

# Resource Summary Report

Generated by [ASWG](#) on Aug 3, 2026

## 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, software resource, data processing software, sequence analysis software, software application, data analysis 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:** 20260803T040527+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 [ASWG](#) .

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.

Kim T, et al. (2025) Evolution of NAC transcription factors from early land plants to domesticated crops. *Plant & cell physiology*, 66(4), 566.

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

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.

Dodd GK, et al. (2025) In silico functional analysis of the human, chimpanzee, and gorilla MHC-A repertoires. *Immunogenetics*, 77(1), 12.

Kuchma SL, et al. (2025) Genetic analysis of flagellar-mediated surface sensing by *Pseudomonas aeruginosa* PA14. *Journal of bacteriology*, 207(7), e0052024.

Casas E, et al. (2025) Genetic polymorphisms lead to major, locus-specific, variation in piRNA production in mouse. *The EMBO journal*, 44(14), 4104.

Lu W, et al. (2025) Metagenomic sequencing reveals the taxonomic and functional characteristics of rumen microorganisms in Dongliu buffalo. *Scientific reports*, 15(1), 18398.

Nilsen J, et al. (2025) Enhanced plasma half-life and efficacy of engineered human albumin-fused GLP-1 despite enzymatic cleavage of its C-terminal end. *Communications biology*, 8(1), 810.

Dias PJ, et al. (2025) Molecular evolution of the members of the Snq2/Pdr18 subfamily of Pdr transporters in the Hemiascomycete yeasts. *FEMS yeast research*, 25.

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

Fischer NM, et al. (2025) Two distinct host-specialized fungal species cause white-nose disease in bats. *Nature*, 642(8069), 1034.

Prescott MA, et al. (2025) Development of a rapid point-of-care dengue virus type 2 infection diagnostic assay using recombinase polymerase amplification and lateral flow device. *Frontiers in cellular and infection microbiology*, 15, 1578549.

Midlovets K, et al. (2025) Bioinformatic Analysis of WNT Family Proteins. *Bioinformatics and biology insights*, 19, 11779322251353347.

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.

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