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	Twelve years of SAMtools and BCFtools. GigaScience, 2021, 10, .	6.4	4,546
2	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	27.8	2,421
3	2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans. Nature, 1994, 368, 32-38.	27.8	1,578
4	The Staden Package, 1998. , 2000, 132, 115-130.		881
5	A new DNA sequence assembly program. Nucleic Acids Research, 1995, 23, 4992-4999.	14.5	842
6	Gap5â€”editing the billion fragment sequence assembly. Bioinformatics, 2010, 26, 1699-1703.	4.1	214
7	HTSlib: C library for reading/writing high-throughput sequencing data. GigaScience, 2021, 10, .	6.4	191
8	Compression of FASTQ and SAM Format Sequencing Data. PLoS ONE, 2013, 8, e59190.	2.5	167
9	De novo yeast genome assemblies from MinION, PacBio and MiSeq platforms. Scientific Reports, 2017, 7, 3935.	3.3	146
10	A genome-wide, end-sequenced 129Sv BAC library resource for targeting vector construction. Genomics, 2005, 86, 753-758.	2.9	105
11	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	6.5	94
12	Comparison of high-throughput sequencing data compression tools. Nature Methods, 2016, 13, 1005-1008.	19.0	91
13	Petabyte-scale innovations at the European Nucleotide Archive. Nucleic Acids Research, 2009, 37, D19-D25.	14.5	82
14	Experiment files and their application during large-scale sequencing projects. DNA Sequence, 1996, 6, 109-117.	0.7	81
15	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
16	Automated detection of point mutations using fluorescent sequence trace subtraction. Nucleic Acids Research, 1998, 26, 3404-3409.	14.5	68
17	Improvements to services at the European Nucleotide Archive. Nucleic Acids Research, 2010, 38, D39-D45.	14.5	67
18	Complex haplotypes, copy number polymorphisms and coding variation in two recently divergent mouse strains. Nature Genetics, 2005, 37, 532-536.	21.4	66

#	Article	IF	Citations
19	Sequence Assembly and Finishing Methods. Methods of Biochemical Analysis, 2002, 43, 303-322.	0.2	48
20	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
21	The Scramble conversion tool. Bioinformatics, 2014, 30, 2818-2819.	4.1	45
22	The application of numerical estimates of base calling accuracy to DNA sequencing projects. Nucleic Acids Research, 1995, 23, 1406-1410.	14.5	37
23	ZTR: a new format for DNA sequence trace data. Bioinformatics, 2002, 18, 3-10.	4.1	26
24	Crumble: reference free lossy compression of sequence quality values. Bioinformatics, 2019, 35, 337-339.	4.1	21
25	Trev: a DNA trace editor and viewer. Bioinformatics, 2002, 18, 194-195.	4.1	16
26	Genome-wide end-sequenced BAC resources for the NOD/MrkTacâ˜† and NOD/ShiLtJâ˜†â˜† mouse genomes. Genomics, 2010, 95, 105-110.	2.9	14
27	CRAM 3.1: advances in the CRAM file format. Bioinformatics, 2022, 38, 1497-1503.	4.1	12
28	Managing Sequencing Projects in the GAP4 Environment. , 2003, , 327-344.		9
29	Shotgun haplotyping: a novel method for surveying allelic sequence variation. Nucleic Acids Research, 2005, 33, e152-e152.	14.5	7