

Milot Mirdita

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1743008/publications.pdf>

Version: 2024-02-01

14
papers

6,687
citations

623734

14
h-index

1058476

14
g-index

23
all docs

23
docs citations

23
times ranked

4317
citing authors

#	ARTICLE	IF	CITATIONS
1	ColabFold: making protein folding accessible to all. <i>Nature Methods</i> , 2022, 19, 679-682.	19.0	3,242
2	DescribePROT: database of amino acid-level protein structure and function predictions. <i>Nucleic Acids Research</i> , 2021, 49, D298-D308.	14.5	46
3	Fast and sensitive taxonomic assignment to metagenomic contigs. <i>Bioinformatics</i> , 2021, 37, 3029-3031.	4.1	110
4	SpacePHARER: sensitive identification of phages from CRISPR spacers in prokaryotic hosts. <i>Bioinformatics</i> , 2021, 37, 3364-3366.	4.1	36
5	PredictProtein - Predicting Protein Structure and Function for 29 Years. <i>Nucleic Acids Research</i> , 2021, 49, W535-W540.	14.5	135
6	Going to extremes – a metagenomic journey into the dark matter of life. <i>FEMS Microbiology Letters</i> , 2021, 368, .	1.8	16
7	MetaEuk – sensitive, high-throughput gene discovery, and annotation for large-scale eukaryotic metagenomics. <i>Microbiome</i> , 2020, 8, 48.	11.1	119
8	Protein Sequence Analysis Using the MPI Bioinformatics Toolkit. <i>Current Protocols in Bioinformatics</i> , 2020, 72, e108.	25.8	458
9	HH-suite3 for fast remote homology detection and deep protein annotation. <i>BMC Bioinformatics</i> , 2019, 20, 473.	2.6	706
10	Protein-level assembly increases protein sequence recovery from metagenomic samples manifold. <i>Nature Methods</i> , 2019, 16, 603-606.	19.0	262
11	MMseqs2 desktop and local web server app for fast, interactive sequence searches. <i>Bioinformatics</i> , 2019, 35, 2856-2858.	4.1	321
12	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. <i>Scientific Reports</i> , 2018, 8, 9939.	3.3	19
13	Uniclust databases of clustered and deeply annotated protein sequences and alignments. <i>Nucleic Acids Research</i> , 2017, 45, D170-D176.	14.5	520
14	Cloud Prediction of Protein Structure and Function with PredictProtein for Debian. <i>BioMed Research International</i> , 2013, 2013, 1-6.	1.9	16