**Wise2DBA (REST)**

**Description**

The Wise2 DNA Block Aligner (DBA) aligns two DNA sequences using the assumption that the sequences share a number of colinear blocks of conservation separated by potentially large and varied lengths of DNA in the two sequences.

For more information see:

- Web form: [http://www.ebi.ac.uk/Tools/psa/wise2dba/](http://www.ebi.ac.uk/Tools/psa/wise2dba/)
- Document/literal SOAP service
- Wise2 homepage

**Important**

*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.*

**Clients**

Sample clients are provided for a number of programming languages. For details of how to use these clients, download the client and run the program without any arguments.

<table>
<thead>
<tr>
<th>Language</th>
<th>Download</th>
<th>Requirements</th>
</tr>
</thead>
<tbody>
<tr>
<td>Perl</td>
<td>wise2dba_lwp.pl</td>
<td>LWP and XML::Simple</td>
</tr>
</tbody>
</table>

For an introduction on how to run these clients and use them in workflows please see the "EMBL-EBI, programmatically: take a REST from manual searches" webinar series.

**WADL**

The WADL for the Wise2DBA (REST) service: [http://www.ebi.ac.uk/Tools/services/rest/wise2dba?wadl](http://www.ebi.ac.uk/Tools/services/rest/wise2dba?wadl)

**Resources**

parameters

List parameter names.

Request

<table>
<thead>
<tr>
<th>URL</th>
<th><a href="http://www.ebi.ac.uk/Tools/services/rest/wise2dba/parameters/">http://www.ebi.ac.uk/Tools/services/rest/wise2dba/parameters/</a></th>
</tr>
</thead>
<tbody>
<tr>
<td>Parameters</td>
<td>none</td>
</tr>
</tbody>
</table>

Response
An XML document containing a list of parameter names.

For example: http://www.ebi.ac.uk/Tools/services/rest/wise2dba/parameters/

**parameterdetails**
Get detailed information about a parameter.

**Request**

<table>
<thead>
<tr>
<th>URL</th>
<th><a href="http://www.ebi.ac.uk/Tools/services/rest/wise2dba/parameterdetails/$parameterId">http://www.ebi.ac.uk/Tools/services/rest/wise2dba/parameterdetails/$parameterId</a></th>
</tr>
</thead>
<tbody>
<tr>
<td>Parameters</td>
<td>$parameterId: the name of the parameter</td>
</tr>
</tbody>
</table>

**Response**
An XML document providing details about the parameter.

For example: http://www.ebi.ac.uk/Tools/services/rest/wise2dba/parameterdetails/asequence.

**run**
Submit a job with the specified parameters.

**Request**

| URL | http://www.ebi.ac.uk/Tools/services/rest/wise2dba/run/ |
| POST | email User e-mail address. See Why do you need my e-mail address? |
| | title an optional title for the job. |
| | para Enable/disable parameter display in output. |
| | pretty Enable/disable pretty ASCII alignment in output. |
| | asequence First sequence. |
| | bsequence Second sequence. |

More detailed information about each parameter, including valid values can be obtained using the getParameterDetails(parameterId) operation.

**Response**
A plain text document containing the job identifier.

**status**
Get the status of a submitted job.

**Request**

| URL | http://www.ebi.ac.uk/Tools/services/rest/wise2dba/status/$jobId |
| Parameters | $jobId: job identifier |

**Response**
A plain text document containing the job status.

The values for the status are:

- **RUNNING**: the job is currently being processed.
- **FINISHED**: job has finished, and the results can then be retrieved.
- **ERROR**: an error occurred attempting to get the job status.
- **FAILURE**: the job failed.
- **NOT_FOUND**: the job cannot be found.

**resulttypes**
Get available result types for a finished job.
An XML document detailing the available result types.

Get the job result of the specified type.

A document containing the result in the requested format. The MIME type of the returned document is set according to the format.