Matthew Huentelman

List of Publications by Year
in descending order

162	20,942	23500 58	11288 136
papers	citations	h-index	g-index

171	171	171	27643
all docs	docs citations	times ranked	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.	9.4	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.	9.4	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.	9.4	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.	9.4	783
5	Recessive Symptomatic Focal Epilepsy and Mutant Contactin-Associated Protein-like 2. New England Journal of Medicine, 2006, 354, 1370-1377.	13.9	576
6	A survey of genetic human cortical gene expression. Nature Genetics, 2007, 39, 1494-1499.	9.4	488
7	GAB2 Alleles Modify Alzheimer's Risk in APOE É›4 Carriers. Neuron, 2007, 54, 713-720.	3.8	451
8	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
9	Common Kibra Alleles Are Associated with Human Memory Performance. Science, 2006, 314, 475-478.	6.0	391
10	A TOMM40 variable-length polymorphism predicts the age of late-onset Alzheimer's disease. Pharmacogenomics Journal, 2010, 10, 375-384.	0.9	351
11	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
12	Resistance to autosomal dominant Alzheimerâ€™s disease in an APOE3 Christchurch homozygote: a case report. Nature Medicine, 2019, 25, 1680-1683.	15.2	328
13	Necroptosis activation in Alzheimer's disease. Nature Neuroscience, 2017, 20, 1236-1246.	7.1	305
14	Genetic Control of Human Brain Transcript Expression in Alzheimer Disease. American Journal of Human Genetics, 2009, 84, 445-458.	2.6	290
15	Identification of genetic variants using bar-coded multiplexed sequencing. Nature Methods, 2008, 5, 887-893.	9.0	285
16	A novel Alzheimer disease locus located near the gene encoding tau protein. Molecular Psychiatry, 2016, 21, 108-117.	4.1	260
17	Voxelwise genome-wide association study (vGWAS). NeuroImage, 2010, 53, 1160-1174.	2.1	239
18	Whole-Genome Analysis of Sporadic Amyotrophic Lateral Sclerosis. New England Journal of Medicine, 2007, 357, 775-788.	13.9	234

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19	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
20	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
21	Brain Differences in Infants at Differential Genetic Risk for Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 11.	4.5	221
22	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
23	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
24	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	9.4	192
25	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
26	GRM7 variants confer susceptibility to age-related hearing impairment. Human Molecular Genetics, 2009, 18, 785-796.	1.4	174
27	Assessment of the genetic variance of late-onset Alzheimer's disease. Neurobiology of Aging, 2016, 41, 200.e13-200.e20.	1.5	174
28	Structure-Based Discovery of a Novel Angiotensin-Converting Enzyme 2 Inhibitor. Hypertension, 2004, 44, 903-906.	1.3	171
29	Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 1394.	4.5	166
30	Genetic analysis of quantitative phenotypes in AD and MCI: imaging, cognition and biomarkers. Brain Imaging and Behavior, 2014, 8, 183-207.	1.1	161
31	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	1.1	155
32	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
33	CR1 is associated with amyloid plaque burden and ageâ€related cognitive decline. Annals of Neurology, 2011, 69, 560-569.	2.8	148
34	Associations Between Biomarkers and Age in the Presenilin 1 E280A Autosomal Dominant Alzheimer Disease Kindred. JAMA Neurology, 2015, 72, 316.	4.5	145
35	Genetic Susceptibility for Alzheimer Disease Neuritic Plaque Pathology. JAMA Neurology, 2013, 70, 1150.	4.5	143
36	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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37	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
38	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
39	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
40	Voxelwise gene-wide association study (vGeneWAS): Multivariate gene-based association testing in 731 elderly subjects. NeuroImage, 2011, 56, 1875-1891.	2.1	116
41	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
42	Mechanisms of CO₂/H⁺Sensitivity of Astrocytes. Journal of Neuroscience, 2016, 36, 10750-10758.	1.7	101
43	Evidence for an association between KIBRA and late-onset Alzheimer's disease. Neurobiology of Aging, 2010, 31, 901-909.	1.5	100
44	SNiPer-HD: improved genotype calling accuracy by an expectation-maximization algorithm for high-density SNP arrays. Bioinformatics, 2007, 23, 57-63.	1.8	93
45	A coding variant in CR1 interacts with APOE-É›4 to influence cognitive decline. Human Molecular Genetics, 2012, 21, 2377-2388.	1.4	90
46	Peripheral delivery of a ROCK inhibitor improves learning and working memory.. Behavioral Neuroscience, 2009, 123, 218-223.	0.6	89
47	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
48	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
49	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
50	ACE2: A novel therapeutic target for cardiovascular diseases. Progress in Biophysics and Molecular Biology, 2006, 91, 163-198.	1.4	81
51	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
52	KIBRA: a new gateway to learning and memory?. Frontiers in Aging Neuroscience, 2010, 2, 4.	1.7	77
53	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
54	<i>Sorl1</i> as an Alzheimerâ€™s Disease Predisposition Gene?. Neurodegenerative Diseases, 2008, 5, 60-64.	0.8	73

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55	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
56	Calmodulin-binding transcription activator 1 (CAMTA1) alleles predispose human episodic memory performance. Human Molecular Genetics, 2007, 16, 1469-1477.	1.4	66
57	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
58	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
59	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
60	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
61	Transcriptome response of human skeletal muscle to divergent exercise stimuli. Journal of Applied Physiology, 2018, 124, 1529-1540.	1.2	61
62	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
63	Characterization of Mitotic Neurons Derived From Adult Rat Hypothalamus and Brain Stem. Journal of Neurophysiology, 2002, 87, 1076-1085.	0.9	58
64	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	2.8	56
65	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
66	Prevention of Cardiac Hypertrophy by Angiotensin II Type-2 Receptor Gene Transfer. Hypertension, 2004, 43, 1233-1238.	1.3	55
67	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
68	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
69	Extracellular microRNAs in blood differentiate between ischaemic and haemorrhagic stroke subtypes. Journal of Extracellular Vesicles, 2020, 9, 1713540.	5.5	53
70	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
71	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
72	A comprehensive catalogue of the coding and non-coding transcripts of the human inner ear. Hearing Research, 2016, 333, 266-274.	0.9	51

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73	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
74	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
75	Protective variant for hippocampal atrophy identified by whole exome sequencing. Annals of Neurology, 2015, 77, 547-552.	2.8	48
76	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
77	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
78	A Frame-Shift Mutation in CAV1 Is Associated with a Severe Neonatal Progeroid and Lipodystrophy Syndrome. PLoS ONE, 2015, 10, e0131797.	1.1	46
79	Hippocampal Transcriptomic Profiles: Subfield Vulnerability to Age and Cognitive Impairment. Frontiers in Aging Neuroscience, 2017, 9, 383.	1.7	45
80	The Future of Hypertension Therapy: Sense, Antisense, or Nonsense?. Hypertension, 2001, 37, 357-364.	1.3	44
81	Cloning and characterization of a secreted form of angiotensin-converting enzyme 2. Regulatory Peptides, 2004, 122, 61-67.	1.9	43
82	Novel pathogenic variants and genes for myopathies identified by whole exome sequencing. Molecular Genetics & Genomic Medicine, 2015, 3, 283-301.	0.6	43
83	Association of SNPs in EGR3 and ARC with Schizophrenia Supports a Biological Pathway for Schizophrenia Risk. PLoS ONE, 2015, 10, e0135076.	1.1	42
84	Initial Assessment of the Pathogenic Mechanisms of the Recently Identified Alzheimer Risk Loci. Annals of Human Genetics, 2013, 77, 85-105.	0.3	41
85	MET Receptor Tyrosine Kinase as an Autism Genetic Risk Factor. International Review of Neurobiology, 2013, 113, 135-165.	0.9	38
86	The Autism Genome Project. Molecular Diagnosis and Therapy, 2005, 5, 233-246.	3.3	37
87	Hippocampal gene expression changes during age-related cognitive decline. Brain Research, 2009, 1256, 101-110.	1.1	37
88	Genetic Implication of a Novel Thiamine Transporter in Human Hypertension. Journal of the American College of Cardiology, 2014, 63, 1542-1555.	1.2	36
89	Decreased serum arylesterase activity in autism spectrum disorders. Psychiatry Research, 2010, 180, 105-113.	1.7	33
90	DNA Methylation and Expression Profiles of Whole Blood in Parkinsonâ€™s Disease. Frontiers in Genetics, 2021, 12, 640266.	1.1	33

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91	Accessible pediatric neuroimaging using a low field strength MRI scanner. NeuroImage, 2021, 238, 118273.	2.1	32
92	Identification of Risk Loci for Necrotizing Meningoencephalitis in Pug Dogs. Journal of Heredity, 2011, 102, S40-S46.	1.0	31
93	The human brainome: network analysis identifies HSPA2 as a novel Alzheimerâ€™s disease target. Brain, 2018, 141, 2721-2739.	3.7	31
94	Family history of Alzheimerâ€™s disease alters cognition and is modified by medical and genetic factors. ELife, 2019, 8, .	2.8	30
95	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
96	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
97	SNiPer: Improved SNP genotype calling for Affymetrix 10K GeneChip microarray data. BMC Genomics, 2005, 6, 149.	1.2	26
98	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
99	Induction of pluripotent stem cells from autopsy donor-derived somatic cells. Neuroscience Letters, 2011, 502, 219-224.	1.0	25
100	Next-generation profiling to identify the molecular etiology of Parkinson dementia. Neurology: Genetics, 2016, 2, e75.	0.9	25
101	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
102	Characterization of X Chromosome Inactivation Using Integrated Analysis of Whole-Exome and mRNA Sequencing. PLoS ONE, 2014, 9, e113036.	1.1	24
103	De novo variants in GREB1L are associated with non-syndromic inner ear malformations and deafness. Human Genetics, 2018, 137, 459-470.	1.8	24
104	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
105	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
106	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
107	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
108	A De Novo Mutation inTEAD1Causes Nonâ€“X-Linked Aicardi Syndrome. , 2015, 56, 3896.		22

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109	Associations of MAP2K3 Gene Variants With Superior Memory in SuperAgers. Frontiers in Aging Neuroscience, 2018, 10, 155.	1.7	22
110	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
111	Gene Therapy for Cardiovascular Disorders. Is There a Future?. Annals of the New York Academy of Sciences, 2001, 953a, 31-42.	1.8	19
112	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
113	In vitro-differentiated neural cell cultures progress towards donor-identical brain tissue. Human Molecular Genetics, 2013, 22, 3534-3546.	1.4	19
114	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
115	Peripheral Biomarkers in Schizophrenia: A Meta-Analysis of Microarray Gene Expression Datasets. International Journal of Neuropsychopharmacology, 2019, 22, 186-193.	1.0	19
116	Family SES Is Associated with the Gut Microbiome in Infants and Children. Microorganisms, 2021, 9, 1608.	1.6	19
117	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
118	A cellular model of amyloid precursor protein processing and amyloid-Î² peptide production. Journal of Neuroscience Methods, 2014, 223, 114-122.	1.3	16
119	Two additional males with Xâ€linked, syndromic mental retardation carry de novo mutations in HNRNPH2. Clinical Genetics, 2019, 96, 183-185.	1.0	16
120	Dopaminergic gene methylation is associated with cognitive performance in a childhood monozygotic twin study. Epigenetics, 2019, 14, 310-323.	1.3	16
121	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
122	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
123	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
124	Compound heterozygous mutations in SNAP29 is associated with Pelizaeus-Merzbacher-like disorder (PMLD). Human Genetics, 2019, 138, 1409-1417.	1.8	14
125	Longitudinal white matter and cognitive development in pediatric carriers of the apolipoprotein Îµ4 allele. NeuroImage, 2020, 222, 117243.	2.1	14
126	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

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127	Transient ACE (Angiotensin-Converting Enzyme) Inhibition Suppresses Future Fibrogenic Capacity and Heterogeneity of Cardiac Fibroblast Subpopulations. Hypertension, 2021, 77, 904-918.	1.3	13
128	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
129	[32] Large-scale production of retroviral vectors for systemic gene delivery. Methods in Enzymology, 2002, 346, 562-573.	0.4	11
130	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
131	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
132	SNP-based chromosomal copy number ascertainment following multiple displacement whole-genome amplification. BioTechniques, 2007, 42, 77-83.	0.8	9
133	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
134	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
135	Identification of functional variants from whole-exome sequencing, combined with neuroimaging genetics. Molecular Psychiatry, 2013, 18, 739-739.	4.1	8
136	Exploring genome-wide DNA methylation patterns in Aicardi syndrome. Epigenomics, 2017, 9, 1373-1386.	1.0	8
137	Congenital myasthenic syndrome caused by a frameshift insertion mutation in GFPT1. Neurology: Genetics, 2020, 6, e468.	0.9	8
138	Telomere Length and Autism Spectrum Disorder Within the Family: Relationships With Cognition and Sensory Symptoms. Autism Research, 2020, 13, 1094-1101.	2.1	8
139	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
140	Compound heterozygous mutations in MASP1 in a deaf child with absent cochlear nerves. Neurology: Genetics, 2017, 3, e153.	0.9	6
141	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
142	Genes Implicated in Rare Congenital Inner Ear and Cochleovestibular Nerve Malformations. Ear and Hearing, 2020, 41, 983-989.	1.0	6
143	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
144	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

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145	The PKC-Î² selective inhibitor, Enzastaurin, impairs memory in middle-aged rats. PLoS ONE, 2018, 13, e0198256.	1.1	5
146	Gradual hypertension induction in middleâ€aged Cyp1a1â€Ren2 transgenic rats produces significant impairments in spatial learning. Physiological Reports, 2019, 7, e14010.	0.7	4
147	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
148	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
149	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
150	Rare Variants in Cardiomyopathy Genes Associated With Stress-Induced Cardiomyopathy. Neurosurgery, 2016, 78, 835-843.	0.6	3
151	Seizure-Induced Arc mRNA Expression Thresholds in Rat Hippocampus and Perirhinal Cortex. Frontiers in Systems Neuroscience, 2018, 12, 53.	1.2	3
152	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
153	Leukocyte and cytokine variables in asymptomatic Pugs at genetic risk of necrotizing meningoencephalitis. Journal of Veterinary Internal Medicine, 2021, , .	0.6	3
154	Multi-scale study of normal aging predicts novel late-onset Alzheimer's disease risk variants. BMC Bioinformatics, 2015, 16, P11.	1.2	2
155	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
156	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
157	Molecular biomarkers to track clinical improvement following an integrative treatment model in autistic toddlers. Acta Neuropsychiatrica, 2021, 33, 267-272.	1.0	2
158	Longitudinal Assessment of Intravoxel Incoherent Motion <scp>Diffusionâ€Weighted MRI</scp> Metrics in Cognitive Decline. Journal of Magnetic Resonance Imaging, 2022, , .	1.9	2
159	[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
160	A potential early clinical phenotype of necrotizing meningoencephalitis in genetically atâ€risk pug dogs. Journal of Veterinary Internal Medicine, 0, , .	0.6	1
161	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
162	Epigenetics of Cognition and Neurodegenerative Disorders. Neuromethods, 2015, , 285-298.	0.2	0