

Service Documentation	Web services for the Regulatory Sequence Analysis Tools (RSAT). Tools developed by Jacques van Helden (jvanheld@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	<p data-bbox="437 448 580 470">Input Parameters</p> <p data-bbox="437 477 1455 591">output Return type. Accepted values: 'server' (result is stored on a file on the server) or 'both' (result is stored on a file on the server and also returned in the output). Default is 'both'. Type = String</p> <p data-bbox="437 607 1455 696">organism (required) Organism. Words need to be underscore separated (example: Escherichia coli). Type = String</p> <p data-bbox="437 712 826 790">query A list of query genes. Type = String</p> <p data-bbox="437 806 1455 884">all Return sequences for all the genes of the organism if value = 1. Incase of a list of query genes, return sequences for all genes. Type = Integer</p> <p data-bbox="437 900 1455 978">noorf Prevent overlap with upstream open reading frames (ORF) if value = 1. Type = Integer</p> <p data-bbox="437 994 1455 1084">from Inferior limit of the region to retrieve. Default is organism dependent. Type = Integer</p> <p data-bbox="437 1099 1262 1178">to Superior limit of the region to retrieve. Default is '-1'. Type = Integer</p> <p data-bbox="437 1193 1455 1272">feattype Type of genome features to load. Supported: CDS, mRNA, tRNA, rRNA, ncRNA, ORF, UTR, repeat, intergenic, intron, exon, promoter, enhancer, silencer, insulator, CpG island, polycomb target, histone mark, histone mark target, histone mark enhancer, histone mark silencer, histone mark insulator, histone mark CpG island, histone mark polycomb target. Type = String</p> <p data-bbox="437 1288 1455 1377">type Sequence type. Supported: upstream, downstream, ORF (unspliced), ORF (spliced), CDS, mRNA, tRNA, rRNA, ncRNA, UTR, repeat, intergenic, intron, exon, promoter, enhancer, silencer, insulator, CpG island, polycomb target, histone mark, histone mark target, histone mark enhancer, histone mark silencer, histone mark insulator, histone mark CpG island, histone mark polycomb target. Type = String</p> <p data-bbox="437 1393 1455 1471">format Sequence format. Supported: IG (Intelligenetics), WC (wconsensus), F (FASTA), G (Genbank), P (Phylo), S (SwissProt), T (TrEMBL), U (Uniprot), V (VISTA), W (WormBase), Y (Yeast), Z (Zebrafish). Type = String</p> <p data-bbox="437 1487 1166 1576">lw Line width (0 for whole sequence on one line). Type = Integer</p> <p data-bbox="437 1592 1455 1738">label Field(s) to be used in the sequence label. Multiple fields can be specified. Supported: id, name, organism_name, sequence_type, current_from, current_to, current_length, current_start, current_end, current_start_end, current_start_end_length, current_start_end_length_start, current_start_end_length_end, current_start_end_length_start_end, current_start_end_length_start_end_length. Default: name. Type = String</p> <p data-bbox="437 1753 1378 1832">label_sep Separator between the label fields. Default: (pipe character). Type = String</p> <p data-bbox="437 1848 1455 1962">nocom No comments if value = 1. Only the identifier and the sequence are returned. By default, the comment indicates the ORF and upstream sequence. Type = Integer</p>

