

Fergal J Martin

List of Publications by Citations

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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.

30
papers

9,429
citations

22
h-index

36
g-index

36
ext. papers

14,280
ext. citations

17.6
avg, IF

4.86
L-index

#	Paper	IF	Citations
30	Ensembl 2018. <i>Nucleic Acids Research</i> , 2018 , 46, D754-D761	20.1	1822
29	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019 , 47, D766-D773	20.1	1140
28	Ensembl 2016. <i>Nucleic Acids Research</i> , 2016 , 44, D710-6	20.1	1094
27	Ensembl 2014. <i>Nucleic Acids Research</i> , 2014 , 42, D749-55	20.1	1087
26	Ensembl 2015. <i>Nucleic Acids Research</i> , 2015 , 43, D662-9	20.1	1013
25	Ensembl 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D682-D688	20.1	645
24	Ensembl 2019. <i>Nucleic Acids Research</i> , 2019 , 47, D745-D751	20.1	554
23	The Ensembl gene annotation system. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	537
22	Ensembl 2017. <i>Nucleic Acids Research</i> , 2017 , 45, D635-D642	20.1	404
21	Ensembl 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D884-D891	20.1	324
20	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746	64.4	161
19	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D916-D923	20.1	82
18	Ensembl 2022. <i>Nucleic Acids Research</i> , 2021 ,	20.1	72
17	The comparative genomics and complex population history of baboons. <i>Science Advances</i> , 2019 , 5, eaau6947	64.7	69
16	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020 , 9,	7.6	60
15	Repeat associated mechanisms of genome evolution and function revealed by the and genomes. <i>Genome Research</i> , 2018 , 28, 448-459	9.7	57
14	A chromosome-level assembly of the Atlantic herring genome-detection of a supergene and other signals of selection. <i>Genome Research</i> , 2019 , 29, 1919-1928	9.7	49

13	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020 , 584, 403-409	50.4	49
12	Consensus coding sequence (CCDS) database: a standardized set of human and mouse protein-coding regions supported by expert curation. <i>Nucleic Acids Research</i> , 2018 , 46, D221-D228	20.1	46
11	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. <i>Nature Communications</i> , 2020 , 11, 2071	17.4	38
10	Towards complete and error-free genome assemblies of all vertebrate species		38
9	Divergence in gene expression within and between two closely related flycatcher species. <i>Molecular Ecology</i> , 2016 , 25, 2015-28	5.7	37
8	An improved pig reference genome sequence to enable pig genetics and genomics research		15
7	Population genomics of the critically endangered kakapo. <i>Cell Genomics</i> , 2021 , 100002		15
6	LINE retrotransposons characterize mammalian tissue-specific and evolutionarily dynamic regulatory regions. <i>Genome Biology</i> , 2021 , 22, 62	18.3	9
5	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes		3
4	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , 2021 ,	20.1	3
3	Accessing Livestock Resources in Ensembl. <i>Frontiers in Genetics</i> , 2021 , 12, 650228	4.5	2
2	Three chromosome-level duck genome assemblies provide insights into genomic variation during domestication. <i>Nature Communications</i> , 2021 , 12, 5932	17.4	1
1	Gaur genome reveals expansion of sperm odorant receptors in domesticated cattle.. <i>BMC Genomics</i> , 2022 , 23, 344	4.5	0