

Yixue Li

List of Publications by Year in descending order

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Version: 2024-02-01

174
papers

8,247
citations

76196

40
h-index

56606

83
g-index

176
all docs

176
docs citations

176
times ranked

13905
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulation of Cellular Metabolism by Protein Lysine Acetylation. <i>Science</i> , 2010, 327, 1000-1004.	6.0	1,642
2	Whole-genome sequencing of 128 camels across Asia reveals origin and migration of domestic Bactrian camels. <i>Communications Biology</i> , 2020, 3, 1.	2.0	809
3	Cytosine base editor generates substantial off-target single-nucleotide variants in mouse embryos. <i>Science</i> , 2019, 364, 289-292.	6.0	573
4	Off-target RNA mutation induced by DNA base editing and its elimination by mutagenesis. <i>Nature</i> , 2019, 571, 275-278.	13.7	330
5	Whole-genome sequencing of six dog breeds from continuous altitudes reveals adaptation to high-altitude hypoxia. <i>Genome Research</i> , 2014, 24, 1308-1315.	2.4	235
6	Genome sequences of wild and domestic bactrian camels. <i>Nature Communications</i> , 2012, 3, 1202.	5.8	176
7	CRISPR/Cas9-mediated targeted chromosome elimination. <i>Genome Biology</i> , 2017, 18, 224.	3.8	142
8	Prediction of lysine ubiquitination with mRMR feature selection and analysis. <i>Amino Acids</i> , 2012, 42, 1387-1395.	1.2	129
9	A Pharmacogenomic Landscape in Human Liver Cancers. <i>Cancer Cell</i> , 2019, 36, 179-193.e11.	7.7	127
10	Refined phylogenetic profiles method for predicting protein-protein interactions. <i>Bioinformatics</i> , 2005, 21, 3409-3415.	1.8	117
11	Molecular Modeling of Two CYP2C19 SNPs and Its Implications for Personalized Drug Design. <i>Protein and Peptide Letters</i> , 2008, 15, 27-32.	0.4	117
12	Predicting rRNA-, RNA-, and DNA-binding proteins from primary structure with support vector machines. <i>Journal of Theoretical Biology</i> , 2006, 240, 175-184.	0.8	111
13	SysPTM: A Systematic Resource for Proteomic Research on Post-translational Modifications. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1839-1849.	2.5	107
14	Effects of Metformin on Metabolite Profiles and LDL Cholesterol in Patients With Type 2 Diabetes. <i>Diabetes Care</i> , 2015, 38, 1858-1867.	4.3	97
15	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.	9.0	97
16	Integrative analysis of DNA methylation and gene expression reveals hepatocellular carcinoma-specific diagnostic biomarkers. <i>Genome Medicine</i> , 2018, 10, 42.	3.6	95
17	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.	1.8	92
18	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, .	3.3	90

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19	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.	5.2	88
20	Predicting O-glycosylation sites in mammalian proteins by using SVMs. <i>Computational Biology and Chemistry</i> , 2006, 30, 203-208.	1.1	83
21	Big Biological Data: Challenges and Opportunities. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 187-189.	3.0	83
22	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.	0.8	83
23	Improved Prediction of Lysine Acetylation by Support Vector Machines. <i>Protein and Peptide Letters</i> , 2009, 16, 977-983.	0.4	78
24	LAcPeP: Lysine Acetylation Site Prediction Using Logistic Regression Classifiers. <i>PLoS ONE</i> , 2014, 9, e89575.	1.1	77
25	miR-27b synergizes with anticancer drugs via p53 activation and CYP1B1 suppression. <i>Cell Research</i> , 2015, 25, 477-495.	5.7	75
26	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.	3.5	75
27	Identifying novel associations between small molecules and miRNAs based on integrated molecular networks. <i>Bioinformatics</i> , 2015, 31, 3638-3644.	1.8	72
28	Prediction of Deleterious Non-Synonymous SNPs Based on Protein Interaction Network and Hybrid Properties. <i>PLoS ONE</i> , 2010, 5, e11900.	1.1	70
29	SysPTM 2.0: an updated systematic resource for post-translational modification. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau025-bau025.	1.4	58
30	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.	0.8	58
31	A novel computational method to predict transcription factor DNA binding preference. <i>Biochemical and Biophysical Research Communications</i> , 2006, 348, 1034-1037.	1.0	55
32	Single-cell RNA sequencing of peripheral blood mononuclear cells from acute Kawasaki disease patients. <i>Nature Communications</i> , 2021, 12, 5444.	5.8	55
33	Comparison of normalization methods with microRNA microarray. <i>Genomics</i> , 2008, 92, 122-128.	1.3	52
34	Aldehyde dehydrogenase 2 (ALDH2) opposes hepatocellular carcinoma progression by regulating AMP-activated protein kinase signaling in mice. <i>Hepatology</i> , 2017, 65, 1628-1644.	3.6	52
35	Hepatocellular carcinoma cell lines retain the genomic and transcriptomic landscapes of primary human cancers. <i>Scientific Reports</i> , 2016, 6, 27411.	1.6	49
36	Metformin Effect on Nontargeted Metabolite Profiles in Patients With Type 2 Diabetes and in Multiple Murine Tissues. <i>Diabetes</i> , 2016, 65, 3776-3785.	0.3	49

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37	MKRN3 regulates the epigenetic switch of mammalian puberty via ubiquitination of MBD3. <i>National Science Review</i> , 2020, 7, 671-685.	4.6	48
38	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.	1.0	47
39	Global Prioritizing Disease Candidate lncRNAs via a Multi-level Composite Network. <i>Scientific Reports</i> , 2017, 7, 39516.	1.6	47
40	ECS: An automatic enzyme classifier based on functional domain composition. <i>Computational Biology and Chemistry</i> , 2007, 31, 226-232.	1.1	46
41	Complex networks theory for analyzing metabolic networks. <i>Science Bulletin</i> , 2006, 51, 1529-1537.	1.7	44
42	Differential combinatorial regulatory network analysis related to venous metastasis of hepatocellular carcinoma. <i>BMC Genomics</i> , 2012, 13, S14.	1.2	43
43	Prediction of Tyrosine Sulfation with mRMR Feature Selection and Analysis. <i>Journal of Proteome Research</i> , 2010, 9, 6490-6497.	1.8	40
44	CanProVar 2.0: An Updated Database of Human Cancer Proteome Variation. <i>Journal of Proteome Research</i> , 2017, 16, 421-432.	1.8	36
45	Using GeneReg to construct time delay gene regulatory networks. <i>BMC Research Notes</i> , 2010, 3, 142.	0.6	33
46	Comparing Computational Methods for Identification of Allele-Specific Expression based on Next Generation Sequencing Data. <i>Genetic Epidemiology</i> , 2014, 38, 591-598.	0.6	33
47	Neuraminidase 1 (NEU1) promotes proliferation and migration as a diagnostic and prognostic biomarker of hepatocellular carcinoma. <i>Oncotarget</i> , 2016, 7, 64957-64966.	0.8	32
48	The Domain Landscape of Virus-Host Interactomes. <i>BioMed Research International</i> , 2014, 2014, 1-13.	0.9	30
49	Prioritizing functional phosphorylation sites based on multiple feature integration. <i>Scientific Reports</i> , 2016, 6, 24735.	1.6	30
50	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.	0.9	30
51	Systematic pathway engineering of <i>Corynebacterium glutamicum</i> S9114 for l-ornithine production. <i>Microbial Cell Factories</i> , 2017, 16, 158.	1.9	30
52	Predicting the protein SUMO modification sites based on Properties Sequential Forward Selection (PSFS). <i>Biochemical and Biophysical Research Communications</i> , 2007, 358, 136-139.	1.0	29
53	The Evolution and Expression Pattern of Human Overlapping lncRNA and Protein-coding Gene Pairs. <i>Scientific Reports</i> , 2017, 7, 42775.	1.6	29
54	The combination approach of SVM and ECOC for powerful identification and classification of transcription factor. <i>BMC Bioinformatics</i> , 2008, 9, 282.	1.2	28

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55	Protein sumoylation sites prediction based on two-stage feature selection. <i>Molecular Diversity</i> , 2010, 14, 81-86.	2.1	28
56	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.	3.8	28
57	Optimization of C-to-G base editors with sequence context preference predictable by machine learning methods. <i>Nature Communications</i> , 2021, 12, 4902.	5.8	28
58	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.	1.2	27
59	Tree of Life Based on Genome Context Networks. <i>PLoS ONE</i> , 2008, 3, e3357.	1.1	26
60	Classification of protein quaternary structure by functional domain composition. <i>BMC Bioinformatics</i> , 2006, 7, 187.	1.2	25
61	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.	1.2	25
62	Enrichment of the fetal fraction in non-invasive prenatal screening reduces maternal background interference. <i>Scientific Reports</i> , 2018, 8, 17675.	1.6	25
63	Chromosome-level assembly of wild Bactrian camel genome reveals organization of immune gene loci. <i>Molecular Ecology Resources</i> , 2020, 20, 770-780.	2.2	25
64	Hyperlipidemia-associated gene variations and expression patterns revealed by whole-genome and transcriptome sequencing of rabbit models. <i>Scientific Reports</i> , 2016, 6, 26942.	1.6	24
65	A Genome-Wide Study of Allele-Specific Expression in Colorectal Cancer. <i>Frontiers in Genetics</i> , 2018, 9, 570.	1.1	24
66	GOTI, a method to identify genome-wide off-target effects of genome editing in mouse embryos. <i>Nature Protocols</i> , 2020, 15, 3009-3029.	5.5	24
67	Automatic transcription factor classifier based on functional domain composition. <i>Biochemical and Biophysical Research Communications</i> , 2006, 347, 141-144.	1.0	23
68	Gene expression module-based chemical function similarity search. <i>Nucleic Acids Research</i> , 2008, 36, e137-e137.	6.5	23
69	Evolution of Protein Phosphorylation for Distinct Functional Modules in Vertebrate Genomes. <i>Molecular Biology and Evolution</i> , 2011, 28, 1131-1140.	3.5	22
70	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.	1.0	22
71	Epididymal Region-Specific miRNA Expression and DNA Methylation and Their Roles in Controlling Gene Expression in Rats. <i>PLoS ONE</i> , 2015, 10, e0124450.	1.1	21
72	Comparative Genome of GK and Wistar Rats Reveals Genetic Basis of Type 2 Diabetes. <i>PLoS ONE</i> , 2015, 10, e0141859.	1.1	21

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73	Identification and analysis of the mouse basic/Helix-Loop-Helix transcription factor family. <i>Biochemical and Biophysical Research Communications</i> , 2006, 350, 648-656.	1.0	20
74	Association between the CYP11 family and six cancer types. <i>Oncology Letters</i> , 2016, 12, 35-40.	0.8	20
75	Adaptive evolution of proteins in hepatitis B virus during divergence of genotypes. <i>Scientific Reports</i> , 2017, 7, 1990.	1.6	20
76	Bow-tie topological features of metabolic networks and the functional significance. <i>Science Bulletin</i> , 2007, 52, 1036-1045.	1.7	19
77	Functional association between influenza A (H1N1) virus and human. <i>Biochemical and Biophysical Research Communications</i> , 2009, 390, 1111-1113.	1.0	19
78	dbDEPC: a database of Differentially Expressed Proteins in human Cancers. <i>Nucleic Acids Research</i> , 2010, 38, D658-D664.	6.5	19
79	The discovery of novel protein-coding features in mouse genome based on mass spectrometry data. <i>Genomics</i> , 2011, 98, 343-351.	1.3	19
80	Large-scale pharmacogenomic studies and drug response prediction for personalized cancer medicine. <i>Journal of Genetics and Genomics</i> , 2021, 48, 540-551.	1.7	19
81	SySAP: a system-level predictor of deleterious single amino acid polymorphisms. <i>Protein and Cell</i> , 2012, 3, 38-43.	4.8	18
82	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.	1.8	17
83	Integrative analysis reveals novel driver genes and molecular subclasses of hepatocellular carcinoma. <i>Aging</i> , 2020, 12, 23849-23871.	1.4	17
84	A model for the 3D chromatin architecture of pro and eukaryotes. <i>Methods</i> , 2012, 58, 307-314.	1.9	16
85	The 3DGD: a database of genome 3D structure. <i>Bioinformatics</i> , 2014, 30, 1640-1642.	1.8	16
86	Differential Regulatory Analysis Based on Coexpression Network in Cancer Research. <i>BioMed Research International</i> , 2016, 2016, 1-8.	0.9	16
87	Exploring mitochondrial evolution and metabolism organization principles by comparative analysis of metabolic networks. <i>Genomics</i> , 2010, 95, 339-344.	1.3	15
88	Reconstruction and Analysis of Human Liver-Specific Metabolic Network Based on CNHLPP Data. <i>Journal of Proteome Research</i> , 2010, 9, 1648-1658.	1.8	15
89	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
90	Combining ZHENG Theory and High-Throughput Expression Data to Predict New Effects of Chinese Herbal Formulae. <i>Evidence-based Complementary and Alternative Medicine</i> , 2012, 2012, 1-8.	0.5	15

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91	EPGD: a comprehensive web resource for integrating and displaying eukaryotic paralog/paralogue information. <i>Nucleic Acids Research</i> , 2007, 36, D255-D262.	6.5	14
92	Prediction of functional phosphorylation sites by incorporating evolutionary information. <i>Protein and Cell</i> , 2012, 3, 675-690.	4.8	14
93	RabGTD: a comprehensive database of rabbit genome and transcriptome. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	14
94	Docking and molecular dynamics studies on CYP2D6. <i>Science Bulletin</i> , 2010, 55, 1877-1880.	1.7	13
95	SyStemCell: A Database Populated with Multiple Levels of Experimental Data from Stem Cell Differentiation Research. <i>PLoS ONE</i> , 2012, 7, e35230.	1.1	13
96	Panel of seven long noncoding RNA as a candidate prognostic biomarker for ovarian cancer. <i>OncoTargets and Therapy</i> , 2017, Volume 10, 2805-2813.	1.0	13
97	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.	1.0	13
98	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.	1.4	13
99	Systematic analysis reveals molecular characteristics of ERG-negative prostate cancer. <i>Scientific Reports</i> , 2018, 8, 12868.	1.6	13
100	Evolution of oncogenic signatures of mutation hotspots in tyrosine kinases supports the atavistic hypothesis of cancer. <i>Scientific Reports</i> , 2018, 8, 8256.	1.6	13
101	Association between Alcohol, Smoking and HLA-DQA1⁰²⁰¹ Genotype in Psoriasis. <i>Acta Biochimica Et Biophysica Sinica</i> , 2004, 36, 597-602.	0.9	12
102	TF-centered downstream gene set enrichment analysis: Inference of causal regulators by integrating TF-DNA interactions and protein post-translational modifications information. <i>BMC Bioinformatics</i> , 2010, 11, S5.	1.2	12
103	Construction and Deciphering of Human Phosphorylation-Mediated Signaling Transduction Networks. <i>Journal of Proteome Research</i> , 2015, 14, 2745-2757.	1.8	12
104	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.	1.8	12
105	Identifying Prognostic Features by Bottom-Up Approach and Correlating to Drug Repositioning. <i>PLoS ONE</i> , 2015, 10, e0118672.	1.1	12
106	Insights into the Coupling of Duplication Events and Macroevolution from an Age Profile of Animal Transmembrane Gene Families. <i>PLoS Computational Biology</i> , 2006, 2, e102.	1.5	11
107	Predicting Protein N-glycosylation by Combining Functional Domain and Secretion Information. <i>Journal of Biomolecular Structure and Dynamics</i> , 2007, 25, 49-54.	2.0	11
108	Prediction of protein coding regions by combining Fourier and Wavelet Transform. , 2010, , .		11

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109	iGepros: an integrated gene and protein annotation server for biological nature exploration. BMC Bioinformatics, 2011, 12, S6.	1.2	11
110	Identifying Key Genes for Nasopharyngeal Carcinoma by Prioritized Consensus Differentially Expressed Genes Caused by Aberrant Methylation. Journal of Cancer, 2021, 12, 874-884.	1.2	11
111	Structural Relationships between Highly Conserved Elements and Genes in Vertebrate Genomes. PLoS ONE, 2008, 3, e3727.	1.1	10
112	Prediction of Protein Modification Sites of Pyrrolidone Carboxylic Acid Using mRMR Feature Selection and Analysis. PLoS ONE, 2011, 6, e28221.	1.1	10
113	Prediction of protein amidation sites by feature selection and analysis. Molecular Genetics and Genomics, 2013, 288, 391-400.	1.0	10
114	PhenoModifier: a genetic modifier database for elucidating the genetic basis of human phenotypic variation. Nucleic Acids Research, 2019, 48, D977-D982.	6.5	10
115	The Safety of Ovarian Preservation in Stage I Endometrial Endometrioid Adenocarcinoma Based on Propensity Score Matching. Combinatorial Chemistry and High Throughput Screening, 2017, 20, 647-655.	0.6	10
116	The 14th Ile residue is essential for Leptin function in regulating energy homeostasis in rat. Scientific Reports, 2016, 6, 28508.	1.6	9
117	Multiple transcription factors contribute to inter-chromosomal interaction in yeast. BMC Systems Biology, 2018, 12, 140.	3.0	9
118	Evaluation of functionality for serine and threonine phosphorylation with different evolutionary ages in human and mouse. BMC Genomics, 2018, 19, 431.	1.2	9
119	Integrated Analysis of Transcriptome in Cancer Patient-Derived Xenografts. PLoS ONE, 2015, 10, e0124780.	1.1	9
120	An interactive viral genome evolution network analysis system enabling rapid large-scale molecular tracing of SARS-CoV-2. Science Bulletin, 2022, 67, 665-669.	4.3	9
121	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.	1.1	8
122	Population-based study of effectiveness of neoadjuvant radiotherapy on survival in US rectal cancer patients according to age. Scientific Reports, 2017, 7, 3471.	1.6	8
123	Transcriptomic sequencing reveals diverse adaptive gene expression responses of human vascular smooth muscle cells to nitro-conjugated linoleic acid. Physiological Genomics, 2018, 50, 287-295.	1.0	8
124	Effects of gut microbiota and fatty acid metabolism on dyslipidemia following weight-loss diets in women: Results from a randomized controlled trial. Clinical Nutrition, 2021, 40, 5511-5520.	2.3	8
125	Gene-Centric Characteristics of Genome-Wide Association Studies. PLoS ONE, 2007, 2, e1262.	1.1	7
126	A cross-species analysis method to analyze animal models' similarity to human's disease state. BMC Systems Biology, 2012, 6, S18.	3.0	7

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127	Improving the genome assembly of rabbits with long-read sequencing. <i>Genomics</i> , 2021, 113, 3216-3223.	1.3	7
128	Cell type specificity of signaling: view from membrane receptors distribution and their downstream transduction networks. <i>Protein and Cell</i> , 2012, 3, 701-713.	4.8	6
129	Integrative Analysis of Transcriptional Regulatory Network and Copy Number Variation in Intrahepatic Cholangiocarcinoma. <i>PLoS ONE</i> , 2014, 9, e98653.	1.1	6
130	Comparative Transcriptomic Analysis of Primary Duck Hepatocytes Provides Insight into Differential Susceptibility to DHBV Infection. <i>PLoS ONE</i> , 2016, 11, e0149702.	1.1	6
131	The accelerated aging model reveals critical mechanisms of late-onset Parkinson's disease. <i>BioData Mining</i> , 2020, 13, 4.	2.2	6
132	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.	1.1	6
133	The structure of phospholamban and its MD simulations. <i>Science Bulletin</i> , 2010, 55, 1619-1624.	1.7	5
134	A knowledge-based method to predict the cooperative relationship between transcription factors. <i>Molecular Diversity</i> , 2010, 14, 815-819.	2.1	5
135	Comparative Transcriptomes and EVO-DEVO Studies Depending on Next Generation Sequencing. <i>Computational and Mathematical Methods in Medicine</i> , 2015, 2015, 1-10.	0.7	5
136	Gene Coexpression and Evolutionary Conservation Analysis of the Human Preimplantation Embryos. <i>BioMed Research International</i> , 2015, 2015, 1-11.	0.9	5
137	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.	0.7	5
138	A novel domain-based method for predicting the functional classes of proteins. <i>Science Bulletin</i> , 2004, 49, 2379-2384.	1.7	4
139	Genomic regions with distinct genomic distance conservation in vertebrate genomes. <i>BMC Genomics</i> , 2009, 10, 133.	1.2	4
140	ASSOCIATION OF FEATURE GENE EXPRESSION WITH STRUCTURAL FINGERPRINTS OF CHEMICAL COMPOUNDS. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 503-519.	0.3	4
141	Towards biological characters of interactions between transcription factors and their DNA targets in mammals. <i>BMC Genomics</i> , 2012, 13, 388.	1.2	4
142	A comparative analysis of tissue gene expression data from high-throughput studies. <i>Science Bulletin</i> , 2012, 57, 2920-2927.	1.7	4
143	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.	0.9	4
144	Protein coding gene CRNKL1 as a potential prognostic biomarker in esophageal adenocarcinoma. <i>Artificial Intelligence in Medicine</i> , 2017, 76, 1-6.	3.8	4

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145	Association of a novel point mutation in MSH2 gene with familial multiple primary cancers. <i>Journal of Hematology and Oncology</i> , 2017, 10, 158.	6.9	4
146	Reconstruction of kidney renal clear cell carcinoma evolution across pathological stages. <i>Scientific Reports</i> , 2018, 8, 3339.	1.6	4
147	Comparative analysis of whole-genome sequences of <i>Streptococcus suis</i> . <i>Science Bulletin</i> , 2006, 51, 1199-1209.	1.7	3
148	Functional analysis of schistosomes EF-hand domain-containing tegument proteins. <i>Science Bulletin</i> , 2007, 52, 2100-2107.	1.7	3
149	Subtyping of type A influenza by sequencing the variable regions of HA gene specifically amplified with RT-PCR. <i>Science Bulletin</i> , 2009, 54, 2164-2167.	1.7	3
150	A novel strategy for deciphering dynamic conservation of gene expression relationship. <i>Journal of Molecular Cell Biology</i> , 2012, 4, 177-179.	1.5	3
151	Inter- and Intra-Chain Disulfide Bond Prediction Based on Optimal Feature Selection. <i>Protein and Peptide Letters</i> , 2013, 20, 324-335.	0.4	3
152	Comparative transcriptomics reveals specific responding genes associated with atherosclerosis in rabbit and mouse models. <i>PLoS ONE</i> , 2018, 13, e0201618.	1.1	3
153	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.	1.5	3
154	Prediction and systematic study of protein-protein interaction networks of <i>Leptospira interrogans</i> . <i>Science Bulletin</i> , 2006, 51, 1296-1305.	1.7	2
155	Modeling the age distribution of gene duplications in vertebrate genome using mixture density. <i>Genomics</i> , 2009, 93, 146-151.	1.3	2
156	Quantitative Dynamic Modelling of the Gene Regulatory Network Controlling Adipogenesis. <i>PLoS ONE</i> , 2014, 9, e110563.	1.1	2
157	Allele frequency of somatic mutations in individuals reveals signatures of cancer-related genes. <i>Acta Biochimica Et Biophysica Sinica</i> , 2015, 47, 657-660.	0.9	2
158	A genome-wide loss-of-function screening method for minimizing false-negatives caused by functional redundancy. <i>Cell Research</i> , 2016, 26, 1067-1070.	5.7	2
159	Systematic identification of rabbit lncRNAs reveals functional roles in atherosclerosis. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 2266-2273.	1.8	2
160	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.	1.7	2
161	Genetic insight of the H5N1 hemagglutinin cleavage site. <i>Science Bulletin</i> , 2007, 52, 2374-2379.	1.7	1
162	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;65:3776-3785. <i>Diabetes</i> , 2017, 66, e3-e4.	0.3	1

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163	The self-organization model reveals systematic characteristics of aging. <i>Theoretical Biology and Medical Modelling</i> , 2020, 17, 4.	2.1	1
164	Comparison of immune profiles between hepatocellular carcinoma subtypes. <i>Biophysics Reports</i> , 2020, 6, 19-32.	0.2	1
165	Integrative Analysis Identified a 6-miRNA Prognostic Signature in Nasopharyngeal Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 661105.	1.8	1
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174	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.	1.8	0