Lukas Forer

List of Publications by Year in descending order

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Version: 2024-02-01

58 papers	11,158 citations	201674 27 h-index	182427 51 g-index
70 all docs	70 docs citations	70 times ranked	22069 citing authors

#	Article	IF	Citations
1	Lipoprotein(a) and SARSâ€CoVâ€2 infections: Susceptibility to infections, ischemic heart disease and thromboembolic events. Journal of Internal Medicine, 2022, 291, 101-107.	6.0	25
2	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
3	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
4	PCSK9 and Cardiovascular Disease in Individuals with Moderately Decreased Kidney Function. Clinical Journal of the American Society of Nephrology: CJASN, 2022, 17, 809-818.	4.5	4
5	The effect of LPA Thr3888Pro on lipoprotein(a) and coronary artery disease is modified by the LPA KIV-2 variant 4925G>A. Atherosclerosis, 2022, 349, 151-159.	0.8	6
6	Meta-imputation: An efficient method to combine genotype data after imputation with multiple reference panels. American Journal of Human Genetics, 2022, 109, 1007-1015.	6.2	15
7	Association between a polygenic and family risk score on the prevalence and incidence of myocardial infarction in the KORA-F3 study. Atherosclerosis, 2022, 352, 10-17.	0.8	6
8	Analyzing Low-Level mtDNA Heteroplasmyâ€"Pitfalls and Challenges from Bench to Benchmarking. International Journal of Molecular Sciences, 2021, 22, 935.	4.1	15
9	Contamination detection in sequencing studies using the mitochondrial phylogeny. Genome Research, 2021, 31, 309-316.	5.5	44
10	Association of mitochondrial DNA copy number with metabolic syndrome and type 2 diabetes in 14Â176 individuals. Journal of Internal Medicine, 2021, 290, 190-202.	6.0	61
11	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
12	Urine Metabolite Levels, Adverse Kidney Outcomes, and Mortality in CKD Patients: A Metabolome-wide Association Study. American Journal of Kidney Diseases, 2021, 78, 669-677.e1.	1.9	22
13	Complex regional pain syndrome: role of contralateral sensitisation. British Journal of Anaesthesia, 2021, 127, e1-e3.	3.4	11
14	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
15	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
16	Persistence of immunity to SARS-CoV-2 over time in the ski resort Ischgl. EBioMedicine, 2021, 70, 103534.	6.1	15
17	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
18	Apolipoprotein Aâ€IV concentrations and clinical outcomes in a large chronic kidney disease cohort: Results from the GCKD study. Journal of Internal Medicine, 2021, , .	6.0	5

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19	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
20	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
21	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
22	Genetic studies of urinary metabolites illuminate mechanisms of detoxification and excretion in humans. Nature Genetics, 2020, 52, 167-176.	21.4	101
23	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
24	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
25	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
26	A Comprehensive Map Of The Variability In The Lipoprotein(A) Kiv 2 Repeat Region And Follow-Up Of The Kiv-2 Arg20ter Mutation In 11,000 Individuals. Atherosclerosis, 2019, 287, e58.	0.8	0
27	The GenomeAsia 100K Project enables genetic discoveries across Asia. Nature, 2019, 576, 106-111.	27.8	265
28	What is normal trauma healing and what is complex regional pain syndrome I? An analysis of clinical and experimental biomarkers. Pain, 2019, 160, 2278-2289.	4.2	35
29	Identification of African-Specific Admixture between Modern and Archaic Humans. American Journal of Human Genetics, 2019, 105, 1254-1261.	6.2	16
30	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
31	A novel but frequent variant in LPA KIV-2 is associated with a pronounced Lp(a) and cardiovascular risk reduction. European Heart Journal, 2017, 38, 1823-1831.	2.2	66
32	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
33	Sensory phenotype and risk factors for painful diabetic neuropathy: a cross-sectional observational study. Pain, 2017, 158, 2340-2353.	4.2	116
34	LASER server: ancestry tracing with genotypes or sequence reads. Bioinformatics, 2017, 33, 2056-2058.	4.1	30
35	Glycaemic control and antidiabetic therapy in patients with diabetes mellitus and chronic kidney disease â€“ cross-sectional data from the German Chronic Kidney Disease (GCKD) cohort. BMC Nephrology, 2016, 17, 59.	1.8	18
36	HaploGrep 2: mitochondrial haplogroup classification in the era of high-throughput sequencing. Nucleic Acids Research, 2016, 44, W58-W63.	14.5	688

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37	mtDNA-Server: next-generation sequencing data analysis of human mitochondrial DNA in the cloud. Nucleic Acids Research, 2016, 44, W64-W69.	14.5	144
38	Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 2016, 48, 1443-1448.	21.4	1,357
39	Next-generation genotype imputation service and methods. Nature Genetics, 2016, 48, 1284-1287.	21.4	2,828
40	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
41	A genome-wide association meta-analysis on apolipoprotein A-IV concentrations. Human Molecular Genetics, 2016, 25, 3635-3646.	2.9	46
42	Cloudflow - enabling faster biomedical pipelines with MapReduce and Spark. Scalable Computing, 2016, 17, .	1.0	0
43	Experiences with workflows for automating data-intensive bioinformatics. Biology Direct, 2015, 10, 43.	4.6	52
44	Prevalence and correlates of gout in a large cohort of patients with chronic kidney disease: the German Chronic Kidney Disease (GCKD) study. Nephrology Dialysis Transplantation, 2015, 30, 613-621.	0.7	85
45	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
46	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
47	Cloudflow - A framework for MapReduce pipeline development in Biomedical Research. , 2015, , .		3
48	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
49	Large-scale mitochondrial DNA analysis in Southeast Asia reveals evolutionary effects of cultural isolation in the multi-ethnic population of Myanmar. BMC Evolutionary Biology, 2014, 14, 17.	3.2	56
50	Delivering bioinformatics MapReduce applications in the cloud. , 2014, , .		7
51	SNPflow: A Lightweight Application for the Processing, Storing and Automatic Quality Checking of Genotyping Assays. PLoS ONE, 2013, 8, e59508.	2.5	6
52	Evaluation of geneâ€“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
53	Cloudgene: A graphical execution platform for MapReduce programs on private and public clouds. BMC Bioinformatics, 2012, 13, 200.	2.6	43
54	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. Nature, 2011, 478, 97-102.	27.8	394

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55	CONAN: copy number variation analysis software for genome-wide association studies. BMC Bioinformatics, 2010, 11, 318.	2.6	17
56	Visual Analytical Methods to Identify Family Clustered Diseases. , 2008, , .		1
57	PedVizApi: a Java API for the interactive, visual analysis of extended pedigrees. Bioinformatics, 2008, 24, 279-281.	4.1	8
58	South Asian Patient Population Genetics Reveal Strong Founder Effects and High Rates of Homozygosity â€“ New Resources for Precision Medicine. SSRN Electronic Journal, 0, , .	0.4	2