Yong Wang

List of Publications by Year
in descending order

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	Modeling gene regulation from paired expression and chromatin accessibility data. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4914-E4923.	7.1	167
2	Integrative analysis of single-cell genomics data by coupled nonnegative matrix factorizations. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7723-7728.	7.1	156
3	Drug Repositioning by Kernel-Based Integration of Molecular Structure, Molecular Activity, and Phenotype Data. PLoS ONE, 2013, 8, e78518.	2.5	110
4	TFAP2C- and p63-Dependent Networks Sequentially Rearrange Chromatin Landscapes to Drive Human Epidermal Lineage Commitment. Cell Stem Cell, 2019, 24, 271-284.e8.	11.1	76
5	A new trust region method for nonlinear equations. Mathematical Methods of Operations Research, 2003, 58, 283-298.	1.0	68
6	Optimization meets systems biology. BMC Systems Biology, 2010, 4, S1.	3.0	61
7	Kernel-based data fusion improves the drug–protein interaction prediction. Computational Biology and Chemistry, 2011, 35, 353-362.	2.3	58
8	DC3 is a method for deconvolution and coupled clustering from bulk and single-cell genomics data. Nature Communications, 2019, 10, 4613.	12.8	57
9	Chromatin accessibility landscape and regulatory network of high-altitude hypoxia adaptation. Nature Communications, 2020, 11, 4928.	12.8	43
10	Time course regulatory analysis based on paired expression and chromatin accessibility data. Genome Research, 2020, 30, 622-634.	5.5	35
11	Modelling biological systems from molecules to dynamical networks. BMC Systems Biology, 2012, 6, S1.	3.0	33
12	Revealing metabolite biomarkers for acupuncture treatment by linear programming based feature selection. BMC Systems Biology, 2012, 6, S15.	3.0	29
13	ERG orchestrates chromatin interactions to drive prostate cell fate reprogramming. Journal of Clinical Investigation, 2020, 130, 5924-5941.	8.2	29
14	A Network Biology Study on Circadian Rhythm by Integrating Various Omics Data. OMICS A Journal of Integrative Biology, 2009, 13, 313-324.	2.0	27
15	Integrated profiling of human pancreatic cancer organoids reveals chromatin accessibility features associated with drug sensitivity. Nature Communications, 2022, 13, 2169.	12.8	27
16	A combinatorial model and algorithm for globally searching community structure in complex networks. Journal of Combinatorial Optimization, 2012, 23, 425-442.	1.3	20
17	A novel mixed integer programming for multi-biomarker panel identification by distinguishing malignant from benign colorectal tumors. Methods, 2015, 83, 3-17.	3.8	20
18	Revealing transcription factor and histone modification co-localization and dynamics across cell lines by integrating ChIP-seq and RNA-seq data. BMC Genomics, 2018, 19, 914.	2.8	17

#	Article	IF	Citations
19	Computational Study of Drugs by Integrating Omics Data with Kernel Methods. Molecular Informatics, 2013, 32, 930-941.	2.5	16
20	The cell-surface 5â€²-nucleotidase CD73 defines a functional T memory cell subset that declines with age. Cell Reports, 2021, 37, 109981.	6.4	15
21	Evaluating Protein Similarity from Coarse Structures. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 583-593.	3.0	14
22	hReg-CNCC reconstructs a regulatory network in human cranial neural crest cells and annotates variants in a developmental context. Communications Biology, 2021, 4, 442.	4.4	10
23	Lipid-gene regulatory network reveals coregulations of triacylglycerol with phosphatidylinositol/lysophosphatidylinositol and with hexosyl-ceramide. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2019, 1864, 168-180.	2.4	9
24	Drug repositioning framework by incorporating functional information. IET Systems Biology, 2013, 7, 188-194.	1.5	7
25	Comparison of chromatin accessibility landscapes during early development of prefrontal cortex between rhesus macaque and human. Nature Communications, 2022, 13, .	12.8	7
26	ZokorDB: tissue specific regulatory network annotation for nonâ€coding elements of plateau zokor. Quantitative Biology, 2020, 8, 43-50.	0.5	6
27	Supervised classification of protein structures based on convex hull representation. International Journal of Bioinformatics Research and Applications, 2007, 3, 123.	0.2	4
28	Reusability report: Compressing regulatory networks to vectors for interpreting gene expression and genetic variants. Nature Machine Intelligence, 2021, 3, 576-580.	16.0	3
29	Annotating regulatory elements by heterogeneous network embedding. Bioinformatics, 2022, 38, 2899-2911.	4.1	2
30	A new geometric-topological method to measure protein fold similarity. Chemical Physics Letters, 2007, 433, 432-438.	2.6	1
31	MIMIC: an optimization method to identify cell type-specific marker panel for cell sorting. Briefings in Bioinformatics, 2021, 22, .	6.5	1
32	Systems biology intertwines with single cell and AI. BMC Bioinformatics, 2019, 20, 204.	2.6	0