Lukas Habegger

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/11492294/publications.pdf

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31	8,332	218381	433756
papers	citations	26 h-index	31 g-index

34	34	34	16129
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. Cell, 2012, 148, 1293-1307.	13.5	1,134
2	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	6.0	1,095
3	Integrative Analysis of the Caenorhabditis elegans Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	6.0	912
4	Genetic and Pharmacologic Inactivation of ANGPTL3 and Cardiovascular Disease. New England Journal of Medicine, 2017, 377, 211-221.	13.9	633
5	Variation in Transcription Factor Binding Among Humans. Science, 2010, 328, 232-235.	6.0	521
6	Distribution and clinical impact of functional variants in 50,726 whole-exome sequences from the DiscovEHR study. Science, 2016, 354, .	6.0	464
7	Computationally efficient whole-genome regression for quantitative and binary traits. Nature Genetics, 2021, 53, 1097-1103.	9.4	457
8	Inactivating Variants in ANGPTL4 and Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 1123-1133.	13.9	411
9	Exome sequencing and analysis of 454,787 UK Biobank participants. Nature, 2021, 599, 628-634.	13.7	377
10	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. Nature, 2020, 586, 749-756.	13.7	369
11	The GENCODE pseudogene resource. Genome Biology, 2012, 13, R51.	13.9	273
12	Advancing human genetics research and drug discovery through exome sequencing of the UK Biobank. Nature Genetics, 2021, 53, 942-948.	9.4	234
13	Discovery of non-ETS gene fusions in human prostate cancer using next-generation RNA sequencing. Genome Research, 2011, 21, 56-67.	2.4	179
14	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, 5254-5259.	3.3	168
15	FusionSeq: a modular framework for finding gene fusions by analyzing paired-end RNA-sequencing data. Genome Biology, 2010, 11, R104.	3.8	137
16	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	5.8	99
17	Comparison and calibration of transcriptome data from RNA-Seq and tiling arrays. BMC Genomics, 2010, 11, 383.	1.2	97
18	Genome-wide analysis provides genetic evidence that ACE2 influences COVID-19 risk and yields risk scores associated with severe disease. Nature Genetics, 2022, 54, 382-392.	9.4	97

#	Article	IF	Citations
19	RSEQtools: a modular framework to analyze RNA-Seq data using compact, anonymized data summaries. Bioinformatics, 2011, 27, 281-283.	1.8	93
20	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. American Journal of Human Genetics, 2021, 108, 1350-1355.	2.6	72
21	Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank. Nature Genetics, 2022, 54, 240-250.	9.4	68
22	VAT: a computational framework to functionally annotate variants in personal genomes within a cloud-computing environment. Bioinformatics, 2012, 28, 2267-2269.	1.8	65
23	Accurate Identification and Analysis of Human mRNA Isoforms Using Deep Long Read Sequencing. G3: Genes, Genomes, Genetics, 2013, 3, 387-397.	0.8	59
24	Profiling and Leveraging Relatedness in a Precision Medicine Cohort of 92,455 Exomes. American Journal of Human Genetics, 2018, 102, 874-889.	2.6	58
25	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. Genome Research, 2013, 23, 2042-2052.	2.4	52
26	Identification of Neuropsychiatric Copy Number Variants in a Health Care System Population. JAMA Psychiatry, 2020, 77, 1276.	6.0	46
27	Gene inactivation and its implications for annotation in the era of personal genomics. Genes and Development, 2011, 25, 1-10.	2.7	29
28	GWAS of serum ALT and AST reveals an association of SLC30A10 Thr95Ile with hypermanganesemia symptoms. Nature Communications, 2021, 12, 4571.	5.8	26
29	Population-scale analysis of common and rare genetic variation associated with hearing loss in adults. Communications Biology, 2022, 5, .	2.0	12
30	IQSeq: Integrated Isoform Quantification Analysis Based on Next-Generation Sequencing. PLoS ONE, 2012, 7, e29175.	1.1	7
31	Medical manifestations and healthcare utilization among adult MyCode participants with neurodevelopmental psychiatric copy number variants. Genetics in Medicine, 2021, , .	1.1	2