

Fergal J Martin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3195889/publications.pdf>

Version: 2024-02-01

27
papers

17,463
citations

279487

23
h-index

525886

27
g-index

36
all docs

36
docs citations

36
times ranked

36112
citing authors

#	ARTICLE	IF	CITATIONS
1	Ensembl 2018. Nucleic Acids Research, 2018, 46, D754-D761.	6.5	2,710
2	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	6.5	2,350
3	Ensembl 2016. Nucleic Acids Research, 2016, 44, D710-D716.	6.5	1,372
4	Ensembl 2021. Nucleic Acids Research, 2021, 49, D884-D891.	6.5	1,231
5	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	6.5	1,211
6	Ensembl 2015. Nucleic Acids Research, 2015, 43, D662-D669.	6.5	1,145
7	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	13.7	1,139
8	Ensembl 2022. Nucleic Acids Research, 2022, 50, D988-D995.	6.5	1,103
9	Ensembl 2020. Nucleic Acids Research, 2020, 48, D682-D688.	6.5	1,076
10	The Ensembl gene annotation system. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw093.	1.4	912
11	Ensembl 2019. Nucleic Acids Research, 2019, 47, D745-D751.	6.5	879
12	GENCODE 2021. Nucleic Acids Research, 2021, 49, D916-D923.	6.5	633
13	Ensembl 2017. Nucleic Acids Research, 2017, 45, D635-D642.	6.5	535
14	An improved pig reference genome sequence to enable pig genetics and genomics research. GigaScience, 2020, 9, .	3.3	187
15	The comparative genomics and complex population history of <i>Papio</i> baboons. Science Advances, 2019, 5, eaau6947.	4.7	115
16	Population genomics of the critically endangered <i>Arctophila</i> . Cell Genomics, 2021, 1, 100002.	3.0	106
17	The tuatara genome reveals ancient features of amniote evolution. Nature, 2020, 584, 403-409.	13.7	105
18	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes. Genome Research, 2018, 28, 448-459.	2.4	99

#	ARTICLE	IF	CITATIONS
19	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.	6.5	97
20	A chromosome-level assembly of the Atlantic herring genomeâ€”detection of a supergene and other signals of selection. <i>Genome Research</i> , 2019, 29, 1919-1928.	2.4	84
21	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. <i>Nature Communications</i> , 2020, 11, 2071.	5.8	84
22	Divergence in gene expression within and between two closely related flycatcher species. <i>Molecular Ecology</i> , 2016, 25, 2015-2028.	2.0	57
23	LINE retrotransposons characterize mammalian tissue-specific and evolutionarily dynamic regulatory regions. <i>Genome Biology</i> , 2021, 22, 62.	3.8	38
24	Three chromosome-level duck genome assemblies provide insights into genomic variation during domestication. <i>Nature Communications</i> , 2021, 12, 5932.	5.8	27
25	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , 2022, 50, D765-D770.	6.5	10
26	Accessing Livestock Resources in Ensembl. <i>Frontiers in Genetics</i> , 2021, 12, 650228.	1.1	3
27	Gaur genome reveals expansion of sperm odorant receptors in domesticated cattle. <i>BMC Genomics</i> , 2022, 23, 344.	1.2	3