Ellen M Schmidt

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7754824/publications.pdf

Version: 2024-02-01

22 papers	12,652 citations	393982 19 h-index	610482 24 g-index
26 all docs	26 docs citations	26 times ranked	20390 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
3	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.	9.4	1,331
4	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
5	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	9.4	547
6	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
7	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
8	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
9	Systematic evaluation of coding variation identifies a candidate causal variant in TM6SF2 influencing total cholesterol and myocardial infarction risk. Nature Genetics, 2014, 46, 345-351.	9.4	268
10	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
11	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
12	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
13	Association of Polygenic Risk Scores for Multiple Cancers in a Phenome-wide Study: Results from The Michigan Genomics Initiative. American Journal of Human Genetics, 2018, 102, 1048-1061.	2.6	147
14	GREGOR: evaluating global enrichment of trait-associated variants in epigenomic features using a systematic, data-driven approach. Bioinformatics, 2015, 31, 2601-2606.	1.8	146
15	Exploring and visualizing large-scale genetic associations by using PheWeb. Nature Genetics, 2020, 52, 550-552.	9.4	129
16	A Fast and Accurate Algorithm to Test for Binary Phenotypes and Its Application to PheWAS. American Journal of Human Genetics, 2017, 101, 37-49.	2.6	116
17	Genome-wide association study of delay discounting in 23,217 adult research participants of European ancestry. Nature Neuroscience, 2018, 21, 16-18.	7.1	98
18	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. American Journal of Human Genetics, 2018, 102, 103-115.	2.6	86

#	Article	IF	Citations
19	Chromosome 1q21.2 and additional loci influence risk of spontaneous coronary artery dissection and myocardial infarction. Nature Communications, 2020, 11, 4432.	5.8	60
20	No large-effect low-frequency coding variation found for myocardial infarction. Human Molecular Genetics, 2014, 23, 4721-4728.	1.4	16
21	LabWAS: Novel findings and study design recommendations from a meta-analysis of clinical labs in two independent biobanks. PLoS Genetics, 2020, 16, e1009077.	1.5	14
22	Insights into blood lipids from rare variant discovery. Current Opinion in Genetics and Development, 2015, 33, 25-31.	1.5	4