

An-Yuan Guo

List of Publications by Year in descending order

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Version: 2024-02-01

117
papers

12,276
citations

57758

44
h-index

29157

104
g-index

120
all docs

120
docs citations

120
times ranked

17598
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | EVAtlas: a comprehensive database for ncRNA expression in human extracellular vesicles. <i>Nucleic Acids Research</i> , 2022, 50, D111-D117. | 14.5 | 27 |
| 2 | ImmuCellAI-mouse: a tool for comprehensive prediction of mouse immune cell abundance and immune microenvironment depiction. <i>Bioinformatics</i> , 2022, 38, 785-791. | 4.1 | 53 |
| 3 | A comprehensive platelet expression atlas (PEA) resource and platelet transcriptome landscape. <i>American Journal of Hematology</i> , 2022, 97, E18. | 4.1 | 3 |
| 4 | Genetic, Pharmacogenomic, and Immune Landscapes of Enhancer RNAs Across Human Cancers. <i>Cancer Research</i> , 2022, 82, 785-790. | 0.9 | 11 |
| 5 | CBX2 and EZH2 cooperatively promote the growth and metastasis of lung adenocarcinoma. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 670-684. | 5.1 | 22 |
| 6 | Tumor-derived extracellular vesicles induce invalid cytokine release and exhaustion of CD19 CAR-T Cells. <i>Cancer Letters</i> , 2022, 536, 215668. | 7.2 | 11 |
| 7 | Abstract LB168: Platelet RNA signature enables early and accurate detection of ovarian cancer: An intercontinental, biomarker identification study. <i>Cancer Research</i> , 2022, 82, LB168-LB168. | 0.9 | 1 |
| 8 | A miR-9-5p/FOXO1/CPEB3 Feed-Forward Loop Drives the Progression of Hepatocellular Carcinoma. <i>Cells</i> , 2022, 11, 2116. | 4.1 | 4 |
| 9 | An integrative multi-omics approach uncovers the regulatory role of CDK7 and CDK4 in autophagy activation induced by silica nanoparticles. <i>Autophagy</i> , 2021, 17, 1426-1447. | 9.1 | 33 |
| 10 | CCLA: an accurate method and web server for cancer cell line authentication using gene expression profiles. <i>Briefings in Bioinformatics</i> , 2021, 22, . | 6.5 | 6 |
| 11 | miRNASNP-v3: a comprehensive database for SNPs and disease-related variations in miRNAs and miRNA targets. <i>Nucleic Acids Research</i> , 2021, 49, D1276-D1281. | 14.5 | 80 |
| 12 | TCRdb: a comprehensive database for T-cell receptor sequences with powerful search function. <i>Nucleic Acids Research</i> , 2021, 49, D468-D474. | 14.5 | 43 |
| 13 | Germline Mutation of PLCD1 Contributes to Human Multiple Pilomatricomas through Protein Kinase D/Extracellular Signal-Regulated Kinase1/2 Cascade and TRPV6. <i>Journal of Investigative Dermatology</i> , 2021, 141, 533-544. | 0.7 | 5 |
| 14 | Expression profile of immune checkpoint genes and their roles in predicting immunotherapy response. <i>Briefings in Bioinformatics</i> , 2021, 22, . | 6.5 | 147 |
| 15 | A folate receptor 3 SNP promotes mitochondria-induced clonogenicity of CML leukemia cells: Implications for treatment free remission. <i>Clinical and Translational Medicine</i> , 2021, 11, e317. | 4.0 | 6 |
| 16 | A comprehensive survey for human transcription factors on expression, regulation, interaction, phenotype and cancer survival. <i>Briefings in Bioinformatics</i> , 2021, 22, . | 6.5 | 8 |
| 17 | Quercetin Ameliorates Gut Microbiota Dysbiosis That Drives Hypothalamic Damage and Hepatic Lipogenesis in Monosodium Glutamate-Induced Abdominal Obesity. <i>Frontiers in Nutrition</i> , 2021, 8, 671353. | 3.7 | 19 |
| 18 | Hypothalamic long noncoding RNA AK044061 is involved in the development of dietary obesity in mice. <i>International Journal of Obesity</i> , 2021, 45, 2638-2647. | 3.4 | 4 |

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|----|---|------|-----------|
| 19 | Case Report: Multi-Omics Analysis and CAR-T Treatment of a Chronic Myeloid Leukemia Blast Crisis Case 5 Years After the Discontinuation of TKI. <i>Frontiers in Oncology</i> , 2021, 11, 739871. | 2.8 | 7 |
| 20 | Extracellular vesicles deposit <i>PCNA</i> to rejuvenate aged bone marrow-derived mesenchymal stem cells and slow age-related degeneration. <i>Science Translational Medicine</i> , 2021, 13, . | 12.4 | 65 |
| 21 | Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33. | 14.5 | 165 |
| 22 | tRiC: a user-friendly data portal to explore the expression landscape of tRNAs in human cancers. <i>RNA Biology</i> , 2020, 17, 1674-1679. | 3.1 | 18 |
| 23 | A 6-Membrane Protein Gene score for prognostic prediction of cytogenetically normal acute myeloid leukemia in multiple cohorts. <i>Journal of Cancer</i> , 2020, 11, 251-259. | 2.5 | 12 |
| 24 | Landscape of cancer diagnostic biomarkers from specifically expressed genes. <i>Briefings in Bioinformatics</i> , 2020, 21, 2175-2184. | 6.5 | 41 |
| 25 | FFLtool: a web server for transcription factor and miRNA feed forward loop analysis in human. <i>Bioinformatics</i> , 2020, 36, 2605-2607. | 4.1 | 19 |
| 26 | Comparison of chronic myeloid leukemia stem cells and hematopoietic stem cells by global proteomic analysis. <i>Biochemical and Biophysical Research Communications</i> , 2020, 522, 362-367. | 2.1 | 7 |
| 27 | Systematic Transcriptome and Regulatory Network Analyses Reveal the Hypoglycemic Mechanism of <i>Dendrobium fimbriatum</i> . <i>Molecular Therapy - Nucleic Acids</i> , 2020, 19, 1-14. | 5.1 | 11 |
| 28 | hTFtarget: A Comprehensive Database for Regulations of Human Transcription Factors and Their Targets. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 120-128. | 6.9 | 201 |
| 29 | p.His16Arg of STXBP1 (MUNC18-1) Associated With Syntaxin 3B Causes Autosomal Dominant Congenital Nystagmus. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 591781. | 3.7 | 6 |
| 30 | Integrated omics in <i>Drosophila</i> uncover a circadian kinome. <i>Nature Communications</i> , 2020, 11, 2710. | 12.8 | 23 |
| 31 | An ultra-sensitive T-cell receptor detection method for TCR-Seq and RNA-Seq data. <i>Bioinformatics</i> , 2020, 36, 4255-4262. | 4.1 | 13 |
| 32 | The expression and regulation of HOX genes and membrane proteins among different cytogenetic groups of acute myeloid leukemia. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1365. | 1.2 | 9 |
| 33 | SNP2APA: a database for evaluating effects of genetic variants on alternative polyadenylation in human cancers. <i>Nucleic Acids Research</i> , 2020, 48, D226-D232. | 14.5 | 37 |
| 34 | Genome-Wide DNA Methylation Enhances Stemness in the Mechanical Selection of Tumor-Repopulating Cells. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 88. | 4.1 | 10 |
| 35 | ImmuCellAI: A Unique Method for Comprehensive Cell Subsets Abundance Prediction and its Application in Cancer Immunotherapy. <i>Advanced Science</i> , 2020, 7, 1902880. | 11.2 | 558 |
| 36 | Time serial transcriptome reveals <i>Cyp2c29</i> as a key gene in hepatocellular carcinoma development. <i>Cancer Biology and Medicine</i> , 2020, 17, 401-417. | 3.0 | 20 |

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|----|---|------|-----------|
| 37 | Regulatory networks in mechanotransduction reveal key genes in promoting cancer cell stemness and proliferation. <i>Oncogene</i> , 2019, 38, 6818-6834. | 5.9 | 34 |
| 38 | GEDS: A Gene Expression Display Server for mRNAs, miRNAs and Proteins. <i>Cells</i> , 2019, 8, 675. | 4.1 | 20 |
| 39 | Identification of STAB1 in Multiple Datasets as a Prognostic Factor for Cytogenetically Normal AML: Mechanism and Drug Indications. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 476-484. | 5.1 | 22 |
| 40 | Tumor-derived extracellular vesicles inhibit osteogenesis and exacerbate myeloma bone disease. <i>Theranostics</i> , 2019, 9, 196-209. | 10.0 | 50 |
| 41 | Comprehensive characterization of circular RNAs in ~1000 human cancer cell lines. <i>Genome Medicine</i> , 2019, 11, 55. | 8.2 | 116 |
| 42 | Regulatory network analysis reveals the oncogenesis roles of feed-forward loops and therapeutic target in T-cell acute lymphoblastic leukemia. <i>BMC Medical Genomics</i> , 2019, 12, 8. | 1.5 | 7 |
| 43 | Transcriptome and Regulatory Network Analyses of CD19-CAR-T Immunotherapy for B-ALL. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 190-200. | 6.9 | 33 |
| 44 | High IL2RA mRNA expression is an independent adverse prognostic biomarker in core binding factor and intermediate-risk acute myeloid leukemia. <i>Journal of Translational Medicine</i> , 2019, 17, 191. | 4.4 | 18 |
| 45 | Tumor necrosis factor α knockout impaired tumorigenesis in chronic myeloid leukemia cells partly by metabolism modification and miRNA regulation. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 2355-2364. | 2.0 | 8 |
| 46 | Transcriptome profiling reveals the anti-diabetic molecular mechanism of <i>Cyclocarya paliurus</i> polysaccharides. <i>Journal of Functional Foods</i> , 2019, 55, 1-8. | 3.4 | 17 |
| 47 | Pancan-meQTL: a database to systematically evaluate the effects of genetic variants on methylation in human cancer. <i>Nucleic Acids Research</i> , 2019, 47, D1066-D1072. | 14.5 | 45 |
| 48 | AnimalTFDB 3.0: a comprehensive resource for annotation and prediction of animal transcription factors. <i>Nucleic Acids Research</i> , 2019, 47, D33-D38. | 14.5 | 592 |
| 49 | EVmiRNA: a database of miRNA profiling in extracellular vesicles. <i>Nucleic Acids Research</i> , 2019, 47, D89-D93. | 14.5 | 209 |
| 50 | Database Resources of the BIG Data Center in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D8-D14. | 14.5 | 157 |
| 51 | SAGD: a comprehensive sex-associated gene database from transcriptomes. <i>Nucleic Acids Research</i> , 2019, 47, D835-D840. | 14.5 | 21 |
| 52 | SEGreg: a database for human specifically expressed genes and their regulations in cancer and normal tissue. <i>Briefings in Bioinformatics</i> , 2019, 20, 1322-1328. | 6.5 | 18 |
| 53 | iUUCD 2.0: an update with rich annotations for ubiquitin and ubiquitin-like conjugations. <i>Nucleic Acids Research</i> , 2018, 46, D447-D453. | 14.5 | 57 |
| 54 | The Genomic Landscape and Pharmacogenomic Interactions of Clock Genes in Cancer Chronotherapy. <i>Cell Systems</i> , 2018, 6, 314-328.e2. | 6.2 | 183 |

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|----|--|------|-----------|
| 55 | Leukemia cell-derived microvesicles induce T cell exhaustion via miRNA delivery. <i>Oncolmmunology</i> , 2018, 7, e1448330. | 4.6 | 24 |
| 56 | SEGtool: a specifically expressed gene detection tool and applications in human tissue and single-cell sequencing data. <i>Briefings in Bioinformatics</i> , 2018, 19, 1325-1336. | 6.5 | 20 |
| 57 | PancanQTL: systematic identification of cis-eQTLs and trans-eQTLs in 33 cancer types. <i>Nucleic Acids Research</i> , 2018, 46, D971-D976. | 14.5 | 191 |
| 58 | lncRNASNP2: an updated database of functional SNPs and mutations in human and mouse lncRNAs. <i>Nucleic Acids Research</i> , 2018, 46, D276-D280. | 14.5 | 199 |
| 59 | dbCoRC: a database of core transcriptional regulatory circuitries modeled by H3K27ac ChIP-seq signals. <i>Nucleic Acids Research</i> , 2018, 46, D71-D77. | 14.5 | 37 |
| 60 | Global analysis of tRNA and translation factor expression reveals a dynamic landscape of translational regulation in human cancers. <i>Communications Biology</i> , 2018, 1, 234. | 4.4 | 58 |
| 61 | Integrating Transcriptome and Experiments Reveals the Anti-diabetic Mechanism of Cyclocarya paliurus Formula. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 13, 419-430. | 5.1 | 12 |
| 62 | GSCALite: a web server for gene set cancer analysis. <i>Bioinformatics</i> , 2018, 34, 3771-3772. | 4.1 | 671 |
| 63 | Differential Co-expression and Regulatory Network Analysis Uncover the Relapse Factor and Mechanism of T Cell Acute Leukemia. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 12, 184-194. | 5.1 | 20 |
| 64 | Investigating the Molecular Mechanism of Aqueous Extract of Cyclocarya paliurus on Ameliorating Diabetes by Transcriptome Profiling. <i>Frontiers in Pharmacology</i> , 2018, 9, 912. | 3.5 | 9 |
| 65 | Genomic landscape and mutational impacts of recurrently mutated genes in cancers. <i>Molecular Genetics & Genomic Medicine</i> , 2018, 6, 910-923. | 1.2 | 15 |
| 66 | The ASH1-miR-375-YWHAZ Signaling Axis Regulates Tumor Properties in Hepatocellular Carcinoma. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 11, 538-553. | 5.1 | 45 |
| 67 | lncRInter: A database of experimentally validated long non-coding RNA interaction. <i>Journal of Genetics and Genomics</i> , 2017, 44, 265-268. | 3.9 | 35 |
| 68 | Interferon- β alters the immune-related miRNA expression of microvesicles derived from mesenchymal stem cells. <i>Journal of Huazhong University of Science and Technology [Medical Sciences]</i> , 2017, 37, 179-184. | 1.0 | 14 |
| 69 | Ablation of EYS in zebrafish causes mislocalisation of outer segment proteins, F-actin disruption and cone-rod dystrophy. <i>Scientific Reports</i> , 2017, 7, 46098. | 3.3 | 52 |
| 70 | A Pan-cancer Analysis of the Expression and Clinical Relevance of Small Nucleolar RNAs in Human Cancer. <i>Cell Reports</i> , 2017, 21, 1968-1981. | 6.4 | 186 |
| 71 | LNCEditing: a database for functional effects of RNA editing in lncRNAs. <i>Nucleic Acids Research</i> , 2017, 45, D79-D84. | 14.5 | 111 |
| 72 | Microvesicles as Potential Biomarkers for the Identification of Senescence in Human Mesenchymal Stem Cells. <i>Theranostics</i> , 2017, 7, 2673-2689. | 10.0 | 82 |

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|----|---|------|-----------|
| 73 | Tumor Cell-Derived Microvesicles Induced Not Epithelial-Mesenchymal Transition but Apoptosis in Human Proximal Tubular (HK-2) Cells: Implications for Renal Impairment in Multiple Myeloma. <i>International Journal of Molecular Sciences</i> , 2017, 18, 513. | 4.1 | 6 |
| 74 | Gene expression, regulation of DEN and HBx induced HCC mice models and comparisons of tumor, para-tumor and normal tissues. <i>BMC Cancer</i> , 2017, 17, 862. | 2.6 | 19 |
| 75 | MicroRNA regulatory pathway analysis identifies miR-142-5p as a negative regulator of TGF- β 2 pathway via targeting SMAD3. <i>Oncotarget</i> , 2016, 7, 71504-71513. | 1.8 | 48 |
| 76 | Mesenchymal Stem Cell-Derived Microvesicles Support Ex Vivo Expansion of Cord Blood-Derived CD34 ⁺ Cells. <i>Stem Cells International</i> , 2016, 2016, 1-13. | 2.5 | 40 |
| 77 | Loss-of-function Mutation in PMVK Causes Autosomal Dominant Disseminated Superficial Porokeratosis. <i>Scientific Reports</i> , 2016, 6, 24226. | 3.3 | 21 |
| 78 | miR-146b-5p within BCR-ABL1 ⁺ Positive Microvesicles Promotes Leukemic Transformation of Hematopoietic Cells. <i>Cancer Research</i> , 2016, 76, 2901-2911. | 0.9 | 88 |
| 79 | A clinical observation of Chinese chronic myelogenous leukemia patients after discontinuation of tyrosine kinase inhibitors. <i>Oncotarget</i> , 2016, 7, 58234-58243. | 1.8 | 7 |
| 80 | Transcription factor and miRNA co-regulatory network reveals shared and specific regulators in the development of B cell and T cell. <i>Scientific Reports</i> , 2015, 5, 15215. | 3.3 | 60 |
| 81 | Scoring the correlation of genes by their shared properties using OScal, an improved overlap quantification model. <i>Scientific Reports</i> , 2015, 5, 10583. | 3.3 | 1 |
| 82 | An update of miRNASNP database for better SNP selection by GWAS data, miRNA expression and online tools. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav029. | 3.0 | 110 |
| 83 | Impact of collection, isolation and storage methodology of circulating microvesicles on flow cytometric analysis. <i>Experimental and Therapeutic Medicine</i> , 2015, 10, 2093-2101. | 1.8 | 12 |
| 84 | GSDS 2.0: an upgraded gene feature visualization server. <i>Bioinformatics</i> , 2015, 31, 1296-1297. | 4.1 | 3,092 |
| 85 | lncRNASNP: a database of SNPs in lncRNAs and their potential functions in human and mouse. <i>Nucleic Acids Research</i> , 2015, 43, D181-D186. | 14.5 | 204 |
| 86 | MiRNA and TF co-regulatory network analysis for the pathology and recurrence of myocardial infarction. <i>Scientific Reports</i> , 2015, 5, 9653. | 3.3 | 41 |
| 87 | AnimalTFDB 2.0: a resource for expression, prediction and functional study of animal transcription factors. <i>Nucleic Acids Research</i> , 2015, 43, D76-D81. | 14.5 | 287 |
| 88 | The regulation of microRNA expression by DNA methylation in hepatocellular carcinoma. <i>Molecular BioSystems</i> , 2015, 11, 532-539. | 2.9 | 64 |
| 89 | Transcription factor and microRNA co-regulatory loops: important regulatory motifs in biological processes and diseases. <i>Briefings in Bioinformatics</i> , 2015, 16, 45-58. | 6.5 | 175 |
| 90 | Integrative Genomic Analysis Identifies That SERPINA6-rs1998056 Regulated by FOXA/ER α Is Associated with Female Hepatocellular Carcinoma. <i>PLoS ONE</i> , 2014, 9, e107246. | 2.5 | 9 |

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|-----|--|------|-----------|
| 91 | Comprehensive analysis of human small RNA sequencing data provides insights into expression profiles and miRNA editing. <i>RNA Biology</i> , 2014, 11, 1375-1385. | 3.1 | 78 |
| 92 | The evolutionary analysis reveals domain fusion of proteins with Frizzled-like CRD domain. <i>Gene</i> , 2014, 533, 229-239. | 2.2 | 23 |
| 93 | Evolution, functional divergence and conserved exon-intron structure of bHLH/PAS gene family. <i>Molecular Genetics and Genomics</i> , 2014, 289, 25-36. | 2.1 | 20 |
| 94 | EKPD: a hierarchical database of eukaryotic protein kinases and protein phosphatases. <i>Nucleic Acids Research</i> , 2014, 42, D496-D502. | 14.5 | 52 |
| 95 | A genetic variant in microRNA target site of TGF- β 2 signaling pathway increases the risk of colorectal cancer in a Chinese population. <i>Tumor Biology</i> , 2014, 35, 4301-4306. | 1.8 | 14 |
| 96 | CPLM: a database of protein lysine modifications. <i>Nucleic Acids Research</i> , 2014, 42, D531-D536. | 14.5 | 155 |
| 97 | Bioinformatics analysis identifies miR-221 as a core regulator in hepatocellular carcinoma and its silencing suppresses tumor properties. <i>Oncology Reports</i> , 2014, 32, 1200-1210. | 2.6 | 44 |
| 98 | Exome Sequencing Identified NRG3 as a Novel Susceptible Gene of Hirschsprung's Disease in a Chinese Population. <i>Molecular Neurobiology</i> , 2013, 47, 957-966. | 4.0 | 30 |
| 99 | The sacred lotus genome provides insights into the evolution of flowering plants. <i>Plant Journal</i> , 2013, 76, 557-567. | 5.7 | 75 |
| 100 | Identification of Novel and Differentially Expressed MicroRNAs in the Ovaries of Laying and Non-Laying Ducks. <i>Journal of Integrative Agriculture</i> , 2013, 12, 136-146. | 3.5 | 14 |
| 101 | Phylogenetic analysis reveals the evolution and diversification of cyclins in eukaryotes. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 1002-1010. | 2.7 | 33 |
| 102 | UUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. <i>Nucleic Acids Research</i> , 2013, 41, D445-D451. | 14.5 | 99 |
| 103 | Integration of Transcriptome, Proteome and Metabolism Data Reveals the Alkaloids Biosynthesis in <i>Macleaya cordata</i> and <i>Macleaya microcarpa</i> . <i>PLoS ONE</i> , 2013, 8, e53409. | 2.5 | 61 |
| 104 | MLL1, a Histone H3K4 Methyltransferase, Regulates the Expression of TNF α -mediated NF- κ B Downstream Genes. <i>Journal of Cell Science</i> , 2012, 125, 4058-66. | 2.0 | 63 |
| 105 | AnimalTFDB: a comprehensive animal transcription factor database. <i>Nucleic Acids Research</i> , 2012, 40, D144-D149. | 14.5 | 265 |
| 106 | The Genome of <i>Ganderma lucidum</i> Provide Insights into Triterpense Biosynthesis and Wood Degradation. <i>PLoS ONE</i> , 2012, 7, e36146. | 2.5 | 78 |
| 107 | Comparative and Evolutionary Analysis of the HES/HEY Gene Family Reveal Exon/Intron Loss and Teleost Specific Duplication Events. <i>PLoS ONE</i> , 2012, 7, e40649. | 2.5 | 26 |
| 108 | Meta-analyses of genome-wide linkage scans of anxiety-related phenotypes. <i>European Journal of Human Genetics</i> , 2012, 20, 1078-1084. | 2.8 | 28 |

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|-----|--|------|-----------|
| 109 | MicroRNA and transcription factor co-regulatory network analysis reveals miR-19 inhibits CYLD in T-cell acute lymphoblastic leukemia. <i>Nucleic Acids Research</i> , 2012, 40, 5201-5214. | 14.5 | 119 |
| 110 | Genome-wide identification of SNPs in microRNA genes and the SNP effects on microRNA target binding and biogenesis. <i>Human Mutation</i> , 2012, 33, 254-263. | 2.5 | 343 |
| 111 | Prioritization and Association Analysis of Murine-Derived Candidate Genes in Anxiety-Spectrum Disorders. <i>Biological Psychiatry</i> , 2011, 70, 888-896. | 1.3 | 25 |
| 112 | Network Analysis of EtOH-Related Candidate Genes. <i>Chemistry and Biodiversity</i> , 2010, 7, 1142-1152. | 2.1 | 3 |
| 113 | New Genomic Structure for Prostate Cancer Specific Gene PCA3 within BMCC1: Implications for Prostate Cancer Detection and Progression. <i>PLoS ONE</i> , 2009, 4, e4995. | 2.5 | 74 |
| 114 | Genome-wide identification and evolutionary analysis of the plant specific SBP-box transcription factor family. <i>Gene</i> , 2008, 418, 1-8. | 2.2 | 227 |
| 115 | PlantTFDB: a comprehensive plant transcription factor database. <i>Nucleic Acids Research</i> , 2007, 36, D966-D969. | 14.5 | 210 |
| 116 | Identification of a Naturally Occurring Recombinant Isolate of Sugarcane Mosaic Virus Causing Maize Dwarf Mosaic Disease. <i>Virus Genes</i> , 2005, 30, 75-83. | 1.6 | 33 |
| 117 | DATF: a database of Arabidopsis transcription factors. <i>Bioinformatics</i> , 2005, 21, 2568-2569. | 4.1 | 296 |