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 analysis of dietary intake identifies new loci and functional links with metabolic traits. Nature Human Behaviour, 2022, 6, 155-163.	12.0	22
2	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
3	Meta-analysis of genome-wide association studies identifies ancestry-specific associations underlying circulating total tau levels. Communications Biology, 2022, 5, 336.	4.4	6
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	JEM: A joint test to estimate the effect of multiple genetic variants on DNA methylation. Genetic Epidemiology, 2021, 45, 280-292.	1.3	0
7	Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. Nature Communications, 2021, 12, 654.	12.8	75
8	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
9	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
10	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
11	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
12	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
13	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
14	Whole genome sequence association analyses of brain volumes in the TOPMed program. Alzheimer's and Dementia, 2020, 16, e040627.	0.8	0
15	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
16	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
17	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
18	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	12.8	89

#	Article	IF	Citations
19	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
20	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
21	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
22	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
23	Whole genome sequence analyses of brain imaging measures in the Framingham Study. Neurology, 2018, 90, e188-e196.	1.1	34
24	Genetic variants associated with earlier age at menopause increase the risk of cardiovascular events in women. Menopause, 2018, 25, 451-457.	2.0	22
25	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
26	Investigation of parent-of-origin effects induced by fenofibrate treatment on triglycerides levels. BMC Genetics, 2018, 19, 83.	2.7	2
27	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
28	Do changes in DNA methylation mediate or interact with SNP variation? A pharmacoepigenetic analysis. BMC Genetics, 2018, 19, 70.	2.7	9
29	Comparison of novel and existing methods for detecting differentially methylated regions. BMC Genetics, 2018, 19, 84.	2.7	10
30	Impact of Genetic Determinants of HbA1c on Type 2 Diabetes Risk and Diagnosis. Current Diabetes Reports, 2018, 18, 52.	4.2	12
31	[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
32	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