

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

FASTA

RRID:SCR_011819

Type: Tool

Proper Citation

FASTA (RRID:SCR_011819)

Resource Information

URL: <http://www.ebi.ac.uk/Tools/sss/fasta/>

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Description: Software package for DNA and protein sequence alignment to find regions of local or global similarity between Protein or DNA sequences, either by searching Protein or DNA databases, or by identifying local duplications within a sequence.

Abbreviations: FASTA

Synonyms: Federal Acquisition Streamlining Act

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Keywords: sequence, alignment, DNA, protein, similarity, searching

Availability: Free, Freely available

Resource Name: FASTA

Resource ID: SCR_011819

Alternate IDs: OMICS_00994

License: Apache2.0

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260905T133003+0000

Ratings and Alerts

No rating or validation information has been found for FASTA.

No alerts have been found for FASTA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 896 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Forshaw TE, et al. (2026) A proteomics and redox proteomics approach to understanding ARDS heterogeneity. *Scientific reports*, 16(1), 6034.

Tessier TM, et al. (2026) Identification of E3 ligase substrates and PROTAC-induced ubiquitylation sites using proximity-based identification of ubiquitin sites (PriUS). *Communications biology*, 9(1).

Nandakumar A, et al. (2026) Genomic diversity analysis enables development of pan-Dengue Toehold RNA sensors. *PLoS neglected tropical diseases*, 20(4), e0014173.

Lundgren JG, et al. (2026) Metastasis suppressing properties of the cell-surface anchored serine protease prostasin: new functional and mechanistic insights from breast cancer. *Oncogenesis*, 15(1).

Morihara N, et al. (2026) Functional Annotation Workflow for Fungal Transcriptomes. *Journal of fungi (Basel, Switzerland)*, 12(2).

Zegers JMS, et al. (2026) Systems acclimation to osmotic stress in zygnematophyte cells. *Nature communications*, 17(1), 755.

Degezelle MM, et al. (2026) Destabilization of cardiac myosin acetylation and sequestration with type 2 diabetes mellitus. *Cardiovascular diabetology*, 25(1).

Loza-Valdes A, et al. (2026) Erk3 deletion drives oxidative adaptations in skeletal muscle. *Molecular metabolism*, 106, 102338.

Mehta S, et al. (2026) iPepGen: a modular, immunopeptidogenomic analysis pipeline for discovery, verification, and prioritization of cancer peptide neoantigen candidates. *Genome biology*, 27(1).

Yan F, et al. (2026) A comprehensive evaluation of long-read de novo transcriptome assembly. *Genome biology*, 27(1).

Li M, et al. (2026) Dynamic profiling of BMSC-dECM reveals accumulation of core matrisome proteins suppresses osteogenic differentiation and bone regeneration. *Journal of advanced research*, 80, 393.

Mostafavi S, et al. (2026) Deciphering Membrane Protein Complexes in Plasmodium falciparum Gametocytes via Integrative Structural Systems Biology. Molecular & cellular proteomics : MCP, 25(5), 101567.

Fowler JH, et al. (2026) Inter- and Intraspecific Venom Variation in the Reclusive Rear-Fanged Black-Striped Snakes (Coniophanes). Toxins, 18(2).

Li Y, et al. (2026) Inhibition of the RORC/GPX4 mediated ferroptosis regulatory axis suppresses tumor growth and alleviates enzalutamide resistance in prostate cancer. Cellular & molecular biology letters, 31(1), 11.

Shah DC, et al. (2026) Exogenous sphingomyelinase mediates MSC-derived EV biogenesis and enhances potency via repackaging of molecular cargo. iScience, 29(3), 114992.

Jachmann C, et al. (2026) The Escherichia coli PeptideAtlas Build: Characterizing the Observed Escherichia coli Pan-Proteome and Its Post-Translational Modifications. Journal of proteome research, 25(2), 1027.

Lennartsson C, et al. (2026) Improved Peptide Search for Identification of SUMO and Sequence-Based Modifiers, in MaxSBM. Molecular & cellular proteomics : MCP, 25(6), 101589.

Petrovskiy DV, et al. (2026) PowerNovo2: A generative flow-based approach to non-autoregressive de novo peptide sequencing. PLoS computational biology, 22(5), e1014298.

Nepal C, et al. (2026) Epigenomic, transcriptomic, and proteomic characterization of breast cancer cell line reference samples. Cell reports methods, 6(1), 101276.

McLean TC, et al. (2026) The conserved two-component systems CutRS and CssRS control the protein secretion stress response in Streptomyces. mBio, 17(1), e0299125.