

Qingbo S Wang

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.

18
papers

3,297
citations

9
h-index

22
g-index

22
ext. papers

6,440
ext. citations

31.8
avg, IF

3.39
L-index

#	Paper	IF	Citations
18	Methods for statistical fine-mapping and their applications to auto-immune diseases.. <i>Seminars in Immunopathology</i> , 2022 , 44, 101	12	0
17	Centers for Mendelian Genomics: A decade of facilitating gene discovery.. <i>Genetics in Medicine</i> , 2022 ,	8.1	5
16	High-resolution Slide-seqV2 spatial transcriptomics enables discovery of disease-specific cell neighborhoods and pathways.. <i>IScience</i> , 2022 , 25, 104097	6.1	1
15	Principles of Spatial Transcriptomics Analysis: A Practical Walk-Through in Kidney Tissue.. <i>Frontiers in Physiology</i> , 2021 , 12, 809346	4.6	2
14	Leveraging supervised learning for functionally-informed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. <i>Nature Communications</i> , 2021 , 12, 3394	17.4	9
13	Mapping the human genetic architecture of COVID-19. <i>Nature</i> , 2021 ,	50.4	162
12	Addendum: The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2021 , 597, E3-E4	50.4	3
11	Evaluating drug targets through human loss-of-function genetic variation. <i>Nature</i> , 2020 , 581, 459-464	50.4	53
10	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020 , 581, 434-443	50.4	2278
9	Landscape of multi-nucleotide variants in 125,748 human exomes and 15,708 genomes. <i>Nature Communications</i> , 2020 , 11, 2539	17.4	51
8	A structural variation reference for medical and population genetics. <i>Nature</i> , 2020 , 581, 444-451	50.4	223
7	Transcript expression-aware annotation improves rare variant interpretation. <i>Nature</i> , 2020 , 581, 452-458	50.4	55
6	The effect of LRRK2 loss-of-function variants in humans. <i>Nature Medicine</i> , 2020 , 26, 869-877	50.5	47
5	High Resolution Slide-seqV2 Spatial Transcriptomics Enables Discovery of Disease-Specific Cell Neighborhoods and Pathways		3
4	Leveraging supervised learning for functionally-informed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs		2
3	The mutational constraint spectrum quantified from variation in 141,456 humans		381
2	Landscape of multi-nucleotide variants in 125,748 human exomes and 15,708 genomes		3

1 Insights from complex trait fine-mapping across diverse populations

5