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