Kathleen E Stirrups

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5661298/publications.pdf

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		516710	677142
18	5,171	16	22
papers	citations	h-index	g-index
23	23	23	11920
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	A comprehensive 1000 Genomes–based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
2	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
3	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
4	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
5	Whole-genome sequencing of patients with rare diseases in a national health system. Nature, 2020, 583, 96-102.	27.8	338
6	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
7	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
8	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
9	Germline selection shapes human mitochondrial DNA diversity. Science, 2019, 364, .	12.6	178
10	Whole-genome sequencing of a sporadic primary immunodeficiency cohort. Nature, 2020, 583, 90-95.	27.8	148
11	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
12	New Blood Pressure–Associated Loci Identified in Meta-Analyses of 475 000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
13	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
14	Development and validation of a universal blood donor genotyping platform: a multinational prospective study. Blood Advances, 2020, 4, 3495-3506.	5.2	31
15	Germline mutations in the transcription factor IKZF5 cause thrombocytopenia. Blood, 2019, 134, 2070-2081.	1.4	29
16	Exome-wide analysis of rare coding variation identifies novel associations with COPD and airflow limitation in <i>MOCS3</i> , <i>IFIT3</i> and <i>SERPINA12</i> . Thorax, 2016, 71, 501-509.	5.6	22
17	Analysis with the exome array identifies multiple new independent variants in lipid loci. Human Molecular Genetics, 2016, 25, 4094-4106.	2.9	19
18	G protein–coupled receptor kinase 5 regulates thrombin signaling in platelets via PAR-1. Blood Advances, 2022, 6, 2319-2330.	5.2	8