

CÃ©line Bellenguez

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

20,678
citations

57758

44
h-index

88630

70
g-index

78
all docs

78
docs citations

78
times ranked

29510
citing authors

#	ARTICLE	IF	CITATIONS
1	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. <i>Nature Genetics</i> , 2013, 45, 1452-1458.	21.4	3,741
2	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011, 476, 214-219.	27.8	2,400
3	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A β , tau, immunity and lipid processing. <i>Nature Genetics</i> , 2019, 51, 414-430.	21.4	1,962
4	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. <i>Nature Genetics</i> , 2013, 45, 1150-1159.	21.4	1,395
5	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. <i>Nature Genetics</i> , 2013, 45, 1353-1360.	21.4	1,213
6	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. <i>Nature Genetics</i> , 2010, 42, 985-990.	21.4	918
7	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. <i>Nature Genetics</i> , 2017, 49, 1373-1384.	21.4	783
8	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. <i>Nature Genetics</i> , 2011, 43, 761-767.	21.4	778
9	New insights into the genetic etiology of Alzheimer's disease and related dementias. <i>Nature Genetics</i> , 2022, 54, 412-436.	21.4	700
10	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , 2018, 173, 1705-1715.e16.	28.9	623
11	Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region. <i>Nature Genetics</i> , 2009, 41, 1330-1334.	21.4	483
12	Common variants near ATM are associated with glycemic response to metformin in type 2 diabetes. <i>Nature Genetics</i> , 2011, 43, 117-120.	21.4	390
13	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. <i>Nature Genetics</i> , 2012, 44, 328-333.	21.4	375
14	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. <i>Nature Neuroscience</i> , 2017, 20, 1052-1061.	14.8	330
15	Increased expression of BIN1 mediates Alzheimer genetic risk by modulating tau pathology. <i>Molecular Psychiatry</i> , 2013, 18, 1225-1234.	7.9	321
16	A novel Alzheimer disease locus located near the gene encoding tau protein. <i>Molecular Psychiatry</i> , 2016, 21, 108-117.	7.9	260
17	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. <i>Nature Genetics</i> , 2018, 50, 834-848.	21.4	239
18	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. <i>Nature Genetics</i> , 2014, 46, 1126-1130.	21.4	212

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19	Dissection of the genetics of Parkinson's disease identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21. <i>Human Molecular Genetics</i> , 2011, 20, 345-353.	2.9	202
20	Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. <i>Molecular Psychiatry</i> , 2020, 25, 1859-1875.	7.9	191
21	Convergent genetic and expression data implicate immunity in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2015, 11, 658-671.	0.8	173
22	Common Genetic Determinants of Intraocular Pressure and Primary Open-Angle Glaucoma. <i>PLoS Genetics</i> , 2012, 8, e1002611.	3.5	164
23	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. <i>Nature Genetics</i> , 2012, 44, 1131-1136.	21.4	162
24	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. <i>PLoS ONE</i> , 2014, 9, e94661.	2.5	155
25	Genetics of Alzheimer's disease: where we are, and where we are going. <i>Current Opinion in Neurobiology</i> , 2020, 61, 40-48.	4.2	144
26	Common variants in Alzheimer's disease and risk stratification by polygenic risk scores. <i>Nature Communications</i> , 2021, 12, 3417.	12.8	140
27	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , The, 2016, 15, 695-707.	10.2	130
28	Contribution to Alzheimer's disease risk of rare variants in TREM2, SORL1, and ABCA7 in 1779 cases and 1273 controls. <i>Neurobiology of Aging</i> , 2017, 59, 220.e1-220.e9.	3.1	116
29	Missense variant in TREML2 protects against Alzheimer's disease. <i>Neurobiology of Aging</i> , 2014, 35, 1510.e19-1510.e26.	3.1	110
30	Meta-analysis of gene-environment-wide association scans accounting for education level identifies additional loci for refractive error. <i>Nature Communications</i> , 2016, 7, 11008.	12.8	104
31	Follow-up of loci from the International Genomics of Alzheimer's Disease Project identifies TRIP4 as a novel susceptibility gene. <i>Translational Psychiatry</i> , 2014, 4, e358-e358.	4.8	98
32	Functional screening of Alzheimer risk loci identifies PTK2B as an in vivo modulator and early marker of Tau pathology. <i>Molecular Psychiatry</i> , 2017, 22, 874-883.	7.9	98
33	SORL1 rare variants: a major risk factor for familial early-onset Alzheimer's disease. <i>Molecular Psychiatry</i> , 2016, 21, 831-836.	7.9	96
34	Zhou et al. reply. <i>Nature Genetics</i> , 2012, 44, 361-362.	21.4	89
35	Biallelic Variants in UBA5 Reveal that Disruption of the UFM1 Cascade Can Result in Early-Onset Encephalopathy. <i>American Journal of Human Genetics</i> , 2016, 99, 695-703.	6.2	87
36	Common variants in the HLA-DRB1- <i>HLA-DQA1</i> HLA class II region are associated with susceptibility to visceral leishmaniasis. <i>Nature Genetics</i> , 2013, 45, 208-213.	21.4	86

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37	Evaluation of a Genetic Risk Score to Improve Risk Prediction for Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2016, 53, 921-932.	2.6	77
38	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. <i>Nature Communications</i> , 2014, 5, 4204.	12.8	72
39	A robust clustering algorithm for identifying problematic samples in genome-wide association studies. <i>Bioinformatics</i> , 2012, 28, 134-135.	4.1	66
40	<i>ABCA7</i> rare variants and Alzheimer disease risk. <i>Neurology</i> , 2016, 86, 2134-2137.	1.1	63
41	Genome-wide association interaction analysis for Alzheimer's disease. <i>Neurobiology of Aging</i> , 2014, 35, 2436-2443.	3.1	61
42	17q21.31 duplication causes prominent tau-related dementia with increased MAPT expression. <i>Molecular Psychiatry</i> , 2017, 22, 1119-1125.	7.9	57
43	Six Novel Loci Associated with Circulating VEGF Levels Identified by a Meta-analysis of Genome-Wide Association Studies. <i>PLoS Genetics</i> , 2016, 12, e1005874.	3.5	56
44	PLD3 and sporadic Alzheimer's disease risk. <i>Nature</i> , 2015, 520, E1-E1.	27.8	54
45	SUCLG2 identified as both a determinant of CSF A β 42 levels and an attenuator of cognitive decline in Alzheimer's disease. <i>Human Molecular Genetics</i> , 2014, 23, 6644-6658.	2.9	45
46	A Genome-wide Association Analysis of a Broad Psychosis Phenotype Identifies Three Loci for Further Investigation. <i>Biological Psychiatry</i> , 2014, 75, 386-397.	1.3	44
47	Integrated clinical and omics approach to rare diseases: novel genes and oligogenic inheritance in holoprosencephaly. <i>Brain</i> , 2019, 142, 35-49.	7.6	44
48	New susceptibility locus for hypertension on chromosome 8q by efficient pedigree-breaking in an Italian isolate. <i>Human Molecular Genetics</i> , 2006, 15, 1735-1743.	2.9	39
49	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. <i>American Journal of Human Genetics</i> , 2016, 98, 1092-1100.	6.2	39
50	Association of variants in <i>HTRA1</i> and <i>NOTCH3</i> with MRI-defined extremes of cerebral small vessel disease in older subjects. <i>Brain</i> , 2019, 142, 1009-1023.	7.6	37
51	Transethnic meta-analysis of rare coding variants in <i>PLCG2</i> , <i>ABI3</i> , and <i>TREM2</i> supports their general contribution to Alzheimer's disease. <i>Translational Psychiatry</i> , 2019, 9, 55.	4.8	32
52	Analysis of Whole-Exome Sequencing Data for Alzheimer Disease Stratified by <i>APOE</i> Genotype. <i>JAMA Neurology</i> , 2019, 76, 1099.	9.0	32
53	Association of Rare <i>APOE</i> Missense Variants V236E and R251G With Risk of Alzheimer Disease. <i>JAMA Neurology</i> , 2022, 79, 652.	9.0	31
54	Comparative assessment of methods for estimating individual genome-wide homozygosity-by-descent from human genomic data. <i>BMC Genomics</i> , 2010, 11, 139.	2.8	29

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55	Genome-wide association study of intraocular pressure identifies the GLCC1/ICA1 region as a glaucoma susceptibility locus. <i>Human Molecular Genetics</i> , 2013, 22, 4653-4660.	2.9	29
56	Genome-wide association study of rate of cognitive decline in Alzheimer's disease patients identifies novel genes and pathways. <i>Alzheimer's and Dementia</i> , 2020, 16, 1134-1145.	0.8	28
57	Strategies for phasing and imputation in a population isolate. <i>Genetic Epidemiology</i> , 2018, 42, 201-213.	1.3	27
58	Accuracy of heritability estimations in presence of hidden population stratification. <i>Scientific Reports</i> , 2016, 6, 26471.	3.3	19
59	Identification and Replication of a Novel Obesity Locus on Chromosome 1q24 in Isolated Populations of Cilento. <i>Diabetes</i> , 2008, 57, 783-790.	0.6	16
60	Linkage Analysis with Dense SNP Maps in Isolated Populations. <i>Human Heredity</i> , 2009, 68, 87-97.	0.8	16
61	Multiomics integrative analysis identifies APOE allele-specific blood biomarkers associated to Alzheimer's disease etiopathogenesis. <i>Aging</i> , 2021, 13, 9277-9329.	3.1	15
62	A multiple splitting approach to linkage analysis in large pedigrees identifies a linkage to asthma on chromosome 12. <i>Genetic Epidemiology</i> , 2009, 33, 207-216.	1.3	13
63	Genetic Variants Modulating CRIPTO Serum Levels Identified by Genome-Wide Association Study in Cilento Isolates. <i>PLoS Genetics</i> , 2015, 11, e1004976.	3.5	13
64	Genetic variation in VAC14 is associated with bacteremia secondary to diverse pathogens in African children. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3601-E3603.	7.1	12
65	Whole-Exome Sequencing in the Isolated Populations of Cilento from South Italy. <i>Scientific Reports</i> , 2019, 9, 4059.	3.3	7
66	Genetically elevated high-density lipoprotein cholesterol through the cholesteryl ester transfer protein gene does not associate with risk of Alzheimer's disease. <i>Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring</i> , 2018, 10, 595-598.	2.4	2
67	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 223-231.	1.7	2
68	TopMed-imputed genome-wide association study of Alzheimer's disease in more than 100,000 European samples from the EADB project. <i>Alzheimer's and Dementia</i> , 2020, 16, e037971.	0.8	0