Caleb Webber

List of Publications by Year
in descending order

69 papers	13,896 citations	94269 37 h-index	95083 68 g-index
76 all docs	76 docs citations	76 times ranked	23098 citing authors

#	Article	IF	Citations
1	Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature, 2005, 438, 803-819.	13.7	2,215
2	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
3	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	13.7	1,803
4	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
5	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	13.7	661
6	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	13.7	657
7	A Physical Map of 30,000 Human Genes. , 1998, 282, 744-746.		605
8	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
9	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. Nature, 2004, 432, 717-722.	13.7	391
10	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
11	Bias of Selection on Human Copy-Number Variants. PLoS Genetics, 2006, 2, e20.	1.5	237
12	A radiation hybrid map of the rat genome containing 5,255 markers. Nature Genetics, 1999, 22, 27-36.	9.4	231
13	GAT: a simulation framework for testing the association of genomic intervals. Bioinformatics, 2013, 29, 2046-2048.	1.8	221
14	Natural genetic variation caused by small insertions and deletions in the human genome. Genome Research, 2011, 21, 830-839.	2.4	212
15	Addressing variability in iPSC-derived models of human disease: guidelines to promote reproducibility. DMM Disease Models and Mechanisms, 2020, 13, .	1.2	205
16	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
17	CSF1R inhibitor JNJ-40346527 attenuates microglial proliferation and neurodegeneration in P301S mice. Brain, 2019, 142, 3243-3264.	3.7	156
18	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

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19	Common Variants in Left/Right Asymmetry Genes and Pathways Are Associated with Relative Hand Skill. PLoS Genetics, 2013, 9, e1003751.	1.5	129
20	Diagnostically relevant facial gestalt information from ordinary photos. ELife, 2014, 3, e02020.	2.8	129
21	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
22	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
23	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
24	Clinical Significance of De Novo and Inherited Copy-Number Variation. Human Mutation, 2013, 34, 1679-1687.	1.1	100
25	Extensive microRNA-mediated crosstalk between lncRNAs and mRNAs in mouse embryonic stem cells. Genome Research, 2015, 25, 655-666.	2.4	95
26	Reduced purifying selection prevails over positive selection in human copy number variant evolution. Genome Research, 2008, 18, 1711-1723.	2.4	73
27	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
28	Phenotype Ontologies and Cross-Species Analysis for Translational Research. PLoS Genetics, 2014, 10, e1004268.	1.5	63
29	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
30	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
31	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
32	Haploinsufficiency predictions without study bias. Nucleic Acids Research, 2015, 43, e101-e101.	6.5	54
33	Network Topologies and Convergent Aetiologies Arising from Deletions and Duplications Observed in Individuals with Autism. PLoS Genetics, 2013, 9, e1003523.	1.5	51
34	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. Nature Communications, 2020, 11, 3368.	5.8	49
35	Unbiased Functional Clustering of Gene Variants with a Phenotypic-Linkage Network. PLoS Computational Biology, 2014, 10, e1003815.	1.5	48
36	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

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37	Hotspots of mutation and breakage in dog and human chromosomes. Genome Research, 2005, 15, 1787-1797.	2.4	47
38	Accurate Distinction of Pathogenic from Benign CNVs in Mental Retardation. PLoS Computational Biology, 2010, 6, e1000752.	1.5	46
39	Pro-maturational Effects of Human iPSC-Derived Cortical Astrocytes upon iPSC-Derived Cortical Neurons. Stem Cell Reports, 2020, 15, 38-51.	2.3	42
40	Forging Links between Human Mental Retardationâ€“Associated CNVs and Mouse Gene Knockout Models. PLoS Genetics, 2009, 5, e1000531.	1.5	40
41	Antiviral activity of bone morphogenetic proteins and activins. Nature Microbiology, 2019, 4, 339-351.	5.9	39
42	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
43	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
44	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
45	The clustering of functionally related genes contributes to CNV-mediated disease. Genome Research, 2015, 25, 802-813.	2.4	31
46	A whole-genome radiation hybrid panel and framework map of the rat genome. Mammalian Genome, 2000, 11, 791-795.	1.0	29
47	Whole-exome sequencing of 228 patients with sporadic Parkinsonâ€™s disease. Scientific Reports, 2017, 7, 41188.	1.6	27
48	Genes and homology. Current Biology, 2004, 14, R332-R333.	1.8	24
49	Elusive Copy Number Variation in the Mouse Genome. PLoS ONE, 2010, 5, e12839.	1.1	24
50	Functional Enrichment Analysis with Structural Variants: Pitfalls and Strategies. Cytogenetic and Genome Research, 2011, 135, 277-285.	0.6	24
51	Genes and biological processes commonly disrupted in rare and heterogeneous developmental delay syndromes. Human Molecular Genetics, 2011, 20, 880-893.	1.4	23
52	Large-scale neuroanatomical study uncovers 198 gene associations in mouse brain morphogenesis. Nature Communications, 2019, 10, 3465.	5.8	23
53	<scp>Humanâ€Specific</scp> Transcriptome of Ventral and Dorsal Midbrain Dopamine Neurons. Annals of Neurology, 2020, 87, 853-868.	2.8	22
54	Epistasis in Neuropsychiatric Disorders. Trends in Genetics, 2017, 33, 256-265.	2.9	18

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55	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	1.7	18
56	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
57	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
58	Multiplex High-Throughput Targeted Proteomic Assay To Identify Induced Pluripotent Stem Cells. Analytical Chemistry, 2017, 89, 2440-2448.	3.2	15
59	Diverse type 2 diabetes genetic risk factors functionally converge in a phenotype-focused gene network. PLoS Computational Biology, 2017, 13, e1005816.	1.5	15
60	GeneNet Toolbox for MATLAB: a flexible platform for the analysis of gene connectivity in biological networks. Bioinformatics, 2015, 31, 442-444.	1.8	14
61	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
62	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
63	Combining multiomics and drug perturbation profiles to identify muscle-specific treatments for spinal muscular atrophy. JCI Insight, 2021, 6, .	2.3	8
64	Increased coverage obtained by combination of methods for protein sequence database searching. Bioinformatics, 2003, 19, 1397-1403.	1.8	7
65	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
66	Elucidating the relationship between migraine risk and brain structure using genetic data. Brain, 2022, 145, 3214-3224.	3.7	7
67	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
68	Candidate genes and biological processes in de novo CNVs from autistic individuals. Genome Biology, 2010, 11, O9.	13.9	0
69	Characterizing epistatic hotspots of human disease. BMC Proceedings, 2012, 6, .	1.8	0