: The vulnerable state of bovine embryonic stem cells. PLoS ONE, 2017, 12, e0173278.	1.1	6
4234	Comparative analysis of genes frequently regulated by drugs based on connectivity map transcriptome data. PLoS ONE, 2017, 12, e0179037.	1.1	11
4235	Titanium biomaterials with complex surfaces induced aberrant peripheral circadian rhythms in bone marrow mesenchymal stromal cells. PLoS ONE, 2017, 12, e0183359.	1.1	18
4236	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
4237	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
4238	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
4239	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
4240	Global gene network exploration based on explainable artificial intelligence approach. PLoS ONE, 2020, 15, e0241508.	1.1	6
4241	The role of the MAD2-TLR4-MyD88 axis in paclitaxel resistance in ovarian cancer. PLoS ONE, 2020, 15, e0243715.	1.1	7
4242	Vectors as Epidemiological Sentinels: Patterns of Within-Tick Borrelia burgdorferi Diversity. PLoS Pathogens, 2016, 12, e1005759.	2.1	28
4243	Dynamic metabolic reprogramming in dendritic cells: An early response to influenza infection that is essential for effector function. PLoS Pathogens, 2020, 16, e1008957.	2.1	13
4244	Meta-analysis of 12 genomic studies in bipolar disorder. Journal of Molecular Neuroscience, 2007, 31, 221-243.	1.1	69
4245	Gene Expression Studies for the Development of Particle Therapy. International Journal of Particle Therapy, 2018, 5, 49-59.	0.9	4
4246	Detecting Positive Selection of Korean Native Goat Populations Using Next-Generation Sequencing. Molecules and Cells, 2016, 39, 862-868.	1.0	13
4247	Key pathways in prostate cancer with SPOP mutation identified by bioinformatic analysis. Open Medicine (Poland), 2020, 15, 1039-1047.	0.6	2

#	ARTICLE	IF	CITATIONS
4248	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
4249	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
4250	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
4251	MicroRNA expression analysis in endometriotic serum treated mesenchymal stem cells. <i>EXCLI Journal</i> , 2017, 16, 852-867.	0.5	6
4252	PPAR β : 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
4253	Molecular links between cellular senescence, longevity and age-related diseases – a systems biology perspective. <i>Aging</i> , 2011, 3, 1178-1191.	1.4	119
4254	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
4255	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
4256	Sirtuin 3 attenuates amyloid- β induced neuronal hypometabolism. <i>Aging</i> , 2018, 10, 2874-2883.	1.4	19
4257	ERK1 indicates good prognosis and inhibits breast cancer progression by suppressing YAP1 signaling. <i>Aging</i> , 2019, 11, 12295-12314.	1.4	16
4258	SLC7A2 serves as a potential biomarker and therapeutic target for ovarian cancer. <i>Aging</i> , 2020, 12, 13281-13296.	1.4	16
4259	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
4260	HMGA1 promotes metastatic processes in basal-like breast cancer regulating EMT and stemness. <i>Oncotarget</i> , 2013, 4, 1293-1308.	0.8	145
4261	Blood RNA expression profiles undergo major changes during the seventh decade. <i>Oncotarget</i> , 2016, 7, 71353-71361.	0.8	1
4262	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
4263	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
4264	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
4265	Systemically identifying and prioritizing risk lncRNAs through integration of pan-cancer phenotype associations. <i>Oncotarget</i> , 2017, 8, 12041-12051.	0.8	12

#	ARTICLE	IF	CITATIONS
4266	Genome-scale analysis identifies GJB2 and ERO1LB as prognosis markers in patients with pancreatic cancer. <i>Oncotarget</i> , 2017, 8, 21281-21289.	0.8	49
4267	iTRAQ-based quantitative proteomic analysis of Yamanaka factors reprogrammed breast cancer cells. <i>Oncotarget</i> , 2017, 8, 34330-34339.	0.8	7
4268	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
4269	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
4270	Autophagy-related gene expression is an independent prognostic indicator of glioma. <i>Oncotarget</i> , 2017, 8, 60987-61000.	0.8	28
4271	Integrative analysis of novel hypomethylation and gene expression signatures in glioblastomas. <i>Oncotarget</i> , 2017, 8, 89607-89619.	0.8	19
4272	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
4273	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
4274	Somatic intronic microsatellite loci differentiate glioblastoma from lower-grade gliomas. <i>Oncotarget</i> , 2014, 5, 6003-6014.	0.8	11
4275	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
4276	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
4277	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
4278	IsomiR expression profiles in human lymphoblastoid cell lines exhibit population and gender dependencies. <i>Oncotarget</i> , 2014, 5, 8790-8802.	0.8	103
4279	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
4280	Somatic mutations in early onset luminal breast cancer. <i>Oncotarget</i> , 2018, 9, 22460-22479.	0.8	25
4281	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
4282	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
4283	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

#	ARTICLE	IF	CITATIONS
4284	Virus-encoded microRNA contributes to the molecular profile of EBV-positive Burkitt lymphomas. <i>Oncotarget</i> , 2016, 7, 224-240.	0.8	33
4285	Time-course gene profiling and networks in demethylated retinoblastoma cell line. <i>Oncotarget</i> , 2015, 6, 23688-23707.	0.8	6
4286	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
4287	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
4288	MicroRNA-708-5p acts as a therapeutic agent against metastatic lung cancer. <i>Oncotarget</i> , 2016, 7, 2417-2432.	0.8	50
4289	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
4290	Cinacalcet inhibits neuroblastoma tumor growth and upregulates cancer-testis antigens. <i>Oncotarget</i> , 2016, 7, 16112-16129.	0.8	19
4291	Age-related changes in the transcriptome of antibody-secreting cells. <i>Oncotarget</i> , 2016, 7, 13340-13353.	0.8	20
4292	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
4293	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
4294	Differential Network Analysis in Human Cancer Research. <i>Current Pharmaceutical Design</i> , 2014, 20, 4-10.	0.9	16
4295	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
4296	Alternatively Spliced Genes as Biomarkers for Schizophrenia, Bipolar Disorder and Psychosis: A Blood-Based Spliceome-Profiling Exploratory Study (Supplementary Table). <i>Current Pharmacogenomics and Personalized Medicine</i> , 2009, 7, 164-188.	0.2	44
4297	Methylated MicroRNA Genes of the Developing Murine Palate. <i>MicroRNA (Shariqah, United Arab) Tj ETQq1 1 0.784314 rgBT /Overlock</i>	0.6	14
4298	Rapid Multiplexed Reduced Representation Bisulfite Sequencing Library Prep (rRRBS). <i>Bio-protocol</i> , 2019, 9, e3171.	0.2	6
4299	Adoption of Clinical Decision Support in Multimorbidity: A Systematic Review. <i>JMIR Medical Informatics</i> , 2015, 3, e4.	1.3	85
4300	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
4301	Manganese Depletion Leads to Multisystem Changes in the Transcriptome of the Opportunistic Pathogen <i>Streptococcus sanguinis</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 592615.	1.5	12

#	ARTICLE	IF	CITATIONS
4302	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
4303	The Effect of 3- ² -Hydroxy-3,4,5,4- ² -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
4304	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
4305	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
4306	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
4307	Transformation of Mature Osteoblasts into Bone Lining Cells and RNA Sequencing-Based Transcriptome Profiling of Mouse Bone during Mechanical Unloading. <i>Endocrinology and Metabolism</i> , 2020, 35, 456-469.	1.3	11
4308	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
4309	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
4310	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
4311	MicroRNA-34a expression in the plasma and in its extracellular vesicle fractions in subjects with Parkinson's disease: An exploratory study. <i>International Journal of Molecular Medicine</i> , 2020, 47, 533-546.	1.8	49
4312	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
4313	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
4314	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
4315	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
4316	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
4317	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
4318	Overexpression of miR-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
4319	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

#	ARTICLE	IF	CITATIONS
4320	Identification of a long non-coding RNA signature for predicting prognosis and biomarkers in lung adenocarcinoma. <i>Oncology Letters</i> , 2020, 19, 2793-2800.	0.8	9
4321	Chemoresistance-associated alternative splicing signatures in serous ovarian cancer. <i>Oncology Letters</i> , 2020, 20, 420-430.	0.8	8
4322	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
4323	Investigation of the association between C&X&C motif chemokine receptor subunits and tumor infiltration levels and prognosis in patients with early-stage pancreatic ductal adenocarcinoma. <i>Oncology Letters</i> , 2020, 20, 16.	0.8	5
4324	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
4325	Comprehensive analysis of the lncRNA-associated competing endogenous RNA network in breast cancer. <i>Oncology Reports</i> , 2019, 42, 2572-2582.	1.2	27
4326	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</i> , Beijing Institute for Cancer Research, 2013, 25, 623-36.	0.7	10
4327	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
4328	MicroRNA alterations in Barrett'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
4329	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
4330	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
4331	MicroRNA regulatory pattern in spinal cord ischemia-reperfusion injury. <i>Neural Regeneration Research</i> , 2020, 15, 2123.	1.6	21
4332	A Proteomic Study of Human Merkel Cell Carcinoma. <i>Journal of Proteomics and Bioinformatics</i> , 2013, 06, 275-282.	0.4	23
4333	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
4334	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
4335	Microarray Analysis of Gene Expression in the Uterine Endometrium during the Implantation Period in Pigs. <i>Asian-Australasian Journal of Animal Sciences</i> , 2012, 25, 1102-1116.	2.4	20
4336	Copy Number Deletion Has Little Impact on Gene Expression Levels in Racehorses. <i>Asian-Australasian Journal of Animal Sciences</i> , 2014, 27, 1345-1354.	2.4	5
4337	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

#	ARTICLE	IF	CITATIONS
4338	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
4339	Integrative analysis of the mouse embryonic transcriptome. <i>Bioinformatics</i> , 2007, 1, 406-413.	0.2	8
4340	DAVID gene ID conversion tool. <i>Bioinformatics</i> , 2008, 2, 428-430.	0.2	156
4341	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
4342	Genes2GO: A web application for querying gene sets for specific GO terms. <i>Bioinformatics</i> , 2016, 12, 231-232.	0.2	4
4343	NOVA-dependent regulation of cryptic NMD exons controls synaptic protein levels after seizure. <i>ELife</i> , 2013, 2, e00178.	2.8	92
4344	Integrative genomic analysis of the human immune response to influenza vaccination. <i>ELife</i> , 2013, 2, e00299.	2.8	126
4345	A component of the mir-17-92 polycistronic oncomir promotes oncogene-dependent apoptosis. <i>ELife</i> , 2013, 2, e00822.	2.8	75
4346	The translational landscape of the splicing factor SRSF1 and its role in mitosis. <i>ELife</i> , 2014, 3, e02028.	2.8	96
4347	Lhx1 maintains synchrony among circadian oscillator neurons of the SCN. <i>ELife</i> , 2014, 3, e03357.	2.8	68
4348	Genome-wide errant targeting by Hairy. <i>ELife</i> , 2015, 4, .	2.8	13
4349	Control of immune ligands by members of a cytomegalovirus gene expansion suppresses natural killer cell activation. <i>ELife</i> , 2017, 6, .	2.8	67
4350	Resolving stem and progenitor cells in the adult mouse incisor through gene co-expression analysis. <i>ELife</i> , 2017, 6, .	2.8	44
4351	Inhibiting the integrated stress response pathway prevents aberrant chondrocyte differentiation thereby alleviating chondrodysplasia. <i>ELife</i> , 2018, 7, .	2.8	59
4352	A new experimental platform facilitates assessment of the transcriptional and chromatin landscapes of aging yeast. <i>ELife</i> , 2018, 7, .	2.8	56
4353	Glucose intake hampers PKA-regulated HSP90 chaperone activity. <i>ELife</i> , 2018, 7, .	2.8	16
4354	Epigenetic silencing of a multifunctional plant stress regulator. <i>ELife</i> , 2019, 8, .	2.8	28
4355	Functional heterogeneity of lymphocytic patterns in primary melanoma dissected through single-cell multiplexing. <i>ELife</i> , 2020, 9, .	2.8	44

#	ARTICLE	IF	CITATIONS
4356	A cross-kingdom conserved ER-phagy receptor maintains endoplasmic reticulum homeostasis during stress. <i>ELife</i> , 2020, 9, .	2.8	139
4357	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
4358	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
4359	miR-21 is upregulated, promoting fibrosis and blocking G2/M in irradiated rat cardiac fibroblasts. <i>PeerJ</i> , 2020, 8, e10502.	0.9	7
4360	Chromosomal rearrangements and protein globularity changes in <i>Mycobacterium tuberculosis</i> isolates from cerebrospinal fluid. <i>PeerJ</i> , 2016, 4, e2484.	0.9	5
4361	Identification of four potential predicting miRNA biomarkers for multiple myeloma from published datasets. <i>PeerJ</i> , 2017, 5, e2831.	0.9	11
4362	Genome methylation and regulatory functions for hypoxic adaptation in Tibetan chicken embryos. <i>PeerJ</i> , 2017, 5, e3891.	0.9	17
4363	Modulation of transcriptional activity in brain lower grade glioma by alternative splicing. <i>PeerJ</i> , 2018, 6, e4686.	0.9	6
4364	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
4365	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
4366	Identification of differentially expressed key genes between glioblastoma and low-grade glioma by bioinformatics analysis. <i>PeerJ</i> , 2019, 7, e6560.	0.9	16
4367	Characterization of bidirectional gene pairs in The Cancer Genome Atlas (TCGA) dataset. <i>PeerJ</i> , 2019, 7, e7107.	0.9	8
4368	Identification of significant gene and pathways involved in HBV-related hepatocellular carcinoma by bioinformatics analysis. <i>PeerJ</i> , 2019, 7, e7408.	0.9	64
4369	Identification of potential biomarkers and pivotal biological pathways for prostate cancer using bioinformatics analysis methods. <i>PeerJ</i> , 2019, 7, e7872.	0.9	35
4370	Identification of key genes and multiple molecular pathways of metastatic process in prostate cancer. <i>PeerJ</i> , 2019, 7, e7899.	0.9	12
4371	Significance of TP53 mutation in bladder cancer disease progression and drug selection. <i>PeerJ</i> , 2019, 7, e8261.	0.9	30
4372	A transcriptional co-expression network-based approach to identify prognostic biomarkers in gastric carcinoma. <i>PeerJ</i> , 2020, 8, e8504.	0.9	6
4373	Weighted gene correlation network analysis reveals novel biomarkers associated with mesenchymal stromal cell differentiation in early phase. <i>PeerJ</i> , 2020, 8, e8907.	0.9	10

#	ARTICLE	IF	CITATIONS
4374	miR-224, miR-147b and miR-31 associated with lymph node metastasis and prognosis for lung adenocarcinoma by regulating PRPF4B, WDR82 or NR3C2. <i>PeerJ</i> , 2020, 8, e9704.	0.9	12
4375	Identification of aberrantly methylated-differentially expressed genes and potential agents for Ewing sarcoma. <i>Annals of Translational Medicine</i> , 2021, 9, 1557-1557.	0.7	0
4376	The Evolution of Clinically Aggressive Triple-Negative Breast Cancer Shows a Large Mutational Diversity and Early Metastasis to Lymph Nodes. <i>Cancers</i> , 2021, 13, 5091.	1.7	4
4377	Maternal High-Fat Diet Disturbs the DNA Methylation Profile in the Brown Adipose Tissue of Offspring Mice. <i>Frontiers in Endocrinology</i> , 2021, 12, 705827.	1.5	9
4378	Brain Cancer Prediction Based on Novel Interpretable Ensemble Gene Selection Algorithm and Classifier. <i>Diagnostics</i> , 2021, 11, 1936.	1.3	4
4379	Extracellular calcium alters calcium-sensing receptor network integrating intracellular calcium-signaling and related key pathway. <i>Scientific Reports</i> , 2021, 11, 20576.	1.6	8
4380	Identification and Characterization of Downy Mildew-Responsive microRNAs in Indian <i>Vitis vinifera</i> by High-Throughput Sequencing. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 899.	1.5	1
4381	Metabolic Analysis of Potential Key Genes Associated with Systemic Lupus Erythematosus Using Liquid Chromatography-Mass Spectrometry. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 1-17.	0.7	2
4382	An In-Silico, In-Vitro and In-Vivo Combined Approach to Identify NMNATs as Potential Protein Targets of ProEGCG for Treatment of Endometriosis. <i>Frontiers in Pharmacology</i> , 2021, 12, 714790.	1.6	4
4383	GNG7 and ADCY1 as diagnostic and prognostic biomarkers for pancreatic adenocarcinoma through bioinformatic-based analyses. <i>Scientific Reports</i> , 2021, 11, 20441.	1.6	10
4384	CD20 positive CD8 T cells are a unique and transcriptionally-distinct subset of T cells with distinct transmigration properties. <i>Scientific Reports</i> , 2021, 11, 20499.	1.6	11
4385	Peripheral Blood-Based Gene Expression Studies in Schizophrenia: A Systematic Review. <i>Frontiers in Genetics</i> , 2021, 12, 736483.	1.1	13
4386	Integrative Systems Biology Analysis Elucidates Mastitis Disease Underlying Functional Modules in Dairy Cattle. <i>Frontiers in Genetics</i> , 2021, 12, 712306.	1.1	18
4387	Exploration of alcohol use disorder-associated brain miRNA-mRNA regulatory networks. <i>Translational Psychiatry</i> , 2021, 11, 504.	2.4	23
4388	Qualitative lysine crotonylome analysis in the ovarian tissue of <i>Harmonia axyridis</i> (Pallas). <i>PLoS ONE</i> , 2021, 16, e0258371.	1.1	0
4389	Integrated bioinformatics analyses of key genes involved in hepatocellular carcinoma immunosuppression. <i>Oncology Letters</i> , 2021, 22, 830.	0.8	10
4390	Unbiased gene expression analysis implicates the huntingtin polyglutamine tract in extra-mitochondrial energy metabolism. <i>PLoS Genetics</i> , 2005, preprint, e135.	1.5	0
4391	Semantic Modeling for SNPs Associated with Ethnic Disparities in HapMap Samples. <i>Genomics and Informatics</i> , 2014, 12, 35.	0.4	0

#	ARTICLE	IF	CITATIONS
4395	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
4397	Exploring the Molecular Mechanism of Thoracic Aortic Aneurysm via Bioinformatics Analysis. <i>Medical Science Monitor</i> , 2018, 24, 1533-1539.	0.5	1
4400	Biomarker identification of thyroid associated ophthalmopathy using microarray data. <i>International Journal of Ophthalmology</i> , 2018, 11, 1482-1488.	0.5	5
4408	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
4409	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
4411	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
4412	Integrated transcriptomic and epigenetic data analysis identifies aberrant expression of genes in acute myeloid leukemia with MLL'AF9 translocation. <i>Molecular Medicine Reports</i> , 2020, 21, 883-893.	1.1	1
4413	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
4416	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
4418	Development of a novel prognostic signature for predicting the overall survival of bladder cancer patients. <i>Bioscience Reports</i> , 2020, 40, .	1.1	3
4419	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
4420	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
4421	G9a/GLP-sensitivity of H3K9me2 Demarcates Two Types of Genomic Compartments. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 359-370.	3.0	4
4422	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
4423	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
4424	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
4425	MiR-181a Targets RSPO2 and Regulates Bone Morphogenetic Protein ' WNT Signaling Crosstalk During Chondrogenic Differentiation of Mesenchymal Stromal Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 747057.	1.8	5
4426	Tet1 Regulates Astrocyte Development and Cognition of Mice Through Modulating GluA1. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 644375.	1.8	4

#	ARTICLE	IF	CITATIONS
4427	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
4428	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
4429	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
4430	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
4431	An organoid-based screen for epigenetic inhibitors that stimulate antigen presentation and potentiate T-cell-mediated cytotoxicity. <i>Nature Biomedical Engineering</i> , 2021, 5, 1320-1335.	11.6	49
4432	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
4433	Identifying Biomarkers to Predict the Progression and Prognosis of Breast Cancer by Weighted Gene Co-expression Network Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 597888.	1.1	6
4436	Human Gene Functional Network-Informed Prediction of HIV-1 Host Dependency Factors. <i>MSystems</i> , 2020, 5, .	1.7	4
4437	Rapid evolution of expression levels in hepatocellular carcinoma. <i>International Journal of Computational Biology and Drug Design</i> , 2020, 13, 454.	0.3	0
4438	HAHmiR.DB: a server platform for high-altitude human miRNA-gene coregulatory networks and associated regulatory circuits. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, .	1.4	5
4439	Circulating MicroRNA Expression Profiles in Patients with Stable and Unstable Angina. <i>Clinics</i> , 2020, 75, e1546.	0.6	4
4442	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
4443	Bioinformatics analysis identifies DYNC111 as prognosis marker in male patients with liver hepatocellular carcinoma. <i>PLoS ONE</i> , 2021, 16, e0258797.	1.1	7
4444	Advances in the application of Let-7 microRNAs in the diagnosis, treatment and prognosis of leukemia (Review). <i>Oncology Letters</i> , 2021, 23, 1.	0.8	15
4445	Analysis of Differentially Expressed Genes That Aggravate Metabolic Diseases in Depression. <i>Life</i> , 2021, 11, 1203.	1.1	1
4446	Comparative methylation and RNA-seq expression analysis in CpG context to identify genes involved in Backfat vs. Liver diversification in Nanchukmacdon Pig. <i>BMC Genomics</i> , 2021, 22, 801.	1.2	4
4447	A gene toolbox for monitoring autophagy transcription. <i>Cell Death and Disease</i> , 2021, 12, 1044.	2.7	46
4448	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

#	ARTICLE	IF	CITATIONS
4451	Discovering biological guilds through topological abstraction. AMIA ... Annual Symposium proceedings, 2006, , 1-5.	0.2	4
4452	Public databases and software for the pathway analysis of cancer genomes. <i>Cancer Informatics</i> , 2007, 3, 379-97.	0.9	6
4453	Time course profiling of the retinal transcriptome after optic nerve transection and optic nerve crush. <i>Molecular Vision</i> , 2008, 14, 1050-63.	1.1	74
4454	Differential expression of anti-angiogenic factors and guidance genes in the developing macula. <i>Molecular Vision</i> , 2009, 15, 45-59.	1.1	48
4455	Data perturbation independent diagnosis and validation of breast cancer subtypes using clustering and patterns. <i>Cancer Informatics</i> , 2007, 2, 243-74.	0.9	9
4456	Bioinformatics resources for cancer research with an emphasis on gene function and structure prediction tools. <i>Cancer Informatics</i> , 2007, 2, 25-35.	0.9	8
4457	Identification and characterization of renal cell carcinoma gene markers. <i>Cancer Informatics</i> , 2007, 3, 65-92.	0.9	24
4458	Characterization of human septic sera induced gene expression modulation in human myocytes. <i>International Journal of Clinical and Experimental Medicine</i> , 2009, 2, 131-48.	1.3	7
4459	Identification of discriminating biomarkers for human disease using integrative network biology. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2009, , 27-38.	0.7	26
4460	Global gene expression profiling of ischemic preconditioning in the rat retina. <i>Molecular Vision</i> , 2007, 13, 1020-30.	1.1	29
4461	GSMA: Gene Set Matrix Analysis, An Automated Method for Rapid Hypothesis Testing of Gene Expression Data. <i>Bioinformatics and Biology Insights</i> , 2009, 1, 49-62.	1.0	5
4463	Temporal ChIP-on-Chip of RNA-Polymerase-II to detect novel gene activation events during photoreceptor maturation. <i>Molecular Vision</i> , 2010, 16, 252-71.	1.1	21
4466	Genomic profiling of genes contributing to metastasis in a mouse model of thyroid follicular carcinoma. <i>American Journal of Cancer Research</i> , 2011, 1, 1-13.	1.4	5
4467	Expression profiling and pathway analysis of KrÄppel-like factor 4 in mouse embryonic fibroblasts. <i>American Journal of Cancer Research</i> , 2011, 1, 85-97.	1.4	9
4468	Using blood gene signatures for assessing effects of exposure to perfluoroalkyl acids (PFAAs) in humans: the NOWAC postgenome study. <i>International Journal of Molecular Epidemiology and Genetics</i> , 2011, 2, 207-16.	0.4	5
4470	The Profile of Human Sperm Proteome; A Mini-review. <i>Journal of Reproduction and Infertility</i> , 2011, 12, 193-9.	1.0	12
4471	Enhanced expression of SOS1 is detected in prostate cancer epithelial cells from African-American men. <i>International Journal of Oncology</i> , 2009, 35, 751-60.	3.9	38
4473	In silico functional profiling of individual prostate cancer tumors: many genes, few functions. <i>Cancer Genomics and Proteomics</i> , 2012, 9, 109-14.	1.0	2

#	ARTICLE	IF	CITATIONS
4474	Generation of a foveomacular transcriptome. <i>Molecular Vision</i> , 2014, 20, 947-54.	1.1	0
4476	Analysis of endoscopic pancreatic function test (ePFT)-collected pancreatic fluid proteins precipitated via ultracentrifugation. <i>JOP: Journal of the Pancreas</i> , 2013, 14, 176-86.	1.5	4
4477	Gene function analysis in osteosarcoma based on microarray gene expression profiling. <i>International Journal of Clinical and Experimental Medicine</i> , 2015, 8, 10401-10.	1.3	13
4478	Screening feature genes of lung carcinoma with DNA microarray analysis. <i>International Journal of Clinical and Experimental Medicine</i> , 2015, 8, 12161-71.	1.3	21
4479	Differential network analysis reveals dysfunctional regulatory networks in gastric carcinogenesis. <i>American Journal of Cancer Research</i> , 2015, 5, 2605-25.	1.4	8
4480	miRNA signature identification of retinoblastoma and the correlations between differentially expressed miRNAs during retinoblastoma progression. <i>Molecular Vision</i> , 2015, 21, 1307-17.	1.1	22
4481	A six-microRNA set as prognostic indicators for bile duct cancer. <i>International Journal of Clinical and Experimental Medicine</i> , 2015, 8, 17261-70.	1.3	25
4482	Analysis of differentially expressed genes based on microarray data of glioma. <i>International Journal of Clinical and Experimental Medicine</i> , 2015, 8, 17321-32.	1.3	8
4483	Dysregulated expression of microRNAs and mRNAs in myocardial infarction. <i>American Journal of Translational Research (discontinued)</i> , 2015, 7, 2291-304.	0.0	25
4486	Interactome analysis of gene expression profiles of cervical cancer reveals dysregulated mitotic gene clusters. <i>American Journal of Translational Research (discontinued)</i> , 2017, 9, 3048-3059.	0.0	13
4487	The Effect of Mammary Extracellular Matrix in Controlling Oral and Mammary Cancer Cells. <i>Asian Pacific Journal of Cancer Prevention</i> , 2018, 19, 57-63.	0.5	0
4488	Cell-type-specific brain methylomes profiled via ultralow-input microfluidics. <i>Nature Biomedical Engineering</i> , 2018, 2, 183-194.	11.6	15
4489	RNA-Seq profiling of circular RNAs and potential function of hsa_circ_0002360 in human lung adenocarcinoma. <i>American Journal of Translational Research (discontinued)</i> , 2019, 11, 160-175.	0.0	16
4490	Arresting proliferation improves the cell identity of corneal endothelial cells in the New Zealand rabbit. <i>Molecular Vision</i> , 2019, 25, 745-755.	1.1	2
4491	A pilot study comparing the genetic molecular biology of gestational and non-gestational choriocarcinoma. <i>American Journal of Translational Research (discontinued)</i> , 2019, 11, 7049-7062.	0.0	5
4492	Cytochrome P450 family proteins as potential biomarkers for ovarian granulosa cell damage in mice with premature ovarian failure. <i>International Journal of Clinical and Experimental Pathology</i> , 2018, 11, 4236-4246.	0.5	1
4493	Discovery of microarray-identified genes associated with the progression of cervical intraepithelial neoplasia. <i>International Journal of Clinical and Experimental Pathology</i> , 2018, 11, 5667-5681.	0.5	2
4494	Role of the axis in the development and progression of keratoconus. <i>Molecular Vision</i> , 2020, 26, 1-13.	1.1	3

#	ARTICLE	IF	CITATIONS
4495	Characterization of the transcriptomes of -induced hair cells in the mouse cochlea. American Journal of Stem Cells, 2020, 9, 1-15.	0.4	2
4496	SMYD2 suppresses APC2 expression to activate the Wnt/ β -catenin pathway and promotes epithelial-mesenchymal transition in colorectal cancer. American Journal of Cancer Research, 2020, 10, 997-1011.	1.4	9
4497	Identification of hub genes associated with esophageal cancer progression using bioinformatics analysis. Oncology Letters, 2020, 20, 214.	0.8	1
4498	Prognostic value of immune related genes in lung adenocarcinoma. Oncology Letters, 2020, 20, 259.	0.8	2
4499	Identification and validation of the prognostic value of immune-related genes in non-small cell lung cancer. American Journal of Translational Research (discontinued), 2020, 12, 5844-5865.	0.0	12
4500	oxLDL-Induced Trained Immunity Is Dependent on Mitochondrial Metabolic Reprogramming. Immunometabolism, 2021, 3, e210025.	6.0	7
4501	Identification of lncRNA-NR_104160 as a biomarker and construction of a lncRNA-related ceRNA network for essential hypertension. American Journal of Translational Research (discontinued), 2020, 12, 6060-6075.	0.0	2
4502	Investigating the human protein-host protein interactome of SARS-CoV-2 infection in the small intestine. Gastroenterology and Hepatology From Bed To Bench, 2020, 13, 374-387.	0.6	3
4503	Silencing reverses acquired resistance to sorafenib in hepatocellular carcinoma. Aging, 2020, 12, 22975-23003.	1.4	0
4504	Identification of key miRNA-gene pairs in gastric cancer through integrated analysis of mRNA and miRNA microarray. American Journal of Translational Research (discontinued), 2021, 13, 253-269.	0.0	4
4505	Identification of candidate targets for the diagnosis and treatment of atherosclerosis by bioinformatics analysis. American Journal of Translational Research (discontinued), 2021, 13, 4137-4151.	0.0	3
4506	Bioinformatics analysis of epigenetic and SNP-related molecular markers in systemic lupus erythematosus. American Journal of Translational Research (discontinued), 2021, 13, 6312-6329.	0.0	0
4507	Evolutionary epigenomic analyses in mammalian early embryos reveal species-specific innovations and conserved principles of imprinting. Science Advances, 2021, 7, eabi6178.	4.7	42
4508	Expression and Prognostic Role of E2F2 in Hepatocellular Carcinoma. International Journal of General Medicine, 2021, Volume 14, 8463-8472.	0.8	5
4509	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
4510	Analysis of miRNA Profiles and the Regulatory Network in Congenital Pulmonary Airway Malformations. Frontiers in Pediatrics, 2021, 9, 671107.	0.9	3
4511	The U1 snRNP component RBP45d regulates temperature-responsive flowering in Arabidopsis. Plant Cell, 2022, 34, 834-851.	3.1	18
4512	Homeoprotein SIX1 compromises antitumor immunity through TGF- β -mediated regulation of collagens. Cellular and Molecular Immunology, 2021, 18, 2660-2672.	4.8	5

#	ARTICLE	IF	CITATIONS
4513	Glioblastoma gene network reconstruction and ontology analysis by online bioinformatics tools. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, .	1.0	4
4514	Deepening into Intracellular Signaling Landscape through Integrative Spatial Proteomics and Transcriptomics in a Lymphoma Model. <i>Biomolecules</i> , 2021, 11, 1776.	1.8	8
4515	Whole Blood Expression Pattern of Inflammation and Redox Genes in Mild Alzheimer's Disease. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 6085-6102.	1.6	9
4516	Hippocampal neurons' cytosolic and membrane-bound ribosomal transcript profiles are differentially regulated by learning and subsequent sleep. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2108534118.	3.3	20
4517	MGEEnrichment: A web application for microglia gene list enrichment analysis. <i>PLoS Computational Biology</i> , 2021, 17, e1009160.	1.5	5
4518	Changes in Methylation across Structural and MicroRNA Genes Relevant for Progression and Metastasis in Colorectal Cancer. <i>Cancers</i> , 2021, 13, 5951.	1.7	5
4519	LIMD2 is a Prognostic and Predictive Marker in Patients With Esophageal Cancer Based on a ceRNA Network Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 774432.	1.1	5
4520	Exploring the Mechanisms of Arsenic Trioxide (Pishuang) in Hepatocellular Carcinoma Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-9.	0.5	3
4521	Web-based transcriptome analysis determines a sixteen-gene signature and associated drugs on hearing loss patients: A bioinformatics approach. <i>Journal of Clinical Laboratory Analysis</i> , 2021, 35, e24065.	0.9	6
4522	Sodium Selenite Enhances Antibiotics Sensitivity of <i>Pseudomonas aeruginosa</i> and Decreases Its Pathogenicity by Inducing Oxidative Stress and Inhibiting Quorum Sensing System. <i>Antioxidants</i> , 2021, 10, 1873.	2.2	1
4523	Genome-wide DNA methylation analysis of pulmonary function in middle and old-aged Chinese monozygotic twins. <i>Respiratory Research</i> , 2021, 22, 300.	1.4	7
4524	CD153/CD30 signaling promotes age-dependent tertiary lymphoid tissue expansion and kidney injury. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	36
4525	Combined Metabolomics and Network Toxicology to Explore the Molecular Mechanism of <i>Phytolacca acinose</i> Roxb-Induced Hepatotoxicity in Zebrafish Larvae in Vivo. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-13.	0.5	2
4526	Integrative investigation of the TF-miRNA coregulatory network involved in the inhibition of breast cancer cell proliferation by resveratrol. <i>FEBS Open Bio</i> , 2021, , .	1.0	6
4527	Association of Circulating Biomarkers of Inc-IGSF3-1:1, SCOC-AS1, and SLC8A1-AS1 with Salt Sensitivity of Blood Pressure in Chinese Population. <i>Journal of Cardiovascular Translational Research</i> , 2021, , 1.	1.1	5
4528	Identification of LIG1 and LIG3 as prognostic biomarkers in breast cancer. <i>Open Medicine (Poland)</i> , 2021, 16, 1705-1717.	0.6	2
4529	Key genes associated with prognosis and metastasis of clear cell renal cell carcinoma. <i>PeerJ</i> , 2022, 10, e12493.	0.9	5
4530	Prognostic value of immune related genes in lung adenocarcinoma. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	5

#	ARTICLE	IF	CITATIONS
4531	Identification of hub genes associated with esophageal cancer progression using bioinformatics analysis. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	3
4532	Silencing <i>KIF14</i> reverses acquired resistance to sorafenib in hepatocellular carcinoma. <i>Aging</i> , 2020, 12, 22975-23003.	1.4	6
4533	Genetic Parameter Estimation and Genome-Wide Association Study-Based Loci Identification of Milk-Related Traits in Chinese Holstein. <i>Frontiers in Genetics</i> , 2021, 12, 799664.	1.1	9
4534	Mitochondrial incompatibility as a hidden driver behind the genome ancestry of African admixed cattle. <i>BMC Biology</i> , 2022, 20, 20.	1.7	3
4535	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
4536	Lentian Supplementation Protects the Gut-Liver Axis and Prevents Steatohepatitis: The Role of Gut Microbiota Involved. <i>Frontiers in Nutrition</i> , 2021, 8, 803691.	1.6	23
4537	Gene Ontology Groups and Signaling Pathways Regulating the Process of Avian Satellite Cell Differentiation. <i>Genes</i> , 2022, 13, 242.	1.0	8
4538	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
4539	Identification of key regulators in Sarcoidosis through multidimensional systems biological approach. <i>Scientific Reports</i> , 2022, 12, 1236.	1.6	4
4540	Identification of four novel hub genes as monitoring biomarkers for colorectal cancer. <i>Hereditas</i> , 2022, 159, 11.	0.5	3
4541	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
4542	Molecular Mechanism of <i>Gelsemium elegans</i> (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
4543	PBK/TOPK Inhibitor Suppresses the Progression of Prolactinomas. <i>Frontiers in Endocrinology</i> , 2021, 12, 706909.	1.5	1
4544	The diagnostic and prognostic significance of small nuclear ribonucleoprotein Sm D1 aberrantly high expression in hepatocellular carcinoma. <i>Journal of Cancer</i> , 2022, 13, 184-201.	1.2	13
4545	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
4546	Computational analyses of mechanism of action (MoA): data, methods and integration. <i>RSC Chemical Biology</i> , 2022, 3, 170-200.	2.0	32
4547	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
4548	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

#	ARTICLE	IF	CITATIONS
4549	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
4550	Chrysin, which targets PLA2, protects PC12 cells from OGD/R-stimulated damage through repressing the NF- κ B signaling pathway. <i>Regenerative Therapy</i> , 2022, 19, 69-76.	1.4	4
4551	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
4552	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
4553	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
4554	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
4555	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. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-16.	0.5	5
4556	Biological response of adrenal carcinoma and melanoma cells to mitotane treatment. <i>Oncology Letters</i> , 2022, 23, 120.	0.8	6
4557	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
4559	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
4560	An instructive role for Interleukin-7 receptor $\hat{1}\pm$ in the development of human B-cell precursor leukemia. <i>Nature Communications</i> , 2022, 13, 659.	5.8	12
4561	Clinical Significance of TET2 in Female Cancers. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, 790605.	2.0	6
4562	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
4563	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
4564	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
4565	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
4566	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
4567	Evolutionary impacts of purine metabolism genes on mammalian oxidative stress adaptation. <i>Zoological Research</i> , 2022, 43, 241-254.	0.9	21

#	ARTICLE	IF	CITATIONS
4568	Prognostic Values and Underlying Regulatory Network of Cohesin Subunits in Esophageal Carcinoma. <i>Journal of Cancer</i> , 2022, 13, 1588-1602.	1.2	2
4569	Multi-omics reveals mitochondrial metabolism proteins susceptible for drug discovery in AML. <i>Leukemia</i> , 2022, . .	3.3	7
4570	Gene expression profiling reveals candidate biomarkers and probable molecular mechanisms in chronic stress. <i>Bioengineered</i> , 2022, 13, 6048-6060.	1.4	3
4571	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
4572	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
4573	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
4574	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
4575	Human APOE ϵ 3 and APOE ϵ 4 Alleles Have Differential Effects on Mouse Olfactory Epithelium. <i>Journal of Alzheimer's Disease</i> , 2022, 85, 1481-1494.	1.2	3
4576	Comprehensive Analysis of LncRNA AC010789.1 Delays Androgenic Alopecia Progression by Targeting MicroRNA-21 and the Wnt/ β -Catenin Signaling Pathway in Hair Follicle Stem Cells. <i>Frontiers in Genetics</i> , 2022, 13, 782750.	1.1	4
4577	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
4578	Lichen Secondary Metabolites Inhibit the Wnt/ β -Catenin Pathway in Glioblastoma Cells and Improve the Anticancer Effects of Temozolomide. <i>Cells</i> , 2022, 11, 1084.	1.8	17
4579	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
4580	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
4581	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
4582	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
4583	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
4584	Transcriptional atlas analysis from multiple tissues reveals the expression specificity patterns in beef cattle. <i>BMC Biology</i> , 2022, 20, 79.	1.7	12
4586	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
4587	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
4588	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
4589	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
4590	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
4591	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
4592	Anticancer Activity of Erianin: Cancer-Specific Target Prediction Based on Network Pharmacology. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 862932.	1.6	13
4593	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
4594	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
4595	Circ_0001174 facilitates osteosarcoma cell proliferation, migration, and invasion by targeting the miR-186-5p/MAC1 axis. <i>Journal of Orthopaedic Surgery and Research</i> , 2022, 17, 159.	0.9	5
4596	<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
4597	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
4598	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
4599	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
4600	Survival analysis of pathway activity as a prognostic determinant in breast cancer. <i>PLoS Computational Biology</i> , 2022, 18, e1010020.	1.5	4
4601	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
4602	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
4603	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
4604	Adult mouse fibroblasts retain organ-specific transcriptomic identity. <i>ELife</i> , 2022, 11, .	2.8	14

#	ARTICLE	IF	CITATIONS
4605	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
4606	Multi-Omics Characterization of Early- and Adult-Onset Major Depressive Disorder. <i>Journal of Personalized Medicine</i> , 2022, 12, 412.	1.1	7
4607	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
4608	Comprehensive proteomic profiling of plasma and serum phosphatidylserine-positive extracellular vesicles reveals tissue-specific proteins. <i>IScience</i> , 2022, 25, 104012.	1.9	24
4609	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
4610	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
4611	Structure-based design of CDC42 effector interaction inhibitors for the treatment of cancer. <i>Cell Reports</i> , 2022, 39, 110641.	2.9	5
4612	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
4613	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
4614	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
4615	Cytokine and Nitric Oxide-Dependent Gene Regulation in Islet Endocrine and Nonendocrine Cells. <i>Function</i> , 2021, 3, zqab063.	1.1	5
4616	Methylome inheritance and enhancer dememorization reset an epigenetic gate safeguarding embryonic programs. <i>Science Advances</i> , 2021, 7, eabl3858.	4.7	12
4617	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
4618	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
4619	(20S) Ginsenoside Rh2 Exerts Its Anti-Tumor Effect by Disrupting the HSP90A-Cdc37 System in Human Liver Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13170.	1.8	14
4620	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
4621	Combination of Wnt/ β -Catenin Targets S100A4 and DKK1 Improves Prognosis of Human Colorectal Cancer. <i>Cancers</i> , 2022, 14, 37.	1.7	7
4622	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

#	ARTICLE	IF	CITATIONS
4623	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
4624	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
4625	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
4626	Somatic DNA demethylation generates tissue-specific methylation states and impacts flowering time. <i>Plant Cell</i> , 2022, 34, 1189-1206.	3.1	24
4627	Promising novel biomarkers and candidate small-molecule drugs for lung adenocarcinoma: Evidence from bioinformatics analysis of high-throughput data. <i>Open Medicine (Poland)</i> , 2021, 17, 96-112.	0.6	1
4628	A Meta-Analysis of Human Transcriptomics Data in the Context of Peritoneal Dialysis Identifies Novel Receptor-Ligand Interactions as Potential Therapeutic Targets. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13277.	1.8	3
4629	The establishment of a hub differential gene model to predict prognosis in stage II and III right- and left-sided colon cancer patients. <i>Annals of Translational Medicine</i> , 2021, 9, 1763-1763.	0.7	1
4630	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
4631	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
4632	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
4633	oxLDL-Induced Trained Immunity Is Dependent on Mitochondrial Metabolic Reprogramming. <i>Immunometabolism</i> , 2021, 3, e210025.	0.7	20
4634	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
4635	Transcriptome alterations in spermatogonial stem cells exposed to bisphenol A. <i>Animal Cells and Systems</i> , 2022, 26, 70-83.	0.8	5
4636	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
4637	Macrophage inflammation resolution requires CPEB4-directed offsetting of mRNA degradation. <i>ELife</i> , 2022, 11, .	2.8	13
4638	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
4639	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
4640	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

#	ARTICLE	IF	CITATIONS
4641	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
4642	Identity of <i>MMP1</i> and its effects on tumor progression in head and neck squamous cell carcinoma. <i>Cancer Medicine</i> , 2022, 11, 2516-2530.	1.3	10
4643	H3K4 demethylase KDM5B regulates cancer cell identity and epigenetic plasticity. <i>Oncogene</i> , 2022, 41, 2958-2972.	2.6	8
4644	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
4645	Identification of novel prognostic targets in glioblastoma using bioinformatics analysis. <i>BioMedical Engineering OnLine</i> , 2022, 21, 26.	1.3	19
4647	Bioinformatics: Novel Insights from Genomic Information. <i>Nestle Nutrition Institute Workshop Series</i> , 2016, 84, 35-46.	1.5	1
4648	Screening the components of <i>Saussurea involucreta</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
4650	Complete Genome Sequence Analysis of <i>Ralstonia solanacearum</i> Strain PeaF1 Provides Insights Into Its Strong Virulence in Peanut Plants. <i>Frontiers in Microbiology</i> , 2022, 13, 830900.	1.5	10
4652	Integrated analysis of differentially expressed genes and a ceRNA network to identify hub lncRNAs and potential drugs for multiple sclerosis.. <i>American Journal of Translational Research (discontinued)</i> , 2022, 14, 772-787.	0.0	0
4653	Identification of hub genes and pathways in bladder cancer using bioinformatics analysis.. <i>American Journal of Clinical and Experimental Urology</i> , 2022, 10, 13-24.	0.4	0
4654	Gut microbiota and differential genes-maintained homeostasis is key to maintaining health of individuals with Yang-deficiency constitution.. <i>Journal of Traditional Chinese Medicine</i> , 2022, 42, 96-101.	0.1	0
4655	Glomerular Expression of S100A8 in Lupus Nephritis: An Integrated Bioinformatics Analysis. <i>Frontiers in Immunology</i> , 2022, 13, 843576.	2.2	3
4656	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
4657	Dominant transcript expression profiles of human protein-coding genes interrogated with GTEx dataset. <i>Scientific Reports</i> , 2022, 12, 6969.	1.6	2
4658	Role of spt23 in <i>Saccharomyces cerevisiae</i> thermal tolerance. <i>Applied Microbiology and Biotechnology</i> , 2022, , 1.	1.7	2
4659	Gene Expression Profiling of Glioblastoma to Recognize Potential Biomarker Candidates. <i>Frontiers in Genetics</i> , 2022, 13, 832742.	1.1	3
4660	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
4661	LINC00922 promotes deterioration of gastric cancer. <i>PLoS ONE</i> , 2022, 17, e0267798.	1.1	1

#	ARTICLE	IF	CITATIONS
4662	Combinatorial Treatment with PARP-1 Inhibitors and Cisplatin Attenuates Cervical Cancer Growth through Fos-Driven Changes in Gene Expression. <i>Molecular Cancer Research</i> , 2022, 20, 1183-1192.	1.5	7
4663	Identification of functionally important miRNA targeted genes associated with child obesity trait in genome-wide association studies. <i>BMC Genomics</i> , 2022, 23, 360.	1.2	4
4664	Bioinformatic approach for the discovery of cis-eQTL signals during fruit ripening of a woody species as grape (<i>Vitis vinifera</i> L.). <i>Scientific Reports</i> , 2022, 12, 7481.	1.6	0
4665	Translocon-associated Protein Subunit SSR3 Determines and Predicts Susceptibility to Paclitaxel in Breast Cancer and Glioblastoma. <i>Clinical Cancer Research</i> , 2022, 28, 3156-3169.	3.2	4
4666	Profiling the Human Phosphoproteome to Estimate the True Extent of Protein Phosphorylation. <i>Journal of Proteome Research</i> , 2022, 21, 1510-1524.	1.8	15
4667	A novel hypoxia-driven gene signature that can predict the prognosis of hepatocellular carcinoma. <i>Bioengineered</i> , 2022, 13, 12193-12210.	1.4	6
4668	Breast Cancer-Stromal Interactions: Adipose-Derived Stromal/Stem Cell Age and Cancer Subtype Mediated Remodeling. <i>Stem Cells and Development</i> , 2022, 31, 604-620.	1.1	3
4669	ERBB3 methylation and immune infiltration in tumor microenvironment of cervical cancer. <i>Scientific Reports</i> , 2022, 12, 8112.	1.6	5
4670	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
4671	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
4672	Curcumin treats endometriosis in mice by the HIF signaling pathway.. <i>American Journal of Translational Research (discontinued)</i> , 2022, 14, 2184-2198.	0.0	0
4673	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
4678	Investigation of molecular mechanisms underlying JAK/STAT signaling pathway in HPV-induced cervical carcinogenesis using "omics" approach. , 2022, 39, .		1