

RSATWSPortType

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

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

organism (required)

Organism. Words need to be underscore separated (example: Escherichia_coli_K12).
Type = String

query

A list of query genes.
Type = String

all

Return sequences for all the genes of the organism if value = 1. Incompatible with query.
Type = Integer

noorf

Prevent overlap with upstream open reading frames (ORF) if value = 1.
Type = Integer

from

Inferior limit of the region to retrieve. Default is organism dependant (example: Saccharomyces cerevisiae = -800).
Type = Integer

to

Superior limit of the region to retrieve. Default is '-1'.
Type = Integer

featype

Type of genome features to load. Supported: CDS, mRNA, tRNA, rRNA.
Type = String

type	Sequence type. Supported: upstream, downstream, ORF (unspliced open reading frame). Type = String
format	Sequence format. Supported: IG (Intelligenetics), WC (wconsensus), raw, FastA Type = String
lw	Line width (0 for whole sequence on one line). 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. Type = String
label_sep	Separator between the label fields. Default: (pipe character). 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. Type = Integer
repeat	Use the repeat masked version of the genome if value = 1. Attention: repeated regions are annotated for some genomes only. Type = Integer
imp_pos	Admit imprecise positions if value = 1. Type = Integer

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

Method**Description****Parameters****purge_seq**

Mask repeated fragments of an input sequence.

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

sequence Sequence to purge. You need to supply either this parameter or the next one (tmp_infile).
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).
Type = String

format Sequence format. Supported: IG (Intelligenetics), WC (wconsensus), raw, FastA.
Type = String

match_length Minimal match length. Default is 40.
Type = Integer

mismatch Number of mismatches allowed. Default is 3.
Type = Integer

str Discard duplications on the direct strand only (1) or on the reverse complement as well (2). Default is 2.
Type = Integer

delete Delete repeats instead of masking them if value = 1.
Type = Integer

mask_short Mask (replace by N characters) sequences shorter than the specified length.
Type = Integer

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

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'. Type = String
sequence	Input sequence. You need to supply either this parameter or the next one (tmp_infile). 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). Type = String
format	Input sequence format. Supported: IG (Intelligenetics), WC (wconsensus), raw, fasta. Default is fasta. Type = String
length (required)	Oligomer length. Type = Integer
organism (required)	Organism. Words need to be underscore separated (example: Escherichia_coli_K12). Type = String
background	Background model: Type of sequences used as background model for estimating expected oligonucleotide frequencies. Supported: upstream, upstreamL, upstream-noorf, intergenic, input. Type = String

stats	List of statistics to return. Supported:occ, mseq, freq, proba, ratio, zscore, like, pos, rank. Type = String
noov	No overlapping of oligos allowed if value = 1. Disable the detection of overlapping matches for self-overlapping patterns (ex TATATA, GATAGA). Type = Integer
str	Oligonucleotide occurrences found on both stands are summed (2) or not (1). Default is 2. Type = Integer
sort	Sort oligomers according to overrepresentation if value = 1. Type = Integer
lth	Lower threshold on some parameter. Format='param value'. 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

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'. Type = String
organism (required)	Organism. Words need to be underscore separated (example: Escherichia_coli_K12). 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). Type = String
full	Full match only (no substring matching) if value = 1. Type = Integer
noquery	Do not print the query at the begining of each line if value = 1. Type = Integer
descr	Match query against the description, too, not just against gene ID and name if value = 1. Type = Integer
featype	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