

Crystallography demand

User Identity Protein Description Plate Selection Experimental Details

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Industry - No

Comments

save profil

load profil

validate

Figure 1S *User Identity*: There are fields that the user must fill, to associate the crystallization request to its demander.

Protein Description

Number of proteins: 1 2 3

1

Name:

Origin:

Category:

Expression:

Fusion protein:

Volume:

Concent.:

Buffer:

Comments:

Preliminary characterisations:

- ☐ Activity test
- ☐ DLS
- ☐ CD
- ☐ mass spectrometry
- ☐ Sequencing
- ☐ Gel filtration

Protein crystallized:

Homologue or mutant crystallized:

Toxic risk:

Conservation:

load protein

save protein

modify

validate

Figure 2S *Protein Description*: Different fields concerning the protein are needed during the experiment request. As for other data, protein information can be loaded and saved.

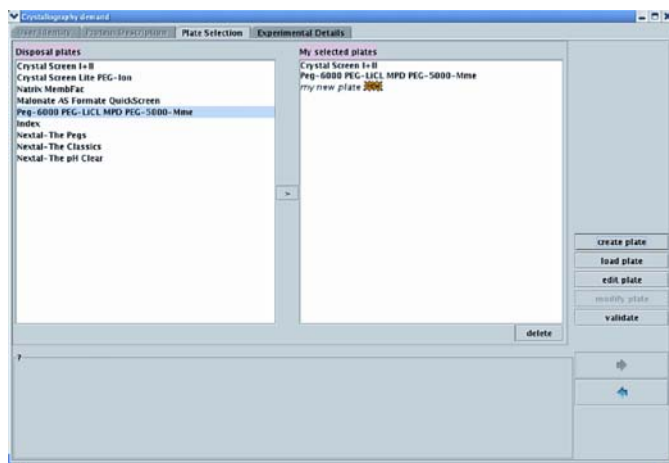


Figure 3S *Plate Selection*: It is possible to select plates from a list of pre-installed already existing crystallization kits, or to create personalized ones.

The image shows a software window titled "New plate" with a tabbed interface. The "Description" tab is active, showing the following fields:

- Plate type:** A dropdown menu currently set to "Vapor Batch Douglas L 96 wells".
- Plate name:** A text input field containing "my new plate".
- Well volume:** A text input field containing "100" followed by a unit dropdown menu set to "µl".
- Comments:** A large, empty text area for additional notes.

At the bottom right of the dialog, there are two buttons: "validate" and a button with a plus icon.

Figure 4S *New Plate Description*: A plate is specified by its type (*e.g.* 24 or 96 well), its name and the well volume.

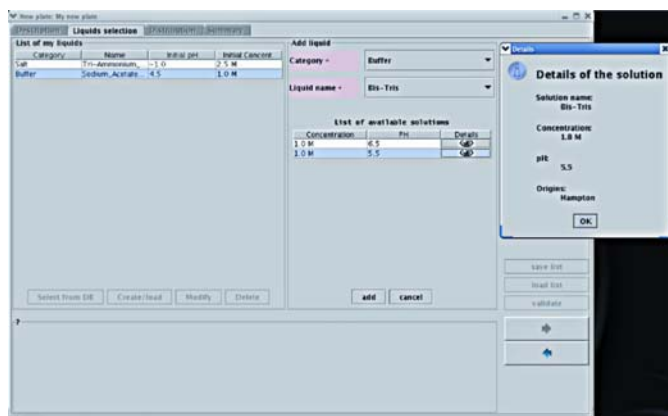


Figure 5S *New Plate Solution Manager*: The experimentalist selects the solutions to be used to fill his plate. He can select them from the data base or create his own new stock solutions.

