EMBOSS
RRID:SCR_008493
Type: Tool

Proper Citation
EMBOSS (RRID:SCR_008493)

Resource Information

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

Description: A software analysis package specially developed for the needs of the molecular biology (e.g. EMBnet) user community. The software automatically copes with data in a variety of formats and even allows transparent retrieval of sequence data from the web. Also, as extensive libraries are provided with the package, it is a platform to allow other scientists to develop and release software in true open source spirit. EMBOSS also integrates a range of currently available packages and tools for sequence analysis into a seamless whole. EMBOSS has: a properly constructed toolkit for creating robust bioinformatics applications or workflows; a comprehensive set of sequence analysis programs; all sequence and many alignment and structural formats are handled; extensive programming library for common sequence analysis tasks; and additional programming libraries for many other areas. Within EMBOSS are programs (applications) covering 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.

Resource Name: EMBOSS

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

Resource ID: SCR_008493

Related resources: BioExtract
**Availability:** Free, Open unspecified license

**Website Status:** Last checked up

**Alternate IDs:** nif-0000-30488

**Old URLs:** http://www.emboss.org

**Abbreviations:** EMBOSS

**Mentions Count:** 2809

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**Ratings and Alerts**

No rating or validation information has been found for EMBOSS.

No alerts have been found for EMBOSS.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 2809 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch Infrastructure](https://fdilab.scicrunch.org).


Renny-Byfield S, et al. (2020) Repetitive DNA content in the maize genome is uncoupled from population stratification at SNP loci. BMC genomics, 21(1), 98.


Adrian-Kalchhauser I, et al. (2020) The round goby genome provides insights into mechanisms that may facilitate biological invasions. BMC biology, 18(1), 11.


Frost HR, et al. (2020) Analysis of Global Collection of Group AGenomes Reveals that the Majority Encode a Trio of M and M-Like Proteins. mSphere, 5(1).