Zhongming Zhao

List of Publications by Year
in descending order

199 papers	10,943 citations	30070 54 h-index	42399 92 g-index
203 all docs	203 docs citations	203 times ranked	19869 citing authors

#	Article	IF	Citations
1	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
2	Protein tyrosine phosphatase receptor Î´ serves as the orexigenic asprosin receptor. Cell Metabolism, 2022, 34, 549-563.e8.	16.2	20
3	Landscape of drug-resistance mutations in kinase regulatory hotspots. Briefings in Bioinformatics, 2021, 22, .	6.5	15
4	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
5	KinaseMD: kinase mutations and drug response database. Nucleic Acids Research, 2021, 49, D552-D561.	14.5	43
6	Deep generative neural network for accurate drug response imputation. Nature Communications, 2021, 12, 1740.	12.8	43
7	DeepVISP: Deep Learning for Virus Site Integration Prediction and Motif Discovery. Advanced Science, 2021, 8, 2004958.	11.2	9
8	Investigating Cellular Trajectories in the Severity of COVID-19 and Their Transcriptional Programs Using Machine Learning Approaches. Genes, 2021, 12, 635.	2.4	13
9	Rewired Pathways and Disrupted Pathway Crosstalk in Schizophrenia Transcriptomes by Multiple Differential Coexpression Methods. Genes, 2021, 12, 665.	2.4	7
10	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
11	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
12	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
13	Association of CXCR6 with COVID-19 severity: delineating the host genetic factors in transcriptomic regulation. Human Genetics, 2021, 140, 1313-1328.	3.8	33
14	siRNA Mediate RNA Interference Concordant with Early On-Target Transient Transcriptional Interference. Genes, 2021, 12, 1290.	2.4	1
15	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
16	VISDB: a manually curated database of viral integration sites in the human genome. Nucleic Acids Research, 2020, 48, D633-D641.	14.5	39
17	Genome-Wide Meta-Analyses of FTND and TTFC Phenotypes. Nicotine and Tobacco Research, 2020, 22, 900-909.	2.6	17
18	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

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19	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
20	A developmental stage specific network approach for studying dynamic transcription factor-microRNA co-regulation during craniofacial development. Development (Cambridge), 2020, 147, .	2.5	17
21	Temozolomide-Induced RNA Interactome Uncovers Novel LncRNA Regulatory Loops in Glioblastoma. Cancers, 2020, 12, 2583.	3.7	6
22	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
23	Decoding whole-genome mutational signatures in 37 human pan-cancers by denoising sparse autoencoder neural network. Oncogene, 2020, 39, 5031-5041.	5.9	9
24	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
25	Dense module searching for gene networks associated with multiple sclerosis. BMC Medical Genomics, 2020, 13, 48.	1.5	13
26	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
27	Detecting methylation signatures in neurodegenerative disease by density-based clustering of applications with reducing noise. Scientific Reports, 2020, 10, 22164.	3.3	7
28	Subtype-specific signaling pathways and genomic aberrations associated with prognosis of glioblastoma. Neuro-Oncology, 2019, 21, 59-70.	1.2	60
29	Computational Approaches for Modeling Signal Transduction Networks. , 2019, , 856-863.		0
30	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
31	TSEA-DB: a traitâ€“tissue association map for human complex traits and diseases. Nucleic Acids Research, 2019, 48, D1022-D1030.	14.5	23
32	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
33	Network-based identification of critical regulators as putative drivers of human cleft lip. BMC Medical Genomics, 2019, 12, 16.	1.5	15
34	Investigation of multi-trait associations using pathway-based analysis of GWAS summary statistics. BMC Genomics, 2019, 20, 79.	2.8	22
35	Distance based knowledge retrieval through rule mining for complex biomarker recognition from tri-omics profiles. International Journal of Computational Biology and Drug Design, 2019, 12, 105.	0.3	2
36	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

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37	Characterization of Tumor-Suppressor Gene Inactivation Events in 33 Cancer Types. Cell Reports, 2019, 26, 496-506.e3.	6.4	21
38	Translational bioinformatics in mental health: open access data sources and computational biomarker discovery. Briefings in Bioinformatics, 2019, 20, 842-856.	6.5	16
39	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
40	Genes and microRNAs associated with mouse cleft palate: A systematic review and bioinformatics analysis. Mechanisms of Development, 2018, 150, 21-27.	1.7	27
41	TissGDB: tissue-specific gene database in cancer. Nucleic Acids Research, 2018, 46, D1031-D1038.	14.5	63
42	Repurposing sertraline sensitizes nonâ€“small cell lung cancer cells to erlotinib by inducing autophagy. JCI Insight, 2018, 3, .	5.0	51
43	Identification of gene signatures from RNA-seq data using Pareto-optimal cluster algorithm. BMC Systems Biology, 2018, 12, 126.	3.0	27
44	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
45	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
46	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
47	An integrative functional genomics framework for effective identification of novel regulatory variants in genomeâ€“phenome studies. Genome Medicine, 2018, 10, 7.	8.2	29
48	ConGEMs: Condensed Gene Co-Expression Module Discovery Through Rule-Based Clustering and Its Application to Carcinogenesis. Genes, 2018, 9, 7.	2.4	18
49	Lung Cancer: One Disease or Many. Human Heredity, 2018, 83, 65-70.	0.8	6
50	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
51	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
52	Decoding critical long non-coding RNA in ovarian cancer epithelial-to-mesenchymal transition. Nature Communications, 2017, 8, 1604.	12.8	159
53	Asprosin is a centrally acting orexigenic hormone. Nature Medicine, 2017, 23, 1444-1453.	30.7	216
54	SZGR 2.0: a one-stop shop of schizophrenia candidate genes. Nucleic Acids Research, 2017, 45, D915-D924.	14.5	44

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55	mutLBSgeneDB: mutated ligand binding site gene DataBase. Nucleic Acids Research, 2017, 45, D256-D263.	14.5	21
56	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
57	Circular RNA expression profiles and features in human tissues: a study using RNA-seq data. BMC Genomics, 2017, 18, 680.	2.8	193
58	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
59	Investigating MicroRNA and transcription factor co-regulatory networks in colorectal cancer. BMC Bioinformatics, 2017, 18, 388.	2.6	35
60	Domain retention in transcription factor fusion genes and its biological and clinical implications: a pan-cancer study. Oncotarget, 2017, 8, 110103-110117.	1.8	15
61	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
62	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
63	Genetic Relationship between Schizophrenia and Nicotine Dependence. Scientific Reports, 2016, 6, 25671.	3.3	67
64	Concordance of copy number loss and down-regulation of tumor suppressor genes: a pan-cancer study. BMC Genomics, 2016, 17, 532.	2.8	37
65	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
66	The Potential Roles of Long Noncoding RNAs (lncRNA) in Glioblastoma Development. Molecular Cancer Therapeutics, 2016, 15, 2977-2986.	4.1	51
67	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
68	Investigating cellular network heterogeneity and modularity in cancer: a network entropy and unbalanced motif approach. BMC Systems Biology, 2016, 10, 65.	3.0	36
69	TSGene 2.0: an updated literature-based knowledgebase for tumor suppressor genes. Nucleic Acids Research, 2016, 44, D1023-D1031.	14.5	332
70	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
71	Critical Genomic Networks and Vasoreactive Variants in Idiopathic Pulmonary Arterial Hypertension. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 464-475.	5.6	69
72	Systematic dissection of dysregulated transcription factorâ€“miRNA feed-forward loops across tumor types. Briefings in Bioinformatics, 2016, 17, 996-1008.	6.5	54

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73	ccmGDB: a database for cancer cell metabolism genes. Nucleic Acids Research, 2016, 44, D959-D968.	14.5	41
74	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
75	Systems Biology-Based Investigation of Cellular Antiviral Drug Targets Identified by Gene-Trap Insertional Mutagenesis. PLoS Computational Biology, 2016, 12, e1005074.	3.2	52
76	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
77	Discovery and characterization of long intergenic non-coding RNAs (lincRNA) module biomarkers in prostate cancer: an integrative analysis of RNA-Seq data. BMC Genomics, 2015, 16, S3.	2.8	50
78	Oncogenes and tumor suppressor genes: comparative genomics and network perspectives. BMC Genomics, 2015, 16, S8.	2.8	41
79	Classification of Cancer Primary Sites Using Machine Learning and Somatic Mutations. BioMed Research International, 2015, 2015, 1-9.	1.9	20
80	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
81	Rare Variants in RTEL1 Are Associated with Familial Interstitial Pneumonia. American Journal of Respiratory and Critical Care Medicine, 2015, 191, 646-655.	5.6	170
82	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
83	VERSE: a novel approach to detect virus integration in host genomes through reference genome customization. Genome Medicine, 2015, 7, 2.	8.2	68
84	Whole-genome sequencing reveals oncogenic mutations in mycosis fungoides. Blood, 2015, 126, 508-519.	1.4	193
85	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
86	In-depth genomic data analyses revealed complex transcriptional and epigenetic dysregulations of BRAF V600E in melanoma. Molecular Cancer, 2015, 14, 60.	19.2	30
87	EW_dmGWAS: edge-weighted dense module search for genome-wide association studies and gene expression profiles. Bioinformatics, 2015, 31, 2591-2594.	4.1	57
88	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
89	Common Variants in the MKL1 Gene Confer Risk of Schizophrenia. Schizophrenia Bulletin, 2015, 41, 715-727.	4.3	15
90	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

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91	ERBB activation modulates sensitivity to MEK1/2 inhibition in a subset of driver-negative melanoma. Oncotarget, 2015, 6, 22348-22360.	1.8	12
92	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
93	Algorithms for network-based identification of differential regulators from transcriptome data: a systematic evaluation. Science China Life Sciences, 2014, 57, 1090-1102.	4.9	7
94	VarWalker: Personalized Mutation Network Analysis of Putative Cancer Genes from Next-Generation Sequencing Data. PLoS Computational Biology, 2014, 10, e1003460.	3.2	96
95	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
96	MSEA: detection and quantification of mutation hotspots through mutation set enrichment analysis. Genome Biology, 2014, 15, 489.	8.8	54
97	Functional consequences of somatic mutations in cancer using protein pocket-based prioritization approach. Genome Medicine, 2014, 6, 81.	8.2	31
98	Network-assisted analysis to prioritize GWAS results: principles, methods and perspectives. Human Genetics, 2014, 133, 125-138.	3.8	86
99	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
100	Beyond Histology: Translating Tumor Genotypes into Clinically Effective Targeted Therapies. Clinical Cancer Research, 2014, 20, 2264-2275.	7.0	60
101	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
102	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
103	Linking Biochemical Pathways and Networks to Adverse Drug Reactions. IEEE Transactions on Nanobioscience, 2014, 13, 131-137.	3.3	12
104	Studying Tumorigenesis through Network Evolution and Somatic Mutational Perturbations in the Cancer Interactome. Molecular Biology and Evolution, 2014, 31, 2156-2169.	8.9	79
105	Reproducible combinatorial regulatory networks elucidate novel oncogenic microRNAs in non-small cell lung cancer. Rna, 2014, 20, 1356-1368.	3.5	47
106	Patterns and processes of somatic mutations in nine major cancers. BMC Medical Genomics, 2014, 7, 11.	1.5	57
107	Rationale for co-targeting IGF-1R and ALK in ALK fusionâ€“positive lung cancer. Nature Medicine, 2014, 20, 1027-1034.	30.7	243
108	Evaluating four major algorithms for identifying differential regulators in condition-specific transcriptional responses. BMC Bioinformatics, 2014, 15, .	2.6	0

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109	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
110	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
111	Exploring drug-target interaction networks of illicit drugs. BMC Genomics, 2013, 14, S1.	2.8	10
112	Detecting somatic point mutations in cancer genome sequencing data: a comparison of mutation callers. Genome Medicine, 2013, 5, 91.	8.2	146
113	Synergetic regulatory networks mediated by oncogene-driven microRNAs and transcription factors in serous ovarian cancer. Molecular BioSystems, 2013, 9, 3187.	2.9	40
114	Application of next generation sequencing to human gene fusion detection: computational tools, features and perspectives. Briefings in Bioinformatics, 2013, 14, 506-519.	6.5	102
115	TSGene: a web resource for tumor suppressor genes. Nucleic Acids Research, 2013, 41, D970-D976.	14.5	295
116	VirusFinder: Software for Efficient and Accurate Detection of Viruses and Their Integration Sites in Host Genomes through Next Generation Sequencing Data. PLoS ONE, 2013, 8, e64465.	2.5	139
117	DCGL v2.0: An R Package for Unveiling Differential Regulation from Differential Co-expression. PLoS ONE, 2013, 8, e79729.	2.5	83
118	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
119	Association Signals Unveiled by a Comprehensive Gene Set Enrichment Analysis of Dental Caries Genome-Wide Association Studies. PLoS ONE, 2013, 8, e72653.	2.5	15
120	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
121	Multi-Dimensional Prioritization of Dental Caries Candidate Genes and Its Enriched Dense Network Modules. PLoS ONE, 2013, 8, e76666.	2.5	24
122	CNVannotator: A Comprehensive Annotation Server for Copy Number Variation in the Human Genome. PLoS ONE, 2013, 8, e80170.	2.5	26
123	Uncovering MicroRNA and Transcription Factor Mediated Regulatory Networks in Glioblastoma. PLoS Computational Biology, 2012, 8, e1002488.	3.2	124
124	Network-Assisted Investigation of Combined Causal Signals from Genome-Wide Association Studies in Schizophrenia. PLoS Computational Biology, 2012, 8, e1002587.	3.2	98
125	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
126	Enriched pathways for major depressive disorder identified from a genome-wide association study. International Journal of Neuropsychopharmacology, 2012, 15, 1401-1411.	2.1	34

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127	BRAF L597 Mutations in Melanoma Are Associated with Sensitivity to MEK Inhibitors. Cancer Discovery, 2012, 2, 791-797.	9.4	194
128	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
129	Comprehensive analyses of tumor suppressor genes in protein-protein interaction networks: A topological perspective. , 2012, , .		2
130	Role of Insulin-Like Growth Factor-1 Signaling Pathway in Cisplatin-Resistant Lung Cancer Cells. International Journal of Radiation Oncology Biology Physics, 2012, 82, e563-e572.	0.8	60
131	Investigating association of four gene regions (GABRB3, MAOB, PAH, and SLC6A4) with five symptoms in schizophrenia. Psychiatry Research, 2012, 198, 202-206.	3.3	20
132	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
133	GenRev: Exploring functional relevance of genes in molecular networks. Genomics, 2012, 99, 183-188.	2.9	45
134	A network and functional investigation of illicit drugs and their targets. , 2012, , .		1
135	Investigating the relationship of DNA methylation with mutation rate and allele frequency in the human genome. BMC Genomics, 2012, 13, S7.	2.8	92
136	RNA-Seq analysis implicates dysregulation of the immune system in schizophrenia. BMC Genomics, 2012, 13, S2.	2.8	63
137	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
138	Searching joint association signals in CATIE schizophrenia genome-wide association studies through a refined integrative network approach. BMC Genomics, 2012, 13, S15.	2.8	8
139	Integrative pathway analysis of genome-wide association studies and gene expression data in prostate cancer. BMC Systems Biology, 2012, 6, S13.	3.0	27
140	Distinct and Competitive Regulatory Patterns of Tumor Suppressor Genes and Oncogenes in Ovarian Cancer. PLoS ONE, 2012, 7, e44175.	2.5	27
141	L-arginine Supplementation Improves Responses to Injury and Inflammation in Dextran Sulfate Sodium Colitis. PLoS ONE, 2012, 7, e33546.	2.5	129
142	NGS catalog: A database of next generation sequencing studies in humans. Human Mutation, 2012, 33, E2341-E2355.	2.5	32
143	Genetic overlap of schizophrenia and bipolar disorder in a highâ€density linkage survey in the Portuguese Island population. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 383-391.	1.7	12
144	DNA Methylation Profiling Distinguishes Three Clusters of Breast Cancer Cell Lines. Chemistry and Biodiversity, 2012, 9, 848-856.	2.1	3

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145	DTome: a web-based tool for drug-target interactome construction. BMC Bioinformatics, 2012, 13, S7.	2.6	39
146	Personalized Pathway Enrichment Map of Putative Cancer Genes from Next Generation Sequencing Data. PLoS ONE, 2012, 7, e37595.	2.5	10
147	Integrative analysis of common neurodegenerative diseases using gene association, interaction networks and mRNA expression data. AMIA Summits on Translational Science Proceedings, 2012, 2012, 62-71.	0.4	11
148	Network-assisted causal gene detection in genome-wide association studies: an improved module search algorithm. , 2011, , 131-134.		4
149	Gene set analysis of genome-wide association studies: Methodological issues and perspectives. Genomics, 2011, 98, 1-8.	2.9	180
150	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
151	Prioritization of Epilepsy Associated Candidate Genes by Convergent Analysis. PLoS ONE, 2011, 6, e17162.	2.5	24
152	Prioritization and Evaluation of Depression Candidate Genes by Combining Multidimensional Data Resources. PLoS ONE, 2011, 6, e18696.	2.5	27
153	Virus interactions with human signal transduction pathways. International Journal of Computational Biology and Drug Design, 2011, 4, 83.	0.3	19
154	IL-15 Regulates Homeostasis and Terminal Maturation of NKT Cells. Journal of Immunology, 2011, 187, 6335-6345.	0.8	139
155	A comprehensive network and pathway analysis of candidate genes in major depressive disorder. BMC Systems Biology, 2011, 5, S12.	3.0	89
156	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
157	Functional complementation between transcriptional methylation regulation and post-transcriptional microRNA regulation in the human genome. BMC Genomics, 2011, 12, S15.	2.8	52
158	Do cancer proteins really interact strongly in the human proteinâ€“protein interaction network?. Computational Biology and Chemistry, 2011, 35, 121-125.	2.3	38
159	dmGWAS: dense module searching for genome-wide association studies in proteinâ€“protein interaction networks. Bioinformatics, 2011, 27, 95-102.	4.1	253
160	Conservation and divergence of DNA methylation in eukaryotes. Epigenetics, 2011, 6, 134-140.	2.7	65
161	Pathway-based analysis of GWAS datasets: effective but caution required. International Journal of Neuropsychopharmacology, 2011, 14, 567-572.	2.1	60
162	An efficient hierarchical generalized linear mixed model for pathway analysis of genome-wide association studies. Bioinformatics, 2011, 27, 686-692.	4.1	50

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163	Identifying genes progressively silenced in preneoplastic and neoplastic liver tissues. International Journal of Computational Biology and Drug Design, 2010, 3, 52.	0.3	4
164	Assessing gene length biases in gene set analysis of Genome-Wide Association Studies. International Journal of Computational Biology and Drug Design, 2010, 3, 297.	0.3	9
165	A comparative study of cancer proteins in the human protein-protein interaction network. BMC Genomics, 2010, 11, S5.	2.8	84
166	Gene- and evidence-based candidate gene selection for schizophrenia and gene feature analysis. Artificial Intelligence in Medicine, 2010, 48, 99-106.	6.5	11
167	Hdac3 Is Essential for the Maintenance of Chromatin Structure and Genome Stability. Cancer Cell, 2010, 18, 436-447.	16.8	305
168	A Novel microRNA and transcription factor mediated regulatory network in schizophrenia. BMC Systems Biology, 2010, 4, 10.	3.0	145
169	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
170	Discovering Disease-specific Biomarker Genes for Cancer Diagnosis and Prognosis. Technology in Cancer Research and Treatment, 2010, 9, 219-229.	1.9	32
171	Features of Recent Codon Evolution: A Comparative Polymorphism-Fixation Study. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-9.	3.0	3
172	Common variants conferring risk of schizophrenia: A pathway analysis of GWAS data. Schizophrenia Research, 2010, 122, 38-42.	2.0	190
173	Schizophrenia Gene Networks and Pathways and Their Applications for Novel Candidate Gene Selection. PLoS ONE, 2010, 5, e11351.	2.5	110
174	New Genomic Structure for Prostate Cancer Specific Gene PCA3 within BMCC1: Implications for Prostate Cancer Detection and Progression. PLoS ONE, 2009, 4, e4995.	2.5	74
175	Apoptotic Engulfment Pathway and Schizophrenia. PLoS ONE, 2009, 4, e6875.	2.5	35
176	Pathway and Network Analysis of Schizophrenia Candidate Genes under Meta-Analysis Linkage Peaks. , 2009, , .		0
177	A multi-dimensional evidence-based candidate gene prioritization approach for complex diseasesâ€“schizophrenia as a case. Bioinformatics, 2009, 25, 2595-6602.	4.1	72
178	CpG islands or CpG clusters: how to identify functional GC-rich regions in a genome?. BMC Bioinformatics, 2009, 10, 65.	2.6	46
179	CpG islands: Algorithms and applications in methylation studies. Biochemical and Biophysical Research Communications, 2009, 382, 643-645.	2.1	49
180	Contrast features of CpG islands in the promoter and other regions in the dog genome. Genomics, 2009, 94, 117-124.	2.9	21

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