ChloÃ© Sarnowski

List of Publications by Year
in descending order

32 papers	6,424 citations	471509 17 h-index	477307 29 g-index
37 all docs	37 docs citations	37 times ranked	11434 citing authors

#	Article	IF	Citations
1	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
2	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331
3	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
4	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
5	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
6	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
7	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
8	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
9	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	12.8	89
10	Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. Nature Communications, 2021, 12, 654.	12.8	75
11	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. Molecular Psychiatry, 2019, 24, 1920-1932.	7.9	44
12	Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. American Journal of Human Genetics, 2019, 105, 706-718.	6.2	44
13	Whole genome sequence analyses of brain imaging measures in the Framingham Study. Neurology, 2018, 90, e188-e196.	1.1	34
14	Type 2 Diabetes Partitioned Polygenic Scores Associate With Disease Outcomes in 454,193 Individuals Across 13 Cohorts. Diabetes Care, 2022, 45, 674-683.	8.6	29
15	DNA methylation within melatonin receptor 1A (MTNR1A) mediates paternally transmitted genetic variant effect on asthma plus rhinitis. Journal of Allergy and Clinical Immunology, 2016, 138, 748-753.	2.9	25
16	Genetic variants associated with earlier age at menopause increase the risk of cardiovascular events in women. Menopause, 2018, 25, 451-457.	2.0	22
17	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits. Nature Human Behaviour, 2022, 6, 155-163.	12.0	22
18	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. Stroke, 2021, , STROKEAHA120031792.	2.0	16

#	Article	IF	Citations
19	Impact of Genetic Determinants of HbA1c on Type 2 Diabetes Risk and Diagnosis. Current Diabetes Reports, 2018, 18, 52.	4.2	12
20	Comparison of novel and existing methods for detecting differentially methylated regions. BMC Genetics, 2018, 19, 84.	2.7	10
21	Large trans-ethnic meta-analysis identifies AKR1C4 as a novel gene associated with age at menarche. Human Reproduction, 2021, 36, 1999-2010.	0.9	10
22	Do changes in DNA methylation mediate or interact with SNP variation? A pharmacoepigenetic analysis. BMC Genetics, 2018, 19, 70.	2.7	9
23	Meta-analysis of genome-wide association studies identifies ancestry-specific associations underlying circulating total tau levels. Communications Biology, 2022, 5, 336.	4.4	6
24	Identification of novel and rare variants associated with handgrip strength using whole genome sequence data from the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. PLoS ONE, 2021, 16, e0253611.	2.5	4
25	Investigation of parent-of-origin effects induced by fenofibrate treatment on triglycerides levels. BMC Genetics, 2018, 19, 83.	2.7	2
26	Application of novel and existing methods to identify genes with evidence of epigenetic association: results from GAW20. BMC Genetics, 2018, 19, 72.	2.7	1
27	[O1â€“11â€“04]: TOPMED WHOLE GENOME SEQUENCE (WGS) ASSOCIATIONS WITH BRAIN MRI MEASURES IN THE FRAMINGHAM STUDY. Alzheimer's and Dementia, 2017, 13, P219.	0.8	0
28	Whole genome sequence association analyses of brain volumes in the TOPMed program. Alzheimer's and Dementia, 2020, 16, e040627.	0.8	0
29	Comparative transâ€ethnic metaâ€analysis of whole exome sequencing variation for Alzheimerâ€™s disease (AD) in 18,402 individuals of the Alzheimerâ€™s Disease Sequencing Project (ADSP). Alzheimer's and Dementia, 2020, 16, e041583.	0.8	0
30	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.	0.8	0
31	Frequency of familial Alzheimerâ€™s disease gene mutations within the Alzheimer Disease Sequencing Project (ADSP). Alzheimer's and Dementia, 2020, 16, e046203.	0.8	0
32	JEM: A joint test to estimate the effect of multiple genetic variants on DNA methylation. Genetic Epidemiology, 2021, 45, 280-292.	1.3	0