Stephen J Newhouse

List of Publications by Year
in descending order

90 papers	17,827 citations	53660 45 h-index	60497 81 g-index
96 all docs	96 docs citations	96 times ranked	26961 citing authors

#	Article	IF	Citations
1	The effects of genotype on inflammatory response in hippocampal progenitor cells: A computational approach. Brain, Behavior, & Immunity - Health, 2021, 15, 100286.	1.3	2
2	A recessive S174X mutation in Optineurin causes amyotrophic lateral sclerosis through a loss of function via allele-specific nonsense-mediated decay. Neurobiology of Aging, 2021, 106, 1-6.	1.5	3
3	An epigenome-wide association study of Alzheimer's disease blood highlights robust DNA hypermethylation in the HOXB6 gene. Neurobiology of Aging, 2020, 95, 26-45.	1.5	51
4	Working Towards a Blood-Derived Gene Expression Biomarker Specific for Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2020, 74, 545-561.	1.2	9
5	Genome-wide Meta-analysis Finds the ACSL5-ZDHHC6 Locus Is Associated with ALS and Links Weight Loss to the Disease Genetics. Cell Reports, 2020, 33, 108323.	2.9	41
6	Genomeâ€wide association study of rate of cognitive decline in Alzheimer's disease patients identifies novel genes and pathways. Alzheimer's and Dementia, 2020, 16, 1134-1145.	0.4	28
7	C9orf72 intermediate expansions of 24â€“30 repeats are associated with ALS. Acta Neuropathologica Communications, 2019, 7, 115.	2.4	75
8	Genetic associations with radiological damage in rheumatoid arthritis: Meta-analysis of seven genome-wide association studies of 2,775 cases. PLoS ONE, 2019, 14, e0223246.	1.1	11
9	Differential gene expression analysis in blood of first episode psychosis patients. Schizophrenia Research, 2019, 209, 88-97.	1.1	27
10	Transcriptomic analysis of probable asymptomatic and symptomatic alzheimer brains. Brain, Behavior, and Immunity, 2019, 80, 644-656.	2.0	72
11	A Meta-Analysis of Alzheimerâ€™s Disease Brain Transcriptomic Data. Journal of Alzheimer's Disease, 2019, 68, 1635-1656.	1.2	67
12	ALSgeneScanner: a pipeline for the analysis and interpretation of DNA sequencing data of ALS patients. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2019, 20, 207-215.	1.1	11
13	A genome-wide association study for extremely high intelligence. Molecular Psychiatry, 2018, 23, 1226-1232.	4.1	54
14	New insights into the pharmacogenomics of antidepressant response from the GENDEP and STAR*D studies: rare variant analysis and high-density imputation. Pharmacogenomics Journal, 2018, 18, 413-421.	0.9	40
15	Multi-polygenic score approach to trait prediction. Molecular Psychiatry, 2018, 23, 1368-1374.	4.1	167
16	Applying polygenic risk scoring for psychiatric disorders to a large family with bipolar disorder and major depressive disorder. Communications Biology, 2018, 1, 163.	2.0	17
17	Exome array analysis of adverse reactions to fluoropyrimidine-based therapy for gastrointestinal cancer. PLoS ONE, 2018, 13, e0188911.	1.1	3
18	Polygenic risk score analyses of symptoms and treatment response in an antipsychotic-naive first episode of psychosis cohort. Translational Psychiatry, 2018, 8, 174.	2.4	49

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19	g(HbF): a genetic model of fetal hemoglobin in sickle cell disease. Blood Advances, 2018, 2, 235-239.	2.5	33
20	Identification of new risk factors for rolandic epilepsy: CNV at Xp22.31 and alterations at cholinergic synapses. Journal of Medical Genetics, 2018, 55, 607-616.	1.5	22
21	Effect of cytochrome CYP2C19 metabolizing activity on antidepressant response and side effects: Meta-analysis of data from genome-wide association studies. European Neuropsychopharmacology, 2018, 28, 945-954.	0.3	64
22	Reversal of Agingâ€Induced Increases in Aortic Stiffness by Targeting Cytoskeletal Proteinâ€Protein Interfaces. Journal of the American Heart Association, 2018, 7, .	1.6	17
23	Loss of Trem2 in microglia leads to widespread disruption of cell coexpression networks in mouse brain. Neurobiology of Aging, 2018, 69, 151-166.	1.5	25
24	Mitochondrial genes are altered in blood early in Alzheimer's disease. Neurobiology of Aging, 2017, 53, 36-47.	1.5	132
25	Pharmacogenetics of antidepressant response: A polygenic approach. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2017, 75, 128-134.	2.5	71
26	Genetic and environmental risk factors for rheumatoid arthritis in a UK African ancestry population: the GENRA caseâ€“control study. Rheumatology, 2017, 56, 1282-1292.	0.9	18
27	Genetics of stroke in a UK African ancestry case-control study. Neurology: Genetics, 2017, 3, e142.	0.9	19
28	An Examination of Polygenic Score Risk Prediction in Individuals With First-Episode Psychosis. Biological Psychiatry, 2017, 81, 470-477.	0.7	176
29	[O2â€“13â€“06]: ASSESSING TREM2 FUNCTION IN ALZHEIMER's DISEASE WITH RNAâ€SEQ. Alzheimer's and Dementia, 2017, 13, P590.	0.4	0
30	Meta-analysis of CYP2C19 association with efficacy and side effects of citalopram and escitalopram. European Neuropsychopharmacology, 2017, 27, S582-S583.	0.3	0
31	Brain Transcriptome Sequencing of a Natural Model of Alzheimer's Disease. Frontiers in Aging Neuroscience, 2017, 9, 64.	1.7	14
32	Trajectories of dementia-related cognitive decline in a large mental health records derived patient cohort. PLoS ONE, 2017, 12, e0178562.	1.1	30
33	P1â€127: Assessing Trem2 Risk Variants in Alzheimer's Disease with RNAâ€SEQ. Alzheimer's and Dementia, 2016, 12, P452.	0.4	0
34	P4-115: Electronic Records for Dementia Research: Do Behavioural Disturbances, Antihypertensives and Antidepressants Influence Decline Trajectories?. , 2016, 12, P1056-P1057.		0
35	P1â€039: Assessment of an Alzheimerâ€™s Gene Expression Signature. Alzheimer's and Dementia, 2016, 12, P415	0.4	0
36	Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 645-653.	0.4	72

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37	Immune signatures and disorder-specific patterns in a cross-disorder gene expression analysis. British Journal of Psychiatry, 2016, 209, 202-208.	1.7	31
38	Genetic Risk as a Marker of Amyloid-Î² and Tau Burden in Cerebrospinal Fluid. Journal of Alzheimer's Disease, 2016, 55, 1417-1427.	1.2	16
39	Quality control, imputation and analysis of genome-wide genotyping data from the Illumina HumanCoreExome microarray. Briefings in Functional Genomics, 2016, 15, 298-304.	1.3	65
40	Genome-Wide Association of Heroin Dependence in Han Chinese. PLoS ONE, 2016, 11, e0167388.	1.1	30
41	No Evidence to Suggest that the Use of Acetylcholinesterase Inhibitors Confounds the Results of Two Blood-Based Biomarker Studies in Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2015, 47, 741-750.	1.2	2
42	A Pathway Based Classification Method for Analyzing Gene Expression for Alzheimerâ€™s Disease Diagnosis. Journal of Alzheimer's Disease, 2015, 49, 659-669.	1.2	43
43	Circulating Proteomic Signatures of Chronological Age. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2015, 70, 809-816.	1.7	106
44	Linking Genetics of Brain Changes to Alzheimer's Disease: Sparse Whole Genome Association Scan of Regional MRI Volumes in the ADNI and AddNeuroMed Cohorts. Journal of Alzheimer's Disease, 2015, 45, 851-864.	1.2	10
45	Plasma protein biomarkers of Alzheimerâ€™s disease endophenotypes in asymptomatic older twins: early cognitive decline and regional brain volumes. Translational Psychiatry, 2015, 5, e584-e584.	2.4	39
46	A Subset of Cerebrospinal Fluid Proteins from a Multi-Analyte Panel Associated with Brain Atrophy, Disease Classification and Prediction in Alzheimerâ€™s Disease. PLoS ONE, 2015, 10, e0134368.	1.1	26
47	Genetic Predisposition to Increased Blood Cholesterol and Triglyceride Lipid Levels and Risk of Alzheimer Disease: A Mendelian Randomization Analysis. PLoS Medicine, 2014, 11, e1001713.	3.9	75
48	Assessment of ZnT3 and PSD95 protein levels in Lewy body dementias and Alzheimer's disease: association with cognitive impairment. Neurobiology of Aging, 2014, 35, 2836-2844.	1.5	94
49	Alleles that increase risk for type 2 diabetes mellitus are not associated with increased risk for Alzheimer's disease. Neurobiology of Aging, 2014, 35, 2883.e3-2883.e10.	1.5	9
50	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	2.6	73
51	No Differences in Hippocampal Volume between Carriers and Non-Carriers of the ApoE Îµ4 and Îµ2 Alleles in Young Healthy Adolescents. Journal of Alzheimer's Disease, 2014, 40, 37-43.	1.2	51
52	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
53	Alzheimer's disease biomarker discovery using SOMAscan multiplexed protein technology. Alzheimer's and Dementia, 2014, 10, 724-734.	0.4	182
54	Pharmacogenetics of pemetrexed combination therapy in lung cancer: pathway analysis reveals novel toxicity associations. Pharmacogenomics Journal, 2014, 14, 411-417.	0.9	16

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55	Calibrating Longitudinal Cognition in Alzheimer's Disease Across Diverse Test Batteries and Datasets. Neuroepidemiology, 2014, 43, 194-205.	1.1	43
56	Detecting epistasis in the presence of linkage disequilibrium: A focused comparison. , 2013, , .		2
57	Candidate Blood Proteome Markers of Alzheimer's Disease Onset and Progression: A Systematic Review and Replication Study. Journal of Alzheimer's Disease, 2013, 38, 515-531.	1.2	160
58	The C9ORF72 expansion mutation is a common cause of ALS+/â˜FTD in Europe and has a single founder. European Journal of Human Genetics, 2013, 21, 102-108.	1.4	201
59	Gene-centric meta-analyses of 108 912 individuals confirm known body mass index loci and reveal three novel signals. Human Molecular Genetics, 2013, 22, 184-201.	1.4	82
60	Microarray, qPCR, andKCNJ5Sequencing of Aldosterone-Producing Adenomas Reveal Differences in Genotype and Phenotype between Zona Glomerulosa- and Zona Fasciculata-Like Tumors. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E819-E829.	1.8	164
61	Common Genetic Variation in the 3â€²- BCL11B Gene Desert Is Associated With Carotid-Femoral Pulse Wave Velocity and Excess Cardiovascular Disease Risk. Circulation: Cardiovascular Genetics, 2012, 5, 81-90.	5.1	90
62	Mitochondrial Dysfunction and Immune Activation are Detectable in Early Alzheimer's Disease Blood. Journal of Alzheimer's Disease, 2012, 30, 685-710.	1.2	141
63	Screening for OPTN mutations in a cohort of British amyotrophic lateral sclerosis patients. Neurobiology of Aging, 2012, 33, 2948.e15-2948.e17.	1.5	18
64	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	2.6	227
65	Plasma Based Markers of [11C] PiB-PET Brain Amyloid Burden. PLoS ONE, 2012, 7, e44260.	1.1	89
66	Identification of cis-regulatory variation influencing protein abundance levels in human plasma. Human Molecular Genetics, 2012, 21, 3719-3726.	1.4	94
67	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	2.6	239
68	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2012, 90, 1116-1117.	2.6	0
69	An MND/ALS phenotype associated with C9orf72 repeat expansion: Abundant p62â€positive, TDPâ€43â€negative inclusions in cerebral cortex, hippocampus and cerebellum but without associated cognitive decline. Neuropathology, 2012, 32, 505-514.	0.7	110
70	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	2.6	122
71	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	2.6	159
72	Chromosome 9p21 in sporadic amyotrophic lateral sclerosis in the UK and seven other countries: a genome-wide association study. Lancet Neurology, The, 2010, 9, 986-994.	4.9	205

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73	Polymorphisms in the WNK1 Gene Are Associated with Blood Pressure Variation and Urinary Potassium Excretion. PLoS ONE, 2009, 4, e5003.	1.1	43
74	Targeting 160 Candidate Genes for Blood Pressure Regulation with a Genome-Wide Genotyping Array. PLoS ONE, 2009, 4, e6034.	1.1	98
75	Genome-wide scan identifies CDH13 as a novel susceptibility locus contributing to blood pressure determination in two European populations. Human Molecular Genetics, 2009, 18, 2288-2296.	1.4	170
76	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
77	Gene-centric Association Signals for Lipids and Apolipoproteins Identified via the HumanCVD BeadChip. American Journal of Human Genetics, 2009, 85, 628-642.	2.6	183
78	Common Genetic Variation Near the Phospholamban Gene Is Associated with Cardiac Repolarisation: Meta-Analysis of Three Genome-Wide Association Studies. PLoS ONE, 2009, 4, e6138.	1.1	53
79	Genome-wide Association Study Identifies Genes for Biomarkers of Cardiovascular Disease: Serum Urate and Dyslipidemia. American Journal of Human Genetics, 2008, 82, 139-149.	2.6	397
80	SLC2A9 Is a High-Capacity Urate Transporter in Humans. PLoS Medicine, 2008, 5, e197.	3.9	305
81	Monogenic Forms of Human Hypertension. , 2007, , 417-428.		1
82	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	9.4	1,298
83	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature, 2007, 447, 661-678.	13.7	8,895
84	Linkage Analysis Using Co-Phenotypes in the BRIGHT Study Reveals Novel Potential Susceptibility Loci for Hypertension. American Journal of Human Genetics, 2006, 79, 323-331.	2.6	22
85	Increased Support for Linkage of a Novel Locus on Chromosome 5q13 for Essential Hypertension in the British Genetics of Hypertension Study. Hypertension, 2006, 48, 105-111.	1.3	22
86	Haplotypes of the WNK1 gene associate with blood pressure variation in a severely hypertensive population from the British Genetics of Hypertension study. Human Molecular Genetics, 2005, 14, 1805-1814.	1.4	91
87	Association ofWNK1Gene Polymorphisms and Haplotypes With Ambulatory Blood Pressure in the General Population. Circulation, 2005, 112, 3423-3429.	1.6	124
88	NO ASSOCIATION OF THE WNK1 GENE WITH ESSENTIAL HYPERTENSION IN THE MRC BRIGHT STUDY. Journal of Hypertension, 2004, 22, S212.	0.3	0
89	Genome-wide mapping of human loci for essential hypertension. Lancet, The, 2003, 361, 2118-2123.	6.3	247
90	Genes and Hypertension. Current Pharmaceutical Design, 2003, 9, 1679-1689.	0.9	57