

# Aaron K Wong

## List of Publications by Citations

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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	Understanding multicellular function and disease with human tissue-specific networks. <i>Nature Genetics</i> , <b>2015</b> , 47, 569-76	36.3	473
37	Coat variation in the domestic dog is governed by variants in three genes. <i>Science</i> , <b>2009</b> , 326, 150-3	33.3	226
36	Tracking footprints of artificial selection in the dog genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 1160-5	11.5	222
35	Genome-wide prediction and functional characterization of the genetic basis of autism spectrum disorder. <i>Nature Neuroscience</i> , <b>2016</b> , 19, 1454-1462	25.5	214
34	Deep learning sequence-based ab initio prediction of variant effects on expression and disease risk. <i>Nature Genetics</i> , <b>2018</b> , 50, 1171-1179	36.3	155
33	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> , <b>2004</b> , 101, 11725-30	11.5	139
32	Whole-genome deep-learning analysis identifies contribution of noncoding mutations to autism risk. <i>Nature Genetics</i> , <b>2019</b> , 51, 973-980	36.3	122
31	Tissue-specific functional networks for prioritizing phenotype and disease genes. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002694	5	114
30	Targeted exploration and analysis of large cross-platform human transcriptomic compendia. <i>Nature Methods</i> , <b>2015</b> , 12, 211-4, 3 p following 214	21.6	92
29	IMP: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, W484-90	20.1	76
28	A comprehensive linkage map of the dog genome. <i>Genetics</i> , <b>2010</b> , 184, 595-605	4	71
27	Tissue-aware data integration approach for the inference of pathway interactions in metazoan organisms. <i>Bioinformatics</i> , <b>2015</b> , 31, 1093-101	7.2	63
26	IMP 2.0: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W128-33	20.1	44
25	Functional knowledge transfer for high-accuracy prediction of under-studied biological processes. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1002957	5	44
24	Interactive Big Data Resource to Elucidate Human Immune Pathways and Diseases. <i>Immunity</i> , <b>2015</b> , 43, 605-14	32.3	41
23	SARS-CoV-2 receptor networks in diabetic and COVID-19-associated kidney disease. <i>Kidney International</i> , <b>2020</b> , 98, 1502-1518	9.9	33
22	GIANT 2.0: genome-scale integrated analysis of gene networks in tissues. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, W65-W70	20.1	33

21	An integrative tissue-network approach to identify and test human disease genes. <i>Nature Biotechnology</i> , <b>2018</b> ,	44.5	31
20	An ADAMTSL2 founder mutation causes Musladin-Lueke Syndrome, a heritable disorder of beagle dogs, featuring stiff skin and joint contractures. <i>PLoS ONE</i> , <b>2010</b> , 5, e12817	3.7	22
19	Network-based analysis of genetic variants associated with hippocampal volume in Alzheimer's disease: a study of ADNI cohorts. <i>BioData Mining</i> , <b>2016</b> , 9, 3	4.3	21
18	FNTM: a server for predicting functional networks of tissues in mouse. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W182-7	20.1	16
17	Low-variance RNAs identify Parkinson's disease molecular signature in blood. <i>Movement Disorders</i> , <b>2015</b> , 30, 813-21	7	14
16	Enabling Precision Medicine through Integrative Network Models. <i>Journal of Molecular Biology</i> , <b>2018</b> , 430, 2913-2923	6.5	11
15	Genome-wide landscape of RNA-binding protein target site dysregulation reveals a major impact on psychiatric disorder risk. <i>Nature Genetics</i> , <b>2021</b> , 53, 166-173	36.3	10
14	Spatial transcriptional mapping of the human nephrogenic program. <i>Developmental Cell</i> , <b>2021</b> , 56, 2381-2398.e6	10.1	7
13	Decoding disease: from genomes to networks to phenotypes. <i>Nature Reviews Genetics</i> , <b>2021</b> , 22, 774-790.e1	10.1	7
12	Spatial Transcriptional Mapping of the Human Nephrogenic Program		6
11	Tissue-specific enhancer functional networks for associating distal regulatory regions to disease. <i>Cell Systems</i> , <b>2021</b> , 12, 353-362.e6	10.6	6
10	GIANT API: an application programming interface for functional genomics. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, W587-92	20.1	2
9	SARS-CoV-2 receptor networks in diabetic and COVID-19 associated kidney disease <b>2020</b> ,		2
8	Genome-wide characterization of genetic and functional dysregulation in autism spectrum disorder		2
7	Modeling transcriptional regulation of model species with deep learning. <i>Genome Research</i> , <b>2021</b> , 31, 1097-1105	9.7	2
6	Interpretation of an individual functional genomics experiment guided by massive public data. <i>Nature Methods</i> , <b>2018</b> , 15, 1049-1052	21.6	2
5	A sequence-based global map of regulatory activity for deciphering human genetics		2
4	Marker panels for genealogy-based mapping, breed demographics, and inference-of-ancestry in the dog. <i>Animal Biotechnology</i> , <b>2012</b> , 23, 241-52	1.4	1

- 3 Tribe: The collaborative platform for reproducible web-based analysis of gene sets 1
- 2 DeepArk: modeling cis-regulatory codes of model species with deep learning 1
- 1 Machine learning methods to model multicellular complexity and tissue specificity. *Nature Reviews Materials*, **2021**, 6, 717-729 733 ○