Lukas Forer

List of Publications by Year in descending order

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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	Next-generation genotype imputation service and methods. Nature Genetics, 2016, 48, 1284-1287.	21.4	2,828
2	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
3	Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 2016, 48, 1443-1448.	21.4	1,357
4	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
5	HaploGrep 2: mitochondrial haplogroup classification in the era of high-throughput sequencing. Nucleic Acids Research, 2016, 44, W58-W63.	14.5	688
6	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. Nature, 2011, 478, 97-102.	27.8	394
7	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
8	The GenomeAsia 100K Project enables genetic discoveries across Asia. Nature, 2019, 576, 106-111.	27.8	265
9	mtDNA-Server: next-generation sequencing data analysis of human mitochondrial DNA in the cloud. Nucleic Acids Research, 2016, 44, W64-W69.	14.5	144
10	Sensory phenotype and risk factors for painful diabetic neuropathy: a cross-sectional observational study. Pain, 2017, 158, 2340-2353.	4.2	116
11	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
12	Genetic studies of urinary metabolites illuminate mechanisms of detoxification and excretion in humans. Nature Genetics, 2020, 52, 167-176.	21.4	101
13	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
14	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
15	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
16	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
17	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
18	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

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19	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
20	Experiences with workflows for automating data-intensive bioinformatics. Biology Direct, 2015, 10, 43.	4.6	52
21	A genome-wide association meta-analysis on apolipoprotein A-IV concentrations. Human Molecular Genetics, 2016, 25, 3635-3646.	2.9	46
22	Contamination detection in sequencing studies using the mitochondrial phylogeny. Genome Research, 2021, 31, 309-316.	5.5	44
23	Cloudgene: A graphical execution platform for MapReduce programs on private and public clouds. BMC Bioinformatics, 2012, 13, 200.	2.6	43
24	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
25	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
26	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
27	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
28	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
29	LASER server: ancestry tracing with genotypes or sequence reads. Bioinformatics, 2017, 33, 2056-2058.	4.1	30
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	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
32	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
33	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
34	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
35	CONAN: copy number variation analysis software for genome-wide association studies. BMC Bioinformatics, 2010, 11, 318.	2.6	17
36	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

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37	Identification of African-Specific Admixture between Modern and Archaic Humans. American Journal of Human Genetics, 2019, 105, 1254-1261.	6.2	16
38	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
39	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
40	Analyzing Low-Level mtDNA Heteroplasmyâ€”Pitfalls and Challenges from Bench to Benchmarking. International Journal of Molecular Sciences, 2021, 22, 935.	4.1	15
41	Persistence of immunity to SARS-CoV-2 over time in the ski resort Ischgl. EBioMedicine, 2021, 70, 103534.	6.1	15
42	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
43	Complex regional pain syndrome: role of contralateral sensitisation. British Journal of Anaesthesia, 2021, 127, e1-e3.	3.4	11
44	PedVizApi: a Java API for the interactive, visual analysis of extended pedigrees. Bioinformatics, 2008, 24, 279-281.	4.1	8
45	Delivering bioinformatics MapReduce applications in the cloud. , 2014, , .		7
46	SNPflow: A Lightweight Application for the Processing, Storing and Automatic Quality Checking of Genotyping Assays. PLoS ONE, 2013, 8, e59508.	2.5	6
47	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
48	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
49	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
50	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
51	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
52	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
53	Cloudflow - A framework for MapReduce pipeline development in Biomedical Research. , 2015, , .		3
54	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

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55	Visual Analytical Methods to Identify Family Clustered Diseases. , 2008, , .		1
56	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
57	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
58	Cloudflow - enabling faster biomedical pipelines with MapReduce and Spark. Scalable Computing, 2016, 17, .	1.0	0