

# Koon-Kiu Yan

## List of Publications by Year in descending order

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Version: 2024-02-01

46  
papers

21,379  
citations

279487

23  
h-index

264894

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. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
2	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012, 489, 91-100.	13.7	1,384
3	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	2.6	1,257
4	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	6.0	912
5	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014, 512, 445-448.	13.7	289
6	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014, 512, 453-456.	13.7	184
7	Ranking scientific publications using a model of network traffic. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2007, 2007, P06010-P06010.	0.9	168
8	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	2.4	166
9	The ModERN Resource: Genome-Wide Binding Profiles for Hundreds of <i>Drosophila</i> and <i>Caenorhabditis elegans</i> Transcription Factors. <i>Genetics</i> , 2018, 208, 937-949.	1.2	164
10	Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , 2019, 20, 57.	3.8	125
11	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. <i>Genome Biology</i> , 2011, 12, R15.	13.9	118
12	Improved Reconstruction of In Silico Gene Regulatory Networks by Integrating Knockout and Perturbation Data. <i>PLoS ONE</i> , 2010, 5, e8121.	1.1	97
13	Measuring the Evolutionary Rewiring of Biological Networks. <i>PLoS Computational Biology</i> , 2011, 7, e1001050.	1.5	96
14	An integrative ENCODE resource for cancer genomics. <i>Nature Communications</i> , 2020, 11, 3696.	5.8	95
15	Construction and Analysis of an Integrated Regulatory Network Derived from High-Throughput Sequencing Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002190.	1.5	92
16	HiC-spector: a matrix library for spectral and reproducibility analysis of Hi-C contact maps. <i>Bioinformatics</i> , 2017, 33, 2199-2201.	1.8	92
17	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, 9186-9191.	3.3	75
18	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. <i>Nature Methods</i> , 2020, 17, 807-814.	9.0	71

#	ARTICLE	IF	CITATIONS
19	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, 6841-6846.	3.3	65
20	Upstream plasticity and downstream robustness in evolution of molecular networks. <i>BMC Evolutionary Biology</i> , 2004, 4, 9.	3.2	62
21	OrthoClust: an orthology-based network framework for clustering data across multiple species. <i>Genome Biology</i> , 2014, 15, R100.	13.9	46
22	MrTADFinder: A network modularity based approach to identify topologically associating domains in multiple resolutions. <i>PLoS Computational Biology</i> , 2017, 13, e1005647.	1.5	42
23	The Spread of Scientific Information: Insights from the Web Usage Statistics in PLoS Article-Level Metrics. <i>PLoS ONE</i> , 2011, 6, e19917.	1.1	39
24	Network Approaches for Dissecting the Immune System. <i>IScience</i> , 2020, 23, 101354.	1.9	28
25	An approach for determining and measuring network hierarchy applied to comparing the phosphorylome and the regulome. <i>Genome Biology</i> , 2015, 16, 63.	3.8	27
26	Analysis of Combinatorial Regulation: Scaling of Partnerships between Regulators with the Number of Governed Targets. <i>PLoS Computational Biology</i> , 2010, 6, e1000755.	1.5	21
27	Cellular Superspreaders: An Epidemiological Perspective on HIV Infection inside the Body. <i>PLoS Pathogens</i> , 2014, 10, e1004092.	2.1	20
28	An improved upper bound for the critical car density of the two-dimensional Bhamâ€“Middletonâ€“Levine traffic model. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1998, 254, 117-121.	1.2	18
29	Loregic: A Method to Characterize the Cooperative Logic of Regulatory Factors. <i>PLoS Computational Biology</i> , 2015, 11, e1004132.	1.5	18
30	Cross-Disciplinary Network Comparison: Matchmaking between Hairballs. <i>Cell Systems</i> , 2016, 2, 147-157.	2.9	13
31	Cross-talk between GLI transcription factors and FOXC1 promotes T-cell acute lymphoblastic leukemia dissemination. <i>Leukemia</i> , 2021, 35, 984-1000.	3.3	12
32	ONE DIMENSIONAL nARY DENSITY CLASSIFICATION USING TWO CELLULAR AUTOMATON RULES. <i>International Journal of Modern Physics C</i> , 1999, 10, 883-889.	0.8	10
33	Temporal Dynamics of Collaborative Networks in Large Scientific Consortia. <i>Trends in Genetics</i> , 2016, 32, 251-253.	2.9	10
34	Parameters of proteome evolution from histograms of amino-acid sequence identities of paralogous proteins. <i>Biology Direct</i> , 2007, 2, 32.	1.9	8
35	Fluctuations in Mass-Action Equilibrium of Protein Binding Networks. <i>Physical Review Letters</i> , 2008, 101, 268102.	2.9	7
36	Classifying rational densities using two one-dimensional cellular automata. <i>Physical Review E</i> , 1998, 57, 1367-1369.	0.8	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. <i>Molecular Cancer Therapeutics</i> , 2021, 20, 2151-2165.	1.9	6
38	Optimal ranking in networks with community structure. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007, 373, 831-836.	1.2	5
39	The miR-424(322)/503 gene cluster regulates pro- versus anti-inflammatory skin DC subset differentiation by modulating TGF- $\beta$ 2 signaling. <i>Cell Reports</i> , 2021, 35, 109049.	2.9	4
40	The corrected gene proximity map for analyzing the 3D genome organization using Hi-C data. <i>BMC Bioinformatics</i> , 2020, 21, 222.	1.2	2
41	miR-424/503 modulates Wnt/ $\beta$ -catenin signaling in the mammary epithelium by targeting LRP6. <i>EMBO Reports</i> , 2021, 22, e53201.	2.0	2
42	Single-cell analysis reveals the Comma-1D cell line as a unique model for mammary gland development and breast cancer. <i>Journal of Cell Science</i> , 2022, 135, .	1.2	2
43	FINDING THE SIGN OF A FUNCTION VALUE BY BINARY CELLULAR AUTOMATON. <i>International Journal of Modern Physics C</i> , 2002, 13, 1347-1364.	0.8	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. <i>Cell Systems</i> , 2020, 10, 219-222.	2.9	0
46	Abstract 237: Inferring spatial organization of tumor microenvironment from single-cell RNA sequencing data using graph embedding. , 2021, , .		0