Zhong-Ming Zhao

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4060369/publications.pdf

Version: 2024-02-01

285 papers	12,969 citations	31902 53 h-index	37111 96 g-index
310 all docs	310 docs citations	310 times ranked	22527 citing authors

#	Article	IF	Citations
1	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
2	Computational tools for copy number variation (CNV) detection using next-generation sequencing data: features and perspectives. BMC Bioinformatics, 2013, 14, S1.	1.2	452
3	Alveolar regeneration through a Krt8+ transitional stem cell state that persists in human lung fibrosis. Nature Communications, 2020, 11, 3559.	5.8	378
4	TSGene 2.0: an updated literature-based knowledgebase for tumor suppressor genes. Nucleic Acids Research, 2016, 44, D1023-D1031.	6.5	332
5	TSGene: a web resource for tumor suppressor genes. Nucleic Acids Research, 2013, 41, D970-D976.	6.5	295
6	Machine learning-based prediction of drugâ€“drug interactions by integrating drug phenotypic, therapeutic, chemical, and genomic properties. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, e278-e286.	2.2	264
7	dmGWAS: dense module searching for genome-wide association studies in proteinâ€“protein interaction networks. Bioinformatics, 2011, 27, 95-102.	1.8	253
8	Rationale for co-targeting IGF-1R and ALK in ALK fusionâ€“positive lung cancer. Nature Medicine, 2014, 20, 1027-1034.	15.2	243
9	Moderate mutation rate in the SARS coronavirus genome and its implications. BMC Evolutionary Biology, 2004, 4, 21.	3.2	235
10	Large-scale prediction of adverse drug reactions using chemical, biological, and phenotypic properties of drugs. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, e28-e35.	2.2	233
11	Interaction with WDR5 Promotes Target Gene Recognition and Tumorigenesis by MYC. Molecular Cell, 2015, 58, 440-452.	4.5	224
12	Asprosin is a centrally acting orexigenic hormone. Nature Medicine, 2017, 23, 1444-1453.	15.2	216
13	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	2.9	204
14	Whole-genome sequencing reveals oncogenic mutations in mycosis fungoides. Blood, 2015, 126, 508-519.	0.6	193
15	Circular RNA expression profiles and features in human tissues: a study using RNA-seq data. BMC Genomics, 2017, 18, 680.	1.2	193
16	Common variants conferring risk of schizophrenia: A pathway analysis of GWAS data. Schizophrenia Research, 2010, 122, 38-42.	1.1	190
17	Gene set analysis of genome-wide association studies: Methodological issues and perspectives. Genomics, 2011, 98, 1-8.	1.3	180
18	Mutations in GDF6 are associated with vertebral segmentation defects in Klippel-Feil syndrome. Human Mutation, 2008, 29, 1017-1027.	1.1	170

#	Article	IF	Citations
19	Decoding critical long non-coding RNA in ovarian cancer epithelial-to-mesenchymal transition. Nature Communications, 2017, 8, 1604.	5.8	159
20	Investigating single nucleotide polymorphism (SNP) density in the human genome and its implications for molecular evolution. Gene, 2003, 312, 207-213.	1.0	146
21	A meta-analysis of oxidative stress markers in schizophrenia. Science China Life Sciences, 2010, 53, 112-124.	2.3	146
22	Detecting somatic point mutations in cancer genome sequencing data: a comparison of mutation callers. Genome Medicine, 2013, 5, 91.	3.6	146
23	A Novel microRNA and transcription factor mediated regulatory network in schizophrenia. BMC Systems Biology, 2010, 4, 10.	3.0	145
24	Neighboring-Nucleotide Effects on Single Nucleotide Polymorphisms: A Study of 2.6 Million Polymorphisms Across the Human Genome. Genome Research, 2002, 12, 1679-1686.	2.4	127
25	Uncovering MicroRNA and Transcription Factor Mediated Regulatory Networks in Glioblastoma. PLoS Computational Biology, 2012, 8, e1002488.	1.5	124
26	Transcriptome sequencing and genome-wide association analyses reveal lysosomal function and actin cytoskeleton remodeling in schizophrenia and bipolar disorder. Molecular Psychiatry, 2015, 20, 563-572.	4.1	124
27	Advances in computational approaches for prioritizing driver mutations and significantly mutated genes in cancer genomes. Briefings in Bioinformatics, 2016, 17, 642-656.	3.2	120
28	Schizophrenia Gene Networks and Pathways and Their Applications for Novel Candidate Gene Selection. PLoS ONE, 2010, 5, e11351.	1.1	110
29	The allergy mediator histamine confers resistance to immunotherapy in cancer patients via activation of the macrophage histamine receptor H1. Cancer Cell, 2022, 40, 36-52.e9.	7.7	101
30	Candidate genes for schizophrenia: A survey of association studies and gene ranking. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 1173-1181.	1.1	98
31	Network-Assisted Investigation of Combined Causal Signals from Genome-Wide Association Studies in Schizophrenia. PLoS Computational Biology, 2012, 8, e1002587.	1.5	98
32	VarWalker: Personalized Mutation Network Analysis of Putative Cancer Genes from Next-Generation Sequencing Data. PLoS Computational Biology, 2014, 10, e1003460.	1.5	96
33	Quantitative network mapping of the human kinome interactome reveals new clues for rational kinase inhibitor discovery and individualized cancer therapy. Oncotarget, 2014, 5, 3697-3710.	0.8	96
34	MET Exon 14 Skipping in Non-Small Cell Lung Cancer. Oncologist, 2016, 21, 481-486.	1.9	94
35	A comprehensive network and pathway analysis of candidate genes in major depressive disorder. BMC Systems Biology, 2011, 5, S12.	3.0	89
36	Gene2vec: distributed representation of genes based on co-expression. BMC Genomics, 2019, 20, 82.	1.2	87

#	Article	IF	Citations
37	Network-assisted analysis to prioritize GWAS results: principles, methods and perspectives. Human Genetics, 2014, 133, 125-138.	1.8	86
38	A Meta-analysis of Somatic Mutations from Next Generation Sequencing of 241 Melanomas: A Road Map for the Study of Genes with Potential Clinical Relevance. Molecular Cancer Therapeutics, 2014, 13, 1918-1928.	1.9	84
39	DCGL v2.0: An R Package for Unveiling Differential Regulation from Differential Co-expression. PLoS ONE, 2013, 8, e79729.	1.1	83
40	scRNASeqDB: A Database for RNA-Seq Based Gene Expression Profiles in Human Single Cells. Genes, 2017, 8, 368.	1.0	80
41	Studying Tumorigenesis through Network Evolution and Somatic Mutational Perturbations in the Cancer Interactome. Molecular Biology and Evolution, 2014, 31, 2156-2169.	3.5	79
42	Extracellular Matrix/Integrin Signaling Promotes Resistance to Combined Inhibition of HER2 and PI3K in HER2+ Breast Cancer. Cancer Research, 2017, 77, 3280-3292.	0.4	76
43	A multi-dimensional evidence-based candidate gene prioritization approach for complex diseasesâ€“schizophrenia as a case. Bioinformatics, 2009, 25, 2595-6602.	1.8	72
44	Proteome-Scale Investigation of Protein Allosteric Regulation Perturbed by Somatic Mutations in 7,000 Cancer Genomes. American Journal of Human Genetics, 2017, 100, 5-20.	2.6	72
45	A bias-reducing pathway enrichment analysis of genome-wide association data confirmed association of the MHC region with schizophrenia. Journal of Medical Genetics, 2012, 49, 96-103.	1.5	68
46	VERSE: a novel approach to detect virus integration in host genomes through reference genome customization. Genome Medicine, 2015, 7, 2.	3.6	68
47	Genetic Relationship between Schizophrenia and Nicotine Dependence. Scientific Reports, 2016, 6, 25671.	1.6	67
48	Multi-level transcriptome sequencing identifies COL1A1 as a candidate marker in human heart failure progression. BMC Medicine, 2020, 18, 2.	2.3	65
49	A Gene Gravity Model for the Evolution of Cancer Genomes: A Study of 3,000 Cancer Genomes across 9 Cancer Types. PLoS Computational Biology, 2015, 11, e1004497.	1.5	65
50	Acquired Resistance of EGFR-Mutant Lung Adenocarcinomas to Afatinib plus Cetuximab Is Associated with Activation of mTORC1. Cell Reports, 2014, 7, 999-1008.	2.9	64
51	RNA-Seq analysis implicates dysregulation of the immune system in schizophrenia. BMC Genomics, 2012, 13, S2.	1.2	63
52	TissGDB: tissue-specific gene database in cancer. Nucleic Acids Research, 2018, 46, D1031-D1038.	6.5	63
53	MBSTAR: multiple instance learning for predicting specific functional binding sites in microRNA targets. Scientific Reports, 2015, 5, 8004.	1.6	62
54	Pathway-based analysis of GWAS datasets: effective but caution required. International Journal of Neuropsychopharmacology, 2011, 14, 567-572.	1.0	60

#	Article	IF	Citations
55	Subtype-specific signaling pathways and genomic aberrations associated with prognosis of glioblastoma. Neuro-Oncology, 2019, 21, 59-70.	0.6	60
56	Patterns and processes of somatic mutations in nine major cancers. BMC Medical Genomics, 2014, 7, 11.	0.7	57
57	EW_dmGWAS: edge-weighted dense module search for genome-wide association studies and gene expression profiles. Bioinformatics, 2015, 31, 2591-2594.	1.8	57
58	MSEA: detection and quantification of mutation hotspots through mutation set enrichment analysis. Genome Biology, 2014, 15, 489.	3.8	54
59	Systematic dissection of dysregulated transcription factorâ€“miRNA feed-forward loops across tumor types. Briefings in Bioinformatics, 2016, 17, 996-1008.	3.2	54
60	Functional complementation between transcriptional methylation regulation and post-transcriptional microRNA regulation in the human genome. BMC Genomics, 2011, 12, S15.	1.2	52
61	Systems Biology-Based Investigation of Cellular Antiviral Drug Targets Identified by Gene-Trap Insertional Mutagenesis. PLoS Computational Biology, 2016, 12, e1005074.	1.5	52
62	The Potential Roles of Long Noncoding RNAs (lncRNA) in Glioblastoma Development. Molecular Cancer Therapeutics, 2016, 15, 2977-2986.	1.9	51
63	Repurposing sertraline sensitizes nonâ€“small cell lung cancer cells to erlotinib by inducing autophagy. JCI Insight, 2018, 3, .	2.3	51
64	deTS: tissue-specific enrichment analysis to decode tissue specificity. Bioinformatics, 2019, 35, 3842-3845.	1.8	51
65	An efficient hierarchical generalized linear mixed model for pathway analysis of genome-wide association studies. Bioinformatics, 2011, 27, 686-692.	1.8	50
66	CpG islands: Algorithms and applications in methylation studies. Biochemical and Biophysical Research Communications, 2009, 382, 643-645.	1.0	49
67	Deep4mC: systematic assessment and computational prediction for DNA N4-methylcytosine sites by deep learning. Briefings in Bioinformatics, 2021, 22, .	3.2	49
68	Next-generation sequencing of paired tyrosine kinase inhibitor-sensitive and -resistant EGFR mutant lung cancer cell lines identifies spectrum of DNA changes associated with drug resistance. Genome Research, 2013, 23, 1434-1445.	2.4	48
69	Systematic Integration of Brain eQTL and GWAS IdentifiesZNF323as a Novel Schizophrenia Risk Gene and Suggests Recent Positive Selection Based on Compensatory Advantage on Pulmonary Function. Schizophrenia Bulletin, 2015, 41, 1294-1308.	2.3	48
70	Estrogen receptor-Î± expressing neurons in the ventrolateral VMH regulate glucose balance. Nature Communications, 2020, 11, 2165.	5.8	48
71	Reproducible combinatorial regulatory networks elucidate novel oncogenic microRNAs in non-small cell lung cancer. Rna, 2014, 20, 1356-1368.	1.6	47
72	CpG islands or CpG clusters: how to identify functional GC-rich regions in a genome?. BMC Bioinformatics, 2009, 10, 65.	1.2	46

#	Article	IF	Citations
73	A network-based drug repositioning infrastructure for precision cancer medicine through targeting significantly mutated genes in the human cancer genomes. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 681-691.	2.2	46
74	SZGR 2.0: a one-stop shop of schizophrenia candidate genes. Nucleic Acids Research, 2017, 45, D915-D924.	6.5	44
75	Clonal architectures predict clinical outcome in clear cell renal cell carcinoma. Nature Communications, 2019, 10, 1245.	5.8	44
76	Systematic Prioritization of Druggable Mutations in â^¼5000 Genomes Across 16 Cancer Types Using a Structural Genomics-based Approach. Molecular and Cellular Proteomics, 2016, 15, 642-656.	2.5	43
77	MicroRNA and transcription factor co-regulatory networks and subtype classification of seminoma and non-seminoma in testicular germ cell tumors. Scientific Reports, 2020, 10, 852.	1.6	43
78	KinaseMD: kinase mutations and drug response database. Nucleic Acids Research, 2021, 49, D552-D561.	6.5	43
79	Deep generative neural network for accurate drug response imputation. Nature Communications, 2021, 12, 1740.	5.8	43
80	ccmGDB: a database for cancer cell metabolism genes. Nucleic Acids Research, 2016, 44, D959-D968.	6.5	41
81	Synergetic regulatory networks mediated by oncogene-driven microRNAs and transcription factors in serous ovarian cancer. Molecular BioSystems, 2013, 9, 3187.	2.9	40
82	Impacts of somatic mutations on gene expression: an association perspective. Briefings in Bioinformatics, 2017, 18, bbw037.	3.2	40
83	Targeted next-generation sequencing of DNA regions proximal to a conserved GXGXXG signaling motif enables systematic discovery of tyrosine kinase fusions in cancer. Nucleic Acids Research, 2010, 38, 6985-6996.	6.5	39
84	DTome: a web-based tool for drug-target interactome construction. BMC Bioinformatics, 2012, 13, S7.	1.2	39
85	VISDB: a manually curated database of viral integration sites in the human genome. Nucleic Acids Research, 2020, 48, D633-D641.	6.5	39
86	Age-associated telomere attrition in adipocyte progenitors predisposes to metabolic disease. Nature Metabolism, 2020, 2, 1482-1497.	5.1	39
87	Integrative network analysis identifies key genes and pathways in the progression of hepatitis C virus induced hepatocellular carcinoma. BMC Medical Genomics, 2011, 4, 62.	0.7	38
88	Machine Learning to Predict Delayed Cerebral Ischemia and Outcomes in Subarachnoid Hemorrhage. Neurology, 2021, 96, e553-e562.	1.5	38
89	ERGR: An ethanol-related gene resource. Nucleic Acids Research, 2009, 37, D840-D845.	6.5	37
90	Concordance of copy number loss and down-regulation of tumor suppressor genes: a pan-cancer study. BMC Genomics, 2016, 17, 532.	1.2	37

#	Article	IF	Citations
91	Sequence context analysis of 8.2 million single nucleotide polymorphisms in the human genome. Gene, 2006, 366, 316-324.	1.0	36
92	Concordant dysregulation of miR-5p and miR-3p arms of the same precursor microRNA may be a mechanism in inducing cell proliferation and tumorigenesis: a lung cancer study. Rna, 2015, 21, 1055-1065.	1.6	36
93	Investigating cellular network heterogeneity and modularity in cancer: a network entropy and unbalanced motif approach. BMC Systems Biology, 2016, 10, 65.	3.0	36
94	Investigating MicroRNA and transcription factor co-regulatory networks in colorectal cancer. BMC Bioinformatics, 2017, 18, 388.	1.2	35
95	Enriched pathways for major depressive disorder identified from a genome-wide association study. International Journal of Neuropsychopharmacology, 2012, 15, 1401-1411.	1.0	34
96	Features of Methylation and Gene Expression in the Promoter-Associated CpG Islands Using Human Methylome Data. Comparative and Functional Genomics, 2012, 2012, 1-8.	2.0	34
97	Toward Repurposing Metformin as a Precision Anti-Cancer Therapy Using Structural Systems Pharmacology. Scientific Reports, 2016, 6, 20441.	1.6	34
98	Graph- and rule-based learning algorithms: a comprehensive review of their applications for cancer type classification and prognosis using genomic data. Briefings in Bioinformatics, 2020, 21, 368-394.	3.2	34
99	Differential Expression of Viral Transcripts From Single-Cell RNA Sequencing of Moderate and Severe COVID-19 Patients and Its Implications for Case Severity. Frontiers in Microbiology, 2020, 11, 603509.	1.5	34
100	6mA-Finder: a novel online tool for predicting DNA N6-methyladenine sites in genomes. Bioinformatics, 2020, 36, 3257-3259.	1.8	34
101	Inconsistency and features of single nucleotide variants detected in whole exome sequencing versus transcriptome sequencing: A case study in lung cancer. Methods, 2015, 83, 118-127.	1.9	33
102	Association of CXCR6 with COVID-19 severity: delineating the host genetic factors in transcriptomic regulation. Human Genetics, 2021, 140, 1313-1328.	1.8	33
103	Discovering Disease-specific Biomarker Genes for Cancer Diagnosis and Prognosis. Technology in Cancer Research and Treatment, 2010, 9, 219-229.	0.8	32
104	Weak sharing of genetic association signals in three lung cancer subtypes: evidence at the SNP, gene, regulation, and pathway levels. Genome Medicine, 2018, 10, 16.	3.6	32
105	Functional consequences of somatic mutations in cancer using protein pocket-based prioritization approach. Genome Medicine, 2014, 6, 81.	3.6	31
106	Anemia and Red Blood Cell Indices Predict HIV-Associated Neurocognitive Impairment in the Highly Active Antiretroviral Therapy Era. Journal of Infectious Diseases, 2016, 213, 1065-1073.	1.9	31
107	Circular RNA expression profiles during the differentiation of mouse neural stem cells. BMC Systems Biology, 2018, 12, 128.	3.0	31
108	Angiogenic gene networks are dysregulated in opioid use disorder: evidence from multi-omics and imaging of postmortem human brain. Molecular Psychiatry, 2021, 26, 7803-7812.	4.1	31

#	Article	IF	Citations
109	In-depth genomic data analyses revealed complex transcriptional and epigenetic dysregulations of BRAF V600E in melanoma. Molecular Cancer, 2015, 14, 60.	7.9	30
110	Critical microRNAs and regulatory motifs in cleft palate identified by a conserved miRNAâ€“TFâ€“gene network approach in humans and mice. Briefings in Bioinformatics, 2020, 21, 1465-1478.	3.2	30
111	Genetic Variation in Iron Metabolism Is Associated with Neuropathic Pain and Pain Severity in HIV-Infected Patients on Antiretroviral Therapy. PLoS ONE, 2014, 9, e103123.	1.1	29
112	Tissue-Specific Signaling Networks Rewired by Major Somatic Mutations in Human Cancer Revealed by Proteome-Wide Discovery. Cancer Research, 2017, 77, 2810-2821.	0.4	29
113	An integrative functional genomics framework for effective identification of novel regulatory variants in genomeâ€“phenome studies. Genome Medicine, 2018, 10, 7.	3.6	29
114	Cell-type deconvolution analysis identifies cancer-associated myofibroblast component as a poor prognostic factor in multiple cancer types. Oncogene, 2021, 40, 4686-4694.	2.6	29
115	Genome-Wide Correlation of DNA Methylation and Gene Expression in Postmortem Brain Tissues of Opioid Use Disorder Patients. International Journal of Neuropsychopharmacology, 2021, 24, 879-891.	1.0	29
116	WebCSEA: web-based cell-type-specific enrichment analysis of genes. Nucleic Acids Research, 2022, 50, W782-W790.	6.5	29
117	Multi-species data integration and gene ranking enrich significant results in an alcoholism genome-wide association study. BMC Genomics, 2012, 13, S16.	1.2	28
118	Optimizing the Sequence of Anti-EGFRâ€“Targeted Therapy in EGFR-Mutant Lung Cancer. Molecular Cancer Therapeutics, 2015, 14, 542-552.	1.9	28
119	Distinct and Competitive Regulatory Patterns of Tumor Suppressor Genes and Oncogenes in Ovarian Cancer. PLoS ONE, 2012, 7, e44175.	1.1	27
120	Targeted activation of <scp>CREB</scp> in reactive astrocytes is neuroprotective in focal acute cortical injury. Glia, 2016, 64, 853-874.	2.5	27
121	Genes and microRNAs associated with mouse cleft palate: A systematic review and bioinformatics analysis. Mechanisms of Development, 2018, 150, 21-27.	1.7	27
122	Identification of gene signatures from RNA-seq data using Pareto-optimal cluster algorithm. BMC Systems Biology, 2018, 12, 126.	3.0	27
123	Nucleotide Variation and Haplotype Diversity in a 10-kb Noncoding Region in Three Continental Human Populations. Genetics, 2006, 174, 399-409.	1.2	26
124	Application of systems biology approach identifies and validates GRB2 as a risk gene for schizophrenia in the Irish Case Control Study of Schizophrenia (ICCSS) sample. Schizophrenia Research, 2011, 125, 201-208.	1.1	26
125	MicroRNA-138 suppresses glioblastoma proliferation through downregulation of CD44. Scientific Reports, 2021, 11, 9219.	1.6	26
126	CNVannotator: A Comprehensive Annotation Server for Copy Number Variation in the Human Genome. PLoS ONE, 2013, 8, e80170.	1.1	26

#	Article	IF	Citations
127	NOTCH-Induced MDSC Recruitment after oHSV Virotherapy in CNS Cancer Models Modulates Antitumor Immunotherapy. Clinical Cancer Research, 2022, 28, 1460-1473.	3.2	26
128	H19, a Long Non-coding RNA, Mediates Transcription Factors and Target Genes through Interference of MicroRNAs in Pan-Cancer. Molecular Therapy - Nucleic Acids, 2020, 21, 180-191.	2.3	25
129	An integrative genomics approach for identifying novel functional consequences of PBRM1 truncated mutations in clear cell renal cell carcinoma (ccRCC). BMC Genomics, 2016, 17, 515.	1.2	24
130	Unique protein expression signatures of survival time in kidney renal clear cell carcinoma through a pan-cancer screening. BMC Genomics, 2017, 18, 678.	1.2	24
131	A Linear Regression and Deep Learning Approach for Detecting Reliable Genetic Alterations in Cancer Using DNA Methylation and Gene Expression Data. Genes, 2020, 11, 931.	1.0	24
132	Convergent genomic and pharmacological evidence of PI3K/GSK3 signaling alterations in neurons from schizophrenia patients. Neuropsychopharmacology, 2021, 46, 673-682.	2.8	24
133	Multi-Dimensional Prioritization of Dental Caries Candidate Genes and Its Enriched Dense Network Modules. PLoS ONE, 2013, 8, e76666.	1.1	24
134	Sequence context analysis in the mouse genome: Single nucleotide polymorphisms and CpG island sequences. Genomics, 2006, 87, 68-74.	1.3	23
135	TSEA-DB: a traitâ€“tissue association map for human complex traits and diseases. Nucleic Acids Research, 2019, 48, D1022-D1030.	6.5	23
136	Presence of three different paternal lineages among North Indians: A study of 560 Y chromosomes. Annals of Human Biology, 2009, 36, 46-59.	0.4	22
137	Dynamic protein interaction modules in human hepatocellular carcinoma progression. BMC Systems Biology, 2013, 7, S2.	3.0	22
138	Investigation of multi-trait associations using pathway-based analysis of GWAS summary statistics. BMC Genomics, 2019, 20, 79.	1.2	22
139	Distinct telomere length and molecular signatures in seminoma and non-seminoma of testicular germ cell tumor. Briefings in Bioinformatics, 2019, 20, 1502-1512.	3.2	22
140	Single-Cell RNA Sequencing Uncovers Paracrine Functions of the Epicardial-Derived Cells in Arrhythmogenic Cardiomyopathy. Circulation, 2021, 143, 2169-2187.	1.6	22
141	mutLBSgeneDB: mutated ligand binding site gene DataBase. Nucleic Acids Research, 2017, 45, D256-D263.	6.5	21
142	MicroRNA-374a, -4680, and -133b suppress cell proliferation through the regulation of genes associated with human cleft palate in cultured human palate cells. BMC Medical Genomics, 2019, 12, 93.	0.7	21
143	Characterization of Tumor-Suppressor Gene Inactivation Events in 33 Cancer Types. Cell Reports, 2019, 26, 496-506.e3.	2.9	21
144	CSEA-DB: an omnibus for human complex trait and cell type associations. Nucleic Acids Research, 2021, 49, D862-D870.	6.5	21

#	Article	IF	Citations
145	Classification of Cancer Primary Sites Using Machine Learning and Somatic Mutations. BioMed Research International, 2015, 2015, 1-9.	0.9	20
146	MicroRNA-655-3p and microRNA-497-5p inhibit cell proliferation in cultured human lip cells through the regulation of genes related to human cleft lip. BMC Medical Genomics, 2019, 12, 70.	0.7	20
147	Protein tyrosine phosphatase receptor Î´ serves as the orexigenic asprosin receptor. Cell Metabolism, 2022, 34, 549-563.e8.	7.2	20
148	Virus interactions with human signal transduction pathways. International Journal of Computational Biology and Drug Design, 2011, 4, 83.	0.3	19
149	Regulation rewiring analysis reveals mutual regulation between STAT1 and miR-155-5p in tumor immunosurveillance in seven major cancers. Scientific Reports, 2015, 5, 12063.	1.6	19
150	Kinase impact assessment in the landscape of fusion genes that retain kinase domains: a pan-cancer study. Briefings in Bioinformatics, 2016, 19, bbw127.	3.2	19
151	A Convergent Study of Genetic Variants Associated With Crohnâ€™s Disease: Evidence From GWAS, Gene Expression, Methylation, eQTL and TWAS. Frontiers in Genetics, 2019, 10, 318.	1.1	19
152	Integration of millions of transcriptomes using batch-aware triplet neural networks. Nature Machine Intelligence, 2021, 3, 705-715.	8.3	19
153	Top associated SNPs in prostate cancer are significantly enriched in cis-expression quantitative trait loci and at transcription factor binding sites. Oncotarget, 2014, 5, 6168-6177.	0.8	19
154	microRNA regulation in cancer: One arm or two arms?. International Journal of Cancer, 2015, 137, 1516-1518.	2.3	18
155	ConGEMs: Condensed Gene Co-Expression Module Discovery Through Rule-Based Clustering and Its Application to Carcinogenesis. Genes, 2018, 9, 7.	1.0	18
156	Glucocorticoids enhance the antileukemic activity of FLT3 inhibitors in FLT3-mutant acute myeloid leukemia. Blood, 2020, 136, 1067-1079.	0.6	18
157	The homing and inhibiting effects of hNSCs-BMP4 on human glioma stem cells. Oncotarget, 2016, 7, 17920-17931.	0.8	18
158	A developmental stage specific network approach for studying dynamic transcription factor-microRNA co-regulation during craniofacial development. Development (Cambridge), 2020, 147, .	1.2	17
159	Predicting regulatory variants using a dense epigenomic mapped CNN model elucidated the molecular basis of trait-tissue associations. Nucleic Acids Research, 2021, 49, 53-66.	6.5	17
160	Mega-analysis of Odds Ratio: A Convergent Method for a Deep Understanding of the Genetic Evidence in Schizophrenia. Schizophrenia Bulletin, 2019, 45, 698-708.	2.3	17
161	Deciphering Signaling Pathway Networks to Understand the Molecular Mechanisms of Metformin Action. PLoS Computational Biology, 2015, 11, e1004202.	1.5	17
162	Genome-wide CRISPR screens using isogenic cells reveal vulnerabilities conferred by loss of tumor suppressors. Science Advances, 2022, 8, eabm6638.	4.7	17

#	Article	IF	Citations
163	An evidence-based knowledgebase of pulmonary arterial hypertension to identify genes and pathways relevant to pathogenesis. Molecular BioSystems, 2014, 10, 732-740.	2.9	16
164	Clinically relevant genes and regulatory pathways associated with NRASQ61 mutations in melanoma through an integrative genomics approach. Oncotarget, 2015, 6, 2496-2508.	0.8	16
165	Towards integrated oncogenic marker recognition through mutual informationâ€based statistically significant feature extraction: an association rule mining based study on cancer expression and methylation profiles. Quantitative Biology, 2017, 5, 302-327.	0.3	16
166	MicroRNA-124-3p suppresses mouse lip mesenchymal cell proliferation through the regulation of genes associated with cleft lip in the mouse. BMC Genomics, 2019, 20, 852.	1.2	16
167	Translational bioinformatics in mental health: open access data sources and computational biomarker discovery. Briefings in Bioinformatics, 2019, 20, 842-856.	3.2	16
168	An integrative, genomic, transcriptomic and network-assisted study to identify genes associated with human cleft lip with or without cleft palate. BMC Medical Genomics, 2020, 13, 39.	0.7	16
169	Heterogeneous DNA methylation contributes to tumorigenesis through inducing the loss of coexpression connectivity in colorectal cancer. Genes Chromosomes and Cancer, 2015, 54, 110-121.	1.5	15
170	Common Variants in the MKL1 Gene Confer Risk of Schizophrenia. Schizophrenia Bulletin, 2015, 41, 715-727.	2.3	15
171	Distinct lithium-induced gene expression effects in lymphoblastoid cell lines from patients with bipolar disorder. European Neuropsychopharmacology, 2017, 27, 1110-1119.	0.3	15
172	p52 expression enhances lung cancer progression. Scientific Reports, 2018, 8, 6078.	1.6	15
173	Network-based identification of critical regulators as putative drivers of human cleft lip. BMC Medical Genomics, 2019, 12, 16.	0.7	15
174	Landscape of drug-resistance mutations in kinase regulatory hotspots. Briefings in Bioinformatics, 2021, 22, .	3.2	15
175	Progression of prostate carcinoma is promoted by adipose stromal cell-secreted CXCL12 signaling in prostate epithelium. Npj Precision Oncology, 2021, 5, 26.	2.3	15
176	Estrogenâ€related receptor Î± is involved in angiogenesis and skeletal muscle revascularization in hindlimb ischemia. FASEB Journal, 2021, 35, e21480.	0.2	15
177	DeepFun: a deep learning sequence-based model to decipher non-coding variant effect in a tissue- and cell type-specific manner. Nucleic Acids Research, 2021, 49, W131-W139.	6.5	15
178	Association Study of 167 Candidate Genes for Schizophrenia Selected by a Multi-Domain Evidence-Based Prioritization Algorithm and Neurodevelopmental Hypothesis. PLoS ONE, 2013, 8, e67776.	1.1	15
179	Charting the proteome landscape in major psychiatric disorders: From biomarkers to biological pathways towards drug discovery. European Neuropsychopharmacology, 2022, 61, 43-59.	0.3	15
180	ANCO-GeneDB: annotations and comprehensive analysis of candidate genes for alcohol, nicotine, cocaine and opioid dependence. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	14

#	Article	IF	Citations
181	Multi-Objective Optimized Fuzzy Clustering for Detecting Cell Clusters from Single-Cell Expression Profiles. Genes, 2019, 10, 611.	1.0	14
182	Oncolytic HSV Therapy Modulates Vesicular Trafficking Inducing Cisplatin Sensitivity and Antitumor Immunity. Clinical Cancer Research, 2021, 27, 542-553.	3.2	14
183	Computational learning of features for automated colonic polyp classification. Scientific Reports, 2021, 11, 4347.	1.6	14
184	Characterization of Schizophrenia Adverse Drug Interactions through a Network Approach and Drug Classification. BioMed Research International, 2013, 2013, 1-10.	0.9	13
185	Transcriptome- and proteome-oriented identification of dysregulated eIF4G, STAT3, and Hippo pathways altered by PIK3CA H1047R in HER2/ER-positive breast cancer. Breast Cancer Research and Treatment, 2016, 160, 457-474.	1.1	13
186	Convergent roles of de novo mutations and common variants in schizophrenia in tissue-specific and spatiotemporal co-expression network. Translational Psychiatry, 2018, 8, 105.	2.4	13
187	Changes in the Microbial Community Diversity of Oil Exploitation. Genes, 2019, 10, 556.	1.0	13
188	FOXK1 Participates in DNA Damage Response by Controlling 53BP1 Function. Cell Reports, 2020, 32, 108018.	2.9	13
189	Dense module searching for gene networks associated with multiple sclerosis. BMC Medical Genomics, 2020, 13, 48.	0.7	13
190	Investigating Cellular Trajectories in the Severity of COVID-19 and Their Transcriptional Programs Using Machine Learning Approaches. Genes, 2021, 12, 635.	1.0	13
191	Genome-wide CRISPR screens reveal cyclin C as synthetic survival target of BRCA2. Nucleic Acids Research, 2021, 49, 7476-7491.	6.5	13
192	Hereditary retinoblastoma iPSC model reveals aberrant spliceosome function driving bone malignancies. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2117857119.	3.3	13
193	Molecular signatures identified by integrating gene expression and methylation in non-seminoma and seminoma of testicular germ cell tumours. Epigenetics, 2021, 16, 162-176.	1.3	12
194	White matter deficits in cocaine use disorder: convergent evidence from in vivo diffusion tensor imaging and ex vivo proteomic analysis. Translational Psychiatry, 2021, 11, 252.	2.4	12
195	ERBB activation modulates sensitivity to MEK1/2 inhibition in a subset of driver-negative melanoma. Oncotarget, 2015, 6, 22348-22360.	0.8	12
196	Adipose tissueâ€“specific ablation of Ces1d causes metabolic dysregulation in mice. Life Science Alliance, 2022, 5, e202101209.	1.3	12
197	Networkâ€Assisted Investigation of Antipsychotic Drugs and Their Targets. Chemistry and Biodiversity, 2012, 9, 900-910.	1.0	11
198	deCS: A Tool for Systematic Cell Type Annotations of Single-Cell RNA Sequencing Data Among Human Tissues. Genomics, Proteomics and Bioinformatics, 2023, 21, 370-384.	3.0	11

#	Article	IF	Citations
199	Exploring drug-target interaction networks of illicit drugs. BMC Genomics, 2013, 14, S1.	1.2	10
200	Identification and Diagnostic Performance of a Small RNA within the PCA3 and BMCC1 Gene Locus That Potentially Targets mRNA. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 268-275.	1.1	10
201	DrivAER: Identification of driving transcriptional programs in single-cell RNA sequencing data. GigaScience, 2020, 9, .	3.3	10
202	Diverse types of genomic evidence converge on alcohol use disorder risk genes. Journal of Medical Genetics, 2020, 57, 733-743.	1.5	10
203	Gene expression imputation and cell-type deconvolution in human brain with spatiotemporal precision and its implications for brain-related disorders. Genome Research, 2021, 31, 146-158.	2.4	10
204	Personalized Pathway Enrichment Map of Putative Cancer Genes from Next Generation Sequencing Data. PLoS ONE, 2012, 7, e37595.	1.1	10
205	Network-Assisted Prediction of Potential Drugs for Addiction. BioMed Research International, 2014, 2014, 1-9.	0.9	9
206	A cross-cancer differential co-expression network reveals microRNA-regulated oncogenic functional modules. Molecular BioSystems, 2015, 11, 3244-3252.	2.9	9
207	Multiple transcription factors contribute to inter-chromosomal interaction in yeast. BMC Systems Biology, 2018, 12, 140.	3.0	9
208	Splicing QTL of human adipose-related traits. Scientific Reports, 2018, 8, 318.	1.6	9
209	Decoding whole-genome mutational signatures in 37 human pan-cancers by denoising sparse autoencoder neural network. Oncogene, 2020, 39, 5031-5041.	2.6	9
210	Overexpression of miR-1306-5p, miR-3195, and miR-3914 Inhibits Ameloblast Differentiation through Suppression of Genes Associated with Human Amelogenesis Imperfecta. International Journal of Molecular Sciences, 2021, 22, 2202.	1.8	9
211	DeepVISP: Deep Learning for Virus Site Integration Prediction and Motif Discovery. Advanced Science, 2021, 8, 2004958.	5.6	9
212	EmptyNN: A neural network based on positive and unlabeled learning to remove cell-free droplets and recover lost cells in scRNA-seq data. Patterns, 2021, 2, 100311.	3.1	9
213	Effects of tamoxifen inducible MerCreMer on gene expression in cardiac myocytes in mice. , 2022, 2, .		9
214	Patient-derived iPSCs link elevated mitochondrial respiratory complex I function to osteosarcoma in Rothmund-Thomson syndrome. PLoS Genetics, 2021, 17, e1009971.	1.5	9
215	Advances on PPARÎ³ Research in the Emerging Era of Precision Medicine. Current Drug Targets, 2018, 19, 663-673.	1.0	8
216	A Frameshift Variant in the CHST9 Gene Identified by Family-Based Whole Genome Sequencing Is Associated with Schizophrenia in Chinese Population. Scientific Reports, 2019, 9, 12717.	1.6	8

#	Article	IF	Citations
217	Genomic landscape of a metastatic malignant proliferating tricholemmal tumor and its response to PI3K inhibition. Npj Precision Oncology, 2019, 3, 5.	2.3	8
218	Decoding regulatory structures and features from epigenomics profiles: A Roadmap-ENCODE Variational Auto-Encoder (RE-VAE) model. Methods, 2021, 189, 44-53.	1.9	8
219	Distinct effect of prenatal and postnatal brain expression across 20 brain disorders and anthropometric social traits: a systematic study of spatiotemporal modularity. Briefings in Bioinformatics, 2021, 22, .	3.2	8
220	An integrative study of genetic variants with brain tissue expression identifies viral etiology and potential drug targets of multiple sclerosis. Molecular and Cellular Neurosciences, 2021, 115, 103656.	1.0	8
221	In silico ranking of phenolics for therapeutic effectiveness on cancer stem cells. BMC Bioinformatics, 2020, 21, 499.	1.2	8
222	Characterization of genome-wide association study data reveals spatiotemporal heterogeneity of mental disorders. BMC Medical Genomics, 2020, 13, 192.	0.7	8
223	Comparison of five supervised feature selection algorithms leading to top features and gene signatures from multi-omics data in cancer. BMC Bioinformatics, 2022, 23, 153.	1.2	8
224	Algorithms for network-based identification of differential regulators from transcriptome data: a systematic evaluation. Science China Life Sciences, 2014, 57, 1090-1102.	2.3	7
225	CNet: a multi-omics approach to detecting clinically associated, combinatory genomic signatures. Bioinformatics, 2019, 35, 5207-5215.	1.8	7
226	TET2 stabilization by 14-3-3 binding to the phosphorylated Serine 99 is deregulated by mutations in cancer. Cell Research, 2019, 29, 248-250.	5.7	7
227	Rewired Pathways and Disrupted Pathway Crosstalk in Schizophrenia Transcriptomes by Multiple Differential Coexpression Methods. Genes, 2021, 12, 665.	1.0	7
228	Co-delivery of novel bispecific and trispecific engagers by an amplicon vector augments the therapeutic effect of an HSV-based oncolytic virotherapy. , 2021, 9, e002454.		7
229	CleftGeneDB: a resource for annotating genes associated with cleft lip and cleft palate. Science Bulletin, 2021, 66, 2340-2342.	4.3	7
230	Detecting methylation signatures in neurodegenerative disease by density-based clustering of applications with reducing noise. Scientific Reports, 2020, 10, 22164.	1.6	7
231	Big data - a 21st century science Maginot Line? No-boundary thinking: shifting from the big data paradigm. BioData Mining, 2015, 8, 7.	2.2	6
232	Lung Cancer: One Disease or Many. Human Heredity, 2018, 83, 65-70.	0.4	6
233	Temozolomide-Induced RNA Interactome Uncovers Novel LncRNA Regulatory Loops in Glioblastoma. Cancers, 2020, 12, 2583.	1.7	6
234	An Integrative Transcriptomic and Methylation Approach for Identifying Differentially Expressed Circular RNAs Associated with DNA Methylation Change. Biomedicines, 2021, 9, 657.	1.4	6

#	Article	IF	Citations
235	Identification of microRNAs and gene regulatory networks in cleft lip common in humans and mice. Human Molecular Genetics, 2021, 30, 1881-1893.	1.4	6
236	A Deep Learningâ€“Based Framework for Supporting Clinical Diagnosis of Glioblastoma Subtypes. Frontiers in Genetics, 2022, 13, 855420.	1.1	6
237	Unsupervised Learning for Feature Representation Using Spatial Distribution of Amino Acids in Aldehyde Dehydrogenase (ALDH2) Protein Sequences. Mathematics, 2022, 10, 2228.	1.1	6
238	Snowball: resampling combined with distance-based regression to discover transcriptional consequences of a driver mutation. Bioinformatics, 2015, 31, 84-93.	1.8	5
239	MicroRNA-138 Increases Chemo-Sensitivity of Glioblastoma through Downregulation of Survivin. Biomedicines, 2021, 9, 780.	1.4	5
240	Crucial Roles of microRNA-16-5p and microRNA-27b-3p in Ameloblast Differentiation Through Regulation of Genes Associated With Amelogenesis Imperfecta. Frontiers in Genetics, 2022, 13, 788259.	1.1	5
241	TrapRM: Transcriptomic and proteomic rule mining using weighted shortest distance based multiple minimum supports for multi-omics dataset. , 2017, , .		4
242	The International Conference on Intelligent Biology and Medicine (ICIBM) 2016: summary and innovation in genomics. BMC Genomics, 2017, 18, 703.	1.2	4
243	Comprehensive characterization of tumor immune landscape following oncolytic virotherapy by single-cell RNA sequencing. Cancer Immunology, Immunotherapy, 2022, 71, 1479-1495.	2.0	4
244	Prioritization of risk genes in multiple sclerosis by a refined Bayesian framework followed by tissue-specificity and cell type feature assessment. BMC Genomics, 2022, 23, 362.	1.2	4
245	Features of Recent Codon Evolution: A Comparative Polymorphism-Fixation Study. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-9.	3.0	3
246	Translational Biomedical Informatics and Computational Systems Medicine. BioMed Research International, 2013, 2013, 1-2.	0.9	3
247	Functional Implications of Biochemical and Molecular Characteristics of Donation After Circulatory Death Livers. Transplantation Direct, 2015, 1, 1-9.	0.8	3
248	The International Conference on Intelligent Biology and Medicine (ICIBM) 2019: bioinformatics methods and applications for human diseases. BMC Bioinformatics, 2019, 20, 676.	1.2	3
249	A Tri-Component Conservation Strategy Reveals Highly Confident MicroRNA-mRNA Interactions and Evolution of MicroRNA Regulatory Networks. PLoS ONE, 2014, 9, e103142.	1.1	3
250	KCOSS: an ultra-fast k-mer counter for assembled genome analysis. Bioinformatics, 2022, 38, 933-940.	1.8	3
251	Identifying candidate genes and drug targets for Alzheimerâ€™s disease by an integrative network approach using genetic and brain region-specific proteomic data. Human Molecular Genetics, 2022, 31, 3341-3354.	1.4	3
252	Comprehensive analyses of tumor suppressor genes in protein-protein interaction networks: A topological perspective. , 2012, , .		2

#	Article	IF	Citations
253	The oncogenic and prognostic potential of eight microRNAs identified by a synergetic regulatory network approach in lung cancer. International Journal of Computational Biology and Drug Design, 2014, 7, 384.	0.3	2
254	Frontiers in Integrative Genomics and Translational Bioinformatics. BioMed Research International, 2015, 2015, 1-3.	0.9	2
255	Bioinformatics drives the applications of next-generation sequencing in translational biomedical research. Methods, 2015, 79-80, 1-2.	1.9	2
256	Whole-Genome Differentially Hydroxymethylated DNA Regions among Twins Discordant for Cardiovascular Death. Genes, 2021, 12, 1183.	1.0	2
257	The International Conference on Intelligent Biology and Medicine (ICIBM) 2020: Data-driven analytics in biomedical genomics. BMC Medical Genomics, 2020, 13, 189.	0.7	2
258	Accelerating bioinformatics research with International Conference on Intelligent Biology and Medicine 2020. BMC Bioinformatics, 2020, 21, 563.	1.2	2
259	Cell-Type-Specific Profibrotic Scores across Multi-Organ Systems Predict Cancer Prognosis. Cancers, 2021, 13, 6024.	1.7	2
260	GDF5+ chondroprogenitors derived from human pluripotent stem cells preferentially form permanent chondrocytes. Development (Cambridge), 2022, 149, .	1.2	2
261	Pathway-assisted investigation of atypical antipsychotic drugs and serotonin receptors in schizophrenia. , 2010, , .		1
262	A comparative study of methods for detecting small somatic variants in disease-normal paired next generation sequencing data. , 2012, , .		1
263	Integrated Approach in Systems Biology. Computational and Mathematical Methods in Medicine, 2014, 2014, 1-2.	0.7	1
264	Integrative Genomics and Computational Systems Medicine. BioMed Research International, 2014, 2014, 1-3.	0.9	1
265	The International Conference on Intelligent Biology and Medicine (ICIBM) 2016: from big data to big analytical tools. BMC Bioinformatics, 2017, 18, 405.	1.2	1
266	The International Conference on Intelligent Biology and Medicine 2018: Medical Informatics Thematic Track (MedicalInfo2018). BMC Medical Informatics and Decision Making, 2019, 19, 21.	1.5	1
267	A Multi-classifier Model to Identify Mitochondrial Respiratory Gene Signatures in Human Cancer. , 2019, , .		1
268	The International Conference on Intelligent Biology and Medicine 2019 (ICIBM 2019): computational methods and applications in medical genomics. BMC Medical Genomics, 2020, 13, 47.	0.7	1
269	Unsupervised Feature Selection Using an Integrated Strategy of Hierarchical Clustering with Singular Value Decomposition: An Integrative Biomarker Discovery Method with Application to Acute Myeloid Leukemia. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	1
270	Fostering precision psychiatry through bioinformatics. Revista Brasileira De Psiquiatria, 2021, , .	0.9	1

#	Article	IF	Citations
271	siRNA Mediate RNA Interference Concordant with Early On-Target Transient Transcriptional Interference. Genes, 2021, 12, 1290.	1.0	1
272	Single-cell RNA sequencing reveals a strong connection between Gadd45g upregulation and oncolytic HSV infection in tumor tissue. Molecular Therapy - Oncolytics, 2021, 23, 330-341.	2.0	1
273	SmartWarf - A portable automated warfarin dosing tool. , 2009, , .		0
274	Global Network Features of Cancer Genes in the Human Interactome. , 2009, , .		0
275	5.7: Presentation session: Neuroscience informatics: “Pathway-assisted investigation of atypical antipsychotic drugs and serotonin receptors in schizophrenia”. , 2010, , .		0
276	Development and implementation of a novel computational tool for an efficient construction of drug-target interactome. , 2011, , .		0
277	Next-Generation Sequencing in Human Genetic Studies: Genome Technologies and Applications to Human Genetic Studies. Human Heredity, 2018, 83, 105-106.	0.4	0
278	Computational Approaches for Modeling Signal Transduction Networks. , 2019, , 856-863.		0
279	Innovating Computational Biology and Intelligent Medicine: ICIBM 2019 Special Issue. Genes, 2020, 11, 437.	1.0	0
280	Distinct Murine Pancreatic Transcriptomic Signatures during Chronic Pancreatitis Recovery. Mediators of Inflammation, 2021, 2021, 1-13.	1.4	0
281	The International Conference on Intelligent Biology and Medicine (ICIBM) 2020: Scalable techniques and algorithms for computational genomics. BMC Genomics, 2020, 21, 831.	1.2	0
282	Negatively-Associated Maximal Frequent Geneset Mining on DNA Methylation Profile. , 2021, , .		0
283	Computational methods for omics data. International Journal of Computational Biology and Drug Design, 2014, 7, 97-101.	0.3	0
284	A Method for Bridging Population-Specific Genotypes to Detect Gene Modules Associated with Alzheimerâ€™s Disease. Cells, 2022, 11, 2219.	1.8	0
285	Drug-Target Network Study Reveals the Core Target-Protein Interactions of Various COVID-19 Treatments. Genes, 2022, 13, 1210.	1.0	0