



Overall workflow description

This workflow takes the list of Gene Identifier numbers of a given BLAST report and retrieves the corresponding Gene Ontology identifier.

Inputs:

- ① blast_report: blast result
- ② gi_number: gi to retrieve GI numbers
- ③ regex: regex value to use for split_by_regex operation
- ④ separator: separator to use between strings

Outputs:

- ⑨ Gi_numbers: list of GI numbers
- ⑩ GO_id: list of GO id

Service descriptions

- ⑤ **blastsimplifier**: Simplifies BLAST output by specifying elements (seq_id, gi, acc, desc, Score, bits, per, p, exp) to be displayed in the blast result output. [filtering].

Input:

new_direct_data: blast report file [BLAST_report].
 Parameter mutually exclusive with the "new_url" parameter
 new_url: url of the blast report file [BLAST_report]
 To choose one of the following input, pass the name of the input as parameter value.
 seq_id: sequence identifier
 gi: For GI number
 acc: For accession number
 desc: for descriptions
 score: for score value
 bits: for bits score
 per: for percentage of identity.
 p: for p-value
 exp: for E-value

Output:

report: a brief summary of the result
 output: list of specified element. Here, list of GI numbers.

- ⑥ **split_by_regex (Split string into string list by regular expression)**: split a given string with a specified regular expression (regex)

Input:

String: string to split
 Regex: regular expression

Output:

split: return split string

- ⑦ **Merge_string_list_to_string**: Merge a list of string

Input:

stringlist: string list to merge
 separator: separator used for merging the list of string

Output:

concatenated: Return concatenated string

- ⑧ **GOIDFromGiList**: retrieves an array of GO id for a specified array of GI's [retrieving]

Input:

giList: list of GI number [genbank_GI]

Output:

result: list of GO id [Gene_Ontology_term_id]