Lukas Habegger

List of Publications by Citations

31 papers	5,510 citations	24 h-index	34 g-index
34 ext. papers	7,144 ext. citations	23.2 avg, IF	4.23 L-index

#	Paper	IF	Citations
31	Personal omics profiling reveals dynamic molecular and medical phenotypes. *Cell*, **2012**, 148, 1293-307	56.2	921
30	A systematic survey of loss-of-function variants in human protein-coding genes. *Science*, **2012**, 335, 823-8	33.3	880
29	Integrative analysis of the Caenorhabditis elegans genome by the modENCODE project. *Science*, **2010**, 330, 1775-87	33.3	744
28	Variation in transcription factor binding among humans. *Science*, **2010**, 328, 232-5	33.3	447
27	Genetic and Pharmacologic Inactivation of ANGPTL3 and Cardiovascular Disease. *New England Journal of Medicine*, **2017**, 377, 211-221	59.2	416
26	Distribution and clinical impact of functional variants in 50,726 whole-exome sequences from the DiscovEHR study. *Science*, **2016**, 354,	33.3	320
25	Inactivating Variants in ANGPTL4 and Risk of Coronary Artery Disease. *New England Journal of Medicine*, **2016**, 374, 1123-33	59.2	305
24	The GENCODE pseudogene resource. *Genome Biology*, **2012**, 13, R51	18.3	232
23	Discovery of non-ETS gene fusions in human prostate cancer using next-generation RNA sequencing. *Genome Research*, **2011**, 21, 56-67	9.7	156
22	Dynamic transcriptomes during neural differentiation of human embryonic stem cells revealed by short, long, and paired-end sequencing. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 5254-9	11.5	142
21	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. *Nature*, **2020**, 586, 749-756	50.4	122
20	FusionSeq: a modular framework for finding gene fusions by analyzing paired-end RNA-sequencing data. *Genome Biology*, **2010**, 11, R104	18.3	121
19	RSEQtools: a modular framework to analyze RNA-Seq data using compact, anonymized data summaries. *Bioinformatics*, **2011**, 27, 281-3	7.2	89
18	Comparison and calibration of transcriptome data from RNA-Seq and tiling arrays. *BMC Genomics*, **2010**, 11, 383	4.5	88
17	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. *Nature Communications*, **2018**, 9, 2252	17.4	71
16	Whole exome sequencing and characterization of coding variation in 49,960 individuals in the UK Biobank		56
15	VAT: a computational framework to functionally annotate variants in personal genomes within a cloud-computing environment. *Bioinformatics*, **2012**, 28, 2267-9	7.2	55

List of Publications

14	Computationally efficient whole-genome regression for quantitative and binary traits. *Nature Genetics*, **2021**, 53, 1097-1103	36.3	51
13	Accurate identification and analysis of human mRNA isoforms using deep long read sequencing. *G3: Genes, Genomes, Genetics*, **2013**, 3, 387-97	3.2	47
12	Advancing human genetics research and drug discovery through exome sequencing of the UK Biobank. *Nature Genetics*, **2021**, 53, 942-948	36.3	42
11	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. *Genome Research*, **2013**, 23, 2042-52	9.7	41
10	Profiling and Leveraging Relatedness in a Precision Medicine Cohort of 92,455 Exomes. *American Journal of Human Genetics*, **2018**, 102, 874-889	11	38
9	Exome sequencing and analysis of 454,787 UK Biobank participants. *Nature*, **2021**, 599, 628-634	50.4	34
8	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. *American Journal of Human Genetics*, **2021**, 108, 1350-1355	11	25
7	Gene inactivation and its implications for annotation in the era of personal genomics. *Genes and Development*, **2011**, 25, 1-10	12.6	23
6	Identification of Neuropsychiatric Copy Number Variants in a Health Care System Population. *JAMA Psychiatry*, **2020**, 77, 1276-1285	14.5	17
5	Genome-wide analysis provides genetic evidence that ACE2 influences COVID-19 risk and yields risk scores associated with severe disease.. *Nature Genetics*, **2022**,	36.3	9
4	GWAS of serum ALT and AST reveals an association of SLC30A10 Thr95Ile with hypermanganesemia symptoms. *Nature Communications*, **2021**, 12, 4571	17.4	6
3	IQSeq: integrated isoform quantification analysis based on next-generation sequencing. *PLoS ONE*, **2012**, 7, e29175	3.7	5
2	Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank.. *Nature Genetics*, **2022**,	36.3	4
1	Profiling copy number variation and disease associations from 50,726 DiscovEHR Study exomes		3