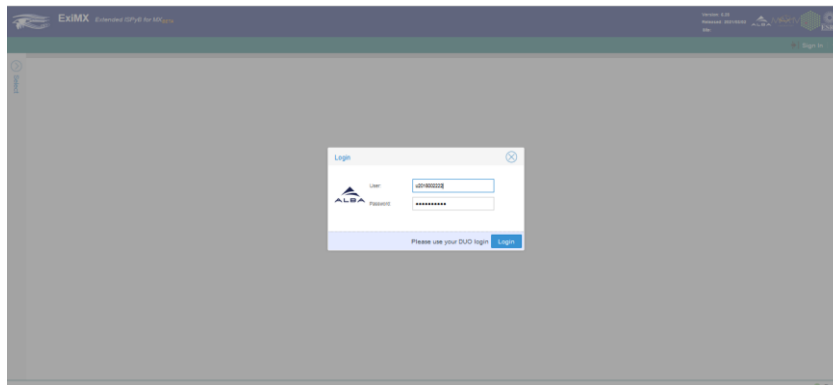
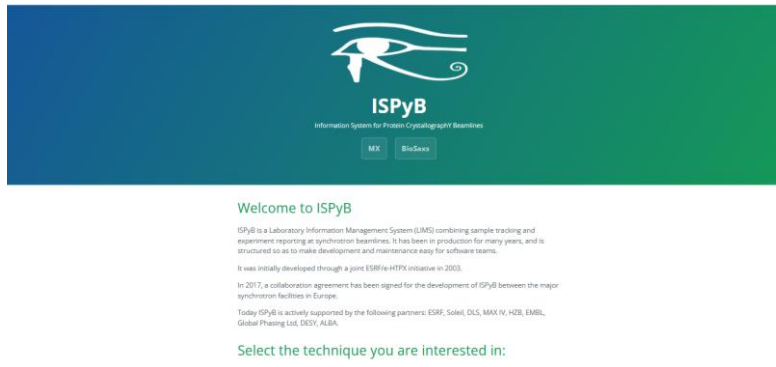
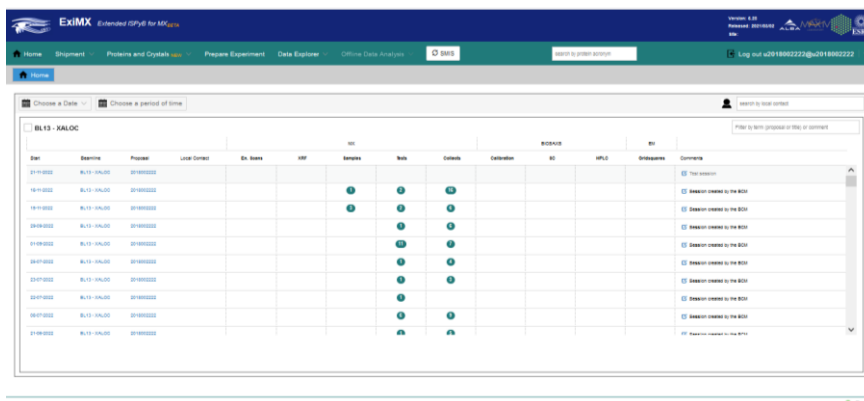


ISPyB EXI User Manual XALOC Beamline

- In your favourite web browser go to <https://ispyb.cells.es/> and choose MX.



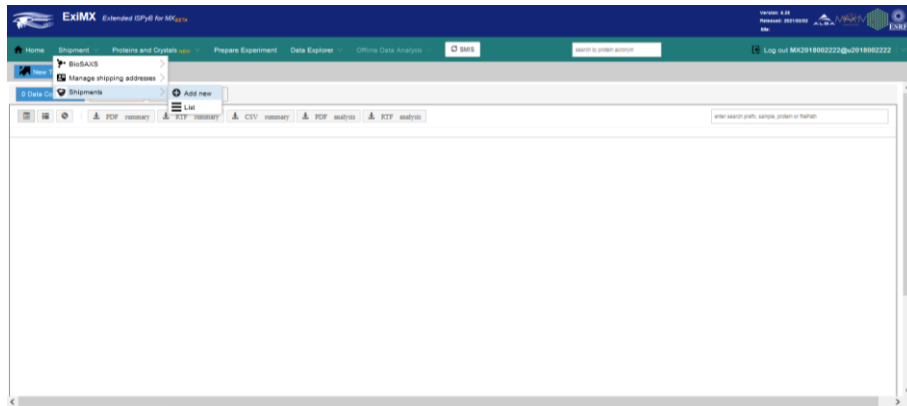
- Login to EXI using the credentials of your proposal
- In order to load your samples in EXI, first enter in the session corresponding to your beamtime (in the example shown, 21/11/2022)



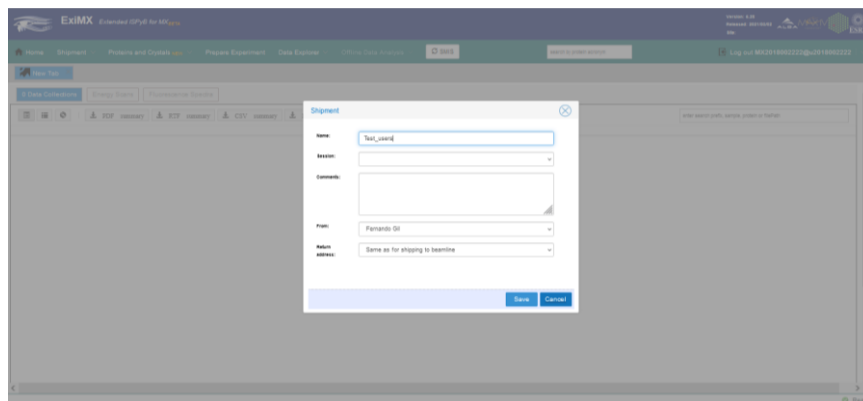
Date	Beamline	Proposal	Local Contact	Ex. beam	AMP	Samples	Note	Controls	Calibration	ID	URL	Outcomes	Comments
21/11/2022	BL13-KALOC	01180222				1	1	1					This session
18/11/2022	BL13-KALOC	01180222				1	1	1					Session created by the BCH
18/11/2022	BL13-KALOC	01180222				1	1	1					Session created by the BCH
04/08/2022	BL13-KALOC	01180222				1	1	1					Session created by the BCH
01/08/2022	BL13-KALOC	01180222				1	1	1					Session created by the BCH
04/07/2022	BL13-KALOC	01180222				1	1	1					Session created by the BCH
23/07/2022	BL13-KALOC	01180222				1	1	1					Session created by the BCH
08/07/2022	BL13-KALOC	01180222				1	1	1					Session created by the BCH
08/07/2022	BL13-KALOC	01180222				1	1	1					Session created by the BCH
01/08/2022	BL13-KALOC	01180222				1	1	1					Session created by the BCH



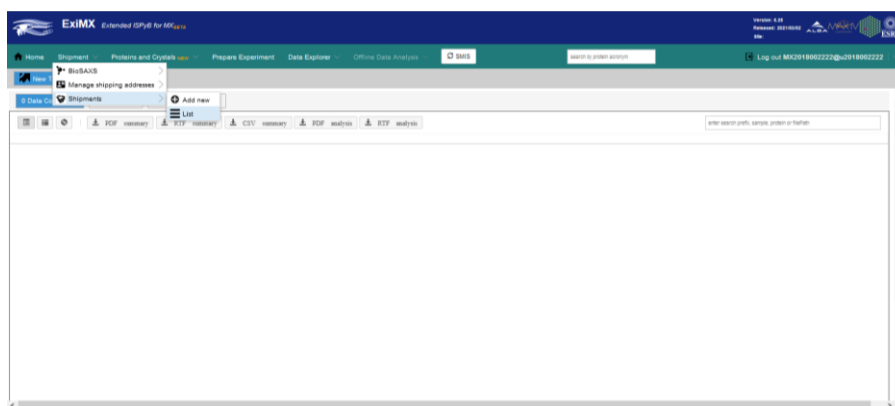
- Create a new shipment: To do that go to shipment in the upper menu and press Shipment>Add new



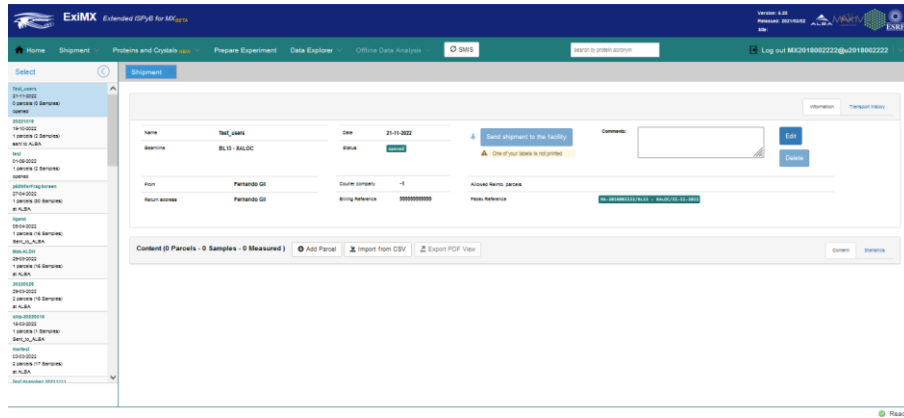
- Create the new shipment by adding a name, a contact person and choosing the corresponding session in the pull down menu.



- Go to the list of shipments in the Shipment menu: Shipment>list.



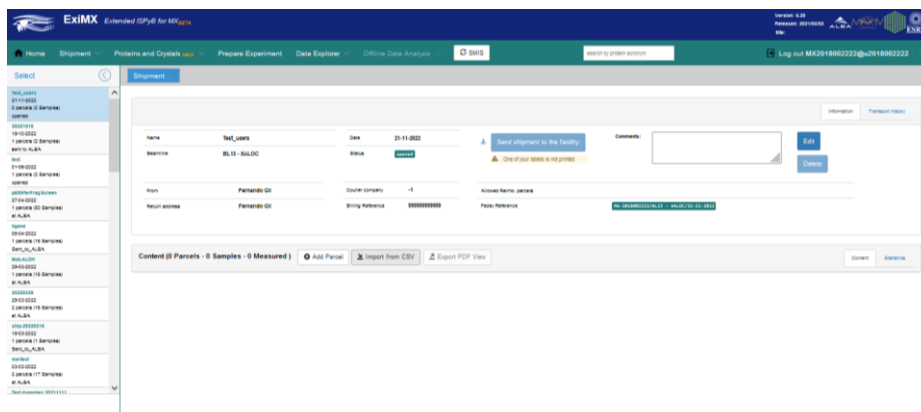
- Select your shipment from the list on the left. Now it is time to load your parcel (dewar) and samples information in EXI.



- The easier option to load your samples would be the use of the CSV template provided (here) filling the different fields. It is not required to fill everything but there are several mandatory fields. Information in columns A to F is mandatory.

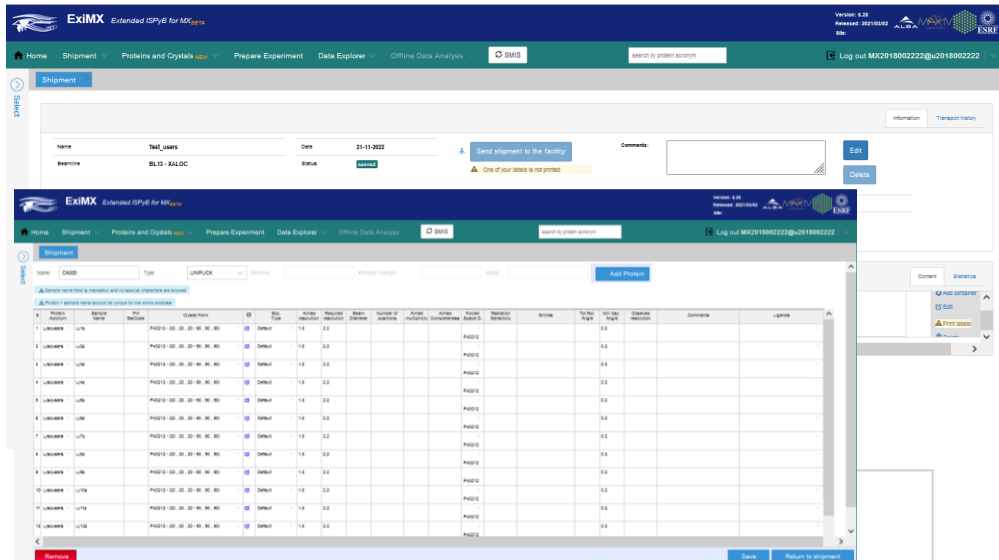
A	B	C	D	E	F	G	H	I	
2	Facial name	container name	container type	container position	protein acronym	sample acronym	pin barcode	SPG	cell
3	Dewar10	CA300	Unspuck		1Lysosmers	Ly1z		P43212	20
4	Dewar10	CA300	Unspuck		2Lysosmers	Ly2z		P43212	20
5	Dewar10	CA300	Unspuck		3Lysosmers	Ly3z		P43212	20
6	Dewar10	CA300	Unspuck		4Lysosmers	Ly4z		P43212	20
7	Dewar10	CA300	Unspuck		5Lysosmers	Ly5z		P43212	20
8	Dewar10	CA300	Unspuck		6Lysosmers	Ly6z		P43212	20
9	Dewar10	CA300	Unspuck		7Lysosmers	Ly7z		P43212	20
10	Dewar10	CA300	Unspuck		8Lysosmers	Ly8z		P43212	20
11	Dewar10	CA300	Unspuck		9Lysosmers	Ly9z		P43212	20
12	Dewar10	CA300	Unspuck		10Lysosmers	Ly10z		P43212	20
13	Dewar10	CA300	Unspuck		11Lysosmers	Ly11z		P43212	20
14	Dewar10	CA300	Unspuck		12Lysosmers	Ly12z		P43212	20
15	Dewar10	CA300	Unspuck		13Lysosmers	Ly13z		P43212	20
16	Dewar10	CA300	Unspuck		14Lysosmers	Ly14z		P43212	20
17	Dewar10	CA300	Unspuck		15Lysosmers	Ly15z		P43212	20
18	Dewar10	CA300	Unspuck		16Lysosmers	Ly16z		P43212	20
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									

- Use the “Import from CSV” option to load your CSV file.





- Once you are happy with your samples it is time to send the shipment to the facility but first you have to print the labels (menu on the right of the samples) and attach it to the dewars.



LABEL INSTRUCTIONS

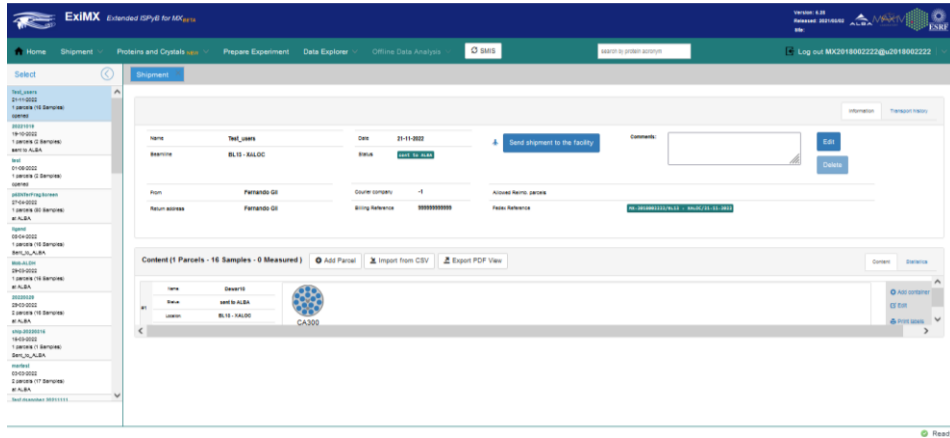
Please print the following three labels and use as follows:

- 1) Dewar Label:** affix this label to your dewar which ensures it can be identified at all times at ALBA
- 2) Outward bound Address label:** To be attached to the outside of your transport container for shipment to ALBA
- 3) Return bound address label:** The return address for your shipment (Please include this in your shipment, e.g. put it behind the outward bound address or in the transport container)

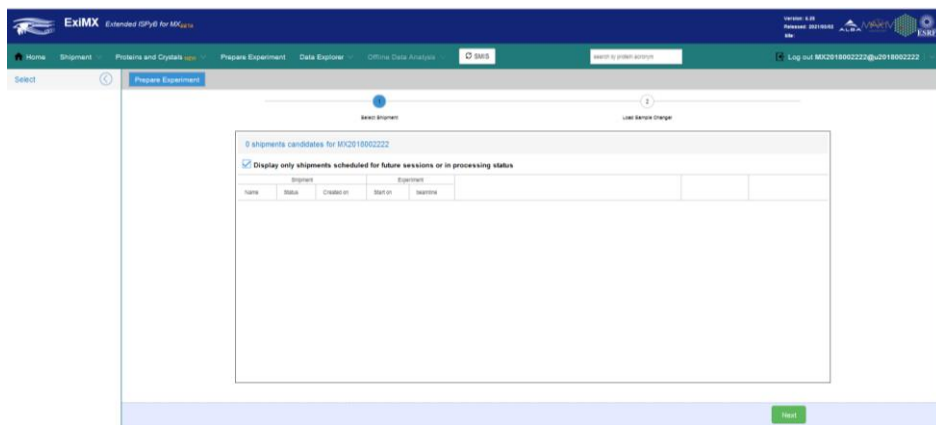
1) DEWAR LABEL: affix this to your DEWAR



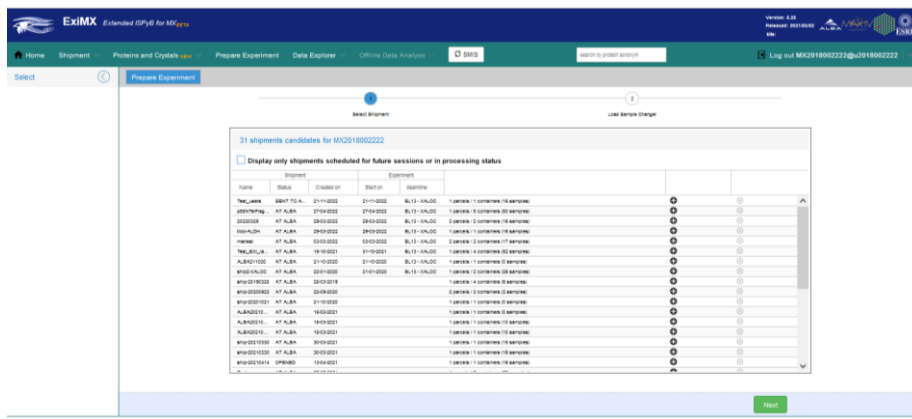
- Now you can proceed to Send Shipment to the Facility by pressing the blue button. The status of the shipment will change from OPENED to SENT TO ALBA. If the blue button is not active refresh the web page or go again to Shipment>List and choose your shipment.



- When the day of your beamtime has arrived it is time for preparing your experiment. To do that, go to the Prepare experiment tab in the main menu.

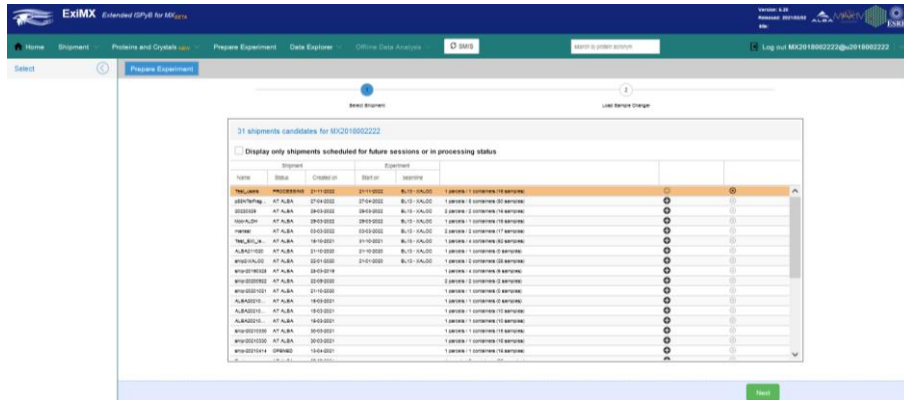


- After unclicking the “Display only shipments scheduled for future sessions or in processing status” check, you will see your shipment.

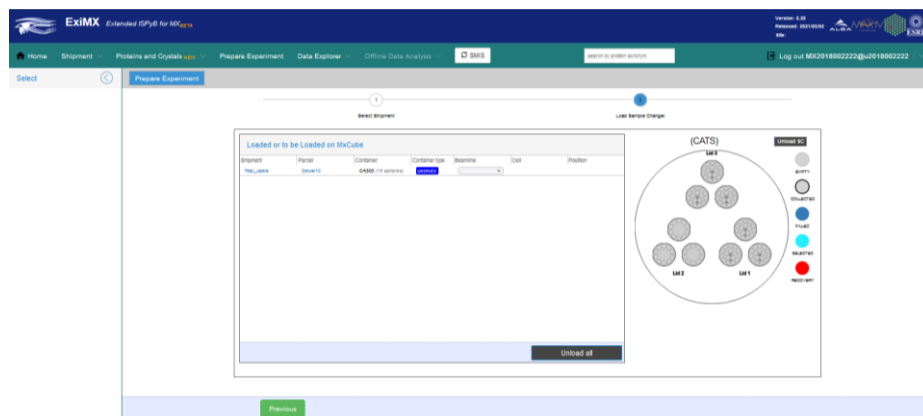




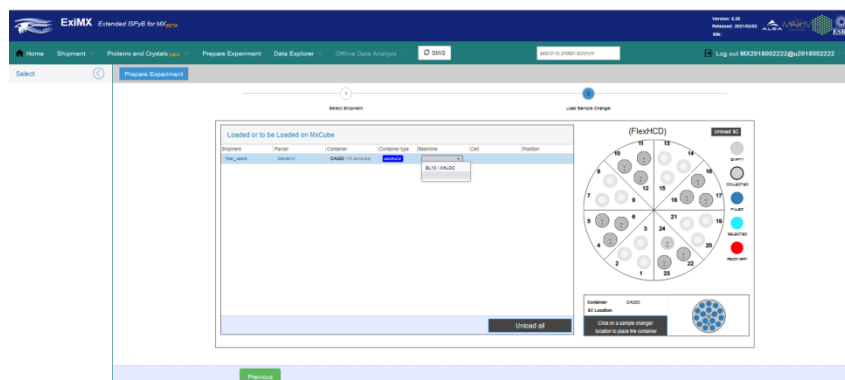
- Choose your shipment by pressing the add icon on the right. The line will change to orange and press Next (green button below)



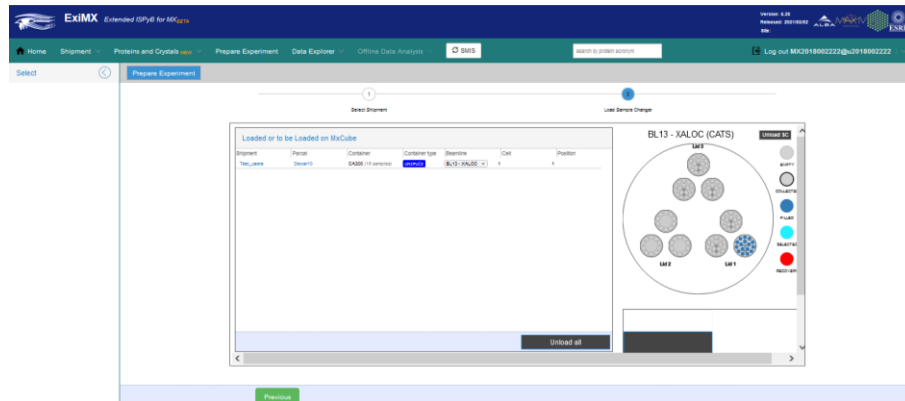
- In the second step we are going to proceed to Load the Sample Changer.



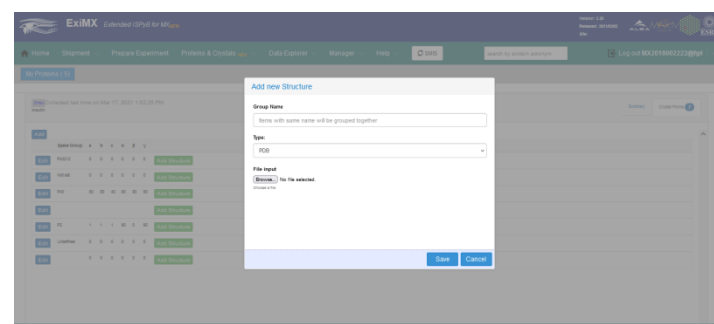
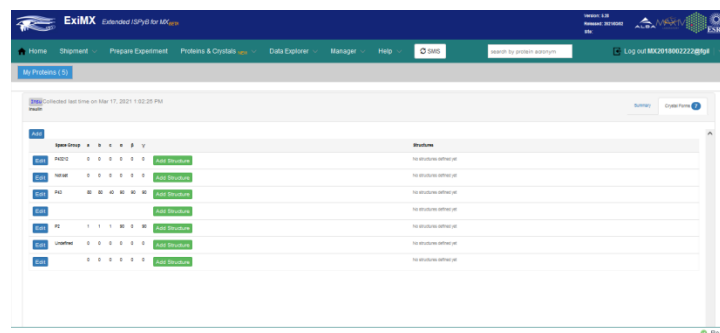
- Select the appropriate beamline, in that case BL13-XALOC



- Afterwards choose the position of your pucks following the instructions of your local contact.



- At any time before the data collection you can add a PDB code of your protein for MR through the Dimple pipeline. Go to the tab Proteins&Crystals>List. Go to a protein previously declared and click the the “Crystal forms” tab. Press the “Structure” button corresponding to your crystal form and upload the PDB code.



- Download your Dimple results from:
 - Enter to your ISPyB session in the Home page

