Eden R Martin

List of Publications by Year
in descending order

208 papers	22,464 citations	18482 62 h-index	9861 141 g-index
235 all docs	235 docs citations	235 times ranked	28174 citing authors

#	Article	IF	Citations
1	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nature Genetics, 2013, 45, 1452-1458.	21.4	3,741
2	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.	21.4	1,962
3	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. Nature Genetics, 2011, 43, 436-441.	21.4	1,676
4	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
5	A multiple testing correction method for genetic association studies using correlated single nucleotide polymorphisms. Genetic Epidemiology, 2008, 32, 361-369.	1.3	646
6	A Test for Linkage and Association in General Pedigrees: The Pedigree Disequilibrium Test. American Journal of Human Genetics, 2000, 67, 146-154.	6.2	588
7	Mitochondrial Polymorphisms Significantly Reduce the Risk of Parkinson Disease. American Journal of Human Genetics, 2003, 72, 804-811.	6.2	507
8	Comprehensive Research Synopsis and Systematic Meta-Analyses in Parkinson's Disease Genetics: The PDGene Database. PLoS Genetics, 2012, 8, e1002548.	3.5	495
9	No Gene Is an Island: The Flip-Flop Phenomenon. American Journal of Human Genetics, 2007, 80, 531-538.	6.2	437
10	Variation in the miRNA-433 Binding Site of FGF20 Confers Risk for Parkinson Disease by Overexpression of Î±-Synuclein. American Journal of Human Genetics, 2008, 82, 283-289.	6.2	437
11	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.	0.8	417
12	Meta-analysis Confirms CR1, CLU, and PICALM as Alzheimer Disease Risk Loci and Reveals Interactions With APOE Genotypes. Archives of Neurology, 2010, 67, 1473.	4.5	376
13	SNPing Away at Complex Diseases: Analysis of Single-Nucleotide Polymorphisms around APOE in Alzheimer Disease. American Journal of Human Genetics, 2000, 67, 383-394.	6.2	342
14	Genome-wide Studies of Copy Number Variation and Exome Sequencing Identify Rare Variants in BAG3 as a Cause of Dilated Cardiomyopathy. American Journal of Human Genetics, 2011, 88, 273-282.	6.2	320
15	Genome-Wide Association Meta-analysis of Neuropathologic Features of Alzheimer's Disease and Related Dementias. PLoS Genetics, 2014, 10, e1004606.	3.5	305
16	Reconstructing the Population Genetic History of the Caribbean. PLoS Genetics, 2013, 9, e1003925.	3.5	296
17	Analysis of European mitochondrial haplogroups with Alzheimer disease risk. Neuroscience Letters, 2004, 365, 28-32.	2.1	264
18	Metaâ€analysis of Parkinson's Disease: Identification of a novel locus, RIT2. Annals of Neurology, 2012, 71, 370-384.	5.3	264

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19	Exome sequencing of extended families with autism reveals genes shared across neurodevelopmental and neuropsychiatric disorders. Molecular Autism, 2014, 5, 1.	4.9	246
20	Large-scale GWAS reveals insights into the genetic architecture of same-sex sexual behavior. Science, 2019, 365, .	12.6	245
21	Genome-wide Association Study Implicates a Chromosome 12 Risk Locus for Late-Onset Alzheimer Disease. American Journal of Human Genetics, 2009, 84, 35-43.	6.2	242
22	Convergence of miRNA Expression Profiling, Î±-Synuclein Interacton and GWAS in Parkinson's Disease. PLoS ONE, 2011, 6, e25443.	2.5	235
23	Glutathione S-transferase omega-1 modifiesage-at-onset of Alzheimer disease and Parkinson disease. Human Molecular Genetics, 2003, 12, 3259-3267.	2.9	208
24	A Genomeâ€wide Association Study of Autism Reveals a Common Novel Risk Locus at 5p14.1. Annals of Human Genetics, 2009, 73, 263-273.	0.8	207
25	A noise-reduction GWAS analysis implicates altered regulation of neurite outgrowth and guidance in autism. Molecular Autism, 2011, 2, 1.	4.9	191
26	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.	7.9	191
27	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.8	173
28	Association of Single-Nucleotide Polymorphisms of the Tau Gene With Late-Onset Parkinson Disease. JAMA - Journal of the American Medical Association, 2001, 286, 2245.	7.4	171
29	Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 1394.	9.0	166
30	Evaluation of copy number variations reveals novel candidate genes in autism spectrum disorder-associated pathways. Human Molecular Genetics, 2012, 21, 3513-3523.	2.9	158
31	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	2.5	155
32	Correcting for a Potential Bias in the Pedigree Disequilibrium Test. American Journal of Human Genetics, 2001, 68, 1065-1067.	6.2	154
33	Association Analysis of Chromosome 15 GABA_AReceptor Subunit Genes in Autistic Disorder. Journal of Neurogenetics, 2001, 15, 245-259.	1.4	154
34	Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel. JAMA Neurology, 2021, 78, 102.	9.0	144
35	Investigation of autism and GABA receptor subunit genes in multiple ethnic groups. Neurogenetics, 2006, 7, 167-174.	1.4	141
36	Fibroblast Growth Factor 20 Polymorphisms and Haplotypes Strongly Influence Risk of Parkinson Disease. American Journal of Human Genetics, 2004, 74, 1121-1127.	6.2	136

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37	Sibling-Based Tests of Linkage and Association for Quantitative Traits. American Journal of Human Genetics, 1999, 64, 1754-1764.	6.2	133
38	Dementia Revealed: Novel Chromosome 6 Locus for Late-Onset Alzheimer Disease Provides Genetic Evidence for Folate-Pathway Abnormalities. PLoS Genetics, 2010, 6, e1001130.	3.5	130
39	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.	6.2	125
40	Ancestral origin of ApoE Îµ4 Alzheimer disease risk in Puerto Rican and African American populations. PLoS Genetics, 2018, 14, e1007791.	3.5	117
41	An Î±-2-macroglobulin insertion-deletion polymorphism in Alzheimer disease. Nature Genetics, 1999, 22, 19-21.	21.4	115
42	Evaluating Pathogenicity of Rare Variants From Dilated Cardiomyopathy in the Exome Era. Circulation: Cardiovascular Genetics, 2012, 5, 167-174.	5.1	112
43	Smoking, Caffeine, and Nonsteroidal Anti-inflammatory Drugs in Families With Parkinson Disease. Archives of Neurology, 2007, 64, 576.	4.5	107
44	Circumventing multiple testing: A multilocus Monte Carlo approach to testing for association. Genetic Epidemiology, 2000, 19, 18-29.	1.3	96
45	Vitamin D Receptor Gene as a Candidate Gene for Parkinson Disease. Annals of Human Genetics, 2011, 75, 201-210.	0.8	95
46	Exome Sequencing and Genome-Wide Linkage Analysis in 17 Families Illustrate the Complex Contribution of TTN Truncating Variants to Dilated Cardiomyopathy. Circulation: Cardiovascular Genetics, 2013, 6, 144-153.	5.1	95
47	Nitric oxide synthase genes and their interactions with environmental factors in Parkinsonâ€™s disease. Neurogenetics, 2008, 9, 249-262.	1.4	91
48	Accounting for Linkage in Family-Based Tests of Association with Missing Parental Genotypes. American Journal of Human Genetics, 2003, 73, 1016-1026.	6.2	89
49	Dry eye symptom severity and persistence are associated with symptoms of neuropathic pain. British Journal of Ophthalmology, 2015, 99, 665-668.	3.9	81
50	Chronic Dry Eye Symptoms after LASIK: Parallels and Lessons to be Learned from other Persistent Post-Operative Pain Disorders. Molecular Pain, 2015, 11, s12990-015-0020.	2.1	80
51	Dry eye symptoms align more closely to non-ocular conditions than to tear film parameters. British Journal of Ophthalmology, 2015, 99, 1126-1129.	3.9	78
52	Neuropathic Ocular Pain due to Dry Eye Is Associated With Multiple Comorbid Chronic Pain Syndromes. Journal of Pain, 2016, 17, 310-318.	1.4	77
53	Epigenome-wide meta-analysis of DNA methylation differences in prefrontal cortex implicates the immune processes in Alzheimerâ€™s disease. Nature Communications, 2020, 11, 6114.	12.8	75
54	Linkage Disequilibrium Inflates Type I Error Rates in Multipoint Linkage Analysis when Parental Genotypes Are Missing. Human Heredity, 2005, 59, 220-227.	0.8	74

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55	ABCA7 frameshift deletion associated with Alzheimer disease in African Americans. Neurology: Genetics, 2016, 2, e79.	1.9	74
56	Identifying Consensus Disease Pathways in Parkinson's Disease Using an Integrative Systems Biology Approach. PLoS ONE, 2011, 6, e16917.	2.5	72
57	Incomplete response to artificial tears is associated with features of neuropathic ocular pain. British Journal of Ophthalmology, 2016, 100, 745-749.	3.9	71
58	Genomic convergence to identify candidate genes for Alzheimer Disease on chromosome 10. Human Mutation, 2009, 30, 463-471.	2.5	69
59	C9ORF72 Intermediate Repeat Copies Are a Significant Risk Factor for Parkinson Disease. Annals of Human Genetics, 2013, 77, 351-363.	0.8	69
60	Exome Sequencing of a Multigenerational Human Pedigree. PLoS ONE, 2009, 4, e8232.	2.5	69
61	Whole exome sequencing of rare variants in EIF4G1 and VPS35 in Parkinson disease. Neurology, 2013, 80, 982-989.	1.1	68
62	Novel variants identified in methyl-CpG-binding domain genes in autistic individuals. Neurogenetics, 2010, 11, 291-303.	1.4	67
63	Two knockdown models of the autism genes SYNGAP1 and SHANK3 in zebrafish produce similar behavioral phenotypes associated with embryonic disruptions of brain morphogenesis. Human Molecular Genetics, 2015, 24, 4006-4023.	2.9	67
64	Comparison of Three Targeted Enrichment Strategies on the SOLiD Sequencing Platform. PLoS ONE, 2011, 6, e18595.	2.5	66
65	Multiple susceptibility loci for multiple sclerosis. Human Molecular Genetics, 2002, 11, 2251-2256.	2.9	65
66	Rare variant mutations identified in pediatric patients with dilated cardiomyopathy. Progress in Pediatric Cardiology, 2011, 31, 39-47.	0.4	65
67	Sex differences in the genetic predictors of Alzheimerâ€™s pathology. Brain, 2019, 142, 2581-2589.	7.6	65
68	Integrated Whole Transcriptome and DNA Methylation Analysis Identifies Gene Networks Specific to Late-Onset Alzheimer's Disease. Journal of Alzheimer's Disease, 2015, 44, 977-987.	2.6	62
69	Vitamin D from different sources is inversely associated with Parkinson disease. Movement Disorders, 2015, 30, 560-566.	3.9	61
70	Analysis of Association at Single Nucleotide Polymorphisms in the APOE Region. Genomics, 2000, 63, 7-12.	2.9	60
71	Revealing the role of glutathione S-transferase omega in age-at-onset of Alzheimer and Parkinson diseases. Neurobiology of Aging, 2006, 27, 1087-1093.	3.1	60
72	Targeted massively parallel sequencing of autism spectrum disorder-associated genes in a case control cohort reveals rare loss-of-function risk variants. Molecular Autism, 2015, 6, 43.	4.9	57

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73	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	5.3	56
74	Association Study of Parkin Gene Polymorphisms With Idiopathic Parkinson Disease. Archives of Neurology, 2003, 60, 975.	4.5	51
75	Genome-wide brain DNA methylation analysis suggests epigenetic reprogramming in Parkinson disease. Neurology: Genetics, 2019, 5, e342.	1.9	50
76	Strong association of a novel Tau promoter haplotype in progressive supranuclear palsy. Neuroscience Letters, 2001, 311, 145-148.	2.1	49
77	The APL Test: Extension to General Nuclear Families and Haplotypes and Examination of Its Robustness. Human Heredity, 2006, 61, 189-199.	0.8	48
78	PARK10 is a major locus for sporadic neuropathologically confirmed Parkinson disease. Neurology, 2015, 84, 972-980.	1.1	48
79	Using Allele Sharing Distance for Detecting Human Population Stratification. Human Heredity, 2009, 68, 182-191.	0.8	47
80	The transcription factor orthodenticle homeobox 2 influences axonal projections and vulnerability of midbrain dopaminergic neurons. Brain, 2010, 133, 2022-2031.	7.6	47
81	Investigation of potential geneâ€“gene interactions between apoe and reln contributing to autism risk. Psychiatric Genetics, 2007, 17, 221-226.	1.1	44
82	Genome-Wide Association Study of Male Sexual Orientation. Scientific Reports, 2017, 7, 16950.	3.3	44
83	Genomic convergence: identifying candidate genes for Parkinson's disease by combining serial analysis of gene expression and genetic linkage. Human Molecular Genetics, 2003, 12, 671-7.	2.9	44
84	Global and local ancestry in Africanâ€Americans: Implications for Alzheimer's disease risk. Alzheimer's and Dementia, 2016, 12, 233-243.	0.8	42
85	Whole genome sequencing of Caribbean Hispanic families with lateâ€onset Alzheimer's disease. Annals of Clinical and Translational Neurology, 2018, 5, 406-417.	3.7	42
86	Rarity of the Alzheimer Diseaseâ€“ProtectiveAPPA673T Variant in the United States. JAMA Neurology, 2015, 72, 209.	9.0	41
87	Segregation of a rare TTC3 variant in an extended family with late-onset Alzheimer disease. Neurology: Genetics, 2016, 2, e41.	1.9	41
88	Early-Onset Alzheimer Disease and Candidate Risk Genes Involved in Endolysosomal Transport. JAMA Neurology, 2017, 74, 1113.	9.0	41
89	Toward Genetics-Driven Early Intervention in Dilated Cardiomyopathy. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	41
90	Discovery of gene-gene interactions across multiple independent data sets of late onset Alzheimer disease from the Alzheimer Disease Genetics Consortium. Neurobiology of Aging, 2016, 38, 141-150.	3.1	39

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91	NOS2Aand the modulating effect of cigarette smoking in Parkinson's disease. Annals of Neurology, 2006, 60, 366-373.	5.3	38
92	Analysis of association between Alzheimer disease and the K variant of butyrylcholinesterase (BCHE-K). Neuroscience Letters, 1999, 269, 115-119.	2.1	37
93	Properties of globalâ€•and localâ€ancestry adjustments in genetic association tests in admixed populations. Genetic Epidemiology, 2018, 42, 214-229.	1.3	37
94	Lack of Association Between Autism andSLC25A12. American Journal of Psychiatry, 2006, 163, 929-931.	7.2	36
95	Evaluating Mitochondrial DNA Variation in Autism Spectrum Disorders. Annals of Human Genetics, 2013, 77, 9-21.	0.8	36
96	Geneâ€Gene Interaction Between FGF20 and MAOB in Parkinson Disease. Annals of Human Genetics, 2008, 72, 157-162.	0.8	34
97	Reconsidering Association Testing Methods Using Single-Variant Test Statistics as Alternatives to Pooling Tests for Sequence Data with Rare Variants. PLoS ONE, 2012, 7, e30238.	2.5	34
98	Evidence that dry eye represents a chronic overlapping pain condition. Molecular Pain, 2017, 13, 174480691772930.	2.1	34
99	Linkage and association analysis of chromosome 19q13 in multiple sclerosis. Neurogenetics, 2001, 3, 195-201.	1.4	33
100	Analysis of the autism chromosome 2 linkage region: GAD1 and other candidate genes. Neuroscience Letters, 2004, 372, 209-214.	2.1	32
101	Analysis of Whole-Exome Sequencing Data for Alzheimer Disease Stratified by APOE Genotype. JAMA Neurology, 2019, 76, 1099.	9.0	32
102	Modulation of the BP Response to Diet by Genes in the Renin-Angiotensin System and the Adrenergic Nervous System. American Journal of Hypertension, 2011, 24, 209-217.	2.0	31
103	Overlap between Parkinson disease and Alzheimer disease in ABCA7 functional variants. Neurology: Genetics, 2016, 2, e44.	1.9	31
104	Linkage disequilibrium and haplotype tagging polymorphisms in the Tau H1 haplotype. Neurogenetics, 2004, 5, 147-155.	1.4	30
105	Carbonic Anhydrase-8 Regulates Inflammatory Pain by Inhibiting the ITPR1-Cytosolic Free Calcium Pathway. PLoS ONE, 2015, 10, e0118273.	2.5	30
106	Genomewide Association Studies of <scp>LRRK2</scp> Modifiers of Parkinson's Disease. Annals of Neurology, 2021, 90, 76-88.	5.3	30
107	Maternal lineages and Alzheimer disease risk in the Old Order Amish. Human Genetics, 2005, 118, 115-122.	3.8	29
108	A rare novel deletion of the tyrosine hydroxylase gene in Parkinson disease. Human Mutation, 2010, 31, E1767-E1771.	2.5	29

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109	An X chromosome-wide association study in autism families identifies TBL1X as a novel autism spectrum disorder candidate gene in males. Molecular Autism, 2011, 2, 18.	4.9	29
110	coMethDMR: accurate identification of co-methylated and differentially methylated regions in epigenome-wide association studies with continuous phenotypes. Nucleic Acids Research, 2019, 47, e98-e98.	14.5	28
111	No evidence supporting MTHFR as a risk factor in the development of familial NSCLP. American Journal of Medical Genetics Part A, 2000, 92, 370-371.	2.4	27
112	The Ubiquilin 1 Gene and Alzheimer's Disease. New England Journal of Medicine, 2005, 352, 2752-2753.	27.0	27
113	A modifier locus on chromosome 5 contributes to L1 cell adhesion molecule X-linked hydrocephalus in mice. Neurogenetics, 2010, 11, 53-71.	1.4	27
114	Rare genetic variation implicated in non-Hispanic white families with Alzheimer disease. Neurology: Genetics, 2018, 4, e286.	1.9	27
115	Genomic evidence consistent with antagonistic pleiotropy may help explain the evolutionary maintenance of same-sex sexual behaviour in humans. Nature Human Behaviour, 2021, 5, 1251-1258.	12.0	27
116	Common Susceptibility Variants Examined for Association with Dilated Cardiomyopathy. Annals of Human Genetics, 2010, 74, 110-116.	0.8	26
117	Quality control and integration of genotypes from two calling pipelines for whole genome sequence data in the Alzheimer's disease sequencing project. Genomics, 2019, 111, 808-818.	2.9	26
118	Sex-specific DNA methylation differences in Alzheimerâ€™s disease pathology. Acta Neuropathologica Communications, 2021, 9, 77.	5.2	26
119	Resolving the relationship between ApolipoproteinE and depression. Neuroscience Letters, 2009, 455, 116-119.	2.1	25
120	X-APL: An Improved Family-Based Test of Association in the Presence of Linkage for the X Chromosome. American Journal of Human Genetics, 2007, 80, 59-68.	6.2	24
121	Absence of C9ORF72 expanded or intermediate repeats in autopsyâ€confirmed Parkinson's disease. Movement Disorders, 2014, 29, 827-830.	3.9	24
122	Genomeâ€wide linkage analyses of nonâ€Hispanic white families identify novel loci for familial lateâ€onset Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 2-10.	0.8	24
123	Comprehensive association analysis of APOE regulatory region polymorphisms in Alzheimer disease. Neurogenetics, 2004, 5, 201-208.	1.4	22
124	Dopaminergic variants in siblings at high risk for autism: Associations with initiating joint attention. Autism Research, 2016, 9, 1142-1150.	3.8	22
125	Genetic Variants of Microtubule Actin Cross-linking Factor 1 (MACF1) Confer Risk for Parkinsonâ€™s Disease. Molecular Neurobiology, 2017, 54, 2878-2888.	4.0	22
126	Genetic Variation in Genes Underlying Diverse Dementias May Explain a Small Proportion of Cases in the Alzheimerâ€™s Disease Sequencing Project. Dementia and Geriatric Cognitive Disorders, 2018, 45, 1-17.	1.5	22

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127	Genome-wide enriched pathway analysis of acute post-radiotherapy pain in breast cancer patients: a prospective cohort study. Human Genomics, 2019, 13, 28.	2.9	20
128	RNA editing alterations in a multi-ethnic Alzheimer disease cohort converge on immune and endocytic molecular pathways. Human Molecular Genetics, 2019, 28, 3053-3061.	2.9	19
129	Response to Zaykin and Shibata. American Journal of Human Genetics, 2008, 82, 796-797.	6.2	18
130	Association Test for X-Linked QTL in Family-Based Designs. American Journal of Human Genetics, 2009, 84, 431-444.	6.2	17
131	Detecting Genetic Interactions in Pathwayâ€Based Genomeâ€Wide Association Studies. Genetic Epidemiology, 2014, 38, 300-309.	1.3	17
132	Power Calculations for a General Class of Tests of Linkage and Association That Use Nuclear Families with Affected and Unaffected Sibs. Theoretical Population Biology, 2001, 60, 193-201.	1.1	15
133	Effect of heterogeneity on the chromosome 10 risk in late-onset Alzheimer disease. Human Mutation, 2007, 28, 1065-1073.	2.5	15
134	CAPL: a novel association test using caseâ€control and family data and accounting for population stratification. Genetic Epidemiology, 2010, 34, 747-755.	1.3	15
135	APOE is not Associated with Alzheimer Disease: a Cautionary tale of Genotype Imputation. Annals of Human Genetics, 2010, 74, 189-194.	0.8	13
136	High-Resolution Survey in Familial Parkinson Disease Genes Reveals Multiple Independent Copy Number Variation Events in PARK2. Human Mutation, 2013, 34, 1071-1074.	2.5	13
137	Family-Based Association Test Using Both Common and Rare Variants and Accounting for Directions of Effects for Sequencing Data. PLoS ONE, 2014, 9, e107800.	2.5	13
138	A General Framework for Formal Tests of Interaction after Exhaustive Search Methods with Applications to MDR and MDR-PDT. PLoS ONE, 2010, 5, e9363.	2.5	13
139	The Q7R Saitohin gene polymorphism is not associated with Alzheimer disease. Neuroscience Letters, 2003, 347, 143-146.	2.1	12
140	Manifestations of Alzheimerâ€™s disease genetic risk in the blood are evident in a multiomic analysis in healthy adults aged 18 to 90. Scientific Reports, 2022, 12, 6117.	3.3	12
141	Genome-wide Linkage Screen in Familial Parkinson Disease Identifies Loci on Chromosomes 3 and 18. American Journal of Human Genetics, 2009, 84, 499-504.	6.2	11
142	DNA variants in CACNA1C modify Parkinson disease risk only when vitamin D level is deficient. Neurology: Genetics, 2016, 2, e72.	1.9	11
143	hVMAT2: A Target of Individualized Medication for Parkinson's Disease. Neurotherapeutics, 2016, 13, 623-634.	4.4	11
144	Association Between Polymorphisms in DNA Damage Repair Genes and Radiation Therapyâ€“Induced Early Adverse Skin Reactions in a Breast Cancer Population: A Polygenic Risk Score Approach. International Journal of Radiation Oncology Biology Physics, 2020, 106, 948-957.	0.8	11

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145	Orderedâ€subset analysis (OSA) for familyâ€based association mapping of complex traits. Genetic Epidemiology, 2008, 32, 627-637.	1.3	10
146	Increased NigralSLC6A3Activity in Schizophrenia Patients: Findings From the Torontoâ€“McLean Cohorts. Schizophrenia Bulletin, 2016, 42, 772-781.	4.3	10
147	MethReg: estimating the regulatory potential of DNA methylation in gene transcription. Nucleic Acids Research, 2022, 50, e51-e51.	14.5	8
148	Parsing the genetic heterogeneity of chromosome 12q susceptibility genes for Alzheimer disease by family-based association analysis. Neurogenetics, 2006, 7, 157-165.	1.4	7
149	Car8 dorsal root ganglion expression and genetic regulation of analgesic responses are associated with a cis-eQTL in mice. Mammalian Genome, 2017, 28, 407-415.	2.2	7
150	Analysis of Single Nucleotide Polymorphisms in Candidate Genes Using the Pedigree Disequilibrium Test. Genetic Epidemiology, 2001, 21, S441-6.	1.3	6
151	Impact of human CA8 on thermal antinociception in relation to morphine equivalence in mice. NeuroReport, 2017, 28, 1215-1220.	1.2	6
152	Human carbonic anhydrase-8 AAV8 gene therapy inhibits nerve growth factor signaling producing prolonged analgesia and anti-hyperalgesia in mice. Gene Therapy, 2018, 25, 297-311.	4.5	6
153	Immune and Inflammatory Pathways Implicated by Whole Blood Transcriptomic Analysis in a Diverse Ancestry Alzheimerâ€™s Disease Cohort. Journal of Alzheimer's Disease, 2020, 76, 1047-1060.	2.6	6
154	Life After the Screen: Making Sense of Many Pâ€Values. Genetic Epidemiology, 2001, 21, S546-51.	1.3	5
155	Increased Efficiency of Case-Control Association Analysis by Using Allele-Sharing and Covariate Information. Human Heredity, 2008, 65, 154-165.	0.8	5
156	Response to Comment on â€œLarge-scale GWAS reveals insights into the genetic architecture of same-sex sexual behaviorâ€. Science, 2021, 371, .	12.6	5
157	An association test of the spatial distribution of rare missense variants within protein structures identifies Alzheimer's diseaseâ€“related patterns. Genome Research, 2022, 32, 778-790.	5.5	5
158	[O1â€“03â€“01]: GENOMEâ€WIDE RARE VARIANT IMPUTATION AND TISSUEâ€SPECIFIC TRANSCRIPTOMIC ANALYSIS IDENTIFY NOVEL RARE VARIANT CANDIDATE LOCI IN LATEâ€ONSET ALZHEIMER's DISEASE: THE ALZHEIMER's DISEASE GENETICS CONSORTIUM. Alzheimer's and Dementia, 2017, 13, P189.	0.8	4
159	Profound analgesia is associated with a truncated peptide resulting from tissue specific alternative splicing of DRG CA8-204 regulated by an exon-level cis-eQTL. PLoS Genetics, 2019, 15, e1008226.	3.5	4
160	Genome studies must account for historyâ€”Response. Science, 2019, 366, 1461-1462.	12.6	4
161	Neuropathological lesions and their contribution to dementia and cognitive impairment in a heterogeneous clinical population. Alzheimer's and Dementia, 2022, 18, 2403-2412.	0.8	4
162	A test for linkage and association in general pedigrees. GeneScreen, 2000, 1, 65-67.	0.6	3

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163	Valid Monte Carlo Permutation Tests for Genetic Caseâ€Control Studies With Missing Genotypes. Genetic Epidemiology, 2014, 38, 325-344.	1.3	3
164	The Alzheimerâ€™s disease sequencing projectâ€“follow up study (ADSPâ€FUS): Increasing ethnic diversity in Alzheimerâ€™s genetics research with addition of potential new cohorts. Alzheimer's and Dementia, 2020, 16, e046400.	0.8	3
165	Genome-Wide Linkage Study Meta-Analysis of Male Sexual Orientation. Archives of Sexual Behavior, 2021, 50, 3371-3375.	1.9	3
166	Genome-Wide Linkage and Association Study of Childhood Gender Nonconformity in Males. Archives of Sexual Behavior, 2021, 50, 3377-3383.	1.9	3
167	O1-03-03: Identification of Novel Candidate Genes for Early-Onset Alzheimer's Disease Through Integrated Whole-Exome Sequencing and Exome Chip Array Association Analysis. , 2016, 12, P177-P178.		2
168	Impact of Genetic Ancestry on Prognostic Biomarkers in Uveal Melanoma. Cancers, 2020, 12, 3208.	3.7	2
169	An exploration of genetic association tests for disease risk and age at onset. Genetic Epidemiology, 2021, 45, 249-279.	1.3	2
170	Genetic architecture of RNA editing regulation in Alzheimerâ€™s disease across diverse ancestral populations. Human Molecular Genetics, 2022, 31, 2876-2886.	2.9	2
171	APOEâ€stratified genomeâ€wide association analysis identifies novel Alzheimer disease candidate risk loci for African Americans. Alzheimer's and Dementia, 2021, 17, e056383.	0.8	2
172	A Monte Carlo permutation approach to choosing an affection status model for bipolar affective disorder. Genetic Epidemiology, 1997, 14, 681-686.	1.3	1
173	Response to Ding and Lin. American Journal of Human Genetics, 2008, 82, 530-531.	6.2	1
174	The Future Is Now â€“ Will the Real Disease Gene Please Stand Up?. Human Heredity, 2008, 66, 127-135.	0.8	1
175	[O2â€“08â€“03]: WHOLEâ€GENOME SEQUENCING IN FAMILIAL LATEâ€ONSET ALZHEIMER's DISEASE IDENTIFIES RARE VARIATION IN AD CANDIDATE GENES. Alzheimer's and Dementia, 2017, 13, P571.	0.8	1
176	Family History of Eating Disorder and the Broad Autism Phenotype in Autism. Autism Research, 2020, 13, 1573-1581.	3.8	1
177	Reversion mutation of cDNA CA8-204 minigene construct produces a truncated functional peptide that regulates calcium release in vitro and produces profound analgesia in vivo. Mammalian Genome, 2020, 31, 287-294.	2.2	1
178	Gene-Environment Interactions in Progressive Supranuclear Palsy. Frontiers in Neurology, 2021, 12, 664796.	2.4	1
179	Alzheimerâ€™s disease risk prediction using automated machine learning. Alzheimer's and Dementia, 2021, 17, .	0.8	1
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