

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