

Brian P Walenz

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

35,131
citations

186209

28
h-index

454834

30
g-index

38
all docs

38
docs citations

38
times ranked

36597
citing authors

#	ARTICLE	IF	CITATIONS
1	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation. Nature Methods, 2022, 19, 696-704.	9.0	30
2	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
3	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	13.7	1,139
4	Weighted minimizer sampling improves long read mapping. Bioinformatics, 2020, 36, i111-i118.	1.8	116
5	Mercury: reference-free quality, completeness, and phasing assessment for genome assemblies. Genome Biology, 2020, 21, 245.	3.8	975
6	HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. Genome Research, 2020, 30, 1291-1305.	2.4	440
7	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. Nature Communications, 2020, 11, 2288.	5.8	39
8	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. PLoS Computational Biology, 2019, 15, e1007273.	1.5	509
9	De novo assembly of haplotype-resolved genomes with trio binning. Nature Biotechnology, 2018, 36, 1174-1182.	9.4	352
10	Canu: scalable and accurate long-read assembly via adaptive <i>k</i> -mer weighting and repeat separation. Genome Research, 2017, 27, 722-736.	2.4	5,620
11	The Atlantic salmon genome provides insights into rediploidization. Nature, 2016, 533, 200-205.	13.7	1,021
12	The Genome of Anopheles darlingi , the main neotropical malaria vector. Nucleic Acids Research, 2013, 41, 7387-7400.	6.5	102
13	A Rickettsia Genome Overrun by Mobile Genetic Elements Provides Insight into the Acquisition of Genes Characteristic of an Obligate Intracellular Lifestyle. Journal of Bacteriology, 2012, 194, 376-394.	1.0	152
14	The bonobo genome compared with the chimpanzee and human genomes. Nature, 2012, 486, 527-531.	13.7	445
15	Hybrid error correction and de novo assembly of single-molecule sequencing reads. Nature Biotechnology, 2012, 30, 693-700.	9.4	946
16	Genetic diversity and population structure of the endangered marsupial <i>Sarcophilus harrisii</i> (Tasmanian devil). Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12348-12353.	3.3	189
17	The dynamic genome of Hydra. Nature, 2010, 464, 592-596.	13.7	743
18	Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12168-12173.	3.3	482

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19	Genetic Variation in an Individual Human Exome. PLoS Genetics, 2008, 4, e1000160.	1.5	248
20	Aggressive assembly of pyrosequencing reads with mates. Bioinformatics, 2008, 24, 2818-2824.	1.8	498
21	The Diploid Genome Sequence of an Individual Human. PLoS Biology, 2007, 5, e254.	2.6	1,491
22	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	6.0	1,283
23	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	13.7	1,886
24	A Space-Efficient Construction of the Burrowsâ€“Wheeler Transform for Genomic Data. Journal of Computational Biology, 2005, 12, 943-951.	0.8	28
25	A Tool for Analyzing Mate Pairs in Assemblies (TAMPA). Journal of Computational Biology, 2005, 12, 497-513.	0.8	19
26	Gene and alternative splicing annotation with AIR. Genome Research, 2005, 15, 54-66.	2.4	70
27	Whole-genome shotgun assembly and comparison of human genome assemblies. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1916-1921.	3.3	164
28	1001 Optimal PDB Structure Alignments: Integer Programming Methods for Finding the Maximum Contact Map Overlap. Journal of Computational Biology, 2004, 11, 27-52.	0.8	138
29	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . Science, 2002, 298, 129-149.	6.0	1,859
30	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	6.0	12,623