Eden R Martin

List of Publications by Year
in descending order

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208 papers	22,464 citations	21215 62 h-index	11282 141 g-index
235 all docs	235 docs citations	235 times ranked	31231 citing authors

#	Article	IF	Citations
1	MethReg: estimating the regulatory potential of DNA methylation in gene transcription. Nucleic Acids Research, 2022, 50, e51-e51.	6.5	8
2	Neuropathological lesions and their contribution to dementia and cognitive impairment in a heterogeneous clinical population. Alzheimer's and Dementia, 2022, 18, 2403-2412.	0.4	4
3	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.	2.4	5
4	Genetic architecture of RNA editing regulation in Alzheimerâ€™s disease across diverse ancestral populations. Human Molecular Genetics, 2022, 31, 2876-2886.	1.4	2
5	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.	1.6	12
6	An exploration of genetic association tests for disease risk and age at onset. Genetic Epidemiology, 2021, 45, 249-279.	0.6	2
7	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
8	Response to Comment on â€œLarge-scale GWAS reveals insights into the genetic architecture of same-sex sexual behaviorâ€. Science, 2021, 371, .	6.0	5
9	Sex-specific DNA methylation differences in Alzheimerâ€™s disease pathology. Acta Neuropathologica Communications, 2021, 9, 77.	2.4	26
10	Gene-Environment Interactions in Progressive Supranuclear Palsy. Frontiers in Neurology, 2021, 12, 664796.	1.1	1
11	Genomewide Association Studies of <scp>LRRK2</scp> Modifiers of Parkinson's Disease. Annals of Neurology, 2021, 90, 76-88.	2.8	30
12	Genome-Wide Linkage Study Meta-Analysis of Male Sexual Orientation. Archives of Sexual Behavior, 2021, 50, 3371-3375.	1.2	3
13	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.	6.2	27
14	Genome-Wide Linkage and Association Study of Childhood Gender Nonconformity in Males. Archives of Sexual Behavior, 2021, 50, 3377-3383.	1.2	3
15	Alzheimerâ€™s disease risk prediction using automated machine learning. Alzheimer's and Dementia, 2021, 17, .	0.4	1
16	Sexâ€specific analysis of DNA methylation changes implicates new loci in Alzheimerâ€™s disease pathology. Alzheimer's and Dementia, 2021, 17, e049363.	0.4	0
17	Estimating the regulatory potential of DNA methylation in Alzheimer's disease. Alzheimer's and Dementia, 2021, 17, e049365.	0.4	0
18	Heritability analyses show partial genetic overlap between (nonâ€Mendelian) early and late onset Alzheimer disease due to an intriguing APOE effect. Alzheimer's and Dementia, 2021, 17, e056143.	0.4	0

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19	APOEâ€stratified genomeâ€wide association analysis identifies novel Alzheimer disease candidate risk loci for African Americans. Alzheimer's and Dementia, 2021, 17, e056383.	0.4	2
20	Genome-wide association and multi-omics studies identify MGMT as a novel risk gene for Alzheimer disease among women.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e054483.	0.4	0
21	Multiple viruses detected in human DNA are associated with Alzheimer disease risk.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e054585.	0.4	0
22	Exome sequencing identifies rare damaging variants in the ATB8B4 and ABCA1 genes as novel risk factors for Alzheimer's disease.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e055982.	0.4	1
23	The Alzheimer's Disease Sequencing Project - Follow Up Study (ADSP-FUS): Increasing ethnic diversity in Alzheimer's genetics research with the addition of potential new cohorts.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e056101.	0.4	0
24	Linkage analysis identifies novel loci in early-onset Alzheimer disease in non-Hispanic white families.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e056427.	0.4	0
25	Admixture mapping identifies novel regions influencing Alzheimer disease in African Americans.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e056443.	0.4	0
26	A large-scale, whole genome sequencing study of unexplained early-onset Alzheimer disease.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e056664.	0.4	0
27	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
28	Epigenome-wide meta-analysis of DNA methylation differences in prefrontal cortex implicates the immune processes in Alzheimerâ€™s disease. Nature Communications, 2020, 11, 6114.	5.8	75
29	Impact of Genetic Ancestry on Prognostic Biomarkers in Uveal Melanoma. Cancers, 2020, 12, 3208.	1.7	2
30	Family History of Eating Disorder and the Broad Autism Phenotype in Autism. Autism Research, 2020, 13, 1573-1581.	2.1	1
31	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.	1.0	1
32	Comparative transâ€ethnic metaâ€analysis of whole exome sequencing variation for Alzheimerâ€™s disease (AD) in 18,402 individuals of the Alzheimerâ€™s Disease Sequencing Project (ADSP). Alzheimer's and Dementia, 2020, 16, e041583.	0.4	0
33	A multiancestry analysis of Alzheimerâ€™s disease coexpressed gene networks identifies a common immune signaling pathway regulated by granulocyteâ€colony stimulating factor (Gâ€CSF). Alzheimer's and Dementia, 2020, 16, e045361.	0.4	0
34	Assessing whole genome sequencing variation for Alzheimerâ€™s disease in 4707 individuals from the Alzheimerâ€™s Disease Sequencing Project (ADSP). Alzheimer's and Dementia, 2020, 16, e045548.	0.4	0
35	The effect of global ancestry and diabetes on the 3MS score in older Puerto Ricans. Alzheimer's and Dementia, 2020, 16, e046051.	0.4	0
36	Mapping Alzheimer diseaseâ€“associated regions in the African American population. Alzheimer's and Dementia, 2020, 16, e046072.	0.4	0

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37	Genomeâ€wide association analyses identify genes modifying ageâ€atâ€onset of Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e046264.	0.4	0
38	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.	0.4	3
39	Structural characterization of rare missense variants within known neurodegenerative disease proteins. Alzheimer's and Dementia, 2020, 16, e046405.	0.4	0
40	Analysis of individual families implicates noncoding DNA variation and multiple biological pathways in Alzheimerâ€™s disease risk. Alzheimer's and Dementia, 2020, 16, e046456.	0.4	0
41	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.	1.2	6
42	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.	0.4	11
43	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.	1.3	26
44	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.	6.5	28
45	Sex differences in the genetic predictors of Alzheimerâ€™s pathology. Brain, 2019, 142, 2581-2589.	3.7	65
46	Genome-wide brain DNA methylation analysis suggests epigenetic reprogramming in Parkinson disease. Neurology: Genetics, 2019, 5, e342.	0.9	50
47	Large-scale GWAS reveals insights into the genetic architecture of same-sex sexual behavior. Science, 2019, 365, .	6.0	245
48	Genome-wide enriched pathway analysis of acute post-radiotherapy pain in breast cancer patients: a prospective cohort study. Human Genomics, 2019, 13, 28.	1.4	20
49	Analysis of Whole-Exome Sequencing Data for Alzheimer Disease Stratified by APOE Genotype. JAMA Neurology, 2019, 76, 1099.	4.5	32
50	RNA editing alterations in a multi-ethnic Alzheimer disease cohort converge on immune and endocytic molecular pathways. Human Molecular Genetics, 2019, 28, 3053-3061.	1.4	19
51	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.	1.5	4
52	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
53	Genome studies must account for historyâ€”Response. Science, 2019, 366, 1461-1462.	6.0	4
54	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.	0.7	22

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55	Whole genome sequencing of Caribbean Hispanic families with lateâ€onset Alzheimer's disease. Annals of Clinical and Translational Neurology, 2018, 5, 406-417.	1.7	42
56	Properties of globalâ€and localâ€ancestry adjustments in genetic association tests in admixed populations. Genetic Epidemiology, 2018, 42, 214-229.	0.6	37
57	Rare genetic variation implicated in non-Hispanic white families with Alzheimer disease. Neurology: Genetics, 2018, 4, e286.	0.9	27
58	P1â€154: GENOMEâ€WIDE LINKAGE ANALYSES OF AFRICAN AMERICAN FAMILIES SUPPORTS EVIDENCE OF LINKAGE TO CHROMOSOME 12. Alzheimer's and Dementia, 2018, 14, P336.	0.4	0
59	P2â€108: WHOLEâ€GENOME SEQUENCING IN NONâ€HISPANIC WHITE FAMILIES IMPLICATES RARE VARIATION IN LATEâ€ONSET ALZHEIMER'S DISEASE RISK. Alzheimer's and Dementia, 2018, 14, P710.	0.4	0
60	O2â€01â€05: MULTIâ€ETHNIC ALZHEIMER'S DISEASE RELATED CHANGES OF RNA EDITING AFFECT IMMUNE REGULATION, ENDOCYTOSIS, AND AMYLOID PRECURSOR PROTEIN CATABOLISM. Alzheimer's and Dementia, 2018, 14, P609.	0.4	0
61	Ancestral origin of ApoE Îµ4 Alzheimer disease risk in Puerto Rican and African American populations. PLoS Genetics, 2018, 14, e1007791.	1.5	117
62	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.	2.3	6
63	Genetic Variants of Microtubule Actin Cross-linking Factor 1 (MACF1) Confer Risk for Parkinsonâ€™s Disease. Molecular Neurobiology, 2017, 54, 2878-2888.	1.9	22
64	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.	1.0	7
65	Single Marker Family-Based Association Analysis Conditional on Parental Information. Methods in Molecular Biology, 2017, 1666, 391-407.	0.4	0
66	Impact of human CA8 on thermal antinociception in relation to morphine equivalence in mice. NeuroReport, 2017, 28, 1215-1220.	0.6	6
67	Evidence that dry eye represents a chronic overlapping pain condition. Molecular Pain, 2017, 13, 174480691772930.	1.0	34
68	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
69	Early-Onset Alzheimer Disease and Candidate Risk Genes Involved in Endolysosomal Transport. JAMA Neurology, 2017, 74, 1113.	4.5	41
70	[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.	0.4	4
71	Toward Genetics-Driven Early Intervention in Dilated Cardiomyopathy. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	41
72	Genome-Wide Association Study of Male Sexual Orientation. Scientific Reports, 2017, 7, 16950.	1.6	44

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73	[P2â€“105]: COLLECTION OF MULTIPLEX FAMILIES WITH UNEXPLAINED EARLYâ€ONSET ALZHEIMER's DISEASE FOR GENOMIC RESEARCH. Alzheimer's and Dementia, 2017, 13, P647.	0.4	0
74	[O2â€“08â€“02]: SEXâ€SPECIFIC ANALYSIS OF THE ADSP CASEâ€CONTROL WHOLEâ€EXOME SEQUENCING DATASET. Alzheimer's and Dementia, 2017, 13, P571.	0.4	0
75	[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.	0.4	1
76	Dopaminergic variants in siblings at high risk for autism: Associations with initiating joint attention. Autism Research, 2016, 9, 1142-1150.	2.1	22
77	DNA variants in CACNA1C modify Parkinson disease risk only when vitamin D level is deficient. Neurology: Genetics, 2016, 2, e72.	0.9	11
78	O1â€03â€02: ABCA7 Frameshift Deletion Associated with Alzheimerâ€™s Disease in African Americans. Alzheimer's and Dementia, 2016, 12, P177.	0.4	0
79	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
80	O1-03-05: High-Resolution Imputation in Genome-Wide Association Studies of Late-Onset Alzheimer's Disease Identifies Novel Rare Variant Associations. , 2016, 12, P178-P179.		0
81	O1-09-02: Whole Exome Sequencing of Late Onset Multiplex Families Identifies Rare Coding Variants in Known and Novel Alzheimerâ€™s Disease Genes. , 2016, 12, P196-P197.		0
82	O1â€09â€03: Whole Genome Sequencing in Familial Lateâ€Onset Alzheimerâ€™s Disease Identifies Variations in TTC3 and FSIP2. Alzheimer's and Dementia, 2016, 12, P197.	0.4	0
83	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.	0.4	24
84	hVMAT2: A Target of Individualized Medication for Parkinson's Disease. Neurotherapeutics, 2016, 13, 623-634.	2.1	11
85	Segregation of a rare TTC3 variant in an extended family with late-onset Alzheimer disease. Neurology: Genetics, 2016, 2, e41.	0.9	41
86	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	2.8	56
87	ABCA7 frameshift deletion associated with Alzheimer disease in African Americans. Neurology: Genetics, 2016, 2, e79.	0.9	74
88	Increased NigralSLC6A3Activity in Schizophrenia Patients: Findings From the Torontoâ€“McLean Cohorts. Schizophrenia Bulletin, 2016, 42, 772-781.	2.3	10
89	Overlap between Parkinson disease and Alzheimer disease in ABCA7 functional variants. Neurology: Genetics, 2016, 2, e44.	0.9	31
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.	1.5	39

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91	Neuropathic Ocular Pain due to Dry Eye Is Associated With Multiple Comorbid Chronic Pain Syndromes. Journal of Pain, 2016, 17, 310-318.	0.7	77
92	Incomplete response to artificial tears is associated with features of neuropathic ocular pain. British Journal of Ophthalmology, 2016, 100, 745-749.	2.1	71
93	Global and local ancestry in Africanâ€Americans: Implications for Alzheimer's disease risk. Alzheimer's and Dementia, 2016, 12, 233-243.	0.4	42
94	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.	2.6	57
95	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.	1.0	80
96	Carbonic Anhydrase-8 Regulates Inflammatory Pain by Inhibiting the ITPR1-Cytosolic Free Calcium Pathway. PLoS ONE, 2015, 10, e0118273.	1.1	30
97	Rarity of the Alzheimer Diseaseâ€"ProtectiveAPPA673T Variant in the United States. JAMA Neurology, 2015, 72, 209.	4.5	41
98	PARK10 is a major locus for sporadic neuropathologically confirmed Parkinson disease. Neurology, 2015, 84, 972-980.	1.5	48
99	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.	1.2	62
100	Vitamin D from different sources is inversely associated with Parkinson disease. Movement Disorders, 2015, 30, 560-566.	2.2	61
101	Dry eye symptoms align more closely to non-ocular conditions than to tear film parameters. British Journal of Ophthalmology, 2015, 99, 1126-1129.	2.1	78
102	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.	1.4	67
103	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.4	173
104	Dry eye symptom severity and persistence are associated with symptoms of neuropathic pain. British Journal of Ophthalmology, 2015, 99, 665-668.	2.1	81
105	Family-Based Association Test Using Both Common and Rare Variants and Accounting for Directions of Effects for Sequencing Data. PLoS ONE, 2014, 9, e107800.	1.1	13
106	Genome-Wide Association Meta-analysis of Neuropathologic Features of Alzheimer's Disease and Related Dementias. PLoS Genetics, 2014, 10, e1004606.	1.5	305
107	Valid Monte Carlo Permutation Tests for Genetic Caseâ€Control Studies With Missing Genotypes. Genetic Epidemiology, 2014, 38, 325-344.	0.6	3
108	Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 1394.	4.5	166

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109	Exome sequencing of extended families with autism reveals genes shared across neurodevelopmental and neuropsychiatric disorders. Molecular Autism, 2014, 5, 1.	2.6	246
110	Detecting Genetic Interactions in Pathwayâ€Based Genomeâ€Wide Association Studies. Genetic Epidemiology, 2014, 38, 300-309.	0.6	17
111	Absence of C9ORF72 expanded or intermediate repeats in autopsyâ€confirmed Parkinson's disease. Movement Disorders, 2014, 29, 827-830.	2.2	24
112	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	1.1	155
113	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
114	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
115	C9ORF72 Intermediate Repeat Copies Are a Significant Risk Factor for Parkinson Disease. Annals of Human Genetics, 2013, 77, 351-363.	0.3	69
116	Evaluating Mitochondrial DNA Variation in Autism Spectrum Disorders. Annals of Human Genetics, 2013, 77, 9-21.	0.3	36
117	High-Resolution Survey in Familial Parkinson Disease Genes Reveals Multiple Independent Copy Number Variation Events in PARK2. Human Mutation, 2013, 34, 1071-1074.	1.1	13
118	Reconstructing the Population Genetic History of the Caribbean. PLoS Genetics, 2013, 9, e1003925.	1.5	296
119	Whole exome sequencing of rare variants in EIF4G1 and VPS35 in Parkinson disease. Neurology, 2013, 80, 982-989.	1.5	68
120	Comprehensive Research Synopsis and Systematic Meta-Analyses in Parkinson's Disease Genetics: The PDGene Database. PLoS Genetics, 2012, 8, e1002548.	1.5	495
121	Evaluating Pathogenicity of Rare Variants From Dilated Cardiomyopathy in the Exome Era. Circulation: Cardiovascular Genetics, 2012, 5, 167-174.	5.1	112
122	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
123	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.	1.1	34
124	Metaâ€analysis of Parkinson's Disease: Identification of a novel locus, RIT2. Annals of Neurology, 2012, 71, 370-384.	2.8	264
125	Identifying Consensus Disease Pathways in Parkinson's Disease Using an Integrative Systems Biology Approach. PLoS ONE, 2011, 6, e16917.	1.1	72
126	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.	1.0	31

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127	Comparison of Three Targeted Enrichment Strategies on the SOLiD Sequencing Platform. PLoS ONE, 2011, 6, e18595.	1.1	66
128	Vitamin D Receptor Gene as a Candidate Gene for Parkinson Disease. Annals of Human Genetics, 2011, 75, 201-210.	0.3	95
129	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
130	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.	2.6	320
131	Rare variant mutations identified in pediatric patients with dilated cardiomyopathy. Progress in Pediatric Cardiology, 2011, 31, 39-47.	0.2	65
132	A noise-reduction GWAS analysis implicates altered regulation of neurite outgrowth and guidance in autism. Molecular Autism, 2011, 2, 1.	2.6	191
133	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.	2.6	29
134	Convergence of miRNA Expression Profiling, Î±-Synuclein Interacton and GWAS in Parkinson's Disease. PLoS ONE, 2011, 6, e25443.	1.1	235
135	A modifier locus on chromosome 5 contributes to L1 cell adhesion molecule X-linked hydrocephalus in mice. Neurogenetics, 2010, 11, 53-71.	0.7	27
136	Novel variants identified in methyl-CpG-binding domain genes in autistic individuals. Neurogenetics, 2010, 11, 291-303.	0.7	67
137	CAPL: a novel association test using caseâ€control and family data and accounting for population stratification. Genetic Epidemiology, 2010, 34, 747-755.	0.6	15
138	A rare novel deletion of the tyrosine hydroxylase gene in Parkinson disease. Human Mutation, 2010, 31, E1767-E1771.	1.1	29
139	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
140	Common Susceptibility Variants Examined for Association with Dilated Cardiomyopathy. Annals of Human Genetics, 2010, 74, 110-116.	0.3	26
141	APOE is not Associated with Alzheimer Disease: a Cautionary tale of Genotype Imputation. Annals of Human Genetics, 2010, 74, 189-194.	0.3	13
142	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
143	The transcription factor orthodenticle homeobox 2 influences axonal projections and vulnerability of midbrain dopaminergic neurons. Brain, 2010, 133, 2022-2031.	3.7	47
144	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

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145	A General Framework for Formal Tests of Interaction after Exhaustive Search Methods with Applications to MDR and MDR-PDT. PLoS ONE, 2010, 5, e9363.	1.1	13
146	Using Allele Sharing Distance for Detecting Human Population Stratification. Human Heredity, 2009, 68, 182-191.	0.4	47
147	Genomic convergence to identify candidate genes for Alzheimer Disease on chromosome 10. Human Mutation, 2009, 30, 463-471.	1.1	69
148	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
149	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
150	Association Test for X-Linked QTL in Family-Based Designs. American Journal of Human Genetics, 2009, 84, 431-444.	2.6	17
151	Genome-wide Linkage Screen in Familial Parkinson Disease Identifies Loci on Chromosomes 3 and 18. American Journal of Human Genetics, 2009, 84, 499-504.	2.6	11
152	Resolving the relationship between ApolipoproteinE and depression. Neuroscience Letters, 2009, 455, 116-119.	1.0	25
153	Exome Sequencing of a Multigenerational Human Pedigree. PLoS ONE, 2009, 4, e8232.	1.1	69
154	Nitric oxide synthase genes and their interactions with environmental factors in Parkinsonâ€™s disease. Neurogenetics, 2008, 9, 249-262.	0.7	91
155	A multiple testing correction method for genetic association studies using correlated single nucleotide polymorphisms. Genetic Epidemiology, 2008, 32, 361-369.	0.6	646
156	Orderedâ€subset analysis (OSA) for familyâ€based association mapping of complex traits. Genetic Epidemiology, 2008, 32, 627-637.	0.6	10
157	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.	2.6	437
158	Response to Ding and Lin. American Journal of Human Genetics, 2008, 82, 530-531.	2.6	1
159	Response to Zaykin and Shibata. American Journal of Human Genetics, 2008, 82, 796-797.	2.6	18
160	Geneâ€Gene Interaction Between FGF20 and MAOB in Parkinson Disease. Annals of Human Genetics, 2008, 72, 157-162.	0.3	34
161	Increased Efficiency of Case-Control Association Analysis by Using Allele-Sharing and Covariate Information. Human Heredity, 2008, 65, 154-165.	0.4	5
162	The Future Is Now â€“ Will the Real Disease Gene Please Stand Up?. Human Heredity, 2008, 66, 127-135.	0.4	1

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163	Smoking, Caffeine, and Nonsteroidal Anti-inflammatory Drugs in Families With Parkinson Disease. Archives of Neurology, 2007, 64, 576.	4.9	107
164	Investigation of potential geneâ€“gene interactions between apoe and reln contributing to autism risk. Psychiatric Genetics, 2007, 17, 221-226.	0.6	44
165	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.	2.6	24
166	No Gene Is an Island: The Flip-Flop Phenomenon. American Journal of Human Genetics, 2007, 80, 531-538.	2.6	437
167	Effect of heterogeneity on the chromosome 10 risk in late-onset Alzheimer disease. Human Mutation, 2007, 28, 1065-1073.	1.1	15
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