

Kevin Y Yip

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.

107 papers	18,339 citations	37 h-index	135 g-index
146 ext. papers	22,536 ext. citations	12 avg, IF	8.16 L-index

#	Paper	IF	Citations
107	Sirtuin 7 super-enhancer drives epigenomic reprogramming in hepatocarcinogenesis. <i>Cancer Letters</i> , 2022 , 525, 115-130	9.9	2
106	Reusability report: Capturing properties of biological objects and their relationships using graph neural networks. <i>Nature Machine Intelligence</i> , 2022 , 4, 222-226	22.5	1
105	A proof-of-concept study for the pathogenetic role of enhancer hypomethylation of MYBPHL in multiple myeloma. <i>Scientific Reports</i> , 2021 , 11, 7009	4.9	1
104	A selective HDAC8 inhibitor potentiates antitumor immunity and efficacy of immune checkpoint blockade in hepatocellular carcinoma. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	11
103	Whole-genome profiling of nasopharyngeal carcinoma reveals viral-host co-operation in inflammatory NF- κ B activation and immune escape. <i>Nature Communications</i> , 2021 , 12, 4193	17.4	10
102	Horseshoe crab genomes reveal the evolution of genes and microRNAs after three rounds of whole genome duplication. <i>Communications Biology</i> , 2021 , 4, 83	6.7	8
101	Identification and characterization of a novel Epstein-Barr Virus-encoded circular RNA from LMP-2 Gene. <i>Scientific Reports</i> , 2021 , 11, 14392	4.9	3
100	Jellyfish genomes reveal distinct homeobox gene clusters and conservation of small RNA processing. <i>Nature Communications</i> , 2020 , 11, 3051	17.4	17
99	A general near-exact k-mer counting method with low memory consumption enables de novo assembly of 106 human sequence data in 2.7 hours. <i>Bioinformatics</i> , 2020 , 36, i625-i633	7.2	0
98	Flexible k-mers with variable-length indels for identifying binding sequences of protein dimers. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1787-1797	13.4	0
97	An integrative ENCODE resource for cancer genomics. <i>Nature Communications</i> , 2020 , 11, 3696	17.4	28
96	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. <i>Nature Methods</i> , 2020 , 17, 807-814	21.6	24
95	A unified framework for integrative study of heterogeneous gene regulatory mechanisms. <i>Nature Machine Intelligence</i> , 2020 , 2, 447-456	22.5	1
94	G9a Plays Distinct Roles in Maintaining DNA Methylation, Retrotransposon Silencing, and Chromatin Looping. <i>Cell Reports</i> , 2020 , 33, 108315	10.6	14
93	Whole-genome analysis of noncoding genetic variations identifies multiscale regulatory element perturbations associated with Hirschsprung disease. <i>Genome Research</i> , 2020 , 30, 1618-1632	9.7	4
92	Shaping the nebulous enhancer in the era of high-throughput assays and genome editing. <i>Briefings in Bioinformatics</i> , 2020 , 21, 836-850	13.4	3
91	Genome maps across 26 human populations reveal population-specific patterns of structural variation. <i>Nature Communications</i> , 2019 , 10, 1025	17.4	70

90	OMMA enables population-scale analysis of complex genomic features and phylogenomic relationships from nanochannel-based optical maps. <i>GigaScience</i> , 2019 , 8,	7.6	3
89	Reply to Tnflated performance measures in enhancer-promoter interaction-prediction methodsT <i>Nature Genetics</i> , 2019 , 51, 1201-1202	36.3	
88	New guidelines for DNA methylome studies regarding 5-hydroxymethylcytosine for understanding transcriptional regulation. <i>Genome Research</i> , 2019 , 29, 543-553	9.7	8
87	Comparative analysis of single-cell parallel sequencing approaches in oocyte application. <i>International Journal of Biochemistry and Cell Biology</i> , 2019 , 107, 1-5	5.6	6
86	Aberrant enhancer hypomethylation contributes to hepatic carcinogenesis through global transcriptional reprogramming. <i>Nature Communications</i> , 2019 , 10, 335	17.4	49
85	A comprehensive web tool for toehold switch design. <i>Bioinformatics</i> , 2018 , 34, 2862-2864	7.2	19
84	A network approach to exploring the functional basis of gene-gene epistatic interactions in disease susceptibility. <i>Bioinformatics</i> , 2018 , 34, 1741-1749	7.2	10
83	Loss of tumor suppressor IGFBP4 drives epigenetic reprogramming in hepatic carcinogenesis. <i>Nucleic Acids Research</i> , 2018 , 46, 8832-8847	20.1	16
82	Case Report: Exome sequencing reveals recurrent mutations and a loss-of-function mutation in a rare undifferentiated tongue sarcoma. <i>F1000Research</i> , 2018 , 7, 499	3.6	4
81	EBV-encoded miRNAs target ATM-mediated response in nasopharyngeal carcinoma. <i>Journal of Pathology</i> , 2018 , 244, 394-407	9.4	30
80	Establishment and characterization of new tumor xenografts and cancer cell lines from EBV-positive nasopharyngeal carcinoma. <i>Nature Communications</i> , 2018 , 9, 4663	17.4	63
79	Identification of Genes Associated With Hirschsprung Disease, Based on Whole-Genome Sequence Analysis, and Potential Effects on Enteric Nervous System Development. <i>Gastroenterology</i> , 2018 , 155, 1908-1922.e5	13.3	38
78	Exome and genome sequencing of nasopharynx cancer identifies NF- κ B pathway activating mutations. <i>Nature Communications</i> , 2017 , 8, 14121	17.4	163
77	OMTools: a software package for visualizing and processing optical mapping data. <i>Bioinformatics</i> , 2017 , 33, 2933-2935	7.2	14
76	OMSV enables accurate and comprehensive identification of large structural variations from nanochannel-based single-molecule optical maps. <i>Genome Biology</i> , 2017 , 18, 230	18.3	15
75	START: a system for flexible analysis of hundreds of genomic signal tracks in few lines of SQL-like queries. <i>BMC Genomics</i> , 2017 , 18, 749	4.5	2
74	Reconstruction of enhancer-target networks in 935 samples of human primary cells, tissues and cell lines. <i>Nature Genetics</i> , 2017 , 49, 1428-1436	36.3	124
73	OMBlast: alignment tool for optical mapping using a seed-and-extend approach. <i>Bioinformatics</i> , 2017 , 33, 311-319	7.2	22

72	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
71	Integrating Information in Biological Ontologies and Molecular Networks to Infer Novel Terms. <i>Scientific Reports</i> , 2016 , 6, 39237	4.9	3
70	A novel method for discovering local spatial clusters of genomic regions with functional relationships from DNA contact maps. <i>Bioinformatics</i> , 2016 , 32, i111-i120	7.2	7
69	Towards a More Accurate Error Model for BioNano Optical Maps. <i>Lecture Notes in Computer Science</i> , 2016 , 67-79	0.9	7
68	Genome-Wide Structural Variation Detection by Genome Mapping on Nanochannel Arrays. <i>Genetics</i> , 2016 , 202, 351-62	4	103
67	Analysis of sequencing data for probing RNA secondary structures and protein-RNA binding in studying posttranscriptional regulations. <i>Briefings in Bioinformatics</i> , 2016 , 17, 1032-1043	13.4	6
66	Yin Yang 1-mediated epigenetic silencing of tumour-suppressive microRNAs activates nuclear factor- B in hepatocellular carcinoma. <i>Journal of Pathology</i> , 2016 , 238, 651-64	9.4	35
65	Interactome-transcriptome analysis discovers signatures complementary to GWAS Loci of Type 2 Diabetes. <i>Scientific Reports</i> , 2016 , 6, 35228	4.9	16
64	A Survey of the Computational Methods for Enhancers and Enhancer-target Predictions 2016 , 3-27		1
63	Improved prediction of RNA secondary structure by integrating the free energy model with restraints derived from experimental probing data. <i>Nucleic Acids Research</i> , 2015 , 43, 7247-59	20.1	55
62	A common set of distinct features that characterize noncoding RNAs across multiple species. <i>Nucleic Acids Research</i> , 2015 , 43, 104-14	20.1	27
61	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014 , 512, 445-8	50.4	207
60	Whole-genome bisulfite sequencing of multiple individuals reveals complementary roles of promoter and gene body methylation in transcriptional regulation. <i>Genome Biology</i> , 2014 , 15, 408	18.3	131
59	Identification of a major determinant for serine-threonine kinase phosphoacceptor specificity. <i>Molecular Cell</i> , 2014 , 53, 140-7	17.6	64
58	The Essential Component in DNA-Based Information Storage System: Robust Error-Tolerating Module. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014 , 2, 49	5.8	10
57	FunSeq2: a framework for prioritizing noncoding regulatory variants in cancer. <i>Genome Biology</i> , 2014 , 15, 480	18.3	209
56	VAS: a convenient web portal for efficient integration of genomic features with millions of genetic variants. <i>BMC Genomics</i> , 2014 , 15, 886	4.5	1
55	ECplot: an online tool for making standardized plots from large datasets for bioinformatics publications. <i>Bioinformatics</i> , 2014 , 30, 1467-8	7.2	

54	Computational identification of protein binding sites on RNAs using high-throughput RNA structure-probing data. <i>Bioinformatics</i> , 2014 , 30, 1049-1055	7.2	5
53	Are special read alignment strategies necessary and cost-effective when handling sequencing reads from patient-derived tumor xenografts?. <i>BMC Genomics</i> , 2014 , 15, 1172	4.5	22
52	Systematic exploration of autonomous modules in noisy microRNA-target networks for testing the generality of the ceRNA hypothesis. <i>BMC Genomics</i> , 2014 , 15, 1178	4.5	9
51	Complete genomic sequence of Epstein-Barr virus in nasopharyngeal carcinoma cell line C666-1. <i>Infectious Agents and Cancer</i> , 2013 , 8, 29	3.5	32
50	Mining Order-Preserving Submatrices from Data with Repeated Measurements. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2013 , 25, 1587-1600	4.2	5
49	Machine learning and genome annotation: a match meant to be?. <i>Genome Biology</i> , 2013 , 14, 205	18.3	56
48	Identification of a recurrent transforming UBR5-ZNF423 fusion gene in EBV-associated nasopharyngeal carcinoma. <i>Journal of Pathology</i> , 2013 , 231, 158-67	9.4	35
47	Sustained antidiabetic effects of a berberine-containing Chinese herbal medicine through regulation of hepatic gene expression. <i>Diabetes</i> , 2012 , 61, 933-43	0.9	88
46	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. <i>Genome Biology</i> , 2012 , 13, R48	18.3	194
45	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
44	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012 , 489, 91-100	50.4	1104
43	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012 , 22, 1658-67	9.7	133
42	Decision Trees for Uncertain Data. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2011 , 23, 64-78	4.2	116
41	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
40	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , 2011 , 9, e1001046	9.7	1060
39	Identification of specificity determining residues in peptide recognition domains using an information theoretic approach applied to large-scale binding maps. <i>BMC Biology</i> , 2011 , 9, 53	7.3	14
38	Genome-wide analysis of chromatin features identifies histone modification sensitive and insensitive yeast transcription factors. <i>Genome Biology</i> , 2011 , 12, R111	18.3	16
37	Metric and trigonometric pruning for clustering of uncertain data in 2D geometric space. <i>Information Systems</i> , 2011 , 36, 476-497	2.7	6

36	ACT: aggregation and correlation toolbox for analyses of genome tracks. <i>Bioinformatics</i> , 2011 , 27, 1152-4.2	31
35	Prediction and characterization of noncoding RNAs in <i>C. elegans</i> by integrating conservation, secondary structure, and high-throughput sequencing and array data. <i>Genome Research</i> , 2011 , 21, 276-83.7	55
34	Improved reconstruction of in silico gene regulatory networks by integrating knockout and perturbation data. <i>PLoS ONE</i> , 2010 , 5, e8121	3.7 73
33	Analysis of membrane proteins in metagenomics: networks of correlated environmental features and protein families. <i>Genome Research</i> , 2010 , 20, 960-71	9.7 33
32	Integrative analysis of the <i>Caenorhabditis elegans</i> genome by the modENCODE project. <i>Science</i> , 2010 , 330, 1775-87	33.3 744
31	Extensive in vivo metabolite-protein interactions revealed by large-scale systematic analyses. <i>Cell</i> , 2010 , 143, 639-50	56.2 162
30	Training set expansion: an approach to improving the reconstruction of biological networks from limited and uneven reliable interactions. <i>Bioinformatics</i> , 2009 , 25, 243-50	7.2 18
29	Multi-level learning: improving the prediction of protein, domain and residue interactions by allowing information flow between levels. <i>BMC Bioinformatics</i> , 2009 , 10, 241	3.6 7
28	Decision Trees for Uncertain Data. <i>Proceedings - International Conference on Data Engineering</i> , 2009 ,	2 45
27	A semi-supervised approach to projected clustering with applications to microarray data. <i>International Journal of Data Mining and Bioinformatics</i> , 2009 , 3, 229-59	0.5 6
26	HCLS 2.0/3.0: health care and life sciences data mashup using Web 2.0/3.0. <i>Journal of Biomedical Informatics</i> , 2008 , 41, 694-705	10.2 67
25	Development of grid-like applications for public health using Web 2.0 mashup techniques. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2008 , 15, 783-6	8.6 18
24	Mining Order-Preserving Submatrices from Data with Repeated Measurements 2008 ,	7
23	An integrated system for studying residue coevolution in proteins. <i>Bioinformatics</i> , 2008 , 24, 290-2	7.2 60
22	LinkHub: a Semantic Web system that facilitates cross-database queries and information retrieval in proteomics. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 3, S5	3.6 22
21	Comparing classical pathways and modern networks: towards the development of an edge ontology. <i>Trends in Biochemical Sciences</i> , 2007 , 32, 320-31	10.3 49
20	Mining periodic patterns with gap requirement from sequences. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2007 , 1, 7	4 62
19	On mining micro-array data by Order-Preserving Submatrix. <i>International Journal of Bioinformatics Research and Applications</i> , 2007 , 3, 42-64	0.9 17

18	The tYNA platform for comparative interactomics: a web tool for managing, comparing and mining multiple networks. <i>Bioinformatics</i> , 2006 , 22, 2968-70	7.2	61
17	Input Validation for Semi-supervised Clustering 2006 ,		2
16	Efficient Clustering of Uncertain Data. <i>IEEE International Conference on Data Mining</i> , 2006 ,		102
15	Progressive skylining over Web-accessible databases. <i>Data and Knowledge Engineering</i> , 2006 , 57, 122-147.5	7.5	40
14	On Mining Micro-array data by Order-Preserving Submatrix 2005 ,		1
13	YeastHub: a semantic web use case for integrating data in the life sciences domain. <i>Bioinformatics</i> , 2005 , 21 Suppl 1, i85-96	7.2	74
12	CLUSTAG: hierarchical clustering and graph methods for selecting tag SNPs. <i>Bioinformatics</i> , 2005 , 21, 1735-6	7.2	59
11	Mining periodic patterns with gap requirement from sequences 2005 ,		26
10	HARP: a practical projected clustering algorithm. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2004 , 16, 1387-1397	4.2	96
9	A web services choreography scenario for interoperating bioinformatics applications. <i>BMC Bioinformatics</i> , 2004 , 5, 25	3.6	11
8	Identifying projected clusters from gene expression profiles. <i>Journal of Biomedical Informatics</i> , 2004 , 37, 345-57	10.2	8
7	Biosphere: the interoperation of web services in microarray cluster analysis. <i>Applied Bioinformatics</i> , 2004 , 3, 253-6		7
6	On discovery of extremely low-dimensional clusters using semi-supervised projected clustering		26
5	Identifying projected clusters from gene expression profiles		1
4	A cross-organism framework for supervised enhancer prediction with epigenetic pattern recognition and targeted validation		5
3	An integrative ENCODE resource for cancer genomics		2
2	Deep learning identifies and quantifies recombination hotspot determinants		1
1	Quantifying full-length circular RNAs in cancer		1

