Matthew Huentelman

List of Publications by Year
in descending order

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Version: 2024-02-01

162 papers	20,942 citations	23500 58 h-index	11288 136 g-index
171 all docs	171 docs citations	171 times ranked	27643 citing authors

#	Article	IF	Citations
1	Longitudinal Assessment of Intravoxel Incoherent Motion <scp>Diffusionâ€Weighted MRI</scp> Metrics in Cognitive Decline. Journal of Magnetic Resonance Imaging, 2022, , .	1.9	2
2	Adenosine triphosphate Binding Cassette subfamily C member 1 (ABCC1) overexpression reduces APP processing and increases alpha- versus beta-secretase activity, in vitro. Biology Open, 2021, 10, .	0.6	2
3	Harsh Parenting Predicts Novel HPA Receptor Gene Methylation and NR3C1 Methylation Predicts Cortisol Daily Slope in Middle Childhood. Cellular and Molecular Neurobiology, 2021, 41, 783-793.	1.7	23
4	Influence of regional white matter hyperintensity volume and apolipoprotein E Îµ4 status on hippocampal volume in healthy older adults. Hippocampus, 2021, 31, 469-480.	0.9	13
5	Transient ACE (Angiotensin-Converting Enzyme) Inhibition Suppresses Future Fibrogenic Capacity and Heterogeneity of Cardiac Fibroblast Subpopulations. Hypertension, 2021, 77, 904-918.	1.3	13
6	DNA Methylation and Expression Profiles of Whole Blood in Parkinsonâ€™s Disease. Frontiers in Genetics, 2021, 12, 640266.	1.1	33
7	Molecular biomarkers to track clinical improvement following an integrative treatment model in autistic toddlers. Acta Neuropsychiatrica, 2021, 33, 267-272.	1.0	2
8	Integration of peripheral transcriptomics, genomics, and interactomics following trauma identifies causal genes for symptoms of post-traumatic stress and major depression. Molecular Psychiatry, 2021, 26, 3077-3092.	4.1	15
9	Identification of retinoblastoma binding protein 7 (Rbbp7) as a mediator against tau acetylation and subsequent neuronal loss in Alzheimerâ€™s disease and related tauopathies. Acta Neuropathologica, 2021, 142, 279-294.	3.9	13
10	Transcriptome-wide association study of post-trauma symptom trajectories identified GRIN3B as a potential biomarker for PTSD development. Neuropsychopharmacology, 2021, 46, 1811-1820.	2.8	15
11	Two separate, large cohorts reveal potential modifiers of age-associated variation in visual reaction time performance. Npj Aging and Mechanisms of Disease, 2021, 7, 14.	4.5	9
12	Family SES Is Associated with the Gut Microbiome in Infants and Children. Microorganisms, 2021, 9, 1608.	1.6	19
13	Accessible pediatric neuroimaging using a low field strength MRI scanner. NeuroImage, 2021, 238, 118273.	2.1	32
14	Autobiographical Memory Fluency Reductions in Cognitively Unimpaired Middle-Aged and Older Adults at Increased Risk for Alzheimerâ€™s Disease Dementia. Journal of the International Neuropsychological Society, 2021, 27, 905-915.	1.2	6
15	Leukocyte and cytokine variables in asymptomatic Pugs at genetic risk of necrotizing meningoencephalitis. Journal of Veterinary Internal Medicine, 2021, , .	0.6	3
16	Remote, Unsupervised Functional Motor Task Evaluation in Older Adults across the United States Using the MindCrowd Electronic Cohort. Developmental Neuropsychology, 2021, 46, 435-446.	1.0	6
17	Maternal choline supplementation ameliorates Alzheimerâ€™s disease pathology by reducing brain homocysteine levels across multiple generations. Molecular Psychiatry, 2020, 25, 2620-2629.	4.1	54
18	Utilizing RNA and outlier analysis to identify an intronic spliceâ€altering variant in AP4S1 in a sibling pair with progressive spastic paraplegia. Human Mutation, 2020, 41, 412-419.	1.1	7

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19	Congenital myasthenic syndrome caused by a frameshift insertion mutation in GFPT1. Neurology: Genetics, 2020, 6, e468.	0.9	8
20	Longitudinal white matter and cognitive development in pediatric carriers of the apolipoprotein Îµ4 allele. NeuroImage, 2020, 222, 117243.	2.1	14
21	Genetic and epigenetic MTHFR gene variants in the mothers of attention-deficit/hyperactivity disorder affected children as possible risk factors for neurodevelopmental disorders. Epigenomics, 2020, 12, 813-823.	1.0	2
22	Transcriptional profiling of multiple system atrophy cerebellar tissue highlights differences between the parkinsonian and cerebellar sub-types of the disease. Acta Neuropathologica Communications, 2020, 8, 76.	2.4	20
23	Association of Common Genetic Variants in the CPSF7 and SDHAF2 Genes with Canine Idiopathic Pulmonary Fibrosis in the West Highland White Terrier. Genes, 2020, 11, 609.	1.0	3
24	Genes Implicated in Rare Congenital Inner Ear and Cochleovestibular Nerve Malformations. Ear and Hearing, 2020, 41, 983-989.	1.0	6
25	Cell death and survival pathways in Alzheimer's disease: an integrative hypothesis testing approach utilizing -omic data sets. Neurobiology of Aging, 2020, 95, 15-25.	1.5	23
26	Extracellular microRNAs in blood differentiate between ischaemic and haemorrhagic stroke subtypes. Journal of Extracellular Vesicles, 2020, 9, 1713540.	5.5	53
27	Telomere Length and Autism Spectrum Disorder Within the Family: Relationships With Cognition and Sensory Symptoms. Autism Research, 2020, 13, 1094-1101.	2.1	8
28	ESHRD: deconvolution of brain homogenate RNA expression data to identify cell-type-specific alterations in Alzheimerâ€™s disease. Aging, 2020, 12, 4124-4162.	1.4	4
29	Transcriptome Changes in the Alzheimerâ€™s Disease Middle Temporal Gyrus: Importance of RNA Metabolism and Mitochondria-Associated Membrane Genes. Journal of Alzheimer's Disease, 2019, 70, 691-713.	1.2	51
30	Two additional males with Xâ€linked, syndromic mental retardation carry de novo mutations in HNRNPH2. Clinical Genetics, 2019, 96, 183-185.	1.0	16
31	A de novo SIX1 variant in a patient with a rare nonsyndromic cochleovestibular nerve abnormality, cochlear hypoplasia, and bilateral sensorineural hearing loss. Molecular Genetics & Genomic Medicine, 2019, 7, e995.	0.6	6
32	Association of AEBP1 and NRN1 RNA expression with Alzheimerâ€™s disease and neurofibrillary tangle density in middle temporal gyrus. Brain Research, 2019, 1719, 217-224.	1.1	15
33	Dopaminergic gene methylation is associated with cognitive performance in a childhood monozygotic twin study. Epigenetics, 2019, 14, 310-323.	1.3	16
34	Exome Sequencing of Two Siblings with Sporadic Autism Spectrum Disorder and Severe Speech Sound Disorder Suggests Pleiotropic and Complex Effects. Behavior Genetics, 2019, 49, 399-414.	1.4	18
35	Gradual hypertension induction in middleâ€aged Cyp1a1â€Ren2 transgenic rats produces significant impairments in spatial learning. Physiological Reports, 2019, 7, e14010.	0.7	4
36	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

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37	Compound heterozygous mutations in SNAP29 is associated with Pelizaeus-Merzbacher-like disorder (PMLD). Human Genetics, 2019, 138, 1409-1417.	1.8	14
38	Resistance to autosomal dominant Alzheimerâ€™s disease in an APOE3 Christchurch homozygote: a case report. Nature Medicine, 2019, 25, 1680-1683.	15.2	328
39	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	9.4	192
40	Peripheral Biomarkers in Schizophrenia: A Meta-Analysis of Microarray Gene Expression Datasets. International Journal of Neuropsychopharmacology, 2019, 22, 186-193.	1.0	19
41	Family history of Alzheimerâ€™s disease alters cognition and is modified by medical and genetic factors. ELife, 2019, 8, .	2.8	30
42	Big data collision: the internet of things, wearable devices and genomics in the study of neurological traits and disease. Human Molecular Genetics, 2018, 27, R35-R39.	1.4	23
43	Neonatal epileptic encephalopathy caused by de novo GNAO1 mutation misdiagnosed as atypical Rett syndrome: Cautions in interpretation of genomic test results. Seminars in Pediatric Neurology, 2018, 26, 28-32.	1.0	10
44	Seizure-Induced Arc mRNA Expression Thresholds in Rat Hippocampus and Perirhinal Cortex. Frontiers in Systems Neuroscience, 2018, 12, 53.	1.2	3
45	The PKC-Î² selective inhibitor, Enzastaurin, impairs memory in middle-aged rats. PLoS ONE, 2018, 13, e0198256.	1.1	5
46	Somatic inactivating PTPRJ mutations and dysregulated pathways identified in canine malignant melanoma by integrated comparative genomic analysis. PLoS Genetics, 2018, 14, e1007589.	1.5	56
47	De novo variants in GREB1L are associated with non-syndromic inner ear malformations and deafness. Human Genetics, 2018, 137, 459-470.	1.8	24
48	Transcriptome response of human skeletal muscle to divergent exercise stimuli. Journal of Applied Physiology, 2018, 124, 1529-1540.	1.2	61
49	Associations of MAP2K3 Gene Variants With Superior Memory in SuperAgers. Frontiers in Aging Neuroscience, 2018, 10, 155.	1.7	22
50	The human brainome: network analysis identifies HSPA2 as a novel Alzheimerâ€™s disease target. Brain, 2018, 141, 2721-2739.	3.7	31
51	Whole transcriptome profiling of the human hippocampus suggests an involvement of the KIBRA rs17070145 polymorphism in differential activation of the MAPK signaling pathway. Hippocampus, 2017, 27, 784-793.	0.9	19
52	Exploring genome-wide DNA methylation patterns in Aicardi syndrome. Epigenomics, 2017, 9, 1373-1386.	1.0	8
53	De Novo Missense Mutations in DHX30 Impair Global Translation and Cause a Neurodevelopmental Disorder. American Journal of Human Genetics, 2017, 101, 716-724.	2.6	66
54	Pattern of gene expression in different stages of schizophrenia: Down-regulation of NPTX2 gene revealed by a meta-analysis of microarray datasets. European Neuropsychopharmacology, 2017, 27, 1054-1063.	0.3	28

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55	Necroptosis activation in Alzheimer's disease. Nature Neuroscience, 2017, 20, 1236-1246.	7.1	305
56	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
57	Compound heterozygous mutations in MASP1 in a deaf child with absent cochlear nerves. Neurology: Genetics, 2017, 3, e153.	0.9	6
58	[P4â€"081]: ASSOCIATION OF MAP2K3 GENE VARIATION AND THE SUPERAGING PHENOTYPE DETECTED BY WHOLE EXOME SEQUENCING. Alzheimer's and Dementia, 2017, 13, P1290.	0.4	1
59	Hippocampal Transcriptomic Profiles: Subfield Vulnerability to Age and Cognitive Impairment. Frontiers in Aging Neuroscience, 2017, 9, 383.	1.7	45
60	Rare Variants in Cardiomyopathy Genes Associated With Stress-Induced Cardiomyopathy. Neurosurgery, 2016, 78, 835-843.	0.6	3
61	DNA Diagnostics of Hereditary Hearing Loss: A Targeted Resequencing Approach Combined with a Mutation Classification System. Human Mutation, 2016, 37, 812-819.	1.1	76
62	Mechanisms of CO₂/H⁺Sensitivity of Astrocytes. Journal of Neuroscience, 2016, 36, 10750-10758.	1.7	101
63	Assessment of the genetic variance of late-onset Alzheimer's disease. Neurobiology of Aging, 2016, 41, 200.e13-200.e20.	1.5	174
64	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	2.8	56
65	Next-generation profiling to identify the molecular etiology of Parkinson dementia. Neurology: Genetics, 2016, 2, e75.	0.9	25
66	A comprehensive catalogue of the coding and non-coding transcripts of the human inner ear. Hearing Research, 2016, 333, 266-274.	0.9	51
67	Time course of cardiac inflammation during nitric oxide synthase inhibition in SHR: impact of prior transient ACE inhibition. Hypertension Research, 2016, 39, 8-18.	1.5	10
68	A novel Alzheimer disease locus located near the gene encoding tau protein. Molecular Psychiatry, 2016, 21, 108-117.	4.1	260
69	Novel pathogenic variants and genes for myopathies identified by whole exome sequencing. Molecular Genetics & Genomic Medicine, 2015, 3, 283-301.	0.6	43
70	Meeting report: discussions and preliminary findings on extracellular RNA measurement methods from laboratories in the NIH Extracellular RNA Communication Consortium. Journal of Extracellular Vesicles, 2015, 4, 26533.	5.5	51
71	Multi-scale study of normal aging predicts novel late-onset Alzheimer's disease risk variants. BMC Bioinformatics, 2015, 16, P11.	1.2	2
72	A De Novo Mutation inTEAD1Causes Nonâ€"X-Linked Aicardi Syndrome. , 2015, 56, 3896.		22

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73	A Frame-Shift Mutation in CAV1 Is Associated with a Severe Neonatal Progeroid and Lipodystrophy Syndrome. PLoS ONE, 2015, 10, e0131797.	1.1	46
74	Feasibility of implementing molecularâ€guided therapy for the treatment of patients with relapsed or refractory neuroblastoma. Cancer Medicine, 2015, 4, 871-886.	1.3	26
75	Protective variant for hippocampal atrophy identified by whole exome sequencing. Annals of Neurology, 2015, 77, 547-552.	2.8	48
76	Associations Between Biomarkers and Age in the Presenilin 1 E280A Autosomal Dominant Alzheimer Disease Kindred. JAMA Neurology, 2015, 72, 316.	4.5	145
77	Genome-wide association analysis demonstrates the highly polygenic character of age-related hearing impairment. European Journal of Human Genetics, 2015, 23, 110-115.	1.4	84
78	Comparison against 186 canid whole-genome sequences reveals survival strategies of an ancient clonally transmissible canine tumor. Genome Research, 2015, 25, 1646-1655.	2.4	63
79	Nucleic acid-based risk factors and biomarkers: a future perspective on their use and development in Alzheimer's disease. Personalized Medicine, 2015, 12, 475-482.	0.8	0
80	Whole-genome sequencing suggests a chemokine gene cluster that modifies age at onset in familial Alzheimer's disease. Molecular Psychiatry, 2015, 20, 1294-1300.	4.1	55
81	Association of SNPs in EGR3 and ARC with Schizophrenia Supports a Biological Pathway for Schizophrenia Risk. PLoS ONE, 2015, 10, e0135076.	1.1	42
82	Epigenetics of Cognition and Neurodegenerative Disorders. Neuromethods, 2015, , 285-298.	0.2	0
83	Transcriptomic Analysis of Tail Regeneration in the Lizard Anolis carolinensis Reveals Activation of Conserved Vertebrate Developmental and Repair Mechanisms. PLoS ONE, 2014, 9, e105004.	1.1	112
84	Characterization of X Chromosome Inactivation Using Integrated Analysis of Whole-Exome and mRNA Sequencing. PLoS ONE, 2014, 9, e113036.	1.1	24
85	Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 1394.	4.5	166
86	Genetic analysis of quantitative phenotypes in AD and MCI: imaging, cognition and biomarkers. Brain Imaging and Behavior, 2014, 8, 183-207.	1.1	161
87	A cellular model of amyloid precursor protein processing and amyloid-Î² peptide production. Journal of Neuroscience Methods, 2014, 223, 114-122.	1.3	16
88	Brain Differences in Infants at Differential Genetic Risk for Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 11.	4.5	221
89	Genetic Implication of a Novel Thiamine Transporter in Human Hypertension. Journal of the American College of Cardiology, 2014, 63, 1542-1555.	1.2	36
90	APOE and BCHE as modulators of cerebral amyloid deposition: a florbetapir PET genome-wide association study. Molecular Psychiatry, 2014, 19, 351-357.	4.1	181

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91	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	1.1	155
92	Identification of Novel Genetic Risk Loci in Maltese Dogs with Necrotizing Meningoencephalitis and Evidence of a Shared Genetic Risk across Toy Dog Breeds. PLoS ONE, 2014, 9, e112755.	1.1	27
93	Genetic Susceptibility for Alzheimer Disease Neuritic Plaque Pathology. JAMA Neurology, 2013, 70, 1150.	4.5	143
94	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
95	MET Receptor Tyrosine Kinase as an Autism Genetic Risk Factor. International Review of Neurobiology, 2013, 113, 135-165.	0.9	38
96	A sensitive and specific diagnostic test for hearing loss using a microdroplet PCRâ€based approach and next generation sequencing. American Journal of Medical Genetics, Part A, 2013, 161, 145-152.	0.7	61
97	Variants in triggering receptor expressed on myeloid cells 2 are associated with both behavioral variant frontotemporal lobar degeneration and Alzheimer's disease. Neurobiology of Aging, 2013, 34, 2077.e11-2077.e18.	1.5	124
98	Whole-exome sequencing and imaging genetics identify functional variants for rate of change in hippocampal volume in mild cognitive impairment. Molecular Psychiatry, 2013, 18, 781-787.	4.1	81
99	Identification of functional variants from whole-exome sequencing, combined with neuroimaging genetics. Molecular Psychiatry, 2013, 18, 739-739.	4.1	8
100	In vitro-differentiated neural cell cultures progress towards donor-identical brain tissue. Human Molecular Genetics, 2013, 22, 3534-3546.	1.4	19
101	Initial Assessment of the Pathogenic Mechanisms of the Recently Identified Alzheimer Risk Loci. Annals of Human Genetics, 2013, 77, 85-105.	0.3	41
102	A coding variant in CR1 interacts with APOE-É›4 to influence cognitive decline. Human Molecular Genetics, 2012, 21, 2377-2388.	1.4	90
103	Brain imaging and fluid biomarker analysis in young adults at genetic risk for autosomal dominant Alzheimer's disease in the presenilin 1 E280A kindred: a case-control study. Lancet Neurology, The, 2012, 11, 1048-1056.	4.9	450
104	Florbetapir PET analysis of amyloid-Î² deposition in the presenilin 1 E280A autosomal dominant Alzheimer's disease kindred: a cross-sectional study. Lancet Neurology, The, 2012, 11, 1057-1065.	4.9	209
105	Analysis of Copy Number Variation in Alzheimerâ€™s Disease in a Cohort of Clinically Characterized and Neuropathologically Verified Individuals. PLoS ONE, 2012, 7, e50640.	1.1	49
106	Somitogenesis in the anole lizard and alligator reveals evolutionary convergence and divergence in the amniote segmentation clock. Developmental Biology, 2012, 363, 308-319.	0.9	52
107	Amyloid pathway-based candidate gene analysis of [11C]PiB-PET in the Alzheimerâ€™s Disease Neuroimaging Initiative (ADNI) cohort. Brain Imaging and Behavior, 2012, 6, 1-15.	1.1	47
108	Voxelwise gene-wide association study (vGeneWAS): Multivariate gene-based association testing in 731 elderly subjects. NeuroImage, 2011, 56, 1875-1891.	2.1	116

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109	Association between GAB2 haplotype and higher glucose metabolism in Alzheimer's disease-affected brain regions in cognitively normal APOEÎµ4 carriers. NeuroImage, 2011, 54, 1896-1902.	2.1	22
110	Are Sema5a mutant mice a good model of autism? A behavioral analysis of sensory systems, emotionality and cognition. Behavioural Brain Research, 2011, 225, 142-150.	1.2	24
111	Induction of pluripotent stem cells from autopsy donor-derived somatic cells. Neuroscience Letters, 2011, 502, 219-224.	1.0	25
112	Tonic Premarin dose-dependently enhances memory, affects neurotrophin protein levels and alters gene expression in middle-aged rats. Neurobiology of Aging, 2011, 32, 680-697.	1.5	60
113	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
114	A genome-wide analysis of population structure in the Finnish Saami with implications for genetic association studies. European Journal of Human Genetics, 2011, 19, 347-352.	1.4	19
115	CR1 is associated with amyloid plaque burden and ageâ€related cognitive decline. Annals of Neurology, 2011, 69, 560-569.	2.8	148
116	Targeted next-generation sequencing: microdroplet PCR approach for variant detection in research and clinical samples. Expert Review of Molecular Diagnostics, 2011, 11, 347-349.	1.5	9
117	Identification of Risk Loci for Necrotizing Meningoencephalitis in Pug Dogs. Journal of Heredity, 2011, 102, S40-S46.	1.0	31
118	A genome-wide association study for age-related hearing impairment in the Saami. European Journal of Human Genetics, 2010, 18, 685-693.	1.4	88
119	A TOMM40 variable-length polymorphism predicts the age of late-onset Alzheimer's disease. Pharmacogenomics Journal, 2010, 10, 375-384.	0.9	351
120	KIBRA: a new gateway to learning and memory?. Frontiers in Aging Neuroscience, 2010, 2, 4.	1.7	77
121	Reduced Posterior Cingulate Mitochondrial Activity in Expired Young Adult Carriers of the APOE Îµ4 Allele, the Major Late-Onset Alzheimer's Susceptibility Gene. Journal of Alzheimer's Disease, 2010, 22, 307-313.	1.2	131
122	Association of CR1, CLU and PICALM with Alzheimer's disease in a cohort of clinically characterized and neuropathologically verified individuals. Human Molecular Genetics, 2010, 19, 3295-3301.	1.4	223
123	A commonly carried allele of the obesity-related FTO gene is associated with reduced brain volume in the healthy elderly. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8404-8409.	3.3	227
124	Hypometabolism in Alzheimer-Affected Brain Regions in Cognitively Healthy Latino Individuals Carrying the Apolipoprotein E Îµ4 Allele. Archives of Neurology, 2010, 67, 462-8.	4.9	89
125	Voxelwise genome-wide association study (vGWAS). NeuroImage, 2010, 53, 1160-1174.	2.1	239
126	Genome-wide analysis reveals novel genes influencing temporal lobe structure with relevance to neurodegeneration in Alzheimer's disease. NeuroImage, 2010, 51, 542-554.	2.1	141

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127	Evidence for an association between KIBRA and late-onset Alzheimer's disease. Neurobiology of Aging, 2010, 31, 901-909.	1.5	100
128	Decreased serum arylesterase activity in autism spectrum disorders. Psychiatry Research, 2010, 180, 105-113.	1.7	33
129	Genome-wide SNP analysis reveals no gain in power for association studies of common variants in the Finnish Saami. European Journal of Human Genetics, 2010, 18, 569-574.	1.4	3
130	Whole genome association study of brain-wide imaging phenotypes for identifying quantitative trait loci in MCI and AD: A study of the ADNI cohort. NeuroImage, 2010, 53, 1051-1063.	2.1	340
131	Whole genome association analysis shows that ACE is a risk factor for Alzheimer's disease and fails to replicate most candidates from Meta-analysis. International Journal of Molecular Epidemiology and Genetics, 2010, 1, 19-30.	0.4	4
132	GRM7 variants confer susceptibility to age-related hearing impairment. Human Molecular Genetics, 2009, 18, 785-796.	1.4	174
133	Hippocampal gene expression changes during age-related cognitive decline. Brain Research, 2009, 1256, 101-110.	1.1	37
134	Phenotypic variability of patients homozygous for the GJB2 mutation 35delG cannot be explained by the influence of one major modifier gene. European Journal of Human Genetics, 2009, 17, 517-524.	1.4	46
135	A Genome-wide Analysis Identifies Genetic Variants in the RELN Gene Associated with Otosclerosis. American Journal of Human Genetics, 2009, 84, 328-338.	2.6	66
136	Genetic Control of Human Brain Transcript Expression in Alzheimer Disease. American Journal of Human Genetics, 2009, 84, 445-458.	2.6	290
137	Peripheral delivery of a ROCK inhibitor improves learning and working memory.. Behavioral Neuroscience, 2009, 123, 218-223.	0.6	89
138	Identification of genetic variants using bar-coded multiplexed sequencing. Nature Methods, 2008, 5, 887-893.	9.0	285
139	<i>Sorl1</i> as an Alzheimerâ€™s Disease Predisposition Gene?. Neurodegenerative Diseases, 2008, 5, 60-64.	0.8	73
140	SNiPer-HD: improved genotype calling accuracy by an expectation-maximization algorithm for high-density SNP arrays. Bioinformatics, 2007, 23, 57-63.	1.8	93
141	Whole-Genome Analysis of Sporadic Amyotrophic Lateral Sclerosis. New England Journal of Medicine, 2007, 357, 775-788.	13.9	234
142	GAB2 Alleles Modify Alzheimer's Risk in APOE É›4 Carriers. Neuron, 2007, 54, 713-720.	3.8	451
143	Identification of the Genetic Basis for Complex Disorders by Use of Pooling-Based Genomewide Single-Nucleotideâ€“Polymorphism Association Studies. American Journal of Human Genetics, 2007, 80, 126-139.	2.6	139
144	Identification of a Novel Risk Locus for Progressive Supranuclear Palsy by a Pooled Genomewide Scan of 500,288 Single-Nucleotide Polymorphisms. American Journal of Human Genetics, 2007, 80, 769-778.	2.6	68

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145	Calmodulin-binding transcription activator 1 (CAMTA1) alleles predispose human episodic memory performance. Human Molecular Genetics, 2007, 16, 1469-1477.	1.4	66
146	SNP-based chromosomal copy number ascertainment following multiple displacement whole-genome amplification. BioTechniques, 2007, 42, 77-83.	0.8	9
147	A survey of genetic human cortical gene expression. Nature Genetics, 2007, 39, 1494-1499.	9.4	488
148	Recessive Symptomatic Focal Epilepsy and Mutant Contactin-Associated Protein-like 2. New England Journal of Medicine, 2006, 354, 1370-1377.	13.9	576
149	Common Kibra Alleles Are Associated with Human Memory Performance. Science, 2006, 314, 475-478.	6.0	391
150	ACE2: A novel therapeutic target for cardiovascular diseases. Progress in Biophysics and Molecular Biology, 2006, 91, 163-198.	1.4	81
151	Protection from angiotensin II-induced cardiac hypertrophy and fibrosis by systemic lentiviral delivery of ACE2 in rats. Experimental Physiology, 2005, 90, 783-790.	0.9	214
152	SNiPer: Improved SNP genotype calling for Affymetrix 10K GeneChip microarray data. BMC Genomics, 2005, 6, 149.	1.2	26
153	The Autism Genome Project. Molecular Diagnosis and Therapy, 2005, 5, 233-246.	3.3	37
154	Prevention of Cardiac Hypertrophy by Angiotensin II Type-2 Receptor Gene Transfer. Hypertension, 2004, 43, 1233-1238.	1.3	55
155	Structure-Based Discovery of a Novel Angiotensin-Converting Enzyme 2 Inhibitor. Hypertension, 2004, 44, 903-906.	1.3	171
156	Cloning and characterization of a secreted form of angiotensin-converting enzyme 2. Regulatory Peptides, 2004, 122, 61-67.	1.9	43
157	Efficient large-scale production and concentration of HIV-1-based lentiviral vectors for use in vivo. Physiological Genomics, 2003, 12, 221-228.	1.0	154
158	Characterization of Mitotic Neurons Derived From Adult Rat Hypothalamus and Brain Stem. Journal of Neurophysiology, 2002, 87, 1076-1085.	0.9	58
159	[32] Large-scale production of retroviral vectors for systemic gene delivery. Methods in Enzymology, 2002, 346, 562-573.	0.4	11
160	Gene Therapy for Cardiovascular Disorders. Is There a Future?. Annals of the New York Academy of Sciences, 2001, 953a, 31-42.	1.8	19
161	The Future of Hypertension Therapy: Sense, Antisense, or Nonsense?. Hypertension, 2001, 37, 357-364.	1.3	44
162	A potential early clinical phenotype of necrotizing meningoencephalitis in genetically atâ€risk pug dogs. Journal of Veterinary Internal Medicine, 0, , .	0.6	1