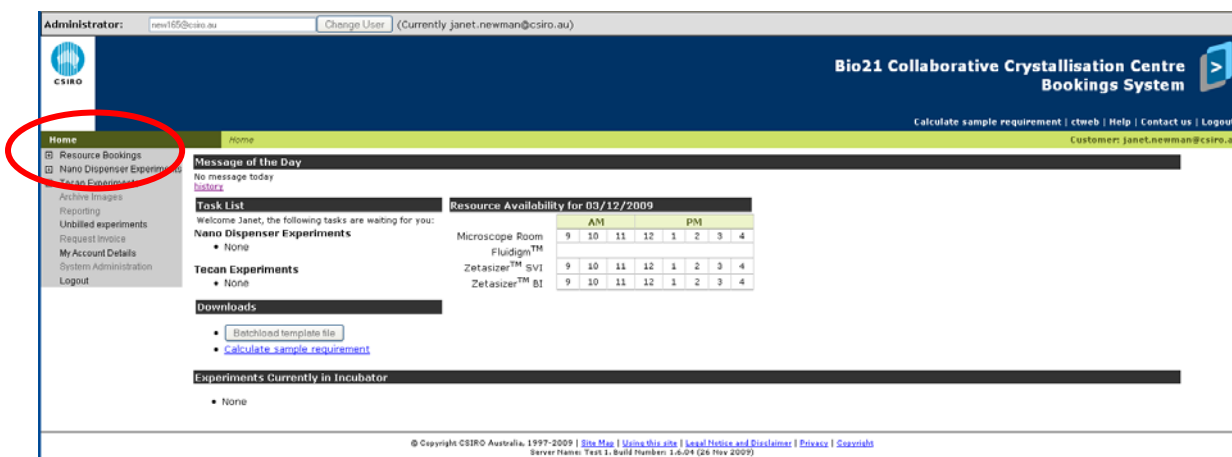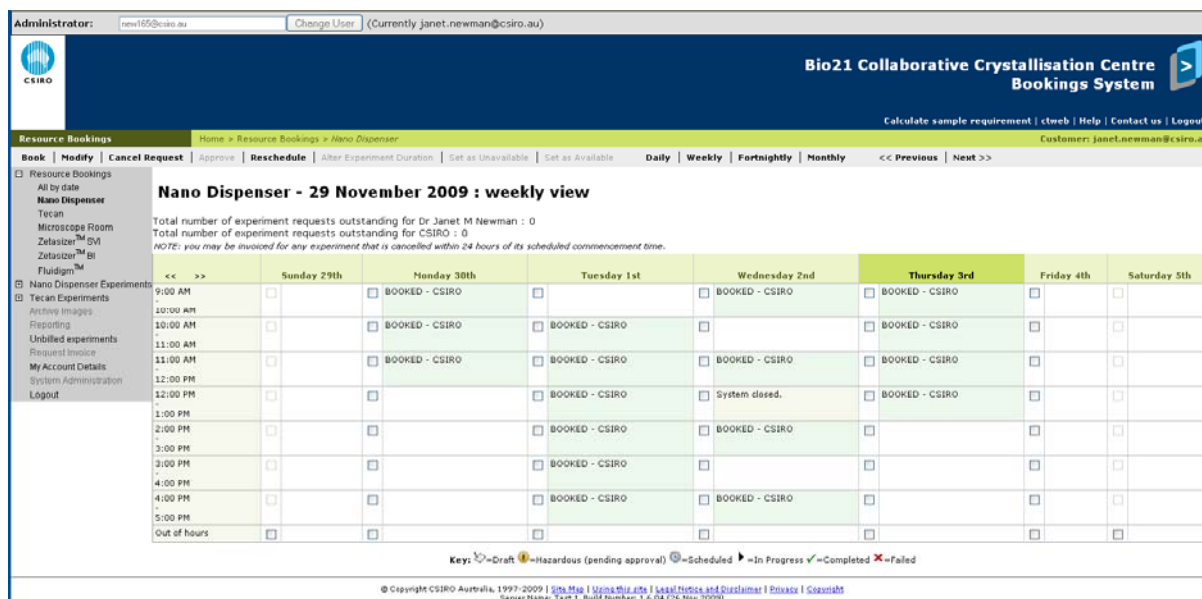# Batchload wizard

The batchload wizard has been implemented to simplify the process of providing us with information about your sample, and what you want us to do with it.

The logic of booking a sample into the C3 is still the same – you log into the booking software (https://c3.csiro.au/login.do), and select **Resource Bookings** from the sidebar (circled below)

This will open up the calendar for the **Nano Dispenser**:

Select a *single* slot (the starting time) for when you would like your sample to be run, irrespective of how many plates your experiment has:

Then click **Book** which is up on the left hand side of the menu toolbar

This opens a booking form, which is the form where you tell us about your sample – there has to be a "batchload file" associated with each booking. This is a tab-delimited text file in a format that can be uploaded directed into our crystallisation database. If you know how to create one of these, you can upload it directly through the booking form (use the "browse" button to locate your batchload on your local file system, and hit "Open" to upload the file once you have located it. If you upload your own batchload file, you must fill in the field "Total Number of Plates for Experiment").

Right above the "browse" button there is a "start" button (circled below in red) – clicking this will open the *batchload wizard*, which will walk you through the creation and attachment of the required batchload file. Once you have created (or uploaded) your batchload file, you need to indicate if the work is commercial or not, if there are hazards associated with the sample, and whether or not the

sample has properties that might make it difficult to dispense. You can also choose NOT to have the Mosquito™ dispenser used in your experiment.

Creating a batchload file using the batchload wizard:

Click on "Start" on the open booking form. This will bring up a new window, with two tabs **Sample Entry** and **Summary**. The window will open up on the **Sample Entry** tab

For each sample that you will be providing to C3 for that booking, you need to provide five pieces of information, and then click "Add Sample" (circled in red, below):

Sample Name

This how you identify the sample that you provide – "Peak2_28Nov2009" for example. The sample name should not include the special characters $,#,/,',*,^

Protein Name

This is the protein that is in the sample – one generally has many samples of the same protein

Protein Concentration

This is the concentration of the protein in the sample, in mg/ml.
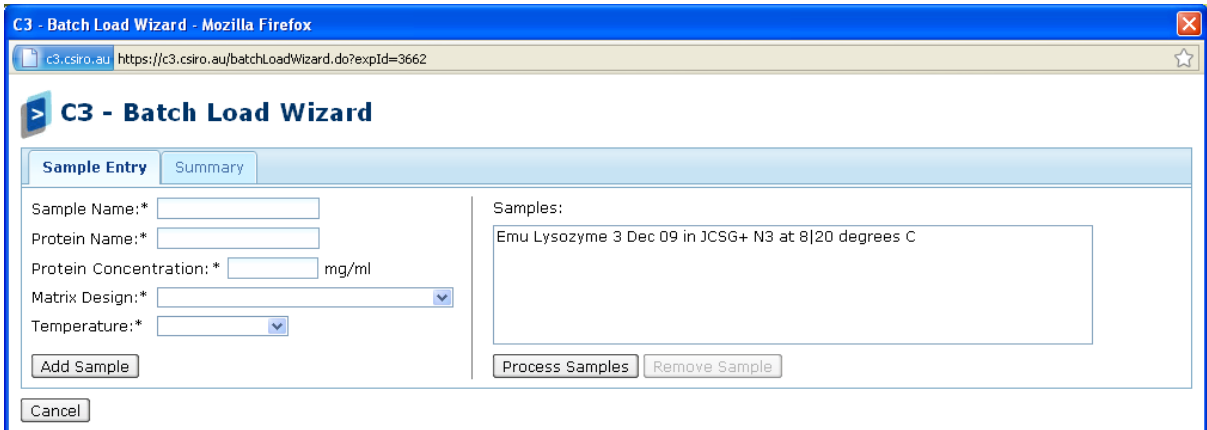
Matrix Design

Matrix design is the screen (or set of screens) that you want to set your sample up against. You select the matrix design from a pulldown selector, which is populated on the fly from the CrystalTrak database. There are four different queries used to populate the menu. The first query returns which screens are available for general use in C3, the second query returns the current design_sets (groups of screens that are run as a single set), the third query returns which screens are available that belong to you, and the fourth query returns your additive screen designs.
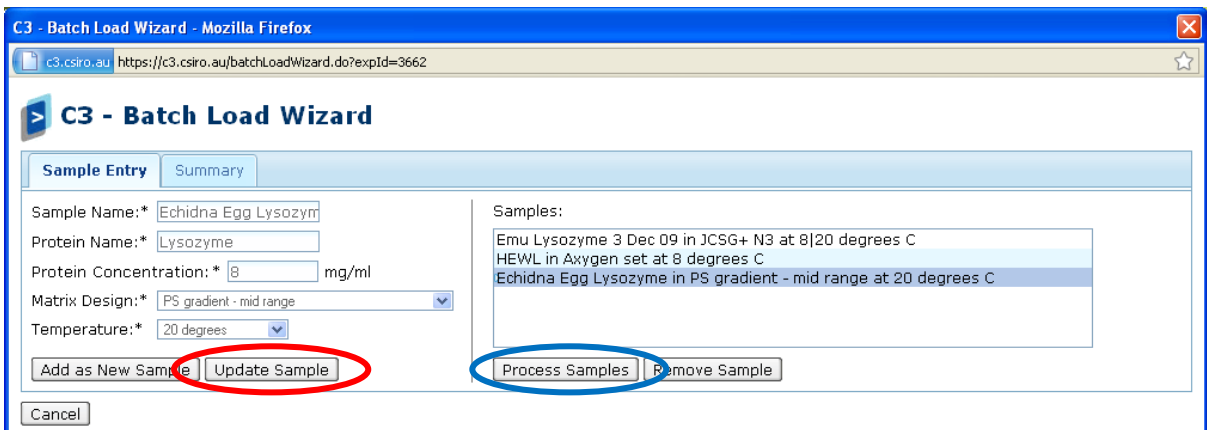
Temperature

Plates may be incubated at either 20 C or 8 C. The option "8 and 20" will create two plates, one to be incubated at 20 C and one to be incubated at 8 C
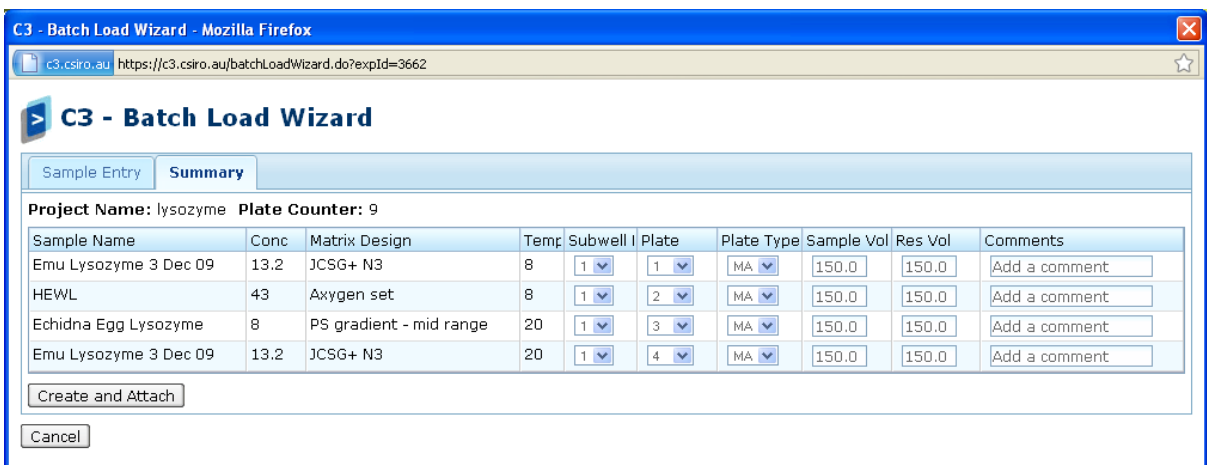

A summary of what you entered will be seen in the "Samples" field on the right hand side
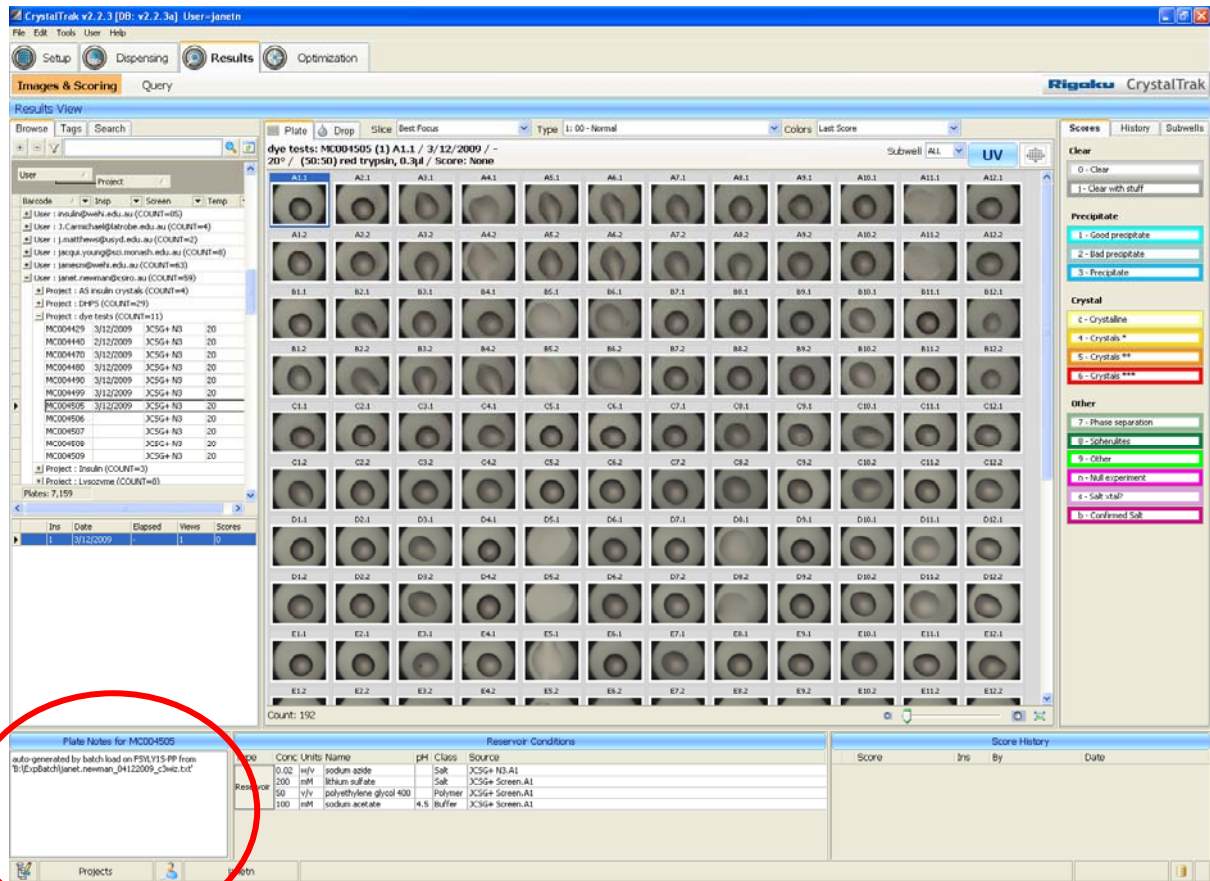
Add further samples the same way, by filling in the five required fields and clicking "Add Sample". If you need to alter a sample, select in the in "Samples" field by clicking on it – this will re-populate the five fields on the left and allows you to edit the sample details. Click "Update Sample" to save your changes.

Once you are happy with your samples, click "Process Samples" (circled in blue, above) to show the **Summary** tab

On this screen you can edit the sample volume and reservoir volume of the drops, and can edit the subwell assignment (Subwell No) for the sample. The wizard will group samples which share a matrix design and temperature onto MC plates automatically. Any text typed into the "Comments" field will be placed in the "Plate Notes" field in the results view in CrystalTrak or CTweb

Once you are satisfied that you have chosen the appropriate sample and reservoir volumes, and have samples grouped together on the plates as you want them, click on "Create and Attach" to generate a batchload file, attach it to that booking, fill in the number plates for the experiment and block out the appropriate amount of time in the calendar. You will be sent an email to confirm your booking.

If you do not receive an email, and if the booking is PINK (not pale green) then your booking Is not valid, and you should try again, or contact c3@csiro.au for help.