



BIONUMERICS Tutorial:

Importing sequences from online repositories

1 Aim

With the BIONUMERICS download routine, sequences can be downloaded from EBI, NCBI, and NIG and imported into BIONUMERICS. In this tutorial you will learn how to download some sequences from an online repository and import into BIONUMERICS.

2 The Import wizard

1. Create a new database (see tutorial "Creating a new database") or open an existing database.
2. In the *Main* window, select **File > Import...** (📁, **Ctrl+I**) to open the *Import* dialog box.
3. Choose the option **Download sequences from internet** under the **Sequence type data** item in the tree and click **<Import>**.
4. Enter the accession codes **X92694** and **X92707** in the **Accession codes** input field, separated by the separation character ",".
5. Specify "," as the **Separation character** and choose one of the available download sites from the list, e.g. **EBI**.
6. With the option **Preview sequences** checked, press **<Next>**.

The import routine fetches the sequences from the selected database and shows detailed information in the next step (see Figure 2).

7. Press **<Next>**.

The next step of the import wizard lists the templates that are present to import sequence information in the database. As this is the first time we import sequences from an online repository, we need to create a new import template by specifying **Import rules**.

8. Click **<Create new>** to create a new import template.

Each header tag (e.g. ID, AC, ...) corresponds to a row in the grid panel.

9. Select **AC - ACCESSION** in the list and click **<Edit destination>** or double-click on **AC - ACCESSION**. Select **Key**, and press **<OK>**.

The grid is updated (see Figure 3).

Import sequences ? X

Download
Download sequences from online repositories.

Accession code(s): X92694,X92707

Separation character: ,

Preferred download site: EBI (EMBL-Bank)

Pick up accession codes from field: Fetch

Search the other sites for unknown accession codes.
 Preview sequences

< Back Next > Cancel

Figure 1: Download sequences from an online repository.

Import sequences ? X

Sequences preview
Double-click on a sequence to open in the Sequence Viewer.

Nr.	File name	Length	Accession	Keywords
<input checked="" type="checkbox"/> 1	EBL_X92694	1372	X92694	16S ribosomal RNA; 16S rRNA gene.
<input checked="" type="checkbox"/> 1	EBL_X92707	1372	X92707	16S ribosomal RNA; 16S rRNA gene.

< Back Next > Cancel

Figure 2: Fetched information.

10. Click **<Next>** and press **<Finish>**.
11. Specify a template name (e.g. **EBI**) and optionally enter a description. Press **<OK>**.
12. Highlight the newly created template and select **Create new** as **Experiment type** (see Figure 4).
13. Press **<Next>**.
14. Specify a sequence type name (e.g. **16S**) and press **<OK>** and confirm the action (see Figure 5).

The *Database links* wizard page will indicate that 2 new entries will be created during import (see Figure 6).

Import template

Import rules
Select import sources and the database destinations

Source type	Source	Destination type	Destination
Sequence header	ID - LOCUS	<None>	<None>
Sequence header	AC - ACCESSION	Entry information	Key
Sequence header	SV - VERSION	<None>	<None>
Sequence header	NI - NID	<None>	<None>
Sequence header	DE - DEFINITION	<None>	<None>
Sequence header	KW - KEYWORDS	<None>	<None>
Sequence header	OS - SOURCE	<None>	<None>
Sequence header	OC - ORGANISM	<None>	<None>
Sequence header	RN - REFERENCE	<None>	<None>
Sequence header	RC - REMARK	<None>	<None>
Sequence header	RX - MEDLINE	<None>	<None>
Sequence header	RA - AUTHORS	<None>	<None>
Sequence header	RT - TITLE	<None>	<None>
Sequence header	RL - JOURNAL	<None>	<None>

Edit destination...
Preview...
 Show advanced options

< Back Next > Cancel

Figure 3: Create a new import template.

Import sequences

Import template
Specify how to import data into the database.

Import templates:

- <Default>
- EBI

EBI

Create new...
Edit...
Preview...
Copy...

Experiment type: <Create new>

< Back Next > Cancel

Figure 4: Select import template.

Create new

Provide a name for the new sequence type:

16S

OK Cancel

Figure 5: Create a new sequence type.

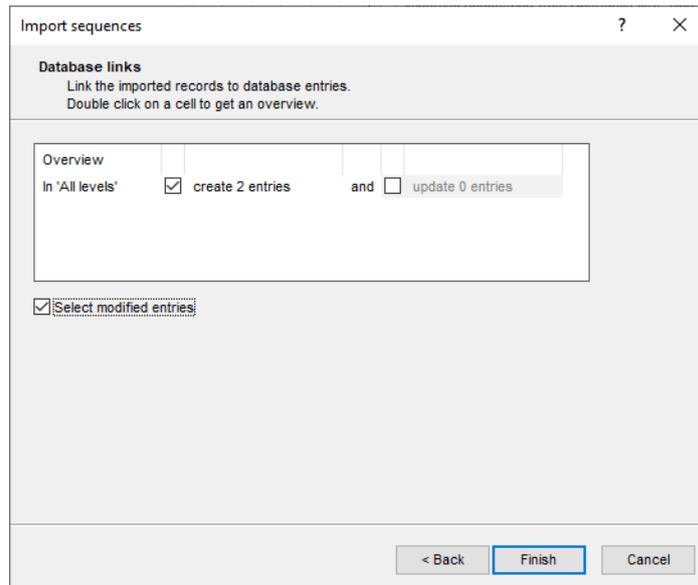


Figure 6: The *Database links* wizard page.

15. Press **<Finish>**.

The two sequences are imported in the database and are automatically selected (see Figure 7).

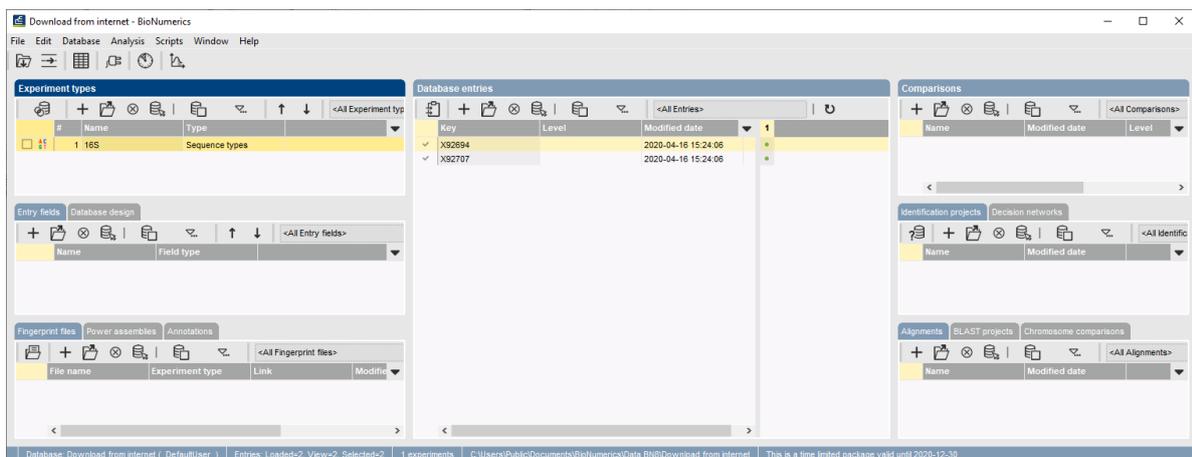


Figure 7: The *Main* window.

16. Click on a green colored dot in the *Experiment presence* panel to open the *Sequence editor* window.

The sequence is displayed in the upper panel and a graphical representation of the sequence is displayed in the panel below. The *Annotation* panel holds the EMBL features, and the header information is stored in the *Header* panel (see Figure 8).

3 Conclusion

In this tutorial you have seen how easy it is to download sequences from online repositories and import them in BIONUMERICS. The sequences can now be analyzed in BIONUMERICS. More information can be found in the analysis tutorials on our website.

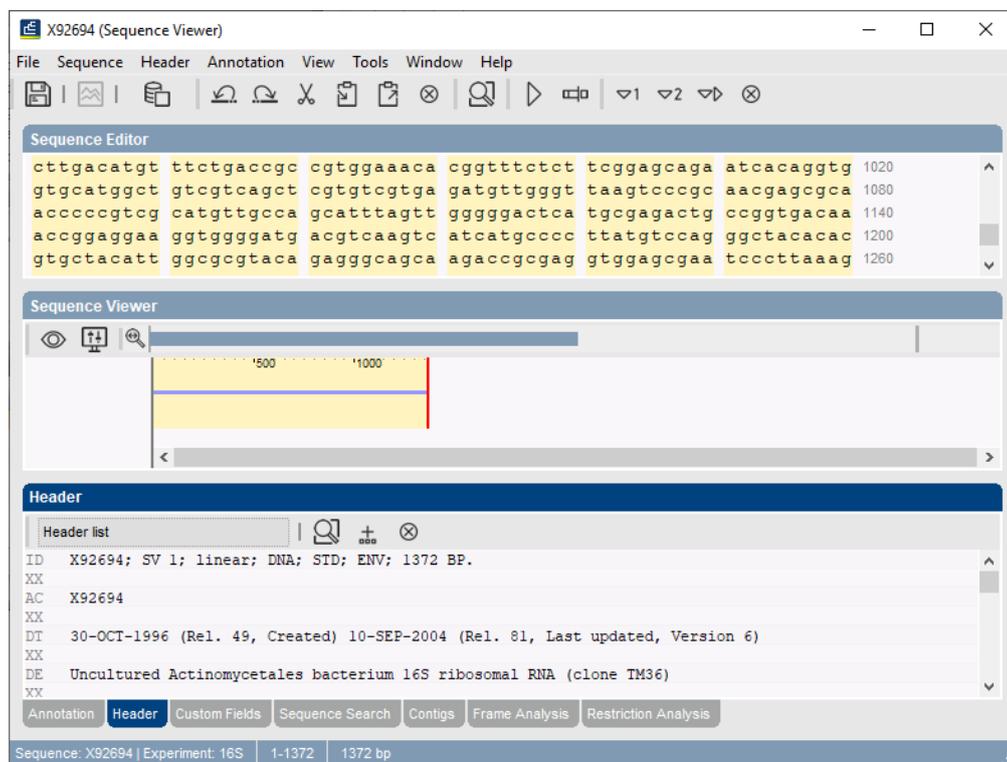


Figure 8: The *Sequence editor* window.