Caleb Webber

List of Publications by Year
in descending order

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69 papers	13,896 citations	94381 37 h-index	95218 68 g-index
76 all docs	76 docs citations	76 times ranked	23098 citing authors

#	Article	IF	Citations
1	Single-Nuclei RNA Sequencing of 5 Regions of the Human Prenatal Brain Implicates Developing Neuron Populations in Genetic Risk for Schizophrenia. Biological Psychiatry, 2023, 93, 157-166.	0.7	11
2	Elucidating the relationship between migraine risk and brain structure using genetic data. Brain, 2022, 145, 3214-3224.	3.7	7
3	Targeted single-cell RNA sequencing of transcription factors enhances the identification of cell types and trajectories. Genome Research, 2021, 31, 1069-1081.	2.4	18
4	Combining multiomics and drug perturbation profiles to identify muscle-specific treatments for spinal muscular atrophy. JCI Insight, 2021, 6, .	2.3	8
5	The genomic basis of mood instability: identification of 46 loci in 363,705 UK Biobank participants, genetic correlation with psychiatric disorders, and association with gene expression and function. Molecular Psychiatry, 2020, 25, 3091-3099.	4.1	48
6	Pro-maturational Effects of Human iPSC-Derived Cortical Astrocytes upon iPSC-Derived Cortical Neurons. Stem Cell Reports, 2020, 15, 38-51.	2.3	42
7	A single-cell atlas of the human substantia nigra reveals cell-specific pathways associated with neurological disorders. Nature Communications, 2020, 11, 4183.	5.8	178
8	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	1.7	18
9	Addressing variability in iPSC-derived models of human disease: guidelines to promote reproducibility. DMM Disease Models and Mechanisms, 2020, 13, .	1.2	205
10	<scp>Humanâ€Specific</scp> Transcriptome of Ventral and Dorsal Midbrain Dopamine Neurons. Annals of Neurology, 2020, 87, 853-868.	2.8	22
11	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. Nature Communications, 2020, 11, 3368.	5.8	49
12	Genomeâ€Wide Association Study of Pain in Parkinson's Disease Implicates TRPM8 as a Risk Factor. Movement Disorders, 2020, 35, 705-707.	2.2	7
13	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. International Journal of Epidemiology, 2020, 49, 1022-1031.	0.9	34
14	Large-scale neuroanatomical study uncovers 198 gene associations in mouse brain morphogenesis. Nature Communications, 2019, 10, 3465.	5.8	23
15	CSF1R inhibitor JNJ-40346527 attenuates microglial proliferation and neurodegeneration in P301S mice. Brain, 2019, 142, 3243-3264.	3.7	156
16	RNA sequencing reveals MMP2 and TGFB1 downregulation in LRRK2 G2019S Parkinson's iPSC-derived astrocytes. Neurobiology of Disease, 2019, 129, 56-66.	2.1	55
17	Cellular Î±-synuclein pathology is associated with bioenergetic dysfunction in Parkinsonâ€™s iPSC-derived dopamine neurons. Human Molecular Genetics, 2019, 28, 2001-2013.	1.4	102
18	Antiviral activity of bone morphogenetic proteins and activins. Nature Microbiology, 2019, 4, 339-351.	5.9	39

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19	Single-Cell Sequencing of iPSC-Dopamine Neurons Reconstructs Disease Progression and Identifies HDAC4 as a Regulator of Parkinson Cell Phenotypes. Cell Stem Cell, 2019, 24, 93-106.e6.	5.2	123
20	Reproducibility of Molecular Phenotypes after Long-Term Differentiation toÂHuman iPSC-Derived Neurons: A Multi-Site Omics Study. Stem Cell Reports, 2018, 11, 897-911.	2.3	135
21	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
22	Transcriptomic profiling of purified patient-derived dopamine neurons identifies convergent perturbations and therapeutics for Parkinsonâ€™s disease. Human Molecular Genetics, 2017, 26, ddw412.	1.4	62
23	Multiplex High-Throughput Targeted Proteomic Assay To Identify Induced Pluripotent Stem Cells. Analytical Chemistry, 2017, 89, 2440-2448.	3.2	15
24	Epistasis in Neuropsychiatric Disorders. Trends in Genetics, 2017, 33, 256-265.	2.9	18
25	Whole-exome sequencing of 228 patients with sporadic Parkinsonâ€™s disease. Scientific Reports, 2017, 7, 41188.	1.6	27
26	Diverse type 2 diabetes genetic risk factors functionally converge in a phenotype-focused gene network. PLoS Computational Biology, 2017, 13, e1005816.	1.5	15
27	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
28	Systematic Phenomics Analysis Deconvolutes Genes Mutated in Intellectual Disability into Biologically Coherent Modules. American Journal of Human Genetics, 2016, 98, 149-164.	2.6	270
29	Duplications in ADHD patients harbour neurobehavioural genes that are coâ€expressed with genes associated with hyperactivity in the mouse. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 97-107.	1.1	2
30	Haploinsufficiency predictions without study bias. Nucleic Acids Research, 2015, 43, e101-e101.	6.5	54
31	GeneNet Toolbox for MATLAB: a flexible platform for the analysis of gene connectivity in biological networks. Bioinformatics, 2015, 31, 442-444.	1.8	14
32	Synergistic Interactions between Drosophila Orthologues of Genes Spanned by De Novo Human CNVs Support Multiple-Hit Models of Autism. PLoS Genetics, 2015, 11, e1004998.	1.5	35
33	Gene Networks Underlying Convergent and Pleiotropic Phenotypes in a Large and Systematically-Phenotyped Cohort with Heterogeneous Developmental Disorders. PLoS Genetics, 2015, 11, e1005012.	1.5	14
34	The clustering of functionally related genes contributes to CNV-mediated disease. Genome Research, 2015, 25, 802-813.	2.4	31
35	Extensive microRNA-mediated crosstalk between lncRNAs and mRNAs in mouse embryonic stem cells. Genome Research, 2015, 25, 655-666.	2.4	95
36	Diagnostically relevant facial gestalt information from ordinary photos. ELife, 2014, 3, e02020.	2.8	129

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37	Unbiased Functional Clustering of Gene Variants with a Phenotypic-Linkage Network. PLoS Computational Biology, 2014, 10, e1003815.	1.5	48
38	Phenotype Ontologies and Cross-Species Analysis for Translational Research. PLoS Genetics, 2014, 10, e1004268.	1.5	63
39	Clinical Significance of De Novo and Inherited Copy-Number Variation. Human Mutation, 2013, 34, 1679-1687.	1.1	100
40	The Roles of FMRP-Regulated Genes in Autism Spectrum Disorder: Single- and Multiple-Hit Genetic Etiologies. American Journal of Human Genetics, 2013, 93, 825-839.	2.6	60
41	Network Topologies and Convergent Aetiologies Arising from Deletions and Duplications Observed in Individuals with Autism. PLoS Genetics, 2013, 9, e1003523.	1.5	51
42	Common Variants in Left/Right Asymmetry Genes and Pathways Are Associated with Relative Hand Skill. PLoS Genetics, 2013, 9, e1003751.	1.5	129
43	GAT: a simulation framework for testing the association of genomic intervals. Bioinformatics, 2013, 29, 2046-2048.	1.8	221
44	Expression profiling of mouse subplate reveals a dynamic gene network and disease association with autism and schizophrenia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3555-3560.	3.3	108
45	Characterizing epistatic hotspots of human disease. BMC Proceedings, 2012, 6, .	1.8	0
46	Large-scale objective association of mouse phenotypes with human symptoms through structural variation identified in patients with developmental disorders. Human Mutation, 2012, 33, 874-883.	1.1	17
47	Functional Enrichment Analysis with Structural Variants: Pitfalls and Strategies. Cytogenetic and Genome Research, 2011, 135, 277-285.	0.6	24
48	Natural genetic variation caused by small insertions and deletions in the human genome. Genome Research, 2011, 21, 830-839.	2.4	212
49	Genes and biological processes commonly disrupted in rare and heterogeneous developmental delay syndromes. Human Molecular Genetics, 2011, 20, 880-893.	1.4	23
50	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	13.7	1,803
51	Elusive Copy Number Variation in the Mouse Genome. PLoS ONE, 2010, 5, e12839.	1.1	24
52	Accurate Distinction of Pathogenic from Benign CNVs in Mental Retardation. PLoS Computational Biology, 2010, 6, e1000752.	1.5	46
53	Candidate genes and biological processes in de novo CNVs from autistic individuals. Genome Biology, 2010, 11, O9.	13.9	0
54	Forging Links between Human Mental Retardationâ€“Associated CNVs and Mouse Gene Knockout Models. PLoS Genetics, 2009, 5, e1000531.	1.5	40

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55	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	13.7	657
56	SCANPS: a web server for iterative protein sequence database searching by dynamic programing, with display in a hierarchical SCOP browser. Nucleic Acids Research, 2008, 36, W25-W29.	6.5	32
57	Reduced purifying selection prevails over positive selection in human copy number variant evolution. Genome Research, 2008, 18, 1711-1723.	2.4	73
58	An analysis of the gene complement of a marsupial, Monodelphis domestica: Evolution of lineage-specific genes and giant chromosomes. Genome Research, 2007, 17, 969-981.	2.4	66
59	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	13.7	661
60	Bias of Selection on Human Copy-Number Variants. PLoS Genetics, 2006, 2, e20.	1.5	237
61	Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature, 2005, 438, 803-819.	13.7	2,215
62	Hotspots of mutation and breakage in dog and human chromosomes. Genome Research, 2005, 15, 1787-1797.	2.4	47
63	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
64	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. Nature, 2004, 432, 717-722.	13.7	391
65	Genes and homology. Current Biology, 2004, 14, R332-R333.	1.8	24
66	Increased coverage obtained by combination of methods for protein sequence database searching. Bioinformatics, 2003, 19, 1397-1403.	1.8	7
67	A whole-genome radiation hybrid panel and framework map of the rat genome. Mammalian Genome, 2000, 11, 791-795.	1.0	29
68	A radiation hybrid map of the rat genome containing 5,255 markers. Nature Genetics, 1999, 22, 27-36.	9.4	231
69	A Physical Map of 30,000 Human Genes. , 1998, 282, 744-746.		605