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List of Publications by Year
in descending order

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Version: 2024-02-01

68	20,678	57758 44	88630 70
papers	citations	h-index	g-index

78	78	78	29510
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
2	Association of Rare APOE Missense Variants V236E and R251G With Risk of Alzheimer Disease. JAMA Neurology, 2022, 79, 652.	9.0	31
3	Multiomics integrative analysis identifies APOE allele-specific blood biomarkers associated to Alzheimerâ€™s disease etiopathogenesis. Aging, 2021, 13, 9277-9329.	3.1	15
4	Common variants in Alzheimerâ€™s disease and risk stratification by polygenic risk scores. Nature Communications, 2021, 12, 3417.	12.8	140
5	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.	7.9	191
6	Genetics of Alzheimerâ€™s disease: where we are, and where we are going. Current Opinion in Neurobiology, 2020, 61, 40-48.	4.2	144
7	TopMedâ€imputed genomeâ€wide association study of Alzheimerâ€™s disease in more than 100,000 European samples from the EADB project. Alzheimer's and Dementia, 2020, 16, e037971.	0.8	0
8	Genomeâ€wide association study of rate of cognitive decline in Alzheimer's disease patients identifies novel genes and pathways. Alzheimer's and Dementia, 2020, 16, 1134-1145.	0.8	28
9	Transethnic meta-analysis of rare coding variants in PLCG2, ABI3, and TREM2 supports their general contribution to Alzheimerâ€™s disease. Translational Psychiatry, 2019, 9, 55.	4.8	32
10	Analysis of Whole-Exome Sequencing Data for Alzheimer Disease Stratified by APOE Genotype. JAMA Neurology, 2019, 76, 1099.	9.0	32
11	Association of variants inHTRA1andNOTCH3with MRI-defined extremes of cerebral small vessel disease in older subjects. Brain, 2019, 142, 1009-1023.	7.6	37
12	Whole-Exome Sequencing in the Isolated Populations of Cilento from South Italy. Scientific Reports, 2019, 9, 4059.	3.3	7
13	Populationâ€based identityâ€byâ€descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 223-231.	1.7	2
14	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.	21.4	1,962
15	Integrated clinical and omics approach to rare diseases: novel genes and oligogenic inheritance in holoprosencephaly. Brain, 2019, 142, 35-49.	7.6	44
16	Strategies for phasing and imputation in a population isolate. Genetic Epidemiology, 2018, 42, 201-213.	1.3	27
17	Genetic variation in VAC14 is associated with bacteremia secondary to diverse pathogens in African children. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3601-E3603.	7.1	12
18	Genetically elevated highâ€density lipoprotein cholesterol through the cholesteryl ester transfer protein gene does not associate with risk of Alzheimer's disease. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2018, 10, 595-598.	2.4	2

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19	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	21.4	239
20	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	28.9	623
21	Functional screening of Alzheimer risk loci identifies PTK2B as an in vivo modulator and early marker of Tau pathology. Molecular Psychiatry, 2017, 22, 874-883.	7.9	98
22	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. Nature Neuroscience, 2017, 20, 1052-1061.	14.8	330
23	17q21.31 duplication causes prominent tau-related dementia with increased MAPT expression. Molecular Psychiatry, 2017, 22, 1119-1125.	7.9	57
24	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
25	Contribution to Alzheimer's disease risk of rare variants in TREM2, SORL1, and ABCA7 in 1779 cases and 1273 controls. Neurobiology of Aging, 2017, 59, 220.e1-220.e9.	3.1	116
26	Evaluation of a Genetic Risk Score to Improve Risk Prediction for Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2016, 53, 921-932.	2.6	77
27	ABCA7 rare variants and Alzheimer disease risk. Neurology, 2016, 86, 2134-2137.	1.1	63
28	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2016, 15, 695-707.	10.2	130
29	Biallelic Variants in UBA5 Reveal that Disruption of the UFM1 Cascade Can Result in Early-Onset Encephalopathy. American Journal of Human Genetics, 2016, 99, 695-703.	6.2	87
30	Meta-analysis of geneâ€“environment-wide association scans accounting for education level identifies additional loci for refractive error. Nature Communications, 2016, 7, 11008.	12.8	104
31	Accuracy of heritability estimations in presence of hidden population stratification. Scientific Reports, 2016, 6, 26471.	3.3	19
32	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. American Journal of Human Genetics, 2016, 98, 1092-1100.	6.2	39
33	SORL1 rare variants: a major risk factor for familial early-onset Alzheimerâ€™s disease. Molecular Psychiatry, 2016, 21, 831-836.	7.9	96
34	A novel Alzheimer disease locus located near the gene encoding tau protein. Molecular Psychiatry, 2016, 21, 108-117.	7.9	260
35	Six Novel Loci Associated with Circulating VEGF Levels Identified by a Meta-analysis of Genome-Wide Association Studies. PLoS Genetics, 2016, 12, e1005874.	3.5	56
36	Genetic Variants Modulating CRIPTO Serum Levels Identified by Genome-Wide Association Study in Cilento Isolates. PLoS Genetics, 2015, 11, e1004976.	3.5	13

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37	PLD3 and sporadic Alzheimer's disease risk. Nature, 2015, 520, E1-E1.	27.8	54
38	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.8	173
39	SUCLG2 identified as both a determinator of CSF AÎ²1â€“42 levels and an attenuator of cognitive decline in Alzheimer's disease. Human Molecular Genetics, 2014, 23, 6644-6658.	2.9	45
40	Follow-up of loci from the International Genomics of Alzheimerâ€™s Disease Project identifies TRIP4 as a novel susceptibility gene. Translational Psychiatry, 2014, 4, e358-e358.	4.8	98
41	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. Nature Genetics, 2014, 46, 1126-1130.	21.4	212
42	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. Nature Communications, 2014, 5, 4204.	12.8	72
43	Missense variant in TREML2 protects against Alzheimer's disease. Neurobiology of Aging, 2014, 35, 1510.e19-1510.e26.	3.1	110
44	A Genome-wide Association Analysis of a Broad Psychosis Phenotype Identifies Three Loci for Further Investigation. Biological Psychiatry, 2014, 75, 386-397.	1.3	44
45	Genome-wide association interaction analysis for Alzheimer's disease. Neurobiology of Aging, 2014, 35, 2436-2443.	3.1	61
46	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	2.5	155
47	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	21.4	1,395
48	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	21.4	1,213
49	Increased expression of BIN1 mediates Alzheimer genetic risk by modulating tau pathology. Molecular Psychiatry, 2013, 18, 1225-1234.	7.9	321
50	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nature Genetics, 2013, 45, 1452-1458.	21.4	3,741
51	Common variants in the HLA-DRB1â€“HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. Nature Genetics, 2013, 45, 208-213.	21.4	86
52	Genome-wide association study of intraocular pressure identifies the GLCCI1/ICA1 region as a glaucoma susceptibility locus. Human Molecular Genetics, 2013, 22, 4653-4660.	2.9	29
53	Common Genetic Determinants of Intraocular Pressure and Primary Open-Angle Glaucoma. PLoS Genetics, 2012, 8, e1002611.	3.5	164
54	A robust clustering algorithm for identifying problematic samples in genome-wide association studies. Bioinformatics, 2012, 28, 134-135.	4.1	66

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55	Zhou et al. reply. Nature Genetics, 2012, 44, 361-362.	21.4	89
56	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. Nature Genetics, 2012, 44, 1131-1136.	21.4	162
57	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. Nature Genetics, 2012, 44, 328-333.	21.4	375
58	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	27.8	2,400
59	Common variants near ATM are associated with glycemic response to metformin in type 2 diabetes. Nature Genetics, 2011, 43, 117-120.	21.4	390
60	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. Nature Genetics, 2011, 43, 761-767.	21.4	778
61	Dissection of the genetics of Parkinson's disease identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21. Human Molecular Genetics, 2011, 20, 345-353.	2.9	202
62	Comparative assessment of methods for estimating individual genome-wide homozygosity-by-descent from human genomic data. BMC Genomics, 2010, 11, 139.	2.8	29
63	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. Nature Genetics, 2010, 42, 985-990.	21.4	918
64	Linkage Analysis with Dense SNP Maps in Isolated Populations. Human Heredity, 2009, 68, 87-97.	0.8	16
65	A multiple splitting approach to linkage analysis in large pedigrees identifies a linkage to asthma on chromosome 12. Genetic Epidemiology, 2009, 33, 207-216.	1.3	13
66	Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region. Nature Genetics, 2009, 41, 1330-1334.	21.4	483
67	Identification and Replication of a Novel Obesity Locus on Chromosome 1q24 in Isolated Populations of Cilento. Diabetes, 2008, 57, 783-790.	0.6	16
68	New susceptibility locus for hypertension on chromosome 8q by efficient pedigree-breaking in an Italian isolate. Human Molecular Genetics, 2006, 15, 1735-1743.	2.9	39