Shan Dong

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1978631/publications.pdf

Version: 2024-02-01

16	10,724	687220 13	940416 16
papers	citations	h-index	g-index

20	20	20	16298
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Exome sequencing of fetuses with congenital diaphragmatic hernia supports a causal role for NR2F2, PTPN11, and WT1 variants. American Journal of Surgery, 2022, 223, 182-186.	0.9	6
2	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	13.5	1,422
3	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. Cell Reports, 2020, 31, 107489.	2.9	91
4	INSIGHTS INTO THE CONTRIBUTION OF RARE NONCODING VARIATION IN AUTISM SPECTRUM DISORDER THROUGH FAMILY-BASED WHOLE-GENOME SEQUENCING. European Neuropsychopharmacology, 2019, 29, S36.	0.3	0
5	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. Nature Genetics, 2018, 50, 727-736.	9.4	235
6	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. Science, 2018, 362, .	6.0	234
7	De Novo Sequence and Copy Number Variants Are Strongly Associated with Tourette Disorder and Implicate Cell Polarity in Pathogenesis. Cell Reports, 2018, 24, 3441-3454.e12.	2.9	91
8	De Novo Coding Variants Are Strongly Associated with Tourette Disorder. Neuron, 2017, 94, 486-499.e9.	3.8	155
9	Whole genome sequencing in psychiatric disorders: the WGSPD consortium. Nature Neuroscience, 2017, 20, 1661-1668.	7.1	122
10	The female protective effect in autism spectrum disorder is not mediated by a single genetic locus. Molecular Autism, 2015, 6, 25.	2.6	50
11	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. Neuron, 2015, 87, 1215-1233.	3.8	1,219
12	De Novo Insertions and Deletions of Predominantly Paternal Origin Are Associated with Autism Spectrum Disorder. Cell Reports, 2014, 9, 16-23.	2.9	151
13	The contribution of de novo coding mutations to autism spectrum disorder. Nature, 2014, 515, 216-221.	13.7	2,188
14	Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. Cell, 2013, 155, 997-1007.	13.5	825
15	H2A.Z Nucleosome Positioning Has No Impact on Genetic Variation in Drosophila Genome. PLoS ONE, 2013, 8, e58295.	1.1	1
16	KOBAS 2.0: a web server for annotation and identification of enriched pathways and diseases. Nucleic Acids Research, 2011, 39, W316-W322.	6.5	3,897