Sebastian Schoenherr

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/435519/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Genome-Wide Characterization of a Highly Penetrant Form of Hyperlipoprotein(a)emia Associated With Genetically Elevated Cardiovascular Risk. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003489.	3.6	5
2	A Family and a Genome-Wide Polygenic Risk Score Are Independently Associated With Stroke in a Population-Based Study. Stroke, 2022, 53, 2331-2339.	2.0	4
3	Contamination detection in sequencing studies using the mitochondrial phylogeny. Genome Research, 2021, 31, 309-316.	5.5	44
4	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
5	Frequent LPA KIV-2 Variants Lower Lipoprotein(a) Concentrations and Protect Against Coronary Artery Disease. Journal of the American College of Cardiology, 2021, 78, 437-449.	2.8	34
6	Discontinuation versus continuation of renin-angiotensin-system inhibitors in COVID-19 (ACEI-COVID): a prospective, parallel group, randomised, controlled, open-label trial. Lancet Respiratory Medicine,the, 2021, 9, 863-872.	10.7	75
7	Persistence of immunity to SARS-CoV-2 over time in the ski resort Ischgl. EBioMedicine, 2021, 70, 103534.	6.1	15
8	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. Nature Genetics, 2021, 53, 1504-1516.	21.4	69
9	Association of changes in bone mineral parameters with mortality in haemodialysis patients: insights from the ARO cohort. Nephrology Dialysis Transplantation, 2020, 35, 478-487.	0.7	19
10	Investigation of a nonsense mutation located in the complex KIV-2 copy number variation region of apolipoprotein(a) in 10,910 individuals. Genome Medicine, 2020, 12, 74.	8.2	19
11	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
12	Extraordinary claims require extraordinary evidence in asserted mtDNA biparental inheritance. Forensic Science International: Genetics, 2020, 47, 102274.	3.1	23
13	Results from the German Chronic Kidney Disease (GCKD) study support association of relative telomere length with mortality in a large cohort of patients with moderate chronic kidney disease. Kidney International, 2020, 98, 488-497.	5.2	16
14	LBP-32-The Natural History of Ferroportin Disease-First Results of the International, Multicenter EASL non-HFE Registry. Journal of Hepatology, 2019, 70, e157.	3.7	0
15	Mitochondrial DNA copy number is associated with mortality and infections in a large cohort of patients with chronic kidney disease. Kidney International, 2019, 96, 480-488.	5.2	53
16	The GenomeAsia 100K Project enables genetic discoveries across Asia. Nature, 2019, 576, 106-111.	27.8	265
17	A comprehensive map of single-base polymorphisms in the hypervariable LPA kringle IV type 2 copy number variation region. Journal of Lipid Research, 2019, 60, 186-199.	4.2	37
18	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356

#	Article	IF	CITATIONS
19	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
20	A novel but frequent variant in <i>LPA</i> KIV-2 is associated with a pronounced Lp(a) and cardiovascular risk reduction. European Heart Journal, 2017, 38, 1823-1831.	2.2	66
21	A genome-wide association meta-analysis on lipoprotein (a) concentrations adjusted for apolipoprotein (a) isoforms. Journal of Lipid Research, 2017, 58, 1834-1844.	4.2	114
22	HaploGrep 2: mitochondrial haplogroup classification in the era of high-throughput sequencing. Nucleic Acids Research, 2016, 44, W58-W63.	14.5	688
23	mtDNA-Server: next-generation sequencing data analysis of human mitochondrial DNA in the cloud. Nucleic Acids Research, 2016, 44, W64-W69.	14.5	144
24	Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 2016, 48, 1443-1448.	21.4	1,357
25	Next-generation genotype imputation service and methods. Nature Genetics, 2016, 48, 1284-1287.	21.4	2,828
26	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
27	A genome-wide association meta-analysis on apolipoprotein A-IV concentrations. Human Molecular Genetics, 2016, 25, 3635-3646.	2.9	46
28	Cloudflow - enabling faster biomedical pipelines with MapReduce and Spark. Scalable Computing, 2016, 17, .	1.0	0
29	Do telomeres have a higher plasticity than thought? Results from the German Chronic Kidney Disease (GCKD) study as a high-risk population. Experimental Gerontology, 2015, 72, 162-166.	2.8	17
30	Association of relative telomere length with cardiovascular disease in a large chronic kidney disease cohort: The GCKD study. Atherosclerosis, 2015, 242, 529-534.	0.8	27
31	Validation of Next-Generation Sequencing of Entire Mitochondrial Genomes and the Diversity of Mitochondrial DNA Mutations in Oral Squamous Cell Carcinoma. PLoS ONE, 2015, 10, e0135643.	2.5	41
32	SNPflow: A Lightweight Application for the Processing, Storing and Automatic Quality Checking of Genotyping Assays. PLoS ONE, 2013, 8, e59508.	2.5	6
33	Evaluation of gene–obesity interaction effects on cholesterol levels: A genetic predisposition score on HDL-cholesterol is modified by obesity. Atherosclerosis, 2012, 225, 363-369.	0.8	15
34	HaploGrep: a fast and reliable algorithm for automatic classification of mitochondrial DNA haplogroups. Human Mutation, 2011, 32, 25-32.	2.5	433