Brian P Walenz

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1643984/publications.pdf

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	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	6.0	12,623
2	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
3	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	13.7	1,886
4	The Genome Sequence of the Malaria MosquitoAnopheles gambiae. Science, 2002, 298, 129-149.	6.0	1,859
5	The Diploid Genome Sequence of an Individual Human. PLoS Biology, 2007, 5, e254.	2.6	1,491
6	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	6.0	1,283
7	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
8	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	13.7	1,139
9	The Atlantic salmon genome provides insights into rediploidization. Nature, 2016, 533, 200-205.	13.7	1,021
10	Merqury: reference-free quality, completeness, and phasing assessment for genome assemblies. Genome Biology, 2020, 21, 245.	3.8	975
11	Hybrid error correction and de novo assembly of single-molecule sequencing reads. Nature Biotechnology, 2012, 30, 693-700.	9.4	946
12	The dynamic genome of Hydra. Nature, 2010, 464, 592-596.	13.7	743
13	Integrating Hi-C links with assembly graphs for chromosome-scale assembly. PLoS Computational Biology, 2019, 15, e1007273.	1.5	509
14	Aggressive assembly of pyrosequencing reads with mates. Bioinformatics, 2008, 24, 2818-2824.	1.8	498
15	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
16	The bonobo genome compared with the chimpanzee and human genomes. Nature, 2012, 486, 527-531.	13.7	445
17	HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. Genome Research, 2020, 30, 1291-1305.	2.4	440
18	De novo assembly of haplotype-resolved genomes with trio binning. Nature Biotechnology, 2018, 36, 1174-1182.	9.4	352

#	ARTICLE	IF	CITATIONS
19	Genetic Variation in an Individual Human Exome. PLoS Genetics, 2008, 4, e1000160.	1.5	248
20	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
21	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
22	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
23	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
24	Weighted minimizer sampling improves long read mapping. Bioinformatics, 2020, 36, i111-i118.	1.8	116
25	The Genome of Anopheles darlingi , the main neotropical malaria vector. Nucleic Acids Research, 2013, 41, 7387-7400.	6.5	102
26	Gene and alternative splicing annotation with AIR. Genome Research, 2005, 15, 54-66.	2.4	70
27	Effect of sequence depth and length in long-read assembly of the maize inbred NC358. Nature Communications, 2020, 11, 2288.	5.8	39
28	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation. Nature Methods, 2022, 19, 696-704.	9.0	30
29	A Space-Efficient Construction of the Burrowsâ€“Wheeler Transform for Genomic Data. Journal of Computational Biology, 2005, 12, 943-951.	0.8	28
30	A Tool for Analyzing Mate Pairs in Assemblies (TAMPA). Journal of Computational Biology, 2005, 12, 497-513.	0.8	19