

# Dong Li

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

1,963  
citations

331670

21  
h-index

289244

40  
g-index

44  
all docs

44  
docs citations

44  
times ranked

3416  
citing authors

#	ARTICLE	IF	CITATIONS
1	CTR-DB, an omnibus for patient-derived gene expression signatures correlated with cancer drug response. <i>Nucleic Acids Research</i> , 2022, 50, D1184-D1199.	14.5	26
2	UbiBrowser 2.0: a comprehensive resource for proteome-wide known and predicted ubiquitin ligase/deubiquitinase-substrate interactions in eukaryotic species. <i>Nucleic Acids Research</i> , 2022, 50, D719-D728.	14.5	46
3	Study on diverse pathological characteristics of heart failure in different stages based on proteomics. <i>Journal of Cellular and Molecular Medicine</i> , 2022, 26, 1169-1182.	3.6	3
4	Exploration of Target Spaces in the Human Genome for Protein and Peptide Drugs. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 780-794.	6.9	2
5	RadAtlas 1.0: a knowledgebase focusing on radiation-associated genes. <i>International Journal of Radiation Biology</i> , 2020, 96, 980-987.	1.8	7
6	In-depth serum proteomics reveals biomarkers of psoriasis severity and response to traditional Chinese medicine. <i>Theranostics</i> , 2019, 9, 2475-2488.	10.0	76
7	UVGD 1.0: a gene-centric database bridging ultraviolet radiation and molecular biology effects in organisms. <i>International Journal of Radiation Biology</i> , 2019, 95, 1172-1177.	1.8	0
8	FibroAtlas: A Database for the Exploration of Fibrotic Diseases and Their Genes. <i>Cardiology Research and Practice</i> , 2019, 2019, 1-7.	1.1	10
9	OsteoporosAtlas: a human osteoporosis-related gene database. <i>PeerJ</i> , 2019, 7, e6778.	2.0	6
10	AllerGAtlas 1.0: a human allergy-related genes database. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	11
11	Functional constraints on adaptive evolution of protein ubiquitination sites. <i>Scientific Reports</i> , 2017, 7, 39949.	3.3	6
12	An integrated bioinformatics platform for investigating the human E3 ubiquitin ligase-substrate interaction network. <i>Nature Communications</i> , 2017, 8, 347.	12.8	151
13	AAGAtlas 1.0: a human autoantigen database. <i>Nucleic Acids Research</i> , 2017, 45, D769-D776.	14.5	48
14	Dammarane Sapogenins Ameliorates Neurocognitive Functional Impairment Induced by Simulated Long-Duration Spaceflight. <i>Frontiers in Pharmacology</i> , 2017, 8, 315.	3.5	42
15	HisgAtlas 1.0: a human immunosuppression gene database. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	44
16	A Cell-type-resolved Liver Proteome. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3190-3202.	3.8	83
17	BATMAN-TCM: a Bioinformatics Analysis Tool for Molecular mechANism of Traditional Chinese Medicine. <i>Scientific Reports</i> , 2016, 6, 21146.	3.3	530
18	CAPER 3.0: A Scalable Cloud-Based System for Data-Intensive Analysis of Chromosome-Centric Human Proteome Project Data Sets. <i>Journal of Proteome Research</i> , 2015, 14, 3720-3728.	3.7	8

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19	Similarity-based prediction for Anatomical Therapeutic Chemical classification of drugs by integrating multiple data sources. <i>Bioinformatics</i> , 2015, 31, 1788-1795.	4.1	59
20	CAPER 2.0: An Interactive, Configurable, and Extensible Workflow-Based Platform to Analyze Data Sets from the Chromosome-centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2014, 13, 99-106.	3.7	10
21	Proteome-wide profiling of activated transcription factors with a concatenated tandem array of transcription factor response elements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6771-6776.	7.1	91
22	First Proteomic Exploration of Protein-Encoding Genes on Chromosome 1 in Human Liver, Stomach, and Colon. <i>Journal of Proteome Research</i> , 2013, 12, 67-80.	3.7	20
23	CAPER: a Chromosome-Assembled human Proteome browsER. <i>Journal of Proteome Research</i> , 2013, 12, 179-186.	3.7	22
24	Proteome-wide Prediction of Self-interacting Proteins Based on Multiple Properties. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1689-1700.	3.8	31
25	General Trends in the Utilization of Structural Factors Contributing to Biological Complexity. <i>Molecular Biology and Evolution</i> , 2012, 29, 1957-1968.	8.9	11
26	Solid State Characterizations and Analysis of Stability in Azelnidipine Polymorphs. <i>Chemical and Pharmaceutical Bulletin</i> , 2012, 60, 995-1002.	1.3	11
27	Evidence for the additions of clustered interacting nodes during the evolution of protein interaction networks from network motifs. <i>BMC Evolutionary Biology</i> , 2011, 11, 133.	3.2	17
28	Toward an understanding of the protein interaction network of the human liver. <i>Molecular Systems Biology</i> , 2011, 7, 536.	7.2	194
29	Insight into Bacterial Virulence Mechanisms against Host Immune Response via the <i>Yersinia pestis</i> -Human Protein-Protein Interaction Network. <i>Infection and Immunity</i> , 2011, 79, 4413-4424.	2.2	52
30	Modular analysis of the probabilistic genetic interaction network. <i>Bioinformatics</i> , 2011, 27, 853-859.	4.1	10
31	A novel parametric approach to mine gene regulatory relationship from microarray datasets. <i>BMC Bioinformatics</i> , 2010, 11, S15.	2.6	3
32	Improving the sensitivity of MASCOT search results validation by combining new features with Bayesian nonparametric model. <i>Proteomics</i> , 2010, 10, 4293-4300.	2.2	14
33	Liverbase: A Comprehensive View of Human Liver Biology. <i>Journal of Proteome Research</i> , 2010, 9, 50-58.	3.7	41
34	Proteome-wide Prediction of Signal Flow Direction in Protein Interaction Networks Based on Interacting Domains. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2063-2070.	3.8	28
35	Protein Interaction Data Set Highlighted with Human Ras-MAPK/PI3K Signaling Pathways. <i>Journal of Proteome Research</i> , 2008, 7, 3879-3889.	3.7	38
36	PRINCESS, a Protein Interaction Confidence Evaluation System with Multiple Data Sources. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1043-1052.	3.8	52

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37	Multi-modality of pI distribution in whole proteome. <i>Proteomics</i> , 2006, 6, 449-455.	2.2	49
38	Protein interaction networks of <i>Saccharomyces cerevisiae</i> , <i>Caenorhabditis elegans</i> and <i>Drosophila melanogaster</i> : Large-scale organization and robustness. <i>Proteomics</i> , 2006, 6, 456-461.	2.2	47
39	A Dataset of Human Fetal Liver Proteome Identified by Subcellular Fractionation and Multiple Protein Separation and Identification Technology. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1703-1707.	3.8	50
40	CPDR: An R Package of Recommending Personalized Drugs for Cancer Patients by Reversing the Individual's Disease-Related Signature. <i>Frontiers in Pharmacology</i> , 0, 13, .	3.5	1