EMBOSS: The European Molecular Biology Open Software Suite Peter Rice (pmr@ebi.ac.uk), Alan Bleasby, Jon Ison, Mahmut Uludag European Bioinformatics Institute, Hinxton, Cambridge, CB10 1SD, United Kingdom.

The European Molecular Biology Open Software Suite (EMBOSS) is a mature package of software tools developed for the molecular biology community. It includes a comprehensive set of applications for molecular sequence analysis and other tasks and integrates popular third-party software packages under a consistent interface. EMBOSS includes extensive C programming libraries and is a platform to develop and release software in the true open source spirit.

A major new stable version is released each year and the current source code tree can be downloaded via CVS. All code is open source and licensed for use by everyone under the GNU Software licenses (GPL with LGPL library code).

There have been many tens of thousands of downloads including site-wide installations all over the world since the project inception. EMBOSS is used extensively in production environments reflecting its mature status and has been incorporated into many web-based, standalone graphical and workflow interfaces including Galaxy, wEMBOSS, EMBOSS Explorer, JEMBOSS, SoapLab, Pise, SRS, Taverna and several commercial workflow packages.

EMBOSS 6.3 will be released on 15th July 2010 (we always release on 15th July). New features include:

- New data formats standard FASTQ Open-Bio parsing
- Use of ontologies new EDAM ontology for data types and methods in EMBOSS
- DAS, BioMart and Ensembl protocol support
- Integration support for Galaxy

Three books are to be published by Cambridge University Press for Users, Developers and Administrators of EMBOSS.

The EMBOSS project has significant new funding for an ambitious programme of extensions and new applications covering:

- Comprehensive coverage of public data (sequence data, linked data resources)
- Access methods for major public data repositories (Ensembl, UCSC, CHADO, BioMart, SOAP, REST)
- Persistent metadata (coordinates, taxonomy, gene ontology, keywords, citations)
- Genome-scale analysis and annotation
- Query language
- 100+ new applications

Project home page: http://emboss.sourceforge.net/

Release download site: ftp://emboss.open-bio.org/pub/EMBOSS/ Anonymous CVS server: http://www.open-bio.org/wiki/SourceCode