Read Sequence from Remote Database Element

Download sequence(s) with the specified ID(s) from one of the remote databases: NCBI, Ensembl, PDB, etc.

The sequences are downloaded with the associated annotations in a file format, specific for the selected database.

The element outputs message(s) with the sequence and annotations data.

Parameters in GUI

Parameter	Description	Default value
Resource IDs (required)	Semicolon-separated list of resource IDs in the database.	
Database (required)	Name of the database to read from.	NCBI Genbank (DNA sequence)
Save file to directory	Directory to store a file loaded from the database.	default
Read resource ID(s) from source	The source to read resource IDs from the list or a local file.	List of TDs

Parameters in Workflow File

Type: fetch-sequence

Parameter	Parameter in the GUI	Type
resource-id	**Resource IDs**	*string*
database	**Database**	*string* Available values are: • ncbi-dna (NCBI GenBank (DNA sequence)) • ncbi-protein (NCBI protein sequence database) • pdb (PDB) • swiss-plot (SWISS-PROT) • uniprot-swiss-prot (UniProtKB/Swiss-Prot) • uniprot-trembl (UniProtKB/TrEMBL)
save-dir	**Save file to directory**	*string*
ids-source	**Read resource ID(s) from source**	*string*

Input/Output Ports

The element has 1 *output port*:

Name in GUI: *Sequence*

Name in Workflow File: out-sequence

Slots:

Slot In GUI	Slot in Workflow File	Type
Sequence	**sequence**	*sequence*
Set of annotations	**annotations**	*annotation-table*