Jason L Stein

List of Publications by Year
in descending order

89 papers	13,338 citations	53794 45 h-index	48315 88 g-index
118 all docs	118 docs citations	118 times ranked	19396 citing authors

#	Article	IF	Citations
1	De novo mutations revealed by whole-exome sequencing are strongly associated with autism. Nature, 2012, 485, 237-241.	27.8	1,863
2	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	27.8	772
3	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. Brain Imaging and Behavior, 2014, 8, 153-182.	2.1	696
4	Advancing the understanding of autism disease mechanisms through genetics. Nature Medicine, 2016, 22, 345-361.	30.7	684
5	Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.	21.4	594
6	Know Your Place: Neural Processing of Social Hierarchy in Humans. Neuron, 2008, 58, 273-283.	8.1	516
7	Chromosome conformation elucidates regulatory relationships in developing human brain. Nature, 2016, 538, 523-527.	27.8	507
8	The genetic architecture of the human cerebral cortex. Science, 2020, 367, .	12.6	450
9	Alzheimer's Disease Neuroimaging Initiative biomarkers as quantitative phenotypes: Genetics core aims, progress, and plans. Alzheimer's and Dementia, 2010, 6, 265-273.	0.8	378
10	ENIGMA and global neuroscience: A decade of large-scale studies of the brain in health and disease across more than 40 countries. Translational Psychiatry, 2020, 10, 100.	4.8	365
11	A Single-Cell Transcriptomic Atlas of Human Neocortical Development during Mid-gestation. Neuron, 2019, 103, 785-801.e8.	8.1	361
12	A validated network of effective amygdala connectivity. NeuroImage, 2007, 36, 736-745.	4.2	360
13	The Dynamic Landscape of Open Chromatin during Human Cortical Neurogenesis. Cell, 2018, 172, 289-304.e18.	28.9	281
14	Circuit-wide Transcriptional Profiling Reveals Brain Region-Specific Gene Networks Regulating Depression Susceptibility. Neuron, 2016, 90, 969-983.	8.1	272
15	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	12.8	250
16	Voxelwise genome-wide association study (vGWAS). NeuroImage, 2010, 53, 1160-1174.	4.2	239
17	A commonly carried allele of the obesity-related FTO gene is associated with reduced brain volume in the healthy elderly. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8404-8409.	7.1	227
18	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213

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19	Common variants at 12q14 and 12q24 are associated with hippocampal volume. Nature Genetics, 2012, 44, 545-551.	21.4	212
20	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431.	14.8	204
21	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192
22	A Quantitative Framework to Evaluate Modeling of Cortical Development by Neural Stem Cells. Neuron, 2014, 83, 69-86.	8.1	184
23	Genetic Control of Expression and Splicing in Developing Human Brain Informs Disease Mechanisms. Cell, 2019, 179, 750-771.e22.	28.9	174
24	ENIGMA and the individual: Predicting factors that affect the brain in 35 countries worldwide. NeuroImage, 2017, 145, 389-408.	4.2	173
25	Obesity is linked with lower brain volume in 700 AD and MCI patients. Neurobiology of Aging, 2010, 31, 1326-1339.	3.1	170
26	Common Alzheimer's Disease Risk Variant Within theCLUGene Affects White Matter Microstructure in Young Adults. Journal of Neuroscience, 2011, 31, 6764-6770.	3.6	157
27	Genome-wide analysis reveals novel genes influencing temporal lobe structure with relevance to neurodegeneration in Alzheimer's disease. NeuroImage, 2010, 51, 542-554.	4.2	141
28	Investigation of Anatomical Thalamo-Cortical Connectivity and fMRI Activation in Schizophrenia. Neuropsychopharmacology, 2012, 37, 499-507.	5.4	133
29	Sparse reduced-rank regression detects genetic associations with voxel-wise longitudinal phenotypes in Alzheimer's disease. NeuroImage, 2012, 60, 700-716.	4.2	121
30	Vasopressin Modulates Medial Prefrontal Cortexâ€“Amygdala Circuitry during Emotion Processing in Humans. Journal of Neuroscience, 2010, 30, 7017-7022.	3.6	118
31	The effects of physical activity, education, and body mass index on the aging brain. Human Brain Mapping, 2011, 32, 1371-1382.	3.6	117
32	Voxelwise gene-wide association study (vGeneWAS): Multivariate gene-based association testing in 731 elderly subjects. NeuroImage, 2011, 56, 1875-1891.	4.2	116
33	Common genetic variation influencing human white matter microstructure. Science, 2021, 372, .	12.6	106
34	Cas9 gene therapy for Angelman syndrome traps Ube3a-ATS long non-coding RNA. Nature, 2020, 587, 281-284.	27.8	92
35	Discovery and replication of gene influences on brain structure using LASSO regression. Frontiers in Neuroscience, 2012, 6, 115.	2.8	91
36	The contribution of genes to cortical thickness and volume. NeuroReport, 2011, 22, 101-105.	1.2	84

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37	Brain structure in healthy adults is related to serum transferrin and the H63D polymorphism in the HFE gene. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E851-9.	7.1	83
38	Genetic variants associated with longitudinal changes in brain structure across the lifespan. Nature Neuroscience, 2022, 25, 421-432.	14.8	75
39	Genetic Markers of ADHD-Related Variations in Intracranial Volume. American Journal of Psychiatry, 2019, 176, 228-238.	7.2	68
40	Comparing 3 T and 1.5 T MRI for tracking Alzheimer's disease progression with tensorâ€based morphometry. Human Brain Mapping, 2010, 31, 499-514.	3.6	66
41	Allelic differences between Europeans and Chinese for CREB1 SNPs and their implications in gene expression regulation, hippocampal structure and function, and bipolar disorder susceptibility. Molecular Psychiatry, 2014, 19, 452-461.	7.9	61
42	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796.	12.8	61
43	Joint genetic analysis of hippocampal size in mouse and human identifies a novel gene linked to neurodegenerative disease. BMC Genomics, 2014, 15, 850.	2.8	59
44	Rare Inherited Variation in Autism: Beginning to See the Forest and a Few Trees. Neuron, 2013, 77, 209-211.	8.1	56
45	Common genetic risk variants identified in the SPARK cohort support DDHD2 as a candidate risk gene for autism. Translational Psychiatry, 2020, 10, 265.	4.8	56
46	Multilocus Genetic Analysis of Brain Images. Frontiers in Genetics, 2011, 2, 73.	2.3	53
47	Genetic Analysis of Cortical Thickness and Fractional Anisotropy of Water Diffusion in the Brain. Frontiers in Neuroscience, 2011, 5, 120.	2.8	52
48	Discovery and replication of dopamine-related gene effects on caudate volume in young and elderly populations (N=1198) using genome-wide search. Molecular Psychiatry, 2011, 16, 927-937.	7.9	52
49	Vasopressin modulates social recognition-related activity in the left temporoparietal junction in humans. Translational Psychiatry, 2011, 1, e3-e3.	4.8	52
50	Predicting White Matter Integrity from Multiple Common Genetic Variants. Neuropsychopharmacology, 2012, 37, 2012-2019.	5.4	49
51	Cell-type-specific effects of genetic variation on chromatin accessibility during human neuronal differentiation. Nature Neuroscience, 2021, 24, 941-953.	14.8	47
52	Memo1-Mediated Tiling of Radial Glial Cells Facilitates Cerebral Cortical Development. Neuron, 2019, 103, 836-852.e5.	8.1	46
53	Relationship of a Variant in theNTRK1Gene to White Matter Microstructure in Young Adults. Journal of Neuroscience, 2012, 32, 5964-5972.	3.6	40
54	Hippocampal structure and human cognition: Key role of spatial processing and evidence supporting the efficiency hypothesis in females. Intelligence, 2013, 41, 129-140.	3.0	40

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55	Common variants contribute to intrinsic human brain functional networks. Nature Genetics, 2022, 54, 508-517.	21.4	37
56	Brain-trait-associated variants impact cell-type-specific gene regulation during neurogenesis. American Journal of Human Genetics, 2021, 108, 1647-1668.	6.2	36
57	Hippocampal volume is related to body mass index in Alzheimer's disease. NeuroReport, 2011, 22, 10-14.	1.2	35
58	EnigmaVis: Online Interactive Visualization of Genome-Wide Association Studies of the Enhancing NeuroImaging Genetics through Meta-Analysis (ENIGMA) Consortium. Twin Research and Human Genetics, 2012, 15, 414-418.	0.6	34
59	JAKMIP1, a Novel Regulator of Neuronal Translation, Modulates Synaptic Function and Autistic-like Behaviors in Mouse. Neuron, 2015, 88, 1173-1191.	8.1	34
60	Common folate gene variant, MTHFR C677T, is associated with brain structure in two independent cohorts of people with mild cognitive impairment. NeuroImage: Clinical, 2012, 1, 179-187.	2.7	29
61	Genome-wide association identifies genetic variants associated with lentiform nucleus volume in Nâ€‰=â€‰1345 young and elderly subjects. Brain Imaging and Behavior, 2013, 7, 102-115.	2.1	26
62	MRLocus: Identifying causal genes mediating a trait through Bayesian estimation of allelic heterogeneity. PLoS Genetics, 2021, 17, e1009455.	3.5	24
63	Predicting temporal lobe volume on MRI from genotypes using L¹-L² regularized regression. , 2012, , 1160-1163.		23
64	Genome-wide interaction analysis reveals replicated epistatic effects on brain structure. Neurobiology of Aging, 2015, 36, S151-S158.	3.1	22
65	Transcriptomic signatures of neuronal differentiation and their association with risk genes for autism spectrum and related neuropsychiatric disorders. Translational Psychiatry, 2016, 6, e864-e864.	4.8	22
66	Mapping causal pathways from genetics to neuropsychiatric disorders using genomeâ€wide imaging genetics: Current status and future directions. Psychiatry and Clinical Neurosciences, 2019, 73, 357-369.	1.8	22
67	The Evolutionary History of Common Genetic Variants Influencing Human Cortical Surface Area. Cerebral Cortex, 2021, 31, 1873-1887.	2.9	21
68	Human neural stem cell-derived cultures in three-dimensional substrates form spontaneously functional neuronal networks. Journal of Tissue Engineering and Regenerative Medicine, 2017, 11, 1022-1033.	2.7	20
69	Structural and functional neuroimaging phenotypes in dysbindin mutant mice. NeuroImage, 2012, 62, 120-129.	4.2	19
70	Ten years of enhancing <scp>neuroâ€imaging</scp> genetics through <scp>metaâ€analysis</scp>: An overview from the <scp>ENIGMA Genetics Working Group</scp>. Human Brain Mapping, 2022, 43, 292-299.	3.6	19
71	Evaluating brain structure traits as endophenotypes using polygenicity and discoverability. Human Brain Mapping, 2022, 43, 329-340.	3.6	19
72	Active fibers: Matching deformable tract templates to diffusion tensor images. NeuroImage, 2009, 47, T82-T89.	4.2	18

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73	Alzheimer's Disease Risk Gene,GAB2, is Associated with Regional Brain Volume Differences in 755 Young Healthy Twins. Twin Research and Human Genetics, 2012, 15, 286-295.	0.6	16
74	Genome engineering of isogenic human ES cells to model autism disorders. Nucleic Acids Research, 2015, 43, e65-e65.	14.5	15
75	Default Patterning Produces Pan-cortical Glutamatergic and CGE/LGE-like GABAergic Neurons from Human Pluripotent Stem Cells. Stem Cell Reports, 2017, 9, 1463-1476.	4.8	14
76	Segmentor: a tool for manual refinement of 3D microscopy annotations. BMC Bioinformatics, 2021, 22, 260.	2.6	11
77	Genetics of the Connectome and the ENIGMA Project. Research and Perspectives in Neurosciences, 2016, , 147-164.	0.4	10
78	Boosting power to detect genetic associations in imaging using multi-locus, genome-wide scans and ridge regression. , 2011, , .		9
79	Exhaustive Search of the SNP-SNP Interactome Identifies Epistatic Effects on Brain Volume in Two Cohorts. Lecture Notes in Computer Science, 2013, 16, 600-607.	1.3	9
80	Genome-wide association reveals dopamine-related genetic effects on caudate volume. Molecular Psychiatry, 2011, 16, 881-881.	7.9	8
81	NuMorph: Tools for cortical cellular phenotyping in tissue-cleared whole-brain images. Cell Reports, 2021, 37, 109802.	6.4	8
82	Neuroimaging and Genetics: Exploring, Searching, and Finding. Twin Research and Human Genetics, 2012, 15, 267-272.	0.6	7
83	Genetic Clustering on the Hippocampal Surface for Genome-Wide Association Studies. Lecture Notes in Computer Science, 2013, 16, 690-697.	1.3	7
84	Copy number variation and brain structure: lessons learned from chromosome 16p11.2. Genome Medicine, 2015, 7, 13.	8.2	6
85	Early developmental gene enhancers affect subcortical volumes in the adult human brain. Human Brain Mapping, 2016, 37, 1788-1800.	3.6	6
86	From base pair to brain. Nature Neuroscience, 2021, 24, 619-621.	14.8	4
87	Imaging Genomics and ENIGMA. , 2016, , 101-115.		3
88	Principal components regression: Multivariate, gene-based tests in imaging genomics. , 2011, , .		2
89	<scp>ToxCast</scp> chemical library Wnt screen identifies diethanolamine as an activator of neural progenitor proliferation. FASEB BioAdvances, 2022, 4, 441-453.	2.4	1