Petr Danecek

List of Publications by Year in descending order

19 papers	37,595 citations	393982 19 h-index	794141 19 g-index
28 all docs	28 docs citations	28 times ranked	59512 citing authors

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

#	Article	IF	Citations
19	The variant call format and VCFtools. Bioinformatics, 2011, 27, 2156-2158.	1.8	11,326