Gerard D Schellenberg

List of Publications by Year
in descending order

176	21,872	30047	15249
papers	citations	54 h-index	126 g-index

195	195	195	25029
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomeâ€wide association and multiâ€omics studies identify MGMT as a novel risk gene for Alzheimer's disease among women. Alzheimer's and Dementia, 2023, 19, 896-908.	0.4	19
2	Alzheimerâ€™s Disease Variant Portal: A Catalog of Genetic Findings for Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2022, 86, 461-477.	1.2	4
3	Protein phosphatase 2A and complement component 4 are linked to the protective effect of APOE É2 for Alzheimer's disease. Alzheimer's and Dementia, 2022, 18, 2042-2054.	0.4	18
4	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
5	Progranulin mutations in clinical and neuropathological Alzheimer's disease. Alzheimer's and Dementia, 2022, 18, 2458-2467.	0.4	12
6	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
7	Genome-wide association study of brain arteriolosclerosis. Journal of Cerebral Blood Flow and Metabolism, 2022, 42, 1437-1450.	2.4	2
8	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	9.4	700
9	Integration of GWAS and brain transcriptomic analyses in a multiethnic sample of 35,245 older adults identifies DCDC2 gene as predictor of episodic memory maintenance. Alzheimer's and Dementia, 2022, 18, 1797-1811.	0.4	5
10	Sex differences in the genetic architecture of cognitive resilience to Alzheimerâ€™s disease. Brain, 2022, 145, 2541-2554.	3.7	26
11	A locus at 19q13.31 significantly reduces the ApoE Îµ4 risk for Alzheimerâ€™s Disease in African Ancestry. PLoS Genetics, 2022, 18, e1009977.	1.5	19
12	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
13	In vitro amplification of pathogenic tau conserves disease-specific bioactive characteristics. Acta Neuropathologica, 2021, 141, 193-215.	3.9	30
14	Latent trait modeling of tau neuropathology in progressive supranuclear palsy. Acta Neuropathologica, 2021, 141, 667-680.	3.9	5
15	Gene-Environment Interactions in Progressive Supranuclear Palsy. Frontiers in Neurology, 2021, 12, 664796.	1.1	1
16	Common variants in Alzheimerâ€™s disease and risk stratification by polygenic risk scores. Nature Communications, 2021, 12, 3417.	5.8	140
17	Association of mitochondrial variants and haplogroups identified by whole exome sequencing with Alzheimer's disease. Alzheimer's and Dementia, 2021, , .	0.4	9
18	Copy Number Variation Identification on 3,800 Alzheimerâ€™s Disease Whole Genome Sequencing Data from the Alzheimerâ€™s Disease Sequencing Project. Frontiers in Genetics, 2021, 12, 752390.	1.1	4

#	Article	IF	Citations
19	TSC1 loss increases risk for tauopathy by inducing tau acetylation and preventing tau clearance via chaperone-mediated autophagy. Science Advances, 2021, 7, eabg3897.	4.7	27
20	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
21	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
22	NIA genetics of Alzheimer's disease data storage site (NIAGADS): 2021 update.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e052258.	0.4	0
23	Copy number variation (CNV) identification and association study on 3,928 Alzheimer's disease whole genome sequencing data from the Alzheimer's Disease Sequencing Project (ADSP).. Alzheimer's and Dementia, 2021, 17 Suppl 3, e052721.	0.4	0
24	Characterization of regulatory roles of genetic signals curated from more than 200 GWA studies in the Alzheimer's Disease Variant Portal (ADVP).. Alzheimer's and Dementia, 2021, 17 Suppl 3, e054255.	0.4	0
25	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
26	Multiple viruses detected in human DNA are associated with Alzheimer disease risk.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e054585.	0.4	0
27	Sex differences in the genetic architecture underlying resilience in AD.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e055010.	0.4	0
28	Sex-specific genetic predictors of memory performance.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e056083.	0.4	0
29	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
30	Admixture mapping identifies novel regions influencing Alzheimer disease in African Americans.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e056443.	0.4	0
31	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
32	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
33	Transmission of tauopathy strains is independent of their isoform composition. Nature Communications, 2020, 11, 7.	5.8	121
34	Fibrillation and molecular characteristics are coherent with clinical and pathological features of 4-repeat tauopathy caused by MAPT variant G273R. Neurobiology of Disease, 2020, 146, 105079.	2.1	4
35	Genetic variants and functional pathways associated with resilience to Alzheimerâ€™s disease. Brain, 2020, 143, 2561-2575.	3.7	93
36	Insoluble Tau From Human FTDP-17 Cases Exhibit Unique Transmission Properties In Vivo. Journal of Neuropathology and Experimental Neurology, 2020, 79, 941-949.	0.9	6

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37	Sex differences in genetic predictors of resilience to Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e043259.	0.4	0
38	Alzheimerâ€™s disease variant portal (ADVP): Harmonized genetics data and evidence collection for Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e044090.	0.4	0
39	Genomeâ€wide metaâ€analysis of lateâ€onset Alzheimerâ€™s disease using rare variant imputation in 65,602 subjects identifies risk loci with roles in memory, neurodevelopment, and cardiometabolic traits: The international genomics of Alzheimerâ€™s project (IGAP). Alzheimer's and Dementia, 2020, 16, e044193.	0.4	1
40	Genomeâ€wide profiling of the noncoding regulatory mechanisms in Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e044268.	0.4	0
41	NIA genetics of Alzheimerâ€™s disease data storage site (NIAGADS): Update 2020. Alzheimer's and Dementia, 2020, 16, e044284.	0.4	1
42	Mechanism for the protective effect of APOE Îµ2 against Alzheimer disease is linked to tau and the classical complement pathway. Alzheimer's and Dementia, 2020, 16, e044881.	0.4	0
43	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
44	Pleiotropy analyses using TADs identify genomic regions affecting risk of AD and stroke. Alzheimer's and Dementia, 2020, 16, e045975.	0.4	0
45	Multimodal genomeâ€wide metaâ€analysis of brain amyloidosis reveals heterogeneity across CSF, PET, and pathological amyloid measures. Alzheimer's and Dementia, 2020, 16, e046009.	0.4	0
46	Mapping Alzheimer diseaseâ€“associated regions in the African American population. Alzheimer's and Dementia, 2020, 16, e046072.	0.4	0
47	Genomeâ€wide interaction study of smoking in Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e046149.	0.4	0
48	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
49	Sex-dependent autosomal effects on clinical progression of Alzheimerâ€™s disease. Brain, 2020, 143, 2272-2280.	3.7	46
50	Exceptionally low likelihood of Alzheimerâ€™s dementia in APOE2 homozygotes from a 5,000-person neuropathological study. Nature Communications, 2020, 11, 667.	5.8	246
51	LRP10 variants in progressive supranuclear palsy. Neurobiology of Aging, 2020, 94, 311.e5-311.e10.	1.5	6
52	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
53	C9orf72 intermediate repeats are associated with corticobasal degeneration, increased C9orf72 expression and disruption of autophagy. Acta Neuropathologica, 2019, 138, 795-811.	3.9	50
54	Gene-based analysis in HRC imputed genome wide association data identifies three novel genes for Alzheimerâ€™s disease. PLoS ONE, 2019, 14, e0218111.	1.1	23

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55	Sex differences in the genetic predictors of Alzheimerâ€™s pathology. Brain, 2019, 142, 2581-2589.	3.7	65
56	Inferring the Molecular Mechanisms of Noncoding Alzheimerâ€™s Disease-Associated Genetic Variants. Journal of Alzheimer's Disease, 2019, 72, 301-318.	1.2	19
57	Polygenic hazard score, amyloid deposition and Alzheimerâ€™s neurodegeneration. Brain, 2019, 142, 460-470.	3.7	63
58	Analysis of Whole-Exome Sequencing Data for Alzheimer Disease Stratified by APOE Genotype. JAMA Neurology, 2019, 76, 1099.	4.5	32
59	CpGâ€related SNPs in the MS4A region have a doseâ€dependent effect on risk of lateâ€“onset Alzheimer disease. Aging Cell, 2019, 18, e12964.	3.0	8
60	Association of Rare Coding Mutations With Alzheimer Disease and Other Dementias Among Adults of European Ancestry. JAMA Network Open, 2019, 2, e191350.	2.8	58
61	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
62	O3â€13â€01: HIGHLY PENETRANT LATEâ€ONSET ALZHEIMER DISEASE VARIANTS IN NOTCH3 IN ASHKENAZI JEWS. Alzheimer's and Dementia, 2019, 15, P918.	0.4	0
63	Activity of the poly(A) binding protein MSUT2 determines susceptibility to pathological tau in the mammalian brain. Science Translational Medicine, 2019, 11, .	5.8	30
64	Dissecting the genetic relationship between cardiovascular risk factors and Alzheimerâ€™s disease. Acta Neuropathologica, 2019, 137, 209-226.	3.9	100
65	A rare missense variant of CASP7 is associated with familial lateâ€onset Alzheimer's disease. Alzheimer's and Dementia, 2019, 15, 441-452.	0.4	39
66	VCPA: genomic variant calling pipeline and data management tool for Alzheimerâ€™s Disease Sequencing Project. Bioinformatics, 2019, 35, 1768-1770.	1.8	23
67	Identification of seven novel loci associated with amino acid levels using single-variant and gene-based tests in 8545 Finnish men from the METSIM study. Human Molecular Genetics, 2018, 27, 1664-1674.	1.4	30
68	CXCR4 involvement in neurodegenerative diseases. Translational Psychiatry, 2018, 8, 73.	2.4	66
69	Selective Genetic Overlap Between Amyotrophic Lateral Sclerosis and Diseases of the Frontotemporal Dementia Spectrum. JAMA Neurology, 2018, 75, 860.	4.5	79
70	Polygenic hazard score: an enrichment marker for Alzheimerâ€™s associated amyloid and tau deposition. Acta Neuropathologica, 2018, 135, 85-93.	3.9	80
71	P4â€044: THE GCAD CLOUDâ€BASED WORKFLOW FOR PROCESSING WHOLE EXOME AND WHOLE GENOME DATA FROM THE ALZHEIMER'S DISEASE SEQUENCING PROJECT. Alzheimer's and Dementia, 2018, 14, P1450.	0.4	0
72	P2â€171: THE POLY(A) BINDING PROTEIN MSUT2 MODULATES GLIOSIS IN TAUOPATHY. Alzheimer's and Dementia, 2018, 14, P734.	0.4	0

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73	P1â€156: GENEâ€BASED ANALYSES IN WHOLE GENOME SEQUENCING OF FAMILIAL LATEâ€ONSET ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2018, 14, P336.	0.4	0
74	P2â€279: CSF SMALL RNA BIOMARKERS FOR ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2018, 14, P785.	0.4	0
75	P2â€106: AFRICAN AMERICAN WHOLE EXOME SEQUENCING SUGGESTS RISK CODING VARIANTS IN IDH1 GENE. Alzheimer's and Dementia, 2018, 14, P709.	0.4	0
76	P1â€139: THE CONTRIBUTION OF SEXâ€SPECIFIC ASSOCIATIONS IN GENETIC STUDIES OF ALZHEIMER'S DISEASE PATHOLOGY. Alzheimer's and Dementia, 2018, 14, P327.	0.4	0
77	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
78	Ancestral origin of ApoE Îµ4 Alzheimer disease risk in Puerto Rican and African American populations. PLoS Genetics, 2018, 14, e1007791.	1.5	117
79	One for all and all for One: Improving replication of genetic studies through network diffusion. PLoS Genetics, 2018, 14, e1007306.	1.5	22
80	Sex-specific genetic predictors of Alzheimerâ€™s disease biomarkers. Acta Neuropathologica, 2018, 136, 857-872.	3.9	87
81	Replication of progressive supranuclear palsy genome-wide association study identifies SLCO1A2 and DUSP10 as new susceptibility loci. Molecular Neurodegeneration, 2018, 13, 37.	4.4	54
82	Impact of apolipoprotein E genotypes on vitamin E and memantine treatment outcomes in Alzheimer's disease. Alzheimer's and Dementia: Translational Research and Clinical Interventions, 2018, 4, 344-349.	1.8	6
83	Genome-wide pleiotropy analysis of neuropathological traits related to Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2018, 10, 22.	3.0	27
84	Sex-Specific Association of Apolipoprotein E With Cerebrospinal Fluid Levels of Tau. JAMA Neurology, 2018, 75, 989.	4.5	223
85	INFERNO: inferring the molecular mechanisms of noncoding genetic variants. Nucleic Acids Research, 2018, 46, 8740-8753.	6.5	46
86	Male-specific epistasis between WWC1 and TLN2 genes is associated with Alzheimer's disease. Neurobiology of Aging, 2018, 72, 188.e3-188.e12.	1.5	24
87	Immune-related genetic enrichment in frontotemporal dementia: An analysis of genome-wide association studies. PLoS Medicine, 2018, 15, e1002487.	3.9	111
88	Genetic architecture of sporadic frontotemporal dementia and overlap with Alzheimer's and Parkinson's diseases. Journal of Neurology, Neurosurgery and Psychiatry, 2017, 88, 152-164.	0.9	107
89	Shared genetic risk between corticobasal degeneration, progressive supranuclear palsy, and frontotemporal dementia. Acta Neuropathologica, 2017, 133, 825-837.	3.9	90
90	Genome-wide association study identifies four novel loci associated with Alzheimerâ€™s endophenotypes and disease modifiers. Acta Neuropathologica, 2017, 133, 839-856.	3.9	199

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91	Clinical diagnosis of progressive supranuclear palsy: The movement disorder society criteria. Movement Disorders, 2017, 32, 853-864.	2.2	1,402
92	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. Nature Neuroscience, 2017, 20, 1052-1061.	7.1	330
93	Genome-wide, high-content siRNA screening identifies the Alzheimerâ€™s genetic risk factor FERMT2 as a major modulator of APP metabolism. Acta Neuropathologica, 2017, 133, 955-966.	3.9	60
94	Genomic variants, genes, and pathways of Alzheimer's disease: An overview. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 5-26.	1.1	147
95	Genetic influences on cognition in progressive supranuclear palsy. Movement Disorders, 2017, 32, 1764-1771.	2.2	6
96	Polygenic hazard scores in preclinical Alzheimer disease. Annals of Neurology, 2017, 82, 484-488.	2.8	49
97	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
98	Early-Onset Alzheimer Disease and Candidate Risk Genes Involved in Endolysosomal Transport. JAMA Neurology, 2017, 74, 1113.	4.5	41
99	[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
100	Two novel loci, COBL and SLC10A2, for Alzheimer's disease in African Americans. Alzheimer's and Dementia, 2017, 13, 119-129.	0.4	87
101	[P3â€“097]: NIA GENETICS OF ALZHEIMER's DISEASE DATA STORAGE SITE (NIAGADS): 2017. Alzheimer's and Dementia, 2017, 13, P971.	0.4	0
102	[P4â€“074]: INTEGRATIVE SYSTEMS BIOLOGY APPROACH TO IDENTIFY NOVEL RISK FACTORS FOR PSP. Alzheimer's and Dementia, 2017, 13, P1286.	0.4	0
103	[P3â€“090]: THE ALZHEIMER's DISEASE SEQUENCING PROJECT (ADSP) DATA UPDATE 2017. Alzheimer's and Dementia, 2017, 13, P968.	0.4	0
104	Caspase-8, association with Alzheimerâ€™s Disease and functional analysis of rare variants. PLoS ONE, 2017, 12, e0185777.	1.1	38
105	Genetic assessment of age-associated Alzheimer disease risk: Development and validation of a polygenic hazard score. PLoS Medicine, 2017, 14, e1002258.	3.9	311
106	F1â€01â€02: Alzheimer's Disease Sequencing Project: Search for Alzheimer's Disease Resilience Genes That May Modify Disease Susceptibility in Specific Apoe Genotype Backgrounds. Alzheimer's and Dementia, 2016, 12, P162.	0.4	0
107	P2â€097: The Alzheimerâ€™s Disease Sequencing Project (ADSP): Data Production, Management, and Availability. Alzheimer's and Dementia, 2016, 12, P648.	0.4	0
108	P2â€077: Alzheimer's Disease Sequencing Project: Search for Alzheimer's Disease Resilience Genes That May Modify Disease Susceptibility in Specific Apoe Genotype Backgrounds. Alzheimer's and Dementia, 2016, 12, P638.	0.4	0

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109	P2-083: Computational Identification of Regulatory Mechanisms Affected By Noncoding Variants Associated with Late-Onset Alzheimer's Disease. , 2016, 12, P640-P641.		0
110	P2â€085: Further Stratification of APOE E4â€Negative Subjects Identifies Novel Genes for Alzheimer's Disease. Alzheimer's and Dementia, 2016, 12, P641.	0.4	0
111	P3â€082: Assessment of the Genetic Variance of Lateâ€Onset Alzheimerâ€™s Disease. Alzheimer's and Dementia, 2016, 12, P849.	0.4	0
112	P3-093: NIA Genetics of Alzheimerâ€™s Disease Data Storage Site (NIAGADS): 2016 Update. , 2016, 12, P855-P856.		0
113	P3â€096: Secondary Analyses of International Genomics of Alzheimer's Project Stage I GWAS Summary Data Identifies Additional Variants Associated With Lateâ€Onset Alzheimer's Disease. Alzheimer's and Dementia, 2016, 12, P856.	0.4	0
114	P4â€048: Convergent Analysis of Endophenotypes in Progressive Supranuclear Palsy. Alzheimer's and Dementia, 2016, 12, P1032.	0.4	0
115	F1-01-03: Rare Deleterious and Loss-of-Function Variants in OPRL1 and GAS2L2 Contribute to the Risk of Late-Onset Alzheimerâ€™s Disease: Alzheimerâ€™s Disease Sequencing Project Case-Control Study. , 2016, 12, P163-P163.		0
116	O1â€03â€02: ABCA7 Frameshift Deletion Associated with Alzheimerâ€™s Disease in African Americans. Alzheimer's and Dementia, 2016, 12, P177.	0.4	0
117	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
118	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
119	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
120	O2â€06â€03: Tissueâ€Specific Genomeâ€Wide Predictions of Genetically Regulated Expression in Alzheimer's Disease. Alzheimer's and Dementia, 2016, 12, P239.	0.4	0
121	O2â€10â€06: A Common Allele in SPI1 Lowers Risk and Delays Age at Onset for Alzheimer's Disease. Alzheimer's and Dementia, 2016, 12, P253.	0.4	0
122	P1â€018: Rare Deleterious And Lossâ€ofâ€Function Variants in OPRL1 and GAS2L2 Contribute to the Risk of Lateâ€Onset Alzheimerâ€™s Disease: Alzheimerâ€™s Disease Sequencing Project Caseâ€Control Study. Alzheimer's and Dementia, 2016, 12, P406.	0.4	1
123	P1â€122: Multivariate Phenotypes Association Study of Neuropathological Features of Alzheimer's Disease and Related Dementias. Alzheimer's and Dementia, 2016, 12, P450.	0.4	0
124	P1-117: Blood Gene Expression Changes Implicated in Alzheimerâ€™s Disease. , 2016, 12, P448-P448.		0
125	P1â€129: Structural Variation (SV) in Heterogenous Wholeâ€Genome Sequencing Data from 111 Families at Risk For Alzheimer's Disease: Alzheimer's Disease Sequencing Project SV Study. Alzheimer's and Dementia, 2016, 12, P453.	0.4	0
126	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

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127	Assessment of the genetic variance of late-onset Alzheimer's disease. Neurobiology of Aging, 2016, 41, 200.e13-200.e20.	1.5	174
128	Association Between Genetic Traits for Immune-Mediated Diseases and Alzheimer Disease. JAMA Neurology, 2016, 73, 691.	4.5	151
129	Gene expression, methylation and neuropathology correlations at progressive supranuclear palsy risk loci. Acta Neuropathologica, 2016, 132, 197-211.	3.9	49
130	NIAGADS: The NIA Genetics of Alzheimer's Disease Data Storage Site. Alzheimer's and Dementia, 2016, 12, 1200-1203.	0.4	24
131	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
132	Global and local ancestry in Africanâ€Americans: Implications for Alzheimer's disease risk. Alzheimer's and Dementia, 2016, 12, 233-243.	0.4	42
133	Rare Functional Variant in TM2D3 is Associated with Late-Onset Alzheimer's Disease. PLoS Genetics, 2016, 12, e1006327.	1.5	47
134	Rarity of the Alzheimer Diseaseâ€“ProtectiveAPPA673T Variant in the United States. JAMA Neurology, 2015, 72, 209.	4.5	41
135	PARK10 is a major locus for sporadic neuropathologically confirmed Parkinson disease. Neurology, 2015, 84, 972-980.	1.5	48
136	Genome-wide association study of corticobasal degeneration identifies risk variants shared with progressive supranuclear palsy. Nature Communications, 2015, 6, 7247.	5.8	170
137	Polygenic Overlap Between C-Reactive Protein, Plasma Lipids, and Alzheimer Disease. Circulation, 2015, 131, 2061-2069.	1.6	145
138	Common polygenic variation enhances risk prediction for Alzheimerâ€™s disease. Brain, 2015, 138, 3673-3684.	3.7	359
139	High copy wildtype human 1N4R tau expression promotes early pathological tauopathy accompanied by cognitive deficits without progressive neurofibrillary degeneration. Acta Neuropathologica Communications, 2015, 3, 33.	2.4	18
140	Association of Long Runs of Homozygosity With Alzheimer Disease Among African American Individuals. JAMA Neurology, 2015, 72, 1313.	4.5	39
141	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.4	173
142	A scoring strategy combining statistics and functional genomics supports a possible role for common polygenic variation in autism. Frontiers in Genetics, 2014, 5, 33.	1.1	10
143	Tau-Mediated NMDA Receptor Impairment Underlies Dysfunction of a Selectively Vulnerable Network in a Mouse Model of Frontotemporal Dementia. Journal of Neuroscience, 2014, 34, 16482-16495.	1.7	60
144	Antisense-mediated Exon Skipping Decreases Tau Protein Expression: A Potential Therapy For Tauopathies. Molecular Therapy - Nucleic Acids, 2014, 3, e180.	2.3	54

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145	Genome-Wide Association Meta-analysis of Neuropathologic Features of Alzheimer's Disease and Related Dementias. PLoS Genetics, 2014, 10, e1004606.	1.5	305
146	Association of MAPT haplotypes with Alzheimerâ€™s disease risk and MAPT brain gene expression levels. Alzheimer's Research and Therapy, 2014, 6, 39.	3.0	106
147	Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 1394.	4.5	166
148	Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. American Journal of Human Genetics, 2014, 94, 677-694.	2.6	819
149	A framework for the interpretation of de novo mutation in human disease. Nature Genetics, 2014, 46, 944-950.	9.4	943
150	Two rare AKAP9 variants are associated with Alzheimer's disease in African Americans. Alzheimer's and Dementia, 2014, 10, 609.	0.4	94
151	Genetic and neuroanatomic associations in sporadic frontotemporal lobar degeneration. Neurobiology of Aging, 2014, 35, 1473-1482.	1.5	43
152	Missense variant in TREML2 protects against Alzheimer's disease. Neurobiology of Aging, 2014, 35, 1510.e19-1510.e26.	1.5	110
153	P1-045: EXOME ARRAY ANALYSIS IDENTIFIES NOVEL RISK VARIANTS FOR ALZHEIMER'S DISEASE WITH ONSET BEFORE 65 YEARS. , 2014, 10, P319-P319.		1
154	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	1.1	155
155	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
156	The genetics and neuropathology of Alzheimerâ€™s disease. Acta Neuropathologica, 2012, 124, 305-323.	3.9	203
157	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
158	APOE mRNA and protein expression in postmortem brain are modulated by an extended haplotype structure. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 409-417.	1.1	62
159	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
160	SUT-2 potentiates tau-induced neurotoxicity in Caenorhabditis elegans. Human Molecular Genetics, 2009, 18, 1825-1838.	1.4	86
161	SUT-1 enables tau-induced neurotoxicity in C . elegans. Human Molecular Genetics, 2007, 16, 1959-1971.	1.4	62
162	Neurodegeneration and defective neurotransmission in a Caenorhabditis elegans model of tauopathy. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9980-9985.	3.3	336

#	Article	IF	Citations
163	Examination of genetic linkage of chromosome 15 to schizophrenia in a large Veterans Affairs Cooperative Study sample. American Journal of Medical Genetics Part A, 2001, 105, 662-668.	2.4	75
164	A novel mutation at position +12 in the intron following Exon 10 of the tau gene in familial frontotemporal dementia (FTD-Kumamoto). Annals of Neurology, 2000, 47, 422-429.	2.8	109
165	A novel mutation at position +12 in the intron following Exon 10 of the tau gene in familial frontotemporal dementia (FTDâ€Kumamoto). Annals of Neurology, 2000, 47, 422-429.	2.8	6
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