

Resource Summary Report

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FASTA

RRID:SCR_011819

Type: Tool

Proper Citation

FASTA (RRID:SCR_011819)

Resource Information

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

Proper Citation: FASTA (RRID:SCR_011819)

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

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: 20260728T043358+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 845 mentions in open access literature.

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

Turner LA, et al. (2025) Differences in gene expression between high and low tolerance rainbow trout (*Oncorhynchus mykiss*) to acute thermal stress. *PloS one*, 20(1), e0312694.

Woo J, et al. (2025) Single-Cell Proteomic Characterization of Drug-Resistant Prostate Cancer Cells Reveals Molecular Signatures Associated with Morphological??Changes. *Molecular & cellular proteomics : MCP*, 24(4), 100949.

Zhang K, et al. (2025) FGF21 protects against HFpEF by improving cardiac mitochondrial bioenergetics in mice. *Nature communications*, 16(1), 1661.

Yu F, et al. (2025) MSFragger-DDA+ enhances peptide identification sensitivity with full isolation window search. *Nature communications*, 16(1), 3329.

Li Z, et al. (2025) Proteomic Analysis of Endemic Viral Infections in Neurons offers Insights into Neurodegenerative Diseases. *bioRxiv : the preprint server for biology*.

Shao C, et al. (2025) Radiotherapy-resistant prostate cancer cells escape immune checkpoint blockade through the senescence-related ataxia telangiectasia and Rad3-related protein. *Cancer communications (London, England)*, 45(3), 218.

Bontempo A, et al. (2025) Yoda1, a Piezo1 agonist, induced latent HIV reactivation associated with upregulation of CD3/TCR complex and HLA genes. *Research square*.

Smith NJ, et al. (2025) Differentiation signals induce APOBEC3A expression via GRHL3 in squamous epithelia and squamous cell carcinoma. *The EMBO journal*, 44(1), 1.

Johnson SR, et al. (2025) Computational scoring and experimental evaluation of enzymes generated by neural networks. *Nature biotechnology*, 43(3), 396.

Ahmad W, et al. (2025) Machine learning driven dashboard for chronic myeloid leukemia prediction using protein sequences. *PloS one*, 20(6), e0321761.

Ramon-Mateu J, et al. (2025) Aboral cell types of *Clytia* and coral larvae have shared features and link taurine to the regulation of settlement. *Science advances*, 11(20), eadv1159.

Pagliarini RA, et al. (2025) STX-721, a Covalent EGFR/HER2 Exon 20 Inhibitor, Utilizes Exon 20-Mutant Dynamic Protein States and Achieves Unique Mutant Selectivity Across Human Cancer Models. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(14), 3002.

Crombez E, et al. (2025) The subordinate role of pseudogenization to recombinative deletion following polyploidization in angiosperms. *Nature communications*, 16(1), 6335.

Schwyster L, et al. (2025) A combination of phenotypic responses and genetic adaptations enables *Staphylococcus aureus* to withstand inhibitory molecules secreted by *Pseudomonas aeruginosa*. *mSystems*, 10(8), e0026225.

Han L, et al. (2025) Extracellular Vesicle Protein Panel Enables Early Lung Cancer Detection in a Large Clinical Cohort. *Journal of extracellular vesicles*, 14(8), e70129.

Karimi I, et al. (2025) The anti-aging potential of antihypertensive peptides of *Pariset*, a dataset of algal peptides. *Frontiers in aging*, 6, 1618082.

Gewurz D, et al. (2025) Plasmid prevalence is independent of antibiotic resistance in environmental *Enterobacteriaceae*. *Microbial genomics*, 11(8).

Lo WC, et al. (2025) SARST2 high-throughput and resource-efficient protein structure alignment against massive databases. *Nature communications*, 16(1), 8691.

Nevers Y, et al. (2025) Quality assessment of gene repertoire annotations with OMArk. *Nature biotechnology*, 43(1), 124.

Majidian S, et al. (2025) EvANI benchmarking workflow for evolutionary distance estimation. *Briefings in bioinformatics*, 26(3).