Jonathan L Haines

List of Publications by Year
in descending order

549	82,612	699 121	515 267
papers	citations	h-index	g-index

613	613	613	69301
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Finding the missing heritability of complex diseases. Nature, 2009, 461, 747-753.	13.7	7,490
2	Mutations in Cu/Zn superoxide dismutase gene are associated with familial amyotrophic lateral sclerosis. Nature, 1993, 362, 59-62.	13.7	6,331
3	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nature Genetics, 2013, 45, 1452-1458.	9.4	3,741
4	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
5	Complement Factor H Variant Increases the Risk of Age-Related Macular Degeneration. Science, 2005, 308, 419-421.	6.0	2,232
6	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
7	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	9.4	1,962
8	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	13.7	1,803
9	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. Nature Genetics, 2011, 43, 436-441.	9.4	1,676
10	Risk Alleles for Multiple Sclerosis Identified by a Genomewide Study. New England Journal of Medicine, 2007, 357, 851-862.	13.9	1,529
11	Mapping autism risk loci using genetic linkage and chromosomal rearrangements. Nature Genetics, 2007, 39, 319-328.	9.4	1,272
12	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	9.4	1,213
13	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nature Genetics, 2016, 48, 134-143.	9.4	1,167
14	Mutations in UBQLN2 cause dominant X-linked juvenile and adult-onset ALS and ALS/dementia. Nature, 2011, 477, 211-215.	13.7	1,016
15	Common genetic variants on 5p14.1 associate with autism spectrum disorders. Nature, 2009, 459, 528-533.	13.7	912
16	Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. Nature Biotechnology, 2013, 31, 1102-1111.	9.4	846
17	Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. American Journal of Human Genetics, 2014, 94, 677-694.	2.6	819
18	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	9.4	783

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19	Meta-analysis of genome scans and replication identify CD6, IRF8 and TNFRSF1A as new multiple sclerosis susceptibility loci. Nature Genetics, 2009, 41, 776-782.	9.4	729
20	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. Science, 2019, 365, .	6.0	710
21	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	9.4	700
22	Seven new loci associated with age-related macular degeneration. Nature Genetics, 2013, 45, 433-439.	9.4	687
23	The Electronic Medical Records and Genomics (eMERGE) Network: past, present, and future. Genetics in Medicine, 2013, 15, 761-771.	1.1	611
24	The PhenX Toolkit: Get the Most From Your Measures. American Journal of Epidemiology, 2011, 174, 253-260.	1.6	610
25	Heterozygosity for a Surfactant Protein C Gene Mutation Associated with Usual Interstitial Pneumonitis and Cellular Nonspecific Interstitial Pneumonitis in One Kindred. American Journal of Respiratory and Critical Care Medicine, 2002, 165, 1322-1328.	2.5	597
26	Interleukin 7 receptor Î± chain (IL7R) shows allelic and functional association with multiple sclerosis. Nature Genetics, 2007, 39, 1083-1091.	9.4	578
27	Isolation of a novel gene underlying batten disease, CLN3. Cell, 1995, 82, 949-957.	13.5	554
28	A genome-wide scan for common alleles affecting risk for autism. Human Molecular Genetics, 2010, 19, 4072-4082.	1.4	538
29	Mitochondrial Polymorphisms Significantly Reduce the Risk of Parkinson Disease. American Journal of Human Genetics, 2003, 72, 804-811.	2.6	507
30	Genome-wide association study identifies a new breast cancer susceptibility locus at 6q25.1. Nature Genetics, 2009, 41, 324-328.	9.4	481
31	Genetic linkage of bilateral acoustic neurofibromatosis to a DNA marker on chromosome 22. Nature, 1987, 329, 246-248.	13.7	478
32	Genetic variants near TIMP3 and high-density lipoproteinâ€“associated loci influence susceptibility to age-related macular degeneration. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7401-7406.	3.3	475
33	Genomeâ€Wide Association Study Confirms SNPs in SNCA and the MAPT Region as Common Risk Factors for Parkinson Disease. Annals of Human Genetics, 2010, 74, 97-109.	0.3	417
34	Linkage of a Gene Causing Familial Amyotrophic Lateral Sclerosis to Chromosome 21 and Evidence of Genetic-Locus Heterogeneity. New England Journal of Medicine, 1991, 324, 1381-1384.	13.9	407
35	Meta-analysis Confirms CR1, CLU, and PICALM as Alzheimer Disease Risk Loci and Reveals Interactions With APOE Genotypes. Archives of Neurology, 2010, 67, 1473.	4.9	376
36	Variants in the ATP-Binding Cassette Transporter (ABCA7), Apolipoprotein E Ïµ4, and the Risk of Late-Onset Alzheimer Disease in African Americans. JAMA - Journal of the American Medical Association, 2013, 309, 1483.	3.8	360

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37	GWAS of Cerebrospinal Fluid Tau Levels Identifies Risk Variants for Alzheimerâ€™s Disease. Neuron, 2013, 78, 256-268.	3.8	344
38	Individual common variants exert weak effects on the risk for autism spectrum disorders. Human Molecular Genetics, 2012, 21, 4781-4792.	1.4	334
39	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. Nature Neuroscience, 2017, 20, 1052-1061.	7.1	330
40	Cigarette Smoking Strongly Modifies the Association of LOC387715 and Age-Related Macular Degeneration. American Journal of Human Genetics, 2006, 78, 852-864.	2.6	316
41	Genomeâ€wide metaâ€analysis identifies novel multiple sclerosis susceptibility loci. Annals of Neurology, 2011, 70, 897-912.	2.8	314
42	Class II HLA interactions modulate genetic risk for multiple sclerosis. Nature Genetics, 2015, 47, 1107-1113.	9.4	312
43	Mapping Multiple Sclerosis Susceptibility to the HLA-DR Locus in African Americans. American Journal of Human Genetics, 2004, 74, 160-167.	2.6	311
44	Genetic assessment of age-associated Alzheimer disease risk: Development and validation of a polygenic hazard score. PLoS Medicine, 2017, 14, e1002258.	3.9	311
45	Genome-Wide Association Meta-analysis of Neuropathologic Features of Alzheimer's Disease and Related Dementias. PLoS Genetics, 2014, 10, e1004606.	1.5	305
46	Common genetic variants in the CLDN2 and PRSS1-PRSS2 loci alter risk for alcohol-related and sporadic pancreatitis. Nature Genetics, 2012, 44, 1349-1354.	9.4	303
47	Robust Replication of Genotype-Phenotype Associations across Multiple Diseases in an Electronic Medical Record. American Journal of Human Genetics, 2010, 86, 560-572.	2.6	302
48	Cardiac Sodium Channel (SCN5A) Variants Associated with Atrial Fibrillation. Circulation, 2008, 117, 1927-1935.	1.6	292
49	Age at Onset in Two Common Neurodegenerative Diseases Is Genetically Controlled. American Journal of Human Genetics, 2002, 70, 985-993.	2.6	291
50	PheKB: a catalog and workflow for creating electronic phenotype algorithms for transportability. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 1046-1052.	2.2	284
51	Heterogeneity at the HLA-DRB1 locus and risk for multiple sclerosis. Human Molecular Genetics, 2006, 15, 2813-2824.	1.4	279
52	Common Variants at 9p21 and 8q22 Are Associated with Increased Susceptibility to Optic Nerve Degeneration in Glaucoma. PLoS Genetics, 2012, 8, e1002654.	1.5	276
53	The genetic defect in familial Alzheimer's disease is not tightly linked to the amyloid Î²-protein gene. Nature, 1987, 329, 156-157.	13.7	275
54	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. Nature Genetics, 2013, 45, 155-163.	9.4	269

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55	A High-Density Screen for Linkage in Multiple Sclerosis. American Journal of Human Genetics, 2005, 77, 454-467.	2.6	268
56	Analysis of European mitochondrial haplogroups with Alzheimer disease risk. Neuroscience Letters, 2004, 365, 28-32.	1.0	264
57	Quality Control Procedures for Genomeâ€Wide Association Studies. Current Protocols in Human Genetics, 2011, 68, Unit1.19.	3.5	259
58	Complete Genomic Screen in Parkinson Disease. JAMA - Journal of the American Medical Association, 2001, 286, 2239.	3.8	257
59	Temperature-sensitive mutations in the IIIâ€“IV cytoplasmic loop region of the skeletal muscle sodium channel gene in paramyotonia congenita. Cell, 1992, 68, 769-774.	13.5	249
60	Human gene for torsion dystonia located on chromosome 9q32-q34. Neuron, 1989, 2, 1427-1434.	3.8	246
61	Exome sequencing of extended families with autism reveals genes shared across neurodevelopmental and neuropsychiatric disorders. Molecular Autism, 2014, 5, 1.	2.6	246
62	Exceptionally low likelihood of Alzheimerâ€™s dementia in APOE2 homozygotes from a 5,000-person neuropathological study. Nature Communications, 2020, 11, 667.	5.8	246
63	Genome-wide Association Study Implicates a Chromosome 12 Risk Locus for Late-Onset Alzheimer Disease. American Journal of Human Genetics, 2009, 84, 35-43.	2.6	242
64	Genetics, statistics and human disease: analytical retooling for complexity. Trends in Genetics, 2004, 20, 640-647.	2.9	230
65	Brain Expression Genome-Wide Association Study (eGWAS) Identifies Human Disease-Associated Variants. PLoS Genetics, 2012, 8, e1002707.	1.5	225
66	Meta-analysis of genome scans of age-related macular degeneration. Human Molecular Genetics, 2005, 14, 2257-2264.	1.4	224
67	Sex-Specific Association of Apolipoprotein E With Cerebrospinal Fluid Levels of Tau. JAMA Neurology, 2018, 75, 989.	4.5	223
68	Linkage of recessive familial amyotrophic lateral sclerosis to chromosome 2q33â€“q35. Nature Genetics, 1994, 7, 425-428.	9.4	221
69	Genome-wide analyses identify 68 new loci associated with intraocular pressure and improve risk prediction for primary open-angle glaucoma. Nature Genetics, 2018, 50, 778-782.	9.4	214
70	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. Nature Genetics, 2014, 46, 1126-1130.	9.4	212
71	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. Nature Genetics, 2016, 48, 189-194.	9.4	211
72	Glutathione S-transferase omega-1 modifiesage-at-onset of Alzheimer disease and Parkinson disease. Human Molecular Genetics, 2003, 12, 3259-3267.	1.4	208

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73	A Genomeâ€wide Association Study of Autism Reveals a Common Novel Risk Locus at 5p14.1. Annals of Human Genetics, 2009, 73, 263-273.	0.3	207
74	Neonatal Pulmonary Hypertension. New England Journal of Medicine, 2001, 344, 1832-1838.	13.9	202
75	Parkin mutations and susceptibility alleles in late-onset Parkinson's disease. Annals of Neurology, 2003, 53, 624-629.	2.8	201
76	Mutations in a Novel CLN6-Encoded Transmembrane Protein Cause Variant Neuronal Ceroid Lipofuscinosis in Man and Mouse. American Journal of Human Genetics, 2002, 70, 324-335.	2.6	199
77	Genome-wide association study identifies four novel loci associated with Alzheimerâ€™s endophenotypes and disease modifiers. Acta Neuropathologica, 2017, 133, 839-856.	3.9	199
78	Evidence for a role of the rare p.A152T variant in MAPT in increasing the risk for FTD-spectrum and Alzheimer's diseases. Human Molecular Genetics, 2012, 21, 3500-3512.	1.4	198
79	Prevalence of Mutations in TIGR/Myocilin in Patients with Adult and Juvenile Primary Open-Angle Glaucoma. American Journal of Human Genetics, 1998, 63, 1549-1552.	2.6	197
80	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	5.8	196
81	Clustering of autoimmune diseases in families with a high-risk for multiple sclerosis: a descriptive study. Lancet Neurology, The, 2006, 5, 924-931.	4.9	194
82	Incorporating language phenotypes strengthens evidence of linkage to autism. American Journal of Medical Genetics Part A, 2001, 105, 539-547.	2.4	192
83	Multitrait analysis of glaucoma identifies new risk loci and enables polygenic prediction of disease susceptibility and progression. Nature Genetics, 2020, 52, 160-166.	9.4	192
84	A noise-reduction GWAS analysis implicates altered regulation of neurite outgrowth and guidance in autism. Molecular Autism, 2011, 2, 1.	2.6	191
85	Whole exome sequencing study identifies novel rare and common Alzheimerâ€™s-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	4.1	191
86	Common variants near ABCA1, AFAP1 and GMDS confer risk of primary open-angle glaucoma. Nature Genetics, 2014, 46, 1120-1125.	9.4	186
87	The role of the CD58 locus in multiple sclerosis. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5264-5269.	3.3	185
88	Construction of a GT polymorphism map of human 9q. Genomics, 1992, 12, 229-240.	1.3	181
89	A novel approach of homozygous haplotype sharing identifies candidate genes in autism spectrum disorder. Human Genetics, 2012, 131, 565-579.	1.8	180
90	Functional Candidate Genes in Age-Related Macular Degeneration: Significant Association withVEGF,VLDLR, andLRP6. , 2006, 47, 329.		178

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91	Protective effect of complement factor B and complement component 2 variants in age-related macular degeneration. Human Molecular Genetics, 2007, 16, 1986-1992.	1.4	175
92	Age-Related Maculopathy: A Genomewide Scan with Continued Evidence of Susceptibility Loci within the 1q31, 10q26, and 17q25 Regions. American Journal of Human Genetics, 2004, 75, 174-189.	2.6	174
93	Assessment of the genetic variance of late-onset Alzheimer's disease. Neurobiology of Aging, 2016, 41, 200.e13-200.e20.	1.5	174
94	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.4	173
95	Genome- and Phenome-Wide Analyses of Cardiac Conduction Identifies Markers of Arrhythmia Risk. Circulation, 2013, 127, 1377-1385.	1.6	167
96	Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 1394.	4.5	166
97	Rapidly progressive Alzheimerâ€™s disease features distinct structures of amyloid-Î². Brain, 2015, 138, 1009-1022.	3.7	166
98	Transethnic genomeâ€wide scan identifies novel Alzheimer's disease loci. Alzheimer's and Dementia, 2017, 13, 727-738.	0.4	166
99	Evidence for Polygenic Susceptibility to Multiple Sclerosisâ€”The Shape of Things to Come. American Journal of Human Genetics, 2010, 86, 621-625.	2.6	162
100	Neurofibromatosis 2: Clinical and DNA Linkage Studies of a Large Kindred. New England Journal of Medicine, 1988, 319, 278-283.	13.9	161
101	The Next PAGE in Understanding Complex Traits: Design for the Analysis of Population Architecture Using Genetics and Epidemiology (PAGE) Study. American Journal of Epidemiology, 2011, 174, 849-859.	1.6	161
102	A highly polymorphic locus very tightly linked to the Huntington's disease gene. Nature, 1988, 332, 734-736.	13.7	159
103	Evaluation of copy number variations reveals novel candidate genes in autism spectrum disorder-associated pathways. Human Molecular Genetics, 2012, 21, 3513-3523.	1.4	158
104	Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. Nature Genetics, 2013, 45, 1375-1379.	9.4	158
105	A second major histocompatibility complex susceptibility locus for multiple sclerosis. Annals of Neurology, 2007, 61, 228-236.	2.8	156
106	Common variants near CAV1 and CAV2 are associated with primary open-angle glaucoma in Caucasians from the USA. Human Molecular Genetics, 2011, 20, 4707-4713.	1.4	156
107	Whole-Exome Sequencing Links a Variant in DHDDS to Retinitis Pigmentosa. American Journal of Human Genetics, 2011, 88, 201-206.	2.6	155
108	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	1.1	155

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109	Linkage Disequilibrium at the Angelman Syndrome Gene UBE3A in Autism Families. Genomics, 2001, 77, 105-113.	1.3	154
110	Meta-analysis of the Association Between Variants in SORL1 and Alzheimer Disease. Archives of Neurology, 2011, 68, 99.	4.9	153
111	A Genomewide Scan for Early-Onset Coronary Artery Disease in 438 Families: The GENECARD Study. American Journal of Human Genetics, 2004, 75, 436-447.	2.6	152
112	Localization of the gene for familial dysautonomia on chromosome 9 and definition of DNA markers for genetic diagnosis. Nature Genetics, 1993, 4, 160-164.	9.4	149
113	SORL1 Is Genetically Associated with Late-Onset Alzheimerâ€™s Disease in Japanese, Koreans and Caucasians. PLoS ONE, 2013, 8, e58618.	1.1	149
114	Polygenic Overlap Between C-Reactive Protein, Plasma Lipids, and Alzheimer Disease. Circulation, 2015, 131, 2061-2069.	1.6	145
115	Novel late-onset Alzheimer disease loci variants associate with brain gene expression. Neurology, 2012, 79, 221-228.	1.5	144
116	Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel. JAMA Neurology, 2021, 78, 102.	4.5	144
117	Rapid Communication: Cu/Zn Superoxide Dismutase Activity in Familial and Sporadic Amyotrophic Lateral Sclerosis. Journal of Neurochemistry, 1994, 62, 384-387.	2.1	143
118	Investigation of autism and GABA receptor subunit genes in multiple ethnic groups. Neurogenetics, 2006, 7, 167-174.	0.7	141
119	Common variants in Alzheimerâ€™s disease and risk stratification by polygenic risk scores. Nature Communications, 2021, 12, 3417.	5.8	140
120	A pooled case-control study of the apolipoprotein E (APOE) gene in age-related maculopathy. Ophthalmic Genetics, 2002, 23, 209-223.	0.5	136
121	A linkage disequilibrium map of the 1-Mb 15q12 GABAAreceptor subunit cluster and association to autism. American Journal of Medical Genetics Part A, 2004, 131B, 51-59.	2.4	135
122	Localization of the huntington's disease gene to a small segment of chromosome 4 flanked by D4S10 and the telomere. Cell, 1987, 50, 565-571.	13.5	130
123	Genome-wide and Ordered-Subset linkage analyses provide support for autism loci on 17q and 19p with evidence of phenotypic and interlocus genetic correlates. BMC Medical Genetics, 2005, 6, 1.	2.1	130
124	Dementia Revealed: Novel Chromosome 6 Locus for Late-Onset Alzheimer Disease Provides Genetic Evidence for Folate-Pathway Abnormalities. PLoS Genetics, 2010, 6, e1001130.	1.5	130
125	Recurrent Tissue-Specific mtDNA Mutations Are Common in Humans. PLoS Genetics, 2013, 9, e1003929.	1.5	130
126	Imputation and quality control steps for combining multiple genome-wide datasets. Frontiers in Genetics, 2014, 5, 370.	1.1	130

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127	Mitochondrial haplogroups and peripheral neuropathy during antiretroviral therapy: an adult AIDS clinical trials group study. Aids, 2005, 19, 1341-1349.	1.0	129
128	Association of Polymorphisms in the Apolipoprotein E Region with Susceptibility to and Progression of Multiple Sclerosis. American Journal of Human Genetics, 2002, 70, 708-717.	2.6	125
129	Genetic susceptibility to Alzheimer disease. Trends in Genetics, 1995, 11, 504-508.	2.9	120
130	C3 R102G polymorphism increases risk of age-related macular degeneration. Human Molecular Genetics, 2008, 17, 1821-1824.	1.4	120
131	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics.. Human Molecular Genetics, 2017, 26, ddw399.	1.4	120
132	Identification of Two Novel Loci for Dominantly Inherited Familial Amyotrophic Lateral Sclerosis. American Journal of Human Genetics, 2003, 73, 397-403.	2.6	119
133	Identification of Genomic Predictors of Atrioventricular Conduction. Circulation, 2010, 122, 2016-2021.	1.6	117
134	Ancestral origin of ApoE Îµ4 Alzheimer disease risk in Puerto Rican and African American populations. PLoS Genetics, 2018, 14, e1007791.	1.5	117
135	A rare mutation in UNC5C predisposes to late-onset Alzheimer's disease and increases neuronal cell death. Nature Medicine, 2014, 20, 1452-1457.	15.2	116
136	An Î±-2-macroglobulin insertion-deletion polymorphism in Alzheimer disease. Nature Genetics, 1999, 22, 19-21.	9.4	115
137	Replication analysis identifies TYK2 as a multiple sclerosis susceptibility factor. European Journal of Human Genetics, 2009, 17, 1309-1313.	1.4	115
138	Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. Cell, 2018, 175, 1679-1687.e7.	13.5	115
139	Distribution ofWDR36DNA Sequence Variants in Patients with Primary Open-Angle Glaucoma. , 2006, 47, 2542.		114
140	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. Nature Genetics, 2017, 49, 993-1004.	9.4	114
141	Exploratory Subsetting of Autism Families Based on Savant Skills Improves Evidence of Genetic Linkage to 15q11-q13. Journal of the American Academy of Child and Adolescent Psychiatry, 2003, 42, 856-863.	0.3	112
142	Genome-wide association study identifies seven novel susceptibility loci for primary open-angle glaucoma. Human Molecular Genetics, 2018, 27, 1486-1496.	1.4	111
143	A comparison of neurological, metabolic, structural, and genetic evaluations in persons at risk for Huntington's disease. Annals of Neurology, 1990, 28, 614-621.	2.8	110
144	Peakwide Mapping on Chromosome 3q13 Identifies the Kalirin Gene as a Novel Candidate Gene for Coronary Artery Disease. American Journal of Human Genetics, 2007, 80, 650-663.	2.6	110

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145	Missense variant in TREML2 protects against Alzheimer's disease. Neurobiology of Aging, 2014, 35, 1510.e19-1510.e26.	1.5	110
146	Genetic Variants Associated with Optic Nerve Vertical Cup-to-Disc Ratio Are Risk Factors for Primary Open Angle Glaucoma in a US Caucasian Population. , 2011, 52, 1788.		109
147	Comprehensive follow-up of the first genome-wide association study of multiple sclerosis identifies KIF21B and TMEM39A as susceptibility loci. Human Molecular Genetics, 2010, 19, 953-962.	1.4	108
148	Endothelial Nitric Oxide Synthase Gene Variants and Primary Open-Angle Glaucoma: Interactions with Sex and Postmenopausal Hormone Use. , 2010, 51, 971.		107
149	Association of MAPT haplotypes with Alzheimerâ€™s disease risk and MAPT brain gene expression levels. Alzheimer's Research and Therapy, 2014, 6, 39.	3.0	106
150	DNA sequence variants in the LOXL1 gene are associated with pseudoexfoliation glaucoma in a U.S. clinic-based population with broad ethnic diversity. BMC Medical Genetics, 2008, 9, 5.	2.1	105
151	A common variant near TGFBR3 is associated with primary open angle glaucoma. Human Molecular Genetics, 2015, 24, 3880-3892.	1.4	105
152	SORCS1 alters amyloid precursor protein processing and variants may increase Alzheimer's disease risk. Annals of Neurology, 2011, 69, 47-64.	2.8	104
153	Dissecting the genetic relationship between cardiovascular risk factors and Alzheimerâ€™s disease. Acta Neuropathologica, 2019, 137, 209-226.	3.9	100
154	Ordered-Subsets Linkage Analysis Detects Novel Alzheimer Disease Loci on Chromosomes 2q34 and 15q22. American Journal of Human Genetics, 2003, 73, 1041-1051.	2.6	99
155	Mitochondrial DNA Polymorphism A4917G Is Independently Associated with Age-Related Macular Degeneration. PLoS ONE, 2008, 3, e2091.	1.1	99
156	Association Between Apolipoprotein E Genotype and Alzheimer Disease in African American Subjects. Archives of Neurology, 2002, 59, 594.	4.9	98
157	Comprehensive Search for Alzheimer Disease Susceptibility Loci in the APOE Region. Archives of Neurology, 2012, 69, 1270.	4.9	97
158	Mapping of the Disease Locus and Identification of ADAMTS10 As a Candidate Gene in a Canine Model of Primary Open Angle Glaucoma. PLoS Genetics, 2011, 7, e1001306.	1.5	96
159	Genetic Linkage of Autosomal Dominant Juvenile Glaucoma to 1q21-q31 in Three Affected Pedigrees. Genomics, 1994, 21, 299-303.	1.3	95
160	Assessing the accuracy of observer-reported ancestry in a biorepository linked to electronic medical records. Genetics in Medicine, 2010, 12, 648-650.	1.1	94
161	Two rare AKAP9 variants are associated with Alzheimer's disease in African Americans. Alzheimer's and Dementia, 2014, 10, 609.	0.4	94
162	Recombination events suggest potential sites for the Huntington's disease gene. Neuron, 1989, 3, 183-190.	3.8	93

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163	Genome-wide association study and meta-analysis of intraocular pressure. Human Genetics, 2014, 133, 41-57.	1.8	93
164	Genetic variants and functional pathways associated with resilience to Alzheimerâ€™s disease. Brain, 2020, 143, 2561-2575.	3.7	93
165	Analysis of the stargardt disease gene (ABCR) in age-related macular degenerationâ˜†. Ophthalmology, 1999, 106, 1531-1536.	2.5	91
166	Drug Transporter and Metabolizing Enzyme Gene Variants and Nonnucleoside Reverse-Transcriptase Inhibitor Hepatotoxicity. Clinical Infectious Diseases, 2006, 43, 779-782.	2.9	91
167	Association of CAV1/CAV2 Genomic Variants with Primary Open-Angle Glaucoma Overall and by Gender and Pattern of Visual Field Loss. Ophthalmology, 2014, 121, 508-516.	2.5	91
168	Meta-analysis of genome-wide association studies identifies novel loci that influence cupping and the glaucomatous process. Nature Communications, 2014, 5, 4883.	5.8	89
169	Apolipoprotein E genotype in patients with alzheimer's disease: Implications for the risk of dementia among relatives. Annals of Neurology, 1995, 38, 797-808.	2.8	87
170	Two novel loci, COBL and SLC10A2, for Alzheimer's disease in African Americans. Alzheimer's and Dementia, 2017, 13, 119-129.	0.4	87
171	Sex-specific genetic predictors of Alzheimerâ€™s disease biomarkers. Acta Neuropathologica, 2018, 136, 857-872.	3.9	87
172	Lack of Association of Mutations in Optineurin With Disease in Patients With Adult-onset Primary Open-angle Glaucoma. JAMA Ophthalmology, 2003, 121, 1181.	2.6	86
173	Early Adult-Onset POAG Linked to 15q11-13 Using Ordered Subset Analysis. , 2005, 46, 2002.		86
174	Deletion of CFHR3 and CFHR1 genes in age-related macular degeneration. Human Molecular Genetics, 2008, 17, 971-977.	1.4	85
175	Localization of Age-Related Macular Degeneration-Associated ARMS2 in Cytosol, Not Mitochondria. , 2009, 50, 3084.		85
176	Distribution of Optineurin Sequence Variations in an Ethnically Diverse Population of Low-tension Glaucoma Patients From the United States. Journal of Glaucoma, 2006, 15, 358-363.	0.8	82
177	GATA2 Is Associated with Familial Early-Onset Coronary Artery Disease. PLoS Genetics, 2006, 2, e139.	1.5	82
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