Resource Summary Report

Generated by dkNET on Apr 28, 2025

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

Defining Citation: DOI:10.1016/S0168-9525(00)02024-2

Keywords: FASEB list

Funding:

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: 20250428T053423+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 4275 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Cesaro S, et al. (2025) A crucial active site network of titratable residues guides catalysis and NAD+ binding in human succinic semialdehyde dehydrogenase. Protein science : a publication of the Protein Society, 34(1), e70024.

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.

Xu ZS, et al. (2025) High-throughput analysis of microbiomes in a meat processing facility: are food processing facilities an establishment niche for persisting bacterial communities? Microbiome, 13(1), 25.

Zakerzade R, et al. (2025) Diversification and recurrent adaptation of the synaptonemal complex in Drosophila. PLoS genetics, 21(1), e1011549.

Hikida H, et al. (2025) BV/ODV-E26 is a conserved baculoviral inhibitory factor for optimizing viral virulence in lepidopteran hosts. iScience, 28(2), 111723.

Chimienti R, et al. (2025) A WFS1 variant disrupting acceptor splice site uncovers the impact of alternative splicing on beta cell apoptosis in a patient with Wolfram syndrome. Diabetologia, 68(1), 128.

Knechtel JW, et al. (2025) KMT5C leverages disorder to optimize cooperation with HP1 for heterochromatin retention. EMBO reports, 26(1), 153.

Mestre B, et al. (2025) An anomalous abundance of tryptophan residues in ceramide synthases based on analysis of all membrane proteins in the Swiss-Prot database. The Journal of biological chemistry, 301(1), 108053.

Gomaa F, et al. (2025) Array of metabolic pathways in a kleptoplastidic foraminiferan protist supports chemoautotrophy in dark, euxinic seafloor sediments. The ISME journal, 19(1).

Tao K, et al. (2025) Complete chloroplast genome of eight Phaius (Orchidaceae) species from China: comparative analysis and phylogenetic relationship. BMC plant biology, 25(1), 37.

Washington JM, et al. (2025) Expanding the Diversity of Actinobacterial Tectiviridae: A Novel Genus from Microbacterium. Viruses, 17(1).

Knutson BA, et al. (2025) Evolutionary and Structural Insights into the RNA Polymerase I A34 Protein Family: A Focus on Intrinsic Disorder and Phase Separation. Genes, 16(1).

Petroll R, et al. (2025) Enhanced sensitivity of TAPscan v4 enables comprehensive analysis of streptophyte transcription factor evolution. The Plant journal : for cell and molecular biology, 121(1), e17184.

Cerasa G, et al. (2025) New Record of Encarsia protransvena and Confirmed Occurrence of Encarsia hispida (Hymenoptera: Aphelinidae) as Parasitoids of Singhiella simplex (Hemiptera: Aleyrodidae) in Italy. Insects, 16(1).

Low SJ, et al. (2025) PathoGD: an integrative genomics approach to primer and guide RNA design for CRISPR-based diagnostics. Communications biology, 8(1), 147.

Shealy EP, et al. (2025) DNA methylation-based age prediction and sex-specific epigenetic aging in a lizard with female-biased longevity. Science advances, 11(5), eadq3589.

Modha S, et al. (2025) Expanding the genomic diversity of human anelloviruses. Virus evolution, 11(1), veaf002.

Sánchez-Serna G, et al. (2025) Less, but More: New Insights From Appendicularians on Chordate Fgf Evolution and the Divergence of Tunicate Lifestyles. Molecular biology and evolution, 42(1).

Brown E, et al. (2024) Inhibitors of the small membrane (M) protein viroporin prevent Zika virus infection. eLife, 13.