Koon-Kiu Yan

List of Publications by Year
in descending order

46 papers	21,379 citations	279798 23 h-index	265206 42 g-index
47 all docs	47 docs citations	47 times ranked	40788 citing authors

#	Article	IF	Citations
1	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
2	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	27.8	1,384
3	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	5.6	1,257
4	Integrative Analysis of the Caenorhabditis elegans Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	12.6	912
5	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	27.8	289
6	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	27.8	184
7	Ranking scientific publications using a model of network traffic. Journal of Statistical Mechanics: Theory and Experiment, 2007, 2007, P06010-P06010.	2.3	168
8	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	5.5	166
9	The ModERN Resource: Genome-Wide Binding Profiles for Hundreds ofDrosophilaandCaenorhabditis elegansTranscription Factors. Genetics, 2018, 208, 937-949.	2.9	164
10	Measuring the reproducibility and quality of Hi-C data. Genome Biology, 2019, 20, 57.	8.8	125
11	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. Genome Biology, 2011, 12, R15.	9.6	118
12	Improved Reconstruction of In Silico Gene Regulatory Networks by Integrating Knockout and Perturbation Data. PLoS ONE, 2010, 5, e8121.	2.5	97
13	Measuring the Evolutionary Rewiring of Biological Networks. PLoS Computational Biology, 2011, 7, e1001050.	3.2	96
14	An integrative ENCODE resource for cancer genomics. Nature Communications, 2020, 11, 3696.	12.8	95
15	Construction and Analysis of an Integrated Regulatory Network Derived from High-Throughput Sequencing Data. PLoS Computational Biology, 2011, 7, e1002190.	3.2	92
16	HiC-spector: a matrix library for spectral and reproducibility analysis of Hi-C contact maps. Bioinformatics, 2017, 33, 2199-2201.	4.1	92
17	Comparing genomes to computer operating systems in terms of the topology and evolution of their regulatory control networks. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9186-9191.	7.1	75
18	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. Nature Methods, 2020, 17, 807-814.	19.0	71

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19	Analysis of diverse regulatory networks in a hierarchical context shows consistent tendencies for collaboration in the middle levels. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6841-6846.	7.1	65
20	Upstream plasticity and downstream robustness in evolution of molecular networks. BMC Evolutionary Biology, 2004, 4, 9.	3.2	62
21	OrthoClust: an orthology-based network framework for clustering data across multiple species. Genome Biology, 2014, 15, R100.	9.6	46
22	MrTADFinder: A network modularity based approach to identify topologically associating domains in multiple resolutions. PLoS Computational Biology, 2017, 13, e1005647.	3.2	42
23	The Spread of Scientific Information: Insights from the Web Usage Statistics in PLoS Article-Level Metrics. PLoS ONE, 2011, 6, e19917.	2.5	39
24	Network Approaches for Dissecting the Immune System. IScience, 2020, 23, 101354.	4.1	28
25	An approach for determining and measuring network hierarchy applied to comparing the phosphorylome and the regulome. Genome Biology, 2015, 16, 63.	8.8	27
26	Analysis of Combinatorial Regulation: Scaling of Partnerships between Regulators with the Number of Governed Targets. PLoS Computational Biology, 2010, 6, e1000755.	3.2	21
27	Cellular Superspreaders: An Epidemiological Perspective on HIV Infection inside the Body. PLoS Pathogens, 2014, 10, e1004092.	4.7	20
28	An improved upper bound for the critical car density of the two-dimensional Bihamâ€"Middletonâ€"Levine traffic model. Physica A: Statistical Mechanics and Its Applications, 1998, 254, 117-121.	2.6	18
29	Loregic: A Method to Characterize the Cooperative Logic of Regulatory Factors. PLoS Computational Biology, 2015, 11, e1004132.	3.2	18
30	Cross-Disciplinary Network Comparison: Matchmaking between Hairballs. Cell Systems, 2016, 2, 147-157.	6.2	13
31	Cross-talk between GLI transcription factors and FOXC1 promotes T-cell acute lymphoblastic leukemia dissemination. Leukemia, 2021, 35, 984-1000.	7.2	12
32	ONE DIMENSIONAL nARY DENSITY CLASSIFICATION USING TWO CELLULAR AUTOMATON RULES. International Journal of Modern Physics C, 1999, 10, 883-889.	1.7	10
33	Temporal Dynamics of Collaborative Networks in Large Scientific Consortia. Trends in Genetics, 2016, 32, 251-253.	6.7	10
34	Parameters of proteome evolution from histograms of amino-acid sequence identities of paralogous proteins. Biology Direct, 2007, 2, 32.	4.6	8
35	Fluctuations in Mass-Action Equilibrium of Protein Binding Networks. Physical Review Letters, 2008, 101, 268102.	7.8	7
36	Classifying rational densities using two one-dimensional cellular automata. Physical Review E, 1998, 57, 1367-1369.	2.1	6

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37	SLFN11 is Widely Expressed in Pediatric Sarcoma and Induces Variable Sensitization to Replicative Stress Caused By DNA-Damaging Agents. Molecular Cancer Therapeutics, 2021, 20, 2151-2165.	4.1	6
38	Optimal ranking in networks with community structure. Physica A: Statistical Mechanics and Its Applications, 2007, 373, 831-836.	2.6	5
39	The miR-424(322)/503 gene cluster regulates pro- versus anti-inflammatory skin DC subset differentiation by modulating TGF-Î² signaling. Cell Reports, 2021, 35, 109049.	6.4	4
40	The corrected gene proximity map for analyzing the 3D genome organization using Hi-C data. BMC Bioinformatics, 2020, 21, 222.	2.6	2
41	miRâ€424/503 modulates Wnt/Î²â€catenin signaling in the mammary epithelium by targeting LRP6. EMBO Reports, 2021, 22, e53201.	4.5	2
42	Single-cell analysis reveals the Comma-1D cell line as a unique model for mammary gland development and breast cancer. Journal of Cell Science, 2022, 135, .	2.0	2
43	FINDING THE SIGN OF A FUNCTION VALUE BY BINARY CELLULAR AUTOMATON. International Journal of Modern Physics C, 2002, 13, 1347-1364.	1.7	0
44	Hierarchical analysis of regulatory networks and cross-disciplinary comparison with the Linux call graph. , 2010, , .		0
45	Comparing Technological Development and Biological Evolution from a Network Perspective. Cell Systems, 2020, 10, 219-222.	6.2	0
46	Abstract 237: Inferring spatial organization of tumor microenvironment from single-cell RNA sequencing data using graph embedding. , 2021, , .		0