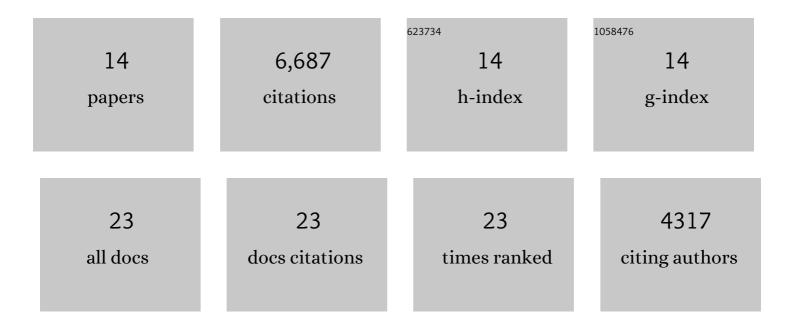
Milot Mirdita

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1743008/publications.pdf Version: 2024-02-01



Μιιότ Μιροιτλ

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