

# Yixue Li

## List of Publications by Citations

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173  
papers

5,607  
citations

35  
h-index

71  
g-index

176  
ext. papers

6,953  
ext. citations

6.6  
avg, IF

5.45  
L-index

#	Paper	IF	Citations
173	Regulation of cellular metabolism by protein lysine acetylation. <i>Science</i> , <b>2010</b> , 327, 1000-4	33.3	1394
172	Cytosine base editor generates substantial off-target single-nucleotide variants in mouse embryos. <i>Science</i> , <b>2019</b> , 364, 289-292	33.3	381
171	Whole-genome sequencing of 128 camels across Asia reveals origin and migration of domestic Bactrian camels. <i>Communications Biology</i> , <b>2020</b> , 3, 1	6.7	215
170	Off-target RNA mutation induced by DNA base editing and its elimination by mutagenesis. <i>Nature</i> , <b>2019</b> , 571, 275-278	50.4	207
169	Whole-genome sequencing of six dog breeds from continuous altitudes reveals adaptation to high-altitude hypoxia. <i>Genome Research</i> , <b>2014</b> , 24, 1308-15	9.7	150
168	Genome sequences of wild and domestic bactrian camels. <i>Nature Communications</i> , <b>2012</b> , 3, 1202	17.4	105
167	Molecular modeling of two CYP2C19 SNPs and its implications for personalized drug design. <i>Protein and Peptide Letters</i> , <b>2008</b> , 15, 27-32	1.9	105
166	Prediction of lysine ubiquitination with mRMR feature selection and analysis. <i>Amino Acids</i> , <b>2012</b> , 42, 1387-95	3.95	101
165	SysPTM: a systematic resource for proteomic research on post-translational modifications. <i>Molecular and Cellular Proteomics</i> , <b>2009</b> , 8, 1839-49	7.6	96
164	Predicting rRNA-, RNA-, and DNA-binding proteins from primary structure with support vector machines. <i>Journal of Theoretical Biology</i> , <b>2006</b> , 240, 175-84	2.3	95
163	Refined phylogenetic profiles method for predicting protein-protein interactions. <i>Bioinformatics</i> , <b>2005</b> , 21, 3409-15	7.2	95
162	CRISPR/Cas9-mediated targeted chromosome elimination. <i>Genome Biology</i> , <b>2017</b> , 18, 224	18.3	93
161	Effects of metformin on metabolite profiles and LDL cholesterol in patients with type 2 diabetes. <i>Diabetes Care</i> , <b>2015</b> , 38, 1858-67	14.6	76
160	Improved prediction of lysine acetylation by support vector machines. <i>Protein and Peptide Letters</i> , <b>2009</b> , 16, 977-83	1.9	73
159	Berberine ameliorates nonalcoholic fatty liver disease by a global modulation of hepatic mRNA and lncRNA expression profiles. <i>Journal of Translational Medicine</i> , <b>2015</b> , 13, 24	8.5	70
158	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> , <b>2016</b> , 7, 85728-85740	3.3	69
157	miR-27b synergizes with anticancer drugs via p53 activation and CYP1B1 suppression. <i>Cell Research</i> , <b>2015</b> , 25, 477-95	24.7	66

156	A Pharmacogenomic Landscape in Human Liver Cancers. <i>Cancer Cell</i> , <b>2019</b> , 36, 179-193.e11	24.3	66
155	Predicting O-glycosylation sites in mammalian proteins by using SVMs. <i>Computational Biology and Chemistry</i> , <b>2006</b> , 30, 203-8	3.6	63
154	LAcEP: lysine acetylation site prediction using logistic regression classifiers. <i>PLoS ONE</i> , <b>2014</b> , 9, e89575	3.7	62
153	Prediction of deleterious non-synonymous SNPs based on protein interaction network and hybrid properties. <i>PLoS ONE</i> , <b>2010</b> , 5, e11900	3.7	61
152	Integrative analysis of DNA methylation and gene expression reveals hepatocellular carcinoma-specific diagnostic biomarkers. <i>Genome Medicine</i> , <b>2018</b> , 10, 42	14.4	60
151	Big biological data: challenges and opportunities. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2014</b> , 12, 187-9	6.5	57
150	SysPTM 2.0: an updated systematic resource for post-translational modification. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2014</b> , 2014, bau025	5	48
149	A rationally engineered cytosine base editor retains high on-target activity while reducing both DNA and RNA off-target effects. <i>Nature Methods</i> , <b>2020</b> , 17, 600-604	21.6	47
148	Comparison of normalization methods with microRNA microarray. <i>Genomics</i> , <b>2008</b> , 92, 122-8	4.3	47
147	A novel computational method to predict transcription factor DNA binding preference. <i>Biochemical and Biophysical Research Communications</i> , <b>2006</b> , 348, 1034-7	3.4	47
146	Identifying novel associations between small molecules and miRNAs based on integrated molecular networks. <i>Bioinformatics</i> , <b>2015</b> , 31, 3638-44	7.2	45
145	Genomic Analysis Reveals Hypoxia Adaptation in the Tibetan Mastiff by Introgression of the Gray Wolf from the Tibetan Plateau. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 734-743	8.3	45
144	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> , <b>2018</b> , 7,	7.6	42
143	A Homeostatic Arid1a-Dependent Permissive Chromatin State Licenses Hepatocyte Responsiveness to Liver-Injury-Associated YAP Signaling. <i>Cell Stem Cell</i> , <b>2019</b> , 25, 54-68.e5	18	42
142	Complex networks theory for analyzing metabolic networks. <i>Science Bulletin</i> , <b>2006</b> , 51, 1529-1537		37
141	Hepatocellular carcinoma cell lines retain the genomic and transcriptomic landscapes of primary human cancers. <i>Scientific Reports</i> , <b>2016</b> , 6, 27411	4.9	36
140	ECS: an automatic enzyme classifier based on functional domain composition. <i>Computational Biology and Chemistry</i> , <b>2007</b> , 31, 226-32	3.6	36
139	Global Prioritizing Disease Candidate lncRNAs via a Multi-level Composite Network. <i>Scientific Reports</i> , <b>2017</b> , 7, 39516	4.9	35

138	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> , <b>2016</b> , 471, 596-602	3.4	35
137	Aldehyde dehydrogenase-2 (ALDH2) opposes hepatocellular carcinoma progression by regulating AMP-activated protein kinase signaling in mice. <i>Hepatology</i> , <b>2017</b> , 65, 1628-1644	11.2	34
136	Prediction of tyrosine sulfation with mRMR feature selection and analysis. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 6490-7	5.6	33
135	Differential combinatorial regulatory network analysis related to venous metastasis of hepatocellular carcinoma. <i>BMC Genomics</i> , <b>2012</b> , 13 Suppl 8, S14	4.5	31
134	Metformin Effect on Nontargeted Metabolite Profiles in Patients With Type 2 Diabetes and in Multiple Murine Tissues. <i>Diabetes</i> , <b>2016</b> , 65, 3776-3785	0.9	30
133	Potential diagnostic and prognostic marker dimethylglycine dehydrogenase (DMGDH) suppresses hepatocellular carcinoma metastasis in vitro and in vivo. <i>Oncotarget</i> , <b>2016</b> , 7, 32607-16	3.3	30
132	Using GeneReg to construct time delay gene regulatory networks. <i>BMC Research Notes</i> , <b>2010</b> , 3, 142	2.3	29
131	CanProVar 2.0: An Updated Database of Human Cancer Proteome Variation. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 421-432	5.6	26
130	Predicting the protein SUMO modification sites based on Properties Sequential Forward Selection (PSFS). <i>Biochemical and Biophysical Research Communications</i> , <b>2007</b> , 358, 136-9	3.4	26
129	Systematic pathway engineering of <i>Corynebacterium glutamicum</i> S9114 for L-ornithine production. <i>Microbial Cell Factories</i> , <b>2017</b> , 16, 158	6.4	24
128	Protein sumoylation sites prediction based on two-stage feature selection. <i>Molecular Diversity</i> , <b>2010</b> , 14, 81-6	3.1	24
127	Genome-wide analysis of homeobox genes from <i>Mesobuthus martensii</i> reveals Hox gene duplication in scorpions. <i>Insect Biochemistry and Molecular Biology</i> , <b>2015</b> , 61, 25-33	4.5	23
126	Neuraminidase 1 (NEU1) promotes proliferation and migration as a diagnostic and prognostic biomarker of hepatocellular carcinoma. <i>Oncotarget</i> , <b>2016</b> , 7, 64957-64966	3.3	23
125	Prioritizing functional phosphorylation sites based on multiple feature integration. <i>Scientific Reports</i> , <b>2016</b> , 6, 24735	4.9	23
124	The Evolution and Expression Pattern of Human Overlapping lncRNA and Protein-coding Gene Pairs. <i>Scientific Reports</i> , <b>2017</b> , 7, 42775	4.9	22
123	Classification of protein quaternary structure by functional domain composition. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 187	3.6	22
122	Hyperlipidemia-associated gene variations and expression patterns revealed by whole-genome and transcriptome sequencing of rabbit models. <i>Scientific Reports</i> , <b>2016</b> , 6, 26942	4.9	21
121	Gene expression module-based chemical function similarity search. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, e1370.1	3.0	21

120	Cancer-Related Triplets of mRNA-lncRNA-miRNA Revealed by Integrative Network in Uterine Corpus Endometrial Carcinoma. <i>BioMed Research International</i> , <b>2017</b> , 2017, 3859582	3	20
119	Evolution of protein phosphorylation for distinct functional modules in vertebrate genomes. <i>Molecular Biology and Evolution</i> , <b>2011</b> , 28, 1131-40	8.3	20
118	The combination approach of SVM and ECOC for powerful identification and classification of transcription factor. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 282	3.6	20
117	Automatic transcription factor classifier based on functional domain composition. <i>Biochemical and Biophysical Research Communications</i> , <b>2006</b> , 347, 141-4	3.4	19
116	MKRN3 regulates the epigenetic switch of mammalian puberty via ubiquitination of MBD3. <i>National Science Review</i> , <b>2020</b> , 7, 671-685	10.8	18
115	SySAP: a system-level predictor of deleterious single amino acid polymorphisms. <i>Protein and Cell</i> , <b>2012</b> , 3, 38-43	7.2	18
114	The domain landscape of virus-host interactomes. <i>BioMed Research International</i> , <b>2014</b> , 2014, 867235	3	18
113	dbDEPC: a database of differentially expressed proteins in human cancers. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D658-64	20.1	18
112	Identification and analysis of the mouse basic/Helix-Loop-Helix transcription factor family. <i>Biochemical and Biophysical Research Communications</i> , <b>2006</b> , 350, 648-56	3.4	18
111	Epididymal Region-Specific miRNA Expression and DNA Methylation and Their Roles in Controlling Gene Expression in Rats. <i>PLoS ONE</i> , <b>2015</b> , 10, e0124450	3.7	18
110	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> , <b>2017</b> , 10, 3095-3105	4.4	17
109	The discovery of novel protein-coding features in mouse genome based on mass spectrometry data. <i>Genomics</i> , <b>2011</b> , 98, 343-51	4.3	17
108	Functional association between influenza A (H1N1) virus and human. <i>Biochemical and Biophysical Research Communications</i> , <b>2009</b> , 390, 1111-3	3.4	17
107	Tree of life based on genome context networks. <i>PLoS ONE</i> , <b>2008</b> , 3, e3357	3.7	16
106	A model for the 3D chromatin architecture of pro and eukaryotes. <i>Methods</i> , <b>2012</b> , 58, 307-14	4.6	15
105	An approach to predict transcription factor DNA binding site specificity based upon gene and transcription factor functional categorization. <i>Bioinformatics</i> , <b>2007</b> , 23, 2449-54	7.2	15
104	Enrichment of the fetal fraction in non-invasive prenatal screening reduces maternal background interference. <i>Scientific Reports</i> , <b>2018</b> , 8, 17675	4.9	15
103	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> , <b>2019</b> , 20, 261	4.5	14

102	Bow-tie topological features of metabolic networks and the functional significance. <i>Science Bulletin</i> , <b>2007</b> , 52, 1036-1045		14
101	EPGD: a comprehensive web resource for integrating and displaying eukaryotic paralog/paralogue information. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D255-62	20.1	14
100	Differential Regulatory Analysis Based on Coexpression Network in Cancer Research. <i>BioMed Research International</i> , <b>2016</b> , 2016, 4241293	3	14
99	Reconstruction and analysis of human liver-specific metabolic network based on CNHLPP data. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 1648-58	5.6	13
98	Combining ZHENG Theory and High-Throughput Expression Data to Predict New Effects of Chinese Herbal Formulae. <i>Evidence-based Complementary and Alternative Medicine</i> , <b>2012</b> , 2012, 986427	2.3	13
97	Panel of seven long noncoding RNA as a candidate prognostic biomarker for ovarian cancer. <i>OncoTargets and Therapy</i> , <b>2017</b> , 10, 2805-2813	4.4	12
96	Association between the CYP11 family and six cancer types. <i>Oncology Letters</i> , <b>2016</b> , 12, 35-40	2.6	12
95	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> , <b>2011</b> , 4, 5-18	0.4	12
94	A Genome-Wide Study of Allele-Specific Expression in Colorectal Cancer. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 570	4.5	12
93	Adaptive evolution of proteins in hepatitis B virus during divergence of genotypes. <i>Scientific Reports</i> , <b>2017</b> , 7, 1990	4.9	11
92	Exploring mitochondrial evolution and metabolism organization principles by comparative analysis of metabolic networks. <i>Genomics</i> , <b>2010</b> , 95, 339-44	4.3	11
91	Comparative Genome of GK and Wistar Rats Reveals Genetic Basis of Type 2 Diabetes. <i>PLoS ONE</i> , <b>2015</b> , 10, e0141859	3.7	11
90	Chromosome-level assembly of wild Bactrian camel genome reveals organization of immune gene loci. <i>Molecular Ecology Resources</i> , <b>2020</b> , 20, 770	8.4	11
89	GOTI, a method to identify genome-wide off-target effects of genome editing in mouse embryos. <i>Nature Protocols</i> , <b>2020</b> , 15, 3009-3029	18.8	11
88	RabGTD: a comprehensive database of rabbit genome and transcriptome. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2018</b> , 2018,	5	11
87	Rabbit models provide insights into bone formation related biological process in atherosclerotic vascular calcification. <i>Biochemical and Biophysical Research Communications</i> , <b>2018</b> , 496, 1369-1375	3.4	10
86	The 3DGD: a database of genome 3D structure. <i>Bioinformatics</i> , <b>2014</b> , 30, 1640-2	7.2	10
85	Construction and Deciphering of Human Phosphorylation-Mediated Signaling Transduction Networks. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 2745-57	5.6	10

84	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> , <b>2010</b> , 11 Suppl 11, S5	3.6	10
83	Predicting protein N-glycosylation by combining functional domain and secretion information. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2007</b> , 25, 49-54	3.6	10
82	Comparing computational methods for identification of allele-specific expression based on next generation sequencing data. <i>Genetic Epidemiology</i> , <b>2014</b> , 38, 591-8	2.6	9
81	Prediction of protein amidation sites by feature selection and analysis. <i>Molecular Genetics and Genomics</i> , <b>2013</b> , 288, 391-400	3.1	9
80	Prediction of functional phosphorylation sites by incorporating evolutionary information. <i>Protein and Cell</i> , <b>2012</b> , 3, 675-90	7.2	9
79	Prediction of protein modification sites of pyrrolidone carboxylic acid using mRMR feature selection and analysis. <i>PLoS ONE</i> , <b>2011</b> , 6, e28221	3.7	9
78	iGepros: an integrated gene and protein annotation server for biological nature exploration. <i>BMC Bioinformatics</i> , <b>2011</b> , 12 Suppl 14, S6	3.6	9
77	Docking and molecular dynamics studies on CYP2D6. <i>Science Bulletin</i> , <b>2010</b> , 55, 1877-1880		9
76	Insights into the coupling of duplication events and macroevolution from an age profile of animal transmembrane gene families. <i>PLoS Computational Biology</i> , <b>2006</b> , 2, e102	5	9
75	Competitive evolution of NSCLC tumor clones and the drug resistance mechanism of first-generation EGFR-TKIs in Chinese NSCLC patients. <i>Heliyon</i> , <b>2018</b> , 4, e01031	3.6	9
74	Evolution of oncogenic signatures of mutation hotspots in tyrosine kinases supports the atavistic hypothesis of cancer. <i>Scientific Reports</i> , <b>2018</b> , 8, 8256	4.9	9
73	The 14th Ile residue is essential for Leptin function in regulating energy homeostasis in rat. <i>Scientific Reports</i> , <b>2016</b> , 6, 28508	4.9	8
72	SyStemCell: a database populated with multiple levels of experimental data from stem cell differentiation research. <i>PLoS ONE</i> , <b>2012</b> , 7, e35230	3.7	8
71	Identifying prognostic features by bottom-up approach and correlating to drug repositioning. <i>PLoS ONE</i> , <b>2015</b> , 10, e0118672	3.7	8
70	Single-cell RNA sequencing of peripheral blood mononuclear cells from acute Kawasaki disease patients. <i>Nature Communications</i> , <b>2021</b> , 12, 5444	17.4	8
69	PhenoModifier: a genetic modifier database for elucidating the genetic basis of human phenotypic variation. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D977-D982	20.1	7
68	Structural relationships between highly conserved elements and genes in vertebrate genomes. <i>PLoS ONE</i> , <b>2008</b> , 3, e3727	3.7	7
67	Integrated analysis of transcriptome in cancer patient-derived xenografts. <i>PLoS ONE</i> , <b>2015</b> , 10, e0124780	3.7	7

66	The Safety of Ovarian Preservation in Stage I Endometrial Endometrioid Adenocarcinoma Based on Propensity Score Matching. <i>Combinatorial Chemistry and High Throughput Screening</i> , <b>2017</b> , 20, 647-655	1.3	7
65	Systematic analysis reveals molecular characteristics of ERG-negative prostate cancer. <i>Scientific Reports</i> , <b>2018</b> , 8, 12868	4.9	7
64	Population-based study of effectiveness of neoadjuvant radiotherapy on survival in US rectal cancer patients according to age. <i>Scientific Reports</i> , <b>2017</b> , 7, 3471	4.9	6
63	cisASE: a likelihood-based method for detecting putative cis-regulated allele-specific expression in RNA sequencing data. <i>Bioinformatics</i> , <b>2016</b> , 32, 3291-3297	7.2	6
62	A cross-species analysis method to analyze animal models similarity to human disease state. <i>BMC Systems Biology</i> , <b>2012</b> , 6 Suppl 3, S18	3.5	6
61	Association between alcohol, smoking and HLA-DQA1*0201 genotype in psoriasis. <i>Acta Biochimica Et Biophysica Sinica</i> , <b>2004</b> , 36, 597-602	2.8	6
60	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> , <b>2021</b> , 22, 4	18.3	6
59	Transcriptomic sequencing reveals diverse adaptive gene expression responses of human vascular smooth muscle cells to nitro-conjugated linoleic acid. <i>Physiological Genomics</i> , <b>2018</b> , 50, 287-295	3.6	5
58	Evaluation of functionality for serine and threonine phosphorylation with different evolutionary ages in human and mouse. <i>BMC Genomics</i> , <b>2018</b> , 19, 431	4.5	5
57	Comparative analysis of viral protein interaction networks in Hepatitis B virus and Hepatitis C virus infected HCC. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2014</b> , 1844, 271-9	4	5
56	Prediction of protein coding regions by combining Fourier and Wavelet Transform <b>2010</b> ,		5
55	Gene-centric characteristics of genome-wide association studies. <i>PLoS ONE</i> , <b>2007</b> , 2, e1262	3.7	5
54	Integrative analysis reveals novel driver genes and molecular subclasses of hepatocellular carcinoma. <i>Aging</i> , <b>2020</b> , 12, 23849-23871	5.6	5
53	High-fidelity base editor with no detectable genome-wide off-target effects		5
52	Optimization of C-to-G base editors with sequence context preference predictable by machine learning methods. <i>Nature Communications</i> , <b>2021</b> , 12, 4902	17.4	5
51	Gene Coexpression and Evolutionary Conservation Analysis of the Human Preimplantation Embryos. <i>BioMed Research International</i> , <b>2015</b> , 2015, 316735	3	4
50	Nonsynonymous Single-Nucleotide Variations on Some Posttranslational Modifications of Human Proteins and the Association with Diseases. <i>Computational and Mathematical Methods in Medicine</i> , <b>2015</b> , 2015, 124630	2.8	4
49	Integrative analysis of transcriptional regulatory network and copy number variation in intrahepatic cholangiocarcinoma. <i>PLoS ONE</i> , <b>2014</b> , 9, e98653	3.7	4



48	Cell type specificity of signaling: view from membrane receptors distribution and their downstream transduction networks. <i>Protein and Cell</i> , <b>2012</b> , 3, 701-13	7.2	4
47	Towards biological characters of interactions between transcription factors and their DNA targets in mammals. <i>BMC Genomics</i> , <b>2012</b> , 13, 388	4.5	4
46	A novel domain-based method for predicting the functional classes of proteins. <i>Science Bulletin</i> , <b>2004</b> , 49, 2379-2384		4
45	Comparative Transcriptomic Analysis of Primary Duck Hepatocytes Provides Insight into Differential Susceptibility to DHBV Infection. <i>PLoS ONE</i> , <b>2016</b> , 11, e0149702	3.7	4
44	Multiple transcription factors contribute to inter-chromosomal interaction in yeast. <i>BMC Systems Biology</i> , <b>2018</b> , 12, 140	3.5	4
43	Large-scale pharmacogenomic studies and drug response prediction for personalized cancer medicine. <i>Journal of Genetics and Genomics</i> , <b>2021</b> , 48, 540-551	4	4
42	Protein coding gene CRNKL1 as a potential prognostic biomarker in esophageal adenocarcinoma. <i>Artificial Intelligence in Medicine</i> , <b>2017</b> , 76, 1-6	7.4	3
41	Association of a novel point mutation in MSH2 gene with familial multiple primary cancers. <i>Journal of Hematology and Oncology</i> , <b>2017</b> , 10, 158	22.4	3
40	Comparative Transcriptomes and EVO-DEVO Studies Depending on Next Generation Sequencing. <i>Computational and Mathematical Methods in Medicine</i> , <b>2015</b> , 2015, 896176	2.8	3
39	A comparative analysis of tissue gene expression data from high-throughput studies. <i>Science Bulletin</i> , <b>2012</b> , 57, 2920-2927		3
38	Inter- and Intra-Chain Disulfide Bond Prediction Based on Optimal Feature Selection. <i>Protein and Peptide Letters</i> , <b>2013</b> , 20, 324-335	1.9	3
37	Genomic regions with distinct genomic distance conservation in vertebrate genomes. <i>BMC Genomics</i> , <b>2009</b> , 10, 133	4.5	3
36	Association of feature gene expression with structural fingerprints of chemical compounds. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2011</b> , 9, 503-19	1	3
35	A novel strategy for deciphering dynamic conservation of gene expression relationship. <i>Journal of Molecular Cell Biology</i> , <b>2012</b> , 4, 177-9	6.3	3
34	The structure of phospholamban and its MD simulations. <i>Science Bulletin</i> , <b>2010</b> , 55, 1619-1624		3
33	A knowledge-based method to predict the cooperative relationship between transcription factors. <i>Molecular Diversity</i> , <b>2010</b> , 14, 815-9	3.1	3
32	Pan-Cancer Analysis of Head-to-Head Gene Pairs in Terms of Transcriptional Activity, Co-expression and Regulation. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 560997	4.5	3
31	The accelerated aging model reveals critical mechanisms of late-onset Parkinson's disease. <i>BioData Mining</i> , <b>2020</b> , 13, 4	4.3	2

30	Reconstruction of kidney renal clear cell carcinoma evolution across pathological stages. <i>Scientific Reports</i> , <b>2018</b> , 8, 3339	4.9	2
29	A genome-wide loss-of-function screening method for minimizing false-negatives caused by functional redundancy. <i>Cell Research</i> , <b>2016</b> , 26, 1067-70	24.7	2
28	Quantitative dynamic modelling of the gene regulatory network controlling adipogenesis. <i>PLoS ONE</i> , <b>2014</b> , 9, e110563	3.7	2
27	Subtyping of type A influenza by sequencing the variable regions of HA gene specifically amplified with RT-PCR. <i>Science Bulletin</i> , <b>2009</b> , 54, 2164-2167		2
26	Modeling the age distribution of gene duplications in vertebrate genome using mixture density. <i>Genomics</i> , <b>2009</b> , 93, 146-51	4.3	2
25	Functional analysis of schistosomes EF-hand domain-containing tegument proteins. <i>Science Bulletin</i> , <b>2007</b> , 52, 2100-2107		2
24	Comparative analysis of whole-genome sequences of <i>Streptococcus suis</i> . <i>Science Bulletin</i> , <b>2006</b> , 51, 1199-1209		2
23	Prediction and systematic study of protein-protein interaction networks of <i>Leptospira interrogans</i> . <i>Science Bulletin</i> , <b>2006</b> , 51, 1296-1305		2
22	DASAF: An R Package for Deep Sequencing-Based Detection of Fetal Autosomal Abnormalities from Maternal Cell-Free DNA. <i>BioMed Research International</i> , <b>2016</b> , 2016, 2714341	3	2
21	Identifying Key Genes for Nasopharyngeal Carcinoma by Prioritized Consensus Differentially Expressed Genes Caused by Aberrant Methylation. <i>Journal of Cancer</i> , <b>2021</b> , 12, 874-884	4.5	2
20	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> <b>2016</b> ;65:3776-3785. <i>Diabetes</i> , <b>2017</b> , 66, e3-e4	0.9	1
19	Comparison of immune profiles between hepatocellular carcinoma subtypes. <i>Biophysics Reports</i> , <b>2020</b> , 6, 19-32	3.5	1
18	Systematic identification of rabbit lncRNAs reveals functional roles in atherosclerosis. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , <b>2018</b> , 1864, 2266-2273	6.9	1
17	Allele frequency of somatic mutations in individuals reveals signatures of cancer-related genes. <i>Acta Biochimica Et Biophysica Sinica</i> , <b>2015</b> , 47, 657-60	2.8	1
16	Genetic insight of the H5N1 hemagglutinin cleavage site. <i>Science Bulletin</i> , <b>2007</b> , 52, 2374-2379		1
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5	Considering Dependencies Amongst Genes Helps to Adjust the Significance Rank of DEGs. <i>Chinese Journal of Chemistry</i> , <b>2010</b> , 28, 1284-1290	4.9	
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2	Integrative Analysis Identified a 6-miRNA Prognostic Signature in Nasopharyngeal Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , <b>2021</b> , 9, 661105	5.7	
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