

# Olivier Fedrigo

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5482876/publications.pdf>

Version: 2024-02-01

30  
papers

2,873  
citations

471509

17  
h-index

454955

30  
g-index

47  
all docs

47  
docs citations

47  
times ranked

3351  
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	A high-quality, long-read genome assembly of the endangered ring-tailed lemur ( <i>Lemur catta</i> ). GigaScience, 2022, 11, .	6.4	1
3	Induction of an immortalized songbird cell line allows for gene characterization and knockout by CRISPR-Cas9. Scientific Reports, 2022, 12, 4369.	3.3	5
4	Single-nuclei isoform RNA sequencing unlocks barcoded exon connectivity in frozen brain tissue. Nature Biotechnology, 2022, 40, 1082-1092.	17.5	52
5	Haplotype-resolved assembly of diploid genomes without parental data. Nature Biotechnology, 2022, 40, 1332-1335.	17.5	139
6	Gfastats: conversion, evaluation and manipulation of genome sequences using assembly graphs. Bioinformatics, 2022, 38, 4214-4216.	4.1	14
7	Reference genome and demographic history of the most endangered marine mammal, the vaquita. Molecular Ecology Resources, 2021, 21, 1008-1020.	4.8	54
8	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. Nature Communications, 2021, 12, 463.	12.8	109
9	Evolutionary and biomedical insights from a marmoset diploid genome assembly. Nature, 2021, 594, 227-233.	27.8	42
10	Extended haplotype-phasing of long-read de novo genome assemblies using Hi-C. Nature Communications, 2021, 12, 1935.	12.8	64
11	Variation in predicted COVID-19 risk among lemurs and lorises. American Journal of Primatology, 2021, 83, e23255.	1.7	7
12	Complete vertebrate mitogenomes reveal widespread repeats and gene duplications. Genome Biology, 2021, 22, 120.	8.8	69
13	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	27.8	1,139
14	The genome sequence of the brown trout, <i>Salmo trutta</i> Linnaeus 1758. Wellcome Open Research, 2021, 6, 108.	1.8	15
15	As above, so below: Whole transcriptome profiling demonstrates strong molecular similarities between avian dorsal and ventral pallial subdivisions. Journal of Comparative Neurology, 2021, 529, 3222-3246.	1.6	15
16	Population genomics of the critically endangered kakapo. Cell Genomics, 2021, 1, 100002.	6.5	106
17	Platypus and echidna genomes reveal mammalian biology and evolution. Nature, 2021, 592, 756-762.	27.8	85
18	A high-quality genome and comparison of short- versus long-read transcriptome of the palaeartic duck <i>Aythya fuligula</i> (tufted duck). GigaScience, 2021, 10, .	6.4	7

#	ARTICLE	IF	CITATIONS
19	Six reference-quality genomes reveal evolution of bat adaptations. <i>Nature</i> , 2020, 583, 578-584.	27.8	210
20	Building genomic infrastructure: Sequencing platinum-standard reference-quality genomes of all cetacean species. <i>Marine Mammal Science</i> , 2020, 36, 1356-1366.	1.8	10
21	Comprehensive identification of mRNA isoforms reveals the diversity of neural cell-surface molecules with roles in retinal development and disease. <i>Nature Communications</i> , 2020, 11, 3328.	12.8	69
22	The genome sequence of the Eurasian red squirrel, <i>Sciurus vulgaris</i> Linnaeus 1758. <i>Wellcome Open Research</i> , 2020, 5, 18.	1.8	3
23	Single-cell isoform RNA sequencing characterizes isoforms in thousands of cerebellar cells. <i>Nature Biotechnology</i> , 2018, 36, 1197-1202.	17.5	253
24	Comparative expression analysis of the phosphocreatine circuit in extant primates: Implications for human brain evolution. <i>Journal of Human Evolution</i> , 2011, 60, 205-212.	2.6	25
25	A Potential Role for Glucose Transporters in the Evolution of Human Brain Size. <i>Brain, Behavior and Evolution</i> , 2011, 78, 315-326.	1.7	28
26	Developmental Evolution: How Beetles Evolved Their Shields. <i>Current Biology</i> , 2010, 20, R64-R66.	3.9	7
27	A Pipeline to Determine RT-QPCR Control Genes for Evolutionary Studies: Application to Primate Gene Expression across Multiple Tissues. <i>PLoS ONE</i> , 2010, 5, e12545.	2.5	25
28	Reply to "Rapidly evolving human promoter regions". <i>Nature Genetics</i> , 2008, 40, 1263-1264.	21.4	1
29	Promoter regions of many neural- and nutrition-related genes have experienced positive selection during human evolution. <i>Nature Precedings</i> , 2007, , .	0.1	2
30	DRUIDS?Detection of regions with unexpected internal deviation from stationarity. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2005, 304B, 119-128.	1.3	6