

Giulio Formenti

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6010650/publications.pdf>

Version: 2024-02-01

17
papers

3,460
citations

759233

12
h-index

940533

16
g-index

32
all docs

32
docs citations

32
times ranked

2580
citing authors

#	ARTICLE	IF	CITATIONS
1	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
2	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	27.8	1,139
3	Long walk to genomics: History and current approaches to genome sequencing and assembly. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 9-19.	4.1	171
4	The era of reference genomes in conservation genomics. <i>Trends in Ecology and Evolution</i> , 2022, 37, 197-202.	8.7	138
5	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	124
6	Population genomics of the critically endangered kākāpō. <i>Cell Genomics</i> , 2021, 1, 100002.	6.5	106
7	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. <i>Genome Biology</i> , 2021, 22, 120.	8.8	69
8	Reference genome and demographic history of the most endangered marine mammal, the vaquita. <i>Molecular Ecology Resources</i> , 2021, 21, 1008-1020.	4.8	54
9	Evolutionary and biomedical insights from a marmoset diploid genome assembly. <i>Nature</i> , 2021, 594, 227-233.	27.8	42
10	Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. <i>Nature Methods</i> , 2022, 19, 687-695.	19.0	42
11	Merfin: improved variant filtering, assembly evaluation and polishing via k-mer validation. <i>Nature Methods</i> , 2022, 19, 696-704.	19.0	30
12	SMRT long reads and Direct Label and Stain optical maps allow the generation of a high-quality genome assembly for the European barn swallow (<i>Hirundo rustica rustica</i>). <i>GigaScience</i> , 2019, 8, .	6.4	23
13	Gfastats: conversion, evaluation and manipulation of genome sequences using assembly graphs. <i>Bioinformatics</i> , 2022, 38, 4214-4216.	4.1	14
14	Inter-generational resemblance of methylation levels at circadian genes and associations with phenology in the barn swallow. <i>Scientific Reports</i> , 2019, 9, 6505.	3.3	8
15	Hi-C scaffolded short- and long-read genome assemblies of the California sea lion are broadly consistent for syntenic inference across 45 million years of evolution. <i>Molecular Ecology Resources</i> , 2021, 21, 2455-2470.	4.8	7
16	The Mitogenome Relationships and Phylogeography of Barn Swallows (<i>Hirundo rustica</i>). <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	4
17	The genome sequence of the European nightjar, <i>Caprimulgus europaeus</i> (Linnaeus, 1758). <i>Wellcome Open Research</i> , 2021, 6, 332.	1.8	0