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List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6755047/publications.pdf

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14 papers	8,701 citations	759233 12 h-index	940533 16 g-index
22 all docs	22 docs citations	22 times ranked	20342 citing authors

#	Article	IF	Citations
1	Methods for statistical fine-mapping and their applications to auto-immune diseases. Seminars in Immunopathology, 2022, 44, 101-113.	6.1	7
2	Centers for Mendelian Genomics: A decade of facilitating gene discovery. Genetics in Medicine, 2022, 24, 784-797.	2.4	44
3	High-resolution Slide-seqV2 spatial transcriptomics enables discovery of disease-specific cell neighborhoods and pathways. IScience, 2022, 25, 104097.	4.1	32
4	Leveraging supervised learning for functionallyÂinformed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. Nature Communications, 2021, 12, 3394.	12.8	44
5	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	27.8	640
6	Addendum: The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2021, 597, E3-E4.	27.8	45
7	A massive effort links protein-coding gene variants to health. Nature, 2021, 599, 561-563.	27.8	1
8	Principles of Spatial Transcriptomics Analysis: A Practical Walk-Through in Kidney Tissue. Frontiers in Physiology, 2021, 12, 809346.	2.8	14
9	Evaluating drug targets through human loss-of-function genetic variation. Nature, 2020, 581, 459-464.	27.8	115
10	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	27.8	6,140
11	Landscape of multi-nucleotide variants in 125,748 human exomes and 15,708 genomes. Nature Communications, 2020, 11, 2539.	12.8	98
12	A structural variation reference for medical and population genetics. Nature, 2020, 581, 444-451.	27.8	614
13	Transcript expression-aware annotation improves rare variant interpretation. Nature, 2020, 581, 452-458.	27.8	142
14	The effect of LRRK2 loss-of-function variants in humans. Nature Medicine, 2020, 26, 869-877.	30.7	79