Read from Remote Database Element

Reads sequences and annotations if any from a remote database.

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

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*

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*