Introduction

EMBL-EBI provides programmatic access to various data resources and analysis tools via Web Services technologies. Web Services is an integration and inter-operation technology. To ensure client and server software from various sources will work well together, the technology is built on open standards:

- Representational state transfer (REST): a software architecture style.
- Web Services Description Language (WSDL): a method for describing Web Services and their capabilities.

For the transport layer Web Services utilise common network protocols, typically the Hypertext Transfer Protocol (HTTP) used to provide access to web sites.

Usage

We kindly ask all users of EMBL-EBI Web Services to submit tool jobs in batches of no more than 30 at a time and not to submit more until the results and processing is complete. Please ensure that a valid email address is provided. Excessive usage of a particular resource will be dealt with in accordance with EMBL-EBI’s Terms of Use. Please contact us if you need further information.

Programs organised by function

| Function                      | Description                                                                 |
|-------------------------------|                                                                            |
| Data Retrieval                | A list of EMBL-EBI Web Services for data retrieval.                       |
| Protein Functional Analysis   | Tools to perform protein functional analysis.                             |
| Sequence Similarity Search    | Identify potentially homologous sequences based on sequence similarity.    |
| Multiple Sequence Alignment   | Alignment of a set of three or more, protein or nucleotide sequences.      |
| Pairwise Sequence Alignment   | Identify regions of similarity that may indicate functional, structural and/or evolutionary relationships between two biological sequences (protein or nucleic acid). |
| Phylogeny                     | Access to phylogenetic tree generation methods.                           |
| RNA                           | RNA Analysis                                                               |
Sequence Format Conversion
Convert between common sequence formats, or verify the formatting of a sequence.

Sequence Statistics
Analyse a sequence to determine its properties and use statistics to assign significance.

Sequence Translation
Translate a coding nucleotide sequence into a protein sequence, or back-translate from a protein sequence to a possible coding nucleotide sequence.

Sequence Operations
Generate checksums for a sequence using a range of checksum/digest methods which can be used to identify potentially identical sequences when searching the corresponding checksum field in sequence databases such as those available from ENA and UniProt.

Literature and Ontologies
Look-up ontology terms and navigate ontology relationships or access and analyse the literature.

Citation
To cite the EMBL-EBI Job Dispatcher Web Services, please refer to the following publication:

DOI: 10.1093/nar/gkac240
EuropePMC: 35412617

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References