

Stephen W Scherer

List of Publications by Year in descending order

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Version: 2024-02-01

308
papers

31,946
citations

9786

73
h-index

5255

165
g-index

318
all docs

318
docs citations

318
times ranked

41845
citing authors

#	ARTICLE	IF	CITATIONS
1	Detection of large-scale variation in the human genome. <i>Nature Genetics</i> , 2004, 36, 949-951.	21.4	2,602
2	Consensus Statement: Chromosomal Microarray Is a First-Tier Clinical Diagnostic Test for Individuals with Developmental Disabilities or Congenital Anomalies. <i>American Journal of Human Genetics</i> , 2010, 86, 749-764.	6.2	2,325
3	Germline and somatic mutations in the tyrosine kinase domain of the MET proto-oncogene in papillary renal carcinomas. <i>Nature Genetics</i> , 1997, 16, 68-73.	21.4	1,461
4	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	12.6	1,085
5	Mutations in the human Sonic Hedgehog gene cause holoprosencephaly. <i>Nature Genetics</i> , 1996, 14, 357-360.	21.4	1,075
6	The human splicing code reveals new insights into the genetic determinants of disease. <i>Science</i> , 2015, 347, 1254806.	12.6	1,053
7	The Database of Genomic Variants: a curated collection of structural variation in the human genome. <i>Nucleic Acids Research</i> , 2014, 42, D986-D992.	14.5	1,033
8	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	21.4	838
9	Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. <i>American Journal of Human Genetics</i> , 2014, 94, 677-694.	6.2	819
10	A copy number variation map of the human genome. <i>Nature Reviews Genetics</i> , 2015, 16, 172-183.	16.3	707
11	Whole genome sequencing resource identifies 18 new candidate genes for autism spectrum disorder. <i>Nature Neuroscience</i> , 2017, 20, 602-611.	14.8	691
12	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. <i>Nature Genetics</i> , 2019, 51, 1207-1214.	21.4	641
13	A gene encoding a putative GTPase regulator is mutated in familial amyotrophic lateral sclerosis 2. <i>Nature Genetics</i> , 2001, 29, 166-173.	21.4	635
14	Meta-analysis of SHANK Mutations in Autism Spectrum Disorders: A Gradient of Severity in Cognitive Impairments. <i>PLoS Genetics</i> , 2014, 10, e1004580.	3.5	501
15	Mutations in a gene encoding a novel protein tyrosine phosphatase cause progressive myoclonus epilepsy. <i>Nature Genetics</i> , 1998, 20, 171-174.	21.4	499
16	Whole-genome sequencing of quartet families with autism spectrum disorder. <i>Nature Medicine</i> , 2015, 21, 185-191.	30.7	457
17	Improved diagnostic yield compared with targeted gene sequencing panels suggests a role for whole-genome sequencing as a first-tier genetic test. <i>Genetics in Medicine</i> , 2018, 20, 435-443.	2.4	404
18	The gene mutated in adult-onset type II citrullinaemia encodes a putative mitochondrial carrier protein. <i>Nature Genetics</i> , 1999, 22, 159-163.	21.4	392

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19	Meta-analysis and multidisciplinary consensus statement: exome sequencing is a first-tier clinical diagnostic test for individuals with neurodevelopmental disorders. <i>Genetics in Medicine</i> , 2019, 21, 2413-2421.	2.4	378
20	Mutations in ATP6N1B, encoding a new kidney vacuolar proton pump 116-kD subunit, cause recessive distal renal tubular acidosis with preserved hearing. <i>Nature Genetics</i> , 2000, 26, 71-75.	21.4	368
21	Molecular Diagnostic Yield of Chromosomal Microarray Analysis and Whole-Exome Sequencing in Children With Autism Spectrum Disorder. <i>JAMA - Journal of the American Medical Association</i> , 2015, 314, 895.	7.4	352
22	Challenges and standards in integrating surveys of structural variation. <i>Nature Genetics</i> , 2007, 39, S7-S15.	21.4	331
23	Single cell-derived clonal analysis of human glioblastoma links functional and genomic heterogeneity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 851-856.	7.1	321
24	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermutated cancers. <i>Nature Genetics</i> , 2015, 47, 257-262.	21.4	306
25	Whole-genome sequencing expands diagnostic utility and improves clinical management in paediatric medicine. <i>Npj Genomic Medicine</i> , 2016, 1, .	3.8	295
26	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014, 46, 826-836.	21.4	281
27	Reliability of the CMT neuropathy score (second version) in Charcot-Marie-Tooth disease. <i>Journal of the Peripheral Nervous System</i> , 2011, 16, 191-198.	3.1	269
28	Fusion of two novel genes, RBM15 and MKL1, in the t(1;22)(p13;q13) of acute megakaryoblastic leukemia. <i>Nature Genetics</i> , 2001, 28, 220-221.	21.4	268
29	FORGE Canada Consortium: Outcomes of a 2-Year National Rare-Disease Gene-Discovery Project. <i>American Journal of Human Genetics</i> , 2014, 94, 809-817.	6.2	219
30	Rates, distribution and implications of postzygotic mosaic mutations in autism spectrum disorder. <i>Nature Neuroscience</i> , 2017, 20, 1217-1224.	14.8	212
31	Genome-wide characteristics of de novo mutations in autism. <i>Npj Genomic Medicine</i> , 2016, 1, 160271-1602710.	3.8	200
32	Human Chromosome 7: DNA Sequence and Biology. <i>Science</i> , 2003, 300, 767-772.	12.6	185
33	A Discovery Resource of Rare Copy Number Variations in Individuals with Autism Spectrum Disorder. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1665-1685.	1.8	175
34	Paternally inherited cis-regulatory structural variants are associated with autism. <i>Science</i> , 2018, 360, 327-331.	12.6	174
35	CHARGE and Kabuki Syndromes: Gene-Specific DNA Methylation Signatures Identify Epigenetic Mechanisms Linking These Clinically Overlapping Conditions. <i>American Journal of Human Genetics</i> , 2017, 100, 773-788.	6.2	166
36	A Comprehensive Workflow for Read Depth-Based Identification of Copy-Number Variation from Whole-Genome Sequence Data. <i>American Journal of Human Genetics</i> , 2018, 102, 142-155.	6.2	156

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37	Genome-wide detection of tandem DNA repeats that are expanded in autism. <i>Nature</i> , 2020, 586, 80-86.	27.8	155
38	Brain-expressed exons under purifying selection are enriched for de novo mutations in autism spectrum disorder. <i>Nature Genetics</i> , 2014, 46, 742-747.	21.4	149
39	Ankrd11 Is a Chromatin Regulator Involved in Autism that Is Essential for Neural Development. <i>Developmental Cell</i> , 2015, 32, 31-42.	7.0	147
40	Phase Separation as a Missing Mechanism for Interpretation of Disease Mutations. <i>Cell</i> , 2020, 183, 1742-1756.	28.9	147
41	Germline Mutation of RPS20, Encoding a Ribosomal Protein, Causes Predisposition to Hereditary Nonpolyposis Colorectal Carcinoma Without DNA Mismatch Repair Deficiency. <i>Gastroenterology</i> , 2014, 147, 595-598.e5.	1.3	143
42	<i>HLA-DRB1*11</i> and variants of the MHC class II locus are strong risk factors for systemic juvenile idiopathic arthritis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15970-15975.	7.1	139
43	Length of Uninterrupted CAG, Independent of Polyglutamine Size, Results in Increased Somatic Instability, Hastening Onset of Huntington Disease. <i>American Journal of Human Genetics</i> , 2019, 104, 1116-1126.	6.2	130
44	Altered TAOK2 activity causes autism-related neurodevelopmental and cognitive abnormalities through RhoA signaling. <i>Molecular Psychiatry</i> , 2019, 24, 1329-1350.	7.9	128
45	Genetic architecture distinguishes systemic juvenile idiopathic arthritis from other forms of juvenile idiopathic arthritis: clinical and therapeutic implications. <i>Annals of the Rheumatic Diseases</i> , 2017, 76, 906-913.	0.9	123
46	Rearrangement bursts generate canonical gene fusions in bone and soft tissue tumors. <i>Science</i> , 2018, 361, .	12.6	121
47	Clinically relevant copy number variations detected in cerebral palsy. <i>Nature Communications</i> , 2015, 6, 7949.	12.8	120
48	A large data resource of genomic copy number variation across neurodevelopmental disorders. <i>Npj Genomic Medicine</i> , 2019, 4, 26.	3.8	118
49	PMP22 antisense oligonucleotides reverse Charcot-Marie-Tooth disease type 1A features in rodent models. <i>Journal of Clinical Investigation</i> , 2017, 128, 359-368.	8.2	117
50	Progress in the genetics of autism spectrum disorder. <i>Developmental Medicine and Child Neurology</i> , 2018, 60, 445-451.	2.1	116
51	ExpansionHunter Denovo: a computational method for locating known and novel repeat expansions in short-read sequencing data. <i>Genome Biology</i> , 2020, 21, 102.	8.8	114
52	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. <i>Biological Psychiatry</i> , 2022, 91, 313-327.	1.3	114
53	Central nervous system dysfunction in a mouse model of Fa2h deficiency. <i>Glia</i> , 2011, 59, 1009-1021.	4.9	112
54	Copy Number Variation in Obsessive-Compulsive Disorder and Tourette Syndrome: A Cross-Disorder Study. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2014, 53, 910-919.	0.5	111

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55	Complete Disruption of Autism-Susceptibility Genes by Gene Editing Predominantly Reduces Functional Connectivity of Isogenic Human Neurons. <i>Stem Cell Reports</i> , 2018, 11, 1211-1225.	4.8	111
56	Expression of multiple neuregulin transcripts in postnatal rat brains. <i>Journal of Comparative Neurology</i> , 1994, 349, 389-400.	1.6	106
57	Biological Overlap of Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder: Evidence From Copy Number Variants. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2014, 53, 761-770.e26.	0.5	105
58	Syndromic autism spectrum disorders: moving from a clinically defined to a molecularly defined approach. <i>Dialogues in Clinical Neuroscience</i> , 2017, 19, 353-371.	3.7	105
59	Compound heterozygous mutations in the noncoding RNU4ATAC cause Roifman Syndrome by disrupting minor intron splicing. <i>Nature Communications</i> , 2015, 6, 8718.	12.8	104
60	Biallelic mutations in DNAJC21 cause Shwachman-Diamond syndrome. <i>Blood</i> , 2017, 129, 1557-1562.	1.4	104
61	Axons modulate the expression of transforming growth factor-betas in Schwann cells. <i>Glia</i> , 1993, 8, 265-276.	4.9	103
62	Delineating the 15q13.3 microdeletion phenotype: a case series and comprehensive review of the literature. <i>Genetics in Medicine</i> , 2015, 17, 149-157.	2.4	103
63	Colorectal carcinomas in mice lacking the catalytic subunit of PI(3)K β . <i>Nature</i> , 2000, 406, 897-902.	27.8	102
64	Risk factors for autism: translating genomic discoveries into diagnostics. <i>Human Genetics</i> , 2011, 130, 123-148.	3.8	102
65	Biallelic mutations in SORD cause a common and potentially treatable hereditary neuropathy with implications for diabetes. <i>Nature Genetics</i> , 2020, 52, 473-481.	21.4	97
66	Physical mapping of the holoprosencephaly critical region on chromosome 7q36. <i>Nature Genetics</i> , 1993, 3, 247-251.	21.4	95
67	Defects of mutant DNMT1 are linked to a spectrum of neurological disorders. <i>Brain</i> , 2015, 138, 845-861.	7.6	94
68	A novel recessive <i>Nefl</i> mutation causes a severe, early-onset axonal neuropathy. <i>Annals of Neurology</i> , 2009, 66, 759-770.	5.3	90
69	Using common genetic variation to examine phenotypic expression and risk prediction in 22q11.2 deletion syndrome. <i>Nature Medicine</i> , 2020, 26, 1912-1918.	30.7	90
70	Periodic reanalysis of whole-genome sequencing data enhances the diagnostic advantage over standard clinical genetic testing. <i>European Journal of Human Genetics</i> , 2018, 26, 740-744.	2.8	88
71	A framework for an evidence-based gene list relevant to autism spectrum disorder. <i>Nature Reviews Genetics</i> , 2020, 21, 367-376.	16.3	83
72	De novo and rare inherited copy-number variations in the hemiplegic form of cerebral palsy. <i>Genetics in Medicine</i> , 2018, 20, 172-180.	2.4	82

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73	OTUD7A Regulates Neurodevelopmental Phenotypes in the 15q13.3 Microdeletion Syndrome. American Journal of Human Genetics, 2018, 102, 278-295.	6.2	81
74	Loss of heterozygosity and reduced expression of the CUTL1 gene in uterine leiomyomas. Oncogene, 1997, 14, 2355-2365.	5.9	80
75	Neurofascin antibodies in autoimmune, genetic, and idiopathic neuropathies. Neurology, 2018, 90, e31-e38.	1.1	78
76	Rare Genome-Wide Copy Number Variation and Expression of Schizophrenia in 22q11.2 Deletion Syndrome. American Journal of Psychiatry, 2017, 174, 1054-1063.	7.2	77
77	Paraoxonase-2 Gene (PON2) G148 Variant Associated with Elevated Fasting Plasma Glucose in Noninsulin-Dependent Diabetes Mellitus 1. Journal of Clinical Endocrinology and Metabolism, 1997, 82, 3373-3377.	3.6	75
78	A high-resolution copy-number variation resource for clinical and population genetics. Genetics in Medicine, 2015, 17, 747-752.	2.4	73
79	CNTN5-/+or EHMT2-/+human iPSC-derived neurons from individuals with autism develop hyperactive neuronal networks. ELife, 2019, 8, .	6.0	72
80	CHD2 haploinsufficiency is associated with developmental delay, intellectual disability, epilepsy and neurobehavioural problems. Journal of Neurodevelopmental Disorders, 2014, 6, 9.	3.1	71
81	Bone marrow failure and developmental delay caused by mutations in poly(A)-specific ribonuclease (<i>PARN</i>). Journal of Medical Genetics, 2015, 52, 738-748.	3.2	71
82	Molecular characterization of NRXN1 deletions from 19,263 clinical microarray cases identifies exons important for neurodevelopmental disease expression. Genetics in Medicine, 2017, 19, 53-61.	2.4	70
83	Genotype-phenotype correlations in <i>SCN8A</i> -related disorders reveal prognostic and therapeutic implications. Brain, 2022, 145, 2991-3009.	7.6	69
84	15q11.2 Duplication Encompassing Only the <i>UBE3A</i> Gene Is Associated with Developmental Delay and Neuropsychiatric Phenotypes. Human Mutation, 2015, 36, 689-693.	2.5	67
85	Lethal Disorder of Mitochondrial Fission Caused by Mutations in DNM1L. Journal of Pediatrics, 2016, 171, 313-316.e2.	1.8	67
86	Delineation of multiple deleted regions in 7q in myeloid disorders. Genes Chromosomes and Cancer, 1999, 25, 384-392.	2.8	65
87	Myopathy associated BAG3 mutations lead to protein aggregation by stalling Hsp70 networks. Nature Communications, 2018, 9, 5342.	12.8	65
88	Molecular specializations at nodes and paranodes in peripheral nerve. , 1996, 34, 452-461.		64
89	Intrathecal gene therapy rescues a model of demyelinating peripheral neuropathy. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2421-9.	7.1	63
90	Structural neuroimaging correlates of social deficits are similar in autism spectrum disorder and attention-deficit/hyperactivity disorder: analysis from the POND Network. Translational Psychiatry, 2019, 9, 72.	4.8	63

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91	A microcosting and cost-consequence analysis of clinical genomic testing strategies in autism spectrum disorder. <i>Genetics in Medicine</i> , 2017, 19, 1268-1275.	2.4	62
92	t(7;12)(q36;p13), a new recurrent translocation involving ETV6 in infant leukemia. <i>Genes Chromosomes and Cancer</i> , 2000, 29, 325-332.	2.8	60
93	Nodes, paranodes and neuropathies. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2018, 89, 61-71.	1.9	60
94	Mutations in ATP1A1 Cause Dominant Charcot-Marie-Tooth Type 2. <i>American Journal of Human Genetics</i> , 2018, 102, 505-514.	6.2	59
95	DNA Methylation Signature for EZH2 Functionally Classifies Sequence Variants in Three PRC2 Complex Genes. <i>American Journal of Human Genetics</i> , 2020, 106, 596-610.	6.2	59
96	Remote Ischemic Preconditioning in Children Undergoing Cardiac Surgery With Cardiopulmonary Bypass: A Single-Center Double-Blinded Randomized Trial. <i>Journal of the American Heart Association</i> , 2014, 3, .	3.7	58
97	<i>PMP22</i> mutations cause abnormal mitochondrial protein processing in patients with non-progressive cerebellar ataxia. <i>Brain</i> , 2015, 138, 1505-1517.	7.6	58
98	Copy Number Variable MicroRNAs in Schizophrenia and Their Neurodevelopmental Gene Targets. <i>Biological Psychiatry</i> , 2015, 77, 158-166.	1.3	58
99	Haploinsufficiency of vascular endothelial growth factor related signaling genes is associated with tetralogy of Fallot. <i>Genetics in Medicine</i> , 2019, 21, 1001-1007.	2.4	58
100	Gene structure of the human MET proto-oncogene. <i>Oncogene</i> , 1997, 15, 1583-1586.	5.9	57
101	The Personal Genome Project Canada: findings from whole genome sequences of the inaugural 56 participants. <i>Cmaj</i> , 2018, 190, E126-E136.	2.0	57
102	Synaptic Dysfunction in Human Neurons With Autism-Associated Deletions in PTCHD1-AS. <i>Biological Psychiatry</i> , 2020, 87, 139-149.	1.3	57
103	Copy number variation in Han Chinese individuals with autism spectrum disorder. <i>Journal of Neurodevelopmental Disorders</i> , 2014, 6, 34.	3.1	55
104	Uncovering obsessive-compulsive disorder risk genes in a pediatric cohort by high-resolution analysis of copy number variation. <i>Journal of Neurodevelopmental Disorders</i> , 2016, 8, 36.	3.1	55
105	Whole-Exome Sequencing and Targeted Copy Number Analysis in Primary Ciliary Dyskinesia. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1775-1781.	1.8	53
106	Axonal pathology in demyelinating diseases. <i>Annals of Neurology</i> , 1999, 45, 6-7.	5.3	52
107	Laforin is a cell membrane and endoplasmic reticulum-associated protein tyrosine phosphatase. <i>Annals of Neurology</i> , 2001, 49, 271-275.	5.3	52
108	Target-enrichment sequencing and copy number evaluation in inherited polyneuropathy. <i>Neurology</i> , 2016, 86, 1762-1771.	1.1	52

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109	Peripheral neuropathy in complex inherited diseases: an approach to diagnosis. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2017, 88, 846-863.	1.9	51
110	The Cardiac Genome Clinic: implementing genome sequencing in pediatric heart disease. <i>Genetics in Medicine</i> , 2020, 22, 1015-1024.	2.4	51
111	New insights into the regulatory function of CYFIP1 in the context of WAVE- and FMRP-containing complexes. <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 463-474.	2.4	49
112	Mutations in RAB39B in individuals with intellectual disability, autism spectrum disorder, and macrocephaly. <i>Molecular Autism</i> , 2017, 8, 59.	4.9	49
113	Complex Copy Number Variation of <i>AMY1</i> does not Associate with Obesity in two East Asian Cohorts. <i>Human Mutation</i> , 2016, 37, 669-678.	2.5	48
114	Frequent appearance of novel protein-coding sequences by frameshift translation. <i>Genomics</i> , 2006, 88, 690-697.	2.9	47
115	Linked Charcot-Marie-Tooth disease. <i>Journal of the Peripheral Nervous System</i> , 2012, 17, 9-13.	3.1	47
116	CAOS—Episodic Cerebellar Ataxia, Areflexia, Optic Atrophy, and Sensorineural Hearing Loss. <i>Journal of Child Neurology</i> , 2015, 30, 1749-1756.	1.4	47
117	Rare Variants in MME, Encoding Metalloprotease Neprilysin, Are Linked to Late-Onset Autosomal-Dominant Axonal Polyneuropathies. <i>American Journal of Human Genetics</i> , 2016, 99, 607-623.	6.2	47
118	Genome Sequencing as a Diagnostic Test in Children With Unexplained Medical Complexity. <i>JAMA Network Open</i> , 2020, 3, e2018109.	5.9	47
119	Complete loss of the DNAJB6 G/F domain and novel missense mutations cause distal-onset DNAJB6 myopathy. <i>Acta Neuropathologica Communications</i> , 2015, 3, 44.	5.2	45
120	Whole-Genome Sequencing Suggests Schizophrenia Risk Mechanisms in Humans with 22q11.2 Deletion Syndrome. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2453-2461.	1.8	43
121	Internodal specializations of myelinated axons in the central nervous system. <i>Cell and Tissue Research</i> , 2001, 305, 53-66.	2.9	42
122	Loss of function of the cytoplasmic isoform of the protein laforin (EPM2A) causes Lafora progressive myoclonus epilepsy. <i>Human Mutation</i> , 2004, 23, 170-176.	2.5	42
123	Analysis of the human Sonic Hedgehog coding and promoter regions in sacral agenesis, triphalangeal thumb, and mirror polydactyly. <i>Human Genetics</i> , 1998, 102, 387-392.	3.8	41
124	Microdeletions of <i>ELP4</i> Are Associated with Language Impairment, Autism Spectrum Disorder, and Mental Retardation. <i>Human Mutation</i> , 2015, 36, 842-850.	2.5	41
125	Genome sequencing as a platform for pharmacogenetic genotyping: a pediatric cohort study. <i>Npj Genomic Medicine</i> , 2017, 2, 19.	3.8	41
126	Germline and somatic mutations in <i>STXBP1</i> with diverse neurodevelopmental phenotypes. <i>Neurology: Genetics</i> , 2017, 3, e199.	1.9	41

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127	Axons modulate the expression of proteolipid protein in the CNS. <i>Journal of Neuroscience Research</i> , 1992, 32, 138-148.	2.9	40
128	Copy-number variations are enriched for neurodevelopmental genes in children with developmental coordination disorder. <i>Journal of Medical Genetics</i> , 2016, 53, 812-819.	3.2	40
129	Implication of <i>LRRC4C</i> and <i>DPP6</i> in neurodevelopmental disorders. <i>American Journal of Medical Genetics, Part A</i> , 2017, 173, 395-406.	1.2	40
130	Prevalence and orthopedic management of foot and ankle deformities in Charcot-Marie-Tooth disease. <i>Muscle and Nerve</i> , 2018, 57, 255-259.	2.2	39
131	Natural history of Charcot-Marie-Tooth disease type 2A: a large international multicentre study. <i>Brain</i> , 2020, 143, 3589-3602.	7.6	39
132	X-linked vacuolar myopathies: Two separate loci and refined genetic mapping. <i>Annals of Neurology</i> , 2000, 47, 666-669.	5.3	38
133	Intra-neural <i>CJB1</i> gene delivery improves nerve pathology in a model of <i>X-linked CMT</i> . <i>Annals of Neurology</i> , 2015, 78, 303-316.	5.3	38
134	<i>De novo PMP2</i> mutations in families with type 1 Charcot-Marie-Tooth disease. <i>Brain</i> , 2016, 139, 1649-1656.	7.6	37
135	Oxytocin Receptor Polymorphisms are Differentially Associated with Social Abilities across Neurodevelopmental Disorders. <i>Scientific Reports</i> , 2017, 7, 11618.	3.3	36
136	Environmental exposures associated with elevated risk for autism spectrum disorder may augment the burden of deleterious <i>de novo</i> mutations among probands. <i>Molecular Psychiatry</i> , 2022, 27, 710-730.	7.9	36
137	Indexing Effects of Copy Number Variation on Genes Involved in Developmental Delay. <i>Scientific Reports</i> , 2016, 6, 28663.	3.3	35
138	<i>ARHGEF9</i> disease. <i>Neurology: Genetics</i> , 2017, 3, e148.	1.9	35
139	A multicenter retrospective study of Charcot-Marie-Tooth disease type 4B (CMT4B) associated with mutations in myotubularin-related proteins (MTMRs). <i>Annals of Neurology</i> , 2019, 86, 55-67.	5.3	35
140	Characterization of the human myeloid leukemia-derived cell line GF-D8 by multiplex fluorescence in situ hybridization, subtelomeric probes, and comparative genomic hybridization. , 1999, 24, 213-221.		34
141	A novel <i>AARS</i> mutation in a family with dominant myeloneuropathy. <i>Neurology</i> , 2015, 84, 2040-2047.	1.1	33
142	Variation in <i>SIPA1L2</i> is correlated with phenotype modification in Charcot-Marie-Tooth disease type 1A. <i>Annals of Neurology</i> , 2019, 85, 316-330.	5.3	33
143	Maturation-dependent apoptotic cell death of oligodendrocytes in myelin-deficient rats. , 1998, 54, 623-634.		32
144	Caspr2 autoantibodies target multiple epitopes. <i>Neurology: Neuroimmunology and Neuroinflammation</i> , 2015, 2, e127.	6.0	32

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145	Care and cost consequences of pediatric whole genome sequencing compared to chromosome microarray. <i>European Journal of Human Genetics</i> , 2017, 25, 1303-1312.	2.8	32
146	Impact of DNA source on genetic variant detection from human whole-genome sequencing data. <i>Journal of Medical Genetics</i> , 2019, 56, 809-817.	3.2	32
147	Control of Long-Term Synaptic Potentiation and Learning by Alternative Splicing of the NMDA Receptor Subunit GluN1. <i>Cell Reports</i> , 2019, 29, 4285-4294.e5.	6.4	32
148	De novo missense variants in RAC3 cause a novel neurodevelopmental syndrome. <i>Genetics in Medicine</i> , 2019, 21, 1021-1026.	2.4	32
149	The Autism Simplex Collection: an international, expertly phenotyped autism sample for genetic and phenotypic analyses. <i>Molecular Autism</i> , 2014, 5, 34.	4.9	31
150	Variable phenotype expression in a family segregating microdeletions of the NRXN1 and MBD5 autism spectrum disorder susceptibility genes. <i>Npj Genomic Medicine</i> , 2017, 2, .	3.8	31
151	Chitayat-Hall and Schaaf-Yang syndromes: a common aetiology: expanding the phenotype of <i>MAGEL2</i>-related disorders. <i>Journal of Medical Genetics</i> , 2018, 55, 316-321.	3.2	31
152	Pathogenic WDFY3 variants cause neurodevelopmental disorders and opposing effects on brain size. <i>Brain</i> , 2019, 142, 2617-2630.	7.6	31
153	Truncating SRCAP variants outside the Floating-Harbor syndrome locus cause a distinct neurodevelopmental disorder with a specific DNA methylation signature. <i>American Journal of Human Genetics</i> , 2021, 108, 1053-1068.	6.2	31
154	Development of a high-resolution Y-chromosome microarray for improved male infertility diagnosis. <i>Fertility and Sterility</i> , 2014, 101, 1079-1085.e3.	1.0	30
155	Prenatal growth restriction, retinal dystrophy, diabetes insipidus and white matter disease: expanding the spectrum of PRPS1-related disorders. <i>European Journal of Human Genetics</i> , 2015, 23, 310-316.	2.8	30
156	De novo exon 1 deletion of <i>AUTS2</i> gene in a patient with autism spectrum disorder and developmental delay: A case report and a brief literature review. <i>American Journal of Medical Genetics, Part A</i> , 2015, 167, 1381-1385.	1.2	30
157	Epileptic Encephalopathy Caused by Mutations in the Guanine Nucleotide Exchange Factor DENND5A. <i>American Journal of Human Genetics</i> , 2016, 99, 1359-1367.	6.2	30
158	Impact of IQ on the diagnostic yield of chromosomal microarray in a community sample of adults with schizophrenia. <i>Genome Medicine</i> , 2017, 9, 105.	8.2	30
159	Myelinated axons fail to develop properly in a genetically authentic mouse model of Charcot-Marie-Tooth disease type 2E. <i>Experimental Neurology</i> , 2018, 308, 13-25.	4.1	30
160	Schwann cell-derived periostin promotes autoimmune peripheral polyneuropathy via macrophage recruitment. <i>Journal of Clinical Investigation</i> , 2018, 128, 4727-4741.	8.2	30
161	Structural organization and chromosomal localization of the human Na,K-ATPase β 3 subunit gene and pseudogene. <i>Mammalian Genome</i> , 1998, 9, 136-143.	2.2	29
162	Expanding the neurodevelopmental phenotypes of individuals with de novo KMT2A variants. <i>Npj Genomic Medicine</i> , 2019, 4, 9.	3.8	29

#	ARTICLE	IF	CITATIONS
163	Subgroup-specific alternative splicing in medulloblastoma. <i>Acta Neuropathologica</i> , 2012, 123, 485-499.	7.7	28
164	DIXDC1 Phosphorylation and Control of Dendritic Morphology Are Impaired by Rare Genetic Variants. <i>Cell Reports</i> , 2016, 17, 1892-1904.	6.4	28
165	Shared genetic risk between eating disorder and substance use related phenotypes: Evidence from genome-wide association studies. <i>Addiction Biology</i> , 2021, 26, e12880.	2.6	28
166	Copy Number Variation Analysis of 100 Twin Pairs Enriched for Neurodevelopmental Disorders. <i>Twin Research and Human Genetics</i> , 2018, 21, 1-11.	0.6	27
167	Communicating complex genomic information: A counselling approach derived from research experience with Autism Spectrum Disorder. <i>Patient Education and Counseling</i> , 2018, 101, 352-361.	2.2	27
168	Microduplications at the pseudoautosomal <i>SHOX</i> locus in autism spectrum disorders and related neurodevelopmental conditions. <i>Journal of Medical Genetics</i> , 2016, 53, 536-547.	3.2	26
169	Genome-wide rare copy number variations contribute to genetic risk for transposition of the great arteries. <i>International Journal of Cardiology</i> , 2016, 204, 115-121.	1.7	26
170	Heterogeneity in clinical sequencing tests marketed for autism spectrum disorders. <i>Npj Genomic Medicine</i> , 2018, 3, 27.	3.8	26
171	DNA Methylation of the Oxytocin Receptor Across Neurodevelopmental Disorders. <i>Journal of Autism and Developmental Disorders</i> , 2021, 51, 3610-3623.	2.7	26
172	Holoprosencephaly, sacral anomalies, and situs ambiguus in an infant with partial monosomy 7q/trisomy 2p and <i>SHH</i> and <i>HLXB9</i> haploinsufficiency. <i>Clinical Genetics</i> , 2000, 57, 388-393.	2.0	25
173	Rare de novo deletion of metabotropic glutamate receptor 7 (<i>GRM7</i>) gene in a patient with autism spectrum disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2015, 168, 258-264.	1.7	25
174	New insights into DNA methylation signatures: SMARCA2 variants in Nicolaides-Baraitser syndrome. <i>BMC Medical Genomics</i> , 2019, 12, 105.	1.5	25
175	Axonal Charcot-Marie-Tooth Disease: from Common Pathogenic Mechanisms to Emerging Treatment Opportunities. <i>Neurotherapeutics</i> , 2021, 18, 2269-2285.	4.4	25
176	Precision Health Resource of Control iPSC Lines for Versatile Multilineage Differentiation. <i>Stem Cell Reports</i> , 2019, 13, 1126-1141.	4.8	24
177	Proteolipid protein mRNA stability is regulated by axonal contact in the rodent peripheral nervous system. <i>Journal of Neurobiology</i> , 2000, 44, 7-19.	3.6	23
178	Genetic variation in paraoxonase 2 is associated with variation in plasma lipoproteins in Canadian Ojibwe. <i>Clinical Genetics</i> , 1998, 54, 394-399.	2.0	23
179	Genome-wide copy number variation analysis identifies novel candidate loci associated with pediatric obesity. <i>European Journal of Human Genetics</i> , 2018, 26, 1588-1596.	2.8	23
180	Genes and Pathways Implicated in Tetralogy of Fallot Revealed by Ultra-Rare Variant Burden Analysis in 231 Genome Sequences. <i>Frontiers in Genetics</i> , 2020, 11, 957.	2.3	23

#	ARTICLE	IF	CITATIONS
181	Chronic multiple paraneoplastic syndromes. <i>Muscle and Nerve</i> , 2000, 23, 1767-1772.	2.2	21
182	Finding the Causes of Inherited Neuropathies. <i>Archives of Neurology</i> , 2006, 63, 812.	4.5	21
183	<i>MED23</i> associated refractory epilepsy successfully treated with the ketogenic diet. <i>American Journal of Medical Genetics, Part A</i> , 2016, 170, 2421-2425.	1.2	21
184	Phenotypic Association Analyses With Copy Number Variation in Recurrent Depressive Disorder. <i>Biological Psychiatry</i> , 2016, 79, 329-336.	1.3	21
185	A Unique Mutation in <i>Connexin32</i> Associated with Severe, Early Onset CMTX in a Heterozygous Female. <i>Annals of the New York Academy of Sciences</i> , 1999, 883, 481-484.	3.8	20
186	Modification of representational difference analysis applied to the isolation of forskolin-regulated genes from Schwann cells. <i>Journal of Neuroscience Research</i> , 2001, 63, 516-524.	2.9	20
187	Integrated Genomics Identifies Convergence of Ankylosing Spondylitis with Global Immune Mediated Disease Pathways. <i>Scientific Reports</i> , 2015, 5, 10314.	3.3	20
188	Genetic test utilization and diagnostic yield in adult patients with neurological disorders. <i>Neurogenetics</i> , 2018, 19, 105-110.	1.4	20
189	A genome-wide linkage study of autism spectrum disorder and the broad autism phenotype in extended pedigrees. <i>Journal of Neurodevelopmental Disorders</i> , 2018, 10, 20.	3.1	20
190	Haploinsufficiency in the <i>ANKS1B</i> gene encoding AIDA-1 leads to a neurodevelopmental syndrome. <i>Nature Communications</i> , 2019, 10, 3529.	12.8	20
191	Genome sequencing as a diagnostic test. <i>Cmaj</i> , 2021, 193, E1626-E1629.	2.0	20
192	Single-cell transcriptome identifies molecular subtype of autism spectrum disorder impacted by de novo loss-of-function variants regulating glial cells. <i>Human Genomics</i> , 2021, 15, 68.	2.9	20
193	Genome-wide tandem repeat expansions contribute to schizophrenia risk. <i>Molecular Psychiatry</i> , 2022, 27, 3692-3698.	7.9	20
194	Identification of an amplified gene cluster in glioma including two novel amplified genes isolated by exon trapping. <i>Human Genetics</i> , 1997, 101, 190-197.	3.8	19
195	Modifier Gene Candidates in Charcot-Marie-Tooth Disease Type 1A: A Case-Only Genome-Wide Association Study. <i>Journal of Neuromuscular Diseases</i> , 2019, 6, 201-211.	2.6	19
196	<i>De Novo</i> Genome and Transcriptome Assembly of the Canadian Beaver (<i>Castor canadensis</i>). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 755-773.	1.8	18
197	<i>STXBP1</i> encephalopathy is associated with awake bruxism. <i>Epilepsy and Behavior</i> , 2019, 92, 121-124.	1.7	18
198	Analysis of recent shared ancestry in a familial cohort identifies coding and noncoding autism spectrum disorder variants. <i>Npj Genomic Medicine</i> , 2022, 7, 13.	3.8	18

#	ARTICLE	IF	CITATIONS
199	The Human Homologue of Flamingo, EGFL2, Encodes a Brain-Expressed Large Cadherin-Like Protein with Epidermal Growth Factor-Like Domains, and Maps to Chromosome 1p13.3-p21.1. <i>DNA Research</i> , 2000, 7, 233-235.	3.4	17
200	Activated immune response in an inherited leukodystrophy disease caused by the loss of oligodendrocyte gap junctions. <i>Neurobiology of Disease</i> , 2015, 82, 86-98.	4.4	17
201	Sleep phenotype of individuals with autism spectrum disorder bearing mutations in the <i>PER2</i> circadian rhythm gene. <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 1120-1130.	1.2	17
202	Whole-genome sequencing suggests mechanisms for 22q11.2 deletion-associated Parkinson's disease. <i>PLoS ONE</i> , 2017, 12, e0173944.	2.5	17
203	Human chromosome 7 circa 2004: a model for structural and functional studies of the human genome. <i>Human Molecular Genetics</i> , 2004, 13, R303-R313.	2.9	16
204	Use of clinical chromosomal microarray in Chinese patients with autism spectrum disorder—implications of a copy number variation involving <i>DPP10</i> . <i>Molecular Autism</i> , 2017, 8, 31.	4.9	16
205	Association of <i>IMMP2L</i> deletions with autism spectrum disorder: A trio family study and meta-analysis. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2018, 177, 93-100.	1.7	16
206	Genome-wide analysis identifies rare copy number variations associated with inflammatory bowel disease. <i>PLoS ONE</i> , 2019, 14, e0217846.	2.5	16
207	A Third Linear Association Between <i>Olduvai</i> (<i>DUF1220</i>) Copy Number and Severity of the Classic Symptoms of Inherited Autism. <i>American Journal of Psychiatry</i> , 2019, 176, 643-650.	7.2	16
208	Maintenance of hypomethylation status and preferential expression of exogenous human <i>MDR1/PGY1</i> gene in mouse L cells by YAC mediated transfer. <i>Somatic Cell and Molecular Genetics</i> , 1997, 23, 259-274.	0.7	15
209	Genomic imbalance in the centromeric 11p15 imprinting center in three families: Further evidence of a role for <i>IC2</i> as a cause of Russell's Silver syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2016, 170, 2731-2739.	1.2	15
210	De novo pathogenic variant in <i>TUBB2A</i> presenting with arthrogryposis multiplex congenita, brain abnormalities, and severe developmental delay. , 2017, 173, 2725-2730.		15
211	Copy number variation in fetal alcohol spectrum disorder. <i>Biochemistry and Cell Biology</i> , 2018, 96, 161-166.	2.0	15
212	Enrichment of loss-of-function and copy number variants in ventricular cardiomyopathy genes in lone atrial fibrillation. <i>Europace</i> , 2021, 23, 844-850.	1.7	15
213	What a finding of gene copy number variation can add to the diagnosis of developmental neuropsychiatric disorders. <i>Current Opinion in Genetics and Development</i> , 2021, 68, 18-25.	3.3	15
214	Clinical Genetic Risk Variants Inform a Functional Protein Interaction Network for Tetralogy of Fallot. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003410.	3.6	15
215	<i>TUBB4A</i> mutations result in both glial and neuronal degeneration in an H-ABC leukodystrophy mouse model. <i>ELife</i> , 2020, 9, .	6.0	15
216	DNA methylation signature associated with Bohring-Opitz syndrome: a new tool for functional classification of variants in <i>ASXL</i> genes. <i>European Journal of Human Genetics</i> , 2022, 30, 695-702.	2.8	15

#	ARTICLE	IF	CITATIONS
217	Carpal tunnel syndrome in inherited neuropathies: A retrospective survey. <i>Muscle and Nerve</i> , 2018, 57, 388-394.	2.2	14
218	Long-Read Sequencing Improves the Detection of Structural Variations Impacting Complex Non-Coding Elements of the Genome. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2060.	4.1	14
219	Whole genome sequencing delineates regulatory, copy number, and cryptic splice variants in early onset cardiomyopathy. <i>Npj Genomic Medicine</i> , 2022, 7, 18.	3.8	14
220	Recurrent duplications of the annexin A1 gene (ANXA1) in autism spectrum disorders. <i>Molecular Autism</i> , 2014, 5, 28.	4.9	13
221	Prevalence of Creatine Deficiency Syndromes in Children With Nonsyndromic Autism. <i>Pediatrics</i> , 2016, 137, .	2.1	13
222	Variant pathogenicity evaluation in the community-driven Inherited Neuropathy Variant Browser. <i>Human Mutation</i> , 2018, 39, 635-642.	2.5	13
223	Copy number variations in a Brazilian cohort with autism spectrum disorders highlight the contribution of cell adhesion genes. <i>Clinical Genetics</i> , 2022, 101, 134-141.	2.0	13
224	Clinical, neurophysiological and morphological study of dominant intermediate Charcot-Marie-Tooth type C neuropathy. <i>Journal of Neurology</i> , 2016, 263, 467-476.	3.6	12
225	A recurrent GARS mutation causes distal hereditary motor neuropathy. <i>Journal of the Peripheral Nervous System</i> , 2019, 24, 320-323.	3.1	12
226	A recessive Trim2 mutation causes an axonal neuropathy in mice. <i>Neurobiology of Disease</i> , 2020, 140, 104845.	4.4	12
227	Temporal trends and yield of clinical diagnostic genetic testing in adult neurology. <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 2922-2928.	1.2	12
228	Contribution of Multiple Inherited Variants to Autism Spectrum Disorder (ASD) in a Family with 3 Affected Siblings. <i>Genes</i> , 2021, 12, 1053.	2.4	12
229	Bone Marrow Failure and Developmental Delay Caused By Mutations in Poly(A)-Specific Ribonuclease. <i>Blood</i> , 2015, 126, 2404-2404.	1.4	11
230	Chromosomal microarray analysis of 410 Han Chinese patients with autism spectrum disorder or unexplained intellectual disability and developmental delay. <i>Npj Genomic Medicine</i> , 2022, 7, 1.	3.8	11
231	Physical mapping of the chromosome 7 breakpoint region in an SLOS patient with t(7;20) (q32.1;q13.2). , 1997, 68, 279-281.		10
232	Rare copy number variations in an adult with transposition of the great arteries emphasize the importance of updated genetic assessments in syndromic congenital cardiac disease. <i>International Journal of Cardiology</i> , 2016, 203, 516-518.	1.7	10
233	<i>HLX</i> is a candidate gene for a pattern of anomalies associated with congenital diaphragmatic hernia, short bowel, and asplenia. <i>American Journal of Medical Genetics, Part A</i> , 2017, 173, 3070-3074.	1.2	10
234	The clinical impact of copy number variants in inherited bone marrow failure syndromes. <i>Npj Genomic Medicine</i> , 2017, 2, .	3.8	10

#	ARTICLE	IF	CITATIONS
235	Characterization of Large Copy Number Variation in Mexican Type 2 Diabetes subjects. Scientific Reports, 2017, 7, 17105.	3.3	10
236	VikNGS: a C++ variant integration kit for next generation sequencing association analysis. Bioinformatics, 2020, 36, 1283-1285.	4.1	10
237	RCL1 copy number variants are associated with a range of neuropsychiatric phenotypes. Molecular Psychiatry, 2021, 26, 1706-1718.	7.9	10
238	Genome sequencing for detection of pathogenic deep intronic variation: A clinical case report illustrating opportunities and challenges. American Journal of Medical Genetics, Part A, 2021, 185, 3129-3135.	1.2	10
239	Molecular Characterization of Distinct Hot Spot Regions on Chromosome 7q in Myeloid Leukemias.. Blood, 2006, 108, 2349-2349.	1.4	10
240	Improving imputation in disease-relevant regions: lessons from cystic fibrosis. Npj Genomic Medicine, 2018, 3, 8.	3.8	9
241	Rare copy number variation in extremely impulsively violent males. Genes, Brain and Behavior, 2019, 18, e12536.	2.2	9
242	Biallelic mutations in EXOC3L2 cause a novel syndrome that affects the brain, kidney and blood. Journal of Medical Genetics, 2019, 56, 340-346.	3.2	9
243	Isoform-specific loss of dystonin causes hereditary motor and sensory neuropathy. Neurology: Genetics, 2020, 6, e496.	1.9	9
244	Discovery of genomic variation across a generation. Human Molecular Genetics, 2021, 30, R174-R186.	2.9	9
245	A recurrent SHANK3 frameshift variant in Autism Spectrum Disorder. Npj Genomic Medicine, 2021, 6, 91.	3.8	9
246	De novo large rare copy-number variations contribute to conotruncal heart disease in Chinese patients. Npj Genomic Medicine, 2016, 1, 16033.	3.8	8
247	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
248	Reliability of the <sc>Charcotâ€Marieâ€Tooth</sc> functional outcome measure. Journal of the Peripheral Nervous System, 2020, 25, 288-291.	3.1	8
249	Whole exome sequencing uncovered highly penetrant recessive mutations for a spectrum of rare genetic pediatric diseases in Bangladesh. Npj Genomic Medicine, 2021, 6, 14.	3.8	8
250	Rare Copy Number Variants Identified Suggest the Regulating Pathways in Hypertension-Related Left Ventricular Hypertrophy. PLoS ONE, 2016, 11, e0148755.	2.5	8
251	Deletion of Loss-of-Functionâ€Intolerant Genes and Risk of 5 Psychiatric Disorders. JAMA Psychiatry, 2022, 79, 78.	11.0	8
252	Febrile ataxia and myokymia broaden the SPG26 hereditary spastic paraplegia phenotype. Neurology: Genetics, 2017, 3, e156.	1.9	7

#	ARTICLE	IF	CITATIONS
253	Hyperventilation-athetosis in <i>ASXL3</i> deficiency (Bainbridge-Ropers) syndrome. <i>Neurology: Genetics</i> , 2017, 3, e189.	1.9	7
254	Yield of next-generation neuropathy gene panels in axonal neuropathies. <i>Journal of the Peripheral Nervous System</i> , 2019, 24, 324-329.	3.1	7
255	Segregating patterns of copy number variations in extended autism spectrum disorder (ASD) pedigrees. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2020, 183, 268-276.	1.7	7
256	Perceived utility of biological testing for autism spectrum disorder is associated with child and family functioning. <i>Research in Developmental Disabilities</i> , 2020, 100, 103605.	2.2	7
257	Adaptation and validation of the Genetic Counseling Outcome Scale for autism spectrum disorders and related conditions. <i>Journal of Genetic Counseling</i> , 2021, 30, 305-318.	1.6	7
258	Inducible knockout of <i>Clec16a</i> in mice results in sensory neurodegeneration. <i>Scientific Reports</i> , 2021, 11, 9319.	3.3	7
259	Mutational Landscape of Autism Spectrum Disorder Brain Tissue. <i>Genes</i> , 2022, 13, 207.	2.4	7
260	Novel Population Specific Autosomal Copy Number Variation and Its Functional Analysis amongst Negritos from Peninsular Malaysia. <i>PLoS ONE</i> , 2014, 9, e100371.	2.5	6
261	Prenatal genomic microarray and sequencing in Canadian medical practice: towards consensus. <i>Journal of Medical Genetics</i> , 2015, 52, 585-586.	3.2	6
262	Copy Number Variation in Tourette Syndrome. <i>Neuron</i> , 2017, 94, 1041-1043.	8.1	6
263	Paternal uniparental disomy of chromosome 19 in a pair of monozygotic diamniotic twins with dysmorphic features and developmental delay. <i>Journal of Medical Genetics</i> , 2018, 55, 847-852.	3.2	6
264	POLG mutations presenting as Charcot-Marie-Tooth disease. <i>Journal of the Peripheral Nervous System</i> , 2019, 24, 213-218.	3.1	6
265	Rare copy number variations affecting the synaptic gene <i>DMXL2</i> in neurodevelopmental disorders. <i>Journal of Neurodevelopmental Disorders</i> , 2019, 11, 3.	3.1	6
266	A Distributed Whole Genome Sequencing Benchmark Study. <i>Frontiers in Genetics</i> , 2020, 11, 612515.	2.3	6
267	Modeling neuronal consequences of autism-associated gene regulatory variants with human induced pluripotent stem cells. <i>Molecular Autism</i> , 2020, 11, 33.	4.9	6
268	Mutations in <i>trp13</i> , the homologue of <i>TRPC6</i> autism candidate gene, causes autism-like behavioral deficits in <i>Drosophila</i> . <i>Molecular Psychiatry</i> , 2022, 27, 3328-3342.	7.9	6
269	A mutation in the heptad repeat 2 domain of <i>MFN2</i> in a large CMT2A family. <i>Journal of the Peripheral Nervous System</i> , 2018, 23, 36-39.	3.1	5
270	Association between distress and knowledge among parents of autistic children. <i>PLoS ONE</i> , 2019, 14, e0223119.	2.5	5

#	ARTICLE	IF	CITATIONS
271	A novel MFN2 mutation causes variable clinical severity in a multi-generational CMT2 family. <i>Neuromuscular Disorders</i> , 2019, 29, 134-137.	0.6	5
272	An Epigenetically Distinct Subset of Children With Autism Spectrum Disorder Resulting From Differences in Blood Cell Composition. <i>Frontiers in Neurology</i> , 2021, 12, 612817.	2.4	5
273	Delineation of a novel neurodevelopmental syndrome associated with <i>PAX5</i> haploinsufficiency. <i>Human Mutation</i> , 2022, 43, 461-470.	2.5	5
274	Chorea-acanthocytosis. <i>Neurology: Genetics</i> , 2018, 4, e242.	1.9	4
275	Critical exon indexing improves clinical interpretation of copy number variants in neurodevelopmental disorders. <i>Neurology: Genetics</i> , 2019, 5, e378.	1.9	4
276	Ancestry and frequency of genetic variants in the general population are confounders in the characterization of germline variants linked to cancer. <i>BMC Medical Genetics</i> , 2020, 21, 92.	2.1	4
277	Biallelic PAN2 variants in individuals with a syndromic neurodevelopmental disorder and multiple congenital anomalies. <i>European Journal of Human Genetics</i> , 2022, 30, 611-618.	2.8	4
278	The 22q11 <i>PRODHDGCR6</i> deletion is frequent in hyperprolinemic subjects but is not a strong risk factor for ASD. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 377-382.	1.7	3
279	Atypical autism in a boy with double duplication of 22q11.2: implications of increasing dosage. <i>Npj Genomic Medicine</i> , 2017, 2, 28.	3.8	3
280	Reanalysing genomic data by normalized coverage values uncovers CNVs in bone marrow failure gene panels. <i>Npj Genomic Medicine</i> , 2019, 4, 30.	3.8	3
281	Analysis of five deep-sequenced trio-genomes of the Peninsular Malaysia Orang Asli and North Borneo populations. <i>BMC Genomics</i> , 2019, 20, 842.	2.8	3
282	A recurrent <i>MORC2</i> mutation causes Charcot-Marie-Tooth disease type 2Z. <i>Journal of the Peripheral Nervous System</i> , 2021, 26, 184-186.	3.1	3
283	Homozygous duplication identified by whole genome sequencing causes LRBA deficiency. <i>Npj Genomic Medicine</i> , 2021, 6, 96.	3.8	3
284	Complex Autism Spectrum Disorder with Epilepsy, Strabismus and Self-Injurious Behaviors in a Patient with a De Novo Heterozygous POLR2A Variant. <i>Genes</i> , 2022, 13, 470.	2.4	3
285	Accelerate Clinical Trials in Charcot-Marie-Tooth Disease (ACT-CMT): A Protocol to Address Clinical Trial Readiness in CMT1A. <i>Frontiers in Neurology</i> , 0, 13, .	2.4	3
286	Discrimination of SNPs in GC-rich regions using a modified hydrolysis probe chemistry protocol. <i>BioTechniques</i> , 2014, 57, 313-6.	1.8	2
287	ISDN2014_0253: High resolution genomic analyses of a clinically defined autism spectrum disorder cohort. <i>International Journal of Developmental Neuroscience</i> , 2015, 47, 76-76.	1.6	2
288	A MT-ATP6 Mutation Causes a Slowly Progressive Myeloneuropathy. <i>Journal of Neuromuscular Diseases</i> , 2019, 6, 385-387.	2.6	2

#	ARTICLE	IF	CITATIONS
289	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
290	Predictors of empowerment in parents of children with autism and related neurodevelopmental disorders who are undergoing genetic testing. Molecular Genetics & Genomic Medicine, 2021, 9, e1803.	1.2	2
291	Chromosomal-level reference genome assembly of the North American wolverine (<i>Gulo gulo</i>) Tj ETQq1 1 0.784314 rgBT /Overlock	1.8	2
292	IDENTIFICATION AND CHARACTERIZATION OF GENES SPANNING TRANSLOCATION BREAKPOINTS ON CHROMOSOME 7q31 IN TWO PATIENTS WITH AUTISTIC DISORDER. Biochemical Society Transactions, 2000, 28, A303-A303.	3.4	1
293	Blocking bad. Brain, 2015, 138, 3132-3133.	7.6	1
294	Subtype-specific therapy for autoimmune neuropathies?. Neurology: Neuroimmunology and Neuroinflammation, 2015, 2, e152.	6.0	1
295	Genomic medicine goes mainstream. Npj Genomic Medicine, 2016, 1, 15001.	3.8	1
296	Chronic multiple paraneoplastic syndromes. Muscle and Nerve, 2000, 23, 1767-1772.	2.2	1
297	A Regional Burden of Sequence-Level Variation in the 22q11.2 Region Influences Schizophrenia Risk and Educational Attainment. Biological Psychiatry, 2022, 91, 718-726.	1.3	1
298	GeneTerpret: a customizable multilayer approach to genomic variant prioritization and interpretation. BMC Medical Genomics, 2022, 15, 31.	1.5	1
299	Disruption of endosomal sorting in Schwann cells leads to defective myelination and endosomal abnormalities observed in Charcot-Marie-Tooth disease. Journal of Neuroscience, 2022, , JN-RM-2481-21.	3.6	1
300	Germline PTPN13 mutations in patients with bone marrow failure and acute lymphoblastic leukemia. Leukemia, 2022, 36, 2132-2135.	7.2	1
301	Fluorescent in situ mapping of the murine deleted in split hand/split foot 1 (<i>dss1</i>) gene to Chromosome 6. Mammalian Genome, 1997, 8, 704-704.	2.2	0
302	MG-108...Beyond the ACMG 56: Parental choices and initial results from a comprehensive whole genome sequencing-based search for predictive genomic variants in children. Journal of Medical Genetics, 2015, 52, A3.2-A4.	3.2	0
303	MG-123...Exonic and intronic NRXN1 deletions: Novel genotype-phenotype correlations. Journal of Medical Genetics, 2015, 52, A9.1-A9.	3.2	0
304	Cover Image, Volume 173A, Number 2, February 2017. American Journal of Medical Genetics, Part A, 2017, 173, i.	1.2	0
305	Genome-wide copy number variant data for inflammatory bowel disease in a caucasian population. Data in Brief, 2019, 25, 104203.	1.0	0
306	Sequencing the Multiple Myeloma Kinome: Absence of Mutation in Known Malignancy-Associated Kinases.. Blood, 2004, 104, 783-783.	1.4	0

#	ARTICLE	IF	CITATIONS
307	Whole Genome Sequencing in Autism: Clinical Translation. , 2014, , 69-97.		0
308	Copy Number Variants Underlying Inherited Bone Marrow Failure Syndromes. Blood, 2015, 126, 2416-2416.	1.4	0