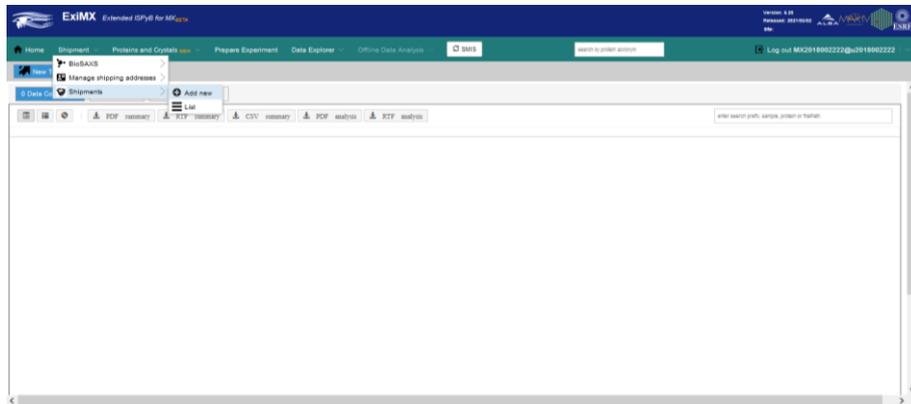
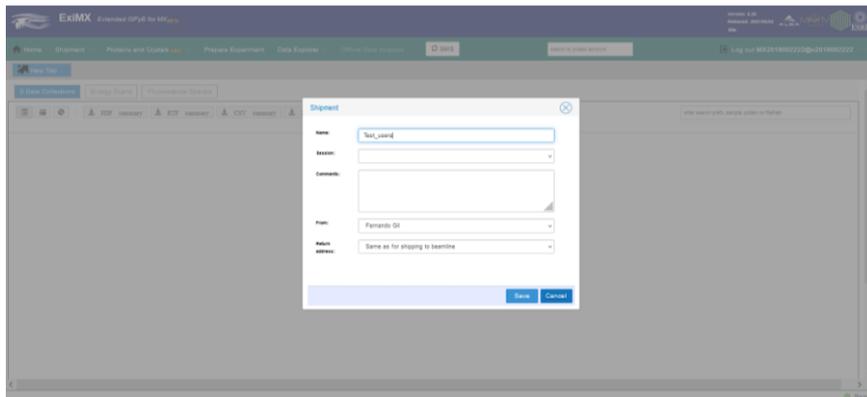




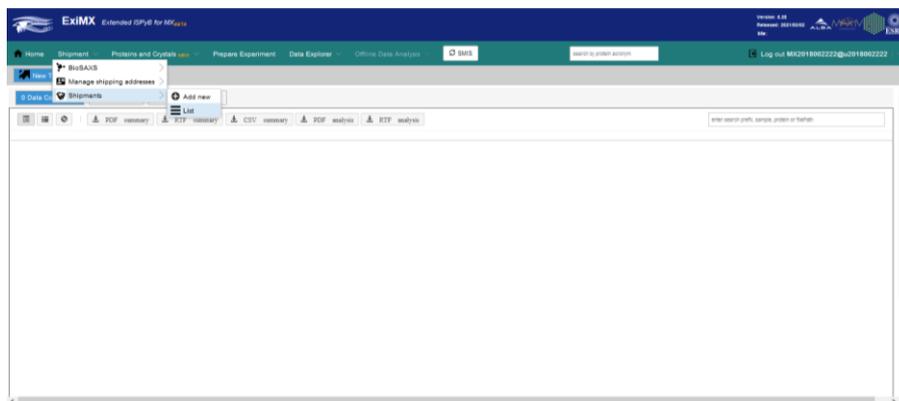
- Create a new shipment: To do that go to shipment in the upper menu and press Shipment>Add new



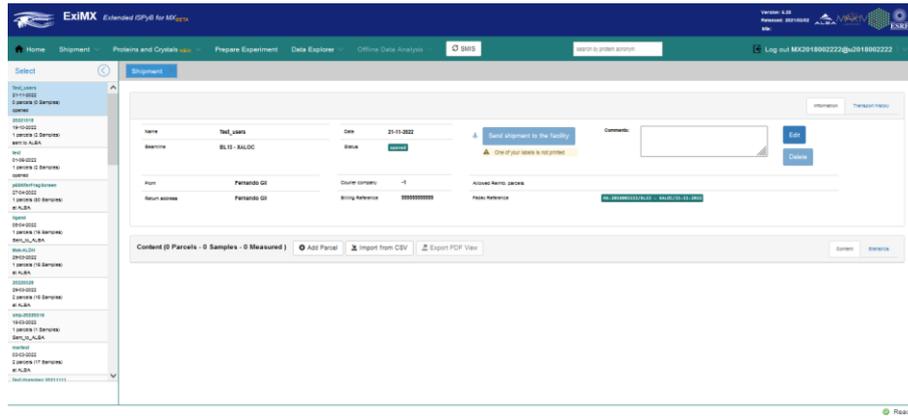
- Create the new shipment by adding a name, a contact person and choosing the corresponding session in the pull down menu.



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



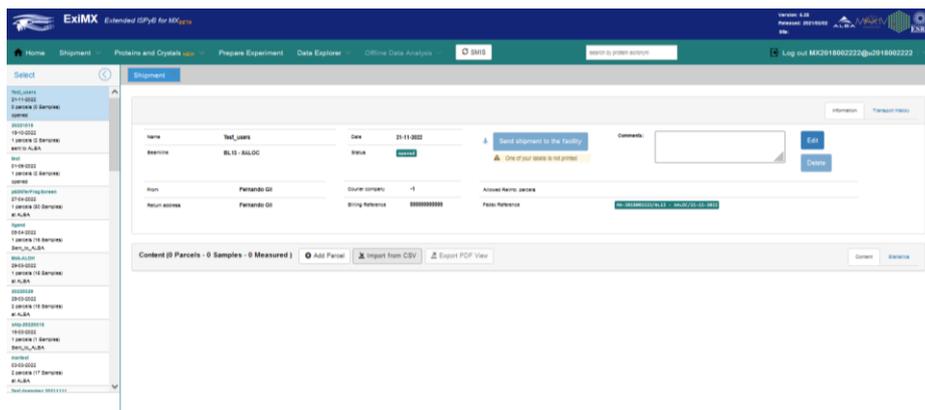
- Select your shipment from the list on the left. Now it is time to load your parcel (dewar) and samples information in EXI.



- 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.

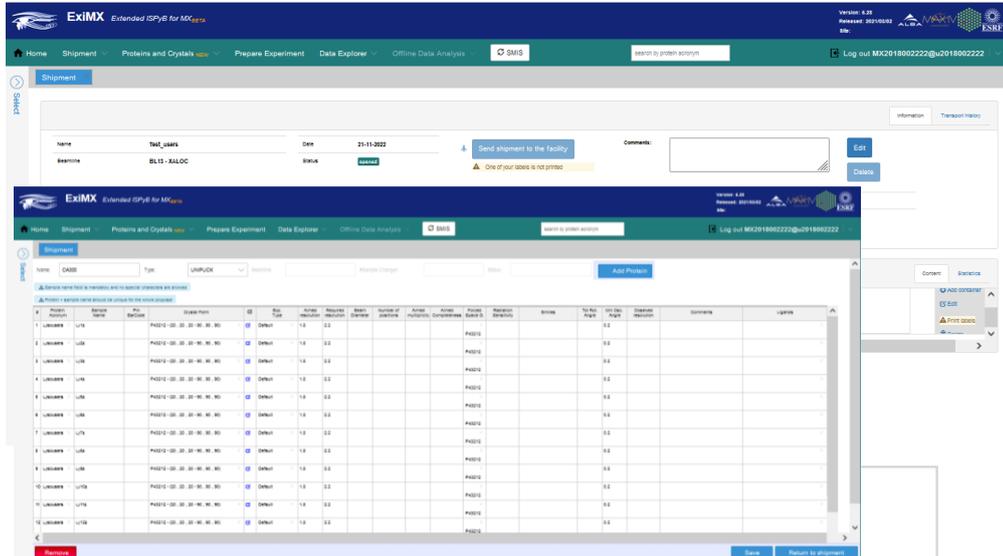
A	B	C	D	E	F	G	H	I		
2	Facial name	container name	container type	container position	protein acronym	sample acronym	pin barcode	SPG	cSEA	cell
3	Dewar10	CA300	Unspuck		1Lysousers	Ly1z		P43212		20
4	Dewar10	CA300	Unspuck		2Lysousers	Ly2z		P43212		20
5	Dewar10	CA300	Unspuck		3Lysousers	Ly3z		P43212		20
6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

- 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)

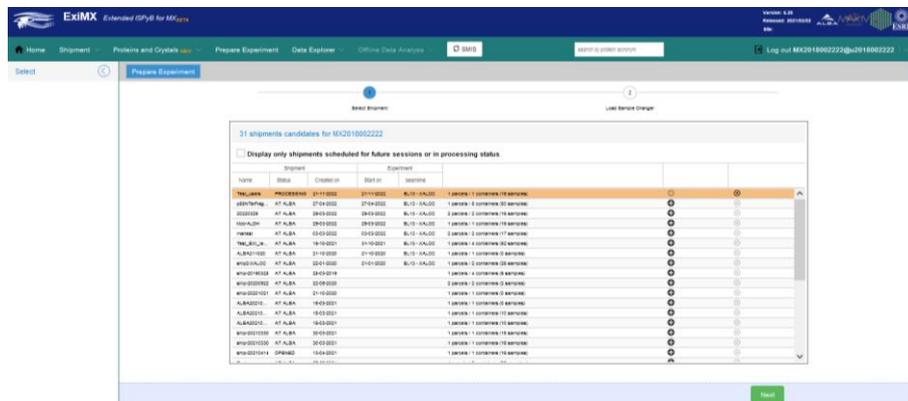
1) DEWAR LABEL: affix this to your DEWAR

"null"

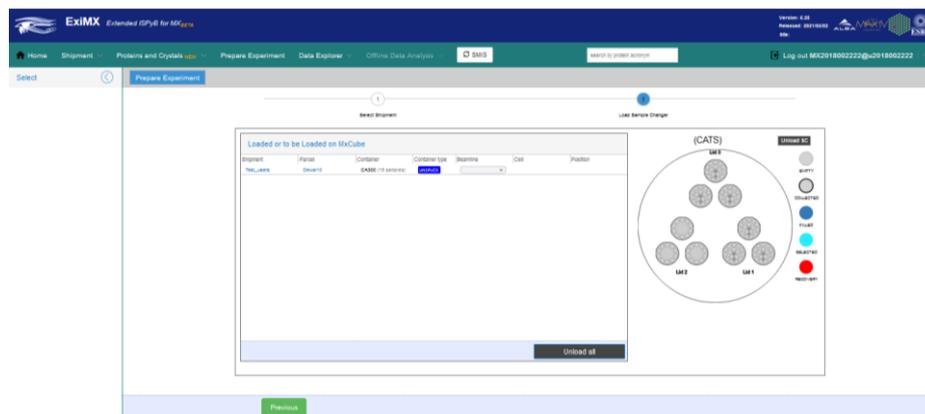
Parcel label	Dewar10
Shipment name	Test_users
Number of parcels	1
Proposal number	MX-2018002222
Laboratory name	XALOC
Local contact	



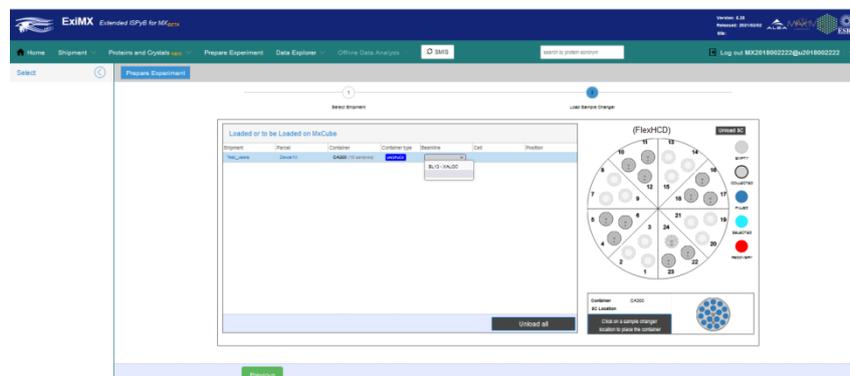
- Choose your shipment by pressing the add icon on the right. The line will change to orange and press Next (green button below)



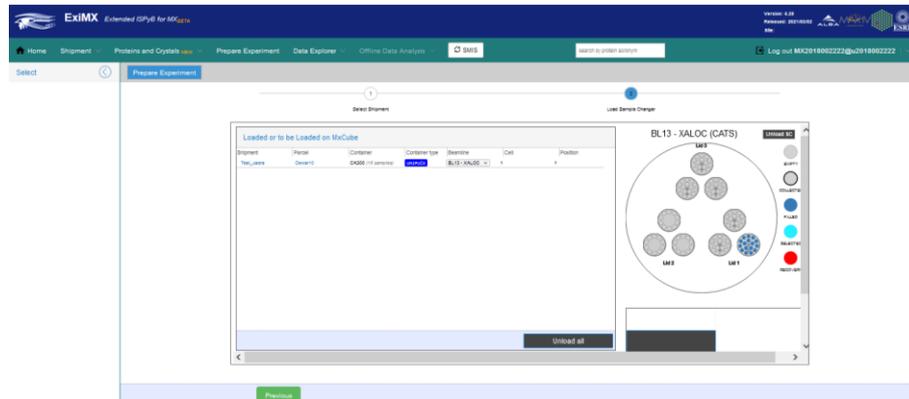
- In the second step we are going to proceed to Load the Sample Changer.



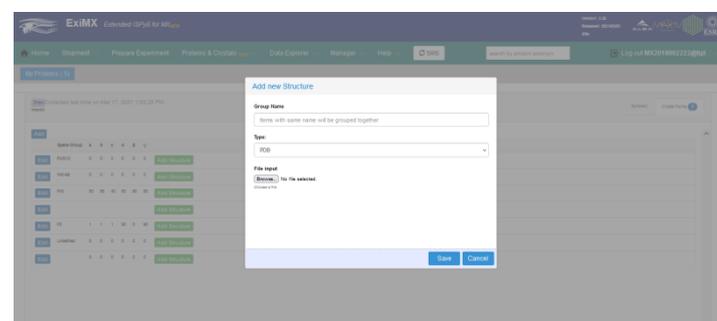
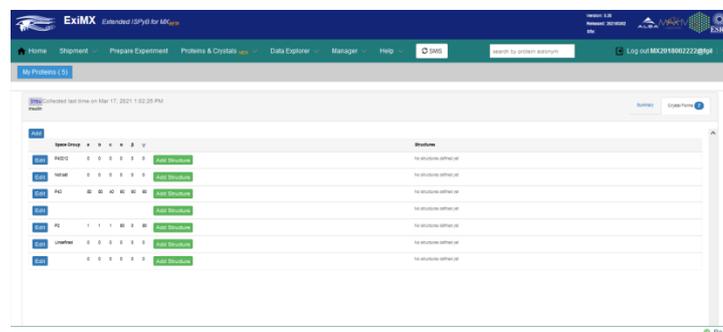
- Select the appropriate beamline, in that case BL13-XALOC



- 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



- Go to the data collection of interest (OSC). If Dimple processing worked nicely you will find the comment: “DIMPLE results available for EDNA_proc DIMPLE results available for AUTO_proc”
- Click the “Last collected results” tab.
- Click the autoPROC or EDNAproc processing. You will find the Dimple outputs at the “Attachments” section.

- Done!

TROUBLESHOOTING

- How can I download a summary of my experiment in .csv format?
 - For the moment this option is not available in EXI, however temporarily you can download the .csv summary from the old version of ISPyB (www.ispyb.cells.es/ispyb): Login>Press GO at MX proposal>Press Data Collection tab>View collections>Reports (first panel above)

