

James S. Sutcliffe

List of Publications by Year in descending order

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134
papers

39,899
citations

12330

69
h-index

13379

130
g-index

137
all docs

137
docs citations

137
times ranked

30024
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of a gene (FMR-1) containing a CCG repeat coincident with a breakpoint cluster region exhibiting length variation in fragile X syndrome. <i>Cell</i> , 1991, 65, 905-914.	28.9	3,285
2	Strong Association of De Novo Copy Number Mutations with Autism. <i>Science</i> , 2007, 316, 445-449.	12.6	2,497
3	Synaptic, transcriptional and chromatin genes disrupted in autism. <i>Nature</i> , 2014, 515, 209-215.	27.8	2,254
4	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. <i>Nature Genetics</i> , 2013, 45, 984-994.	21.4	2,067
5	Variation of the CCG repeat at the fragile X site results in genetic instability: Resolution of the Sherman paradox. <i>Cell</i> , 1991, 67, 1047-1058.	28.9	2,007
6	Functional impact of global rare copy number variation in autism spectrum disorders. <i>Nature</i> , 2010, 466, 368-372.	27.8	1,803
7	Patterns and rates of exonic de novo mutations in autism spectrum disorders. <i>Nature</i> , 2012, 485, 242-245.	27.8	1,597
8	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. <i>Cell</i> , 2020, 180, 568-584.e23.	28.9	1,422
9	Mapping autism risk loci using genetic linkage and chromosomal rearrangements. <i>Nature Genetics</i> , 2007, 39, 319-328.	21.4	1,272
10	Autism genome-wide copy number variation reveals ubiquitin and neuronal genes. <i>Nature</i> , 2009, 459, 569-573.	27.8	1,270
11	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. <i>Neuron</i> , 2015, 87, 1215-1233.	8.1	1,219
12	Multiple Recurrent De Novo CNVs, Including Duplications of the 7q11.23 Williams Syndrome Region, Are Strongly Associated with Autism. <i>Neuron</i> , 2011, 70, 863-885.	8.1	1,146
13	A framework for the interpretation of de novo mutation in human disease. <i>Nature Genetics</i> , 2014, 46, 944-950.	21.4	943
14	Common genetic variants on 5p14.1 associate with autism spectrum disorders. <i>Nature</i> , 2009, 459, 528-533.	27.8	912
15	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
16	De novo truncating mutations in E6-AP ubiquitin-protein ligase gene (UBE3A) in Angelman syndrome. <i>Nature Genetics</i> , 1997, 15, 74-77.	21.4	801
17	DNA methylation represses FMR-1 transcription in fragile X syndrome. <i>Human Molecular Genetics</i> , 1992, 1, 397-400.	2.9	674
18	Recurrent Rearrangements of Chromosome 1q21.1 and Variable Pediatric Phenotypes. <i>New England Journal of Medicine</i> , 2008, 359, 1685-1699.	27.0	663

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19	Microduplications of 16p11.2 are associated with schizophrenia. <i>Nature Genetics</i> , 2009, 41, 1223-1227.	21.4	646
20	Contribution of SHANK3 Mutations to Autism Spectrum Disorder. <i>American Journal of Human Genetics</i> , 2007, 81, 1289-1297.	6.2	604
21	A genome-wide linkage and association scan reveals novel loci for autism. <i>Nature</i> , 2009, 461, 802-808.	27.8	570
22	A genome-wide scan for common alleles affecting risk for autism. <i>Human Molecular Genetics</i> , 2010, 19, 4072-4082.	2.9	538
23	Imprinted expression of the murine Angelman syndrome gene, <i>Ube3a</i> , in hippocampal and Purkinje neurons. <i>Nature Genetics</i> , 1997, 17, 75-78.	21.4	466
24	Deletions of a differentially methylated CpG island at the SNRPN gene define a putative imprinting control region. <i>Nature Genetics</i> , 1994, 8, 52-58.	21.4	418
25	A genetic variant that disrupts <i>MET</i> transcription is associated with autism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 16834-16839.	7.1	389
26	A Multisite Study of the Clinical Diagnosis of Different Autism Spectrum Disorders. <i>Archives of General Psychiatry</i> , 2012, 69, 306.	12.3	385
27	Allelic Heterogeneity at the Serotonin Transporter Locus (<i>SLC6A4</i>) Confers Susceptibility to Autism and Rigid-Compulsive Behaviors. <i>American Journal of Human Genetics</i> , 2005, 77, 265-279.	6.2	378
28	Genome-Wide Analyses of Exonic Copy Number Variants in a Family-Based Study Point to Novel Autism Susceptibility Genes. <i>PLoS Genetics</i> , 2009, 5, e1000536.	3.5	374
29	Tissue specific expression of FMR1 provides evidence for a functional role in fragile X syndrome. <i>Nature Genetics</i> , 1993, 3, 36-43.	21.4	358
30	Common genetic variants, acting additively, are a major source of risk for autism. <i>Molecular Autism</i> , 2012, 3, 9.	4.9	357
31	Individual common variants exert weak effects on the risk for autism spectrum disorders. <i>Human Molecular Genetics</i> , 2012, 21, 4781-4792.	2.9	334
32	Autism gene variant causes hyperserotonemia, serotonin receptor hypersensitivity, social impairment and repetitive behavior. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5469-5474.	7.1	278
33	SPARK: A US Cohort of 50,000 Families to Accelerate Autism Research. <i>Neuron</i> , 2018, 97, 488-493.	8.1	265
34	Integrated Model of De Novo and Inherited Genetic Variants Yields Greater Power to Identify Risk Genes. <i>PLoS Genetics</i> , 2013, 9, e1003671.	3.5	253
35	Human and murine FMR-1: alternative splicing and translational initiation downstream of the CCG repeat. <i>Nature Genetics</i> , 1993, 4, 244-251.	21.4	247
36	Rare Complete Knockouts in Humans: Population Distribution and Significant Role in Autism Spectrum Disorders. <i>Neuron</i> , 2013, 77, 235-242.	8.1	242

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37	Partial and generalized epilepsy with febrile seizures plus and a novel <i>SCN1A</i> mutation. <i>Neurology</i> , 2001, 57, 2265-2272.	1.1	193
38	Analysis of the RELN gene as a genetic risk factor for autism. <i>Molecular Psychiatry</i> , 2005, 10, 563-571.	7.9	181
39	De novo mutation in the dopamine transporter gene associates dopamine dysfunction with autism spectrum disorder. <i>Molecular Psychiatry</i> , 2013, 18, 1315-1323.	7.9	181
40	A novel approach of homozygous haplotype sharing identifies candidate genes in autism spectrum disorder. <i>Human Genetics</i> , 2012, 131, 565-579.	3.8	180
41	Human serotonin transporter variants display altered sensitivity to protein kinase G and p38 mitogen-activated protein kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11545-11550.	7.1	167
42	Linkage Disequilibrium at the Angelman Syndrome Gene UBE3A in Autism Families. <i>Genomics</i> , 2001, 77, 105-113.	2.9	154
43	The spectrum of mutations in UBE3A causing Angelman syndrome. <i>Human Molecular Genetics</i> , 1999, 8, 129-135.	2.9	150
44	Association of oxytocin receptor (OXTR) gene variants with multiple phenotype domains of autism spectrum disorder. <i>Journal of Neurodevelopmental Disorders</i> , 2011, 3, 101-112.	3.1	148
45	Genetic evidence implicating multiple genes in the MET receptor tyrosine kinase pathway in autism spectrum disorder. <i>Autism Research</i> , 2008, 1, 159-168.	3.8	143
46	Distinct Genetic Risk Based on Association of <i>MET</i> in Families With Co-occurring Autism and Gastrointestinal Conditions. <i>Pediatrics</i> , 2009, 123, 1018-1024.	2.1	141
47	A linkage disequilibrium map of the 16Mb 15q12 GABA _A receptor subunit cluster and association to autism. <i>American Journal of Medical Genetics Part A</i> , 2004, 131B, 51-59.	2.4	135
48	Analysis of Rare, Exonic Variation amongst Subjects with Autism Spectrum Disorders and Population Controls. <i>PLoS Genetics</i> , 2013, 9, e1003443.	3.5	133
49	A Genome-wide Association Study of Autism Using the Simons Simplex Collection: Does Reducing Phenotypic Heterogeneity in Autism Increase Genetic Homogeneity?. <i>Biological Psychiatry</i> , 2015, 77, 775-784.	1.3	133
50	Genome-wide and Ordered-Subset linkage analyses provide support for autism loci on 17q and 19p with evidence of phenotypic and interlocus genetic correlates. <i>BMC Medical Genetics</i> , 2005, 6, 1.	2.1	130
51	Imprinting analysis of three genes in the Prader-Willi/Angelman region: SNRPN, E6-associated protein, and PAR-2 (D15S225E). <i>Human Molecular Genetics</i> , 1994, 3, 309-315.	2.9	125
52	Enhanced activity of human serotonin transporter variants associated with autism. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009, 364, 163-173.	4.0	120
53	Linkage and association analysis at the serotonin transporter (SLC6A4) locus in a rigid-compulsive subset of autism. <i>American Journal of Medical Genetics Part A</i> , 2004, 127B, 104-112.	2.4	118
54	A common X-linked inborn error of carnitine biosynthesis may be a risk factor for nondysmorphic autism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7974-7981.	7.1	118

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55	A Bayesian framework that integrates multi-omics data and gene networks predicts risk genes from schizophrenia GWAS data. <i>Nature Neuroscience</i> , 2019, 22, 691-699.	14.8	118
56	Exploratory Subsetting of Autism Families Based on Savant Skills Improves Evidence of Genetic Linkage to 15q11-q13. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2003, 42, 856-863.	0.5	112
57	Autism and 15q11-q13 disorders: Behavioral, genetic, and pathophysiological issues. <i>Mental Retardation and Developmental Disabilities Research Reviews</i> , 2004, 10, 284-291.	3.6	112
58	Shorter sleep duration is associated with social impairment and comorbidities in ASD. <i>Autism Research</i> , 2017, 10, 1221-1238.	3.8	109
59	SLC6A3 coding variant Ala559Val found in two autism probands alters dopamine transporter function and trafficking. <i>Translational Psychiatry</i> , 2014, 4, e464-e464.	4.8	108
60	The E6-AP Ubiquitin-Protein Ligase (<i>UBE3A</i>) Gene Is Localized within a Narrowed Angelman Syndrome Critical Region. <i>Genome Research</i> , 1997, 7, 368-377.	5.5	106
61	Maternal transmission of a rare GABRB3 signal peptide variant is associated with autism. <i>Molecular Psychiatry</i> , 2011, 16, 86-96.	7.9	106
62	Use of array CGH to detect exonic copy number variants throughout the genome in autism families detects a novel deletion in TMLHE. <i>Human Molecular Genetics</i> , 2011, 20, 4360-4370.	2.9	101
63	A complete YAC contig of the Prader-Willi/Angelman chromosome region (15q11-q13) and refined localization of the SNRPN gene. <i>Genomics</i> , 1993, 18, 546-552.	2.9	100
64	Rare familial 16q21 microdeletions under a linkage peak implicate cadherin 8 (CDH8) in susceptibility to autism and learning disability. <i>Journal of Medical Genetics</i> , 2011, 48, 48-54.	3.2	94
65	Validation studies of SNRPN methylation as a diagnostic test for Prader-Willi syndrome. , 1996, 66, 77-80.		87
66	Mouse/human sequence divergence in a region with a paternal-specific methylation imprint at the human H19 locus. <i>Human Molecular Genetics</i> , 1996, 5, 1155-1161.	2.9	85
67	A Novel Human <i>CAMK2A</i> Mutation Disrupts Dendritic Morphology and Synaptic Transmission, and Causes ASD-Related Behaviors. <i>Journal of Neuroscience</i> , 2017, 37, 2216-2233.	3.6	83
68	Characterization of a highly polymorphic dinucleotide repeat 150 KB proximal to the fragile X site. <i>American Journal of Medical Genetics Part A</i> , 1992, 43, 237-243.	2.4	82
69	Variation in ITGB3 is associated with whole-blood serotonin level and autism susceptibility. <i>European Journal of Human Genetics</i> , 2006, 14, 923-931.	2.8	82
70	Association and Mutation Analyses of 16p11.2 Autism Candidate Genes. <i>PLoS ONE</i> , 2009, 4, e4582.	2.5	80
71	Appetitive behavior, compulsivity, and neurochemistry in Prader-Willi syndrome. <i>Mental Retardation and Developmental Disabilities Research Reviews</i> , 2000, 6, 125-130.	3.6	75
72	Integrated YAC Contig Map of the Prader-Willi/Angelman Region on Chromosome 15q11-q13 with Average STS Spacing of 35 kb. <i>Genome Research</i> , 1998, 8, 146-157.	5.5	72

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73	Adjusting Head Circumference for Covariates in Autism: Clinical Correlates of a Highly Heritable Continuous Trait. <i>Biological Psychiatry</i> , 2013, 74, 576-584.	1.3	70
74	Rare Autism-Associated Variants Implicate Syntaxin 1 (STX1 R26Q) Phosphorylation and the Dopamine Transporter (hDAT R51W) in Dopamine Neurotransmission and Behaviors. <i>EBioMedicine</i> , 2015, 2, 135-146.	6.1	70
75	Tissue-specific and allele-specific replication timing control in the imprinted human Prader-Willi syndrome region.. <i>Genes and Development</i> , 1995, 9, 808-820.	5.9	67
76	Intellectual Disability Is Associated with Increased Runs of Homozygosity in Simplex Autism. <i>American Journal of Human Genetics</i> , 2013, 93, 103-109.	6.2	63
77	Dense linkage disequilibrium mapping in the 15q11-q13 maternal expression domain yields evidence for association in autism. <i>Molecular Psychiatry</i> , 2003, 8, 624-634.	7.9	60
78	Modest Impact on Risk for Autism Spectrum Disorder of Rare Copy Number Variants at 15q11.2, Specifically Breakpoints 1 to 2. <i>Autism Research</i> , 2014, 7, 355-362.	3.8	59
79	Molecular Genetics of the Platelet Serotonin System in First-Degree Relatives of Patients with Autism. <i>Neuropsychopharmacology</i> , 2008, 33, 353-360.	5.4	57
80	Examination of NRCAM, LRRN3, KIAA0716, and LAMB1 as autism candidate genes. <i>BMC Medical Genetics</i> , 2004, 5, 12.	2.1	56
81	Neuronally-expressed necdin gene: an imprinted candidate gene in Prader-Willi syndrome. <i>Lancet</i> , The, 1997, 350, 1520-1521.	13.7	53
82	Insights into the Pathogenesis of Autism. <i>Science</i> , 2008, 321, 208-209.	12.6	53
83	Genetics of Childhood Disorders: XLVII. Autism, Part 6: Duplication and Inherited Susceptibility of Chromosome 15q11-q13 Genes in Autism. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2003, 42, 253-256.	0.5	51
84	Genetic analysis of biological pathway data through genomic randomization. <i>Human Genetics</i> , 2011, 129, 563-571.	3.8	50
85	Leveraging blood serotonin as an endophenotype to identify de novo and rare variants involved in autism. <i>Molecular Autism</i> , 2017, 8, 14.	4.9	50
86	Association of <i>MET</i> with social and communication phenotypes in individuals with autism spectrum disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2010, 153B, 438-446.	1.7	49
87	Modeling rare gene variation to gain insight into the oldest biomarker in autism: construction of the serotonin transporter Gly56Ala knock-in mouse. <i>Journal of Neurodevelopmental Disorders</i> , 2009, 1, 158-171.	3.1	43
88	Parent-of-origin effects of the serotonin transporter gene associated with autism. , 2011, 156, 139-144.		41
89	Analysis of <i>CHRNA7</i> rare variants in autism spectrum disorder susceptibility. <i>American Journal of Medical Genetics, Part A</i> , 2015, 167, 715-723.	1.2	41
90	Autosomal Dominant Lateral Temporal Epilepsy: Two Families with Novel Mutations in the LGI1 Gene. <i>Epilepsia</i> , 2004, 45, 218-222.	5.1	39

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91	Gene-ontology enrichment analysis in two independent family-based samples highlights biologically plausible processes for autism spectrum disorders. <i>European Journal of Human Genetics</i> , 2011, 19, 1082-1089.	2.8	39
92	Loci nominally associated with autism from genome-wide analysis show enrichment of brain expression quantitative trait loci but not lymphoblastoid cell line expression quantitative trait loci. <i>Molecular Autism</i> , 2012, 3, 3.	4.9	38
93	Lack of Association Between Autism and <i>SLC25A12</i> . <i>American Journal of Psychiatry</i> , 2006, 163, 929-931.	7.2	36
94	Genetic background modulates phenotypes of serotonin transporter Ala56 knock-in mice. <i>Molecular Autism</i> , 2013, 4, 35.	4.9	35
95	Structural, functional, and behavioral insights of dopamine dysfunction revealed by a deletion in <i>SLC6A3</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3853-3862.	7.1	35
96	Defining the autism minimum candidate gene region on chromosome 7. <i>American Journal of Medical Genetics Part A</i> , 2003, 117B, 90-96.	2.4	32
97	Analysis of the autism chromosome 2 linkage region: <i>GAD1</i> and other candidate genes. <i>Neuroscience Letters</i> , 2004, 372, 209-214.	2.1	32
98	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
99	Colocalization and Regulated Physical Association of Presynaptic Serotonin Transporters with A_{3} Adenosine Receptors. <i>Molecular Pharmacology</i> , 2011, 80, 458-465.	2.3	30
100	Integrin $\beta 3$ Haploinsufficiency Modulates Serotonin Transport and Antidepressant-Sensitive Behavior in Mice. <i>Neuropsychopharmacology</i> , 2015, 40, 2015-2024.	5.4	26
101	Is there sexual dimorphism of hyperserotonemia in autism spectrum disorder?. <i>Autism Research</i> , 2017, 10, 1417-1423.	3.8	24
102	Maternal Serotonin Levels Are Associated With Cognitive Ability and Core Symptoms in Autism Spectrum Disorder. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2018, 57, 867-875.	0.5	24
103	Identification of a novel paternally expressed transcript adjacent to <i>snRPN</i> in the Prader-Willi syndrome critical region. <i>Genome Research</i> , 1996, 6, 742-746.	5.5	23
104	Rare coding variants of the adenosine A3 receptor are increased in autism: on the trail of the serotonin transporter regulome. <i>Molecular Autism</i> , 2013, 4, 28.	4.9	23
105	Novel method for combined linkage and genome-wide association analysis finds evidence of distinct genetic architecture for two subtypes of autism. <i>Journal of Neurodevelopmental Disorders</i> , 2011, 3, 113-123.	3.1	22
106	The Gain-of-Function Integrin $\beta 3$ Pro33 Variant Alters the Serotonin System in the Mouse Brain. <i>Journal of Neuroscience</i> , 2017, 37, 11271-11284.	3.6	22
107	Partial duplication of the <i>APBA2</i> gene in chromosome 15q13 corresponds to duplcon structures. <i>BMC Genomics</i> , 2003, 4, 15.	2.8	20
108	Using extended pedigrees to identify novel autism spectrum disorder (ASD) candidate genes. <i>Human Genetics</i> , 2015, 134, 191-201.	3.8	20

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109	Zn ²⁺ reverses functional deficits in a de novo dopamine transporter variant associated with autism spectrum disorder. <i>Molecular Autism</i> , 2015, 6, 8.	4.9	19
110	Possible dosage effect of maternally expressed genes on visual recognition memory in Prader-Willi syndrome. <i>American Journal of Medical Genetics Part A</i> , 2001, 105, 71-75.	2.4	18
111	Consensus Genotyper for Exome Sequencing (CGES): improving the quality of exome variant genotypes. <i>Bioinformatics</i> , 2015, 31, 187-193.	4.1	18
112	The GABBR1 locus and the G1465A variant is not associated with temporal lobe epilepsy preceded by febrile seizures. <i>BMC Medical Genetics</i> , 2005, 6, 13.	2.1	17
113	Accuracy of phenotyping children with autism based on parent report: what specifically do we gain phenotyping "rapidly"? <i>Autism Research</i> , 2012, 5, 31-38.	3.8	17
114	Sequencing and Functional Analysis of the SNRPN Promoter: In Vitro Methylation Abolishes Promoter Activity. <i>Genome Research</i> , 1997, 7, 642-648.	5.5	16
115	"Severe" Prader-Willi syndrome with a large deletion of chromosome 15 due to an unbalanced t(15,22)(q14;q11.2) translocation. <i>Clinical Genetics</i> , 2003, 63, 79-81.	2.0	14
116	Mutations in GABRA1, GABRA5, GABRG2 and GABRD receptor genes are not a major factor in the pathogenesis of familial focal epilepsy preceded by febrile seizures. <i>Neuroscience Letters</i> , 2006, 394, 74-78.	2.1	14
117	A haplotype-based framework for group-wise transmission/disequilibrium tests for rare variant association analysis. <i>Bioinformatics</i> , 2015, 31, 1452-1459.	4.1	14
118	Detection of imprinting mutations in Angelman syndrome using a probe for exon 1± of SNRPN. <i>American Journal of Medical Genetics Part A</i> , 1996, 63, 414-415.	2.4	13
119	Whole exome sequencing reveals minimal differences between cell line and whole blood derived DNA. <i>Genomics</i> , 2013, 102, 270-277.	2.9	13
120	Strategy for molecular cloning of the fragile X site DNA. <i>American Journal of Medical Genetics Part A</i> , 1988, 30, 613-623.	2.4	12
121	Fine mapping and association studies in a candidate region for autism on chromosome 2q31-q32. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2009, 150B, 535-544.	1.7	12
122	The impact of genotype calling errors on family-based studies. <i>Scientific Reports</i> , 2016, 6, 28323.	3.3	12
123	PCR amplification and analysis of yeast artificial chromosomes. <i>Genomics</i> , 1992, 13, 1303-1306.	2.9	11
124	The Drosophila Gene Sulfateless Modulates Autism-Like Behaviors. <i>Frontiers in Genetics</i> , 2019, 10, 574.	2.3	11
125	Drosophila melanogaster: a novel animal model for the behavioral characterization of autism-associated mutations in the dopamine transporter gene. <i>Molecular Psychiatry</i> , 2013, 18, 1235-1235.	7.9	9
126	Pro32Pro33 Mutations in the Integrin $\alpha 3$ PSI Domain Result in $\alpha 3$ Priming and Enhanced Adhesion: Reversal of the Hypercoagulability Phenotype by the Src Inhibitor SKI-606. <i>Molecular Pharmacology</i> , 2014, 85, 921-931.	2.3	7

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127	Psychometric validation and refinement of the Interoception Sensory Questionnaire (ISQ) in adolescents and adults on the autism spectrum. <i>Molecular Autism</i> , 2021, 12, 42.	4.9	6
128	Angelman syndrome in an inbred family. <i>Human Genetics</i> , 1996, 97, 294-298.	3.8	5
129	Our vision for Autism Research. <i>Autism Research</i> , 2008, 1, 71-72.	3.8	3
130	Heterogeneity and the design of genetic studies in autism. <i>Autism Research</i> , 2008, 1, 205-206.	3.8	3
131	Affiliative Behaviors and Beyond: It's the Phenotype, Stupid. <i>Biological Psychiatry</i> , 2008, 63, 909-910.	1.3	2
132	Advantages of RT-PCR and denaturing gradient gel electrophoresis for analysis of genomic imprinting: Detection of new mouse and human expressed polymorphisms. , 1996, 7, 144-148.		1
133	An Automated Functional Annotation Pipeline That Rapidly Prioritizes Clinically Relevant Genes for Autism Spectrum Disorder. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9029.	4.1	1
134	Calculating genetic risk for dysfunction in pleiotropic biological processes using whole exome sequencing data. <i>Journal of Neurodevelopmental Disorders</i> , 2022, 14, .	3.1	0