

Kathleen E Stirrups

List of Publications by Year in descending order

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

Version: 2024-02-01

18
papers

5,171
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516710

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docs citations

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11920
citing authors

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