

# 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	<p>string</p> <p>Available values are:</p> <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>
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