Stephan J Sanders

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1970353/publications.pdf Version: 2024-02-01



STEDHAN I SANDERS

#	Article	IF	CITATIONS
1	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	13.7	2,254
2	The contribution of de novo coding mutations to autism spectrum disorder. Nature, 2014, 515, 216-221.	13.7	2,188
3	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
4	De novo mutations revealed by whole-exome sequencing are strongly associated with autism. Nature, 2012, 485, 237-241.	13.7	1,863
5	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
6	Predicting Splicing from Primary Sequence with Deep Learning. Cell, 2019, 176, 535-548.e24.	13.5	1,305
7	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. Neuron, 2015, 87, 1215-1233.	3.8	1,219
8	Multiple Recurrent De Novo CNVs, Including Duplications of the 7q11.23 Williams Syndrome Region, Are Strongly Associated with Autism. Neuron, 2011, 70, 863-885.	3.8	1,146
9	Most genetic risk for autism resides with common variation. Nature Genetics, 2014, 46, 881-885.	9.4	977
10	A framework for the interpretation of de novo mutation in human disease. Nature Genetics, 2014, 46, 944-950.	9.4	943
11	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
12	Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. Cell, 2013, 155, 997-1007.	13.5	825
13	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	6.0	805
14	De novo mutations in histone-modifying genes in congenital heart disease. Nature, 2013, 498, 220-223.	13.7	798
15	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	7.1	701
16	De novo mutations in congenital heart disease with neurodevelopmental and other congenital anomalies. Science, 2015, 350, 1262-1266.	6.0	646
17	Contribution of rare inherited and de novo variants in 2,871 congenital heart disease probands. Nature Genetics, 2017, 49, 1593-1601.	9.4	624
18	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	6.0	618

#	Article	IF	CITATIONS
19	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
20	Meta-analysis of GWAS of over 16,000 individuals with autism spectrum disorder highlights a novel locus at 10q24.32 and a significant overlap with schizophrenia. Molecular Autism, 2017, 8, 21.	2.6	495
21	Whole-exome sequencing identifies recessive WDR62 mutations in severe brain malformations. Nature, 2010, 467, 207-210.	13.7	457
22	Sex and gender differences in autism spectrum disorder: summarizing evidence gaps and identifying emerging areas of priority. Molecular Autism, 2015, 6, 36.	2.6	413
23	Polygenic transmission disequilibrium confirms that common and rare variation act additively to create risk for autism spectrum disorders. Nature Genetics, 2017, 49, 978-985.	9.4	401
24	Using Whole-Exome Sequencing to Identify Inherited Causes of Autism. Neuron, 2013, 77, 259-273.	3.8	383
25	Common genetic variants, acting additively, are a major source of risk for autism. Molecular Autism, 2012, 3, 9.	2.6	357
26	Genetic risk for autism spectrum disorders and neuropsychiatric variation in the general population. Nature Genetics, 2016, 48, 552-555.	9.4	326
27	The autism-associated chromatin modifier CHD8 regulates other autism risk genes during human neurodevelopment. Nature Communications, 2015, 6, 6404.	5.8	316
28	L-Histidine Decarboxylase and Tourette's Syndrome. New England Journal of Medicine, 2010, 362, 1901-1908.	13.9	304
29	Refining the role of de novo protein-truncating variants in neurodevelopmental disorders by using population reference samples. Nature Genetics, 2017, 49, 504-510.	9.4	298
30	Deletion 17q12 Is a Recurrent Copy Number Variant that Confers High Risk of Autism and Schizophrenia. American Journal of Human Genetics, 2010, 87, 618-630.	2.6	282
31	Mutations in <i>BCKD-kinase</i> Lead to a Potentially Treatable Form of Autism with Epilepsy. Science, 2012, 338, 394-397.	6.0	272
32	Integrated Model of De Novo and Inherited Genetic Variants Yields Greater Power to Identify Risk Genes. PLoS Genetics, 2013, 9, e1003671.	1.5	253
33	Rare Complete Knockouts in Humans: Population Distribution and Significant Role in Autism Spectrum Disorders. Neuron, 2013, 77, 235-242.	3.8	242
34	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
35	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. Science, 2018, 362, .	6.0	234
36	Increased Frequency of De Novo Copy Number Variants in Congenital Heart Disease by Integrative Analysis of Single Nucleotide Polymorphism Array and Exome Sequence Data. Circulation Research, 2014, 115, 884-896.	2.0	229

#	Article	IF	CITATIONS
37	Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. American Journal of Human Genetics, 2015, 96, 283-294.	2.6	225
38	Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science, 2018, 362, .	6.0	220
39	Progress in Understanding and Treating SCN2A-Mediated Disorders. Trends in Neurosciences, 2018, 41, 442-456.	4.2	210
40	Opposing Effects on Na V 1.2 Function Underlie Differences Between SCN2A Variants Observed in Individuals With Autism Spectrum Disorder or Infantile Seizures. Biological Psychiatry, 2017, 82, 224-232.	0.7	208
41	Copy-Number Disorders Are a Common Cause of Congenital Kidney Malformations. American Journal of Human Genetics, 2012, 91, 987-997.	2.6	201
42	Rare Inherited and De Novo CNVs Reveal Complex Contributions to ASD Risk in Multiplex Families. American Journal of Human Genetics, 2016, 99, 540-554.	2.6	179
43	Modeling non-syndromic autism and the impact of TRPC6 disruption in human neurons. Molecular Psychiatry, 2015, 20, 1350-1365.	4.1	175
44	Genotype to phenotype relationships in autism spectrum disorders. Nature Neuroscience, 2015, 18, 191-198.	7.1	168
45	Rare Copy Number Variants in Tourette Syndrome Disrupt Genes in Histaminergic Pathways and Overlap with Autism. Biological Psychiatry, 2012, 71, 392-402.	0.7	167
46	Genome-wide Transcriptome Profiling Reveals the Functional Impact of Rare De Novo and Recurrent CNVs in Autism Spectrum Disorders. American Journal of Human Genetics, 2012, 91, 38-55.	2.6	160
47	Defining the diverse spectrum of inversions, complex structural variation, and chromothripsis in the morbid humanÂgenome. Genome Biology, 2017, 18, 36.	3.8	159
48	De Novo Coding Variants Are Strongly Associated with Tourette Disorder. Neuron, 2017, 94, 486-499.e9.	3.8	155
49	De Novo Insertions and Deletions of Predominantly Paternal Origin Are Associated with Autism Spectrum Disorder. Cell Reports, 2014, 9, 16-23.	2.9	151
50	The Autism-Associated Gene Scn2a Contributes to Dendritic Excitability and Synaptic Function in the Prefrontal Cortex. Neuron, 2019, 103, 673-685.e5.	3.8	148
51	Loss of δ-catenin function in severe autism. Nature, 2015, 520, 51-56.	13.7	145
52	Using large clinical data sets to infer pathogenicity for rare copy number variants in autism cohorts. Molecular Psychiatry, 2013, 18, 1090-1095.	4.1	140
53	De Novo Mutations in Protein Kinase Genes CAMK2A and CAMK2B Cause Intellectual Disability. American Journal of Human Genetics, 2017, 101, 768-788.	2.6	136
54	A Genome-wide Association Study of Autism Using the Simons Simplex Collection: Does Reducing Phenotypic Heterogeneity in Autism Increase Genetic Homogeneity?. Biological Psychiatry, 2015, 77, 775-784.	0.7	133

#	Article	IF	CITATIONS
55	Whole genome sequencing in psychiatric disorders: the WGSPD consortium. Nature Neuroscience, 2017, 20, 1661-1668.	7.1	122
56	A common X-linked inborn error of carnitine biosynthesis may be a risk factor for nondysmorphic autism. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7974-7981.	3.3	118
57	High rate of disease-related copy number variations in childhood onset schizophrenia. Molecular Psychiatry, 2014, 19, 568-572.	4.1	116
58	Exome Sequencing for Prenatal Diagnosis in Nonimmune Hydrops Fetalis. New England Journal of Medicine, 2020, 383, 1746-1756.	13.9	114
59	DAWN: a framework to identify autism genes and subnetworks using gene expression and genetics. Molecular Autism, 2014, 5, 22.	2.6	111
60	Use of array CGH to detect exonic copy number variants throughout the genome in autism families detects a novel deletion in TMLHE. Human Molecular Genetics, 2011, 20, 4360-4370.	1.4	101
61	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
62	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. Cell Reports, 2020, 31, 107489.	2.9	91
63	A framework for the investigation of rare genetic disorders in neuropsychiatry. Nature Medicine, 2019, 25, 1477-1487.	15.2	90
64	Frequency and Complexity of De Novo Structural Mutation in Autism. American Journal of Human Genetics, 2016, 98, 667-679.	2.6	88
65	De Novo Disruption of the Proteasome Regulatory Subunit PSMD12 Causes a Syndromic Neurodevelopmental Disorder. American Journal of Human Genetics, 2017, 100, 352-363.	2.6	86
66	First glimpses of the neurobiology of autism spectrum disorder. Current Opinion in Genetics and Development, 2015, 33, 80-92.	1.5	79
67	Identification of Developmental and Behavioral Markers Associated With Genetic Abnormalities in Autism Spectrum Disorder. American Journal of Psychiatry, 2017, 174, 576-585.	4.0	73
68	Adjusting Head Circumference for Covariates in Autism: Clinical Correlates of a Highly Heritable Continuous Trait. Biological Psychiatry, 2013, 74, 576-584.	0.7	70
69	A Chromatin Accessibility Atlas of the Developing Human Telencephalon. Cell, 2020, 182, 754-769.e18.	13.5	69
70	Biological concepts in human sodium channel epilepsies and their relevance in clinical practice. Epilepsia, 2020, 61, 387-399.	2.6	65
71	Intellectual Disability Is Associated with Increased Runs of Homozygosity in Simplex Autism. American Journal of Human Genetics, 2013, 93, 103-109.	2.6	63
72	Modest Impact on Risk for Autism Spectrum Disorder of Rare Copy Number Variants at 15 <scp>q</scp> 11.2, Specifically Breakpoints 1 to 2. Autism Research, 2014, 7, 355-362.	2.1	59

#	Article	IF	CITATIONS
73	Whole-exome sequencing in obsessive-compulsive disorder identifies rare mutations in immunological and neurodevelopmental pathways. Translational Psychiatry, 2016, 6, e764-e764.	2.4	59
74	Homozygous loss of DIAPH1 is a novel cause of microcephaly in humans. European Journal of Human Genetics, 2015, 23, 165-172.	1.4	57
75	De novo structural mutation rates and gamete-of-origin biases revealed through genome sequencing of 2,396 families. American Journal of Human Genetics, 2021, 108, 597-607.	2.6	57
76	Paradoxical hyperexcitability from NaV1.2 sodium channel loss in neocortical pyramidal cells. Cell Reports, 2021, 36, 109483.	2.9	57
77	Dual Molecular Effects of Dominant RORA Mutations Cause Two Variants of Syndromic Intellectual Disability with Either Autism or Cerebellar Ataxia. American Journal of Human Genetics, 2018, 102, 744-759.	2.6	51
78	The female protective effect in autism spectrum disorder is not mediated by a single genetic locus. Molecular Autism, 2015, 6, 25.	2.6	50
79	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature Communications, 2021, 12, 3968.	5.8	48
80	No Evidence for Association of Autism with Rare Heterozygous Point Mutations in Contactin-Associated Protein-Like 2 (CNTNAP2), or in Other Contactin-Associated Proteins or Contactins. PLoS Genetics, 2015, 11, e1004852.	1.5	47
81	Paired-Duplication Signatures Mark Cryptic Inversions and Other Complex Structural Variation. American Journal of Human Genetics, 2015, 97, 170-176.	2.6	45
82	DIXDC1 contributes to psychiatric susceptibility by regulating dendritic spine and glutamatergic synapse density via GSK3 and Wnt/β-catenin signaling. Molecular Psychiatry, 2018, 23, 467-475.	4.1	44
83	Peabody Picture Vocabulary Test: Proxy for Verbal IQ in Genetic Studies of Autism Spectrum Disorder. Journal of Autism and Developmental Disorders, 2017, 47, 1073-1085.	1.7	40
84	Body composition at high altitude: a randomized placebo-controlled trial of dietary carbohydrate supplementation. American Journal of Clinical Nutrition, 2009, 90, 1193-1202.	2.2	39
85	Appositions between cocaine and amphetamine-related transcript- and gonadotropin releasing hormone-immunoreactive neurons in the hypothalamus of the Siberian hamster. Neuroscience Letters, 2001, 314, 111-114.	1.0	35
86	Physiological and Psychological Illness Symptoms at High Altitude and Their Relationship With Acute Mountain Sickness: A Prospective Cohort Study. Journal of Travel Medicine, 2012, 19, 210-219.	1.4	30
87	Children with autism spectrum disorder who improve with fever: Insights from the Simons Simplex Collection. Autism Research, 2018, 11, 175-184.	2.1	30
88	Missense Variants in the Histone Acetyltransferase Complex Component Gene TRRAP Cause Autism and Syndromic Intellectual Disability. American Journal of Human Genetics, 2019, 104, 530-541.	2.6	30
89	The female protective effect against autism spectrum disorder. Cell Genomics, 2022, 2, 100134.	3.0	30
90	A balanced t(10;15) translocation in a male patient with developmental language disorder. European Journal of Medical Genetics, 2012, 55, 128-131.	0.7	22

#	Article	IF	CITATIONS
91	Cross-Disorder Comparison of Four Neuropsychiatric CNV Loci. Current Genetic Medicine Reports, 2014, 2, 151-161.	1.9	22
92	Developmental dynamics of voltage-gated sodium channel isoform expression in the human and mouse brain. Genome Medicine, 2021, 13, 135.	3.6	19
93	Standardizing the Next Generation of Bioinformatics Software Development with BioHDF (HDF5). Advances in Experimental Medicine and Biology, 2010, 680, 693-700.	0.8	18
94	A Markov random field-based approach to characterizing human brain development using spatial–temporal transcriptome data. Annals of Applied Statistics, 2015, 9, 429-451.	0.5	18
95	Differential excitatory vs inhibitory SCN expression at single cell level regulates brain sodium channel function in neurodevelopmental disorders. European Journal of Paediatric Neurology, 2020, 24, 129-133.	0.7	18
96	Extrathymic <i>Aire</i> -expressing cells support maternal-fetal tolerance. Science Immunology, 2021, 6, .	5.6	17
97	High-throughput characterization of the role of non-B DNA motifs on promoter function. Cell Genomics, 2022, 2, 100111.	3.0	17
98	Intergenerational Neuroimaging of Human Brain Circuitry. Trends in Neurosciences, 2016, 39, 644-648.	4.2	16
99	Searching for Potocki–Lupski syndrome phenotype: A patient with language impairment and no autism. Brain and Development, 2012, 34, 700-703.	0.6	15
100	Clinical impact of splicing in neurodevelopmental disorders. Genome Medicine, 2020, 12, 36.	3.6	15
101	Constructing and optimizing 3D atlases from 2D data with application to the developing mouse brain. ELife, 2021, 10, .	2.8	15
102	A model and test for coordinated polygenic epistasis in complex traits. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
103	Homeostatic plasticity fails at the intersection of autism-gene mutations and a novel class of common genetic modifiers. ELife, 2020, 9, .	2.8	14
104	Next-Generation Sequencing in Autism Spectrum Disorder. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a026872.	2.9	13
105	Patterns of delay in early gross motor and expressive language milestone attainment in probands with genetic conditions versus idiopathic ASD from SFARI registries. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2021, 62, 1297-1307.	3.1	13
106	Prenatal exposure to paternal smoking and likelihood for autism spectrum disorder. Autism, 2021, 25, 1946-1959.	2.4	12
107	Not All Autism Genes Are Created Equal: A Response to Myers etÂal American Journal of Human Genetics, 2020, 107, 1000-1003.	2.6	11
108	A complex chromosomal rearrangement involving chromosomes 2, 5, and X in autism spectrum disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 529-536.	1.1	10

#	Article	IF	CITATIONS
109	Wholeâ€Brain Image Analysis and Anatomical Atlas 3D Generation Using MagellanMapper. Current Protocols in Neuroscience, 2020, 94, e104.	2.6	9
110	Hereditary hyperferritinaemia-cataract syndrome and differential diagnosis of hereditary haemochromatosis. Postgraduate Medical Journal, 2003, 79, 600-601.	0.9	6
111	Attention Finally Being Paid to Girls at Risk of Autism. Journal of the American Academy of Child and Adolescent Psychiatry, 2016, 55, 159-160.	0.3	6
112	Automating Installation of the Integrating Biology and the Bedside (i2b2) Platform. Biomedical Informatics Insights, 2018, 10, 117822261877774.	4.6	6
113	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
114	Building a Precision Medicine Delivery Platform for Clinics: The University of California, San Francisco, BRIDGE Experience. Journal of Medical Internet Research, 2022, 24, e34560.	2.1	6
115	A biomedical open knowledge network harnesses the power of AI to understand deep human biology. AI Magazine, 2022, 43, 46-58.	1.4	5
116	Appreciating the Population-wide Impact of Copy Number Variants on Cognition. Biological Psychiatry, 2017, 82, 78-80.	0.7	4
117	Detection of subtle white matter lesions in MRI through texture feature extraction and boundary delineation using an embedded clustering strategy. Scientific Reports, 2022, 12, 4433.	1.6	4
118	Deletion 17q12 Is a Recurrent Copy Number Variant that Confers High Risk of Autism and Schizophrenia. American Journal of Human Genetics, 2011, 88, 121.	2.6	3
119	Harnessing rare variants in neuropsychiatric and neurodevelopment disorders—a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, , .	1.8	2
120	Enhancing Clinical Information Display to Improve Patient Encounters: Human-Centered Design and Evaluation of the Parkinson Disease-BRIDGE Platform. JMIR Human Factors, 2022, 9, e33967.	1.0	2
121	Gene coexpression modules in human cognition. Nature Neuroscience, 2016, 19, 173-175.	7.1	1
122	706. Wnt/β-Catenin Pathway Contributions to Dendritic Spine and Clutamatergic Synapse Formation Responsive to Lithium-Mediated GSK3 Inhibition. Biological Psychiatry, 2017, 81, S286.	0.7	1
123	LIMITED CONTRIBUTION OF RARE, NONCODING VARIATION TO AUTISM SPECTRUM DISORDER FROM SEQUENCING OF 2,076 GENOMES IN QUARTET FAMILIES. European Neuropsychopharmacology, 2019, 29, S784-S785.	0.3	1
124	Exome Sequencing for Prenatal Diagnosis in Nonimmune Hydrops Fetalis. Obstetrical and Gynecological Survey, 2021, 76, 139-141.	0.2	1
125	Mental Retardation (Former Term). , 2013, , 1841-1841.		0

#	Article	IF	CITATIONS
127	The Newly Emerging View of the Genome. , 2016, , 3-26.		О
128	Whole-Exome Sequencing in Fetuses with Congenital Diaphragmatic Hernias: Known and Novel Genetic Mutation. Journal of the American College of Surgeons, 2020, 231, S217.	0.2	0
129	7q11.23 Duplications. , 2021, , 10-10.		О
130	Assessing the utility of electronic measures as a proxy for cognitive ability. Autism Research, 0, , .	2.1	0