

Luisa Zini, Proteome Software, Inc

In Scaffold 3.00.06, a new feature, called **Configure Protein Annotation Preferences**, has been added to the **Samples View**. It allows for easier selection of the representative members of protein families included in the list of identified proteins. The new feature acts globally on the list, allowing the user to set a series of preferences that will determine which family member will be viewed in the list.

Most Scaffold users are familiar with the **Samples View**. In this view, once the sample files are loaded, a list of identified proteins is shown. If several proteins are identified by the same peptides, they will be grouped together in a family. The number in parenthesis, appearing next to the protein accession number, gives the count of proteins included in the family in addition to the one showed in the Scaffold list.

3	<input checked="" type="checkbox"/>	(P02522) Beta crystallin B2 (BP)	CRBB2_BOVIN	23 kDa	100%
4	<input checked="" type="checkbox"/>	(P07318) Beta crystallin B1	CRBB1_BOVIN	28 kDa	100%
5	<input checked="" type="checkbox"/>	(PX1842) beta A4 crystallin, new sequenc...	CRBD_BOVIN (+1)	22 kDa	100%
6	<input checked="" type="checkbox"/>	(P26444) Beta crystallin A2 (Beta-A2-cry...	CRBA2_BOVIN	22 kDa	100%

Figure 1 Example of a selected protein family in the Proteins View

The standard way of changing which member of the protein family shows in the list is to select a protein family and then go to the Protein information pane, located at the bottom left corner of the **Samples View**. In this pane it is possible to select, through the preferred accession number pull-down menu, which protein represents a particular family. When the list of identified proteins is quite long, using this type of approach may feel daunting. This is the time when **Configure Protein Annotation Preferences** will help rearrange all the protein family appearances with one click.

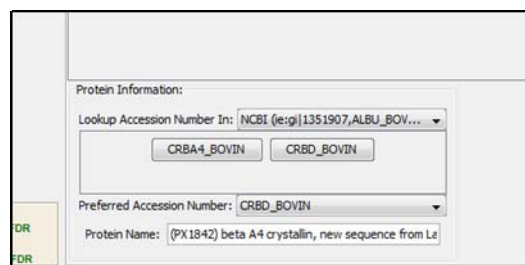


Figure 2 Protein Information Pane

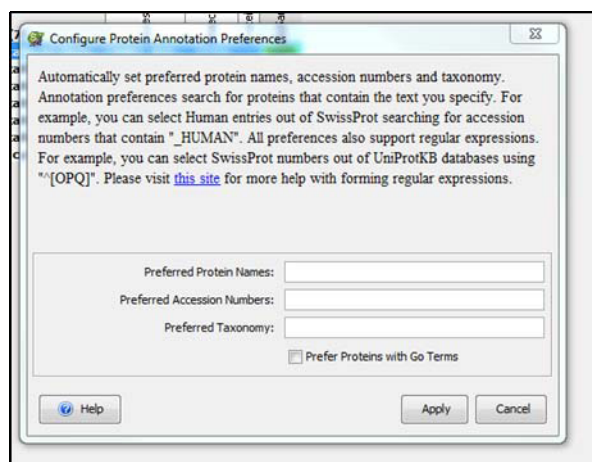


Figure 3 New feature window

To access this feature go to the Experiment menu and select **Apply Protein Annotation Preferences**. The window **Configure Protein Annotation Preferences** will appear. It contains three text boxes that allow performing searches over preferred protein names, accession numbers and taxonomy. Searches can be done over a particular name that is contained in the proteins description, for example. The setting of the preferences also supports regular expressions. In addition, there is a check box that ensures that the preferred protein showed has associated GO terms. Once you have defined your choices click OK and the list of protein will get rearranged showing the desired type of protein for each family included in the list. Please let us know how you like the feature; we appreciate your feedback.