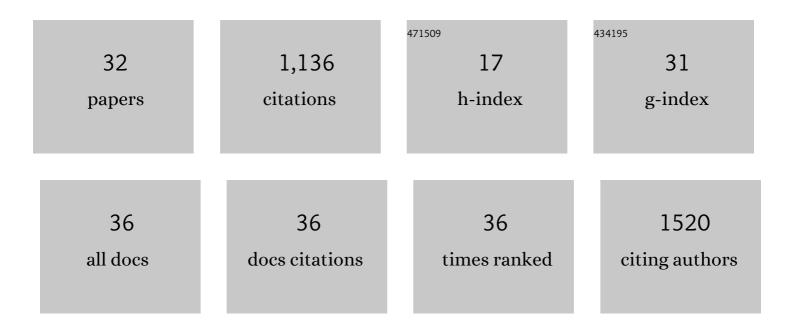
Yong Wang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Annotating regulatory elements by heterogeneous network embedding. Bioinformatics, 2022, 38, 2899-2911.	4.1	2
2	Integrated profiling of human pancreatic cancer organoids reveals chromatin accessibility features associated with drug sensitivity. Nature Communications, 2022, 13, 2169.	12.8	27
3	Comparison of chromatin accessibility landscapes during early development of prefrontal cortex between rhesus macaque and human. Nature Communications, 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. Communications Biology, 2021, 4, 442.	4.4	10
5	MIMIC: an optimization method to identify cell type-specific marker panel for cell sorting. Briefings in Bioinformatics, 2021, 22, .	6.5	1
6	Reusability report: Compressing regulatory networks to vectors for interpreting gene expression and genetic variants. Nature Machine Intelligence, 2021, 3, 576-580.	16.0	3
7	The cell-surface 5′-nucleotidase CD73 defines a functional T memory cell subset that declines with age. Cell Reports, 2021, 37, 109981.	6.4	15
8	Chromatin accessibility landscape and regulatory network of high-altitude hypoxia adaptation. Nature Communications, 2020, 11, 4928.	12.8	43
9	ZokorDB: tissue specific regulatory network annotation for non oding elements of plateau zokor. Quantitative Biology, 2020, 8, 43-50.	0.5	6
10	Time course regulatory analysis based on paired expression and chromatin accessibility data. Genome Research, 2020, 30, 622-634.	5.5	35
11	ERG orchestrates chromatin interactions to drive prostate cell fate reprogramming. Journal of Clinical Investigation, 2020, 130, 5924-5941.	8.2	29
12	DC3 is a method for deconvolution and coupled clustering from bulk and single-cell genomics data. Nature Communications, 2019, 10, 4613.	12.8	57
13	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
14	Systems biology intertwines with single cell and AI. BMC Bioinformatics, 2019, 20, 204.	2.6	0
15	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
16	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
17	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
18	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

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