Tychele N Turner

List of Publications by Year
in descending order

38 papers	3,633 citations	331259 21 h-index	360668 35 g-index
47 all docs	47 docs citations	47 times ranked	7015 citing authors

#	Article	IF	Citations
1	Excess of rare, inherited truncating mutations in autism. Nature Genetics, 2015, 47, 582-588.	9.4	531
2	Targeted sequencing identifies 91 neurodevelopmental-disorder risk genes with autism and developmental-disability biases. Nature Genetics, 2017, 49, 515-526.	9.4	443
3	Genomic Patterns of De Novo Mutation in Simplex Autism. Cell, 2017, 171, 710-722.e12.	13.5	308
4	De novo genic mutations among a Chinese autism spectrum disorder cohort. Nature Communications, 2016, 7, 13316.	5.8	293
5	Genome Sequencing of Autism-Affected Families Reveals Disruption of Putative Noncoding Regulatory DNA. American Journal of Human Genetics, 2016, 98, 58-74.	2.6	248
6	denovo-db: a compendium of humande novovariants. Nucleic Acids Research, 2017, 45, D804-D811.	6.5	173
7	Exome sequencing of 457 autism families recruited online provides evidence for autism risk genes. Npj Genomic Medicine, 2019, 4, 19.	1.7	163
8	Single-cell epigenomics reveals mechanisms of human cortical development. Nature, 2021, 598, 205-213.	13.7	154
9	Hotspots of missense mutation identify neurodevelopmental disorder genes and functional domains. Nature Neuroscience, 2017, 20, 1043-1051.	7.1	152
10	Loss of Î´-catenin function in severe autism. Nature, 2015, 520, 51-56.	13.7	145
11	Molecular Genetic Anatomy and Risk Profile of Hirschsprungâ€™s Disease. New England Journal of Medicine, 2019, 380, 1421-1432.	13.9	131
12	Recurrent de novo mutations in neurodevelopmental disorders: properties and clinical implications. Genome Medicine, 2017, 9, 101.	3.6	112
13	Large-scale targeted sequencing identifies risk genes for neurodevelopmental disorders. Nature Communications, 2020, 11, 4932.	5.8	105
14	Genome sequencing identifies multiple deleterious variants in autism patients with more severe phenotypes. Genetics in Medicine, 2019, 21, 1611-1620.	1.1	88
15	Sex-Based Analysis of De Novo Variants in Neurodevelopmental Disorders. American Journal of Human Genetics, 2019, 105, 1274-1285.	2.6	84
16	Recent ultra-rare inherited variants implicate new autism candidate risk genes. Nature Genetics, 2021, 53, 1125-1134.	9.4	68
17	The Role of De Novo Noncoding Regulatory Mutations in Neurodevelopmental Disorders. Trends in Neurosciences, 2019, 42, 115-127.	4.2	56
18	Clinical phenotype of ASD-associated DYRK1A haploinsufficiency. Molecular Autism, 2017, 8, 54.	2.6	55

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19	The autism spectrum phenotype in ADNP syndrome. Autism Research, 2018, 11, 1300-1310.	2.1	49
20	Revealing rateâ€limiting steps in complex disease biology: The crucial importance of studying rare, extremeâ€phenotype families. BioEssays, 2016, 38, 578-586.	1.2	47
21	Proteins linked to autosomal dominant and autosomal recessive disorders harbor characteristic rare missense mutation distribution patterns. Human Molecular Genetics, 2015, 24, 5995-6002.	1.4	40
22	Clinical Phenotypes of Carriers of Mutations in CHD8 or Its Conserved Target Genes. Biological Psychiatry, 2020, 87, 123-131.	0.7	22
23	Thousands of high-quality sequencing samples fail to show meaningful correlation between 5S and 45S ribosomal DNA arrays in humans. Scientific Reports, 2021, 11, 449.	1.6	19
24	Molecular subtyping and improved treatment of neurodevelopmental disease. Genome Medicine, 2016, 8, 22.	3.6	17
25	Rare and de novo coding variants in chromodomain genes in Chiari I malformation. American Journal of Human Genetics, 2021, 108, 100-114.	2.6	17
26	Coding and noncoding variants in EBF3 are involved in HADDS and simplex autism. Human Genomics, 2021, 15, 44.	1.4	16
27	Altered neuronal physiology, development, and function associated with a common chromosome 15 duplication involving CHRNA7. BMC Biology, 2021, 19, 147.	1.7	9
28	From karyotypes to precision genomics in 9p deletion and duplication syndromes. Human Genetics and Genomics Advances, 2022, 3, 100081.	1.0	9
29	Comorbid symptoms of inattention, autism, and executive cognition in youth with putative genetic risk. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2018, 59, 268-276.	3.1	8
30	Germline mosaicism of a missense variant in <scp>KCNC2</scp> in a multiplex family with autism and epilepsy characterized by longâ€read sequencing. American Journal of Medical Genetics, Part A, 2022, 188, 2071-2081.	0.7	7
31	Differences in the number of de novo mutations between individuals are due to small family-specific effects and stochasticity. Genome Research, 2021, 31, 1513-1518.	2.4	6
32	Precise breakpoint detection in a patient with 9pâ€“ syndrome. Journal of Physical Education and Sports Management, 2020, 6, a005348.	0.5	4
33	Familial Lipomas Without Classic Neurofibromatosis-1 Caused by a Missense Germline NF1 Mutation. Neurology: Genetics, 2021, 7, e582.	0.9	3
34	Ancestry adjustment improves genome-wide estimates of regional intolerance. Genetics, 2022, , .	1.2	2
35	Genetic counseling as preventive intervention: toward individual specification of transgenerational autism risk. Journal of Neurodevelopmental Disorders, 2021, 13, 39.	1.5	1
36	Large-Scale Population-Based Assessment of Psychiatric Comorbidities in Autism Spectrum Disorder and Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2019, 86, e25-e27.	0.7	0

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37	ACES: Analysis of Conservation with an Extensive list of Species. Bioinformatics, 2021, 37, 3920-3922.	1.8	0
38	Genetic etiologies of autism: Unpacking pathogenic mechanisms and characteristics. , 2022, , 197-213.		0