

Matthieu Muffato

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6157005/publications.pdf>

Version: 2024-02-01

35
papers

20,572
citations

159525

30
h-index

302012

39
g-index

43
all docs

43
docs citations

43
times ranked

40661
citing authors

#	ARTICLE	IF	CITATIONS
1	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , 2013, 496, 498-503.	13.7	3,708
2	Ensembl 2018. <i>Nucleic Acids Research</i> , 2018, 46, D754-D761.	6.5	2,710
3	Ensembl 2016. <i>Nucleic Acids Research</i> , 2016, 44, D710-D716.	6.5	1,372
4	Ensembl 2021. <i>Nucleic Acids Research</i> , 2021, 49, D884-D891.	6.5	1,231
5	Ensembl 2014. <i>Nucleic Acids Research</i> , 2014, 42, D749-D755.	6.5	1,211
6	Ensembl 2015. <i>Nucleic Acids Research</i> , 2015, 43, D662-D669.	6.5	1,145
7	Ensembl 2022. <i>Nucleic Acids Research</i> , 2022, 50, D988-D995.	6.5	1,103
8	Ensembl 2020. <i>Nucleic Acids Research</i> , 2020, 48, D682-D688.	6.5	1,076
9	Ensembl 2019. <i>Nucleic Acids Research</i> , 2019, 47, D745-D751.	6.5	879
10	Ensembl 2013. <i>Nucleic Acids Research</i> , 2012, 41, D48-D55.	6.5	856
11	Ensembl 2012. <i>Nucleic Acids Research</i> , 2012, 40, D84-D90.	6.5	840
12	Sequencing of the sea lamprey (<i>Petromyzon marinus</i>) genome provides insights into vertebrate evolution. <i>Nature Genetics</i> , 2013, 45, 415-421.	9.4	588
13	Ensembl 2017. <i>Nucleic Acids Research</i> , 2017, 45, D635-D642.	6.5	535
14	Ensembl Genomes 2020â€”enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020, 48, D689-D695.	6.5	416
15	Ensembl comparative genomics resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav096.	1.4	344
16	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	13.7	320
17	Plasticity of Animal Genome Architecture Unmasked by Rapid Evolution of a Pelagic Tunicate. <i>Science</i> , 2010, 330, 1381-1385.	6.0	251
18	Genomicus: a database and a browser to study gene synteny in modern and ancestral genomes. <i>Bioinformatics</i> , 2010, 26, 1119-1121.	1.8	236

#	ARTICLE	IF	CITATIONS
19	Current Methods for Automated Filtering of Multiple Sequence Alignments Frequently Worsen Single-Gene Phylogenetic Inference. <i>Systematic Biology</i> , 2015, 64, 778-791.	2.7	200
20	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016, 13, 425-430.	9.0	198
21	Genomicus: five genome browsers for comparative genomics in eukaryota. <i>Nucleic Acids Research</i> , 2012, 41, D700-D705.	6.5	141
22	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. <i>Nucleic Acids Research</i> , 2022, 50, D996-D1003.	6.5	141
23	TreeFam v9: a new website, more species and orthology-on-the-fly. <i>Nucleic Acids Research</i> , 2014, 42, D922-D925.	6.5	125
24	The comparative genomics and complex population history of <i>Papio</i> baboons. <i>Science Advances</i> , 2019, 5, eaau6947.	4.7	115
25	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020, 584, 403-409.	13.7	105
26	Genomicus update 2015: KaryoView and MatrixView provide a genome-wide perspective to multispecies comparative genomics. <i>Nucleic Acids Research</i> , 2015, 43, D682-D689.	6.5	100
27	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes. <i>Genome Research</i> , 2018, 28, 448-459.	2.4	99
28	The 3D Organization of Chromatin Explains Evolutionary Fragile Genomic Regions. <i>Cell Reports</i> , 2015, 10, 1913-1924.	2.9	52
29	The Quest for Orthologs benchmark service and consensus calls in 2020. <i>Nucleic Acids Research</i> , 2020, 48, W538-W545.	6.5	41
30	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	1.8	36
31	Paleogenomics in vertebrates, or the recovery of lost genomes from the mist of time. <i>BioEssays</i> , 2008, 30, 122-134.	1.2	35
32	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. <i>Genome Biology and Evolution</i> , 2015, 7, 1988-1999.	1.1	25
33	ncRNA orthologies in the vertebrate lineage. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav127.	1.4	19
34	PhylDiag: identifying complex synteny blocks that include tandem duplications using phylogenetic gene trees. <i>BMC Bioinformatics</i> , 2014, 15, 268.	1.2	10
35	Scripting Analyses of Genomes in Ensembl Plants. <i>Methods in Molecular Biology</i> , 2022, 2443, 27-55.	0.4	6