

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

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: 20260829T182331+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 4742 mentions in open access literature.

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

Shi M, et al. (2026) Transcriptomic landscape of transposable elements reveals LTR7-PLAAT4 as a potential oncogene and therapeutic target in pancreatic adenocarcinoma. *Genome research*, 36(2), 275.

Cisneros AF, et al. (2026) Paralog interference contributes to the preservation of genetic redundancy. *Current biology : CB*, 36(6), 1373.

Hitti E, et al. (2026) Profound alterations of cancer transcriptomes by the RNase L inhibitor ABCE1 through the modulation of UU/UA-dinucleotide rich transcript abundance. *RNA biology*, 23(1), 1.

Sato S, et al. (2026) MET Enhances Amivantamab Binding to EGFR and Antibody-Dependent Cellular Toxicity. *Cancer science*, 117(1), 118.

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.

De Filippo E, et al. (2026) Stepwise recombination suppression around the mating-type locus associated with a diploid-like life cycle in *Schizothecium fungi*. *Molecular biology and evolution*, 43(1).

Gao J, et al. (2026) Polyploidy drives structural and functional evolution in *Camellia* mitochondrial genomes. *BMC genomics*, 27(1), 224.

Zou Y, et al. (2026) Mining and engineering of ene-reductases from marine sediment metagenome for prochiral ACE inhibitor synthesis. *Applied and environmental microbiology*, 92(2), e0233325.

Youssef DG, et al. (2026) Computational characterization of GRP78 binding sites on mitochondrial GPX4: implications for targeting ferroptosis in triple-negative breast cancer. *Scientific reports*, 16(1), 1330.

Ootsuki R, et al. (2026) Minimum virtual dataset for reproducible triploid de novo genome assembly. *Scientific data*, 13(1).

Naveed M, et al. (2026) Immunoinformatics-based design and evaluation of a multi-epitope vaccine against *Vibrio fluvialis*. *Scientific reports*, 16(1), 4100.

Deng X, et al. (2026) Comparative plastome analyses reveal life-form-associated selection signatures in Orchidaceae. *BMC plant biology*, 26(1).

Chen Y, et al. (2026) EBV strain interacts with host HLA to drive nasopharyngeal carcinoma risk. *Nature*, 653(8115), 786.

Smolen C, et al. (2026) Evolutionary instability drives structural diversity and disease susceptibility at the 16p12.2 locus. *bioRxiv : the preprint server for biology*.

Schimke KD, et al. (2026) Sequencing complete plasmids on Oxford Nanopore Technologies sequencers using R2C2 and Chopper. *PloS one*, 21(4), e0345168.

Briggs EJ, et al. (2026) Big Spider, Big Genome: Chromosome-Level Genome of a North American Tarantula (*Aphonopelma marxi*) and Comparative Genomics Across 300 Million Years of Spider Evolution. *Genome biology and evolution*, 18(4).

Qiu Q, et al. (2026) Comparative Analysis of Microbial Community Structure and Function in the Gut of South China Tigers Under Different Dietary Treatments. *Veterinary sciences*, 13(3).

Afshan G, et al. (2026) A mutation-aware proteomics approach for designing a multi-epitope vaccine against multidrug-resistant *Acinetobacter baumannii* and *Pseudomonas aeruginosa*. *Microbiology spectrum*, 14(4), e0309525.

Zhang H, et al. (2026) PON-Del predictor for sequence retaining protein deletions. *PLoS computational biology*, 22(2), e1014020.

Zhou H, et al. (2026) Genome-Wide Analysis of the YUCCA Gene Family in Wheat and the Potential Roles of TaYUCCA19 and Its Homologs in Male Reproductive Development. *Plants (Basel, Switzerland)*, 15(4).