# Zhongming Zhao

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | TSGene 2.0: an updated literature-based knowledgebase for tumor suppressor genes. Nucleic Acids Research, 2016, 44, D1023-D1031. | 14.5 | 332 |
| 2 | Hdac3 Is Essential for the Maintenance of Chromatin Structure and Genome Stability. Cancer Cell, 2010, 18, 436-447. | 16.8 | 305 |
| 3 | TSGene: a web resource for tumor suppressor genes. Nucleic Acids Research, 2013, 41, D970-D976. | 14.5 | 295 |
| 4 | 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 |
| 5 | dmGWAS: dense module searching for genome-wide association studies in proteinâ€“protein interaction networks. Bioinformatics, 2011, 27, 95-102. | 4.1 | 253 |
| 6 | Rationale for co-targeting IGF-1R and ALK in ALK fusionâ€“positive lung cancer. Nature Medicine, 2014, 20, 1027-1034. | 30.7 | 243 |
| 7 | Moderate mutation rate in the SARS coronavirus genome and its implications. BMC Evolutionary Biology, 2004, 4, 21. | 3.2 | 235 |
| 8 | 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 |
| 9 | Asprosin is a centrally acting orexigenic hormone. Nature Medicine, 2017, 23, 1444-1453. | 30.7 | 216 |
| 10 | BRAF L597 Mutations in Melanoma Are Associated with Sensitivity to MEK Inhibitors. Cancer Discovery, 2012, 2, 791-797. | 9.4 | 194 |
| 11 | Whole-genome sequencing reveals oncogenic mutations in mycosis fungoides. Blood, 2015, 126, 508-519. | 1.4 | 193 |
| 12 | Circular RNA expression profiles and features in human tissues: a study using RNA-seq data. BMC Genomics, 2017, 18, 680. | 2.8 | 193 |
| 13 | Common variants conferring risk of schizophrenia: A pathway analysis of GWAS data. Schizophrenia Research, 2010, 122, 38-42. | 2.0 | 190 |
| 14 | Gene set analysis of genome-wide association studies: Methodological issues and perspectives. Genomics, 2011, 98, 1-8. | 2.9 | 180 |
| 15 | Mutations in GDF6 are associated with vertebral segmentation defects in Klippel-Feil syndrome. Human Mutation, 2008, 29, 1017-1027. | 2.5 | 170 |
| 16 | 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 |
| 17 | Decoding critical long non-coding RNA in ovarian cancer epithelial-to-mesenchymal transition. Nature Communications, 2017, 8, 1604. | 12.8 | 159 |
| 18 | Investigating single nucleotide polymorphism (SNP) density in the human genome and its implications for molecular evolution. Gene, 2003, 312, 207-213. | 2.2 | 146 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Detecting somatic point mutations in cancer genome sequencing data: a comparison of mutation callers. Genome Medicine, 2013, 5, 91. | 8.2 | 146 |
| 20 | A Novel microRNA and transcription factor mediated regulatory network in schizophrenia. BMC Systems Biology, 2010, 4, 10. | 3.0 | 145 |
| 21 | IL-15 Regulates Homeostasis and Terminal Maturation of NKT Cells. Journal of Immunology, 2011, 187, 6335-6345. | 0.8 | 139 |
| 22 | 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 |
| 23 | L-arginine Supplementation Improves Responses to Injury and Inflammation in Dextran Sulfate Sodium Colitis. PLoS ONE, 2012, 7, e33546. | 2.5 | 129 |
| 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 | CpG island density and its correlations with genomic features in mammalian genomes. Genome Biology, 2008, 9, R79. | 9.6 | 107 |
| 30 | 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 |
| 31 | 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 |
| 32 | Network-Assisted Investigation of Combined Causal Signals from Genome-Wide Association Studies in Schizophrenia. PLoS Computational Biology, 2012, 8, e1002587. | 3.2 | 98 |
| 33 | VarWalker: Personalized Mutation Network Analysis of Putative Cancer Genes from Next-Generation Sequencing Data. PLoS Computational Biology, 2014, 10, e1003460. | 3.2 | 96 |
| 34 | 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 |
| 35 | Investigating the relationship of DNA methylation with mutation rate and allele frequency in the human genome. BMC Genomics, 2012, 13, S7. | 2.8 | 92 |
| 36 | A comprehensive network and pathway analysis of candidate genes in major depressive disorder. BMC Systems Biology, 2011, 5, S12. | 3.0 | 89 |

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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 comparative study of cancer proteins in the human protein-protein interaction network. BMC Genomics, 2010, 11, S5. | 2.8 | 84 |
| 39 | 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 |
| 40 | DCGL v2.0: An R Package for Unveiling Differential Regulation from Differential Co-expression. PLoS ONE, 2013, 8, e79729. | 2.5 | 83 |
| 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 | 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 |
| 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 | 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 |
| 46 | 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 |
| 47 | VERSE: a novel approach to detect virus integration in host genomes through reference genome customization. Genome Medicine, 2015, 7, 2. | 8.2 | 68 |
| 48 | Genetic Relationship between Schizophrenia and Nicotine Dependence. Scientific Reports, 2016, 6, 25671. | 3.3 | 67 |
| 49 | Conservation and divergence of DNA methylation in eukaryotes. Epigenetics, 2011, 6, 134-140. | 2.7 | 65 |
| 50 | 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 |
| 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 | Pathway-based analysis of GWAS datasets: effective but caution required. International Journal of Neuropsychopharmacology, 2011, 14, 567-572. | 2.1 | 60 |
| 54 | 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 |

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|---|---|---|---|
| 55 | Beyond Histology: Translating Tumor Genotypes into Clinically Effective Targeted Therapies. Clinical Cancer Research, 2014, 20, 2264-2275. | 7.0 | 60 |
| 56 | Subtype-specific signaling pathways and genomic aberrations associated with prognosis of glioblastoma. Neuro-Oncology, 2019, 21, 59-70. | 1.2 | 60 |
| 57 | Patterns and processes of somatic mutations in nine major cancers. BMC Medical Genomics, 2014, 7, 11. | 1.5 | 57 |
| 58 | EW_dmGWAS: edge-weighted dense module search for genome-wide association studies and gene expression profiles. Bioinformatics, 2015, 31, 2591-2594. | 4.1 | 57 |
| 59 | Mutational spectrum in the recent human genome inferred by single nucleotide polymorphisms. Genomics, 2006, 88, 527-534. | 2.9 | 56 |
| 60 | MSEA: detection and quantification of mutation hotspots through mutation set enrichment analysis. Genome Biology, 2014, 15, 489. | 8.8 | 54 |
| 61 | Systematic dissection of dysregulated transcription factorâ€“miRNA feed-forward loops across tumor types. Briefings in Bioinformatics, 2016, 17, 996-1008. | 6.5 | 54 |
| 62 | Functional complementation between transcriptional methylation regulation and post-transcriptional microRNA regulation in the human genome. BMC Genomics, 2011, 12, S15. | 2.8 | 52 |
| 63 | Systems Biology-Based Investigation of Cellular Antiviral Drug Targets Identified by Gene-Trap Insertional Mutagenesis. PLoS Computational Biology, 2016, 12, e1005074. | 3.2 | 52 |
| 64 | The Potential Roles of Long Noncoding RNAs (lncRNA) in Glioblastoma Development. Molecular Cancer Therapeutics, 2016, 15, 2977-2986. | 4.1 | 51 |
| 65 | Repurposing sertraline sensitizes nonâ€“small cell lung cancer cells to erlotinib by inducing autophagy. JCI Insight, 2018, 3, . | 5.0 | 51 |
| 66 | An efficient hierarchical generalized linear mixed model for pathway analysis of genome-wide association studies. Bioinformatics, 2011, 27, 686-692. | 4.1 | 50 |
| 67 | 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 |
| 68 | CpG islands: Algorithms and applications in methylation studies. Biochemical and Biophysical Research Communications, 2009, 382, 643-645. | 2.1 | 49 |
| 69 | 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 |
| 70 | Reproducible combinatorial regulatory networks elucidate novel oncogenic microRNAs in non-small cell lung cancer. Rna, 2014, 20, 1356-1368. | 3.5 | 47 |
| 71 | Features and Trend of Loss of Promoter-Associated CpG Islands in the Human and Mouse Genomes. Molecular Biology and Evolution, 2007, 24, 1991-2000. | 8.9 | 46 |
| 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 | GenRev: Exploring functional relevance of genes in molecular networks. Genomics, 2012, 99, 183-188. | 2.9 | 45 |
| 75 | Comparative Analysis of CpG Islands in Four Fish Genomes. Comparative and Functional Genomics, 2008, 2008, 1-6. | 2.0 | 44 |
| 76 | SZGR 2.0: a one-stop shop of schizophrenia candidate genes. Nucleic Acids Research, 2017, 45, D915-D924. | 14.5 | 44 |
| 77 | 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 |
| 78 | 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 |
| 79 | KinaseMD: kinase mutations and drug response database. Nucleic Acids Research, 2021, 49, D552-D561. | 14.5 | 43 |
| 80 | Deep generative neural network for accurate drug response imputation. Nature Communications, 2021, 12, 1740. | 12.8 | 43 |
| 81 | Oncogenes and tumor suppressor genes: comparative genomics and network perspectives. BMC Genomics, 2015, 16, S8. | 2.8 | 41 |
| 82 | ccmGDB: a database for cancer cell metabolism genes. Nucleic Acids Research, 2016, 44, D959-D968. | 14.5 | 41 |
| 83 | Synergetic regulatory networks mediated by oncogene-driven microRNAs and transcription factors in serous ovarian cancer. Molecular BioSystems, 2013, 9, 3187. | 2.9 | 40 |
| 84 | 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 |
| 85 | DTome: a web-based tool for drug-target interactome construction. BMC Bioinformatics, 2012, 13, S7. | 2.6 | 39 |
| 86 | VISDB: a manually curated database of viral integration sites in the human genome. Nucleic Acids Research, 2020, 48, D633-D641. | 14.5 | 39 |
| 87 | Methylation-Dependent Transition Rates Are Dependent on Local Sequence Lengths and Genomic Regions. Molecular Biology and Evolution, 2007, 24, 23-25. | 8.9 | 38 |
| 88 | 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 |
| 89 | Do cancer proteins really interact strongly in the human proteinâ€“protein interaction network?. Computational Biology and Chemistry, 2011, 35, 121-125. | 2.3 | 38 |
| 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 | Investigating cellular network heterogeneity and modularity in cancer: a network entropy and unbalanced motif approach. BMC Systems Biology, 2016, 10, 65. | 3.0 | 36 |
| 93 | The influence of neighboring-nucleotide composition on single nucleotide polymorphisms (SNPs) in the mouse genome and its comparison with human SNPs. Genomics, 2004, 84, 785-795. | 2.9 | 35 |
| 94 | Apoptotic Engulfment Pathway and Schizophrenia. PLoS ONE, 2009, 4, e6875. | 2.5 | 35 |
| 95 | Investigating MicroRNA and transcription factor co-regulatory networks in colorectal cancer. BMC Bioinformatics, 2017, 18, 388. | 2.6 | 35 |
| 96 | Enriched pathways for major depressive disorder identified from a genome-wide association study. International Journal of Neuropsychopharmacology, 2012, 15, 1401-1411. | 2.1 | 34 |
| 97 | 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 |
| 98 | 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 |
| 99 | 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 |
| 100 | Association of CXCR6 with COVID-19 severity: delineating the host genetic factors in transcriptomic regulation. Human Genetics, 2021, 140, 1313-1328. | 3.8 | 33 |
| 101 | Discovering Disease-specific Biomarker Genes for Cancer Diagnosis and Prognosis. Technology in Cancer Research and Treatment, 2010, 9, 219-229. | 1.9 | 32 |
| 102 | NGS catalog: A database of next generation sequencing studies in humans. Human Mutation, 2012, 33, E2341-E2355. | 2.5 | 32 |
| 103 | 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 |
| 104 | The dystrobrevin binding protein 1 (DTNBP1) gene is associated with schizophrenia in the Irish Case Control Study of Schizophrenia (ICCSS) sample. Schizophrenia Research, 2009, 115, 245-253. | 2.0 | 31 |
| 105 | Functional consequences of somatic mutations in cancer using protein pocket-based prioritization approach. Genome Medicine, 2014, 6, 81. | 8.2 | 31 |
| 106 | In-depth genomic data analyses revealed complex transcriptional and epigenetic dysregulations of BRAF V600E in melanoma. Molecular Cancer, 2015, 14, 60. | 19.2 | 30 |
| 107 | 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 |
| 108 | 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 |

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| 109 | 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 |
| 110 | An integrative functional genomics framework for effective identification of novel regulatory variants in genomeâ€“phenome studies. Genome Medicine, 2018, 10, 7. | 8.2 | 29 |
| 111 | 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 |
| 112 | Prioritization and Evaluation of Depression Candidate Genes by Combining Multidimensional Data Resources. PLoS ONE, 2011, 6, e18696. | 2.5 | 27 |
| 113 | Integrative pathway analysis of genome-wide association studies and gene expression data in prostate cancer. BMC Systems Biology, 2012, 6, S13. | 3.0 | 27 |
| 114 | Distinct and Competitive Regulatory Patterns of Tumor Suppressor Genes and Oncogenes in Ovarian Cancer. PLoS ONE, 2012, 7, e44175. | 2.5 | 27 |
| 115 | Genes and microRNAs associated with mouse cleft palate: A systematic review and bioinformatics analysis. Mechanisms of Development, 2018, 150, 21-27. | 1.7 | 27 |
| 116 | Identification of gene signatures from RNA-seq data using Pareto-optimal cluster algorithm. BMC Systems Biology, 2018, 12, 126. | 3.0 | 27 |
| 117 | Nucleotide Variation and Haplotype Diversity in a 10-kb Noncoding Region in Three Continental Human Populations. Genetics, 2006, 174, 399-409. | 2.9 | 26 |
| 118 | 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 |
| 119 | CNVannotator: A Comprehensive Annotation Server for Copy Number Variation in the Human Genome. PLoS ONE, 2013, 8, e80170. | 2.5 | 26 |
| 120 | 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 |
| 121 | Prioritization of Epilepsy Associated Candidate Genes by Convergent Analysis. PLoS ONE, 2011, 6, e17162. | 2.5 | 24 |
| 122 | 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 |
| 123 | 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 |
| 124 | Multi-Dimensional Prioritization of Dental Caries Candidate Genes and Its Enriched Dense Network Modules. PLoS ONE, 2013, 8, e76666. | 2.5 | 24 |
| 125 | Sequence context analysis in the mouse genome: Single nucleotide polymorphisms and CpG island sequences. Genomics, 2006, 87, 68-74. | 2.9 | 23 |
| 126 | TSEA-DB: a traitâ€“tissue association map for human complex traits and diseases. Nucleic Acids Research, 2019, 48, D1022-D1030. | 14.5 | 23 |

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|---|---|---|---|
| 127 | Directionality of point mutation and 5-methylcytosine deamination rates in the chimpanzee genome. BMC Genomics, 2006, 7, 316. | 2.8 | 22 |
| 128 | Investigation of multi-trait associations using pathway-based analysis of GWAS summary statistics. BMC Genomics, 2019, 20, 79. | 2.8 | 22 |
| 129 | Contrast features of CpG islands in the promoter and other regions in the dog genome. Genomics, 2009, 94, 117-124. | 2.9 | 21 |
| 130 | mutLBSgeneDB: mutated ligand binding site gene DataBase. Nucleic Acids Research, 2017, 45, D256-D263. | 14.5 | 21 |
| 131 | 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 |
| 132 | Characterization of Tumor-Suppressor Gene Inactivation Events in 33 Cancer Types. Cell Reports, 2019, 26, 496-506.e3. | 6.4 | 21 |
| 133 | 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 |
| 134 | Classification of Cancer Primary Sites Using Machine Learning and Somatic Mutations. BioMed Research International, 2015, 2015, 1-9. | 1.9 | 20 |
| 135 | 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 |
| 136 | Protein tyrosine phosphatase receptor Î´ serves as the orexigenic asprosin receptor. Cell Metabolism, 2022, 34, 549-563.e8. | 16.2 | 20 |
| 137 | Virus interactions with human signal transduction pathways. International Journal of Computational Biology and Drug Design, 2011, 4, 83. | 0.3 | 19 |
| 138 | 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 |
| 139 | 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 |
| 140 | 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 |
| 141 | ConGEMs: Condensed Gene Co-Expression Module Discovery Through Rule-Based Clustering and Its Application to Carcinogenesis. Genes, 2018, 9, 7. | 2.4 | 18 |
| 142 | Genome-Wide Meta-Analyses of FTND and TTFC Phenotypes. Nicotine and Tobacco Research, 2020, 22, 900-909. | 2.6 | 17 |
| 143 | A developmental stage specific network approach for studying dynamic transcription factor-microRNA co-regulation during craniofacial development. Development (Cambridge), 2020, 147, . | 2.5 | 17 |
| 144 | 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 |

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|---|---|---|---|
| 145 | 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 |
| 146 | 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 |
| 147 | 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 |
| 148 | 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 |
| 149 | Translational bioinformatics in mental health: open access data sources and computational biomarker discovery. Briefings in Bioinformatics, 2019, 20, 842-856. | 6.5 | 16 |
| 150 | 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 |
| 151 | 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 |
| 152 | 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 |
| 153 | Common Variants in the MKL1 Gene Confer Risk of Schizophrenia. Schizophrenia Bulletin, 2015, 41, 715-727. | 4.3 | 15 |
| 154 | Network-based identification of critical regulators as putative drivers of human cleft lip. BMC Medical Genomics, 2019, 12, 16. | 1.5 | 15 |
| 155 | Landscape of drug-resistance mutations in kinase regulatory hotspots. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 15 |
| 156 | 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 |
| 157 | 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 |
| 158 | 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 |
| 159 | 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 |
| 160 | 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 |
| 161 | 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 |
| 162 | Dense module searching for gene networks associated with multiple sclerosis. BMC Medical Genomics, 2020, 13, 48. | 1.5 | 13 |

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| 163 | Investigating Cellular Trajectories in the Severity of COVID-19 and Their Transcriptional Programs Using Machine Learning Approaches. Genes, 2021, 12, 635. | 2.4 | 13 |
| 164 | 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 |
| 165 | Linking Biochemical Pathways and Networks to Adverse Drug Reactions. IEEE Transactions on Nanobioscience, 2014, 13, 131-137. | 3.3 | 12 |
| 166 | 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 |
| 167 | ERBB activation modulates sensitivity to MEK1/2 inhibition in a subset of driver-negative melanoma. Oncotarget, 2015, 6, 22348-22360. | 1.8 | 12 |
| 168 | Gene- and evidence-based candidate gene selection for schizophrenia and gene feature analysis. Artificial Intelligence in Medicine, 2010, 48, 99-106. | 6.5 | 11 |
| 169 | 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 |
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