Michael Ronemus

List of Publications by Year
in descending order

19 papers	6,732 citations	516215 16 h-index	839053 18 g-index
20 all docs	20 docs citations	20 times ranked	11500 citing authors

#	Article	IF	Citations
1	The contribution of de novo coding mutations to autism spectrum disorder. Nature, 2014, 515, 216-221.	13.7	2,188
2	De Novo Gene Disruptions in Children on the Autistic Spectrum. Neuron, 2012, 74, 285-299.	3.8	1,311
3	De novo mutations in congenital heart disease with neurodevelopmental and other congenital anomalies. Science, 2015, 350, 1262-1266.	6.0	646
4	Rare De Novo Variants Associated with Autism Implicate a Large Functional Network of Genes Involved in Formation and Function of Synapses. Neuron, 2011, 70, 898-907.	3.8	641
5	Rare De Novo and Transmitted Copy-Number Variation in Autistic Spectrum Disorders. Neuron, 2011, 70, 886-897.	3.8	639
6	The role of de novo mutations in the genetics of autism spectrum disorders. Nature Reviews Genetics, 2014, 15, 133-141.	7.7	339
7	Increased Frequency of De Novo Copy Number Variants in Congenital Heart Disease by Integrative Analysis of Single Nucleotide Polymorphism Array and Exome Sequence Data. Circulation Research, 2014, 115, 884-896.	2.0	229
8	Reducing INDEL calling errors in whole genome and exome sequencing data. Genome Medicine, 2014, 6, 89.	3.6	144
9	MicroRNA-Targeted and Small Interfering RNAâ€“Mediated mRNA Degradation Is Regulated by Argonaute, Dicer, and RNA-Dependent RNA Polymerase in Arabidopsis. Plant Cell, 2006, 18, 1559-1574.	3.1	141
10	Low load for disruptive mutations in autism genes and their biased transmission. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5600-7.	3.3	129
11	The contribution of de novo and rare inherited copy number changes to congenital heart disease in an unselected sample of children with conotruncal defects or hypoplastic left heart disease. Human Genetics, 2014, 133, 11-27.	1.8	112
12	Indel variant analysis of short-read sequencing data with Scalpel. Nature Protocols, 2016, 11, 2529-2548.	5.5	99
13	SMASH, a fragmentation and sequencing method for genomic copy number analysis. Genome Research, 2016, 26, 844-851.	2.4	31
14	Methylation mystery. Nature, 2005, 433, 472-473.	13.7	24
15	Rates of contributory de novo mutation in high and low-risk autism families. Communications Biology, 2021, 4, 1026.	2.0	24
16	Rare De Novo Germline Copy-Number Variation in Testicular Cancer. American Journal of Human Genetics, 2012, 91, 379-383.	2.6	21
17	Reducing system noise in copy number data using principal components of self-self hybridizations. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E103-E110.	3.3	8
18	Partial bisulfite conversion for unique template sequencing. Nucleic Acids Research, 2018, 46, e10-e10.	6.5	6

#	Article	IF	Citations
19	Detection of Copy Number Variants by Short Multiply Aggregated Sequence Homologies. Journal of Molecular Diagnostics, 2020, 22, 1476-1481.	1.2	0