

# 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	Highly accurate protein structure prediction with AlphaFold. <i>Nature</i> , 2021, 596, 583-589.	27.8	17,754
2	ColabFold: making protein folding accessible to all. <i>Nature Methods</i> , 2022, 19, 679-682.	19.0	3,242
3	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
4	HH-suite3 for fast remote homology detection and deep protein annotation. <i>BMC Bioinformatics</i> , 2019, 20, 473.	2.6	706
5	Uniclust databases of clustered and deeply annotated protein sequences and alignments. <i>Nucleic Acids Research</i> , 2017, 45, D170-D176.	14.5	520
6	Clustering huge protein sequence sets in linear time. <i>Nature Communications</i> , 2018, 9, 2542.	12.8	497
7	ProtTrans: Toward Understanding the Language of Life Through Self-Supervised Learning. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2022, 44, 7112-7127.	13.9	496
8	Protein Sequence Analysis Using the MPI Bioinformatics Toolkit. <i>Current Protocols in Bioinformatics</i> , 2020, 72, e108.	25.8	458
9	MMseqs2 desktop and local web server app for fast, interactive sequence searches. <i>Bioinformatics</i> , 2019, 35, 2856-2858.	4.1	321
10	Protein-level assembly increases protein sequence recovery from metagenomic samples manyfold. <i>Nature Methods</i> , 2019, 16, 603-606.	19.0	262
11	Applying and improving <scp>AlphaFold</scp> at <scp>CASP14</scp>. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1711-1721.	2.6	231
12	PredictProtein - Predicting Protein Structure and Function for 29 Years. <i>Nucleic Acids Research</i> , 2021, 49, W535-W540.	14.5	135
13	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
14	Terminating contamination: large-scale search identifies more than 2,000,000 contaminated entries in GenBank. <i>Genome Biology</i> , 2020, 21, 115.	8.8	130
15	Fast and sensitive taxonomic assignment to metagenomic contigs. <i>Bioinformatics</i> , 2021, 37, 3029-3031.	4.1	110
16	DescribePROT: database of amino acid-level protein structure and function predictions. <i>Nucleic Acids Research</i> , 2021, 49, D298-D308.	14.5	46
17	Unifying the known and unknown microbial coding sequence space. <i>ELife</i> , 2022, 11, .	6.0	41
18	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	4.1	36

#	ARTICLE	IF	CITATIONS
19	Accurate protein structure prediction: what comes next?. <i>Biodesign</i> , 2021, 9, 47-50.	0.4	25
20	HFSP: high speed homology-driven function annotation of proteins. <i>Bioinformatics</i> , 2018, 34, i304-i312.	4.1	22
21	Cloud Prediction of Protein Structure and Function with PredictProtein for Debian. <i>BioMed Research International</i> , 2013, 2013, 1-6.	1.9	16
22	Going to extremes – a metagenomic journey into the dark matter of life. <i>FEMS Microbiology Letters</i> , 2021, 368, .	1.8	16
23	Evolutionary balance between foldability and functionality of a glucose transporter. <i>Nature Chemical Biology</i> , 2022, 18, 713-723.	8.0	13
24	Highly multiplexed oligonucleotide probe-ligation testing enables efficient extraction-free SARS-CoV-2 detection and viral genotyping. <i>Modern Pathology</i> , 2021, 34, 1093-1103.	5.5	12
25	PhyloCSF++: a fast and user-friendly implementation of PhyloCSF with annotation tools. <i>Bioinformatics</i> , 2022, 38, 1440-1442.	4.1	8
26	Metagenomic Association Analysis of Gut Symbiont <i>Limosilactobacillus reuteri</i> Without Host-Specific Genome Isolation. <i>Frontiers in Microbiology</i> , 2020, 11, 585622.	3.5	4