Dong Li

List of Publications by Year
in descending order

		331670	289244
40 papers	**1,963** citations	**21** h-index	**40** g-index
44 all docs	**44** docs citations	**44** times ranked	**3416** citing authors

#	Article	IF	Citations
1	BATMAN-TCM: a Bioinformatics Analysis Tool for Molecular mechANism of Traditional Chinese Medicine. Scientific Reports, 2016, 6, 21146.	3.3	530
2	Toward an understanding of the protein interaction network of the human liver. Molecular Systems Biology, 2011, 7, 536.	7.2	194
3	An integrated bioinformatics platform for investigating the human E3 ubiquitin ligase-substrate interaction network. Nature Communications, 2017, 8, 347.	12.8	151
4	Proteome-wide profiling of activated transcription factors with a concatenated tandem array of transcription factor response elements. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6771-6776.	7.1	91
5	A Cell-type-resolved Liver Proteome. Molecular and Cellular Proteomics, 2016, 15, 3190-3202.	3.8	83
6	In-depth serum proteomics reveals biomarkers of psoriasis severity and response to traditional Chinese medicine. Theranostics, 2019, 9, 2475-2488.	10.0	76
7	Similarity-based prediction for Anatomical Therapeutic Chemical classification of drugs by integrating multiple data sources. Bioinformatics, 2015, 31, 1788-1795.	4.1	59
8	PRINCESS, a Protein Interaction Confidence Evaluation System with Multiple Data Sources. Molecular and Cellular Proteomics, 2008, 7, 1043-1052.	3.8	52
9	Insight into Bacterial Virulence Mechanisms against Host Immune Response via the Yersinia pestis-Human Protein-Protein Interaction Network. Infection and Immunity, 2011, 79, 4413-4424.	2.2	52
10	A Dataset of Human Fetal Liver Proteome Identified by Subcellular Fractionation and Multiple Protein Separation and Identification Technology. Molecular and Cellular Proteomics, 2006, 5, 1703-1707.	3.8	50
11	Multi-modality of pI distribution in whole proteome. Proteomics, 2006, 6, 449-455.	2.2	49
12	AAgAtlas 1.0: a human autoantigen database. Nucleic Acids Research, 2017, 45, D769-D776.	14.5	48
13	Protein interaction networks ofSaccharomyces cerevisiae,Caenorhabditis elegans andDrosophila melanogaster: Large-scale organization and robustness. Proteomics, 2006, 6, 456-461.	2.2	47
14	UbiBrowser 2.0: a comprehensive resource for proteome-wide known and predicted ubiquitin ligase/deubiquitinase–substrate interactions in eukaryotic species. Nucleic Acids Research, 2022, 50, D719-D728.	14.5	46
15	HisgAtlas 1.0: a human immunosuppression gene database. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	44
16	Dammarane Sapogenins Ameliorates Neurocognitive Functional Impairment Induced by Simulated Long-Duration Spaceflight. Frontiers in Pharmacology, 2017, 8, 315.	3.5	42
17	Liverbase: A Comprehensive View of Human Liver Biology. Journal of Proteome Research, 2010, 9, 50-58.	3.7	41
18	Protein Interaction Data Set Highlighted with Human Ras-MAPK/PI3K Signaling Pathways. Journal of Proteome Research, 2008, 7, 3879-3889.	3.7	38

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19	Proteome-wide Prediction of Self-interacting Proteins Based on Multiple Properties. Molecular and Cellular Proteomics, 2013, 12, 1689-1700.	3.8	31
20	Proteome-wide Prediction of Signal Flow Direction in Protein Interaction Networks Based on Interacting Domains. Molecular and Cellular Proteomics, 2009, 8, 2063-2070.	3.8	28
21	CTR-DB, an omnibus for patient-derived gene expression signatures correlated with cancer drug response. Nucleic Acids Research, 2022, 50, D1184-D1199.	14.5	26
22	CAPER: a Chromosome-Assembled human Proteome browsER. Journal of Proteome Research, 2013, 12, 179-186.	3.7	22
23	First Proteomic Exploration of Protein-Encoding Genes on Chromosome 1 in Human Liver, Stomach, and Colon. Journal of Proteome Research, 2013, 12, 67-80.	3.7	20
24	Evidence for the additions of clustered interacting nodes during the evolution of protein interaction networks from network motifs. BMC Evolutionary Biology, 2011, 11, 133.	3.2	17
25	Improving the sensitivity of MASCOT search results validation by combining new features with Bayesian nonparametric model. Proteomics, 2010, 10, 4293-4300.	2.2	14
26	General Trends in the Utilization of Structural Factors Contributing to Biological Complexity. Molecular Biology and Evolution, 2012, 29, 1957-1968.	8.9	11
27	Solid State Characterizations and Analysis of Stability in Azelnidipine Polymorphs. Chemical and Pharmaceutical Bulletin, 2012, 60, 995-1002.	1.3	11
28	AllerGAtlas 1.0: a human allergy-related genes database. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	11
29	Modular analysis of the probabilistic genetic interaction network. Bioinformatics, 2011, 27, 853-859.	4.1	10
30	CAPER 2.0: An Interactive, Configurable, and Extensible Workflow-Based Platform to Analyze Data Sets from the Chromosome-centric Human Proteome Project. Journal of Proteome Research, 2014, 13, 99-106.	3.7	10
31	FibroAtlas: A Database for the Exploration of Fibrotic Diseases and Their Genes. Cardiology Research and Practice, 2019, 2019, 1-7.	1.1	10
32	CAPER 3.0: A Scalable Cloud-Based System for Data-Intensive Analysis of Chromosome-Centric Human Proteome Project Data Sets. Journal of Proteome Research, 2015, 14, 3720-3728.	3.7	8
33	RadAtlas 1.0: a knowledgebase focusing on radiation-associated genes. International Journal of Radiation Biology, 2020, 96, 980-987.	1.8	7
34	Functional constraints on adaptive evolution of protein ubiquitination sites. Scientific Reports, 2017, 7, 39949.	3.3	6
35	OsteoporosAtlas: a human osteoporosis-related gene database. PeerJ, 2019, 7, e6778.	2.0	6
36	A novel parametric approach to mine gene regulatory relationship from microarray datasets. BMC Bioinformatics, 2010, 11, S15.	2.6	3

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37	Study on diverse pathological characteristics of heart failure in different stages based on proteomics. Journal of Cellular and Molecular Medicine, 2022, 26, 1169-1182.	3.6	3
38	Exploration of Target Spaces in the Human Genome for Protein and Peptide Drugs. Genomics, Proteomics and Bioinformatics, 2022, 20, 780-794.	6.9	2
39	CPDR: An R Package of Recommending Personalized Drugs for Cancer Patients by Reversing the Individual's Disease-Related Signature. Frontiers in Pharmacology, 0, 13, .	3.5	1
40	UVGD 1.0: a gene-centric database bridging ultraviolet radiation and molecular biology effects in organisms. International Journal of Radiation Biology, 2019, 95, 1172-1177.	1.8	0