

Koon-Kiu Yan

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

44
papers

15,921
citations

23
h-index

47
g-index

47
ext. papers

19,557
ext. citations

12
avg, IF

8.14
L-index

#	Paper	IF	Citations
44	miR-424/503 modulates Wnt/ β -catenin signaling in the mammary epithelium by targeting LRP6. <i>EMBO Reports</i> , 2021 , 22, e53201	6.5	1
43	The miR-424(322)/503 gene cluster regulates pro- versus anti-inflammatory skin DC subset differentiation by modulating TGF- β signaling. <i>Cell Reports</i> , 2021 , 35, 109049	10.6	1
42	Cross-talk between GLI transcription factors and FOXC1 promotes T-cell acute lymphoblastic leukemia dissemination. <i>Leukemia</i> , 2021 , 35, 984-1000	10.7	2
41	SLFN11 is Widely Expressed in Pediatric Sarcoma and Induces Variable Sensitization to Replicative Stress Caused By DNA-Damaging Agents. <i>Molecular Cancer Therapeutics</i> , 2021 , 20, 2151-2165	6.1	1
40	The corrected gene proximity map for analyzing the 3D genome organization using Hi-C data. <i>BMC Bioinformatics</i> , 2020 , 21, 222	3.6	1
39	Network Approaches for Dissecting the Immune System. <i>iScience</i> , 2020 , 23, 101354	6.1	11
38	An integrative ENCODE resource for cancer genomics. <i>Nature Communications</i> , 2020 , 11, 3696	17.4	28
37	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. <i>Nature Methods</i> , 2020 , 17, 807-814	21.6	24
36	Comparing Technological Development and Biological Evolution from a Network Perspective. <i>Cell Systems</i> , 2020 , 10, 219-222	10.6	
35	Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , 2019 , 20, 57	18.3	62
34	The ModERN Resource: Genome-Wide Binding Profiles for Hundreds of and Transcription Factors. <i>Genetics</i> , 2018 , 208, 937-949	4	71
33	HiC-spector: a matrix library for spectral and reproducibility analysis of Hi-C contact maps. <i>Bioinformatics</i> , 2017 , 33, 2199-2201	7.2	50
32	MrTADFinder: A network modularity based approach to identify topologically associating domains in multiple resolutions. <i>PLoS Computational Biology</i> , 2017 , 13, e1005647	5	28
31	Temporal Dynamics of Collaborative Networks in Large Scientific Consortia. <i>Trends in Genetics</i> , 2016 , 32, 251-253	8.5	8
30	Cross-Disciplinary Network Comparison: Matchmaking Between Hairballs. <i>Cell Systems</i> , 2016 , 2, 147-157	10.6	12
29	Loregic: a method to characterize the cooperative logic of regulatory factors. <i>PLoS Computational Biology</i> , 2015 , 11, e1004132	5	14
28	An approach for determining and measuring network hierarchy applied to comparing the phosphorolome and the regulome. <i>Genome Biology</i> , 2015 , 16, 63	18.3	21

27	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014 , 512, 445-8	50.4	207
26	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014 , 512, 453-6	50.4	135
25	Cellular superspreaders: an epidemiological perspective on HIV infection inside the body. <i>PLoS Pathogens</i> , 2014 , 10, e1004092	7.6	16
24	OrthoClust: an orthology-based network framework for clustering data across multiple species. <i>Genome Biology</i> , 2014 , 15, R100	18.3	35
23	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
22	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012 , 489, 91-100	50.4	1104
21	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012 , 22, 1658-67	9.7	133
20	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. <i>Genome Biology</i> , 2011 , 12, R15	18.3	96
19	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , 2011 , 9, e1001046	9.7	1060
18	Construction and analysis of an integrated regulatory network derived from high-throughput sequencing data. <i>PLoS Computational Biology</i> , 2011 , 7, e1002190	5	69
17	Measuring the evolutionary rewiring of biological networks. <i>PLoS Computational Biology</i> , 2011 , 7, e1001050	9.5	81
16	The spread of scientific information: insights from the web usage statistics in PLoS article-level metrics. <i>PLoS ONE</i> , 2011 , 6, e19917	3.7	29
15	Improved reconstruction of in silico gene regulatory networks by integrating knockout and perturbation data. <i>PLoS ONE</i> , 2010 , 5, e8121	3.7	73
14	Analysis of diverse regulatory networks in a hierarchical context shows consistent tendencies for collaboration in the middle levels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 6841-6	11.5	56
13	Comparing genomes to computer operating systems in terms of the topology and evolution of their regulatory control networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 9186-91	11.5	60
12	Analysis of combinatorial regulation: scaling of partnerships between regulators with the number of governed targets. <i>PLoS Computational Biology</i> , 2010 , 6, e1000755	5	20
11	Integrative analysis of the <i>Caenorhabditis elegans</i> genome by the modENCODE project. <i>Science</i> , 2010 , 330, 1775-87	33.3	744
10	Fluctuations in mass-action equilibrium of protein binding networks. <i>Physical Review Letters</i> , 2008 , 101, 268102	7.4	6

9	Parameters of proteome evolution from histograms of amino-acid sequence identities of paralogous proteins. <i>Biology Direct</i> , 2007 , 2, 32	7.2	7
8	Optimal ranking in networks with community structure. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007 , 373, 831-836	3.3	4
7	Ranking scientific publications using a model of network traffic. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2007 , 2007, P06010-P06010	1.9	125
6	Upstream plasticity and downstream robustness in evolution of molecular networks. <i>BMC Evolutionary Biology</i> , 2004 , 4, 9	3	41
5	FINDING THE SIGN OF A FUNCTION VALUE BY BINARY CELLULAR AUTOMATON. <i>International Journal of Modern Physics C</i> , 2002 , 13, 1347-1364	1.1	
4	ONE DIMENSIONAL BINARY DENSITY CLASSIFICATION USING TWO CELLULAR AUTOMATON RULES. <i>International Journal of Modern Physics C</i> , 1999 , 10, 883-889	1.1	10
3	An improved upper bound for the critical car density of the two-dimensional Biham-Middleton-Levine traffic model. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1998 , 254, 117-121	3.3	15
2	Classifying rational densities using two one-dimensional cellular automata. <i>Physical Review E</i> , 1998 , 57, 1367-1369	2.4	6
1	A cross-organism framework for supervised enhancer prediction with epigenetic pattern recognition and targeted validation		5