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	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
2	Computational tools for copy number variation (CNV) detection using next-generation sequencing data: features and perspectives. BMC Bioinformatics, 2013, 14, S1.	2.6	452
3	Alveolar regeneration through a Krt8+ transitional stem cell state that persists in human lung fibrosis. Nature Communications, 2020, 11, 3559.	12.8	378
4	TSGene 2.0: an updated literature-based knowledgebase for tumor suppressor genes. Nucleic Acids Research, 2016, 44, D1023-D1031.	14.5	332
5	TSGene: a web resource for tumor suppressor genes. Nucleic Acids Research, 2013, 41, D970-D976.	14.5	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.	4.4	264
7	dmGWAS: dense module searching for genome-wide association studies in proteinâ€“protein interaction networks. Bioinformatics, 2011, 27, 95-102.	4.1	253
8	Rationale for co-targeting IGF-1R and ALK in ALK fusionâ€“positive lung cancer. Nature Medicine, 2014, 20, 1027-1034.	30.7	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.	4.4	233
11	Interaction with WDR5 Promotes Target Gene Recognition and Tumorigenesis by MYC. Molecular Cell, 2015, 58, 440-452.	9.7	224
12	Asprosin is a centrally acting orexigenic hormone. Nature Medicine, 2017, 23, 1444-1453.	30.7	216
13	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
14	Whole-genome sequencing reveals oncogenic mutations in mycosis fungoides. Blood, 2015, 126, 508-519.	1.4	193
15	Circular RNA expression profiles and features in human tissues: a study using RNA-seq data. BMC Genomics, 2017, 18, 680.	2.8	193
16	Common variants conferring risk of schizophrenia: A pathway analysis of GWAS data. Schizophrenia Research, 2010, 122, 38-42.	2.0	190
17	Gene set analysis of genome-wide association studies: Methodological issues and perspectives. Genomics, 2011, 98, 1-8.	2.9	180
18	Mutations in GDF6 are associated with vertebral segmentation defects in Klippel-Feil syndrome. Human Mutation, 2008, 29, 1017-1027.	2.5	170

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19	Decoding critical long non-coding RNA in ovarian cancer epithelial-to-mesenchymal transition. Nature Communications, 2017, 8, 1604.	12.8	159
20	Investigating single nucleotide polymorphism (SNP) density in the human genome and its implications for molecular evolution. Gene, 2003, 312, 207-213.	2.2	146
21	A meta-analysis of oxidative stress markers in schizophrenia. Science China Life Sciences, 2010, 53, 112-124.	4.9	146
22	Detecting somatic point mutations in cancer genome sequencing data: a comparison of mutation callers. Genome Medicine, 2013, 5, 91.	8.2	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.	5.5	127
25	Uncovering MicroRNA and Transcription Factor Mediated Regulatory Networks in Glioblastoma. PLoS Computational Biology, 2012, 8, e1002488.	3.2	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.	7.9	124
27	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
28	Schizophrenia Gene Networks and Pathways and Their Applications for Novel Candidate Gene Selection. PLoS ONE, 2010, 5, e11351.	2.5	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.	16.8	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.	1.7	98
31	Network-Assisted Investigation of Combined Causal Signals from Genome-Wide Association Studies in Schizophrenia. PLoS Computational Biology, 2012, 8, e1002587.	3.2	98
32	VarWalker: Personalized Mutation Network Analysis of Putative Cancer Genes from Next-Generation Sequencing Data. PLoS Computational Biology, 2014, 10, e1003460.	3.2	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.	1.8	96
34	MET Exon 14 Skipping in Non-Small Cell Lung Cancer. Oncologist, 2016, 21, 481-486.	3.7	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.	2.8	87

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37	Network-assisted analysis to prioritize GWAS results: principles, methods and perspectives. Human Genetics, 2014, 133, 125-138.	3.8	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.	4.1	84
39	DCGL v2.0: An R Package for Unveiling Differential Regulation from Differential Co-expression. PLoS ONE, 2013, 8, e79729.	2.5	83
40	scRNASeqDB: A Database for RNA-Seq Based Gene Expression Profiles in Human Single Cells. Genes, 2017, 8, 368.	2.4	80
41	Studying Tumorigenesis through Network Evolution and Somatic Mutational Perturbations in the Cancer Interactome. Molecular Biology and Evolution, 2014, 31, 2156-2169.	8.9	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.	0.9	76
43	A multi-dimensional evidence-based candidate gene prioritization approach for complex diseasesâ€“schizophrenia as a case. Bioinformatics, 2009, 25, 2595-6602.	4.1	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.	6.2	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.	3.2	68
46	VERSE: a novel approach to detect virus integration in host genomes through reference genome customization. Genome Medicine, 2015, 7, 2.	8.2	68
47	Genetic Relationship between Schizophrenia and Nicotine Dependence. Scientific Reports, 2016, 6, 25671.	3.3	67
48	Multi-level transcriptome sequencing identifies COL1A1 as a candidate marker in human heart failure progression. BMC Medicine, 2020, 18, 2.	5.5	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.	3.2	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.	6.4	64
51	RNA-Seq analysis implicates dysregulation of the immune system in schizophrenia. BMC Genomics, 2012, 13, S2.	2.8	63
52	TissGDB: tissue-specific gene database in cancer. Nucleic Acids Research, 2018, 46, D1031-D1038.	14.5	63
53	MBSTAR: multiple instance learning for predicting specific functional binding sites in microRNA targets. Scientific Reports, 2015, 5, 8004.	3.3	62
54	Pathway-based analysis of GWAS datasets: effective but caution required. International Journal of Neuropsychopharmacology, 2011, 14, 567-572.	2.1	60

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55	Subtype-specific signaling pathways and genomic aberrations associated with prognosis of glioblastoma. Neuro-Oncology, 2019, 21, 59-70.	1.2	60
56	Patterns and processes of somatic mutations in nine major cancers. BMC Medical Genomics, 2014, 7, 11.	1.5	57
57	EW_dmGWAS: edge-weighted dense module search for genome-wide association studies and gene expression profiles. Bioinformatics, 2015, 31, 2591-2594.	4.1	57
58	MSEA: detection and quantification of mutation hotspots through mutation set enrichment analysis. Genome Biology, 2014, 15, 489.	8.8	54
59	Systematic dissection of dysregulated transcription factorâ€“miRNA feed-forward loops across tumor types. Briefings in Bioinformatics, 2016, 17, 996-1008.	6.5	54
60	Functional complementation between transcriptional methylation regulation and post-transcriptional microRNA regulation in the human genome. BMC Genomics, 2011, 12, S15.	2.8	52
61	Systems Biology-Based Investigation of Cellular Antiviral Drug Targets Identified by Gene-Trap Insertional Mutagenesis. PLoS Computational Biology, 2016, 12, e1005074.	3.2	52
62	The Potential Roles of Long Noncoding RNAs (lncRNA) in Glioblastoma Development. Molecular Cancer Therapeutics, 2016, 15, 2977-2986.	4.1	51
63	Repurposing sertraline sensitizes nonâ€“small cell lung cancer cells to erlotinib by inducing autophagy. JCI Insight, 2018, 3, .	5.0	51
64	deTS: tissue-specific enrichment analysis to decode tissue specificity. Bioinformatics, 2019, 35, 3842-3845.	4.1	51
65	An efficient hierarchical generalized linear mixed model for pathway analysis of genome-wide association studies. Bioinformatics, 2011, 27, 686-692.	4.1	50
66	CpG islands: Algorithms and applications in methylation studies. Biochemical and Biophysical Research Communications, 2009, 382, 643-645.	2.1	49
67	Deep4mC: systematic assessment and computational prediction for DNA N4-methylcytosine sites by deep learning. Briefings in Bioinformatics, 2021, 22, .	6.5	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.	5.5	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.	4.3	48
70	Estrogen receptor-Î± expressing neurons in the ventrolateral VMH regulate glucose balance. Nature Communications, 2020, 11, 2165.	12.8	48
71	Reproducible combinatorial regulatory networks elucidate novel oncogenic microRNAs in non-small cell lung cancer. Rna, 2014, 20, 1356-1368.	3.5	47
72	CpG islands or CpG clusters: how to identify functional GC-rich regions in a genome?. BMC Bioinformatics, 2009, 10, 65.	2.6	46

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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.	4.4	46
74	SZGR 2.0: a one-stop shop of schizophrenia candidate genes. Nucleic Acids Research, 2017, 45, D915-D924.	14.5	44
75	Clonal architectures predict clinical outcome in clear cell renal cell carcinoma. Nature Communications, 2019, 10, 1245.	12.8	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.	3.8	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.	3.3	43
78	KinaseMD: kinase mutations and drug response database. Nucleic Acids Research, 2021, 49, D552-D561.	14.5	43
79	Deep generative neural network for accurate drug response imputation. Nature Communications, 2021, 12, 1740.	12.8	43
80	ccmGDB: a database for cancer cell metabolism genes. Nucleic Acids Research, 2016, 44, D959-D968.	14.5	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.	6.5	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.	14.5	39
84	DTome: a web-based tool for drug-target interactome construction. BMC Bioinformatics, 2012, 13, S7.	2.6	39
85	VISDB: a manually curated database of viral integration sites in the human genome. Nucleic Acids Research, 2020, 48, D633-D641.	14.5	39
86	Age-associated telomere attrition in adipocyte progenitors predisposes to metabolic disease. Nature Metabolism, 2020, 2, 1482-1497.	11.9	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.	1.5	38
88	Machine Learning to Predict Delayed Cerebral Ischemia and Outcomes in Subarachnoid Hemorrhage. Neurology, 2021, 96, e553-e562.	1.1	38
89	ERGR: An ethanol-related gene resource. Nucleic Acids Research, 2009, 37, D840-D845.	14.5	37
90	Concordance of copy number loss and down-regulation of tumor suppressor genes: a pan-cancer study. BMC Genomics, 2016, 17, 532.	2.8	37

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91	Sequence context analysis of 8.2 million single nucleotide polymorphisms in the human genome. Gene, 2006, 366, 316-324.	2.2	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.	3.5	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.	2.6	35
95	Enriched pathways for major depressive disorder identified from a genome-wide association study. International Journal of Neuropsychopharmacology, 2012, 15, 1401-1411.	2.1	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.	3.3	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.	6.5	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.	3.5	34
100	6mA-Finder: a novel online tool for predicting DNA N6-methyladenine sites in genomes. Bioinformatics, 2020, 36, 3257-3259.	4.1	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.	3.8	33
102	Association of CXCR6 with COVID-19 severity: delineating the host genetic factors in transcriptomic regulation. Human Genetics, 2021, 140, 1313-1328.	3.8	33
103	Discovering Disease-specific Biomarker Genes for Cancer Diagnosis and Prognosis. Technology in Cancer Research and Treatment, 2010, 9, 219-229.	1.9	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.	8.2	32
105	Functional consequences of somatic mutations in cancer using protein pocket-based prioritization approach. Genome Medicine, 2014, 6, 81.	8.2	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.	4.0	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.	7.9	31

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109	In-depth genomic data analyses revealed complex transcriptional and epigenetic dysregulations of BRAF V600E in melanoma. Molecular Cancer, 2015, 14, 60.	19.2	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.	6.5	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.	2.5	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.	0.9	29
113	An integrative functional genomics framework for effective identification of novel regulatory variants in genomeâ€“phenome studies. Genome Medicine, 2018, 10, 7.	8.2	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.	5.9	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.	2.1	29
116	WebCSEA: web-based cell-type-specific enrichment analysis of genes. Nucleic Acids Research, 2022, 50, W782-W790.	14.5	29
117	Multi-species data integration and gene ranking enrich significant results in an alcoholism genome-wide association study. BMC Genomics, 2012, 13, S16.	2.8	28
118	Optimizing the Sequence of Anti-EGFRâ€“Targeted Therapy in EGFR-Mutant Lung Cancer. Molecular Cancer Therapeutics, 2015, 14, 542-552.	4.1	28
119	Distinct and Competitive Regulatory Patterns of Tumor Suppressor Genes and Oncogenes in Ovarian Cancer. PLoS ONE, 2012, 7, e44175.	2.5	27
120	Targeted activation of <scp>CREB</scp> in reactive astrocytes is neuroprotective in focal acute cortical injury. Glia, 2016, 64, 853-874.	4.9	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.	2.9	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.	2.0	26
125	MicroRNA-138 suppresses glioblastoma proliferation through downregulation of CD44. Scientific Reports, 2021, 11, 9219.	3.3	26
126	CNVannotator: A Comprehensive Annotation Server for Copy Number Variation in the Human Genome. PLoS ONE, 2013, 8, e80170.	2.5	26

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127	NOTCH-Induced MDSC Recruitment after oHSV Virotherapy in CNS Cancer Models Modulates Antitumor Immunotherapy. Clinical Cancer Research, 2022, 28, 1460-1473.	7.0	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.	5.1	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.	2.8	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.	2.8	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.	2.4	24
132	Convergent genomic and pharmacological evidence of PI3K/GSK3 signaling alterations in neurons from schizophrenia patients. Neuropsychopharmacology, 2021, 46, 673-682.	5.4	24
133	Multi-Dimensional Prioritization of Dental Caries Candidate Genes and Its Enriched Dense Network Modules. PLoS ONE, 2013, 8, e76666.	2.5	24
134	Sequence context analysis in the mouse genome: Single nucleotide polymorphisms and CpG island sequences. Genomics, 2006, 87, 68-74.	2.9	23
135	TSEA-DB: a traitâ€“tissue association map for human complex traits and diseases. Nucleic Acids Research, 2019, 48, D1022-D1030.	14.5	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.	1.0	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.	2.8	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.	6.5	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.	14.5	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.	1.5	21
143	Characterization of Tumor-Suppressor Gene Inactivation Events in 33 Cancer Types. Cell Reports, 2019, 26, 496-506.e3.	6.4	21
144	CSEA-DB: an omnibus for human complex trait and cell type associations. Nucleic Acids Research, 2021, 49, D862-D870.	14.5	21

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145	Classification of Cancer Primary Sites Using Machine Learning and Somatic Mutations. BioMed Research International, 2015, 2015, 1-9.	1.9	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.	1.5	20
147	Protein tyrosine phosphatase receptor Î´ serves as the orexigenic asprosin receptor. Cell Metabolism, 2022, 34, 549-563.e8.	16.2	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.	3.3	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.	6.5	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.	2.3	19
152	Integration of millions of transcriptomes using batch-aware triplet neural networks. Nature Machine Intelligence, 2021, 3, 705-715.	16.0	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.	1.8	19
154	microRNA regulation in cancer: One arm or two arms?. International Journal of Cancer, 2015, 137, 1516-1518.	5.1	18
155	ConGEMs: Condensed Gene Co-Expression Module Discovery Through Rule-Based Clustering and Its Application to Carcinogenesis. Genes, 2018, 9, 7.	2.4	18
156	Glucocorticoids enhance the antileukemic activity of FLT3 inhibitors in FLT3-mutant acute myeloid leukemia. Blood, 2020, 136, 1067-1079.	1.4	18
157	The homing and inhibiting effects of hNSCs-BMP4 on human glioma stem cells. Oncotarget, 2016, 7, 17920-17931.	1.8	18
158	A developmental stage specific network approach for studying dynamic transcription factor-microRNA co-regulation during craniofacial development. Development (Cambridge), 2020, 147, .	2.5	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.	14.5	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.	4.3	17
161	Deciphering Signaling Pathway Networks to Understand the Molecular Mechanisms of Metformin Action. PLoS Computational Biology, 2015, 11, e1004202.	3.2	17
162	Genome-wide CRISPR screens using isogenic cells reveal vulnerabilities conferred by loss of tumor suppressors. Science Advances, 2022, 8, eabm6638.	10.3	17

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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.	1.8	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.	0.5	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.	2.8	16
167	Translational bioinformatics in mental health: open access data sources and computational biomarker discovery. Briefings in Bioinformatics, 2019, 20, 842-856.	6.5	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.	1.5	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.	2.8	15
170	Common Variants in the MKL1 Gene Confer Risk of Schizophrenia. Schizophrenia Bulletin, 2015, 41, 715-727.	4.3	15
171	Distinct lithium-induced gene expression effects in lymphoblastoid cell lines from patients with bipolar disorder. European Neuropsychopharmacology, 2017, 27, 1110-1119.	0.7	15
172	p52 expression enhances lung cancer progression. Scientific Reports, 2018, 8, 6078.	3.3	15
173	Network-based identification of critical regulators as putative drivers of human cleft lip. BMC Medical Genomics, 2019, 12, 16.	1.5	15
174	Landscape of drug-resistance mutations in kinase regulatory hotspots. Briefings in Bioinformatics, 2021, 22, .	6.5	15
175	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
176	Estrogenâ€related receptor Î± is involved in angiogenesis and skeletal muscle revascularization in hindlimb ischemia. FASEB Journal, 2021, 35, e21480.	0.5	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.	14.5	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.	2.5	15
179	Charting the proteome landscape in major psychiatric disorders: From biomarkers to biological pathways towards drug discovery. European Neuropsychopharmacology, 2022, 61, 43-59.	0.7	15
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