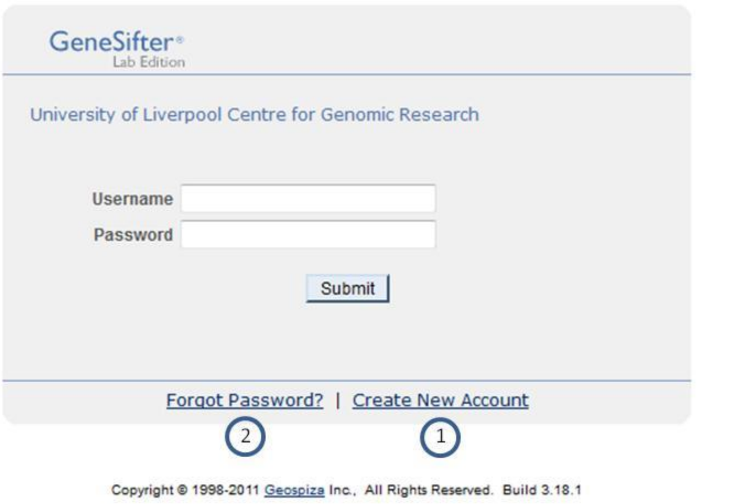
Guide to the Laboratory Information Management System used at the Centre for Genomic Research

Introduction

The Centre for Genomic Research (CGR) is introducing a Laboratory Information Management System (LIMS) for submission and processing of samples for sequencing. The GeneSifter software by Geospiza will streamline our procedures and provide our users with an enhanced service, including tracking progress of orders and samples. This document is a step-by-step guide to help you navigate the GeneSifter LIMS.

To log in or create a new account, please go to http://cgrlms.liv.ac.uk/login and provide the required information (to follow the website link, just hover the mouse above the link, press Crtl and left-click on the mouse).

Figure 1



In figure 1, please log in using your existing username and password, or click

① Create new account if you are a new user and log in using your chosen user name and password.

② Forgot password if you are an existing user, but have forgotten your password.

Figure 2

Figure 2 shows your personal homepage once you have logged in.

The dashboard "My orders" gives an overview of the orders you have placed with the CGR.

The menu on the left is used to navigate LIMS or place new orders.

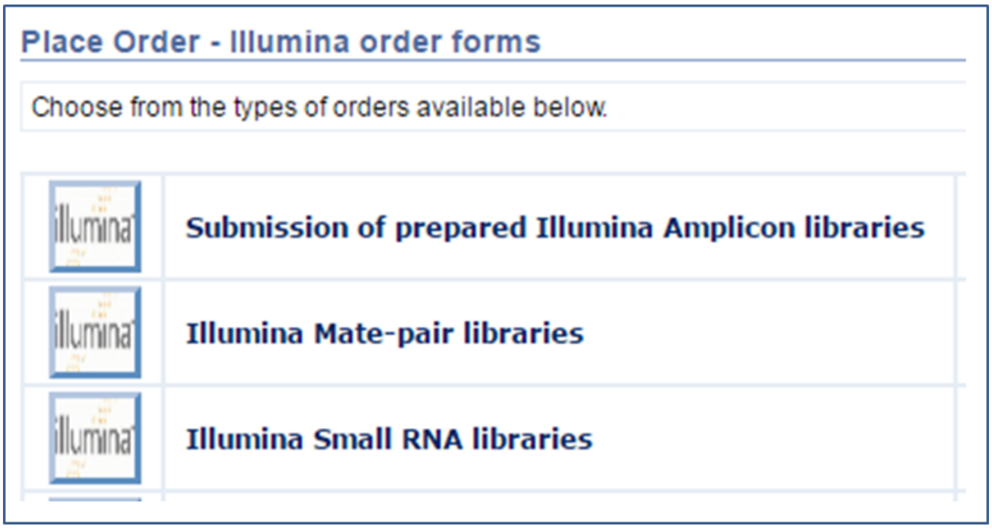
Place an order - Part 1: Open the appropriate sample submission form

To place an order, your user details have to include information about "Groups".

If you are a returning user this information will already be in you details. However, if you are a new user, the Centre for Genomic Research will be notified when you register and we will add this information to your user details. In the meantime, you are able to create an order, but you cannot submit this until you have been assigned to a group.

Step 1: Click on "Place order" in the left hand menu of your homepage (see Figure 2 above) to get an overview of the available sequencing platforms at the CGR:

Step 2: Click on the icon of the platform you require to get an overview of the available library types within the chosen sequencing platform:


Place Order - Illumina order forms

Choose from the types of orders available below.

Submission of prepared Illumina Amplicon libraries

Illumina Mate-pair libraries

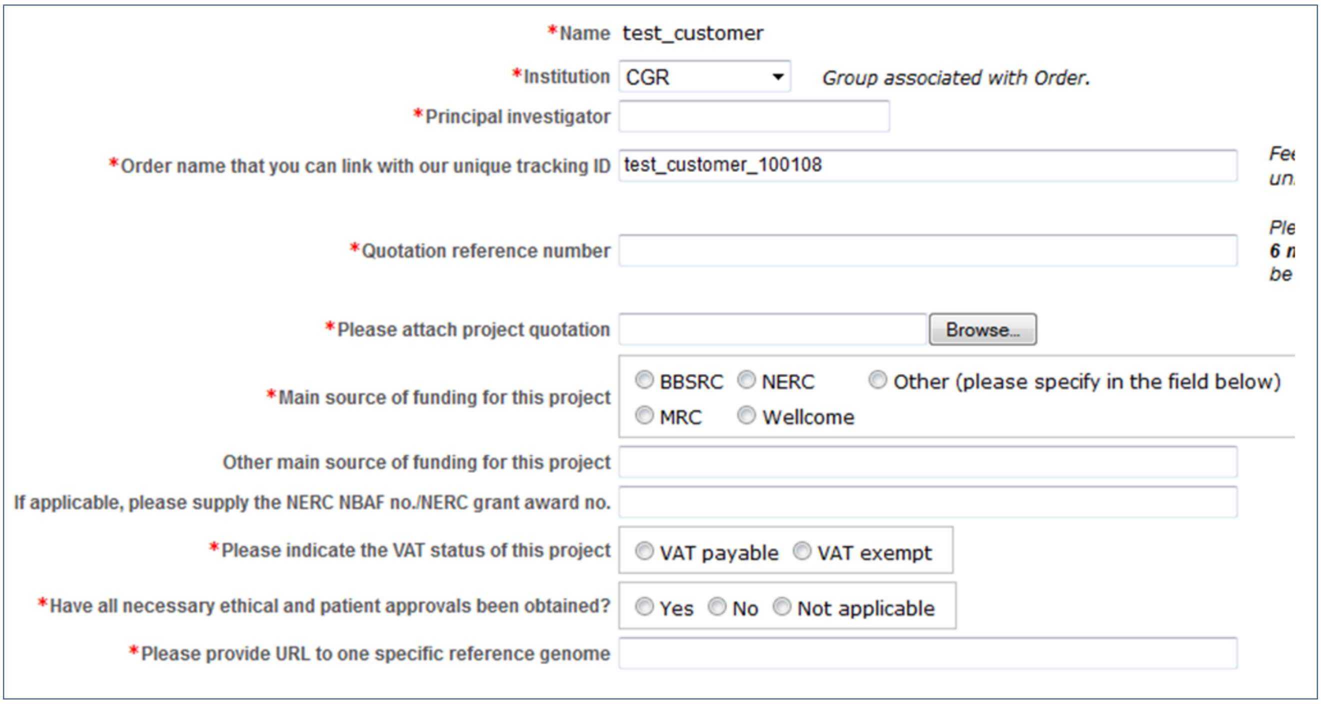
Illumina Small RNA libraries

Step 3: Click on the appropriate library type to open the relevant order form.

If you require multiple types of sequencing, you will need to make multiple orders, using the relevant order form for each.

Place an order - Part 2: Complete the project and sample information form

Figure 3


*Name test_customer

*Institution CGR *Group associated with Order.*

*Principal investigator

*Order name that you can link with our unique tracking ID test_customer_100108

*Quotation reference number

*Please attach project quotation Browse...

*Main source of funding for this project ◯ BBSRC ◯ NERC ◯ Other (please specify in the field below) ◯ MRC ◯ Wellcome

Other main source of funding for this project

If applicable, please supply the NERC NBAF no./NERC grant award no.

*Please indicate the VAT status of this project ◯ VAT payable ◯ VAT exempt

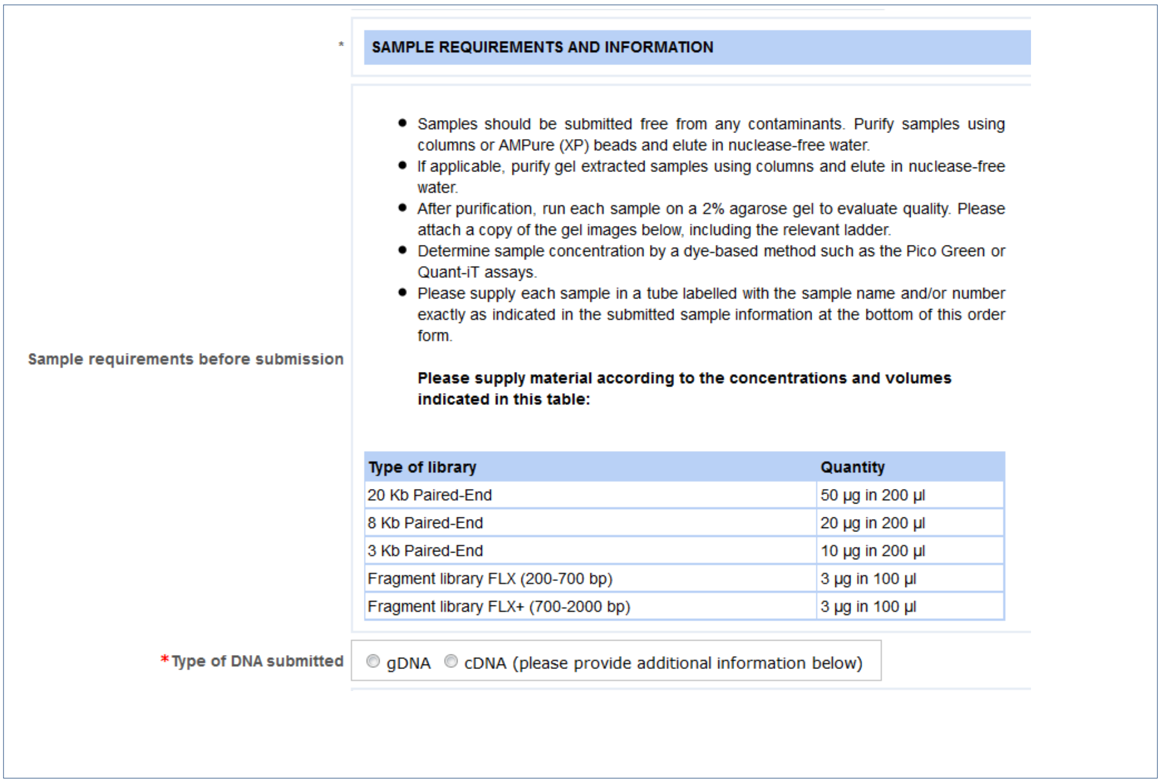
*Have all necessary ethical and patient approvals been obtained? ◯ Yes ◯ No ◯ Not applicable

*Please provide URL to one specific reference genome

Figure 3 shows some information we require for all types of orders.

Note that all required fields are denoted with a red asterisk and you will not be able to submit the order without completion of those.

Figure 4



SAMPLE REQUIREMENTS AND INFORMATION

Sample requirements before submission

- Samples should be submitted free from any contaminants. Purify samples using columns or AMPure (XP) beads and elute in nuclease-free water.
- If applicable, purify gel extracted samples using columns and elute in nuclease-free water.
- After purification, run each sample on a 2% agarose gel to evaluate quality. Please attach a copy of the gel images below, including the relevant ladder.
- Determine sample concentration by a dye-based method such as the Pico Green or Quant-iT assays.
- Please supply each sample in a tube labelled with the sample name and/or number exactly as indicated in the submitted sample information at the bottom of this order form.

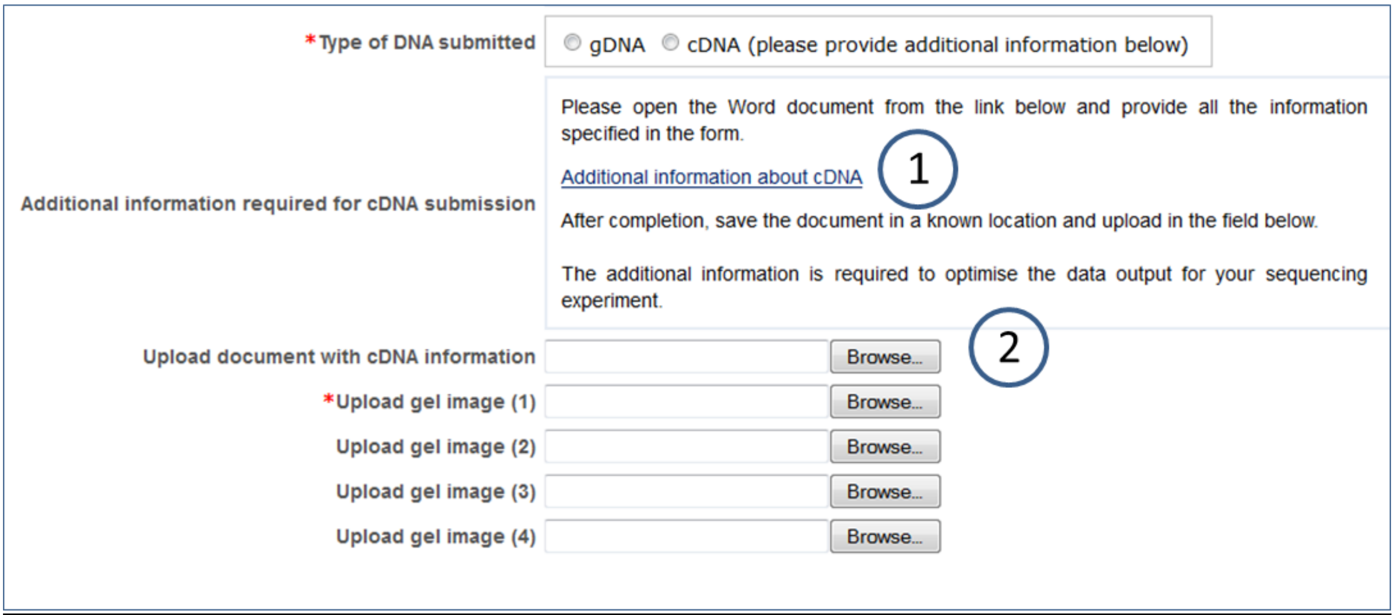
Please supply material according to the concentrations and volumes indicated in this table:

Type of library	Quantity
20 Kb Paired-End	50 µg in 200 µl
8 Kb Paired-End	20 µg in 200 µl
3 Kb Paired-End	10 µg in 200 µl
Fragment library FLX (200-700 bp)	3 µg in 100 µl
Fragment library FLX+ (700-2000 bp)	3 µg in 100 µl

*Type of DNA submitted: gDNA / cDNA (please provide additional information below)

Figure 4 shows an example of sample requirements. These obviously differ depending on the type of samples, libraries and platform. **Please check the specific requirements before you prepare your samples for submission.**

Figure 5



*Type of DNA submitted: gDNA / cDNA (please provide additional information below)

Additional information required for cDNA submission

Please open the Word document from the link below and provide all the information specified in the form.

Additional information about cDNA 1

After completion, save the document in a known location and upload in the field below.

The additional information is required to optimise the data output for your sequencing experiment.

Upload document with cDNA information [Browse...] 2

*Upload gel image (1) [Browse...]

Upload gel image (2) [Browse...]

Upload gel image (3) [Browse...]

Upload gel image (4) [Browse...]

Figure 5 illustrates that for some sample types, we require additional information.

① Details of the additional information is provided in a document that can be downloaded via a link on the order form.

② Once completed and saved, the document can be uploaded using the browsing dialog box.

At the bottom of the order form there is a sample information table that needs to be completed for each sample.

Figure 6

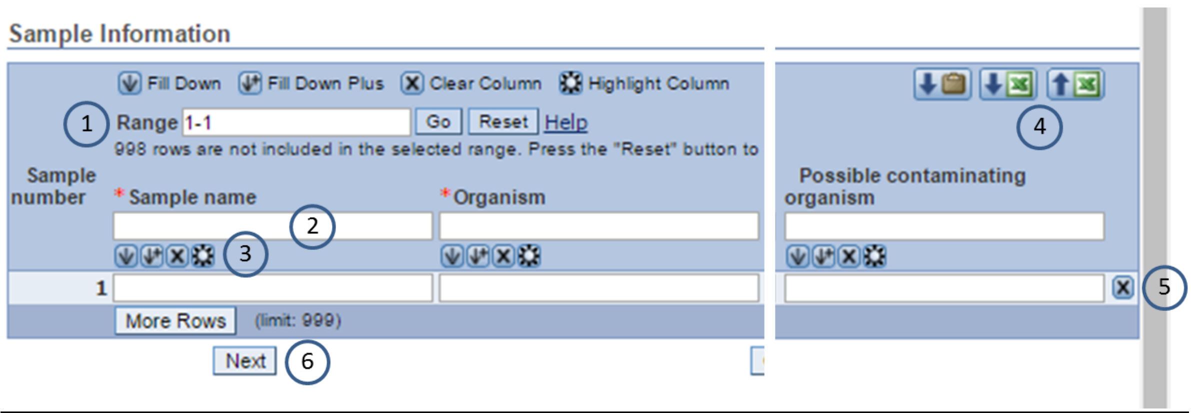


Figure 6 shows a small part of a sample information table. Please read below for information on ① - ⑥.

① Please enter the required range of rows needed for you samples (1-6 for six samples, for example).

You can enter the information in each column and row individually or you can use the Easy fill controls.

To use the Easy fill controls:

② Enter the required information in the field at the top of the column.

③ Fill in the remainder of the column by clicking on one of the Easy fill control icons.

See the table below for a description of their use.

Easy fill control	Description
	Fills every row in the column with the information that was entered in the field at the top of the column ②
	Can be used if the information entered in the field at the top of the column ② ends with a digit. Using the "Fill down plus" icon will automatically increment the last digit of the entry by one for each row.
	Deletes all information entered in the column
	Locks all other columns, allowing you to use the tab key to move to the next row when entering data in the highlighted column

④ You can also use the Excel download/upload Easy fill controls. The table below gives a description of their use.

Easy fill control	Description
	Downloads the input grid (sample information table) into Excel. •If you use this option, you <u>cannot</u> make any changes to the contents of the top row of the grid or to the column number/order. If you make changes to any of those, the grid will not be recognised by GeneSifter and, hence, you will not be able to upload the data entries. •If you choose to complete a sample field with a dropdown menu while in Excel, you have pick one of the options from the menu (**exact** wording). •Once you have completed the grid, save it in a known location and upload the information using the icon described below.
	Uploads a completed input grid (sample information table) from a known location. <u>Note</u> that the table on the bottom may be wider than the screen and, hence, the pop-up window that appears when you click the upload file icon could be out of view on the far left of the screen. <u>Note</u> that other files will need to be uploaded **after** you have uploaded data from Excel.

⑤ If you click the  icon, you remove all the information entered in that row.

⑥ Finally, when all required (indicated by a red asterisk) information has been entered, click Next to complete this part of placing the order.

Place an order - Part 3: Completion of the purchasing information form

When you have submitted the project and sample information form, you will automatically get to a summary page similar to the one in Figure 7.

Figure 7

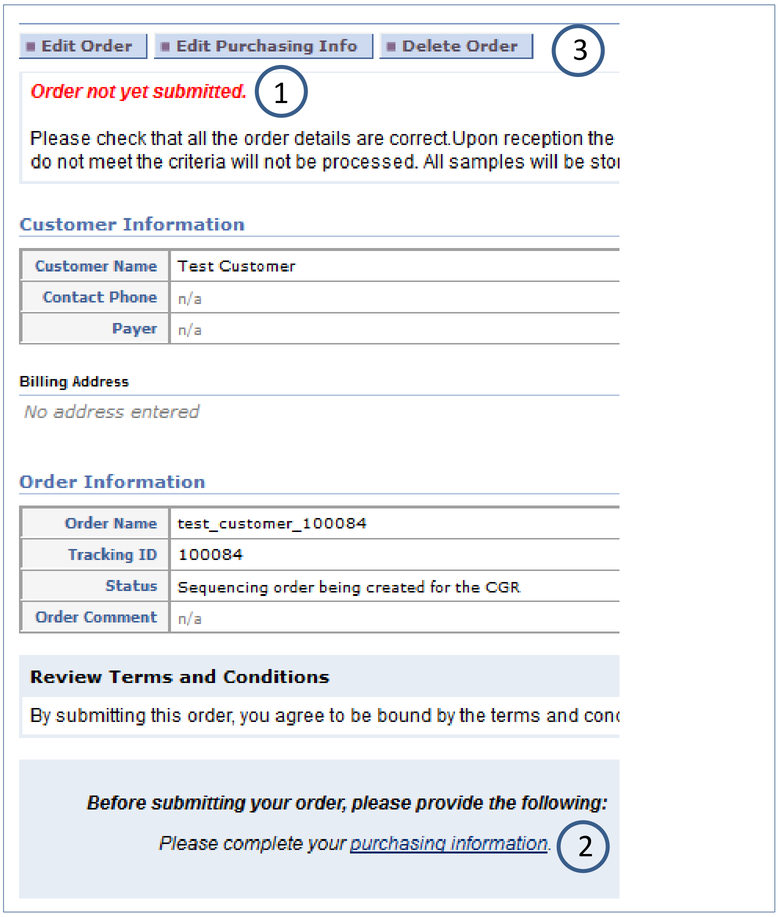


Figure 7 illustrates:

① After completion of the project and sample information form, the order is not yet submitted.

② You are required to provide the purchasing information (see more about this in Figure 8 below).

③ Throughout GeneSifter you will find blue action buttons at the top of the page. Click on these to carry out the labelled functions; for example, to edit or delete an order.

Figure 8

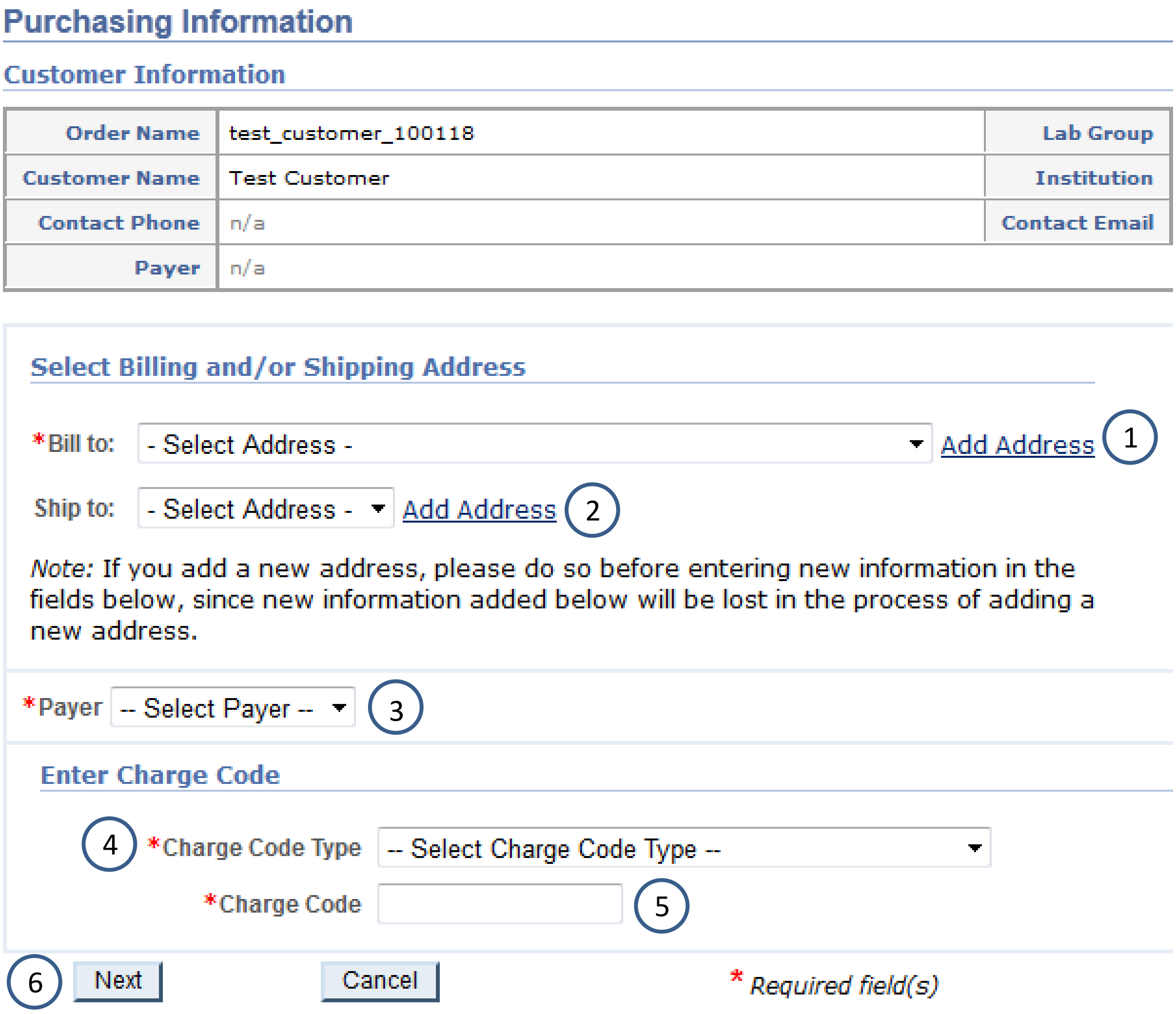


Figure 8 shows the purchasing information that needs to be completed.

① Please select the name and address of your principal investigator in the "Bill to" dropdown menu. If the details are not already there, please add them using the Add address link. This is required for invoicing.

② Enter your own address in the "Ship to" dropdown menu. This is not a required field. However, if you want to complete the information and your details are not already there, or you need to edit them, please use the Add address link. You will only need to do this once unless your details change.

③ Please select the payer of the order from the dropdown menu.

④- ⑤ Enter the Charge code type plus Charge code, depending on where your funding is held. See the table below to decide which type of charge code is appropriate for your order/project.

Charge code type	Charge code description
Purchase order number	For • all users outside the University of Liverpool • NERC NBAF award holders, if the principal investigator holds the funds.
Cost centre code	For University of Liverpool users only. Valid format for the cost centre code is 3 capital letters followed by 5 digits. The complete funds will be charged against your grant when the project is completed.
NERC NBAF number	Please enter the NBAF number only, if NERC or the Centre for Genomic Research hold the funds for this project.

Funds held with the Centre for Genomic Research	Please provide the AGF number for reference. If you have not already obtained this, please contact Lesley Parsons (parsonsl@liv.ac.uk).
Centre for Genomic Research R&D	For R&D projects within the CGR only. Please provide the cost centre code in the format 3 capital letters followed by 5 digits.
TD voucher scheme	Please enter the commitment reference number provided by the Technology Directorate.
MIF-OMIC credit	For projects funded by the MIF-OMIC credit scheme

⑥ Once you have completed the purchasing information and clicked the Next button, you are directed to either:

If you are a returning user: A page similar to Figure 7. However, the "Submit order" button is now active, because you have submitted the purchasing information.

If you are a new user: The order form to complete the field "Institution". Once that is done, please save the order form and you will now get to a page similar to Figure 7. However, the "Submit order" button is now active, because you have submitted the purchasing information and completed the order form.

TO COMPLETE THE SUBMISSION YOU HAVE TO CLICK THE SUBMIT ORDER BUTTON FOUND BELOW THE ORDER INFORMATION TABLE.