

Resource Summary Report

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EMBOSS

RRID:SCR_008493

Type: Tool

Proper Citation

EMBOSS (RRID:SCR_008493)

Resource Information

URL: <http://emboss.sourceforge.net/>

Proper Citation: EMBOSS (RRID:SCR_008493)

Description: Software analysis package for molecular biology community. Automatically copes with data in variety of formats and allows transparent retrieval of sequence data from web. Libraries are provided with package. Provides toolkit for creating bioinformatics applications or workflows. Provides set of sequence analysis programs. Provided programs cover areas such as sequence alignment, rapid database searching with sequence patterns, protein motif identification, nucleotide sequence pattern analysis, codon usage analysis for small genomes, rapid identification of sequence patterns in large scale sequence sets, and presentation tools for publication.

Abbreviations: EMBOSS

Synonyms: The European Molecular Biology Open Software Suite, European Molecular Biology Open Software Suite

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

Defining Citation: [DOI:10.1016/S0168-9525\(00\)02024-2](https://doi.org/10.1016/S0168-9525(00)02024-2)

Keywords: FASEB list

Availability: Free, Freely available

Resource Name: EMBOSS

Resource ID: SCR_008493

Alternate IDs: OMICS_21165, nif-0000-30488

Alternate URLs: <https://sources.debian.org/src/emboss/>

Old URLs: <http://www.emboss.org>

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260801T190332+0000

Ratings and Alerts

No rating or validation information has been found for EMBOSS.

No alerts have been found for EMBOSS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4543 mentions in open access literature.

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

Baldelli V, et al. (2026) The *Pseudomonas aeruginosa* sirB2 gene is a fitness determinant of anaerobic growth and its inactivation affects virulence and rugose small colony variants emergence. *Virulence*, 17(1), 2605800.

Tørresen OK, et al. (2026) Comparison of whole-genome assemblies of European river lamprey (*Lampetra fluviatilis*) and brook lamprey (*Lampetra planeri*). *The Journal of heredity*, 117(1), 96.

El Khalili O, et al. (2026) Development of a Next-Generation Sequencing Protocol for Assessing Lenacapavir Resistance in HIV-1 Capsid. *Journal of medical virology*, 98(1), e70773.

Nath R, et al. (2025) Lineage-Specific Class-A GPCR Dynamics Reflect Diverse Chemosensory Adaptations in Lophotrochozoa. *Molecular biology and evolution*, 42(3).

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Fettig R, et al. (2025) Short internal open reading frames repress the translation of N-terminally truncated proteoforms. *EMBO reports*, 26(6), 1566.

Xu W, et al. (2025) Specificities of Chemosensory Receptors in the Human Gut Microbiota. *bioRxiv : the preprint server for biology*.

Walter JD, et al. (2025) Flycodes enable simultaneous preclinical analysis for dozens of antibodies in single cassette-dosed mice. *Proceedings of the National Academy of Sciences of the United States of America*, 122(12), e2426481122.

Baruah A, et al. (2025) Patho-Ecological Distribution and Genetic Diversity of *Fusarium oxysporum* f. sp. *cubense* in Malbhog Banana Belts of Assam, India. *Journal of fungi* (Basel, Switzerland), 11(3).

Myers ML, et al. (2025) Analysis of polyclonal and monoclonal antibody to the influenza virus nucleoprotein in different oligomeric states. *Virus research*, 355, 199563.

Castellanos-Labarcena J, et al. (2025) Single specimen genome assembly of *Culicoides stellifer* shows evidence of a non-retroviral endogenous viral element. *BMC genomics*, 26(1), 247.

Robène I, et al. (2025) RUNCOV: a one-pot triplex real-time RT-LAMP as a point-of-care diagnostic tool for detecting SARS-CoV-2. *Biology methods & protocols*, 10(1), bpaf010.

Zhang ?? T, et al. (2025) VISTA: A Tool for Fast Taxonomic Assignment of Viral Genome Sequences. *Genomics, proteomics & bioinformatics*, 23(1).

Fornasiero A, et al. (2025) *Oryza* genome evolution through a tetraploid lens. *Nature genetics*, 57(5), 1287.

Lyupina YV, et al. (2025) The divergent intron-containing actin in sponge morphogenetic processes. *NAR genomics and bioinformatics*, 7(2), lqaf071.

Abou-Kandil A, et al. (2025) The proteomic response of *Aspergillus fumigatus* to amphotericin B (AmB) reveals the involvement of the RTA-like protein RtaA in AmB resistance. *microLife*, 6, uqae024.

Schmid EW, et al. (2025) Predictomes, a classifier-curated database of AlphaFold-modeled protein-protein interactions. *Molecular cell*, 85(6), 1216.

Elphinstone C, et al. (2025) RepeatOBserver: Tandem Repeat Visualisation and Putative Centromere Detection. *Molecular ecology resources*, 25(7), e14084.

Tan X, et al. (2025) Decoding codon usage in human papillomavirus type 59. *Virus genes*, 61(3), 313.

Dean AAC, et al. (2025) An algorithm for annotation and classification of *T. cruzi* MASP sequences: towards a better understanding of the parasite genetic variability. *BMC genomics*, 26(1), 194.