

Aaron K Wong

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.

38
papers

2,335
citations

20
h-index

41
g-index

41
ext. papers

3,237
ext. citations

19
avg, IF

4.66
L-index

#	Paper	IF	Citations
38	Tissue-specific enhancer functional networks for associating distal regulatory regions to disease. <i>Cell Systems</i> , 2021 , 12, 353-362.e6	10.6	6
37	Modeling transcriptional regulation of model species with deep learning. <i>Genome Research</i> , 2021 , 31, 1097-1105	9.7	2
36	Machine learning methods to model multicellular complexity and tissue specificity. <i>Nature Reviews Materials</i> , 2021 , 6, 717-729	73.3	0
35	Genome-wide landscape of RNA-binding protein target site dysregulation reveals a major impact on psychiatric disorder risk. <i>Nature Genetics</i> , 2021 , 53, 166-173	36.3	10
34	Spatial transcriptional mapping of the human nephrogenic program. <i>Developmental Cell</i> , 2021 , 56, 2381-2398.e6	23.9	6
33	Decoding disease: from genomes to networks to phenotypes. <i>Nature Reviews Genetics</i> , 2021 , 22, 774-790.1	10.1	7
32	SARS-CoV-2 receptor networks in diabetic and COVID-19 associated kidney disease 2020 ,		2
31	SARS-CoV-2 receptor networks in diabetic and COVID-19-associated kidney disease. <i>Kidney International</i> , 2020 , 98, 1502-1518	9.9	33
30	Whole-genome deep-learning analysis identifies contribution of noncoding mutations to autism risk. <i>Nature Genetics</i> , 2019 , 51, 973-980	36.3	122
29	Deep learning sequence-based ab initio prediction of variant effects on expression and disease risk. <i>Nature Genetics</i> , 2018 , 50, 1171-1179	36.3	155
28	Enabling Precision Medicine through Integrative Network Models. <i>Journal of Molecular Biology</i> , 2018 , 430, 2913-2923	6.5	11
27	Interpretation of an individual functional genomics experiment guided by massive public data. <i>Nature Methods</i> , 2018 , 15, 1049-1052	21.6	2
26	An integrative tissue-network approach to identify and test human disease genes. <i>Nature Biotechnology</i> , 2018 ,	44.5	31
25	GIANT 2.0: genome-scale integrated analysis of gene networks in tissues. <i>Nucleic Acids Research</i> , 2018 , 46, W65-W70	20.1	33
24	GIANT API: an application programming interface for functional genomics. <i>Nucleic Acids Research</i> , 2016 , 44, W587-92	20.1	2
23	Network-based analysis of genetic variants associated with hippocampal volume in Alzheimers disease: a study of ADNI cohorts. <i>BioData Mining</i> , 2016 , 9, 3	4.3	21
22	Genome-wide prediction and functional characterization of the genetic basis of autism spectrum disorder. <i>Nature Neuroscience</i> , 2016 , 19, 1454-1462	25.5	214

21	Targeted exploration and analysis of large cross-platform human transcriptomic compendia. <i>Nature Methods</i> , 2015 , 12, 211-4, 3 p following 214	21.6	92
20	Understanding multicellular function and disease with human tissue-specific networks. <i>Nature Genetics</i> , 2015 , 47, 569-76	36.3	473
19	Tissue-aware data integration approach for the inference of pathway interactions in metazoan organisms. <i>Bioinformatics</i> , 2015 , 31, 1093-101	7.2	63
18	Low-variance RNAs identify Parkinsons disease molecular signature in blood. <i>Movement Disorders</i> , 2015 , 30, 813-21	7	14
17	IMP 2.0: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. <i>Nucleic Acids Research</i> , 2015 , 43, W128-33	20.1	44
16	Interactive Big Data Resource to Elucidate Human Immune Pathways and Diseases. <i>Immunity</i> , 2015 , 43, 605-14	32.3	41
15	FNTM: a server for predicting functional networks of tissues in mouse. <i>Nucleic Acids Research</i> , 2015 , 43, W182-7	20.1	16
14	Functional knowledge transfer for high-accuracy prediction of under-studied biological processes. <i>PLoS Computational Biology</i> , 2013 , 9, e1002957	5	44
13	Marker panels for genealogy-based mapping, breed demographics, and inference-of-ancestry in the dog. <i>Animal Biotechnology</i> , 2012 , 23, 241-52	1.4	1
12	Tissue-specific functional networks for prioritizing phenotype and disease genes. <i>PLoS Computational Biology</i> , 2012 , 8, e1002694	5	114
11	IMP: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. <i>Nucleic Acids Research</i> , 2012 , 40, W484-90	20.1	76
10	An ADAMTSL2 founder mutation causes Musladin-Lueke Syndrome, a heritable disorder of beagle dogs, featuring stiff skin and joint contractures. <i>PLoS ONE</i> , 2010 , 5, e12817	3.7	22
9	Tracking footprints of artificial selection in the dog genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 1160-5	11.5	222
8	A comprehensive linkage map of the dog genome. <i>Genetics</i> , 2010 , 184, 595-605	4	71
7	Coat variation in the domestic dog is governed by variants in three genes. <i>Science</i> , 2009 , 326, 150-3	33.3	226
6	Breed distribution and history of canine mdr1-1Delta, a pharmacogenetic mutation that marks the emergence of breeds from the collie lineage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 11725-30	11.5	139
5	Tribe: The collaborative platform for reproducible web-based analysis of gene sets		1
4	DeepArk: modeling cis-regulatory codes of model species with deep learning		1

3	Spatial Transcriptional Mapping of the Human Nephrogenic Program	6
2	Genome-wide characterization of genetic and functional dysregulation in autism spectrum disorder	2
1	A sequence-based global map of regulatory activity for deciphering human genetics	2