

Fabio Madeira

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1786671/publications.pdf>

Version: 2024-02-01

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