

# Shared Database

The rational storage of biological data is an ever-present issue. It is not only about large data sizes, but also about the requirement of simultaneous access to them by several scientists. For instance, a few researchers from a lab may need to work on the same data, like a set of primers or data produced by sequencing. That information has to be updated and synchronized between different users and kept in a common storage. That is what UGENE Shared Database is intended for.



To start sharing data via UGENE you need to deploy a public database server. MySQL servers are currently supported. See [this paragraph](#) for details about the required server configuration.

After that any UGENE user (who knows the correct login/password, however) can [connect to the database](#). The connected database is shown in the [Project View](#) as a document exactly the same way as if the data were located on the local computer.

As described in [this paragraph](#) the users can have a read-only access to the database or be able to modify its content. A user with a read-only access can:

- Browse the data in the database
- Open the data in the UGENE views
- [Export the data to the local computer](#)

Users with write access, in addition, can:

- [Add new objects to the database](#)
- Create new folders to order the data in the database
- Modify the folders hierarchy inside the database (using [drag'n'drop](#))
- Rename objects and folders
- Delete existed objects
- Delete folders

All UGENE instances connected to a database constantly monitors the state of the database and shows changes, made by other users.



UGENE accesses large remote data, such as NGS assemblies, so that only a viewed part of them is loaded to a client computer. So, if you store the assembly data on a server, the data can be browsed in the UGENE Assembly Browser on a local computer almost instantly, without the need to copy the data on the computer or use the hard disk space.

For details see the documentation below:

- [Configuring Database](#)
- [Connecting to a Shared Database](#)
- [Adding Data to the Database](#)
- [Database in the Project](#)
- [Deleting Data](#)
- [Drag'n'drop in the Database](#)
- [Exporting Objects from the Database](#)