

# 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.

**Element type:** fetch-sequence

## Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
<b>Resource IDs</b> (required)	Semicolon-separated list of resource IDs in the database.		<b>resource-id</b>	<i>string</i>
<b>Database</b> (required)	Name of the database to read from.	NCBI Genbank (DNA sequence)	<b>database</b>	<i>string</i>  Available values are: <ul style="list-style-type: none"><li>• ncbi-dna (NCBI GenBank (DNA sequence))</li><li>• ncbi-protein (NCBI protein sequence database)</li><li>• pdb (PDB)</li><li>• swiss-plot (SWISS-PROT)</li><li>• uniprot-swiss-prot (UniProtKB /Swiss-Prot)</li><li>• uniprot-trembl (UniProtKB /TrEMBL)</li></ul>
<b>Save file to directory</b>	Directory to store a file loaded from the database.	default	<b>save-dir</b>	<i>string</i>
<b>Read resource ID(s) from source</b>	The source to read resource IDs from the list or a local file.	List of TDs	<b>ids-source</b>	<i>string</i>

## 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
<b>Sequence</b>	<b>sequence</b>	<i>sequence</i>
<b>Set of annotations</b>	<b>annotations</b>	<i>annotation-table</i>