# James K Bonfield

List of Publications by Year
in descending order



| 29 | 12,009 | 304743 | 526287 |
|---|---|---|---|
| papers | citations | 22 h-index | 27 g-index |

| 33 | 33 | 33 | 13633 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | CRAM 3.1: advances in the CRAM file format. Bioinformatics, 2022, 38, 1497-1503. | 4.1 | 12 |
| 2 | HTSlib: C library for reading/writing high-throughput sequencing data. GigaScience, 2021, 10, . | 6.4 | 191 |
| 3 | Twelve years of SAMtools and BCFtools. GigaScience, 2021, 10, . | 6.4 | 4,546 |
| 4 | GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029. | 6.5 | 94 |
| 5 | Crumble: reference free lossy compression of sequence quality values. Bioinformatics, 2019, 35, 337-339. | 4.1 | 21 |
| 6 | De novo yeast genome assemblies from MinION, PacBio and MiSeq platforms. Scientific Reports, 2017, 7, 3935. | 3.3 | 146 |
| 7 | Comparison of high-throughput sequencing data compression tools. Nature Methods, 2016, 13, 1005-1008. | 19.0 | 91 |
| 8 | The Scramble conversion tool. Bioinformatics, 2014, 30, 2818-2819. | 4.1 | 45 |
| 9 | Compression of FASTQ and SAM Format Sequencing Data. PLoS ONE, 2013, 8, e59190. | 2.5 | 167 |
| 10 | Improvements to services at the European Nucleotide Archive. Nucleic Acids Research, 2010, 38, D39-D45. | 14.5 | 67 |
| 11 | Gap5â€”editing the billion fragment sequence assembly. Bioinformatics, 2010, 26, 1699-1703. | 4.1 | 214 |
| 12 | Genome-wide end-sequenced BAC resources for the NOD/MrkTacâ˜† and NOD/ShiLtJâ˜†â˜† mouse genomes. Genomics, 2010, 95, 105-110. | 2.9 | 14 |
| 13 | Petabyte-scale innovations at the European Nucleotide Archive. Nucleic Acids Research, 2009, 37, D19-D25. | 14.5 | 82 |
| 14 | Priorities for nucleotide trace, sequence and annotation data capture at the Ensembl Trace Archive and the EMBL Nucleotide Sequence Database. Nucleic Acids Research, 2007, 36, D5-D12. | 14.5 | 46 |
| 15 | Complex haplotypes, copy number polymorphisms and coding variation in two recently divergent mouse strains. Nature Genetics, 2005, 37, 532-536. | 21.4 | 66 |
| 16 | Transcriptome analysis for the chicken based on 19,626 finished cDNA sequences and 485,337 expressed sequence tags. Genome Research, 2005, 15, 174-183. | 5.5 | 79 |
| 17 | Shotgun haplotyping: a novel method for surveying allelic sequence variation. Nucleic Acids Research, 2005, 33, e152-e152. | 14.5 | 7 |
| 18 | A genome-wide, end-sequenced 129Sv BAC library resource for targeting vector construction. Genomics, 2005, 86, 753-758. | 2.9 | 105 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716. | 27.8 | 2,421 |
| 20 | Managing Sequencing Projects in the GAP4 Environment. , 2003, , 327-344. | | 9 |
| 21 | ZTR: a new format for DNA sequence trace data. Bioinformatics, 2002, 18, 3-10. | 4.1 | 26 |
| 22 | Sequence Assembly and Finishing Methods. Methods of Biochemical Analysis, 2002, 43, 303-322. | 0.2 | 48 |
| 23 | Trev: a DNA trace editor and viewer. Bioinformatics, 2002, 18, 194-195. | 4.1 | 16 |
| 24 | The Staden Package, 1998. , 2000, 132, 115-130. | | 881 |
| 25 | Automated detection of point mutations using fluorescent sequence trace subtraction. Nucleic Acids Research, 1998, 26, 3404-3409. | 14.5 | 68 |
| 26 | Experiment files and their application during large-scale sequencing projects. DNA Sequence, 1996, 6, 109-117. | 0.7 | 81 |
| 27 | The application of numerical estimates of base calling accuracy to DNA sequencing projects. Nucleic Acids Research, 1995, 23, 1406-1410. | 14.5 | 37 |
| 28 | A new DNA sequence assembly program. Nucleic Acids Research, 1995, 23, 4992-4999. | 14.5 | 842 |
| 29 | 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans. Nature, 1994, 368, 32-38. | 27.8 | 1,578 |