Introduction

EMBL-EBI provides programmatic access to various data resources and analysis tools via Web Services technologies 1) 2).

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:

- Representation 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

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Retrieval</td>
<td>A list of EMBL-EBI Web Services for data retrieval.</td>
</tr>
<tr>
<td>Protein Functional Analysis</td>
<td>Tools to perform protein functional analysis.</td>
</tr>
<tr>
<td>Sequence Similarity Search</td>
<td>Identify potentially homologous sequences based on sequence similarity.</td>
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<tr>
<td>Multiple Sequence Alignment</td>
<td>Alignment of a set of three or more, protein or nucleotide sequences.</td>
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<tr>
<td>Pairwise Sequence Alignment</td>
<td>Identify regions of similarity that may indicate functional, structural or evolutionary relationships between two biological sequences (protein or nucleic acid).</td>
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<tr>
<td>Phylogeny</td>
<td>Access to phylogenetic tree generation methods.</td>
</tr>
<tr>
<td>RNA</td>
<td>RNA Analysis</td>
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</tbody>
</table>

1) EMBL-EBI Web Services
2) EMBL-EBI Web Services
Sequence Format Conversion | Convert between common sequence formats, or verify the formatting of a sequence.
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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.
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:


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References