# Petr Danecek

## List of Publications by Year in descending order



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|---|---|---|---|
| 19 papers | 37,595 citations | 394390 19 h-index | 794568 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, . | 6.4 | 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. | 6.2 | 42 |
| 3 | Twelve years of SAMtools and BCFtools. GigaScience, 2021, 10, . | 6.4 | 4,546 |
| 4 | Evidence for 28 genetic disorders discovered by combining healthcare and research data. Nature, 2020, 586, 757-762. | 27.8 | 343 |
| 5 | Insights into human genetic variation and population history from 929 diverse genomes. Science, 2020, 367, . | 12.6 | 534 |
| 6 | Contribution of retrotransposition to developmental disorders. Nature Communications, 2019, 10, 4630. | 12.8 | 43 |
| 7 | Very low-depth whole-genome sequencing in complex trait association studies. Bioinformatics, 2019, 35, 2555-2561. | 4.1 | 68 |
| 8 | Ancient human parallel lineages within North America contributed to a coastal expansion. Science, 2018, 360, 1024-1027. | 12.6 | 138 |
| 9 | BCFtools/csq: haplotype-aware variant consequences. Bioinformatics, 2017, 33, 2037-2039. | 4.1 | 289 |
| 10 | Common genetic variation drives molecular heterogeneity in human iPSCs. Nature, 2017, 546, 370-375. | 27.8 | 491 |
| 11 | Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884. | 6.2 | 131 |
| 12 | BCFtools/RoH: a hidden Markov model approach for detecting autozygosity from next-generation sequencing data. Bioinformatics, 2016, 32, 1749-1751. | 4.1 | 506 |
| 13 | Reference-based phasing using the Haplotype Reference Consortium panel. Nature Genetics, 2016, 48, 1443-1448. | 21.4 | 1,357 |
| 14 | A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283. | 21.4 | 2,421 |
| 15 | A Method for Checking Genomic Integrity in Cultured Cell Lines from SNP Genotyping Data. PLoS ONE, 2016, 11, e0155014. | 2.5 | 26 |
| 16 | A global reference for human genetic variation. Nature, 2015, 526, 68-74. | 27.8 | 13,998 |
| 17 | The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90. | 27.8 | 1,014 |
| 18 | A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871. | 12.8 | 62 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | The variant call format and VCFtools. Bioinformatics, 2011, 27, 2156-2158. | 4.1 | 11,326 |