Fabio Madeira

List of Publications by Year
in descending order

18 papers	17,654 citations	623574 14 h-index	887953 17 g-index
21 all docs	21 docs citations	21 times ranked	31582 citing authors

#	Article	IF	Citations
1	The European Nucleotide Archive in 2021. Nucleic Acids Research, 2022, 50, D106-D110.	6.5	62
2	Search and sequence analysis tools services from EMBL-EBI in 2022. Nucleic Acids Research, 2022, 50, W276-W279.	6.5	1,050
3	UniProt: the universal protein knowledgebase in 2021. Nucleic Acids Research, 2021, 49, D480-D489.	6.5	4,709
4	R2DT is a framework for predicting and visualising RNA secondary structure using templates. Nature Communications, 2021, 12, 3494.	5.8	58
5	Cysteine and iron accelerate the formation of ribose-5-phosphate, providing insights into the evolutionary origins of the metabolic network structure. PLoS Biology, 2021, 19, e3001468.	2.6	14
6	PDBe-KB: a community-driven resource for structural and functional annotations. Nucleic Acids Research, 2020, 48, D344-D353.	6.5	87
7	The Dundee Resource for Sequence Analysis and Structure Prediction. Protein Science, 2020, 29, 277-297.	3.1	14
8	The EMBL-EBI search and sequence analysis tools APIs in 2019. Nucleic Acids Research, 2019, 47, W636-W641.	6.5	3,820
9	Using EMBL–EBI Services via Web Interface and Programmatically via Web Services. Current Protocols in Bioinformatics, 2019, 66, e74.	25.8	38
10	UniProt: a worldwide hub of protein knowledge. Nucleic Acids Research, 2019, 47, D506-D515.	6.5	6,185
11	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	6.5	1,291
12	JABAWS 2.2 distributed web services for Bioinformatics: protein disorder, conservation and RNA secondary structure. Bioinformatics, 2018, 34, 1939-1940.	1.8	29
13	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	0.8	27
14	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	0.8	29
15	14-3-3-Pred: improved methods to predict 14-3-3-binding phosphopeptides. Bioinformatics, 2015, 31, 2276-2283.	1.8	177
16	ANIA: ANnotation and Integrated Analysis of the 14-3-3 interactome. Database: the Journal of Biological Databases and Curation, 2014, 2014, bat085.	1.4	51
17	Constraining Protein Docking with Coevolution Data for Medical Research. Lecture Notes in Computer Science, 2013, , 110-114.	1.0	1
18	PYCOEVOL - A Python Workflow to Study Protein-protein Coevolution. , 2012, , .		0