Chunlei Wu

List of Publications by Year
in descending order

37 papers	6,343 citations	236925 25 h-index	315739 38 g-index
55 all docs	55 docs citations	55 times ranked	15891 citing authors

#	ARTICLE	IF	CITATIONS
1	BioThings SDK: a toolkit for building high-performance data APIs in biomedical research. Bioinformatics, 2022, 38, 2077-2079.	4.1	13
2	Generation and network analysis of an RNA-seq transcriptional atlas for the rat. NAR Genomics and Bioinformatics, 2022, 4, lqac017.	3.2	4
3	Demonstrating an approach for evaluating synthetic geospatial and temporal epidemiologic data utility: results from analyzing >1.8 million SARS-CoV-2 tests in the United States National COVID Cohort Collaborative (N3C). Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 1350-1365.	4.4	8
4	Association of Early Aspirin Use With In-Hospital Mortality in Patients With Moderate COVID-19. JAMA Network Open, 2022, 5, e223890.	5.9	31
5	The National COVID Cohort Collaborative (N3C): Rationale, design, infrastructure, and deployment. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 427-443.	4.4	342
6	Clinical Characterization and Prediction of Clinical Severity of SARS-CoV-2 Infection Among US Adults Using Data From the US National COVID Cohort Collaborative. JAMA Network Open, 2021, 4, e2116901.	5.9	179
7	Wikidata as a knowledge graph for the life sciences. ELife, 2020, 9, .	6.0	76
8	Advancing computational biology and bioinformatics research through open innovation competitions. PLoS ONE, 2019, 14, e0222165.	2.5	6
9	ChlamBase: a curated model organism database for the Chlamydia research community. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	5
10	exRNA Atlas Analysis Reveals Distinct Extracellular RNA Cargo Types and Their Carriers Present across Human Biofluids. Cell, 2019, 177, 463-477.e15.	28.9	228
11	Functional Annotation of the Transcriptome of the Pig, Sus scrofa, Based Upon Network Analysis of an RNAseq Transcriptional Atlas. Frontiers in Genetics, 2019, 10, 1355.	2.3	42
12	Cross-linking BioThings APIs through JSON-LD to facilitate knowledge exploration. BMC Bioinformatics, 2018, 19, 30.	2.6	24
13	Combination of novel and public RNA-seq datasets to generate an mRNA expression atlas for the domestic chicken. BMC Genomics, 2018, 19, 594.	2.8	86
14	Diverse reprogramming codes for neuronal identity. Nature, 2018, 557, 375-380.	27.8	94
15	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. Nature Genetics, 2017, 49, 170-174.	21.4	460
16	smartAPI: Towards a More Intelligent Network of Web APIs. Lecture Notes in Computer Science, 2017, , 154-169.	1.3	26
17	WikiGenomes: an open web application for community consumption and curation of gene annotation data in Wikidata. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	25
18	A high resolution atlas of gene expression in the domestic sheep (Ovis aries). PLoS Genetics, 2017, 13, e1006997.	3.5	210

#	Article	IF	Citations
19	Centralizing content and distributing labor: a community model for curating the very long tail of microbial genomes. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw028.	3.0	9
20	dbNSFP v3.0: A One-Stop Database of Functional Predictions and Annotations for Human Nonsynonymous and Splice-Site SNVs. Human Mutation, 2016, 37, 235-241.	2.5	845
21	High-performance web services for querying gene and variant annotation. Genome Biology, 2016, 17, 91.	8.8	166
22	BioGPS: building your own mash-up of gene annotations and expression profiles. Nucleic Acids Research, 2016, 44, D313-D316.	14.5	369
23	The Cure: Design and Evaluation of a Crowdsourcing Game for Gene Selection for Breast Cancer Survival Prediction. JMIR Serious Games, 2014, 2, e7.	3.1	31
24	Stress-Independent Activation of XBP1s and/or ATF6 Reveals Three Functionally Diverse ER Proteostasis Environments. Cell Reports, 2013, 3, 1279-1292.	6.4	436
25	BioGPS and MyGene.info: organizing online, gene-centric information. Nucleic Acids Research, 2013, 41, D561-D565.	14.5	324
26	Circulating microRNAs as a Fingerprint for Liver Cirrhosis. PLoS ONE, 2013, 8, e66577.	2.5	63
27	BioGPS and GXD: mouse gene expression data—the benefits and challenges of data integration. Mammalian Genome, 2012, 23, 550-558.	2.2	7
28	Identification of Serum-Derived Sphingosine-1-Phosphate as a Small Molecule Regulator of YAP. Chemistry and Biology, 2012, 19, 955-962.	6.0	219
29	A gene expression atlas of the domestic pig. BMC Biology, 2012, 10, 90.	3.8	199
30	TCLUST: A Fast Method for Clustering Genome-Scale Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 808-818.	3.0	14
31	CAFET Algorithm Reveals Wnt/PCP Signature in Lung Squamous Cell Carcinoma. PLoS ONE, 2011, 6, e25807.	2.5	7
32	A small molecule accelerates neuronal differentiation in the adult rat. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16542-16547.	7.1	109
33	Screening the mammalian extracellular proteome for regulators of embryonic human stem cell pluripotency. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3552-3557.	7.1	91
34	BioGPS: an extensible and customizable portal for querying and organizing gene annotation resources. Genome Biology, 2009, 10, R130.	8.8	1,216
35	Gene Set Enrichment in eQTL Data Identifies Novel Annotations and Pathway Regulators. PLoS Genetics, 2008, 4, e1000070.	3.5	90
36	A Gene Wiki for Community Annotation of Gene Function. PLoS Biology, 2008, 6, e175.	5.6	104

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37	Genomewide Association Analysis in Diverse Inbred Mice: Power and Population Structure. Genetics, 2007, 176, 675-683.	2.9	68