Mehdi Zarrei

List of Publications by Year
in descending order

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Version: 2024-02-01

48 papers	3,170 citations	394421 19 h-index	206112 48 g-index
52 all docs	52 docs citations	52 times ranked	6843 citing authors

#	Article	IF	Citations
1	Copy number variations in a Brazilian cohort with autism spectrum disorders highlight the contribution of cell adhesion genes. Clinical Genetics, 2022, 101, 134-141.	2.0	13
2	Deletion of Loss-of-Functionâ€“Intolerant Genes and Risk of 5 Psychiatric Disorders. JAMA Psychiatry, 2022, 79, 78.	11.0	8
3	Chromosomal microarray analysis of 410 Han Chinese patients with autism spectrum disorder or unexplained intellectual disability and developmental delay. Npj Genomic Medicine, 2022, 7, 1.	3.8	11
4	Mutations in trpÎ³, the homologue of TRPC6 autism candidate gene, causes autism-like behavioral deficits in Drosophila. Molecular Psychiatry, 2022, 27, 3328-3342.	7.9	6
5	Regionally defined proteomic profiles of human cerebral tissue and organoids reveal conserved molecular modules of neurodevelopment. Cell Reports, 2022, 39, 110846.	6.4	7
6	Rare CACNA1H and RELN variants interact through mTORC1 pathway in oligogenic autism spectrum disorder. Translational Psychiatry, 2022, 12, .	4.8	3
7	RCL1 copy number variants are associated with a range of neuropsychiatric phenotypes. Molecular Psychiatry, 2021, 26, 1706-1718.	7.9	10
8	Inherited duplications of PPP2R3B predispose to nevi and melanoma via a C21orf91-driven proliferative phenotype. Genetics in Medicine, 2021, 23, 1636-1647.	2.4	5
9	Niche Shifts, Hybridization, Polyploidy and Geographic Parthenogenesis in Western North American Hawthorns (Crataegus subg. Sanguineae, Rosaceae). Agronomy, 2021, 11, 2133.	3.0	3
10	A recurrent SHANK3 frameshift variant in Autism Spectrum Disorder. Npj Genomic Medicine, 2021, 6, 91.	3.8	9
11	Homozygous duplication identified by whole genome sequencing causes LRBA deficiency. Npj Genomic Medicine, 2021, 6, 96.	3.8	3
12	Single-cell transcriptome identifies molecular subtype of autism spectrum disorder impacted by de novo loss-of-function variants regulating glial cells. Human Genomics, 2021, 15, 68.	2.9	20
13	Metaâ€Analyses Support Previous and Novel Autism Candidate Genes: Outcomes of an Unexplored Brazilian Cohort. Autism Research, 2020, 13, 199-206.	3.8	25
14	Genes and Pathways Implicated in Tetralogy of Fallot Revealed by Ultra-Rare Variant Burden Analysis in 231 Genome Sequences. Frontiers in Genetics, 2020, 11, 957.	2.3	23
15	Ancestry and frequency of genetic variants in the general population are confounders in the characterization of germline variants linked to cancer. BMC Medical Genetics, 2020, 21, 92.	2.1	4
16	Segregating patterns of copy number variations in extended autism spectrum disorder (ASD) pedigrees. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 268-276.	1.7	7
17	Refining critical regions in 15q24 microdeletion syndrome pertaining to autism. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 217-226.	1.7	2
18	A large data resource of genomic copy number variation across neurodevelopmental disorders. Npj Genomic Medicine, 2019, 4, 26.	3.8	118

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19	Expanding the neurodevelopmental phenotypes of individuals with de novo KMT2A variants. Npj Genomic Medicine, 2019, 4, 9.	3.8	29
20	Intratumoral Genetic and Functional Heterogeneity in Pediatric Glioblastoma. Cancer Research, 2019, 79, 2111-2123.	0.9	28
21	Rare copy number variation in extremely impulsively violent males. Genes, Brain and Behavior, 2019, 18, e12536.	2.2	9
22	Copy number variation in fetal alcohol spectrum disorder. Biochemistry and Cell Biology, 2018, 96, 161-166.	2.0	15
23	Association of IMMP2L deletions with autism spectrum disorder: A trio family study and metaâ€analysis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 93-100.	1.7	16
24	De novo and rare inherited copy-number variations in the hemiplegic form of cerebral palsy. Genetics in Medicine, 2018, 20, 172-180.	2.4	82
25	Rearrangement bursts generate canonical gene fusions in bone and soft tissue tumors. Science, 2018, 361, .	12.6	121
26	A genome-wide linkage study of autism spectrum disorder and the broad autism phenotype in extended pedigrees. Journal of Neurodevelopmental Disorders, 2018, 10, 20.	3.1	20
27	Whole genome sequencing resource identifies 18 new candidate genes for autism spectrum disorder. Nature Neuroscience, 2017, 20, 602-611.	14.8	691
28	A de novo deletion in a boy with cerebral palsy suggests a refined critical region for the 4q21.22 microdeletion syndrome. American Journal of Medical Genetics, Part A, 2017, 173, 1287-1293.	1.2	8
29	Variable phenotype expression in a family segregating microdeletions of the NRXN1 and MBD5 autism spectrum disorder susceptibility genes. Npj Genomic Medicine, 2017, 2, .	3.8	31
30	Mutations in RAB39B in individuals with intellectual disability, autism spectrum disorder, and macrocephaly. Molecular Autism, 2017, 8, 59.	4.9	49
31	Whole-genome sequencing suggests mechanisms for 22q11.2 deletion-associated Parkinsonâ€™s disease. PLoS ONE, 2017, 12, e0173944.	2.5	17
32	Microcephalyâ€capillary malformation syndrome: Brothers with a homozygous STAMBP mutation, uncovered by exome sequencing. American Journal of Medical Genetics, Part A, 2016, 170, 3018-3022.	1.2	16
33	Genome-wide characteristics of de novo mutations in autism. Npj Genomic Medicine, 2016, 1, 160271-1602710.	3.8	200
34	Uncovering obsessive-compulsive disorder risk genes in a pediatric cohort by high-resolution analysis of copy number variation. Journal of Neurodevelopmental Disorders, 2016, 8, 36.	3.1	55
35	Indexing Effects of Copy Number Variation on Genes Involved in Developmental Delay. Scientific Reports, 2016, 6, 28663.	3.3	35
36	Whole-Genome Sequencing Suggests Schizophrenia Risk Mechanisms in Humans with 22q11.2 Deletion Syndrome. G3: Genes, Genomes, Genetics, 2015, 5, 2453-2461.	1.8	43

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37	Whole-genome sequencing of quartet families with autism spectrum disorder. Nature Medicine, 2015, 21, 185-191.	30.7	457
38	A copy number variation map of the human genome. Nature Reviews Genetics, 2015, 16, 172-183.	16.3	707
39	Clinically relevant copy number variations detected in cerebral palsy. Nature Communications, 2015, 6, 7949.	12.8	120
40	DNA barcodes from four loci provide poor resolution of taxonomic groups in the genus Crataegus. AoB PLANTS, 2015, 7, .	2.3	26
41	Crataegus Ã—ninae-celottiae and C. Ã—cogswellii (Rosaceae,ÂMaleae), two spontaneously formedÂintersectional nothospecies. PhytoKeys, 2014, 36, 1-26.	1.0	10
42	Speciation and evolution in the Gagea reticulata species complex (Tulipeae; Liliaceae). Molecular Phylogenetics and Evolution, 2012, 62, 624-639.	2.7	20
43	Gagea calcicola (Liliaceae), a new species from southwestern Iran. Kew Bulletin, 2010, 65, 89-96.	0.9	8
44	Gagea robusta (Liliaceae), a new species from Flora Iranica area. Kew Bulletin, 2010, 65, 327-336.	0.9	10
45	The systematic importance of anatomical data in Gagea (Liliaceae) from the Flora Iranica area. Botanical Journal of the Linnean Society, 2010, 164, 155-177.	1.6	12
46	Systematic revision of the genus Gagea Salisb. (Liliaceae) in Iran. Botanical Journal of the Linnean Society, 2007, 154, 559-588.	1.6	24
47	Pollen morphology of the genus Gagea (Liliaceae) in Iran. Flora: Morphology, Distribution, Functional Ecology of Plants, 2005, 200, 96-108.	1.2	24
48	A new species of Gagea (Liliaceae) from Iran. Nordic Journal of Botany, 2003, 23, 269-274.	0.5	9