

Christian Benner

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7773092/publications.pdf>

Version: 2024-02-01

17
papers

2,970
citations

759233

12
h-index

888059

17
g-index

27
all docs

27
docs citations

27
times ranked

5260
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	27.8	929
2	FINEMAP: efficient variable selection using summary data from genome-wide association studies. <i>Bioinformatics</i> , 2016, 32, 1493-1501.	4.1	584
3	Genetics of 35 blood and urine biomarkers in the UK Biobank. <i>Nature Genetics</i> , 2021, 53, 185-194.	21.4	377
4	Prospects of Fine-Mapping Trait-Associated Genomic Regions by Using Summary Statistics from Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2017, 101, 539-551.	6.2	200
5	Functionally informed fine-mapping and polygenic localization of complex trait heritability. <i>Nature Genetics</i> , 2020, 52, 1355-1363.	21.4	185
6	Interrogation of human hematopoiesis at single-cell and single-variant resolution. <i>Nature Genetics</i> , 2019, 51, 683-693.	21.4	147
7	Genome-wide analysis of 102,084 migraine cases identifies 123 risk loci and subtype-specific risk alleles. <i>Nature Genetics</i> , 2022, 54, 152-160.	21.4	135
8	Polygenic Hyperlipidemias and Coronary Artery Disease Risk. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002725.	3.6	60
9	Genome-wide association meta-analysis of nicotine metabolism and cigarette consumption measures in smokers of European descent. <i>Molecular Psychiatry</i> , 2021, 26, 2212-2223.	7.9	45
10	An effector index to predict target genes at GWAS loci. <i>Human Genetics</i> , 2022, 141, 1431-1447.	3.8	28
11	Genome-Wide Analysis of Evolutionary Markers of Human Influenza A(H1N1)pdm09 and A(H3N2) Viruses May Guide Selection of Vaccine Strain Candidates. <i>Genome Biology and Evolution</i> , 2015, 7, 3472-3483.	2.5	23
12	Genome-Wide Meta-Analysis of Sciatica in Finnish Population. <i>PLoS ONE</i> , 2016, 11, e0163877.	2.5	23
13	An expanded analysis framework for multivariate GWAS connects inflammatory biomarkers to functional variants and disease. <i>European Journal of Human Genetics</i> , 2021, 29, 309-324.	2.8	19
14	biMM: efficient estimation of genetic variances and covariances for cohorts with high-dimensional phenotype measurements. <i>Bioinformatics</i> , 2017, 33, 2405-2407.	4.1	11
15	Comparative Analysis of Whole-Genome Sequences of Influenza A(H1N1)pdm09 Viruses Isolated from Hospitalized and Nonhospitalized Patients Identifies Missense Mutations That Might Be Associated with Patient Hospital Admissions in Finland during 2009 to 2014. <i>Genome Announcements</i> , 2015, 3, .	0.8	8
16	Genetic Loci Associated with Allergic Sensitization in Lithuanians. <i>PLoS ONE</i> , 2015, 10, e0134188.	2.5	4
17	Dissecting the Regulation of Human Hematopoiesis at Single-Cell and Single-Variant Resolution. <i>Blood</i> , 2018, 132, 531-531.	1.4	0