Francoise Thibaud-Nissen

List of Publications by Year
in descending order

28 papers	15,231 citations	236925 25 h-index	501196 28 g-index
34 all docs	34 docs citations	34 times ranked	24232 citing authors

#	Article	IF	Citations
1	Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Research, 2016, 44, D733-D745.	14.5	4,739
2	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
3	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	27.8	1,139
4	Araport11: a complete reannotation of the Arabidopsis thaliana reference genome. Plant Journal, 2017, 89, 789-804.	5.7	925
5	RefSeq: an update on mammalian reference sequences. Nucleic Acids Research, 2014, 42, D756-D763.	14.5	892
6	Database resources of the national center for biotechnology information. Nucleic Acids Research, 2022, 50, D20-D26.	14.5	887
7	RefSeq: an update on prokaryotic genome annotation and curation. Nucleic Acids Research, 2018, 46, D851-D860.	14.5	749
8	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. Genome Research, 2017, 27, 849-864.	5.5	728
9	Telomere-to-telomere assembly of a complete human X chromosome. Nature, 2020, 585, 79-84.	27.8	549
10	RefSeq: expanding the Prokaryotic Genome Annotation Pipeline reach with protein family model curation. Nucleic Acids Research, 2021, 49, D1020-D1028.	14.5	519
11	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2020, 48, D9-D16.	14.5	381
12	De novo assembly of the cattle reference genome with single-molecule sequencing. GigaScience, 2020, 9, .	6.4	380
13	Assembly: a resource for assembled genomes at NCBI. Nucleic Acids Research, 2016, 44, D73-D80.	14.5	292
14	Long-read sequencing and de novo assembly of a Chinese genome. Nature Communications, 2016, 7, 12065.	12.8	242
15	A New Chicken Genome Assembly Provides Insight into Avian Genome Structure. G3: Genes, Genomes, Genetics, 2017, 7, 109-117.	1.8	228
16	The Egyptian Rousette Genome Reveals Unexpected Features of Bat Antiviral Immunity. Cell, 2018, 173, 1098-1110.e18.	28.9	220
17	A joint NCBI and EMBL-EBI transcript set for clinical genomics and research. Nature, 2022, 604, 310-315.	27.8	162
18	Chromosome-level assembly of the water buffalo genome surpasses human and goat genomes in sequence contiguity. Nature Communications, 2019, 10, 260.	12.8	161

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19	The genome of the vervet (Chlorocebus aethiops sabaeus). Genome Research, 2015, 25, 1921-1933.	5.5	114
20	Population genomics of the critically endangered kÄkÄpÅ. Cell Genomics, 2021, 1, 100002.	6.5	106
21	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. Nature Communications, 2020, 11, 2071.	12.8	84
22	Improved reference genome of the arboviral vector Aedes albopictus. Genome Biology, 2020, 21, 215.	8.8	65
23	Genome assembly and transcriptome resource for river buffalo, Bubalus bubalis (2n = 50). GigaScience, 2017, 6, 1-6.	6.4	55
24	The Genome of C57BL/6J â€œEveâ€ the Mother of the Laboratory Mouse Genome Reference Strain. G3: Genes, Genomes, Genetics, 2019, 9, 1795-1805.	1.8	49
25	A high-quality bonobo genome refines the analysis of hominid evolution. Nature, 2021, 594, 77-81.	27.8	39
26	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	33
27	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation. Nature Methods, 2022, 19, 696-704.	19.0	30
28	A guinea fowl genome assembly provides new evidence on evolution following domestication and selection in galliformes. Molecular Ecology Resources, 2019, 19, 997-1014.	4.8	24