

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