Matthew Huentelman

List of Publications by Citations

159 papers	15,300 citations	56 h-index	123 g-index
171 ext. papers	18,702 ext. citations	8.7 avg, IF	5.27 L-index

#	Paper	IF	Citations
159	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. *Nature Genetics*, **2013**, 45, 1452-8	36.3	2714
158	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. *Nature Genetics*, **2011**, 43, 436-41	36.3	1367
157	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A, tau, immunity and lipid processing. *Nature Genetics*, **2019**, 51, 414-430	36.3	917
156	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. *Nature Genetics*, **2017**, 49, 1373-1384	36.3	508
155	Recessive symptomatic focal epilepsy and mutant contactin-associated protein-like 2. *New England Journal of Medicine*, **2006**, 354, 1370-7	59.2	483
154	A survey of genetic human cortical gene expression. *Nature Genetics*, **2007**, 39, 1494-9	36.3	413
153	GAB2 alleles modify Alzheimer's risk in APOE epsilon4 carriers. *Neuron*, **2007**, 54, 713-20	13.9	405
152	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, 1048-56	24.1	347
151	Common Kibra alleles are associated with human memory performance. *Science*, **2006**, 314, 475-8	33.3	342
150	A TOMM40 variable-length polymorphism predicts the age of late-onset Alzheimer's disease. *Pharmacogenomics Journal*, **2010**, 10, 375-84	3.5	270
149	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, 1051-63	7.9	266
148	Identification of genetic variants using bar-coded multiplexed sequencing. *Nature Methods*, **2008**, 5, 887-93	21.6	266
147	Genetic control of human brain transcript expression in Alzheimer disease. *American Journal of Human Genetics*, **2009**, 84, 445-58	11	229
146	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, 8404-9	11.5	202
145	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, 3295-301	5.6	199
144	Voxelwise genome-wide association study (vGWAS). *NeuroImage*, **2010**, 53, 1160-74	7.9	197
143	Whole-genome analysis of sporadic amyotrophic lateral sclerosis. *New England Journal of Medicine*, **2007**, 357, 775-88	59.2	194

142	Protection from angiotensin II-induced cardiac hypertrophy and fibrosis by systemic lentiviral delivery of ACE2 in rats. *Experimental Physiology*, **2005**, 90, 783-90	2.4	186
141	Florbetapir PET analysis of amyloid-β deposition in the presenilin 1 E280A autosomal dominant Alzheimer's disease kindred: a cross-sectional study. *Lancet Neurology, The*, **2012**, 11, 1057-65	24.1	178
140	A novel Alzheimer disease locus located near the gene encoding tau protein. *Molecular Psychiatry*, **2016**, 21, 108-17	15.1	175
139	Necroptosis activation in Alzheimer's disease. *Nature Neuroscience*, **2017**, 20, 1236-1246	25.5	173
138	Resistance to autosomal dominant Alzheimer's disease in an APOE3 Christchurch homozygote: a case report. *Nature Medicine*, **2019**, 25, 1680-1683	50.5	171
137	Brain differences in infants at differential genetic risk for late-onset Alzheimer disease: a cross-sectional imaging study. *JAMA Neurology*, **2014**, 71, 11-22	17.2	166
136	APOE and BCHE as modulators of cerebral amyloid deposition: a florbetapir PET genome-wide association study. *Molecular Psychiatry*, **2014**, 19, 351-7	15.1	145
135	GRM7 variants confer susceptibility to age-related hearing impairment. *Human Molecular Genetics*, **2009**, 18, 785-96	5.6	145
134	Structure-based discovery of a novel angiotensin-converting enzyme 2 inhibitor. *Hypertension*, **2004** , 44, 903-6	8.5	142
133	Efficient large-scale production and concentration of HIV-1-based lentiviral vectors for use in vivo. *Physiological Genomics*, **2003**, 12, 221-8	3.6	139
132	Effects of multiple genetic loci on age at onset in late-onset Alzheimer disease: a genome-wide association study. *JAMA Neurology*, **2014**, 71, 1394-404	17.2	129
131	Identification of the genetic basis for complex disorders by use of pooling-based genomewide single-nucleotide-polymorphism association studies. *American Journal of Human Genetics*, **2007**, 80, 126-39	11	129
130	CR1 is associated with amyloid plaque burden and age-related cognitive decline. *Annals of Neurology*, **2011**, 69, 560-9	9.4	128
129	Genome-wide analysis reveals novel genes influencing temporal lobe structure with relevance to neurodegeneration in Alzheimer's disease. *NeuroImage*, **2010**, 51, 542-54	7.9	119
128	Assessment of the genetic variance of late-onset Alzheimer's disease. *Neurobiology of Aging*, **2016**, 41, 200.e13-200.e20	5.6	119
127	Reduced posterior cingulate mitochondrial activity in expired young adult carriers of the APOE ε4 allele, the major late-onset Alzheimer's susceptibility gene. *Journal of Alzheimer's Disease*, **2010**, 22, 307-13	4.3	118
126	Genetic susceptibility for Alzheimer disease neuritic plaque pathology. *JAMA Neurology*, **2013**, 70, 1150-7	17.2	113
125	Associations between biomarkers and age in the presenilin 1 E280A autosomal dominant Alzheimer disease kindred: a cross-sectional study. *JAMA Neurology*, **2015**, 72, 316-24	17.2	112

124	Genetic analysis of quantitative phenotypes in AD and MCI: imaging, cognition and biomarkers. *Brain Imaging and Behavior*, **2014**, 8, 183-207	4.1	111
123	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.e11-8	5.6	111
122	Voxelwise gene-wide association study (vGeneWAS): multivariate gene-based association testing in 731 elderly subjects. *NeuroImage*, **2011**, 56, 1875-91	7.9	96
121	Transcriptomic analysis of tail regeneration in the lizard Anolis carolinensis reveals activation of conserved vertebrate developmental and repair mechanisms. *PLoS ONE*, **2014**, 9, e105004	3.7	90
120	Gene-wide analysis detects two new susceptibility genes for Alzheimer's disease. *PLoS ONE*, **2014**, 9, e94661	3.7	90
119	SNiPer-HD: improved genotype calling accuracy by an expectation-maximization algorithm for high-density SNP arrays. *Bioinformatics*, **2007**, 23, 57-63	7.2	86
118	Genetic architecture of subcortical brain structures in 38,851 individuals. *Nature Genetics*, **2019**, 51, 1624-1636	30.5	81
117	Evidence for an association between KIBRA and late-onset Alzheimer's disease. *Neurobiology of Aging*, **2010**, 31, 901-9	5.6	78
116	A coding variant in CR1 interacts with APOE-ε4 to influence cognitive decline. *Human Molecular Genetics*, **2012**, 21, 2377-88	5.6	78
115	Mechanisms of CO2/H+ Sensitivity of Astrocytes. *Journal of Neuroscience*, **2016**, 36, 10750-10758	6.6	74
114	Hypometabolism in Alzheimer-affected brain regions in cognitively healthy Latino individuals carrying the apolipoprotein E epsilon4 allele. *Archives of Neurology*, **2010**, 67, 462-8		73
113	Peripheral delivery of a ROCK inhibitor improves learning and working memory. *Behavioral Neuroscience*, **2009**, 123, 218-23	2.1	72
112	A genome-wide association study for age-related hearing impairment in the Saami. *European Journal of Human Genetics*, **2010**, 18, 685-93	5.3	71
111	ACE2: A novel therapeutic target for cardiovascular diseases. *Progress in Biophysics and Molecular Biology*, **2006**, 91, 163-98	4.7	70
110	Genome-wide association analysis demonstrates the highly polygenic character of age-related hearing impairment. *European Journal of Human Genetics*, **2015**, 23, 110-5	5.3	66
109	KIBRA: A New Gateway to Learning and Memory?. *Frontiers in Aging Neuroscience*, **2010**, 2, 4	5.3	64
108	Sorl1 as an Alzheimer's disease predisposition gene?. *Neurodegenerative Diseases*, **2008**, 5, 60-4	2.3	64
107	Whole-exome sequencing and imaging genetics identify functional variants for rate of change in hippocampal volume in mild cognitive impairment. *Molecular Psychiatry*, **2013**, 18, 781-7	15.1	63

106	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, 769-78	11	61
105	DNA Diagnostics of Hereditary Hearing Loss: A Targeted Resequencing Approach Combined with a Mutation Classification System. *Human Mutation*, **2016**, 37, 812-9	4.7	59
104	A sensitive and specific diagnostic test for hearing loss using a microdroplet PCR-based approach and next generation sequencing. *American Journal of Medical Genetics, Part A*, **2013**, 161A, 145-52	2.5	56
103	Calmodulin-binding transcription activator 1 (CAMTA1) alleles predispose human episodic memory performance. *Human Molecular Genetics*, **2007**, 16, 1469-77	5.6	55
102	Tonic Premarin dose-dependently enhances memory, affects neurotrophin protein levels and alters gene expression in middle-aged rats. *Neurobiology of Aging*, **2011**, 32, 680-97	5.6	54
101	A genome-wide analysis identifies genetic variants in the RELN gene associated with otosclerosis. *American Journal of Human Genetics*, **2009**, 84, 328-38	11	52
100	Prevention of cardiac hypertrophy by angiotensin II type-2 receptor gene transfer. *Hypertension*, **2004**, 43, 1233-8	8.5	49
99	Comparison against 186 canid whole-genome sequences reveals survival strategies of an ancient clonally transmissible canine tumor. *Genome Research*, **2015**, 25, 1646-55	9.7	48
98	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	16.4	45
97	Characterization of mitotic neurons derived from adult rat hypothalamus and brain stem. *Journal of Neurophysiology*, **2002**, 87, 1076-85	3.2	45
96	Protective variant for hippocampal atrophy identified by whole exome sequencing. *Annals of Neurology*, **2015**, 77, 547-52	9.4	43
95	Shared genetic contribution to Ischaemic Stroke and Alzheimer's Disease. *Annals of Neurology*, **2016**, 79, 739-747	9.4	42
94	Somitogenesis in the anole lizard and alligator reveals evolutionary convergence and divergence in the amniote segmentation clock. *Developmental Biology*, **2012**, 363, 308-19	3.1	40
93	Initial assessment of the pathogenic mechanisms of the recently identified Alzheimer risk Loci. *Annals of Human Genetics*, **2013**, 77, 85-105	2.2	40
92	Amyloid pathway-based candidate gene analysis of [(11)C]PiB-PET in the Alzheimer's Disease Neuroimaging Initiative (ADNI) cohort. *Brain Imaging and Behavior*, **2012**, 6, 1-15	4.1	39
91	De Novo Missense Mutations in DHX30 Impair Global Translation and Cause a Neurodevelopmental Disorder. *American Journal of Human Genetics*, **2017**, 101, 716-724	11	38
90	A comprehensive catalogue of the coding and non-coding transcripts of the human inner ear. *Hearing Research*, **2016**, 333, 266-274	3.9	37
89	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, 517-24	5.3	37

88	Cloning and characterization of a secreted form of angiotensin-converting enzyme 2. *Regulatory Peptides*, **2004**, 122, 61-7		37
87	Whole-genome sequencing suggests a chemokine gene cluster that modifies age at onset in familial Alzheimer disease. *Molecular Psychiatry*, **2015**, 20, 1294-300	15.1	36
86	Transcriptome response of human skeletal muscle to divergent exercise stimuli. *Journal of Applied Physiology*, **2018**, 124, 1529-1540	3.7	35
85	Analysis of copy number variation in Alzheimer disease in a cohort of clinically characterized and neuropathologically verified individuals. *PLoS ONE*, **2012**, 7, e50640	3.7	35
84	The future of hypertension therapy: sense, antisense, or nonsense?. *Hypertension*, **2001**, 37, 357-64	8.5	35
83	Novel pathogenic variants and genes for myopathies identified by whole exome sequencing. *Molecular Genetics & Genomic Medicine*, **2015**, 3, 283-301	2.3	33
82	Hippocampal gene expression changes during age-related cognitive decline. *Brain Research*, **2009**, 1256, 101-10	3.7	32
81	Somatic inactivating PTPRJ mutations and dysregulated pathways identified in canine malignant melanoma by integrated comparative genomic analysis. *PLoS Genetics*, **2018**, 14, e1007589	6	30
80	MET receptor tyrosine kinase as an autism genetic risk factor. *International Review of Neurobiology*, **2013**, 113, 135-65	4.4	28
79	Decreased serum arylesterase activity in autism spectrum disorders. *Psychiatry Research*, **2010**, 180, 105-13	3.9	28
78	The Autism Genome Project: goals and strategies. *Molecular Diagnosis and Therapy*, **2005**, 5, 233-46		28
77	Association of SNPs in EGR3 and ARC with Schizophrenia Supports a Biological Pathway for Schizophrenia Risk. *PLoS ONE*, **2015**, 10, e0135076	3.7	28
76	Genetic implication of a novel thiamine transporter in human hypertension. *Journal of the American College of Cardiology*, **2014**, 63, 1542-55	15.1	27
75	Hippocampal Transcriptomic Profiles: Subfield Vulnerability to Age and Cognitive Impairment. *Frontiers in Aging Neuroscience*, **2017**, 9, 383	5.3	27
74	A Frame-Shift Mutation in CAV1 Is Associated with a Severe Neonatal Progeroid and Lipodystrophy Syndrome. *PLoS ONE*, **2015**, 10, e0131797	3.7	27
73	Identification of risk loci for necrotizing meningoencephalitis in Pug dogs. *Journal of Heredity*, **2011**, 102 Suppl 1, S40-6	2.4	26
72	Maternal choline supplementation ameliorates Alzheimer disease pathology by reducing brain homocysteine levels across multiple generations. *Molecular Psychiatry*, **2020**, 25, 2620-2629	15.1	24
71	Extracellular microRNAs in blood differentiate between ischaemic and haemorrhagic stroke subtypes. *Journal of Extracellular Vesicles*, **2020**, 9, 1713540	16.4	22

70	Transcriptome Changes in the Alzheimer's Disease Middle Temporal Gyrus: Importance of RNA Metabolism and Mitochondria-Associated Membrane Genes. *Journal of Alzheimer's Disease*, **2019**, 70, 691-713	4.3	22
69	SNiPer: improved SNP genotype calling for Affymetrix 10K GeneChip microarray data. *BMC Genomics*, **2005**, 6, 149	4.5	21
68	Next-generation profiling to identify the molecular etiology of Parkinson dementia. *Neurology: Genetics*, **2016**, 2, e75	3.8	20
67	Feasibility of implementing molecular-guided therapy for the treatment of patients with relapsed or refractory neuroblastoma. *Cancer Medicine*, **2015**, 4, 871-86	4.8	20
66	The human brainome: network analysis identifies HSPA2 as a novel Alzheimer’s disease target. *Brain*, **2018**, 141, 2721-2739	11.2	19
65	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	4.2	19
64	Association between GAB2 haplotype and higher glucose metabolism in Alzheimer's disease-affected brain regions in cognitively normal APOE ε4 carriers. *NeuroImage*, **2011**, 54, 1896-902	7.9	19
63	Induction of pluripotent stem cells from autopsy donor-derived somatic cells. *Neuroscience Letters*, **2011**, 502, 219-24	3.3	19
62	A De Novo Mutation in TEAD1 Causes Non-X-Linked Aicardi Syndrome **2015**, 56, 3896-904		18
61	Are Sema5a mutant mice a good model of autism? A behavioral analysis of sensory systems, emotionality and cognition. *Behavioural Brain Research*, **2011**, 225, 142-50	3.4	18
60	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	3.7	17
59	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	5.6	16
58	In vitro-differentiated neural cell cultures progress towards donor-identical brain tissue. *Human Molecular Genetics*, **2013**, 22, 3534-46	5.6	16
57	A genome-wide analysis of population structure in the Finnish Saami with implications for genetic association studies. *European Journal of Human Genetics*, **2011**, 19, 347-52	5.3	16
56	A cellular model of amyloid precursor protein processing and amyloid-β peptide production. *Journal of Neuroscience Methods*, **2014**, 223, 114-22	3	15
55	De novo variants in GREB1L are associated with non-syndromic inner ear malformations and deafness. *Human Genetics*, **2018**, 137, 459-470	6.3	14
54	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	3.5	12
53	Dopaminergic gene methylation is associated with cognitive performance in a childhood monozygotic twin study. *Epigenetics*, **2019**, 14, 310-323	5.7	12

52	Associations of Gene Variants With Superior Memory in SuperAgers. *Frontiers in Aging Neuroscience*, **2018**, 10, 155	5.3	12
51	Characterization of X chromosome inactivation using integrated analysis of whole-exome and mRNA sequencing. *PLoS ONE*, **2014**, 9, e113036	3.7	12
50	Family history of Alzheimer's disease alters cognition and is modified by medical and genetic factors. *ELife*, **2019**, 8,	8.9	12
49	Gene therapy for cardiovascular disorders: is there a future?. *Annals of the New York Academy of Sciences*, **2001**, 953, 31-42	6.5	11
48	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	7.3	10
47	Two additional males with X-linked, syndromic mental retardation carry de novo mutations in HNRNPH2. *Clinical Genetics*, **2019**, 96, 183-185	4	9
46	SNP-based chromosomal copy number ascertainment following multiple displacement whole-genome amplification. *BioTechniques*, **2007**, 42, 77-83	2.5	9
45	Large-scale production of retroviral vectors for systemic gene delivery. *Methods in Enzymology*, **2002**, 346, 562-73	1.7	9
44	Time course of cardiac inflammation during nitric oxide synthase inhibition in SHR: impact of prior transient ACE inhibition. *Hypertension Research*, **2016**, 39, 8-18	4.7	8
43	Identification of functional variants from whole-exome sequencing, combined with neuroimaging genetics. *Molecular Psychiatry*, **2013**, 18, 739	15.1	8
42	Peripheral Biomarkers in Schizophrenia: A Meta-Analysis of Microarray Gene Expression Datasets. *International Journal of Neuropsychopharmacology*, **2019**, 22, 186-193	5.8	8
41	Exploring genome-wide DNA methylation patterns in Aicardi syndrome. *Epigenomics*, **2017**, 9, 1373-1386	4.4	7
40	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	3.2	7
39	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	2.9	7
38	Compound heterozygous mutations in SNAP29 is associated with Pelizaeus-Merzbacher-like disorder (PMLD). *Human Genetics*, **2019**, 138, 1409-1417	6.3	7
37	Association of AEBP1 and NRN1 RNA expression with Alzheimer's disease and neurofibrillary tangle density in middle temporal gyrus. *Brain Research*, **2019**, 1719, 217-224	3.7	6
36	Compound heterozygous mutations in in a deaf child with absent cochlear nerves. *Neurology: Genetics*, **2017**, 3, e153	3.8	6
35	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	4.6	6

34	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	5.6	5
33	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	2.3	5
32	Family SES Is Associated with the Gut Microbiome in Infants and Children. *Microorganisms*, **2021**, 9,	4.9	5
31	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	0.9	4
30	DNA Methylation and Expression Profiles of Whole Blood in Parkinson's Disease. *Frontiers in Genetics*, **2021**, 12, 640266	4.5	4
29	Transcriptome-wide association study of post-trauma symptom trajectories identified GRIN3B as a potential biomarker for PTSD development. *Neuropsychopharmacology*, **2021**, 46, 1811-1820	8.7	4
28	The PKC-ι selective inhibitor, Enzastaurin, impairs memory in middle-aged rats. *PLoS ONE*, **2018**, 13, e0198256	3.7	4
27	Genes Implicated in Rare Congenital Inner Ear and Cochleovestibular Nerve Malformations. *Ear and Hearing*, **2020**, 41, 983-989	3.4	3
26	Telomere Length and Autism Spectrum Disorder Within the Family: Relationships With Cognition and Sensory Symptoms. *Autism Research*, **2020**, 13, 1094-1101	5.1	3
25	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, 569-74	5.3	3
24	Congenital myasthenic syndrome caused by a frameshift insertion mutation in. *Neurology: Genetics*, **2020**, 6, e468	3.8	3
23	Longitudinal white matter and cognitive development in pediatric carriers of the apolipoprotein ε4 allele. *NeuroImage*, **2020**, 222, 117243	7.9	3
22	Transient ACE (Angiotensin-Converting Enzyme) Inhibition Suppresses Future Fibrogenic Capacity and Heterogeneity of Cardiac Fibroblast Subpopulations. *Hypertension*, **2021**, 77, 904-918	8.5	3
21	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	15.1	3
20	Identification of retinoblastoma binding protein 7 (Rbbp7) as a mediator against tau acetylation and subsequent neuronal loss in Alzheimer's disease and related tauopathies. *Acta Neuropathologica*, **2021**, 142, 279-294	14.3	3
19	Gradual hypertension induction in middle-aged Cyp1a1-Ren2 transgenic rats produces significant impairments in spatial learning. *Physiological Reports*, **2019**, 7, e14010	2.6	2
18	Genetic and epigenetic gene variants in the mothers of attention-deficit/hyperactivity disorder affected children as possible risk factors for neurodevelopmental disorders. *Epigenomics*, **2020**, 12, 813-823	4.4	2
17	ESHRD: deconvolution of brain homogenate RNA expression data to identify cell-type-specific alterations in Alzheimer's disease. *Aging*, **2020**, 12, 4124-4162	5.6	2

16	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	5.5	2
15	Seizure-Induced mRNA Expression Thresholds in Rat Hippocampus and Perirhinal Cortex. *Frontiers in Systems Neuroscience*, **2018**, 12, 53	3.5	2
14	Accessible pediatric neuroimaging using a low field strength MRI scanner. *NeuroImage*, **2021**, 238, 118273	7.9	2
13	Association of Common Genetic Variants in the and Genes with Canine Idiopathic Pulmonary Fibrosis in the West Highland White Terrier. *Genes*, **2020**, 11,	4.2	1
12	[P4081]: ASSOCIATION OF MAP2K3 GENE VARIATION AND THE SUPERAGING PHENOTYPE DETECTED BY WHOLE EXOME SEQUENCING **2017**, 13, P1290-P1290		1
11	Leukocyte and cytokine variables in asymptomatic Pugs at genetic risk of necrotizing meningoencephalitis. *Journal of Veterinary Internal Medicine*, **2021**,	3.1	1
10	Remote, Unsupervised Functional Motor Task Evaluation in Older Adults across the United States Using the MindCrowd Electronic Cohort. *Developmental Neuropsychology*, **2021**, 46, 435-446	1.8	1
9	Utilizing RNA and outlier analysis to identify an intronic splice-altering variant in AP4S1 in a sibling pair with progressive spastic paraplegia. *Human Mutation*, **2020**, 41, 412-419	4.7	1
8	Rare Variants in Cardiomyopathy Genes Associated With Stress-Induced Cardiomyopathy. *Neurosurgery*, **2016**, 78, 835-43	3.2	1
7	Influence of regional white matter hyperintensity volume and apolipoprotein E ε4 status on hippocampal volume in healthy older adults. *Hippocampus*, **2021**, 31, 469-480	3.5	1
6	Olfactory Bulb and Amygdala Gene Expression Changes in Subjects Dying with COVID-19 **2021**,		1
5	Multi-scale study of normal aging predicts novel late-onset Alzheimer's disease risk variants. *BMC Bioinformatics*, **2015**, 16, P11	3.6	0
4	Molecular biomarkers to track clinical improvement following an integrative treatment model in autistic toddlers. *Acta Neuropsychiatrica*, **2021**, 33, 267-272	3.9	0
3	Autobiographical Memory Fluency Reductions in Cognitively Unimpaired Middle-Aged and Older Adults at Increased Risk for Alzheimer's Disease Dementia. *Journal of the International Neuropsychological Society*, **2021**, 27, 905-915	3.1	0
2	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	2.2	
1	Epigenetics of Cognition and Neurodegenerative Disorders. *Neuromethods*, **2015**, 285-298	0.4	