

Yong Wang

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

1,136
citations

471509

17
h-index

434195

31
g-index

36
all docs

36
docs citations

36
times ranked

1520
citing authors

#	ARTICLE	IF	CITATIONS
1	Annotating regulatory elements by heterogeneous network embedding. <i>Bioinformatics</i> , 2022, 38, 2899-2911.	4.1	2
2	Integrated profiling of human pancreatic cancer organoids reveals chromatin accessibility features associated with drug sensitivity. <i>Nature Communications</i> , 2022, 13, 2169.	12.8	27
3	Comparison of chromatin accessibility landscapes during early development of prefrontal cortex between rhesus macaque and human. <i>Nature Communications</i> , 2022, 13, .	12.8	7
4	hReg-CNCC reconstructs a regulatory network in human cranial neural crest cells and annotates variants in a developmental context. <i>Communications Biology</i> , 2021, 4, 442.	4.4	10
5	MIMIC: an optimization method to identify cell type-specific marker panel for cell sorting. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	1
6	Reusability report: Compressing regulatory networks to vectors for interpreting gene expression and genetic variants. <i>Nature Machine Intelligence</i> , 2021, 3, 576-580.	16.0	3
7	The cell-surface 5â€²-nucleotidase CD73 defines a functional T memory cell subset that declines with age. <i>Cell Reports</i> , 2021, 37, 109981.	6.4	15
8	Chromatin accessibility landscape and regulatory network of high-altitude hypoxia adaptation. <i>Nature Communications</i> , 2020, 11, 4928.	12.8	43
9	ZokorDB: tissue specific regulatory network annotation for nonâ€²coding elements of plateau zokor. <i>Quantitative Biology</i> , 2020, 8, 43-50.	0.5	6
10	Time course regulatory analysis based on paired expression and chromatin accessibility data. <i>Genome Research</i> , 2020, 30, 622-634.	5.5	35
11	ERG orchestrates chromatin interactions to drive prostate cell fate reprogramming. <i>Journal of Clinical Investigation</i> , 2020, 130, 5924-5941.	8.2	29
12	DC3 is a method for deconvolution and coupled clustering from bulk and single-cell genomics data. <i>Nature Communications</i> , 2019, 10, 4613.	12.8	57
13	TFAP2C- and p63-Dependent Networks Sequentially Rearrange Chromatin Landscapes to Drive Human Epidermal Lineage Commitment. <i>Cell Stem Cell</i> , 2019, 24, 271-284.e8.	11.1	76
14	Systems biology intertwines with single cell and AI. <i>BMC Bioinformatics</i> , 2019, 20, 204.	2.6	0
15	Lipid-gene regulatory network reveals coregulations of triacylglycerol with phosphatidylinositol/lysophosphatidylinositol and with hexosyl-ceramide. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2019, 1864, 168-180.	2.4	9
16	Revealing transcription factor and histone modification co-localization and dynamics across cell lines by integrating ChIP-seq and RNA-seq data. <i>BMC Genomics</i> , 2018, 19, 914.	2.8	17
17	Integrative analysis of single-cell genomics data by coupled nonnegative matrix factorizations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7723-7728.	7.1	156
18	Modeling gene regulation from paired expression and chromatin accessibility data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4914-E4923.	7.1	167

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19	A novel mixed integer programming for multi-biomarker panel identification by distinguishing malignant from benign colorectal tumors. <i>Methods</i> , 2015, 83, 3-17.	3.8	20
20	Computational Study of Drugs by Integrating Omics Data with Kernel Methods. <i>Molecular Informatics</i> , 2013, 32, 930-941.	2.5	16
21	Drug repositioning framework by incorporating functional information. <i>IET Systems Biology</i> , 2013, 7, 188-194.	1.5	7
22	Drug Repositioning by Kernel-Based Integration of Molecular Structure, Molecular Activity, and Phenotype Data. <i>PLoS ONE</i> , 2013, 8, e78518.	2.5	110
23	A combinatorial model and algorithm for globally searching community structure in complex networks. <i>Journal of Combinatorial Optimization</i> , 2012, 23, 425-442.	1.3	20
24	Modelling biological systems from molecules to dynamical networks. <i>BMC Systems Biology</i> , 2012, 6, S1.	3.0	33
25	Revealing metabolite biomarkers for acupuncture treatment by linear programming based feature selection. <i>BMC Systems Biology</i> , 2012, 6, S15.	3.0	29
26	Kernel-based data fusion improves the drug-protein interaction prediction. <i>Computational Biology and Chemistry</i> , 2011, 35, 353-362.	2.3	58
27	Optimization meets systems biology. <i>BMC Systems Biology</i> , 2010, 4, S1.	3.0	61
28	A Network Biology Study on Circadian Rhythm by Integrating Various Omics Data. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 313-324.	2.0	27
29	Evaluating Protein Similarity from Coarse Structures. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 583-593.	3.0	14
30	Supervised classification of protein structures based on convex hull representation. <i>International Journal of Bioinformatics Research and Applications</i> , 2007, 3, 123.	0.2	4
31	A new geometric-topological method to measure protein fold similarity. <i>Chemical Physics Letters</i> , 2007, 433, 432-438.	2.6	1
32	A new trust region method for nonlinear equations. <i>Mathematical Methods of Operations Research</i> , 2003, 58, 283-298.	1.0	68