Zhong-Ming Zhao

List of Publications by Year
in descending order

285	12,969	31976	37204
papers	citations	53 h-index	96 g-index

310	310	310	22527
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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.	6.9	11
2	Comprehensive characterization of tumor immune landscape following oncolytic virotherapy by single-cell RNA sequencing. Cancer Immunology, Immunotherapy, 2022, 71, 1479-1495.	4.2	4
3	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.	16.8	101
4	KCOSS: an ultra-fast k-mer counter for assembled genome analysis. Bioinformatics, 2022, 38, 933-940.	4.1	3
5	Effects of tamoxifen inducible MerCreMer on gene expression in cardiac myocytes in mice. , 2022, 2, .		9
6	NOTCH-Induced MDSC Recruitment after oHSV Virotherapy in CNS Cancer Models Modulates Antitumor Immunotherapy. Clinical Cancer Research, 2022, 28, 1460-1473.	7.0	26
7	A Deep Learningâ€“Based Framework for Supporting Clinical Diagnosis of Glioblastoma Subtypes. Frontiers in Genetics, 2022, 13, 855420.	2.3	6
8	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.	2.3	5
9	Protein tyrosine phosphatase receptor Î´ serves as the orexigenic asprosin receptor. Cell Metabolism, 2022, 34, 549-563.e8.	16.2	20
10	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.	7.1	13
11	GDF5+ chondroprogenitors derived from human pluripotent stem cells preferentially form permanent chondrocytes. Development (Cambridge), 2022, 149, .	2.5	2
12	Adipose tissueâ€“specific ablation of Ces1d causes metabolic dysregulation in mice. Life Science Alliance, 2022, 5, e202101209.	2.8	12
13	WebCSEA: web-based cell-type-specific enrichment analysis of genes. Nucleic Acids Research, 2022, 50, W782-W790.	14.5	29
14	Genome-wide CRISPR screens using isogenic cells reveal vulnerabilities conferred by loss of tumor suppressors. Science Advances, 2022, 8, eabm6638.	10.3	17
15	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.	2.8	4
16	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.	2.6	8
17	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.	2.9	3
18	Charting the proteome landscape in major psychiatric disorders: From biomarkers to biological pathways towards drug discovery. European Neuropsychopharmacology, 2022, 61, 43-59.	0.7	15

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19	Unsupervised Learning for Feature Representation Using Spatial Distribution of Amino Acids in Aldehyde Dehydrogenase (ALDH2) Protein Sequences. Mathematics, 2022, 10, 2228.	2.2	6
20	A Method for Bridging Population-Specific Genotypes to Detect Gene Modules Associated with Alzheimerâ€™s Disease. Cells, 2022, 11, 2219.	4.1	0
21	Drug-Target Network Study Reveals the Core Target-Protein Interactions of Various COVID-19 Treatments. Genes, 2022, 13, 1210.	2.4	0
22	Landscape of drug-resistance mutations in kinase regulatory hotspots. Briefings in Bioinformatics, 2021, 22, .	6.5	15
23	Deep4mC: systematic assessment and computational prediction for DNA N4-methylcytosine sites by deep learning. Briefings in Bioinformatics, 2021, 22, .	6.5	49
24	Molecular signatures identified by integrating gene expression and methylation in non-seminoma and seminoma of testicular germ cell tumours. Epigenetics, 2021, 16, 162-176.	2.7	12
25	KinaseMD: kinase mutations and drug response database. Nucleic Acids Research, 2021, 49, D552-D561.	14.5	43
26	Oncolytic HSV Therapy Modulates Vesicular Trafficking Inducing Cisplatin Sensitivity and Antitumor Immunity. Clinical Cancer Research, 2021, 27, 542-553.	7.0	14
27	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.	5.5	10
28	Convergent genomic and pharmacological evidence of PI3K/GSK3 signaling alterations in neurons from schizophrenia patients. Neuropsychopharmacology, 2021, 46, 673-682.	5.4	24
29	Machine Learning to Predict Delayed Cerebral Ischemia and Outcomes in Subarachnoid Hemorrhage. Neurology, 2021, 96, e553-e562.	1.1	38
30	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.	14.5	17
31	CSEA-DB: an omnibus for human complex trait and cell type associations. Nucleic Acids Research, 2021, 49, D862-D870.	14.5	21
32	Decoding regulatory structures and features from epigenomics profiles: A Roadmap-ENCODE Variational Auto-Encoder (RE-VAE) model. Methods, 2021, 189, 44-53.	3.8	8
33	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.	3.0	1
34	Computational learning of features for automated colonic polyp classification. Scientific Reports, 2021, 11, 4347.	3.3	14
35	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.	4.1	9
36	Deep generative neural network for accurate drug response imputation. Nature Communications, 2021, 12, 1740.	12.8	43

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37	DeepVISP: Deep Learning for Virus Site Integration Prediction and Motif Discovery. Advanced Science, 2021, 8, 2004958.	11.2	9
38	Progression of prostate carcinoma is promoted by adipose stromal cell-secreted CXCL12 signaling in prostate epithelium. Npj Precision Oncology, 2021, 5, 26.	5.4	15
39	Estrogenâ€related receptor Î± is involved in angiogenesis and skeletal muscle revascularization in hindlimb ischemia. FASEB Journal, 2021, 35, e21480.	0.5	15
40	Investigating Cellular Trajectories in the Severity of COVID-19 and Their Transcriptional Programs Using Machine Learning Approaches. Genes, 2021, 12, 635.	2.4	13
41	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.	4.8	12
42	Rewired Pathways and Disrupted Pathway Crosstalk in Schizophrenia Transcriptomes by Multiple Differential Coexpression Methods. Genes, 2021, 12, 665.	2.4	7
43	MicroRNA-138 suppresses glioblastoma proliferation through downregulation of CD44. Scientific Reports, 2021, 11, 9219.	3.3	26
44	Distinct Murine Pancreatic Transcriptomic Signatures during Chronic Pancreatitis Recovery. Mediators of Inflammation, 2021, 2021, 1-13.	3.0	0
45	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.	14.5	15
46	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, .	6.5	8
47	An Integrative Transcriptomic and Methylation Approach for Identifying Differentially Expressed Circular RNAs Associated with DNA Methylation Change. Biomedicines, 2021, 9, 657.	3.2	6
48	Identification of microRNAs and gene regulatory networks in cleft lip common in humans and mice. Human Molecular Genetics, 2021, 30, 1881-1893.	2.9	6
49	Association of CXCR6 with COVID-19 severity: delineating the host genetic factors in transcriptomic regulation. Human Genetics, 2021, 140, 1313-1328.	3.8	33
50	Cell-type deconvolution analysis identifies cancer-associated myofibroblast component as a poor prognostic factor in multiple cancer types. Oncogene, 2021, 40, 4686-4694.	5.9	29
51	Single-Cell RNA Sequencing Uncovers Paracrine Functions of the Epicardial-Derived Cells in Arrhythmogenic Cardiomyopathy. Circulation, 2021, 143, 2169-2187.	1.6	22
52	Integration of millions of transcriptomes using batch-aware triplet neural networks. Nature Machine Intelligence, 2021, 3, 705-715.	16.0	19
53	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.	2.1	29
54	MicroRNA-138 Increases Chemo-Sensitivity of Glioblastoma through Downregulation of Survivin. Biomedicines, 2021, 9, 780.	3.2	5

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55	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
56	Whole-Genome Differentially Hydroxymethylated DNA Regions among Twins Discordant for Cardiovascular Death. Genes, 2021, 12, 1183.	2.4	2
57	Genome-wide CRISPR screens reveal cyclin C as synthetic survival target of BRCA2. Nucleic Acids Research, 2021, 49, 7476-7491.	14.5	13
58	CleftGeneDB: a resource for annotating genes associated with cleft lip and cleft palate. Science Bulletin, 2021, 66, 2340-2342.	9.0	7
59	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.	7.9	31
60	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.	5.9	9
61	Fostering precision psychiatry through bioinformatics. Revista Brasileira De Psiquiatria, 2021, , .	1.7	1
62	siRNA Mediate RNA Interference Concordant with Early On-Target Transient Transcriptional Interference. Genes, 2021, 12, 1290.	2.4	1
63	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.	2.2	8
64	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.	4.4	1
65	Cell-Type-Specific Profibrotic Scores across Multi-Organ Systems Predict Cancer Prognosis. Cancers, 2021, 13, 6024.	3.7	2
66	Negatively-Associated Maximal Frequent Geneset Mining on DNA Methylation Profile. , 2021, , .		0
67	Patient-derived iPSCs link elevated mitochondrial respiratory complex I function to osteosarcoma in Rothmund-Thomson syndrome. PLoS Genetics, 2021, 17, e1009971.	3.5	9
68	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.	6.5	34
69	VISDB: a manually curated database of viral integration sites in the human genome. Nucleic Acids Research, 2020, 48, D633-D641.	14.5	39
70	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.	6.5	30
71	Multi-level transcriptome sequencing identifies COL1A1 as a candidate marker in human heart failure progression. BMC Medicine, 2020, 18, 2.	5.5	65
72	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.	3.5	34

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73	Alveolar regeneration through a Krt8+ transitional stem cell state that persists in human lung fibrosis. Nature Communications, 2020, 11, 3559.	12.8	378
74	A developmental stage specific network approach for studying dynamic transcription factor-microRNA co-regulation during craniofacial development. Development (Cambridge), 2020, 147, .	2.5	17
75	FOXK1 Participates in DNA Damage Response by Controlling 53BP1 Function. Cell Reports, 2020, 32, 108018.	6.4	13
76	Temozolomide-Induced RNA Interactome Uncovers Novel LncRNA Regulatory Loops in Glioblastoma. Cancers, 2020, 12, 2583.	3.7	6
77	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.	2.4	24
78	Age-associated telomere attrition in adipocyte progenitors predisposes to metabolic disease. Nature Metabolism, 2020, 2, 1482-1497.	11.9	39
79	DrivAER: Identification of driving transcriptional programs in single-cell RNA sequencing data. GigaScience, 2020, 9, .	6.4	10
80	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.	5.1	25
81	Glucocorticoids enhance the antileukemic activity of FLT3 inhibitors in FLT3-mutant acute myeloid leukemia. Blood, 2020, 136, 1067-1079.	1.4	18
82	Decoding whole-genome mutational signatures in 37 human pan-cancers by denoising sparse autoencoder neural network. Oncogene, 2020, 39, 5031-5041.	5.9	9
83	6mA-Finder: a novel online tool for predicting DNA N6-methyladenine sites in genomes. Bioinformatics, 2020, 36, 3257-3259.	4.1	34
84	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.	3.3	43
85	Diverse types of genomic evidence converge on alcohol use disorder risk genes. Journal of Medical Genetics, 2020, 57, 733-743.	3.2	10
86	Estrogen receptor-Î± expressing neurons in the ventrolateral VMH regulate glucose balance. Nature Communications, 2020, 11, 2165.	12.8	48
87	The International Conference on Intelligent Biology and Medicine 2019 (ICIBM 2019): computational methods and applications in medical genomics. BMC Medical Genomics, 2020, 13, 47.	1.5	1
88	Innovating Computational Biology and Intelligent Medicine: ICIBM 2019 Special Issue. Genes, 2020, 11, 437.	2.4	0
89	Dense module searching for gene networks associated with multiple sclerosis. BMC Medical Genomics, 2020, 13, 48.	1.5	13
90	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.	1.5	16

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91	Detecting methylation signatures in neurodegenerative disease by density-based clustering of applications with reducing noise. Scientific Reports, 2020, 10, 22164.	3.3	7
92	In silico ranking of phenolics for therapeutic effectiveness on cancer stem cells. BMC Bioinformatics, 2020, 21, 499.	2.6	8
93	The International Conference on Intelligent Biology and Medicine (ICIBM) 2020: Data-driven analytics in biomedical genomics. BMC Medical Genomics, 2020, 13, 189.	1.5	2
94	The International Conference on Intelligent Biology and Medicine (ICIBM) 2020: Scalable techniques and algorithms for computational genomics. BMC Genomics, 2020, 21, 831.	2.8	0
95	Characterization of genome-wide association study data reveals spatiotemporal heterogeneity of mental disorders. BMC Medical Genomics, 2020, 13, 192.	1.5	8
96	Accelerating bioinformatics research with International Conference on Intelligent Biology and Medicine 2020. BMC Bioinformatics, 2020, 21, 563.	2.6	2
97	Subtype-specific signaling pathways and genomic aberrations associated with prognosis of glioblastoma. Neuro-Oncology, 2019, 21, 59-70.	1.2	60
98	Computational Approaches for Modeling Signal Transduction Networks. , 2019, , 856-863.		0
99	Multi-Objective Optimized Fuzzy Clustering for Detecting Cell Clusters from Single-Cell Expression Profiles. Genes, 2019, 10, 611.	2.4	14
100	Changes in the Microbial Community Diversity of Oil Exploitation. Genes, 2019, 10, 556.	2.4	13
101	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.	1.5	21
102	TSEA-DB: a traitâ€“tissue association map for human complex traits and diseases. Nucleic Acids Research, 2019, 48, D1022-D1030.	14.5	23
103	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.	3.3	8
104	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.	1.5	20
105	CNet: a multi-omics approach to detecting clinically associated, combinatory genomic signatures. Bioinformatics, 2019, 35, 5207-5215.	4.1	7
106	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.	2.3	19
107	Clonal architectures predict clinical outcome in clear cell renal cell carcinoma. Nature Communications, 2019, 10, 1245.	12.8	44
108	deTS: tissue-specific enrichment analysis to decode tissue specificity. Bioinformatics, 2019, 35, 3842-3845.	4.1	51

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109	Gene2vec: distributed representation of genes based on co-expression. BMC Genomics, 2019, 20, 82.	2.8	87
110	Network-based identification of critical regulators as putative drivers of human cleft lip. BMC Medical Genomics, 2019, 12, 16.	1.5	15
111	The International Conference on Intelligent Biology and Medicine 2018: Medical Informatics Thematic Track (MedicalInfo2018). BMC Medical Informatics and Decision Making, 2019, 19, 21.	3.0	1
112	Investigation of multi-trait associations using pathway-based analysis of GWAS summary statistics. BMC Genomics, 2019, 20, 79.	2.8	22
113	Genomic landscape of a metastatic malignant proliferating tricholemmal tumor and its response to PI3K inhibition. Npj Precision Oncology, 2019, 3, 5.	5.4	8
114	A Multi-classifier Model to Identify Mitochondrial Respiratory Gene Signatures in Human Cancer. , 2019, , .		1
115	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.	2.8	16
116	The International Conference on Intelligent Biology and Medicine (ICIBM) 2019: bioinformatics methods and applications for human diseases. BMC Bioinformatics, 2019, 20, 676.	2.6	3
117	TET2 stabilization by 14-3-3 binding to the phosphorylated Serine 99 is deregulated by mutations in cancer. Cell Research, 2019, 29, 248-250.	12.0	7
118	Characterization of Tumor-Suppressor Gene Inactivation Events in 33 Cancer Types. Cell Reports, 2019, 26, 496-506.e3.	6.4	21
119	Distinct telomere length and molecular signatures in seminoma and non-seminoma of testicular germ cell tumor. Briefings in Bioinformatics, 2019, 20, 1502-1512.	6.5	22
120	Translational bioinformatics in mental health: open access data sources and computational biomarker discovery. Briefings in Bioinformatics, 2019, 20, 842-856.	6.5	16
121	Mega-analysis of Odds Ratio: A Convergent Method for a Deep Understanding of the Genetic Evidence in Schizophrenia. Schizophrenia Bulletin, 2019, 45, 698-708.	4.3	17
122	Genes and microRNAs associated with mouse cleft palate: A systematic review and bioinformatics analysis. Mechanisms of Development, 2018, 150, 21-27.	1.7	27
123	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
124	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
125	TissGDB: tissue-specific gene database in cancer. Nucleic Acids Research, 2018, 46, D1031-D1038.	14.5	63
126	Repurposing sertraline sensitizes nonâ€“small cell lung cancer cells to erlotinib by inducing autophagy. JCI Insight, 2018, 3, .	5.0	51

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127	Identification of gene signatures from RNA-seq data using Pareto-optimal cluster algorithm. BMC Systems Biology, 2018, 12, 126.	3.0	27
128	Next-Generation Sequencing in Human Genetic Studies: Genome Technologies and Applications to Human Genetic Studies. Human Heredity, 2018, 83, 105-106.	0.8	0
129	Circular RNA expression profiles during the differentiation of mouse neural stem cells. BMC Systems Biology, 2018, 12, 128.	3.0	31
130	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, .	3.0	14
131	Multiple transcription factors contribute to inter-chromosomal interaction in yeast. BMC Systems Biology, 2018, 12, 140.	3.0	9
132	Convergent roles of de novo mutations and common variants in schizophrenia in tissue-specific and spatiotemporal co-expression network. Translational Psychiatry, 2018, 8, 105.	4.8	13
133	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.	8.2	32
134	An integrative functional genomics framework for effective identification of novel regulatory variants in genomeâ€“phenome studies. Genome Medicine, 2018, 10, 7.	8.2	29
135	Splicing QTL of human adipose-related traits. Scientific Reports, 2018, 8, 318.	3.3	9
136	p52 expression enhances lung cancer progression. Scientific Reports, 2018, 8, 6078.	3.3	15
137	Advances on PPARÎ³ Research in the Emerging Era of Precision Medicine. Current Drug Targets, 2018, 19, 663-673.	2.1	8
138	ConGEMs: Condensed Gene Co-Expression Module Discovery Through Rule-Based Clustering and Its Application to Carcinogenesis. Genes, 2018, 9, 7.	2.4	18
139	Lung Cancer: One Disease or Many. Human Heredity, 2018, 83, 65-70.	0.8	6
140	Impacts of somatic mutations on gene expression: an association perspective. Briefings in Bioinformatics, 2017, 18, bbw037.	6.5	40
141	Extracellular Matrix/Integrin Signaling Promotes Resistance to Combined Inhibition of HER2 and PI3K in HER2+ Breast Cancer. Cancer Research, 2017, 77, 3280-3292.	0.9	76
142	Tissue-Specific Signaling Networks Rewired by Major Somatic Mutations in Human Cancer Revealed by Proteome-Wide Discovery. Cancer Research, 2017, 77, 2810-2821.	0.9	29
143	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.	6.2	72
144	Distinct lithium-induced gene expression effects in lymphoblastoid cell lines from patients with bipolar disorder. European Neuropsychopharmacology, 2017, 27, 1110-1119.	0.7	15

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145	Decoding critical long non-coding RNA in ovarian cancer epithelial-to-mesenchymal transition. Nature Communications, 2017, 8, 1604.	12.8	159
146	Asprosin is a centrally acting orexigenic hormone. Nature Medicine, 2017, 23, 1444-1453.	30.7	216
147	SZGR 2.0: a one-stop shop of schizophrenia candidate genes. Nucleic Acids Research, 2017, 45, D915-D924.	14.5	44
148	mutLBSgeneDB: mutated ligand binding site gene DataBase. Nucleic Acids Research, 2017, 45, D256-D263.	14.5	21
149	The International Conference on Intelligent Biology and Medicine (ICIBM) 2016: from big data to big analytical tools. BMC Bioinformatics, 2017, 18, 405.	2.6	1
150	TrapRM: Transcriptomic and proteomic rule mining using weighted shortest distance based multiple minimum supports for multi-omics dataset. , 2017, , .		4
151	Unique protein expression signatures of survival time in kidney renal clear cell carcinoma through a pan-cancer screening. BMC Genomics, 2017, 18, 678.	2.8	24
152	Circular RNA expression profiles and features in human tissues: a study using RNA-seq data. BMC Genomics, 2017, 18, 680.	2.8	193
153	scRNASeqDB: A Database for RNA-Seq Based Gene Expression Profiles in Human Single Cells. Genes, 2017, 8, 368.	2.4	80
154	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.	0.5	16
155	Investigating MicroRNA and transcription factor co-regulatory networks in colorectal cancer. BMC Bioinformatics, 2017, 18, 388.	2.6	35
156	The International Conference on Intelligent Biology and Medicine (ICIBM) 2016: summary and innovation in genomics. BMC Genomics, 2017, 18, 703.	2.8	4
157	Targeted activation of <scp>CREB</scp> in reactive astrocytes is neuroprotective in focal acute cortical injury. Glia, 2016, 64, 853-874.	4.9	27
158	Kinase impact assessment in the landscape of fusion genes that retain kinase domains: a pan-cancer study. Briefings in Bioinformatics, 2016, 19, bbw127.	6.5	19
159	Toward Repurposing Metformin as a Precision Anti-Cancer Therapy Using Structural Systems Pharmacology. Scientific Reports, 2016, 6, 20441.	3.3	34
160	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.	4.4	46
161	MET Exon 14 Skipping in Non-Small Cell Lung Cancer. Oncologist, 2016, 21, 481-486.	3.7	94
162	Genetic Relationship between Schizophrenia and Nicotine Dependence. Scientific Reports, 2016, 6, 25671.	3.3	67

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163	Concordance of copy number loss and down-regulation of tumor suppressor genes: a pan-cancer study. BMC Genomics, 2016, 17, 532.	2.8	37
164	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.	2.5	13
165	The Potential Roles of Long Noncoding RNAs (lncRNA) in Glioblastoma Development. Molecular Cancer Therapeutics, 2016, 15, 2977-2986.	4.1	51
166	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.	2.8	24
167	Investigating cellular network heterogeneity and modularity in cancer: a network entropy and unbalanced motif approach. BMC Systems Biology, 2016, 10, 65.	3.0	36
168	TSGene 2.0: an updated literature-based knowledgebase for tumor suppressor genes. Nucleic Acids Research, 2016, 44, D1023-D1031.	14.5	332
169	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.	3.8	43
170	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.	4.0	31
171	Systematic dissection of dysregulated transcription factorâ€“miRNA feed-forward loops across tumor types. Briefings in Bioinformatics, 2016, 17, 996-1008.	6.5	54
172	ccmGDB: a database for cancer cell metabolism genes. Nucleic Acids Research, 2016, 44, D959-D968.	14.5	41
173	Advances in computational approaches for prioritizing driver mutations and significantly mutated genes in cancer genomes. Briefings in Bioinformatics, 2016, 17, 642-656.	6.5	120
174	Systems Biology-Based Investigation of Cellular Antiviral Drug Targets Identified by Gene-Trap Insertional Mutagenesis. PLoS Computational Biology, 2016, 12, e1005074.	3.2	52
175	The homing and inhibiting effects of hNSCs-BMP4 on human glioma stem cells. Oncotarget, 2016, 7, 17920-17931.	1.8	18
176	Regulation rewiring analysis reveals mutual regulation between STAT1 and miR-155-5p in tumor immunosurveillance in seven major cancers. Scientific Reports, 2015, 5, 12063.	3.3	19
177	Frontiers in Integrative Genomics and Translational Bioinformatics. BioMed Research International, 2015, 2015, 1-3.	1.9	2
178	Classification of Cancer Primary Sites Using Machine Learning and Somatic Mutations. BioMed Research International, 2015, 2015, 1-9.	1.9	20
179	Clinically relevant genes and regulatory pathways associated with NRASQ61 mutations in melanoma through an integrative genomics approach. Oncotarget, 2015, 6, 2496-2508.	1.8	16
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