

Petr Danecek

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4387217/publications.pdf>

Version: 2024-02-01

19
papers

37,595
citations

448610

19
h-index

889612

19
g-index

28
all docs

28
docs citations

28
times ranked

65140
citing authors

#	ARTICLE	IF	CITATIONS
1	HTSlib: C library for reading/writing high-throughput sequencing data. <i>GigaScience</i> , 2021, 10, .	3.3	191
2	Non-coding region variants upstream of MEF2C cause severe developmental disorder through three distinct loss-of-function mechanisms. <i>American Journal of Human Genetics</i> , 2021, 108, 1083-1094.	2.6	42
3	Twelve years of SAMtools and BCFtools. <i>GigaScience</i> , 2021, 10, .	3.3	4,546
4	Evidence for 28 genetic disorders discovered by combining healthcare and research data. <i>Nature</i> , 2020, 586, 757-762.	13.7	343
5	Insights into human genetic variation and population history from 929 diverse genomes. <i>Science</i> , 2020, 367, .	6.0	534
6	Contribution of retrotransposition to developmental disorders. <i>Nature Communications</i> , 2019, 10, 4630.	5.8	43
7	Very low-depth whole-genome sequencing in complex trait association studies. <i>Bioinformatics</i> , 2019, 35, 2555-2561.	1.8	68
8	Ancient human parallel lineages within North America contributed to a coastal expansion. <i>Science</i> , 2018, 360, 1024-1027.	6.0	138
9	BCFtools/csqs: haplotype-aware variant consequences. <i>Bioinformatics</i> , 2017, 33, 2037-2039.	1.8	289
10	Common genetic variation drives molecular heterogeneity in human iPSCs. <i>Nature</i> , 2017, 546, 370-375.	13.7	491
11	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 865-884.	2.6	131
12	BCFtools/RoH: a hidden Markov model approach for detecting autozygosity from next-generation sequencing data. <i>Bioinformatics</i> , 2016, 32, 1749-1751.	1.8	506
13	Reference-based phasing using the Haplotype Reference Consortium panel. <i>Nature Genetics</i> , 2016, 48, 1443-1448.	9.4	1,357
14	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	9.4	2,421
15	A Method for Checking Genomic Integrity in Cultured Cell Lines from SNP Genotyping Data. <i>PLoS ONE</i> , 2016, 11, e0155014.	1.1	26
16	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
17	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015, 526, 82-90.	13.7	1,014
18	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. <i>Nature Communications</i> , 2014, 5, 4871.	5.8	62

#	ARTICLE	IF	CITATIONS
19	The variant call format and VCFtools. <i>Bioinformatics</i> , 2011, 27, 2156-2158.	1.8	11,326