Matthew Solomonson

List of Publications by Year
in descending order

22	9,716	361413	610901
papers	citations	20 h-index	24 g-index

29	29	29	20970
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	27.8	6,140
2	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	27.8	640
3	A structural variation reference for medical and population genetics. Nature, 2020, 581, 444-451.	27.8	614
4	The ExAC browser: displaying reference data information from over 60 000 exomes. Nucleic Acids Research, 2017, 45, D840-D845.	14.5	587
5	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	27.8	326
6	Ultra-Rare Genetic Variation in the Epilepsies: A Whole-Exome Sequencing Study of 17,606 Individuals. American Journal of Human Genetics, 2019, 105, 267-282.	6.2	237
7	Variant interpretation using population databases: Lessons from gnomAD. Human Mutation, 2022, 43, 1012-1030.	2.5	184
8	Transcript expression-aware annotation improves rare variant interpretation. Nature, 2020, 581, 452-458.	27.8	142
9	Evaluating drug targets through human loss-of-function genetic variation. Nature, 2020, 581, 459-464.	27.8	115
10	Structure of EspB from the ESX-1 Type VII Secretion System and Insights into its Export Mechanism. Structure, 2015, 23, 571-583.	3.3	85
11	Crystal Structure of Sulfide:Quinone Oxidoreductase from Acidithiobacillus ferrooxidans: Insights into Sulfidotrophic Respiration and Detoxification. Journal of Molecular Biology, 2010, 398, 292-305.	4.2	84
12	Pyranopterin conformation defines the function of molybdenum and tungsten enzymes. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14773-14778.	7.1	82
13	Exome sequencing in bipolar disorder identifies AKAP11 as a risk gene shared with schizophrenia. Nature Genetics, 2022, 54, 541-547.	21.4	65
14	Structure and mechanism of Staphylococcus aureus TarM, the wall teichoic acid Î±-glycosyltransferase. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E576-85.	7.1	49
15	Structure of the Mycosin-1 Protease from the Mycobacterial ESX-1 Protein Type VII Secretion System. Journal of Biological Chemistry, 2013, 288, 17782-17790.	3.4	48
16	Addendum: The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2021, 597, E3-E4.	27.8	45
17	Centers for Mendelian Genomics: A decade of facilitating gene discovery. Genetics in Medicine, 2022, 24, 784-797.	2.4	44
18	Distinct Metal Isoforms Underlie Promiscuous Activity Profiles of Metalloenzymes. ACS Chemical Biology, 2015, 10, 1684-1693.	3.4	42

#	Article	IF	Citations
19	Sub-genic intolerance, ClinVar, and the epilepsies: A whole-exome sequencing study of 29,165 individuals. American Journal of Human Genetics, 2021, 108, 965-982.	6.2	35
20	seqr : A webâ€based analysis and collaboration tool for rare disease genomics. Human Mutation, 2022, , .	2.5	31
21	SARS-CoV-2 susceptibility and COVID-19 disease severity are associated with genetic variants affecting gene expression in a variety of tissues. Cell Reports, 2021, 37, 110020.	6.4	25
22	Preliminary X-ray crystallographic analysis of sulfide:quinone oxidoreductase fromAcidithiobacillus ferrooxidans. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 839-842.	0.7	6