# RSATWSPortType

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|---|---|
| **Service Documentation** | **Web services for the Regulatory Sequence Analysis Tools (RSAT). Tools developed by Jacques van Helden (jvanheld@scmbb.ulb.ac.be), SOAP/WSDL interface developed by Olivier Sand (oly@scmbb.ulb.ac.be).** |
| **Server Address** | **http://rsat.scmbb.ulb.ac.be/rsat/web_services/RSATWS.cgi** |

## Method: retrieve_seq

**Description**

**Returns upstream, downstream or coding DNA sequences for list of query genes.**

**Parameters**

### Input Parameters

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|---|---|
| **output** | **Return type. Accepted values: 'server' (result is stored on a file on the server), 'client' (result is directly transferred to the client), or 'both'. Default is 'both'.<br>Type = String** |
| **organism (required)** | **Organism. Words need to be underscore separated (example: Escherichia_coli_K12).<br>Type = String** |
| **query** | **A list of query genes.<br>Type = String** |
| **all** | **Return sequences for all the genes of the organism if value = 1. Incompatible with query.<br>Type = Integer** |
| **noorf** | **Prevent overlap with upstream open reading frames (ORF) if value = 1.<br>Type = Integer** |
| **from** | **Inferior limit of the region to retrieve. Default is organism dependant (example: Saccharomyces cerevisiae = -800).<br>Type = Integer** |
| **to** | **Superior limit of the region to retrieve. Default is '-1'.<br>Type = Integer** |
| **feattype** | **Type of genome features to load. Supported: CDS, mRNA, tRNA, rRNA.<br>Type = String** |
| **type** | **Sequence type. Supported: upstream, downstream, ORF (unspliced open reading frame).<br>Type = String** |

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| format | Sequence format. Supported: IG (Intelligenetics), WC (wconsensus), raw, FastA<br>Type = String |
| lw | Line width (0 for whole sequence on one line).<br>Type = Integer |
| label | Field(s) to be used in the sequence label. Multiple fields can be specified, separated by commas. Supported: id, name, organism_name, sequence_type, current_from, current_to, ctg, orf_strand, reg_left, reg_right. Default: name.<br>Type = String |
| label_sep | Separator between the label fields. Default: \| (pipe character).<br>Type = String |
| nocom | No comments if value = 1. Only the identifier and the sequence are returned. By default, the comment indicates the ORF and upstream sequence coordinates.<br>Type = Integer |
| repeat | Use the repeat masked version of the genome if value = 1. Attention: repeated regions are annotated for some genomes only.<br>Type = Integer |
| imp_pos | Admit imprecise positions if value = 1.<br>Type = Integer |

**Output Parameters**

| | |
|---|---|
| server | Location of the result file on the server. This can be used as input for a further request.<br>Type = String |
| command | The stand alone command executed on the server.<br>Type = String |
| client | The results.<br>Type = String |

## Method purge_seq

**Description** Mask repeated fragments of an input sequence.

**Parameters**

**Input Parameters**

| | |
|---|---|
| output | Return type. Accepted values: 'server' (result is stored on a file on the server), 'client' (result is directly transferred to the client), or 'both'. Default is 'both'.<br>Type = String |

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|---|---|
| sequence | Sequence to purge. You need to supply either this parameter or the next one (tmp_infile).<br>Type = String |
| tmp_infile | Name of the file with input sequence on the server. You need to supply either this parameter or the previous one (sequence).<br>Type = String |
| format | Sequence format. Supported: IG (Intelligenetics), WC (wconsensus), raw, FastA.<br>Type = String |
| match_length | Minimal match length. Default is 40.<br>Type = Integer |
| mismatch | Number of mismatches allowed. Default is 3.<br>Type = Integer |
| str | Discard duplications on the direct strand only (1) or on the reverse complement as well (2). Default is 2.<br>Type = Integer |
| delete | Delete repeats instead of masking them if value = 1.<br>Type = Integer |
| mask_short | Mask (replace by N characters) sequences shorter than the specified length.<br>Type = Integer |

### Output Parameters

| | |
|---|---|
| server | Location of the result file on the server. This can be used as input for a further request.<br>Type = String |
| command | The stand alone command executed on the server.<br>Type = String |
| client | The results.<br>Type = String |

## Method oligo_analysis

**Description**

Analysis of the statistical significance of all the oligomers of a given size in a sequence. Commonly used to detect over-represented oligonucleotides in a set of promoter sequences.

**Parameters**

**Input Parameters**

| | |
|---|---|
| **output** | **Return type. Accepted values: 'server' (result is stored on a file on the server), 'client' (result is directly transferred to the client), or 'both'. Default is 'both'.**<br>**Type = String** |
| **sequence** | **Input sequence. You need to supply either this parameter or the next one (tmp_infile).**<br>**Type = String** |
| **tmp_infile** | **Name of the file with input sequence on the server. You need to supply either this parameter or the previous one (sequence).**<br>**Type = String** |
| **format** | **Input sequence format. Supported: IG (Intelligenetics), WC (wconsensus), raw, fasta. Default is fasta.**<br>**Type = String** |
| **length (required)** | **Oligomer length.**<br>**Type = Integer** |
| **organism (required)** | **Organism. Words need to be underscore separated (example: Escherichia_coli_K12).**<br>**Type = String** |
| **background** | **Background model: Type of sequences used as background model for estimating expected oligonucleotide frequencies. Supported: upstream, upstreamL, upstream-noorf, intergenic, input.**<br>**Type = String** |
| **stats** | **List of statistics to return. Supported:occ, mseq, freq, proba, ratio, zscore, like, pos, rank.**<br>**Type = String** |
| **noov** | **No overlapping of oligos allowed if value = 1. Disable the detection of overlapping matches for self-overlapping patterns (ex TATATA, GATAGA).**<br>**Type = Integer** |
| **str** | **Oligonucleotide occurrences found on both stands are summed (2) or not (1). Default is 2.**<br>**Type = Integer** |
| **sort** | **Sort oligomers according to overrepresentation if value = 1.**<br>**Type = Integer** |
| **lth** | **Lower threshold on some parameter. Format='param value'.**<br>**Type = String** |

**Output Parameters**

| | |
|---|---|
| server | Location of the result file on the server. This can be used as input for a further request.<br>Type = String |
| command | The stand alone command executed on the server.<br>Type = String |
| client | The results.<br>Type = String |

## Method dna_pattern

**Description** Searches all occurrences of a pattern within DNA sequences.

**Parameters**

**Input Parameters**

| | |
|---|---|
| output | Return type. Accepted values: 'server' (result is stored on a file on the server), 'client' (result is directly transferred to the client), or 'both'. Default is 'both'.<br>Type = String |
| sequence | Input sequence. You need to supply either this parameter or the next one (tmp_infile).<br>Type = String |
| tmp_infile | Name of the file with input sequence on the server. You need to supply either this parameter or the previous one (sequence).<br>Type = String |
| format | Input sequence format. Supported: IG (Intelligenetics), WC (wconsensus), raw, fasta. Default is fasta.<br>Type = String |
| subst | Number of substitutions allowed.<br>Type = Integer |
| pattern (required) | Pattern to match.<br>Type = String |
| id | Pattern identifier.<br>Type = String |
| origin | Origin for the calculation of positions (0 for end of sequence).<br>Type = String |
| noov | No overlapping of oligos allowed if value = 1. Disable the detection of overlapping matches for self-overlapping patterns (ex TATATA, GATAGA).<br>Type = Integer |

| | |
|---|---|
| str | Oligonucleotide occurrences found on both stands are summed (2) or not (1). Default is 2.<br>Type = Integer |
| sort | Sort oligomers according to overrepresentation if value = 1.<br>Type = Integer |
| th | Threshold on match count.<br>Type = Integer |

**Output Parameters**

| | |
|---|---|
| server | Location of the result file on the server. This can be used as input for a further request.<br>Type = String |
| command | The stand alone command executed on the server.<br>Type = String |
| client | The results.<br>Type = String |

## Method gene_info

**Description** Get information about genes.

**Parameters**

**Input Parameters**

| | |
|---|---|
| output | Return type. Accepted values: 'server' (result is stored on a file on the server), 'client' (result is directly transferred to the client), or 'both'. Default is 'both'.<br>Type = String |
| organism (required) | Organism. Words need to be underscore separated (example: Escherichia_coli_K12).<br>Type = String |
| query (required) | List of gene(s) for which you want info on or list of keywords to search for (can be regular expressions).<br>Type = String |
| full | Full match only (no substring matching) if value = 1.<br>Type = Integer |
| noquery | Do not print the query at the begining of each line if value = 1.<br>Type = Integer |
| descr | Match query against the description, too, not just against gene ID and name if value = 1.<br>Type = Integer |

**feattype** Feature type (CDS, mRNA, tRNA, rRNA, scRNA).
Type = String

**Output Parameters**

**server** Location of the result file on the server. This can be used as input for a further request.
Type = String

**command** The stand alone command executed on the server.
Type = String

**client** The results.
Type = String

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## Method supported_organisms

**Description** Get a list of supported organisms.

**Parameters** **Input Parameters**

**output** Return type. Accepted values: 'server' (result is stored on a file on the server), 'client' (result is directly transferred to the client), or 'both'. Default is 'both'.
Type = String

**format** Output format (supported: html_list,html_table,array,text,keys,names,sizes,full,tree,html_tree).
Type = String

**taxon** Root taxon.
Type = String

**Output Parameters**

**server** Location of the result file on the server. This can be used as input for a further request.
Type = String

**command** The stand alone command executed on the server.
Type = String

**client** The results.
Type = String

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