

# Yixue Li

## List of Publications by Year in descending order

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174  
papers

8,247  
citations

76326

40  
h-index

56724

83  
g-index

176  
all docs

176  
docs citations

176  
times ranked

13905  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of heavy-chain antibody gene repertoires in Bactrian camels. <i>Journal of Genetics and Genomics</i> , 2023, 50, 38-45.	3.9	1
2	An interactive viral genome evolution network analysis system enabling rapid large-scale molecular tracing of SARS-CoV-2. <i>Science Bulletin</i> , 2022, 67, 665-669.	9.0	9
3	Spatial Multiomics Analysis Reveals Only Minor Genetic and Epigenetic Changes in Human Liver Cancer Stem-Like Cells Compared With Other Tumor Parenchymal Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 810687.	3.7	1
4	Associations of erythrocyte polyunsaturated fatty acids with incidence of stroke and stroke types in adult Chinese: a prospective study of over 8000 individuals. <i>European Journal of Nutrition</i> , 2022, , 1.	3.9	0
5	Gene dysregulation analysis builds a mechanistic signature for prognosis and therapeutic benefit in colorectal cancer. <i>Journal of Molecular Cell Biology</i> , 2021, 12, 881-893.	3.3	3
6	Integrated genomic and transcriptomic analysis reveals unique characteristics of hepatic metastases and pro-metastatic role of complement C1q in pancreatic ductal adenocarcinoma. <i>Genome Biology</i> , 2021, 22, 4.	8.8	28
7	Identifying Key Genes for Nasopharyngeal Carcinoma by Prioritized Consensus Differentially Expressed Genes Caused by Aberrant Methylation. <i>Journal of Cancer</i> , 2021, 12, 874-884.	2.5	11
8	Integrative Analysis Identified a 6-miRNA Prognostic Signature in Nasopharyngeal Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 661105.	3.7	1
9	Large-scale pharmacogenomic studies and drug response prediction for personalized cancer medicine. <i>Journal of Genetics and Genomics</i> , 2021, 48, 540-551.	3.9	19
10	Optimization of C-to-G base editors with sequence context preference predictable by machine learning methods. <i>Nature Communications</i> , 2021, 12, 4902.	12.8	28
11	Effects of gut microbiota and fatty acid metabolism on dyslipidemia following weight-loss diets in women: Results from a randomized controlled trial. <i>Clinical Nutrition</i> , 2021, 40, 5511-5520.	5.0	8
12	Single-cell RNA sequencing of peripheral blood mononuclear cells from acute Kawasaki disease patients. <i>Nature Communications</i> , 2021, 12, 5444.	12.8	55
13	Improving the genome assembly of rabbits with long-read sequencing. <i>Genomics</i> , 2021, 113, 3216-3223.	2.9	7
14	Chromosome-level assembly of wild Bactrian camel genome reveals organization of immune gene loci. <i>Molecular Ecology Resources</i> , 2020, 20, 770-780.	4.8	25
15	GOTI, a method to identify genome-wide off-target effects of genome editing in mouse embryos. <i>Nature Protocols</i> , 2020, 15, 3009-3029.	12.0	24
16	A rationally engineered cytosine base editor retains high on-target activity while reducing both DNA and RNA off-target effects. <i>Nature Methods</i> , 2020, 17, 600-604.	19.0	97
17	The self-organization model reveals systematic characteristics of aging. <i>Theoretical Biology and Medical Modelling</i> , 2020, 17, 4.	2.1	1
18	The accelerated aging model reveals critical mechanisms of late-onset Parkinson's disease. <i>BioData Mining</i> , 2020, 13, 4.	4.0	6

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19	MKRN3 regulates the epigenetic switch of mammalian puberty via ubiquitination of MBD3. <i>National Science Review</i> , 2020, 7, 671-685.	9.5	48
20	Whole-genome sequencing of 128 camels across Asia reveals origin and migration of domestic Bactrian camels. <i>Communications Biology</i> , 2020, 3, 1.	4.4	809
21	Comparison of immune profiles between hepatocellular carcinoma subtypes. <i>Biophysics Reports</i> , 2020, 6, 19-32.	0.8	1
22	Pan-Cancer Analysis of Head-to-Head Gene Pairs in Terms of Transcriptional Activity, Co-expression and Regulation. <i>Frontiers in Genetics</i> , 2020, 11, 560997.	2.3	6
23	Integrative analysis reveals novel driver genes and molecular subclasses of hepatocellular carcinoma. <i>Aging</i> , 2020, 12, 23849-23871.	3.1	17
24	Genome assembly and transcriptome analysis provide insights into the antischistosome mechanism of <i>Microtus fortis</i> . <i>Journal of Genetics and Genomics</i> , 2020, 47, 743-755.	3.9	2
25	Kinase substrate Edge Biomarkers Provide A More Accurate Prognostic Prediction in ER-negative Breast Cancer. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 525-538.	6.9	0
26	A Pharmacogenomic Landscape in Human Liver Cancers. <i>Cancer Cell</i> , 2019, 36, 179-193.e11.	16.8	127
27	Off-target RNA mutation induced by DNA base editing and its elimination by mutagenesis. <i>Nature</i> , 2019, 571, 275-278.	27.8	330
28	A Homeostatic Arid1a-Dependent Permissive Chromatin State Licenses Hepatocyte Responsiveness to Liver-Injury-Associated YAP Signaling. <i>Cell Stem Cell</i> , 2019, 25, 54-68.e5.	11.1	88
29	PhenoModifier: a genetic modifier database for elucidating the genetic basis of human phenotypic variation. <i>Nucleic Acids Research</i> , 2019, 48, D977-D982.	14.5	10
30	Rapid evolution of a retro-transposable hotspot of ovine genome underlies the alteration of BMP2 expression and development of fat tails. <i>BMC Genomics</i> , 2019, 20, 261.	2.8	27
31	Cytosine base editor generates substantial off-target single-nucleotide variants in mouse embryos. <i>Science</i> , 2019, 364, 289-292.	12.6	573
32	Reconstruction of kidney renal clear cell carcinoma evolution across pathological stages. <i>Scientific Reports</i> , 2018, 8, 3339.	3.3	4
33	Systematic identification of rabbit LncRNAs reveals functional roles in atherosclerosis. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2266-2273.	3.8	2
34	Rabbit models provide insights into bone formation related biological process in atherosclerotic vascular calcification. <i>Biochemical and Biophysical Research Communications</i> , 2018, 496, 1369-1375.	2.1	13
35	Whole-genome sequences of 89 Chinese sheep suggest role of RXFP2 in the development of unique horn phenotype as response to semi-feralization. <i>GigaScience</i> , 2018, 7, .	6.4	90
36	A Genome-Wide Study of Allele-Specific Expression in Colorectal Cancer. <i>Frontiers in Genetics</i> , 2018, 9, 570.	2.3	24

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37	Competitive evolution of NSCLC tumor clones and the drug resistance mechanism of first-generation EGFR-TKIs in Chinese NSCLC patients. <i>Heliyon</i> , 2018, 4, e01031.	3.2	13
38	Enrichment of the fetal fraction in non-invasive prenatal screening reduces maternal background interference. <i>Scientific Reports</i> , 2018, 8, 17675.	3.3	25
39	Multiple transcription factors contribute to inter-chromosomal interaction in yeast. <i>BMC Systems Biology</i> , 2018, 12, 140.	3.0	9
40	RabGTD: a comprehensive database of rabbit genome and transcriptome. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	14
41	Systematic analysis reveals molecular characteristics of ERG-negative prostate cancer. <i>Scientific Reports</i> , 2018, 8, 12868.	3.3	13
42	Evolution of oncogenic signatures of mutation hotspots in tyrosine kinases supports the atavistic hypothesis of cancer. <i>Scientific Reports</i> , 2018, 8, 8256.	3.3	13
43	Comparative transcriptomics reveals specific responding genes associated with atherosclerosis in rabbit and mouse models. <i>PLoS ONE</i> , 2018, 13, e0201618.	2.5	3
44	Transcriptomic sequencing reveals diverse adaptive gene expression responses of human vascular smooth muscle cells to nitro-conjugated linoleic acid. <i>Physiological Genomics</i> , 2018, 50, 287-295.	2.3	8
45	Evaluation of functionality for serine and threonine phosphorylation with different evolutionary ages in human and mouse. <i>BMC Genomics</i> , 2018, 19, 431.	2.8	9
46	Integrative analysis of DNA methylation and gene expression reveals hepatocellular carcinoma-specific diagnostic biomarkers. <i>Genome Medicine</i> , 2018, 10, 42.	8.2	95
47	Genomic Analysis Reveals Hypoxia Adaptation in the Tibetan Mastiff by Introgression of the Grey Wolf from the Tibetan Plateau. <i>Molecular Biology and Evolution</i> , 2017, 34, msw274.	8.9	75
48	Global Prioritizing Disease Candidate lncRNAs via a Multi-level Composite Network. <i>Scientific Reports</i> , 2017, 7, 39516.	3.3	47
49	Protein coding gene CRNKL1 as a potential prognostic biomarker in esophageal adenocarcinoma. <i>Artificial Intelligence in Medicine</i> , 2017, 76, 1-6.	6.5	4
50	Response to Comment on Adam et al. Metformin Effect on Nontargeted Metabolite Profiles in Patients With Type 2 Diabetes and in Multiple Murine Tissues. <i>Diabetes</i> 2016;65:3776â€“3785. <i>Diabetes</i> , 2017, 66, e3-e4.	0.6	1
51	CanProVar 2.0: An Updated Database of Human Cancer Proteome Variation. <i>Journal of Proteome Research</i> , 2017, 16, 421-432.	3.7	36
52	Population-based study of effectiveness of neoadjuvant radiotherapy on survival in US rectal cancer patients according to age. <i>Scientific Reports</i> , 2017, 7, 3471.	3.3	8
53	The Evolution and Expression Pattern of Human Overlapping lncRNA and Protein-coding Gene Pairs. <i>Scientific Reports</i> , 2017, 7, 42775.	3.3	29
54	Aldehyde dehydrogenaseâ€² (ALDH2) opposes hepatocellular carcinoma progression by regulating AMPâ€²activated protein kinase signaling in mice. <i>Hepatology</i> , 2017, 65, 1628-1644.	7.3	52

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55	Adaptive evolution of proteins in hepatitis B virus during divergence of genotypes. <i>Scientific Reports</i> , 2017, 7, 1990.	3.3	20
56	Cancer-Related Triplets of mRNA-lncRNA-miRNA Revealed by Integrative Network in Uterine Corpus Endometrial Carcinoma. <i>BioMed Research International</i> , 2017, 2017, 1-7.	1.9	30
57	Panel of seven long noncoding RNA as a candidate prognostic biomarker for ovarian cancer. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 2805-2813.	2.0	13
58	Systematic pathway engineering of <i>Corynebacterium glutamicum</i> S9114 for l-ornithine production. <i>Microbial Cell Factories</i> , 2017, 16, 158.	4.0	30
59	Association of a novel point mutation in MSH2 gene with familial multiple primary cancers. <i>Journal of Hematology and Oncology</i> , 2017, 10, 158.	17.0	4
60	CRISPR/Cas9-mediated targeted chromosome elimination. <i>Genome Biology</i> , 2017, 18, 224.	8.8	142
61	Comprehensive analysis of differential co-expression patterns reveal transcriptional dysregulation mechanism and identify novel prognostic lncRNAs in esophageal squamous cell carcinoma. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 3095-3105.	2.0	22
62	The Safety of Ovarian Preservation in Stage I Endometrial Endometrioid Adenocarcinoma Based on Propensity Score Matching. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 647-655.	1.1	10
63	SysFinder: A customized platform for search, comparison and assisted design of appropriate animal models based on systematic similarity. <i>Journal of Genetics and Genomics</i> , 2017, 44, 251-258.	3.9	0
64	A Two-layer Model to Identify Hepatitis B Virus Related Chronic Hepatitis and Liver Cirrhosis Based on Plasma microRNA Biomarkers. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 123-132.	1.1	1
65	Differential Regulatory Analysis Based on Coexpression Network in Cancer Research. <i>BioMed Research International</i> , 2016, 2016, 1-8.	1.9	16
66	Neuraminidase 1 (NEU1) promotes proliferation and migration as a diagnostic and prognostic biomarker of hepatocellular carcinoma. <i>Oncotarget</i> , 2016, 7, 64957-64966.	1.8	32
67	DASAF: An R Package for Deep Sequencing-Based Detection of Fetal Autosomal Abnormalities from Maternal Cell-Free DNA. <i>BioMed Research International</i> , 2016, 2016, 1-7.	1.9	4
68	Construction of differential mRNA-lncRNA crosstalk networks based on ceRNA hypothesis uncover key roles of lncRNAs implicated in esophageal squamous cell carcinoma. <i>Oncotarget</i> , 2016, 7, 85728-85740.	1.8	83
69	Comparative Transcriptomic Analysis of Primary Duck Hepatocytes Provides Insight into Differential Susceptibility to DHBV Infection. <i>PLoS ONE</i> , 2016, 11, e0149702.	2.5	6
70	Prioritizing functional phosphorylation sites based on multiple feature integration. <i>Scientific Reports</i> , 2016, 6, 24735.	3.3	30
71	A genome-wide loss-of-function screening method for minimizing false-negatives caused by functional redundancy. <i>Cell Research</i> , 2016, 26, 1067-1070.	12.0	2
72	Hepatocellular carcinoma cell lines retain the genomic and transcriptomic landscapes of primary human cancers. <i>Scientific Reports</i> , 2016, 6, 27411.	3.3	49

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73	Hyperlipidemia-associated gene variations and expression patterns revealed by whole-genome and transcriptome sequencing of rabbit models. <i>Scientific Reports</i> , 2016, 6, 26942.	3.3	24
74	Metformin Effect on Nontargeted Metabolite Profiles in Patients With Type 2 Diabetes and in Multiple Murine Tissues. <i>Diabetes</i> , 2016, 65, 3776-3785.	0.6	49
75	cisASE: a likelihood-based method for detecting putative <i>cis</i> -regulated allele-specific expression in RNA sequencing data. <i>Bioinformatics</i> , 2016, 32, 3291-3297.	4.1	12
76	The 14th Ile residue is essential for Leptin function in regulating energy homeostasis in rat. <i>Scientific Reports</i> , 2016, 6, 28508.	3.3	9
77	Association between the CYP11 family and six cancer types. <i>Oncology Letters</i> , 2016, 12, 35-40.	1.8	20
78	Noninvasive diagnosis and monitoring of mutations by deep sequencing of circulating tumor DNA in esophageal squamous cell carcinoma. <i>Biochemical and Biophysical Research Communications</i> , 2016, 471, 596-602.	2.1	47
79	Potential diagnostic and prognostic marker dimethylglycine dehydrogenase (DMGDH) suppresses hepatocellular carcinoma metastasis <i>in vitro</i> and <i>in vivo</i> . <i>Oncotarget</i> , 2016, 7, 32607-32616.	1.8	58
80	Comparative Transcriptomes and EVO-DEVO Studies Depending on Next Generation Sequencing. <i>Computational and Mathematical Methods in Medicine</i> , 2015, 2015, 1-10.	1.3	5
81	Gene Coexpression and Evolutionary Conservation Analysis of the Human Preimplantation Embryos. <i>BioMed Research International</i> , 2015, 2015, 1-11.	1.9	5
82	Nonsynonymous Single-Nucleotide Variations on Some Posttranslational Modifications of Human Proteins and the Association with Diseases. <i>Computational and Mathematical Methods in Medicine</i> , 2015, 2015, 1-12.	1.3	5
83	Construction and Deciphering of Human Phosphorylation-Mediated Signaling Transduction Networks. <i>Journal of Proteome Research</i> , 2015, 14, 2745-2757.	3.7	12
84	Allele frequency of somatic mutations in individuals reveals signatures of cancer-related genes. <i>Acta Biochimica Et Biophysica Sinica</i> , 2015, 47, 657-660.	2.0	2
85	Berberine ameliorates nonalcoholic fatty liver disease by a global modulation of hepatic mRNA and lncRNA expression profiles. <i>Journal of Translational Medicine</i> , 2015, 13, 24.	4.4	92
86	miR-27b synergizes with anticancer drugs via p53 activation and CYP1B1 suppression. <i>Cell Research</i> , 2015, 25, 477-495.	12.0	75
87	Identifying novel associations between small molecules and miRNAs based on integrated molecular networks. <i>Bioinformatics</i> , 2015, 31, 3638-3644.	4.1	72
88	Genome-wide analysis of homeobox genes from <i>Mesobuthus martensii</i> reveals Hox gene duplication in scorpions. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 61, 25-33.	2.7	25
89	Effects of Metformin on Metabolite Profiles and LDL Cholesterol in Patients With Type 2 Diabetes. <i>Diabetes Care</i> , 2015, 38, 1858-1867.	8.6	97
90	Identifying Prognostic Features by Bottom-Up Approach and Correlating to Drug Repositioning. <i>PLoS ONE</i> , 2015, 10, e0118672.	2.5	12

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91	Epididymal Region-Specific miRNA Expression and DNA Methylation and Their Roles in Controlling Gene Expression in Rats. PLoS ONE, 2015, 10, e0124450.	2.5	21
92	Integrated Analysis of Transcriptome in Cancer Patient-Derived Xenografts. PLoS ONE, 2015, 10, e0124780.	2.5	9
93	Comparative Genome of GK and Wistar Rats Reveals Genetic Basis of Type 2 Diabetes. PLoS ONE, 2015, 10, e0141859.	2.5	21
94	LAcEP: Lysine Acetylation Site Prediction Using Logistic Regression Classifiers. PLoS ONE, 2014, 9, e89575.	2.5	77
95	Integrative Analysis of Transcriptional Regulatory Network and Copy Number Variation in Intrahepatic Cholangiocarcinoma. PLoS ONE, 2014, 9, e98653.	2.5	6
96	Quantitative Dynamic Modelling of the Gene Regulatory Network Controlling Adipogenesis. PLoS ONE, 2014, 9, e110563.	2.5	2
97	Big Biological Data: Challenges and Opportunities. Genomics, Proteomics and Bioinformatics, 2014, 12, 187-189.	6.9	83
98	Investigating co-evolution of functionally associated phosphosites in human. Molecular Genetics and Genomics, 2014, 289, 1217-1223.	2.1	0
99	The Domain Landscape of Virus-Host Interactomes. BioMed Research International, 2014, 2014, 1-13.	1.9	30
100	Whole-genome sequencing of six dog breeds from continuous altitudes reveals adaptation to high-altitude hypoxia. Genome Research, 2014, 24, 1308-1315.	5.5	235
101	Comparative analysis of viral protein interaction networks in Hepatitis B Virus and Hepatitis C Virus infected HCC. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 271-279.	2.3	8
102	Comparing Computational Methods for Identification of Allele-Specific Expression based on Next Generation Sequencing Data. Genetic Epidemiology, 2014, 38, 591-598.	1.3	33
103	The 3DGD: a database of genome 3D structure. Bioinformatics, 2014, 30, 1640-1642.	4.1	16
104	SysPTM 2.0: an updated systematic resource for post-translational modification. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau025-bau025.	3.0	58
105	Prediction of protein amidation sites by feature selection and analysis. Molecular Genetics and Genomics, 2013, 288, 391-400.	2.1	10
106	Inter- and Intra-Chain Disulfide Bond Prediction Based on Optimal Feature Selection. Protein and Peptide Letters, 2013, 20, 324-335.	0.9	3
107	Combining ZHENG Theory and High-Throughput Expression Data to Predict New Effects of Chinese Herbal Formulae. Evidence-based Complementary and Alternative Medicine, 2012, 2012, 1-8.	1.2	15
108	cGRNexp: a web platform for building combinatorial gene regulation networks based on user-uploaded gene expression datasets. , 2012, , .		0

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109	A novel strategy for deciphering dynamic conservation of gene expression relationship. <i>Journal of Molecular Cell Biology</i> , 2012, 4, 177-179.	3.3	3
110	Cell type specificity of signaling: view from membrane receptors distribution and their downstream transduction networks. <i>Protein and Cell</i> , 2012, 3, 701-713.	11.0	6
111	Genome sequences of wild and domestic bactrian camels. <i>Nature Communications</i> , 2012, 3, 1202.	12.8	176
112	A model for the 3D chromatin architecture of pro and eukaryotes. <i>Methods</i> , 2012, 58, 307-314.	3.8	16
113	Towards biological characters of interactions between transcription factors and their DNA targets in mammals. <i>BMC Genomics</i> , 2012, 13, 388.	2.8	4
114	A comparative analysis of tissue gene expression data from high-throughput studies. <i>Science Bulletin</i> , 2012, 57, 2920-2927.	1.7	4
115	Differential combinatorial regulatory network analysis related to venous metastasis of hepatocellular carcinoma. <i>BMC Genomics</i> , 2012, 13, S14.	2.8	43
116	A cross-species analysis method to analyze animal models' similarity to human's disease state. <i>BMC Systems Biology</i> , 2012, 6, S18.	3.0	7
117	Prediction of functional phosphorylation sites by incorporating evolutionary information. <i>Protein and Cell</i> , 2012, 3, 675-690.	11.0	14
118	SyStemCell: A Database Populated with Multiple Levels of Experimental Data from Stem Cell Differentiation Research. <i>PLoS ONE</i> , 2012, 7, e35230.	2.5	13
119	SySAP: a system-level predictor of deleterious single amino acid polymorphisms. <i>Protein and Cell</i> , 2012, 3, 38-43.	11.0	18
120	Prediction of lysine ubiquitination with mRMR feature selection and analysis. <i>Amino Acids</i> , 2012, 42, 1387-1395.	2.7	129
121	The discovery of novel protein-coding features in mouse genome based on mass spectrometry data. <i>Genomics</i> , 2011, 98, 343-351.	2.9	19
122	Prediction of Protein Modification Sites of Pyrrolidone Carboxylic Acid Using mRMR Feature Selection and Analysis. <i>PLoS ONE</i> , 2011, 6, e28221.	2.5	10
123	iGepros: an integrated gene and protein annotation server for biological nature exploration. <i>BMC Bioinformatics</i> , 2011, 12, S6.	2.6	11
124	The role of Hepatitis C Virus in the dynamic protein interaction networks of hepatocellular cirrhosis and carcinoma. <i>International Journal of Computational Biology and Drug Design</i> , 2011, 4, 5.	0.3	15
125	ASSOCIATION OF FEATURE GENE EXPRESSION WITH STRUCTURAL FINGERPRINTS OF CHEMICAL COMPOUNDS. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 503-519.	0.8	4
126	Evolution of Protein Phosphorylation for Distinct Functional Modules in Vertebrate Genomes. <i>Molecular Biology and Evolution</i> , 2011, 28, 1131-1140.	8.9	22



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127	Docking and molecular dynamics studies on CYP2D6. Science Bulletin, 2010, 55, 1877-1880.	1.7	13
128	The structure of phospholamban and its MD simulations. Science Bulletin, 2010, 55, 1619-1624.	1.7	5
129	Protein sumoylation sites prediction based on two-stage feature selection. Molecular Diversity, 2010, 14, 81-86.	3.9	28
130	A knowledge-based method to predict the cooperative relationship between transcription factors. Molecular Diversity, 2010, 14, 815-819.	3.9	5
131	TF-centered downstream gene set enrichment analysis: Inference of causal regulators by integrating TF-DNA interactions and protein post-translational modifications information. BMC Bioinformatics, 2010, 11, S5.	2.6	12
132	Using GeneReg to construct time delay gene regulatory networks. BMC Research Notes, 2010, 3, 142.	1.4	33
133	Considering Dependencies Amongst Genes Helps to Adjust the Significance Rank of DEGs. Chinese Journal of Chemistry, 2010, 28, 1284-1290.	4.9	0
134	dbDEPC: a database of Differentially Expressed Proteins in human Cancers. Nucleic Acids Research, 2010, 38, D658-D664.	14.5	19
135	Regulation of Cellular Metabolism by Protein Lysine Acetylation. Science, 2010, 327, 1000-1004.	12.6	1,642
136	Prediction of Tyrosine Sulfation with mRMR Feature Selection and Analysis. Journal of Proteome Research, 2010, 9, 6490-6497.	3.7	40
137	Exploring mitochondrial evolution and metabolism organization principles by comparative analysis of metabolic networks. Genomics, 2010, 95, 339-344.	2.9	15
138	Reconstruction and Analysis of Human Liver-Specific Metabolic Network Based on CNHLPP Data. Journal of Proteome Research, 2010, 9, 1648-1658.	3.7	15
139	Prediction of protein coding regions by combining Fourier and Wavelet Transform. , 2010, , .		11
140	Prediction of Deleterious Non-Synonymous SNPs Based on Protein Interaction Network and Hybrid Properties. PLoS ONE, 2010, 5, e11900.	2.5	70
141	SysPTM: A Systematic Resource for Proteomic Research on Post-translational Modifications. Molecular and Cellular Proteomics, 2009, 8, 1839-1849.	3.8	107
142	Genomic regions with distinct genomic distance conservation in vertebrate genomes. BMC Genomics, 2009, 10, 133.	2.8	4
143	Subtyping of type A influenza by sequencing the variable regions of HA gene specifically amplified with RT-PCR. Science Bulletin, 2009, 54, 2164-2167.	1.7	3
144	Functional association between influenza A (H1N1) virus and human. Biochemical and Biophysical Research Communications, 2009, 390, 1111-1113.	2.1	19

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145	Modeling the age distribution of gene duplications in vertebrate genome using mixture density. <i>Genomics</i> , 2009, 93, 146-151.	2.9	2
146	Improved Prediction of Lysine Acetylation by Support Vector Machines. <i>Protein and Peptide Letters</i> , 2009, 16, 977-983.	0.9	78
147	The combination approach of SVM and ECOC for powerful identification and classification of transcription factor. <i>BMC Bioinformatics</i> , 2008, 9, 282.	2.6	28
148	Comparison of normalization methods with microRNA microarray. <i>Genomics</i> , 2008, 92, 122-128.	2.9	52
149	Molecular Modeling of Two CYP2C19 SNPs and Its Implications for Personalized Drug Design. <i>Protein and Peptide Letters</i> , 2008, 15, 27-32.	0.9	117
150	Gene expression module-based chemical function similarity search. <i>Nucleic Acids Research</i> , 2008, 36, e137-e137.	14.5	23
151	Tree of Life Based on Genome Context Networks. <i>PLoS ONE</i> , 2008, 3, e3357.	2.5	26
152	Structural Relationships between Highly Conserved Elements and Genes in Vertebrate Genomes. <i>PLoS ONE</i> , 2008, 3, e3727.	2.5	10
153	EPCD: a comprehensive web resource for integrating and displaying eukaryotic paralog/paralogue information. <i>Nucleic Acids Research</i> , 2007, 36, D255-D262.	14.5	14
154	An approach to predict transcription factor DNA binding site specificity based upon gene and transcription factor functional categorization. <i>Bioinformatics</i> , 2007, 23, 2449-2454.	4.1	17
155	Predicting Protein N-glycosylation by Combining Functional Domain and Secretion Information. <i>Journal of Biomolecular Structure and Dynamics</i> , 2007, 25, 49-54.	3.5	11
156	Predicting the protein SUMO modification sites based on Properties Sequential Forward Selection (PSFS). <i>Biochemical and Biophysical Research Communications</i> , 2007, 358, 136-139.	2.1	29
157	Gene-Centric Characteristics of Genome-Wide Association Studies. <i>PLoS ONE</i> , 2007, 2, e1262.	2.5	7
158	ECS: An automatic enzyme classifier based on functional domain composition. <i>Computational Biology and Chemistry</i> , 2007, 31, 226-232.	2.3	46
159	Bow-tie topological features of metabolic networks and the functional significance. <i>Science Bulletin</i> , 2007, 52, 1036-1045.	1.7	19
160	Functional analysis of schistosomes EF-hand domain-containing tegument proteins. <i>Science Bulletin</i> , 2007, 52, 2100-2107.	1.7	3
161	Genetic insight of the H5N1 hemagglutinin cleavage site. <i>Science Bulletin</i> , 2007, 52, 2374-2379.	1.7	1
162	Automatic transcription factor classifier based on functional domain composition. <i>Biochemical and Biophysical Research Communications</i> , 2006, 347, 141-144.	2.1	23

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163	A novel computational method to predict transcription factor DNA binding preference. <i>Biochemical and Biophysical Research Communications</i> , 2006, 348, 1034-1037.	2.1	55
164	Identification and analysis of the mouse basic/Helix-Loop-Helix transcription factor family. <i>Biochemical and Biophysical Research Communications</i> , 2006, 350, 648-656.	2.1	20
165	Predicting O-glycosylation sites in mammalian proteins by using SVMs. <i>Computational Biology and Chemistry</i> , 2006, 30, 203-208.	2.3	83
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