

Martin Steinegger

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1812139/publications.pdf>

Version: 2024-02-01

26
papers

28,089
citations

394421

19
h-index

552781

26
g-index

47
all docs

47
docs citations

47
times ranked

15409
citing authors

#	ARTICLE	IF	CITATIONS
1	ProtTrans: Toward Understanding the Language of Life Through Self-Supervised Learning. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2022, 44, 7112-7127.	13.9	496
2	PhyloCSF++: a fast and user-friendly implementation of PhyloCSF with annotation tools. Bioinformatics, 2022, 38, 1440-1442.	4.1	8
3	Unifying the known and unknown microbial coding sequence space. ELife, 2022, 11, .	6.0	41
4	Evolutionary balance between foldability and functionality of a glucose transporter. Nature Chemical Biology, 2022, 18, 713-723.	8.0	13
5	ColabFold: making protein folding accessible to all. Nature Methods, 2022, 19, 679-682.	19.0	3,242
6	DescribePROT: database of amino acid-level protein structure and function predictions. Nucleic Acids Research, 2021, 49, D298-D308.	14.5	46
7	Highly multiplexed oligonucleotide probe-ligation testing enables efficient extraction-free SARS-CoV-2 detection and viral genotyping. Modern Pathology, 2021, 34, 1093-1103.	5.5	12
8	Fast and sensitive taxonomic assignment to metagenomic contigs. Bioinformatics, 2021, 37, 3029-3031.	4.1	110
9	PredictProtein - Predicting Protein Structure and Function for 29 Years. Nucleic Acids Research, 2021, 49, W535-W540.	14.5	135
10	Going to extremes – a metagenomic journey into the dark matter of life. FEMS Microbiology Letters, 2021, 368, .	1.8	16
11	Highly accurate protein structure prediction with AlphaFold. Nature, 2021, 596, 583-589.	27.8	17,754
12	Accurate protein structure prediction: what comes next?. Biodesign, 2021, 9, 47-50.	0.4	25
13	Applying and improving <scp>AlphaFold</scp> at <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1711-1721.	2.6	231
14	Metagenomic Association Analysis of Gut Symbiont Limosilactobacillus reuteri Without Host-Specific Genome Isolation. Frontiers in Microbiology, 2020, 11, 585622.	3.5	4
15	Terminating contamination: large-scale search identifies more than 2,000,000 contaminated entries in GenBank. Genome Biology, 2020, 21, 115.	8.8	130
16	Protein Sequence Analysis Using the MPI Bioinformatics Toolkit. Current Protocols in Bioinformatics, 2020, 72, e108.	25.8	458
17	HH-suite3 for fast remote homology detection and deep protein annotation. BMC Bioinformatics, 2019, 20, 473.	2.6	706
18	Protein-level assembly increases protein sequence recovery from metagenomic samples manyfold. Nature Methods, 2019, 16, 603-606.	19.0	262

#	ARTICLE	IF	CITATIONS
19	MMseqs2 desktop and local web server app for fast, interactive sequence searches. <i>Bioinformatics</i> , 2019, 35, 2856-2858.	4.1	321
20	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	4.1	36
21	Clustering huge protein sequence sets in linear time. <i>Nature Communications</i> , 2018, 9, 2542.	12.8	497
22	HFSP: high speed homology-driven function annotation of proteins. <i>Bioinformatics</i> , 2018, 34, i304-i312.	4.1	22
23	Uniclust databases of clustered and deeply annotated protein sequences and alignments. <i>Nucleic Acids Research</i> , 2017, 45, D170-D176.	14.5	520
24	MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets. <i>Nature Biotechnology</i> , 2017, 35, 1026-1028.	17.5	1,879
25	MMseqs software suite for fast and deep clustering and searching of large protein sequence sets. <i>Bioinformatics</i> , 2016, 32, 1323-1330.	4.1	131
26	Cloud Prediction of Protein Structure and Function with PredictProtein for Debian. <i>BioMed Research International</i> , 2013, 2013, 1-6.	1.9	16