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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☒	☐ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐ A description of all covariates tested
☒	☐ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☒	☐ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☒	☐ For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	The open source softwares DIAMOND (v2.0.0, https://github.com/bbuchfink/diamond), SWIPE (v2.1.0), MMSeqs2 (e9678f625b16a806e1ae0bf04d7daf733f1142f2, https://github.com/soedinglab/MMseqs2/) were used for creation of the query dataset and the SCOP annotation. SpEED (v1.0) was used for computing spaced seeds.
Data analysis	The open source softwares DIAMOND (v2.0.0, v2.0.5, v2.0.7, v0.7.12, v0.4.7, https://github.com/bbuchfink/diamond), MMSeqs2 (e9678f625b16a806e1ae0bf04d7daf733f1142f2, https://github.com/soedinglab/MMseqs2/), BLAST (v2.10.0, v2.2.31), QuickBLAST (v0.0.0) were used for generating and evaluating the benchmark data. EMBOSS needleall v6.6.0.0 was used to compute Needleman Wunsch alignments.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The sequence and annotation data that support the findings of this study are available in figshare with the identifier doi:10.6084/m9.figshare.c.5053112.v1. The SCOPe ASTRAL40 dataset can be downloaded at http://scop.berkeley.edu/downloads/scopeseq-2.07/astral-scopedom-seqres-gd-sel-gs-bib-40-2.07.fa. The download URLs for the two databases UniRef50 and NCBI NR are ftp://ftp.uniprot.org/pub/databases/uniprot/uniref/uniref50/uniref50.fasta.gz and ftp://

ftp.ncbi.nlm.nih.gov/blast/db/FASTA/nr.gz. The sequencing reads of the supplementary benchmarks are part of the samples with ENA accessions SAMEA5383815, SAMEA5383897, SAMEA5383886, SAMEA5383828, SAMEA5383925, SAMEA5383848, SAMEA5383824, SAMEA5383873, SAMEA5384011, SAMEA5383807, SAMEA103892455, SAMEA103892562, SAMEA103892552, SAMEA103892441, SAMEA103892588, SAMEA103892582, SAMEA103892581, SAMEA103892571, SAMEA103892491, SAMEA103892619.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Datasets of less than 100,000 proteins have been considered sufficient to assess the sensitivity of protein aligners in reference literature, for example: Altschul et al., Nucleic Acids Research, 1997, Vol. 25, No. 17 3389–3402 / Altschul et al., FEBS Journal 272 (2005) 5101–5109 / Brenner et al., Proc. Natl. Acad. Sci. USA Vol. 95, pp. 6073–6078, May 1998 / Steinegger et al., Nature Biotechnology 35, 1026–1028 (2017). In comparison, our query and target datasets comprise 1.7 million and 7.7 million proteins respectively.
Data exclusions	No data was excluded.
Replication	The benchmarking computations were repeated independently at least 3 times which successfully verified the consistency of the results.
Randomization	Randomization does not apply because the study does not involve subjects that are assigned to treatment groups.
Blinding	Blinding does not apply because the study does not involve subjects that are assigned to treatment groups.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging