RESEARCH & PUBLICATIONS

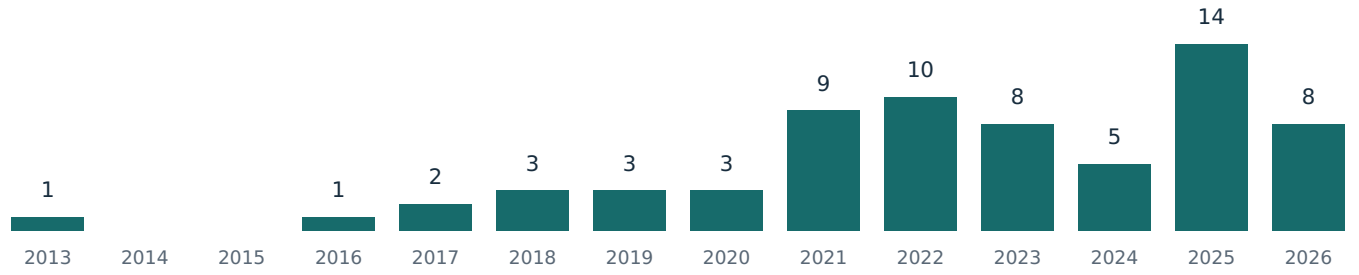
Martin Steinegger

A publication record at a glance

68	60,663	35
ARTICLES	CITATIONS	h-INDEX

PUBLICATION ACTIVITY

Articles by publication year



1 articles have no publication year in the database.

MOST CITED IN THIS LIST

Highly Accurate Protein Structure Prediction With AlphaFold — 37,559
2021 Nature

ColabFold: Making Protein Folding Accessible to All — 7,576
2022 Nature Methods

MMseqs2 Enables Sensitive Protein Sequence Searching for the Analysis of Massive Data Sets — 3,632
2017 Nature Biotechnology

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Ordered by publication year, newest first

2026

01 AlphaFold Protein Structure Database 2025: A Redesigned Interface and Updated Structural Coverage — 51 citations
Nucleic Acids Research · 54, D358-D362
https://exaly.com/article/207370594

02 Protein Structure-Informed Bacteriophage Genome Annotation With Phold — 62 citations
Nucleic Acids Research
https://exaly.com/article/208516594

03 Protein Folding Stability Estimation With Explicit Consideration of Unfolded States — 8 citations
Nature Communications
https://exaly.com/article/209512697

04 Multiple Protein Structure Alignment at Scale With FoldMason — 92 citations
Science · 391, 485-488
https://exaly.com/article/209786036

05 Structural Motif Search Across the Protein Universe With Folddisco — 7 citations
Nature Biotechnology
https://exaly.com/article/214615422

06 Accelign: A GPU-Based Library for Accelerating Pairwise Sequence Alignment — 0 citations
BMC Bioinformatics · 27, 137
https://exaly.com/article/215160444

07 Expanding the Scope of Protein Language Modeling to Protein-Protein Interactions With MSA Pairformer. — 5 citations
Cell · 189, 4964-4979.e8
https://exaly.com/article/216290189

08 Changing Minds: How AI Is Transforming the Life Sciences. — 0 citations
Cell · 189, 5909-5913
https://exaly.com/article/218390988

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09 Easy and Accurate Protein Structure Prediction Using ColabFold — 145 citations
Nature Protocols · 20, 1-23
https://exaly.com/article/193715171

10 BFVD—A Large Repository of Predicted Viral Protein Structures — 68 citations
Nucleic Acids Research · 53, D340-D347
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2025 / continued

11 **Discovery of Highly Active Kynureninases for Cancer Immunotherapy Through Protein Language Model**
Nucleic Acids Research
https://exaly.com/article/196136553
9 citations

12 **Rapid and Sensitive Protein Complex Alignment With Foldseek-Multimer**
Nature Methods · 22, 469-472
https://exaly.com/article/197464776
58 citations

13 **Cutting-Edge Deep-Learning Based Tools for Metagenomic Research**
National Science Review · 12, nwaf056
https://exaly.com/article/197984527
8 citations

14 **FunVIP: Fungal Validation and Identification Pipeline Based on Phylogenetic Analysis**
Journal of Microbiology · 63, e2411017
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11 citations

15 **Unicore Enables Scalable and Accurate Phylogenetic Reconstruction With Structural Core Genes**
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6 citations

16 **Structural Basis of the Catalytic and Allosteric Mechanism of Bacterial Acetyltransferase PatZ**
Proceedings of the National Academy of Sciences of the United States of America · 122, e2419096122
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17 **An Nf-Core Framework for the Systematic Comparison of Alternative Modeling Tools: The Multiple Sequence Alignment Case Study**
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https://exaly.com/article/203422705
1 citations

18 **GPU-Accelerated Homology Search With MMseqs2**
Nature Methods · 22, 2024-2027
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49 citations

19 **Structural Phylogenetics Unravels the Evolutionary Diversification of Communication Systems in Gram-Positive Bacteria and Their Viruses**
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20 **Easy and Interactive Taxonomic Profiling With Metabuli App**
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21 **Democratizing Protein Language Model Training, Sharing and Collaboration**
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22 **CarpeDeam: A De Novo Metagenome Assembler for Heavily Damaged Ancient Datasets**
Genome Biology · 26, 372
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23 **Fast and Accurate Protein Structure Search With Foldseek**
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24 **Petabase-Scale Homology Search for Structure Prediction**
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25 **Metabuli: Sensitive and Specific Metagenomic Classification via Joint Analysis of Amino Acid and DNA**
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26 **Strain-Resolved De-Novo Metagenomic Assembly of Viral Genomes and Microbial 16S rRNAs**
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27 **Bilingual Language Model for Protein Sequence and Structure**
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28 **UFCG: Database of Universal Fungal Core Genes and Pipeline for Genome-Wide Phylogenetic Analysis of Fungi.**
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29 **Novel Machine Learning Approaches Revolutionize Protein Knowledge**
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30 AlphaFold2 Reveals Commonalities and Novelties in Protein Structure Space for 21 Model Organisms

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31 Foldcomp: A Library and Format for Compressing and Indexing Large Protein Structure Sets.

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32 Cross-Phyla Protein Annotation by Structural Prediction and Alignment

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33 Qualitative Metabolomics-Based Characterization of a Phenolic UDP-Xylosyltransferase With a Broad Substrate Spectrum From Lentinus brumalis

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34 Block Aligner: An Adaptive SIMD-Accelerated Aligner for Sequences and Position-Specific Scoring Matrices.

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35 Clustering Predicted Structures at the Scale of the Known Protein Universe

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36 ProtTrans: Toward Understanding the Language of Life Through Self-Supervised Learning

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37 PhyloCSF++: A Fast and User-Friendly Implementation of PhyloCSF With Annotation Tools.

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38 Unifying the Known and Unknown Microbial Coding Sequence Space.

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39 Evolutionary Balance Between Foldability and Functionality of a Glucose Transporter
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40 ColabFold: Making Protein Folding Accessible to All
Nature Methods · 19, 679-682
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41 Metagenome Analysis Using the Kraken Software Suite
Nature Protocols · 17, 2815-2839
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42 Nearest Neighbor Search on Embeddings Rapidly Identifies Distant Protein Relations
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43 3D-Beacons: Decreasing the Gap Between Protein Sequences and Structures Through a Federated Network of Protein Structure Data Resources
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44 Structure-Guided Isoform Identification for the Human Transcriptome.
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45 Author Response: Structure-Guided Isoform Identification for the Human Transcriptome
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2021

46 DescribePROT: Database of Amino Acid-Level Protein Structure and Function Predictions
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47 Highly Multiplexed Oligonucleotide Probe-Ligation Testing Enables Efficient Extraction-Free SARS-CoV-2 Detection and Viral Genotyping
Modern Pathology · 34, 1093-1103
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48 **Fast and Sensitive Taxonomic Assignment to Metagenomic Contigs**
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https://exaly.com/article/79775612

49 **PredictProtein - Predicting Protein Structure and Function for 29 Years**
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Nucleic Acids Research · 49, W535-W540
https://exaly.com/article/80371922

50 **Going to Extremes - A Metagenomic Journey Into the Dark Matter of Life.**
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51 **Highly Accurate Protein Structure Prediction With AlphaFold**
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52 **Accurate Protein Structure Prediction: What Comes Next?**
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Biodesign · 9, 47-50
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53 **Applying and Improving AlphaFold at CASP14**
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Proteins: Structure, Function and Bioinformatics · 89, 1711-1721
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54 **Author Response: Unifying the Known and Unknown Microbial Coding Sequence Space**
1 citations
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55 **Metagenomic Association Analysis of Gut Symbiont Limosilactobacillus reuteri Without Host-Specific Genome Isolation**
5 citations
Frontiers in Microbiology · 11, 585622
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56 **Terminating Contamination: Large-Scale Search Identifies More Than 2,000,000 Contaminated Entries in GenBank**
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Genome Biology · 21, 1-12
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57 **Protein Sequence Analysis Using the MPI Bioinformatics Toolkit**
662 citations
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58 **HH-suite3 for Fast Remote Homology Detection and Deep Protein Annotation** — 885 citations
BMC Bioinformatics · 20, 1-15
https://exaly.com/article/72739598

59 **Protein-Level Assembly Increases Protein Sequence Recovery From Metagenomic Samples Manyfold** — 350 citations
Nature Methods · 16, 603-606
https://exaly.com/article/72984998

60 **MMseqs2 Desktop and Local Web Server App for Fast, Interactive Sequence Searches** — 500 citations
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61 **Gearing Up to Handle the Mosaic Nature of Life in the Quest for Orthologs.** — 37 citations
Bioinformatics · 34, 323-329
https://exaly.com/article/70894297

62 **Clustering Huge Protein Sequence Sets in Linear Time** — 700 citations
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https://exaly.com/article/71200904

63 **HFSP: High Speed Homology-Driven Function Annotation of Proteins.** — 36 citations
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64 **Uniclust Databases of Clustered and Deeply Annotated Protein Sequences and Alignments.** — 579 citations
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65 **MMseqs2 Enables Sensitive Protein Sequence Searching for the Analysis of Massive Data Sets** — 3,632 citations
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66 **MMseqs Software Suite for Fast and Deep Clustering and Searching of Large Protein Sequence Sets.**

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67 **Cloud Prediction of Protein Structure and Function With PredictProtein for Debian**

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