

Matthieu Muffato

List of Publications by Citations

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Version: 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

36
papers

13,753
citations

30
h-index

43
g-index

43
ext. papers

18,176
ext. citations

18.2
avg, IF

5.16
L-index

#	Paper	IF	Citations
36	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , 2013 , 496, 498-503	50.4	2550
35	Ensembl 2018. <i>Nucleic Acids Research</i> , 2018 , 46, D754-D761	20.1	1822
34	Ensembl 2016. <i>Nucleic Acids Research</i> , 2016 , 44, D710-6	20.1	1094
33	Ensembl 2014. <i>Nucleic Acids Research</i> , 2014 , 42, D749-55	20.1	1087
32	Ensembl 2015. <i>Nucleic Acids Research</i> , 2015 , 43, D662-9	20.1	1013
31	Ensembl 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D84-90	20.1	798
30	Ensembl 2013. <i>Nucleic Acids Research</i> , 2013 , 41, D48-55	20.1	797
29	Ensembl 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D682-D688	20.1	645
28	Ensembl 2019. <i>Nucleic Acids Research</i> , 2019 , 47, D745-D751	20.1	554
27	Sequencing of the sea lamprey (<i>Petromyzon marinus</i>) genome provides insights into vertebrate evolution. <i>Nature Genetics</i> , 2013 , 45, 415-21, 421e1-2	36.3	465
26	Ensembl 2017. <i>Nucleic Acids Research</i> , 2017 , 45, D635-D642	20.1	404
25	Ensembl 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D884-D891	20.1	324
24	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014 , 513, 195-201	50.4	241
23	Ensembl Genomes 2020-enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020 , 48, D689-D695	20.1	214
22	Plasticity of animal genome architecture unmasked by rapid evolution of a pelagic tunicate. <i>Science</i> , 2010 , 330, 1381-5	33.3	212
21	Ensembl comparative genomics resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	186
20	Genomicus: a database and a browser to study gene synteny in modern and ancestral genomes. <i>Bioinformatics</i> , 2010 , 26, 1119-21	7.2	182

19	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016 , 13, 425-30	21.6	133
18	Current Methods for Automated Filtering of Multiple Sequence Alignments Frequently Worsen Single-Gene Phylogenetic Inference. <i>Systematic Biology</i> , 2015 , 64, 778-91	8.4	129
17	Genomicus: five genome browsers for comparative genomics in eukaryota. <i>Nucleic Acids Research</i> , 2013 , 41, D700-5	20.1	128
16	TreeFam v9: a new website, more species and orthology-on-the-fly. <i>Nucleic Acids Research</i> , 2014 , 42, D922-5	20.1	96
15	Genomicus update 2015: KaryoView and MatrixView provide a genome-wide perspective to multispecies comparative genomics. <i>Nucleic Acids Research</i> , 2015 , 43, D682-9	20.1	86
14	Ensembl 2022. <i>Nucleic Acids Research</i> , 2021 ,	20.1	72
13	The comparative genomics and complex population history of baboons. <i>Science Advances</i> , 2019 , 5, eaau6947	6.4	69
12	Repeat associated mechanisms of genome evolution and function revealed by the and genomes. <i>Genome Research</i> , 2018 , 28, 448-459	9.7	57
11	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020 , 584, 403-409	50.4	49
10	The 3D organization of chromatin explains evolutionary fragile genomic regions. <i>Cell Reports</i> , 2015 , 10, 1913-24	10.6	36
9	Paleogenomics in vertebrates, or the recovery of lost genomes from the mist of time. <i>BioEssays</i> , 2008 , 30, 122-34	4.1	34
8	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018 , 34, 323-329	2.9	25
7	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. <i>Genome Biology and Evolution</i> , 2015 , 7, 1988-99	3.9	19
6	The Quest for Orthologs benchmark service and consensus calls in 2020. <i>Nucleic Acids Research</i> , 2020 , 48, W538-W545	20.1	17
5	ncRNA orthologies in the vertebrate lineage. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	14
4	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. <i>Nucleic Acids Research</i> , 2021 ,	20.1	12
3	PhylDiag: identifying complex synteny blocks that include tandem duplications using phylogenetic gene trees. <i>BMC Bioinformatics</i> , 2014 , 15, 268	3.6	8
2	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes		3

1 Scripting Analyses of Genomes in Ensembl Plants.. *Methods in Molecular Biology*, **2022**, 2443, 27-55 1.4 ○