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	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	The variant call format and VCFtools. Bioinformatics, 2011, 27, 2156-2158.	1.8	11,326
3	Twelve years of SAMtools and BCFtools. GigaScience, 2021, 10, .	3.3	4,546
4	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
5	Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 2016, 48, 1443-1448.	9.4	1,357
6	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
7	Insights into human genetic variation and population history from 929 diverse genomes. Science, 2020, 367, .	6.0	534
8	BCFtools/RoH: a hidden Markov model approach for detecting autozygosity from next-generation sequencing data. Bioinformatics, 2016, 32, 1749-1751.	1.8	506
9	Common genetic variation drives molecular heterogeneity in human iPSCs. Nature, 2017, 546, 370-375.	13.7	491
10	Evidence for 28 genetic disorders discovered by combining healthcare and research data. Nature, 2020, 586, 757-762.	13.7	343
11	BCFtools/csq: haplotype-aware variant consequences. Bioinformatics, 2017, 33, 2037-2039.	1.8	289
12	HTSlib: C library for reading/writing high-throughput sequencing data. GigaScience, 2021, 10, .	3.3	191
13	Ancient human parallel lineages within North America contributed to a coastal expansion. Science, 2018, 360, 1024-1027.	6.0	138
14	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131
15	Very low-depth whole-genome sequencing in complex trait association studies. Bioinformatics, 2019, 35, 2555-2561.	1.8	68
16	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	5.8	62
17	Contribution of retrotransposition to developmental disorders. Nature Communications, 2019, 10, 4630.	5.8	43
18	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

#	Article	IF	Citations
19	A Method for Checking Genomic Integrity in Cultured Cell Lines from SNP Genotyping Data. PLoS ONE, 2016, 11, e0155014.	1.1	26