ISPyB user manual

June 2015

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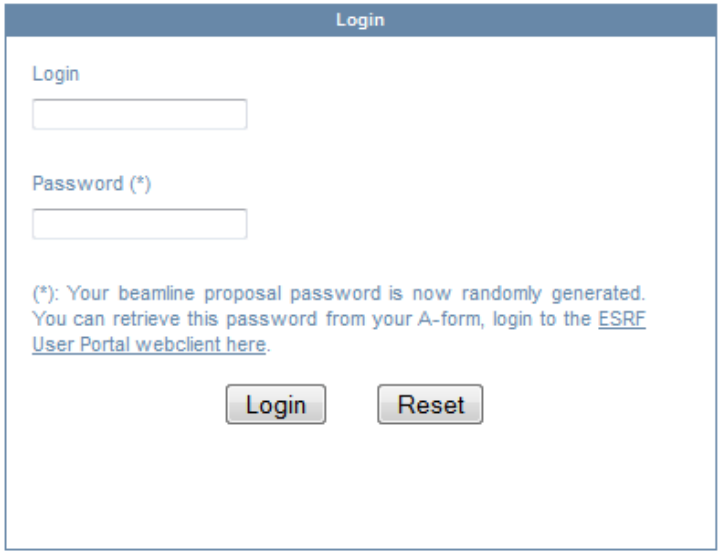
Part I: Click on a title to directly go to the corresponding page

ISPyB user manual

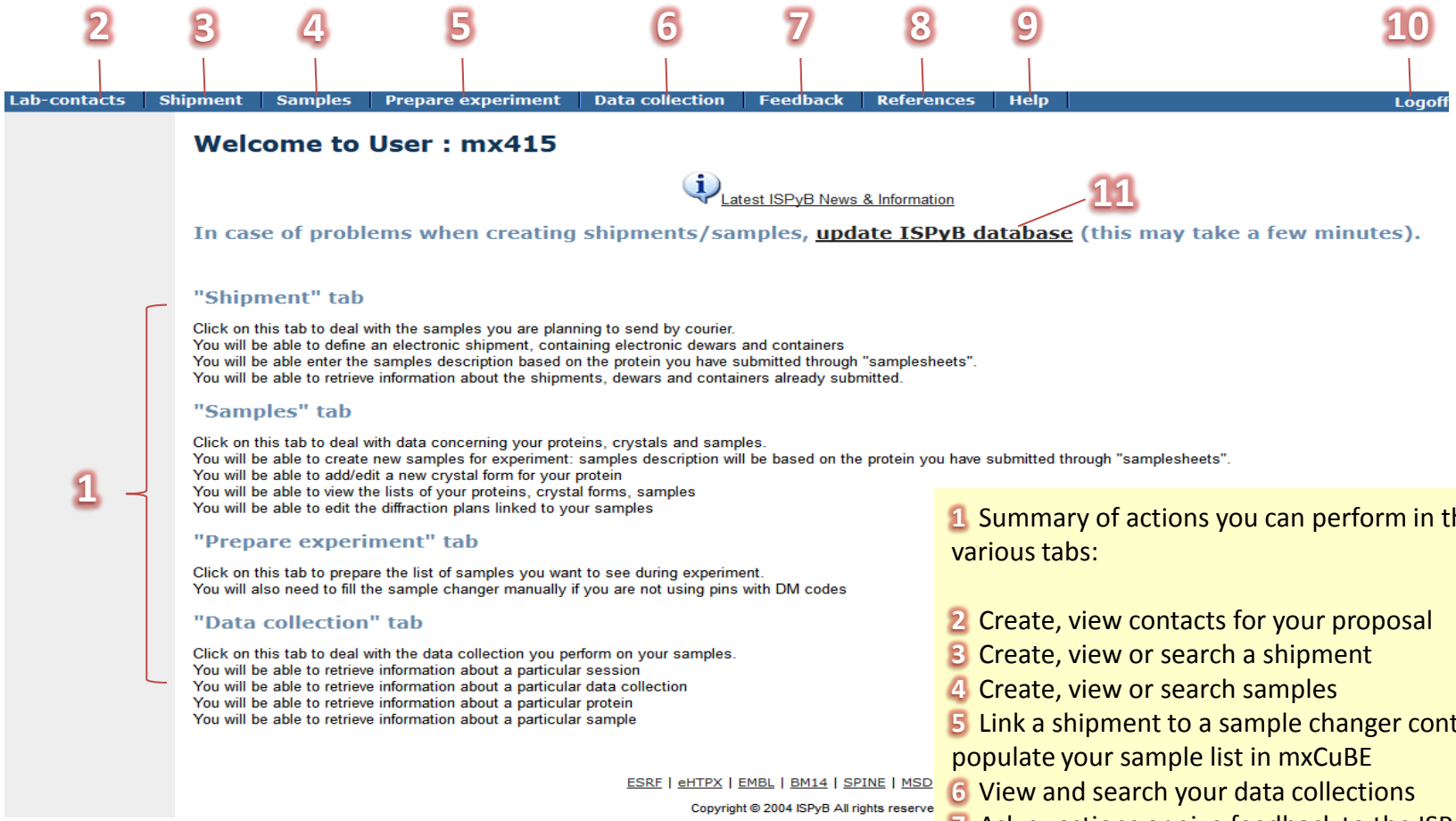
Part I: Web Interface Description

ISPyB Login



Use your ESRF experiment number (i.e. mx123, ix123, fx123) and password to log in

General Homepage

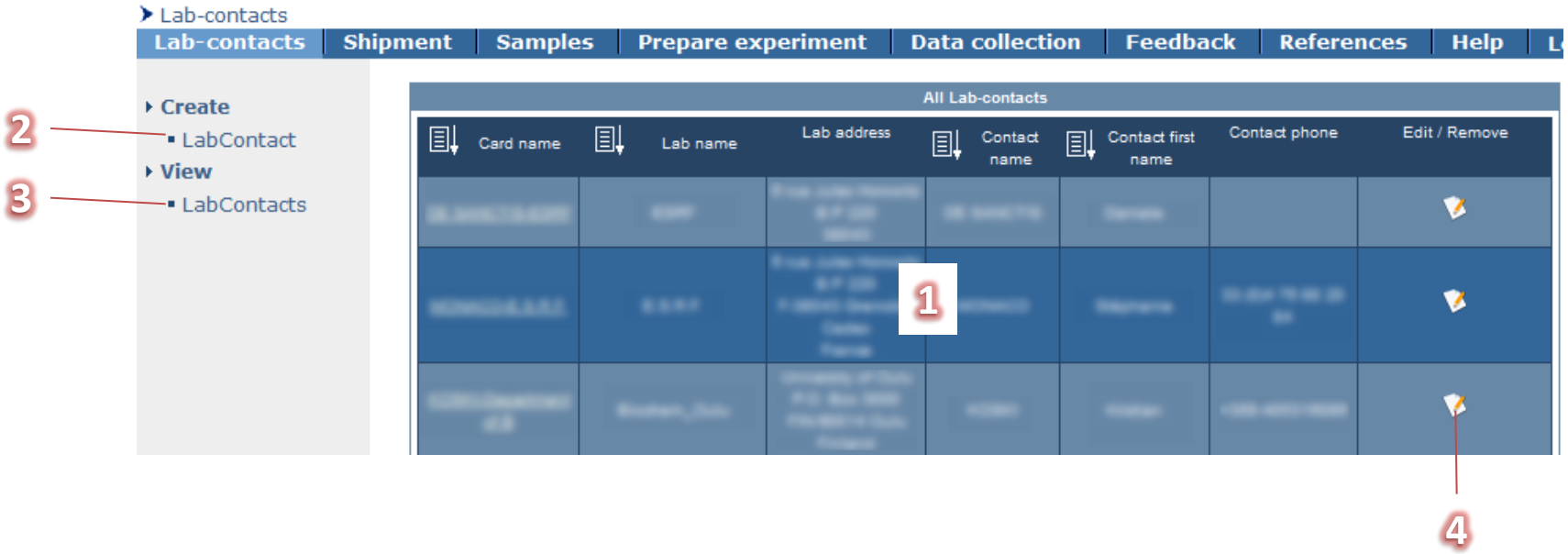


1 Summary of actions you can perform in the various tabs:

2 Create, view contacts for your proposal
3 Create, view or search a shipment
4 Create, view or search samples
5 Link a shipment to a sample changer content to populate your sample list in mxCuBE
6 View and search your data collections
7 Ask questions or give feedback to the ISPyB team
8 Find the references to cite when reporting data measured on ESRF MX beamlines

9 and 11 Go to information and help pages
10 Log out of your ISPyB session

Lab-contacts tab



1 Previously created lab-contacts
2 Create a new lab-contact
3 Go back to you lab-contact table (1)
4 Edit or remove an existing lab-contact

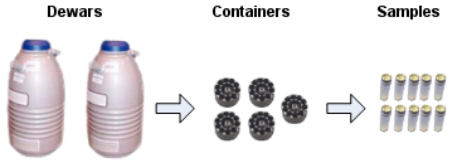
Shipment tab: Homepage

Shipment

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help | Logof

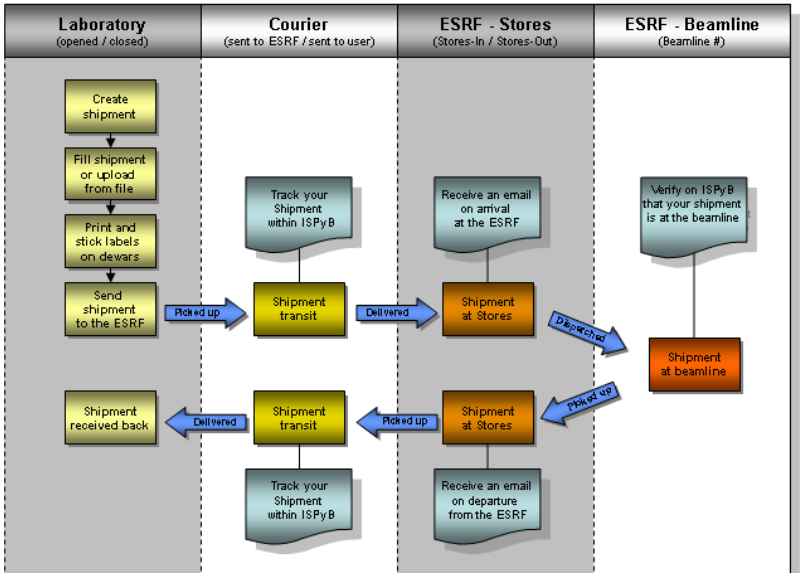
- Create
  - Shipment
  - Puck
  - CSV upload
- View
  - Shipments
  - Dewars
- Search
  - Shipment
  - Dewar

A **Shipment** consists of a set of Dewars which is sent from your home lab to the synchrotron via a courier company. Each dry shipping **Dewar** within the shipment is identified by a label (barcode or sticker). The dewars(s) contains a set of Containers (Baskets or canes). **Containers** (typically Baskets), contain Samples. A **Sample** (Sample Holder) contains the **Crystal**.



Tracking your shipment & contents (Dewars, toolboxes etc) allows you to follow the progress of your shipment from your home Lab to The ESRF. This feature also provides for:

- Generation of Dewar and shipment labels for sending your shipment by courier
- Notification by email of your shipment arrival and departure from The ESRF. Returned shipment notifications also include the courier tracking number to allow you to track the shipment while in transit back to your home laboratory
- Location of your shipment at The ESRF



1 Summary of the shipment tracking system put in place at ESRF
2 Create a shipment or a puck
3 View existing shipments or dewars
4 Search for a shipment or a dewar

Shipment tab: Create-> Shipment

Shipment ➤ Create ➤ Shipment

Home | Lab-contacts | Shipment | Samples | Prepare experiment | Data collection

- Create
  - Shipment
  - Puck
  - CSV upload
- View
  - Shipments
  - Dewars
- Search
  - Shipment
  - Dewar

New/Edit Shipment

Details

Creation date: Fri Mar 13 11:22:41 CET 2015

Shipment label *

Number of dewars *

Number of other components (i.e. toolbox, laser...): 0

Beamline / Experiment: 17-03-2015 ID30A-1 *

Comments

Shipment status: opened

Lab-contacts

Lab-Contact for sending: select a contact card *

Creation/Edition of a Lab-Contact card

Return adress is identical as sending adress (Y/N)

If No, Lab-Contact for Return: select a contact card *

Courier accounts details for return

These informations are relevant for all shipments.

Courier company for return (if ESRF sends a dewar back)

Courier account

Billing reference

Average Customs value of a dewar (Euro)

Average Transport value of a dewar (Euro)

Save | Save and Edit

Details

Creation date: Tue Feb 18 09:08:09 CET 2014

Shipment label *

Number of dewars *

Number of other components (i.e. toolbox, laser...): 0

Beamline / Experiment: No session available

Comments

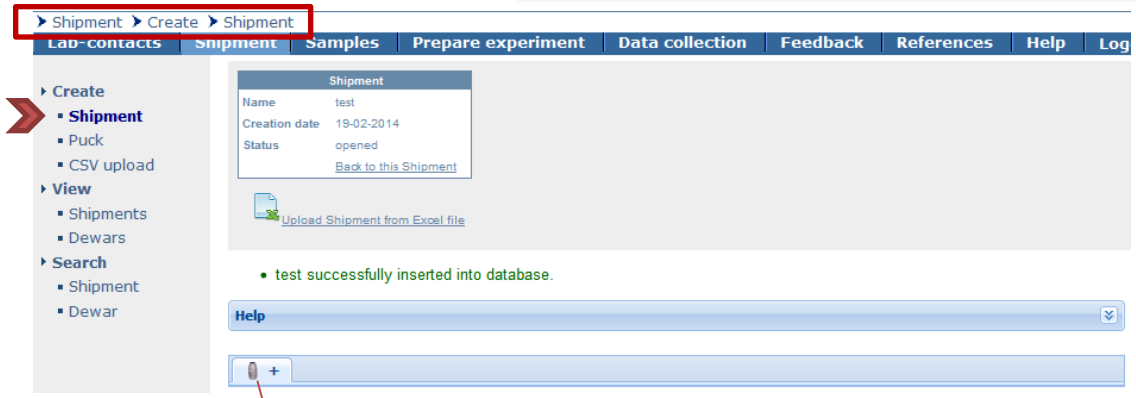
Fill-in the different parameters and save to create a new shipment

1 An experiment session has to be scheduled and selected in the SMIS system in order to link your shipment with that session

2 Save the shipment and redirect you to view that shipment where you can print your tracking label

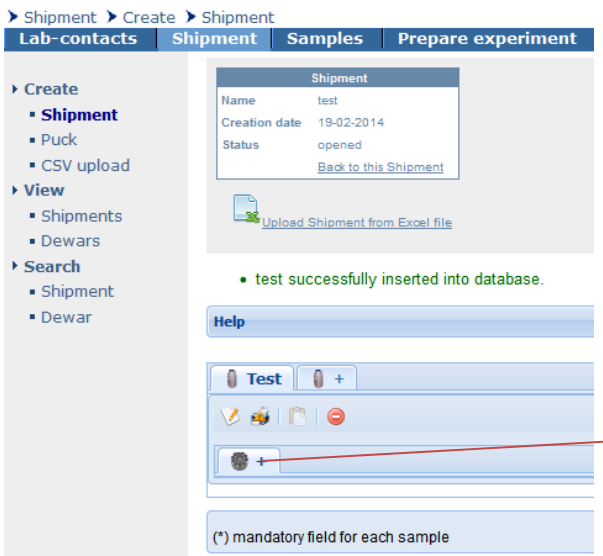
3 Save the shipment and redirect you to the shipment content creation page where you will be able to describe your samples

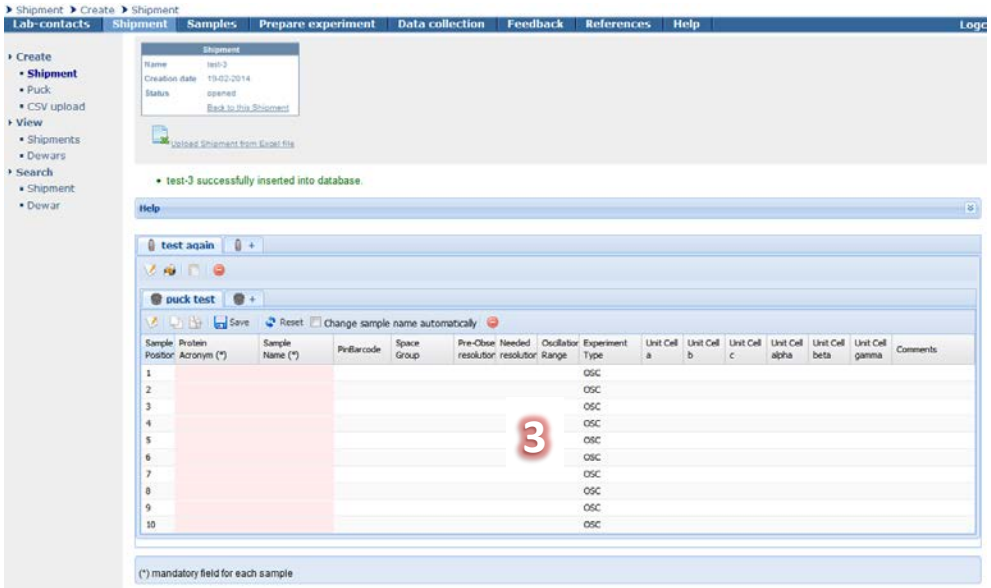
Shipment tab: Create -> Shipment



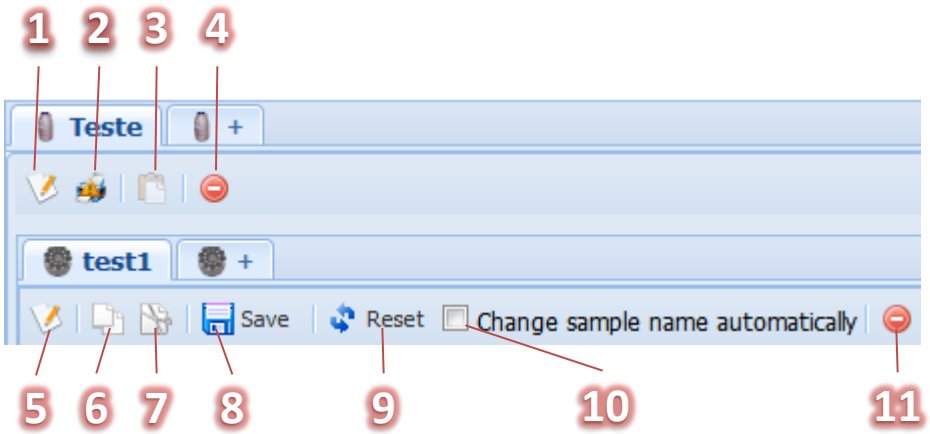
Shipment content creation page:

1 Add a new dewar to this shipment
2 Add and name a new puck
3 Fill-in the different cells and save to create a new puck (see next page)



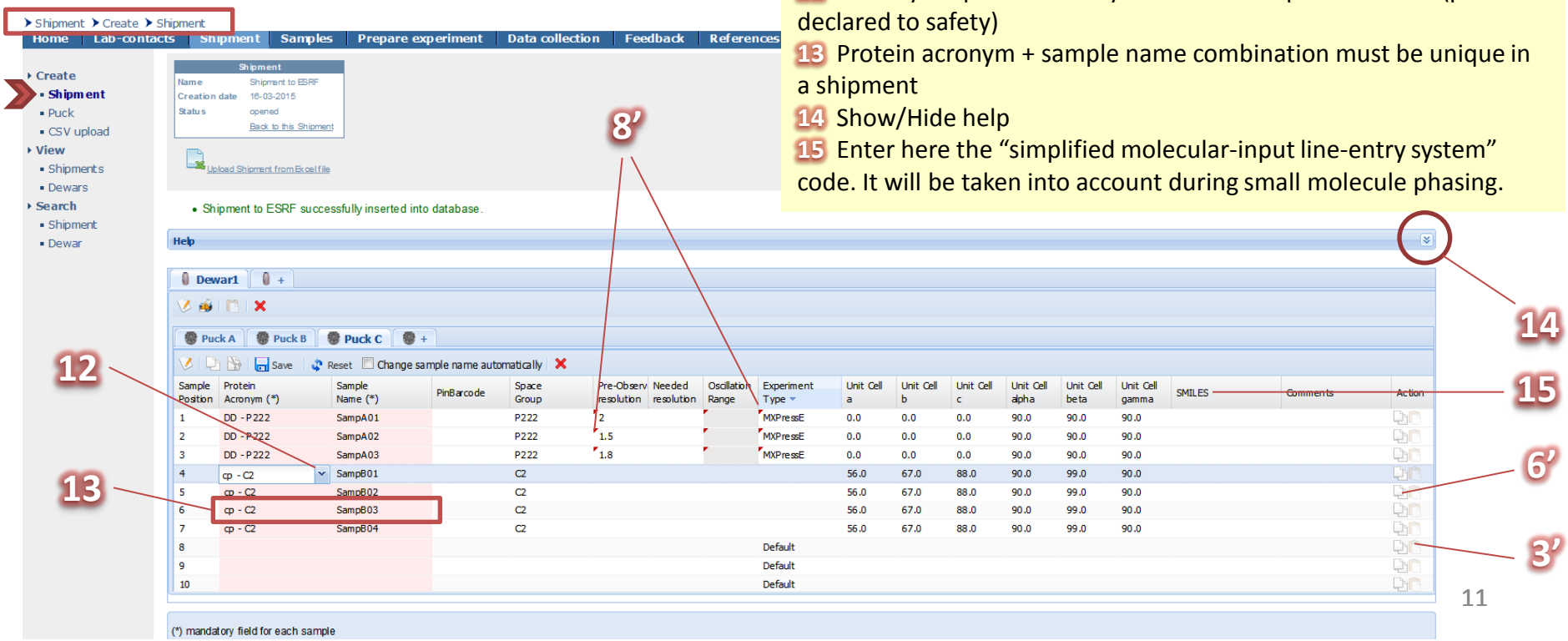


Shipment tab: Create -> Shipment



Fill-in the different cells and save to create a new puck

1 Edit the dewar label
2 Print your component label
3 Paste a copied or cut puck into a new dewar
4 Remove this dewar and its content (pucks)
5 Edit the puck label
6 Copy this puck (or sample 6'). You can then paste it with (3 or 3')
7 Cut this puck. You can then paste it with (3)
8 Save puck content as it is. Red corner on cells indicate that some information needs to be saved (8')
9 Erase all puck content
10 When ticked, adds an incremental number to the "sample name"
11 Delete puck and its content
12 Select your protein acronym from the drop down menu (proteins declared to safety)
13 Protein acronym + sample name combination must be unique in a shipment
14 Show/Hide help
15 Enter here the "simplified molecular-input line-entry system" code. It will be taken into account during small molecule phasing.



Shipment tab: Create-> Puck

Shipment ➤ Create ➤ Puck

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help | Logo

- Create
  - Shipment
  - Puck
  - CSV upload
- View
  - Shipments
  - Dewars
- Search
  - Shipment
  - Dewar

Puck Information

Shipping: ship-20140219

Dewar: Dewar1

Puck: Puck1

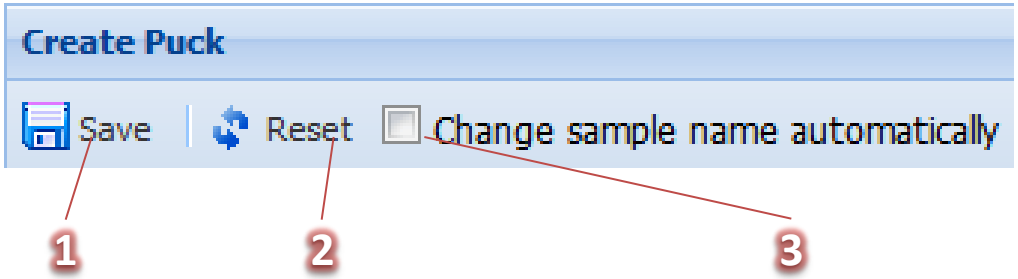
Create Puck

Save | Reset | Change sample name automatically

Sample Position	Protein Acronym (*)	Sample Name (*)	PinBarcode	Space Group	Pre-Observed resolution	Needed resolution	Oscillation Range	Experiment Type	Unit Cell a	Unit Cell b	Unit Cell c	Unit Cell alpha	Unit Cell beta	Unit Cell gamma	Comments
1	[illegible]			P2	0		0	OSC	0	0	0	0	0	0	
2	---							OSC							
3								OSC							
4								OSC							
5								OSC							
6								OSC							
7								OSC							
8								OSC							
9								OSC							
10								OSC							

1'

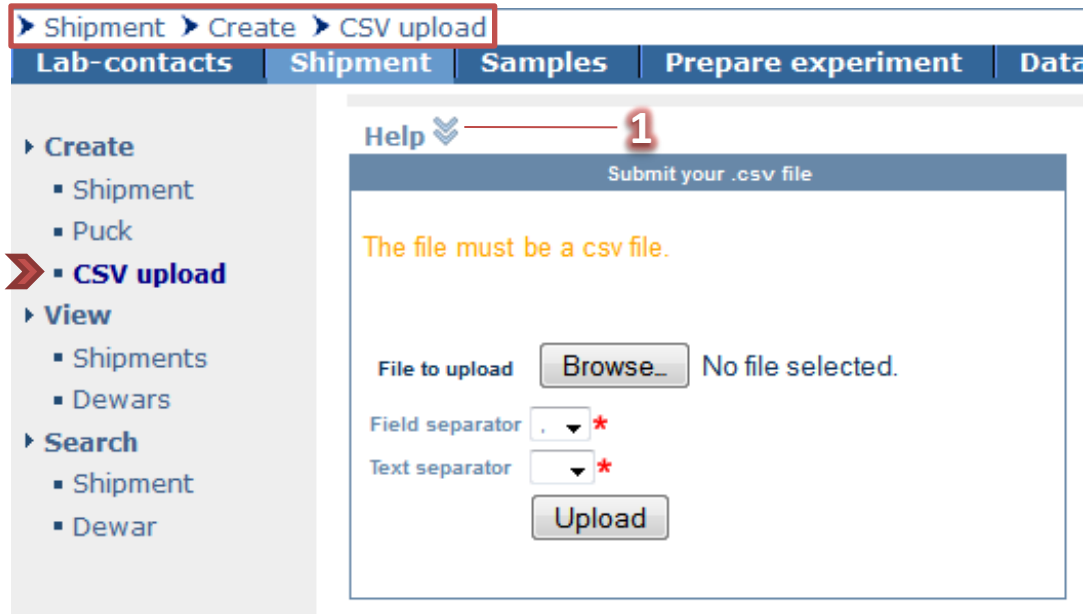
4



Fill-in the different cells and save to create a new puck

1 Save puck content as it is. Red corner on cells indicate that some informations need to be saved (1')
2 Reset puck content
3 When ticked, adds an incremental number to the "sample name"
4 Select your protein acronym from the drop down menu

Shipment tab: Create -> CSV upload



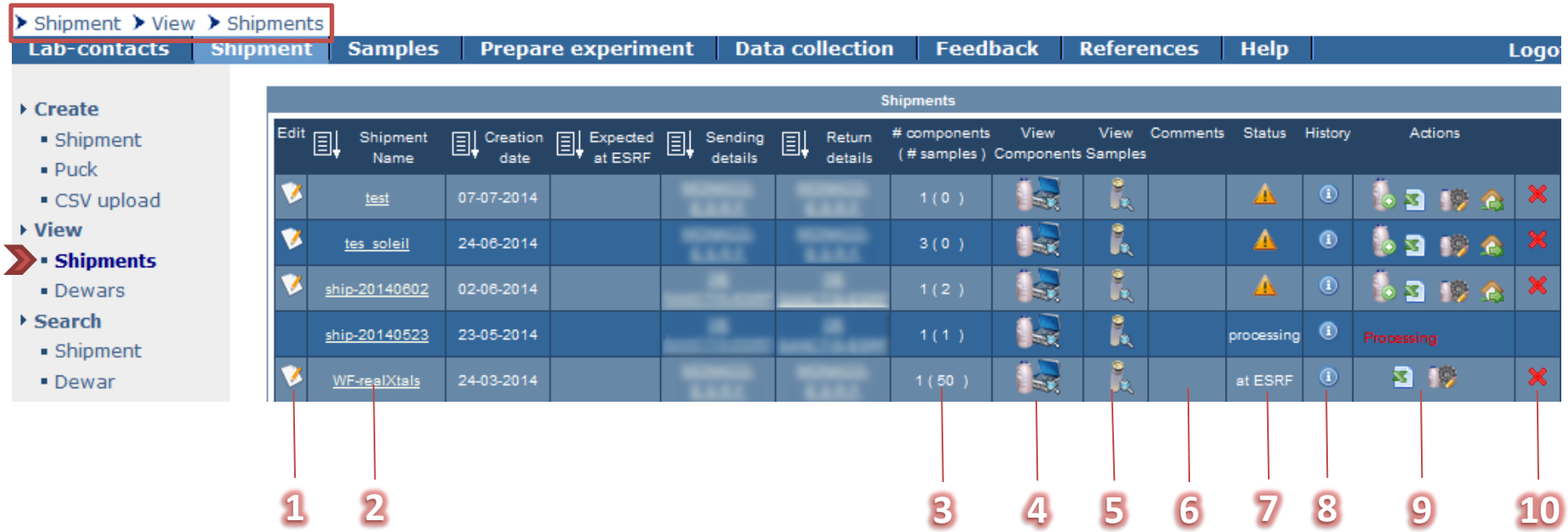
1 Show/Hide help

CSV File example in Excel:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
1	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample01	1		90	90	90	90	90	90
2	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample02	2		90	90	90	90	90	90
3	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample03	3		90	90	90	90	90	90
4	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample04	4		90	90	90	90	90	90
5	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample05	5		90	90	90	90	90	90
6	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample06	6		90	90	90	90	90	90
7	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample07	7		90	90	90	90	90	90
8	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	CMY-10	beta-lactamase	P41212	0	sample08	8		90	90	90	90	90	90
9	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	CMY-10	beta-lactamase	P41212	0	sample09	9		90	90	90	90	90	90
10	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	CMY-10	beta-lactamase	P41212	0	sample10	10		90	90	90	90	90	90
11	mx	123	1	ship-20140214	Dewar1	Puck2	3	2.1	0.5	t2	thiolase	C222	0	s01	1		90	90	90	90	90	90
12	mx	123	1	ship-20140214	Dewar1	Puck2	3	2.1	0.5	t2	thiolase	C222	0	s02	2		90	90	90	90	90	90
13	mx	123	1	ship-20140214	Dewar2	Puck3	3	2.1	0.5	t2	thiolase	C222	0	test01	1		90	90	90	90	90	90
14	mx	123	1	ship-20140214	Dewar2	Puck3	3	2.1	0.5	t2	thiolase	C222	0	test02	2		90	90	90	90	90	90

Upload your CSV file to create a new shipment

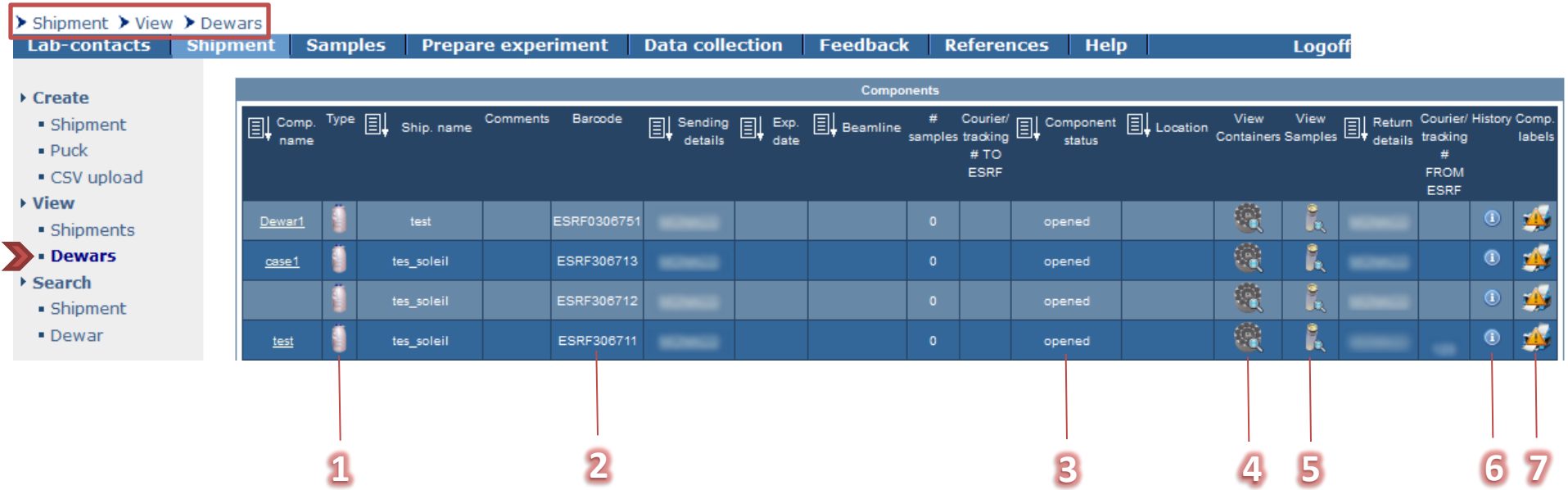
Shipment tab: View -> Shipments



In the Shipment tab-> View -> Shipments page you can :

1 Edit an existing shipment (attach it to another session, change the transport details or comments)
2 and 4 List the component details of that shipment
3 List the number of components and samples already registered for this shipment
5 View all samples of that shipment
6 Comments that can be edited during shipment creation or in (1)
7 View your shipment status (sent to ESRF, at ESRF, not complete or processing)
8 View the shipment information and dewar history
9 Actions that can be performed on your shipment: add a dewar, upload its content from XLS files, edit its content, put it in 'sent to ESRF" mode. These icons are replaced by processing if is has been used on the beamline
10 Delete that shipment ⚠ If you have data collected for this shipment, this will delete them!!

Shipment tab: View -> Dewars



In the Shipment tab -> View -> Dewars page you can :

1 View the type of component included in all your shipments (dewars or other)
2 View the barcode issued for that shipment for tracking purpose (tracking sheet printable from (6))
3 Check your component status (opened, ready to go, at ESRF, sent to user, closed)
4 List the pucks of this dewar
5 List the samples of dewar
6 View your component history
7 Print you component label

Shipment tab:
View -> Shipments or Dewars
-> View samples

Samples

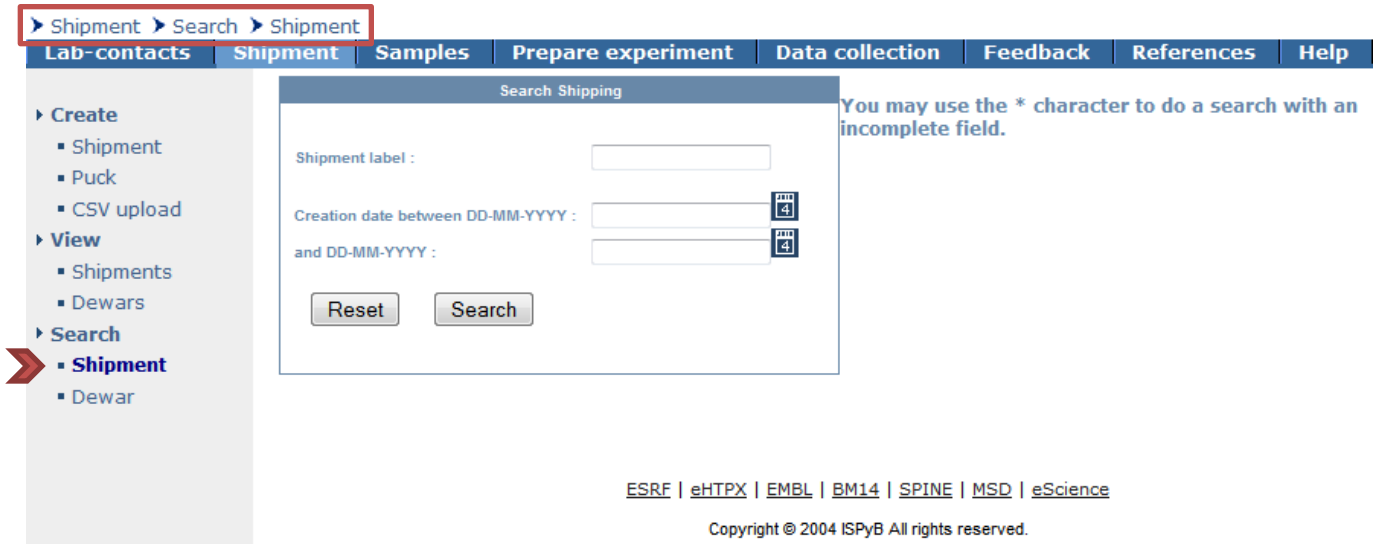
Protein	Space Group	Sample name	Smp code	Shipment	Dewar	Container	Loc. in cont.	Cell a	Cell b	Cell c	Cell alpha	Cell beta	Cell gamma	Crystal comments	Already observed resol.	Required resol.	Minimal resol.	Sample comments	Edit sample	Sample status	Data Collections	Data CollectionGroups
CER	P212121	sampA01	HA00AQ8595	WF-realXtals	dewar1	[illegible]	1	55.0	63.0	69.0	90.0	90.0	90.0			1.5						
CER	P212121	sampA02	HA00AP6006	WF-realXtals	dewar1	[illegible]	2	55.0	63.0	69.0	90.0	90.0	90.0			2						
CER	P212121	sampA03	HA00AQ8103	WF-realXtals	dewar1	[illegible]	3	55.0	63.0	69.0	90.0	90.0	90.0			3						
CER	P212121	sampA04	HA00AQ8573	WF-realXtals	dewar1	[illegible]	4	55.0	63.0	69.0	90.0	90.0	90.0			1.5						
CER	P212121	sampA05	HA00AQ8114	WF-realXtals	dewar1	[illegible]	5	55.0	63.0	69.0	90.0	90.0	90.0			2						
CER	P212121	sampA06	HA00AP6015	WF-realXtals	dewar1	[illegible]	6	55.0	63.0	69.0	90.0	90.0	90.0			3		sans cryo				
CER	P212121	sampA07	HA00AQ8584	WF-realXtals	dewar1	[illegible]	7	55.0	63.0	69.0	90.0	90.0	90.0					sans cryo				
CER	P212121	sampA08	HA00AP9755	WF-realXtals	dewar1	[illegible]	8	55.0	63.0	69.0	90.0	90.0	90.0					sans cryo				
CER	P212121	sampA09	HA00AQ8580	WF-realXtals	dewar1	[illegible]	9	55.0	63.0	69.0	90.0	90.0	90.0					sans cryo				
CER	P212121	sampA10	HA00AB6186	WF-realXtals	dewar1	[illegible]	10	55.0	63.0	69.0	90.0	90.0	90.0					sans cryo				
CER	P212121	sampB01	HA00AQ6589	WF-realXtals	dewar1	CB340A-Steph1	1	55.0	63.0	69.0	90.0	90.0	90.0			1.8						
CER	P212121	sampB02	HA00AC6788	WF-realXtals	dewar1	CB340A-Steph1	2	55.0	63.0	69.0	90.0	90.0	90.0			2		Long pin - Lucid fails				
CER	P212121	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]			[illegible]						

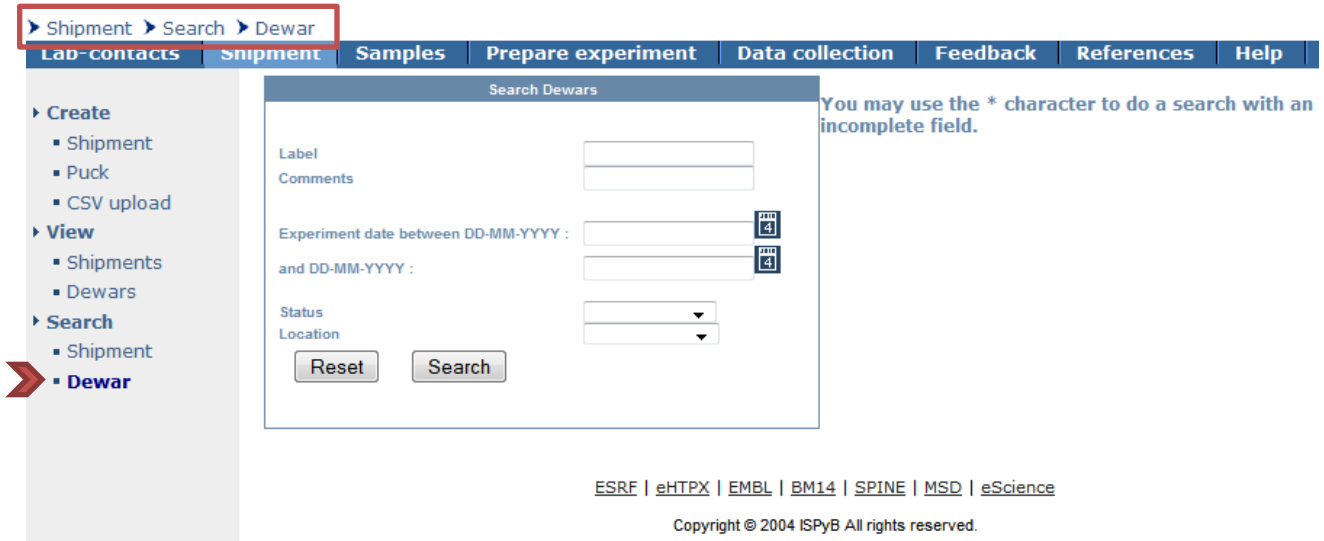
1 2 3 4 5 6 7

From the Shipment-> View -> Shipments page you can go to a summary page of the samples registered in one shipment :

1 Click on link to open the sample detail page
2 Click on link to open the shipment detail page
3 Click on link to view all the samples in this dewar
4 Parameters and comments previously entered when creating the sample
5 Edit or delete this sample
6 View the data collections
7 View collection summary by group (sample name, experiment type…)

Shipment tab: Search





Use these pages to search a particular shipment or a dewar

Samples tab: Homepage

Samples

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help | Logoff

- Create
  - New sample
  - New crystal form
- View
  - Proteins and crystal forms
  - Unassigned Samples
- Search
  - Protein
  - Sample
- Update Database

What you can do in the samples pages

Create

New sample

Note that the **most recommended** way of creating new samples is to create first 1 shipment, then dewars, then containers and add samples to them.

If you want to create an unassigned sample, this sample can be attached later to a shipment/dewar/container you created.
This sample will be attached to a protein and to a crystal form: information is retrieved from the samplesheets you submited to safety.

New Crystal Form

To create new crystal forms you can use later when creating your samples.

View

Proteins and crystal forms

To display all the proteins you have entered through samplesheets and the crystal forms associated.
Click on a protein acronym to retrieve the list of all samples coming from this protein.
Click on crystalForm space group to retrieve the list of all samples coming from this crystal form.

Unassigned Samples

To display the list of samples which are not linked to any shipment.

All samples

To display the list of all your samples
Click on edit to add/update sample parameters after experiment
Click on Diffraction plan to edit the diffraction plan parameters you want (By default the parameters you submitted through samplesheets are kept).
click on the sample name to have all the characteristics of this sample.

Search

Forms to search for a particular protein or a particular sample.

Update Database

If some protein acronyms are missing in the list when creating a sample, you can get them by updating ISPyB database.

1. Summary of the actions you can perform under the samples tabs
2. Create a sample or a crystal form for a protein
3. View existing protein crystal forms or unassigned samples (not attached to a shipment
4. Search for a protein (by its acronym) or a sample (by its barcode or name)
5. Retrieve the protein acronyms from your sample sheets newly submitted in the SMIS database

Samples tab: Create -> New sample

Samples ➤ Create ➤ New sample

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | He

- Create
  - New sample
  - New crystal form
- View
  - Proteins and crystal forms
  - Unassigned Samples
- Search
  - Protein
  - Sample
- Update Database

1'

No samples have been found

1

Create a new Sample

Select a Protein Acronym with a SpaceGroup (1) * -- Please select an acronym+crystal --

Sample Name: *
(the image name will be : 'acronym'-'sample name'_'run number'_'image number')
Authorized characters are a-z, A-Z, 0-9, underscore and dash.

Datamatrix Code:
(needed to use sample changer)
Authorized characters are a-z, A-Z, 0-9.

Location in container:
(position on cane or position in basket)

Holder Length in mm: 22
(typically between 15mm and 27mm, Spine default is 22mm)

Loop Type Nylon

Comments

Reset Save

(1) If you do not see your proteins, update ISPyB database: Update Database menu.

Use this form to create a new sample related to your protein

1 If you don't find your protein in the list on the left, update the database (1')

Samples tab: Create -> New crystal form

Samples ➤ Create ➤ New crystal form

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help

- Create
  - New sample
  - **New crystal form**
- View
  - Proteins and crystal forms
  - Unassigned Samples
- Search
  - Protein
  - Sample
- Update Database

1'

Create a new Crystal Form

Please select a Protein Acronym M031 1
this field is required

Geometry Class: Primitive triclinic, Primitive monoclinic, Centred monoclinic, Primitive orthohombic, C-centred orthohombic, I-centred orthohombic, F-centred orthohombic, Primitive tetragonal, I-centred tetragonal, Primitive trigonal, Primitive hexagonal, Rhombohedral, Primitive cubic, I-centred cubic, F-centred cubic, Unknown

Space Group

a b c
Alpha Beta gamma

Morphology Color

Crystal size X Crystal size Y Crystal size Z

Comments

Reset Save

Use this form to create a new crystal form related to your protein

1 If you don't find your protein here, update your ISPyB database (1')

Samples tab: View-> Protein and crystal forms

Samples ➤ View ➤ Proteins and crystal forms

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help | Lo

- Create
  - New sample
  - New crystal form
- View
  - **Proteins and crystal forms**
- Search
  - Protein
  - Sample
- Update Database

Click on the acronym, or on the space group to see the samples attached to corresponding acronym, space group.

Proteins and Crystal Forms List

Protein Name	Protein Acronym	New Crystal Form	SpaceGroup	A	B	C	Alpha	Beta	Gamma	Comments	Edit	Delete	PDB File	Data Collections
test	test1		Undefined	32.016	33.281	48.002	77.97	70.54	61.28				Upload	View
test				108.666	180.159	101.144	90.0	110.3	90.0				Upload	View
Mnth	Mnth		R32	0.0	0.0	0.0	0.0	0.0	0.0				Upload	View
PA0688	PA0		P21	0.0	0.0	0.0	90.0	0.0	90.0				Upload	View

1 2 3 4 5

Allows you to view all proteins and their associated crystal forms

1. Create a new crystal form for that protein
2. Edit this crystal form
3. Delete this crystal form
4. Upload the corresponding PDB file (for Autoprocessing purposes)
5. View all the data collections measured for that crystal form of that protein

Samples tab: Search -> Protein or sample

Samples ➤ Search ➤ Protein

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback

- Create
  - New sample
  - New crystal form
- View
  - Proteins and crystal forms
  - Unassigned Samples
- Search
  - **Protein**
  - Sample
- Update Database

Search Protein

Acronym

Reset Search

You may use the * character to do a search with an incomplete Acronym.

Samples ➤ Search ➤ Sample

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback

- Create
  - New sample
  - New crystal form
- View
  - Proteins and crystal forms
  - Unassigned Samples
- Search
  - Protein
  - **Sample**
- Update Database

Search Sample

Name

Datamatrix Code

Reset Search

You may use the * character to do a search with an incomplete Name.

ESRF | eHTPX | EMBL | BM14 | SPINE | MSD | eScience

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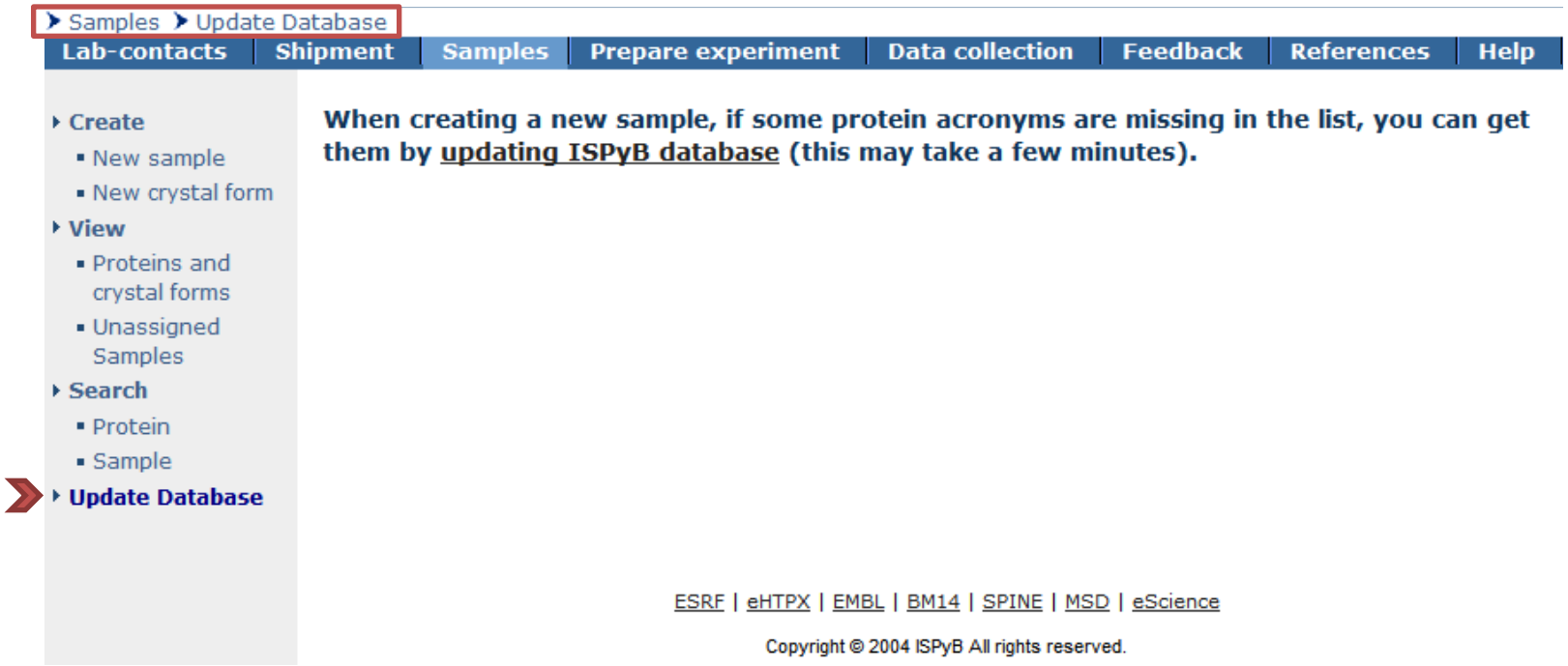
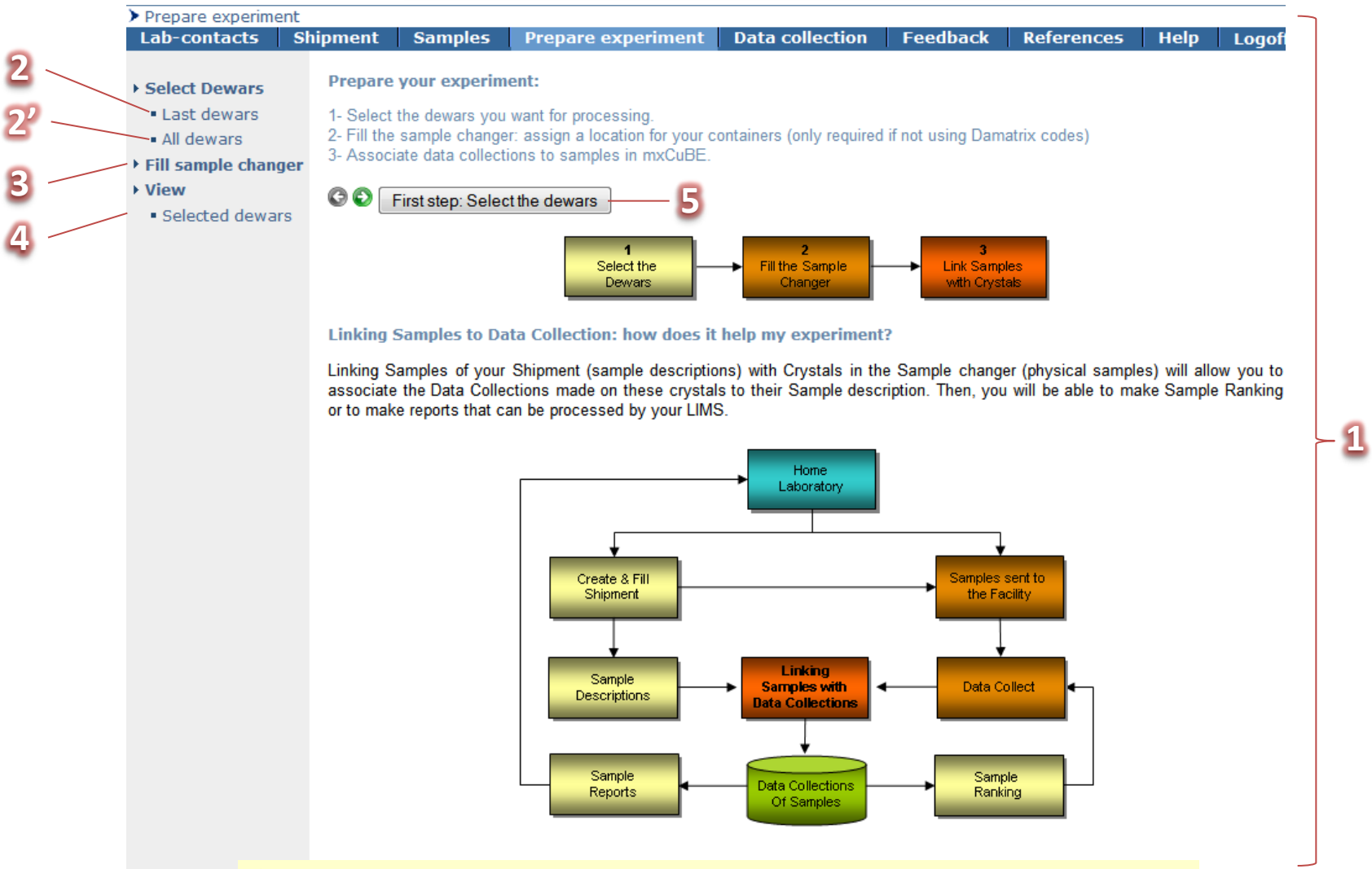
Use these pages to search for a particular protein or a sample

Samples tab: Update Database



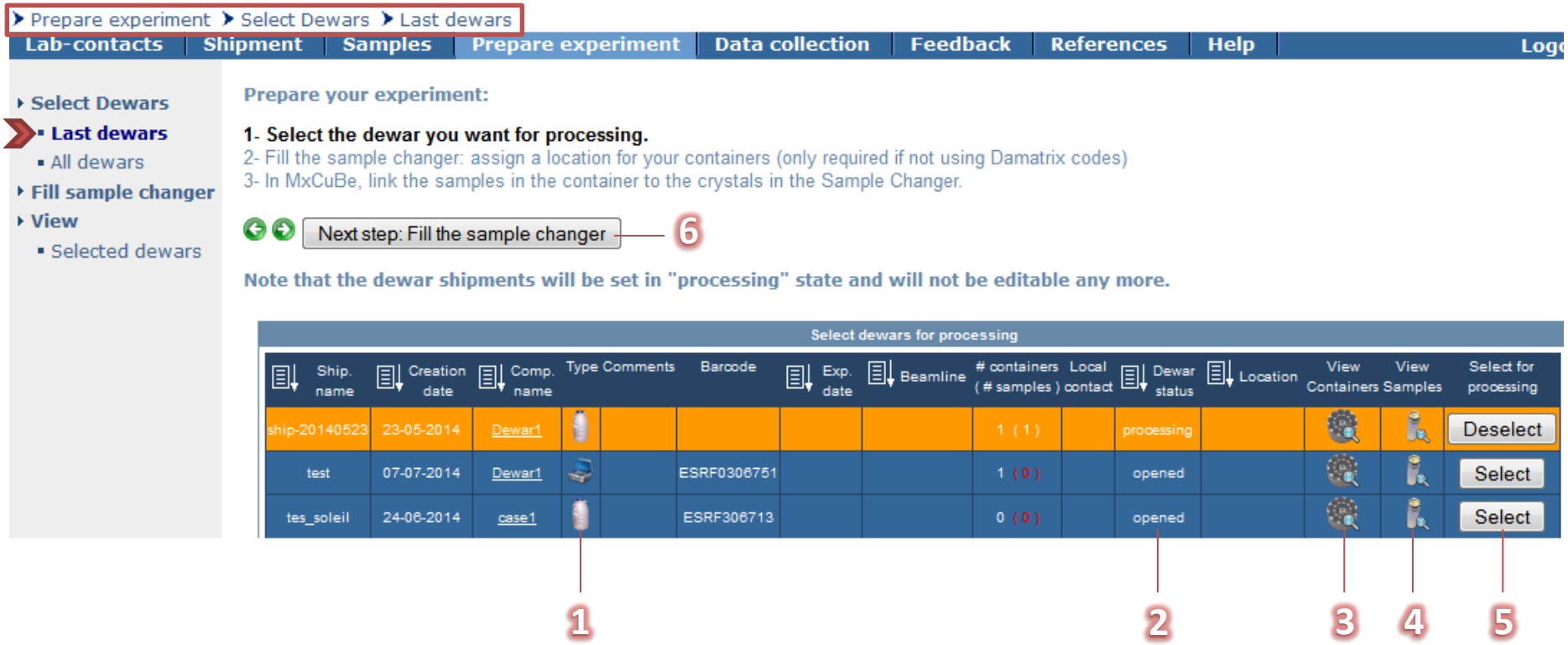
Click on "**updating ISPyB database**" to retrieve protein acronyms from recent submitted safety sheets in the SMIS database (synchronisation with SMIS database)

Prepare experiment tab



1 Describes the purposes of the "prepare experiment" tab (to view your ISPyB samples within the data collection GUI mxCUBE)
2 and 5 Select the dewar you want to put in processing from a shortlist (last 60 days)
2' Same as 2 but showing all dewars in that user account
3 Specify directly where samples are located in the sample changer
6 View dewar(s) selected in 2.

Prepare experiment pages – Select Dewars



In this tab dewars not selected appear in blue and dewars already selected appear in orange

1 View the type of component included in your shipment (dewar or toolbox)
2 Check your component status (opened, ready to go, at ESRF, sent to user, closed)
3 List the pucks of that dewar
4 List the samples of that dewar
5 Select or deselect this dewar for sample changer filling
6 Click to define the positions of the pucks in the sample changer

Tip: If you do not see a dewar that you have already created, click on “All dewars”

Prepare experiment tab: Fill sample changer

Prepare experiment ▸ Fill sample changer

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help

- Select Dewars
  - Last dewars
  - All dewars
- Fill sample changer
- View
  - Selected dewars

Prepare your experiment:

1- Select the dewars you want for processing.

2- Fill the sample changer: assign a location for your containers (only required if not using Damatrix codes)

3- In MxCuBe, link the samples in the container to the crystals in the Sample Changer.

Next step: Link Samples in mxCuBE — 3

This step is not required if you are using Datamatrix code on your samples pins.

Containers to load in sample changer

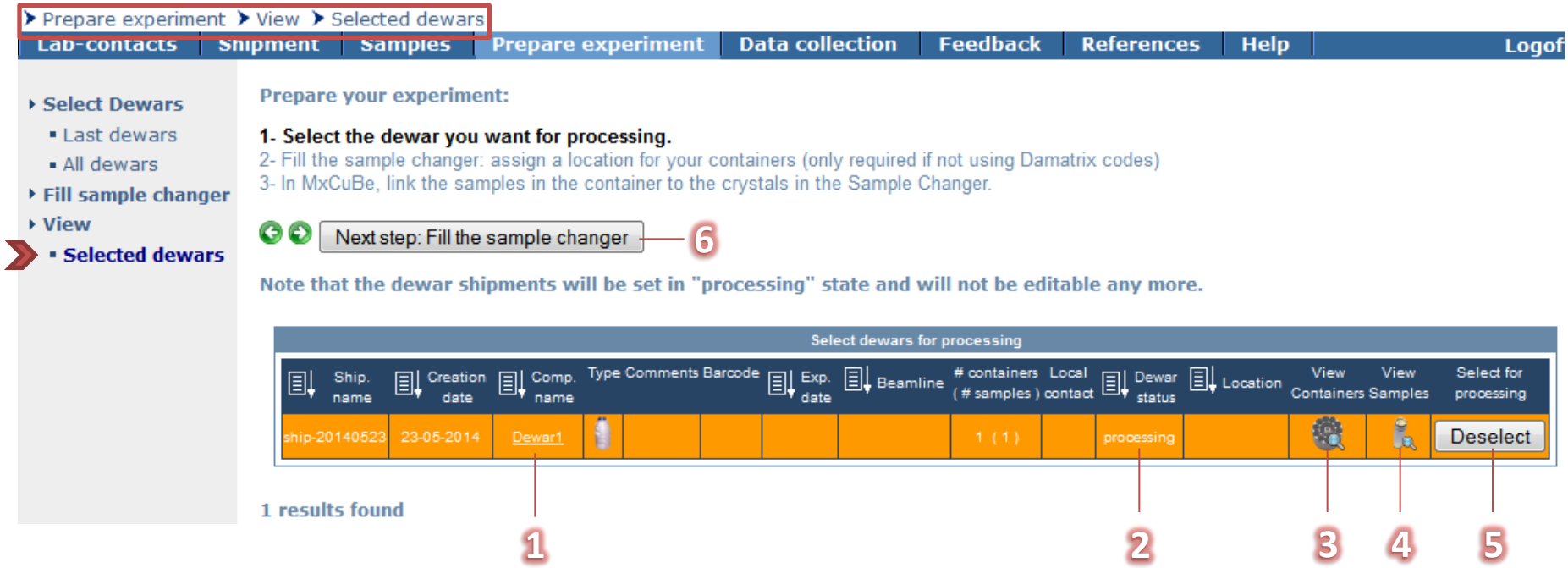
Shipment name	Shipment creation date	Dewar label	Dewar barcode	Container code	Container type	Container capacity	# samples	Beamline Location	Location in Sample Changer
ship-20140206id29	06-02-2014	Dewar1	ESRF0306223	Puck1	Puck	10	6	ID29	1

Save — 2

1

1. Enter the beamline location and the sample changer position of the puck
2. Save the pucks location
3. Click here to view a guide on how to view your selected samples in MXCuBE

Prepare experiment tab: View



Here you can view the list of the previously selected dewars

1 and 3 List the content (pucks) of that dewar
2 Check your dewar status (opened, ready to go, at ESRF, sent to user, processing, closed)
4 View the samples registered in this dewar
5 Select or deselect this dewar to view it in MXCuBE (beamline control software)
6 Click to define the positions of the pucks in the sample changer

Data collection tab

Data collection ➤ View all sessions

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help | Lo

1 View last sessions
2 View all sessions
3 Search data collections

Search Sessions 9

All sessions

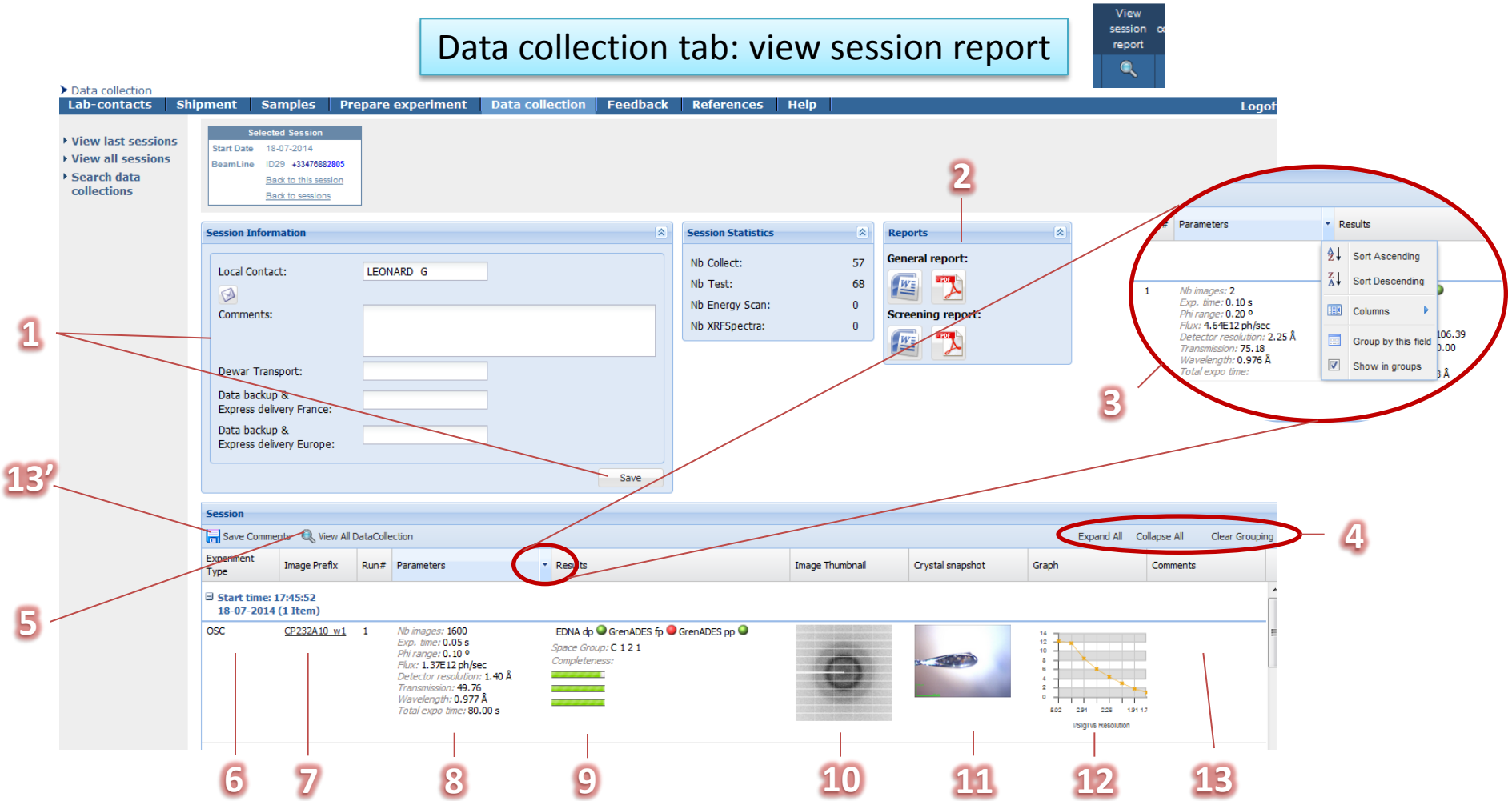
Start Date	End Date	Beamline	Local contact	# Shifts	Comments	Edit	View session report	View collections groups	View collections	SMIS A-Form
26-06-2014	27-06-2014	ID29	POUDEVIGNE E	2						A-Form
28-04-2014	29-04-2014	ID23-1	CARPENTIER P	2						A-Form
18-03-2014	19-03-2014	ID23-1	MONACO S	2						A-Form
17-02-2014	18-02-2014	ID23-1	POPOV A	2						A-Form
13-12-2013	15-12-2013	ID23-1	MUELLER DIECKMANN C	2						A-Form
30-10-2013	01-11-2013	ID23-1	POPOV A	2						A-Form
05-09-2013	07-09-2013	ID23-1	POPOV A	2						A-Form
17-06-2013	19-06-2013	ID23-1	POPOV A	1						A-Form
15-04-2013	17-04-2013	ID23-1	DE SANCTIS D	2						A-Form
21-02-2013	23-02-2013	ID23-1	GORDON E	2						A-Form
03-12-2012	05-12-2012	ID23-1	ALI S	2						
13-09-2012	14-09-2012	ID23-1	RUSSI S	1						
22-06-2012	23-06-2012	ID23-1	LEONARD G	1						
20-06-2012	22-06-2012	ID23-1	FLOT D	1						
03-10-2011	05-10-2011	ID23-1	LEONARD G	1						
29-06-2011	01-07-2011	ID23-1	MONACO S	1						
09-05-2011	11-05-2011	ID23-1	FERRAZ LEAL R	2						
10-03-2011	12-03-2011	ID23-1	CARPENTIER P	2						
02-02-2011	04-02-2011	ID23-1	MCCARTHY A	2						
09-12-2010	10-12-2010	ID23-2		3	Session created by the BCM					

1 2 3 4 >> Go to page

8 10 4 5 6 7 11

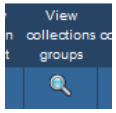
1 View your 20 last sessions
2 View all your sessions
3 Search for a specific data collection or a set of data collections
4 Add comments to this session
5 View reports (parameters, snapshot, autoprocessing...) for a specific session
6 View collection summary by sample
7 View a chronological summary of your collects and detailed autoprocessing results
8 View the A-form (SMIS) corresponding to that session
9 Filter the sessions by date and/or beamtime
10 and 11 View a specific page of the session list

Data collection tab: view session report



1 Add comments about this session and save
2 Download collection reports of different kind and of various formats
3 Click on the right end of the title row to set the parameters grouping/sorting
NB: You can order the columns as you wish by dragging the title where you want
4 Expand/ collapse all lines or clear the parameters grouping
5 View chronological data collection for that session and basic autoprocessing results
6 Experiment type (OSC=standard collection, characterisation…)
7 Click here to view all the details of this experiment (parameters, autoprocessing results…)
8 Experiment parameters
9 View collection autoprocessing status and results
10 Click on the diffraction thumbnail to view full size image
11 Click on the crystal snapshot to view full size image
12 Click on the analytical graph to view full size image
13 Add comments about this data collection and save (13')

Data collection tab: view collections groups



Data collection

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help | Lo

- View last sessions
- View all sessions
- Search data collections

Selected Session

Start Date 20-02-2014
BeamLine ID29 +33476882805
Back to this session
Back to sessions

Session Information

Local Contact:
Comments:
Save

Session Statistics

Nb Collect:	98
Nb Test:	8
Nb Energy Scan:	0
Nb XRFSpectra:	0

DataCollectionGroups | EnergyScans | XRFSpectra

DataCollectionGroups

1 Save Comments | 3 View DataCollection for all groups | Expand All | Collapse All | Clear Grouping

Workflow	Experime Type	Protein Acronym	Image Prefix	Run No	Sample position	Start Time	Comments	Nb Data Collecti	Nb images	View Collections
Sample name: (15 Items)										
XrayCentering	Helical				(1)	20-02-2014 16:...		4	4	
2 XrayCentering	Helical				(1)	20-02-2014 16:...		5	4	
	OSC				(1)	20-02-2014 16:...		7	20	4
	OSC				(1)	20-02-2014 16:...		7	20	
	OSC				(1)	20-02-2014 16:...		7	900	
	Helical			1	(1)	20-02-2014 16:...		1	100	

5 6

1 Save comments
2 Click to view the data collections associated with that of that workflow (collects, images, results)
3 View chronological data collection for that session and basic autoprocessing results
4 View your collections
5 Energy scans for that session
6 XRF spectra for that session

Data collection tab: view collections

Data collection

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help | Logoff

View collections

- View last sessions
- View all sessions
- Search data collections

Selected Session
Start Date 26-06-2014
BeamLine ID29 +33476882805
Back to this session
Back to sessions

Data Collection info...

Reports
General report:
Screening report:

Parameters
Ignore RSymm in the low resolution shell over: 10
Ignore I / Sigma in the low resolution shell under: 1
Update

References
When reporting data collected on ID29 please cite the appropriate references
ID29
EDNA
Workflow
MxCuBE
ISPyB
BEST
AutoProcessing
Download as BibTeX

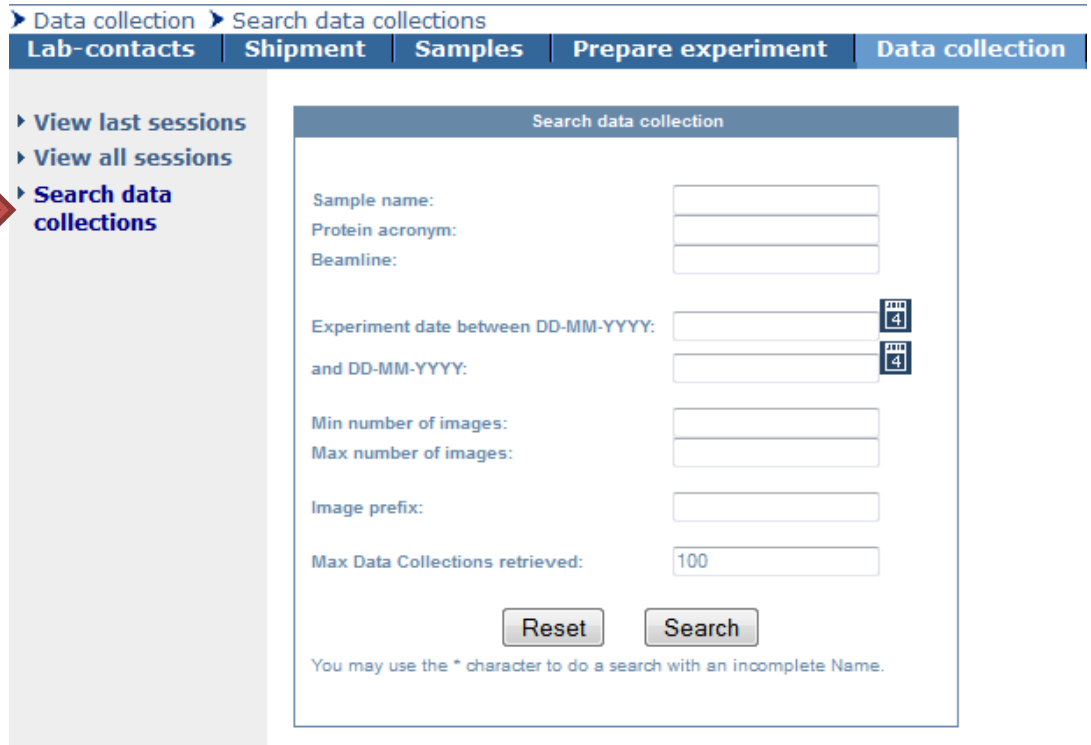
DataCollections
47 DataCollections
Save | Experiment Parameters | Rank EDNA | Expand All | Collapse All | Clear Grouping

Image Prefix	Run No	Experime Type	Protein Acronyr	Start time	# images	Experiment Parameters	Status	Space Group	Completene	Resolution	Rsymm Inner Outer Overall	Unit_cell a, b, c alpha, beta, gamma	Sample Ranking	Skip	Comments	Downloa autoproc files
ref-308	1	Chara...		26-06-2014 18:54:02	2			C2		2.93		271.90, 49.07, 106.39 90.00, 92.61, 90.00				
ref-307	2	Chara...		26-06-2014 18:45:52	2			P222		2.41		40.69, 49.09, 103.69 90.00, 90.00, 90.00				
ref-307	1	Chara...		26-06-2014 18:43:09	2					0.00						
306_w1	2	OSC		26-06-2014 18:35:52	1800			C 2 2 2		100 - 4.95 2.38 - 2.3 100 - 2.3	7.3 153.8 18.1	87.80, 209.30, 50.10 90.00, 90.00, 90.00				
306_w1	1	OSC		26-06-2014 18:31:17	1800			C 2 2 2		100 - 5. 2.77 - 2.... 100 - 2.67	9.2 273.7 26.4	87.70, 208.60, 50.00 90.00, 90.00, 90.00				

1 2 3 4 5 6 7 8 9 10 11

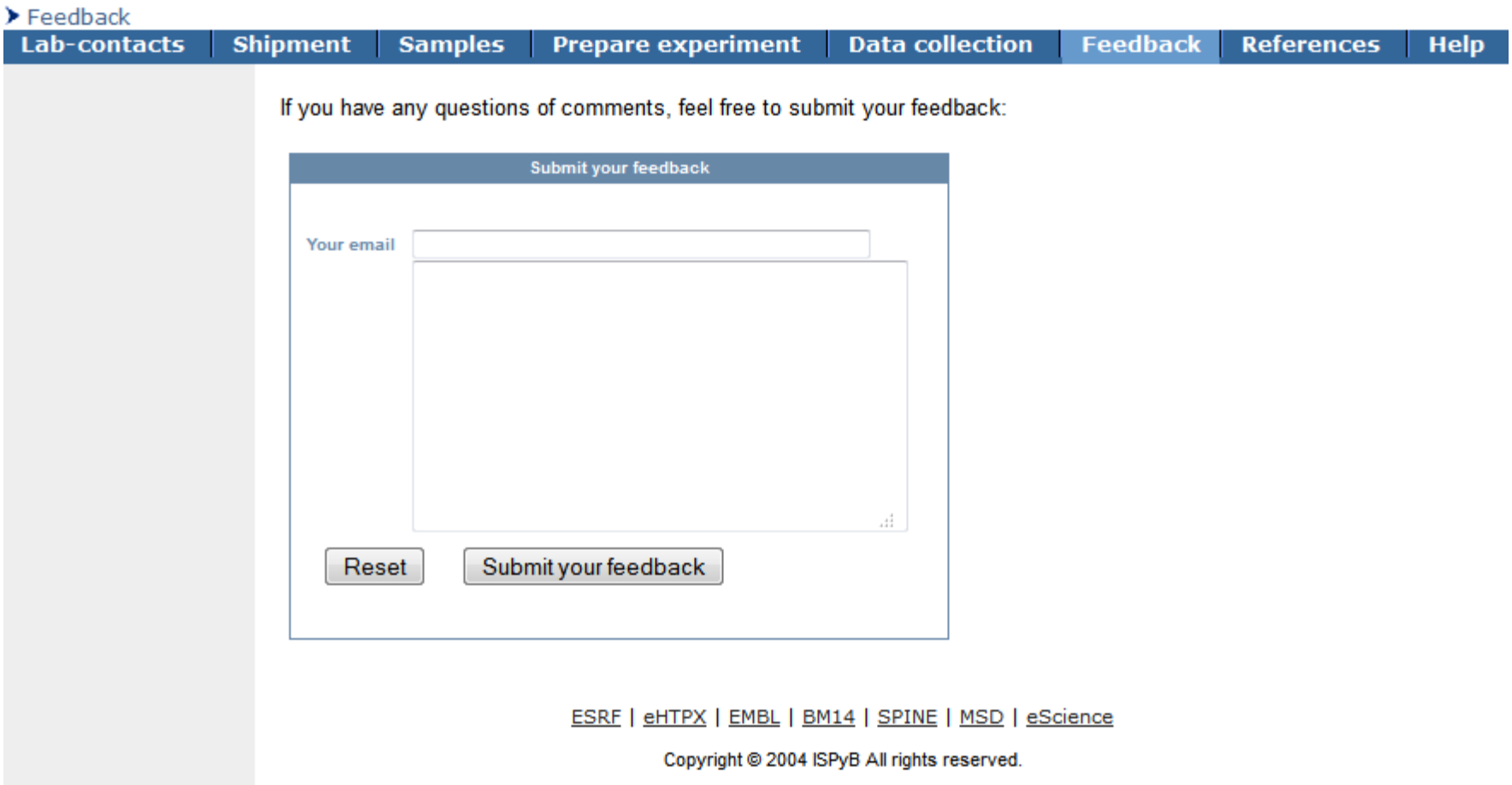
1 Download reports for that session in various formats
2 Tunable parameters for the autoprocessing results summary display
3 References to quote for the publication of your results collected at ESRF
4 Show/ Hide data collection info
5 Show experiment parameters table (wavelength, transmission, exposure time, Phi start, Phi range and detector resolution)
6 View collection status (snapshot, data collection, indexing, autoprocesing)
7 Best autoprocessing summary
8 Select that characterisation for ranking
9 Start sample ranking
10 Download the autoprocessing files for that collect
11 Save your comments

Data collection tab: Search data collections



Use this form to look for specific data collection(s)

Feedback tab



Use this form to give us feedback. We value your opinion and advices on ISPyB and we will use your feedback to improve its operation. We will be happy to help you use ISPyB if necessary.

References tab

References

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References

When reporting data from the ESRF MX beamlines please cite the appropriate references:

- ID23-1
- ID23-2
- ID29
- EDNA
- Workflow
- MxCuBE
- ISPyB
- BEST
- X-ray fluorescence spectra
- AutoProcessing
- Mesh scan

Download as BibTeX

ESRF | eHTPX | EMBL | BM14 | SPINE | MSD | eScience

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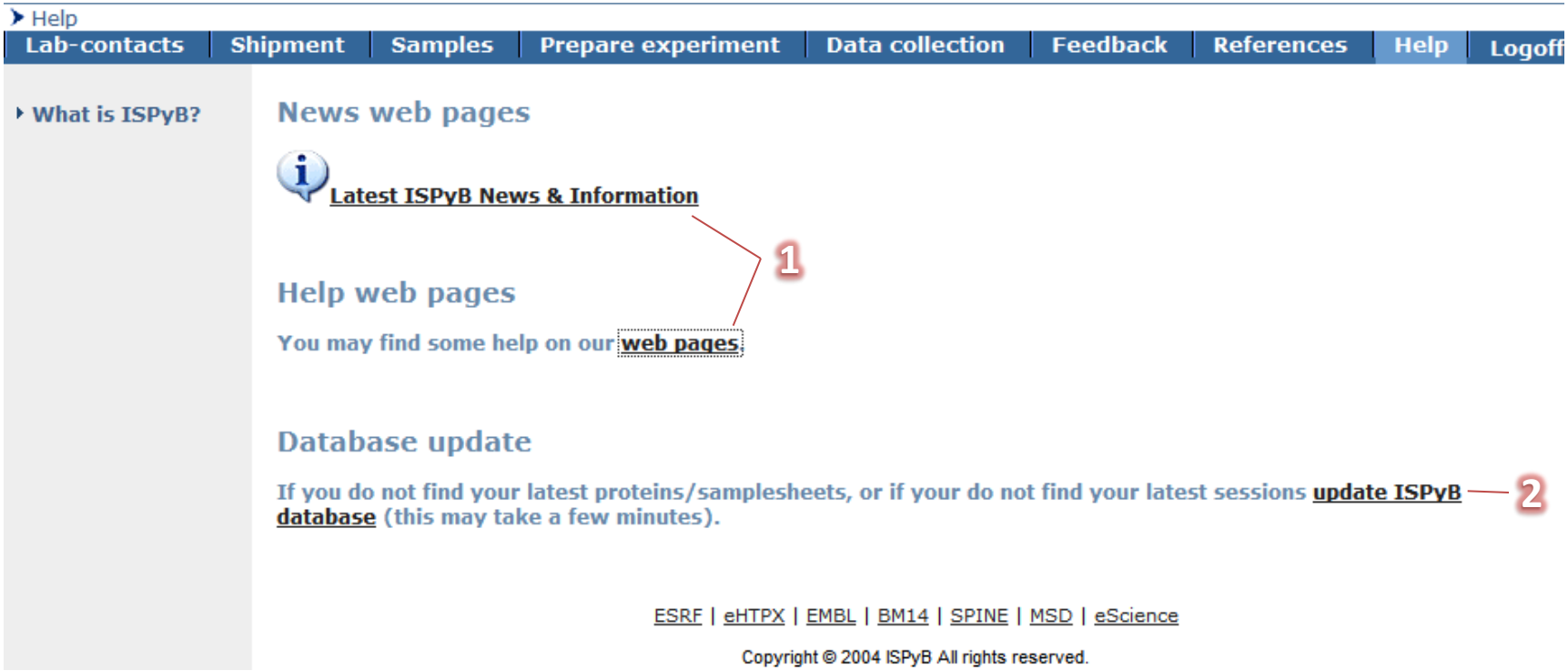
List the references to quote when you report data from the ESRF MX beamlines

Help tab

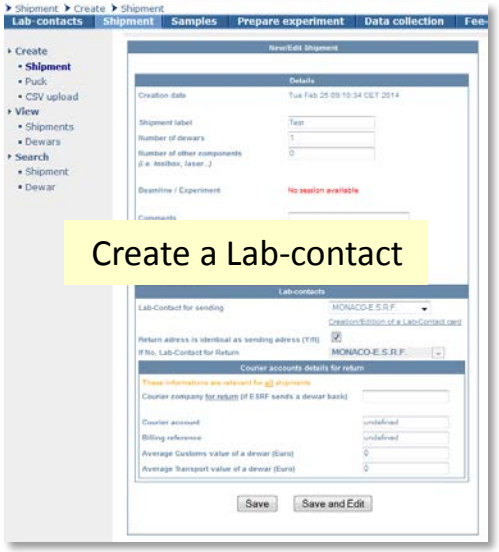


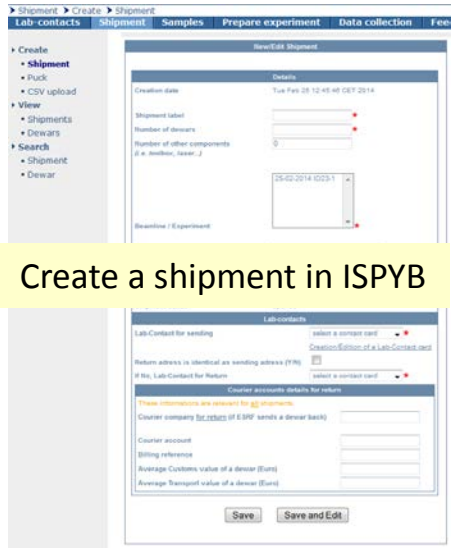
1 Redirection to our web pages where you will find News, information and help pages
2 Click on this link to update the ISPyB database with new proteins (safety sheets) or new session which are stored in the SMIS database (an automatic update takes place every night)

ISPyB user manual

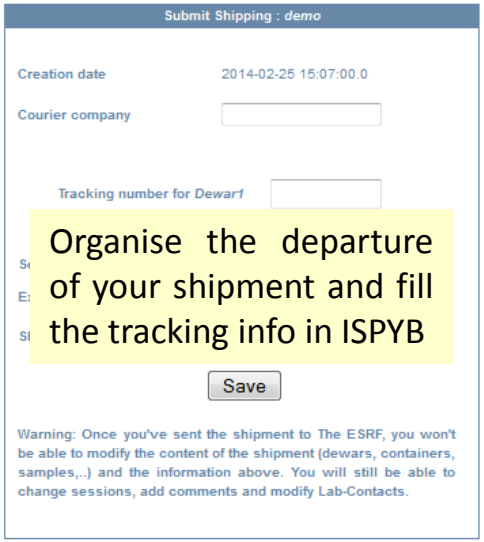
Part II: How to's

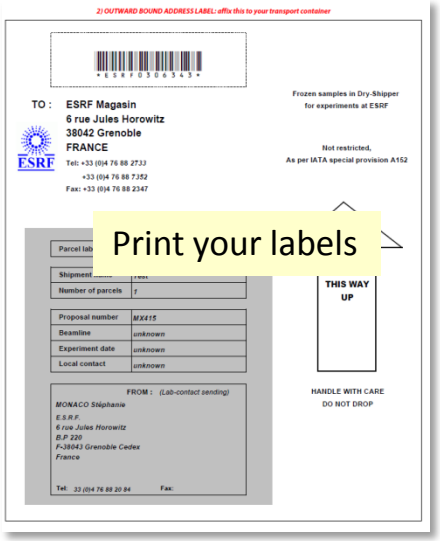
How to:
Track your shipment through ISPyB
Procedure summary





Tracking your shipment & contents (Dewars, toolboxes etc) allows you to follow the progress of your shipment from your home Lab to ESRF and back



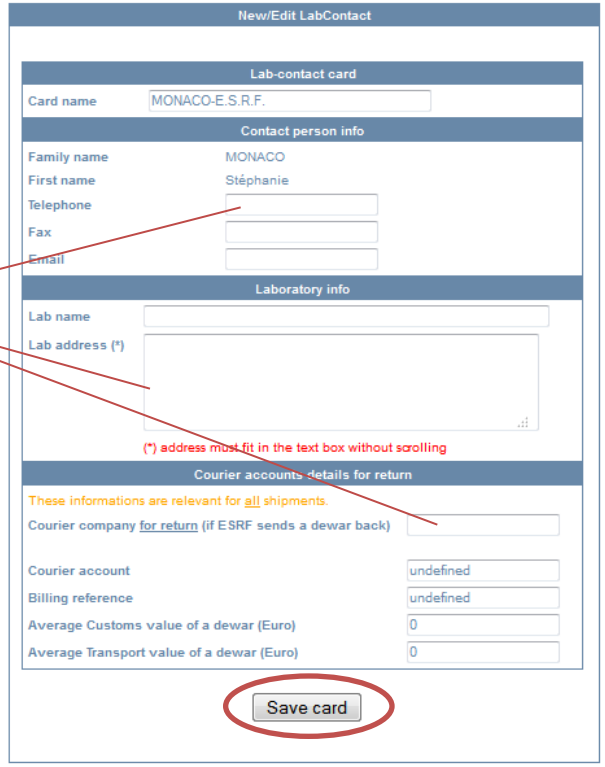


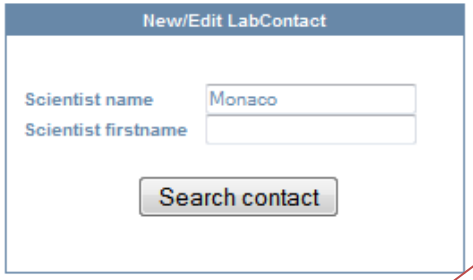
How to:
Track your shipment through ISPyB
Create a lab contact

=> If your lab-contact already exists please go directly to step 2

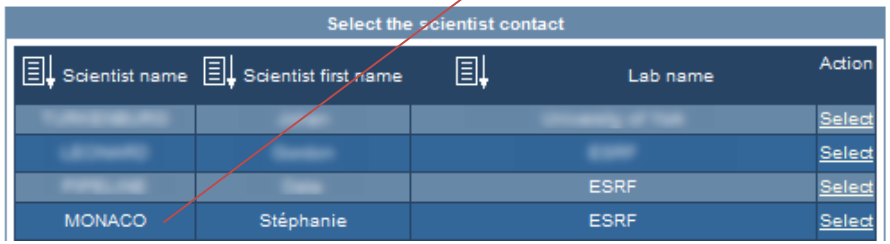
1

3





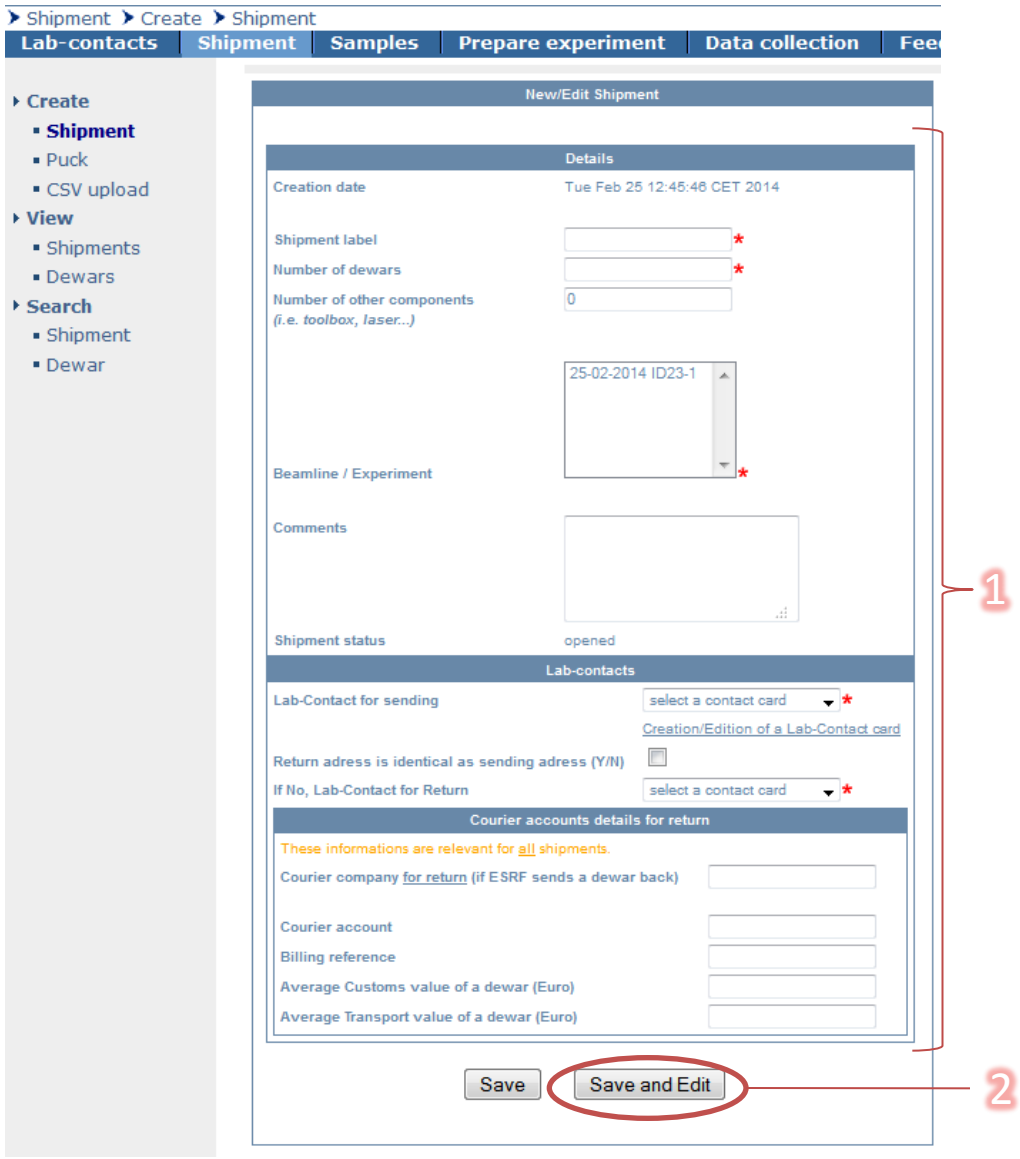
2



1 Fill in scientist name and search the SMIS database for that particular proposal
2 If not found: select one person in your group and go to (3)
3 If found: fill-in & save

NOTE: this needs to be done only ONCE for your proposal and for your LAB address

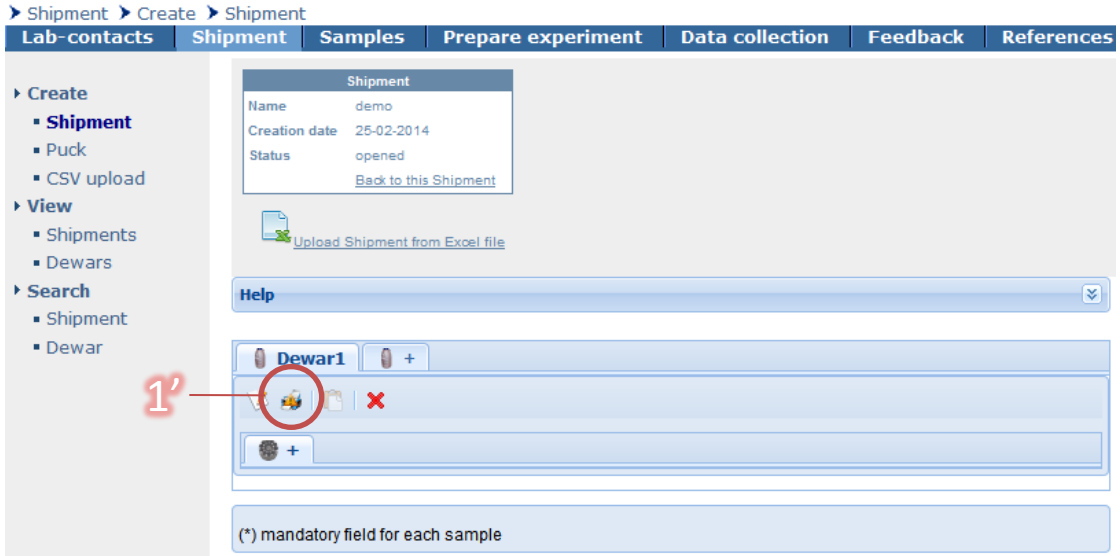
How to:
Track your shipment through ISPyB
Create a shipment

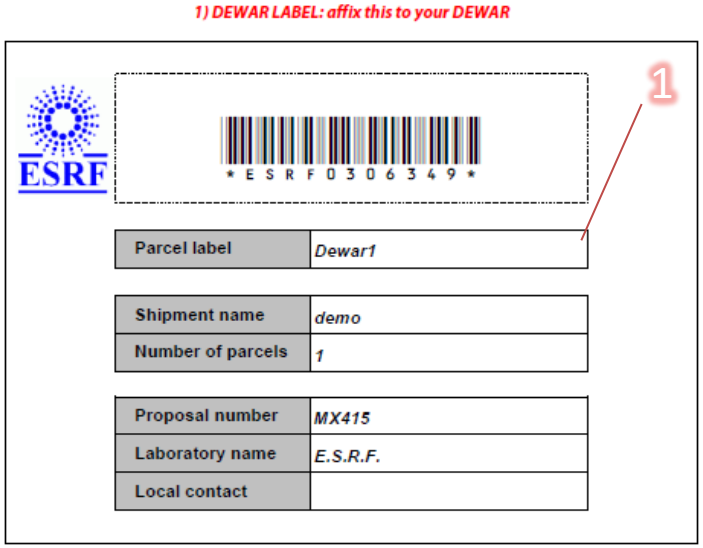


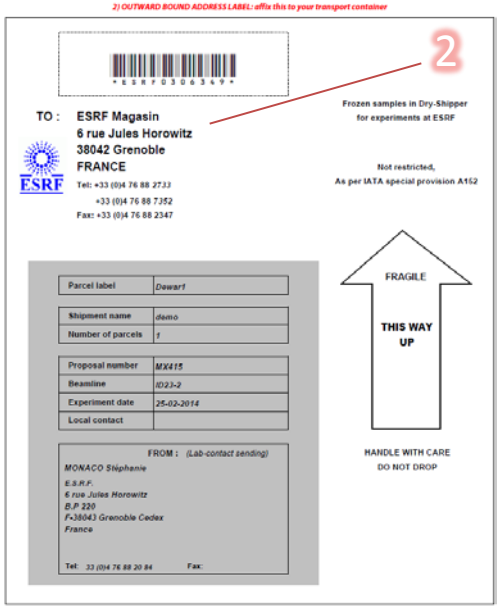
1 Fill in details with components & 2 dewars
2 Save & edit

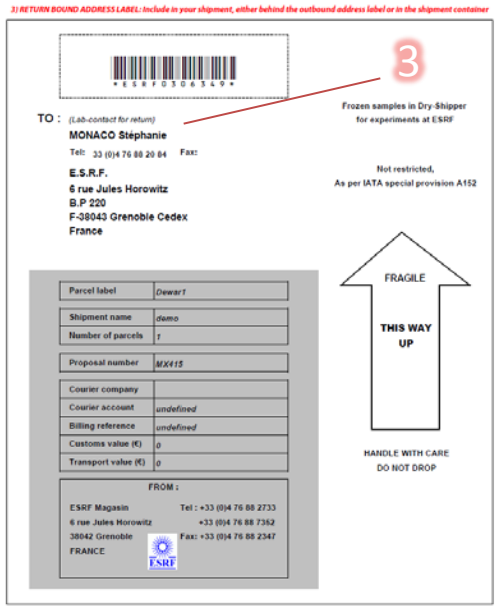
NOTE: if in the field Beamline/Experiment "No session available" appears, please contact deborah.davison@esrf.fr to check that your experiment is scheduled in the SMIS system – If it is already scheduled but this was done during the day of the shipment creation, update ISPYB db with SMIS db info by clicking on 'Help tab' and **update ISPYB database** link

How to:
Track your shipment through ISPyB
Print your labels









1' For each component, print the labels by clicking on the printer icon
NB : This printer icon shows the attention sign until you have opened it once to print the labels

Once printed, stick label 1 and 2 to your dewar and box and put label 3 inside your dewar box for return (same action to do with any other shipment component like a backup in a box, a toolbox..)

How to:
Track your shipment through ISPyB (first option)

Shipment ▸ View ▸ Shipments

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help

- Create
  - Shipment
  - Puck
  - CSV upload
- View
  - Shipments
  - Dewars

1

Shipments

Edit	Shipment Name	Creation date	Expected at ESRF	Sending details	Return details	# components (# samples)	View Dewars	View Samples	Comments	Status	History	Actions
	demo	25-02-2014		MONACO-E.S.R.F.	MONACO-E.S.R.F.	1 (0)						
	ship1	25-02-2014				3 (0)						

2

Submit Shipping : *demo*

Creation date 2014-02-25 15:07:00.0

Courier company

Tracking number for *Dewar1*

Sending Date (DD-MM-YYYY) *

Expected ESRF arrival date *

Shipment status sent to ESRF

Save

Warning: Once you've sent the shipment to The ESRF, you won't be able to modify the content of the shipment (dewars, containers, samples,..) and the information above. You will still be able to change sessions, add comments and modify Lab-Contacts.

3

Shipment Information | Dewar History

Dewar1 history view

Label	Dewar1
Barcode	ESRF0306349
Average customs values (Euro)	0
Average transport values (Euro)	0

Outbound courier

Outbound tracking number

Date	Status	Location
25-02-2014 15:13	ready to go	
25-02-2014 15:13	ready to go	
25-02-2014 15:37	sent to ESRF	

Return courier

Return tracking number

Shipment Information | Dewar History

Details

Label	demo
Number of components	1
Creation date	25-02-2014
Sending date	26-02-2014
Expected arrival date	28-02-2014
Return date	

Lab-contact for sending

Name	MONACO
Firstname	Stéphanie
Phone	33 (0)4 76 88 20 84
Fax	
Email	monaco@esrf.fr
Lab name	E.S.R.F.
Lab address	6 rue Jules Horowitz B.P 220 F-38043 Grenoble Cedex France

Lab-contact for return

Name	MONACO
Firstname	Stéphanie
Phone	33 (0)4 76 88 20 84
Fax	
Email	monaco@esrf.fr
Lab name	E.S.R.F.
Lab address	6 rue Jules Horowitz B.P 220 F-38043 Grenoble Cedex France

1 Send your shipment to ESRF
2 Fill in the details of the courier transport with your tracking number
3 View the history and the information of your shipment

How to:
Track your shipment through ISPyB (second option)

Shipment ▸ View ▸ Shipments

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help | Log

- Create
  - Shipment
  - Puck
  - CSV upload
- View
  - Shipments
  - Dewars

Shipments

Edit	Shipment Name	Creation date	Expected at ESRF	Sending details	Return details	# components (# samples)	View Dewars	View Samples	Comments	Status	History	Actions
	demo	25-02-2014		MONACO-E.S.R.F.	MONACO-E.S.R.F.	1 (0)						
	ship1	25-02-2014		[illegible]	[illegible]	3 (0)						

1

2

All Components in Shipment : demo

Shipment comments :

Type	Comp. name	Comments	Barcode	Exp. date and beamline	tracking # TO Synchrotron	Tracking # FROM Synchrotron	Comp. status	ESRF Location	View Containers	View Samples	History	Comp. labels	Edit Comp. parameters	Other actions
	Dewar1		ESRF0306349	25/02/2014 ID23-2			sent to ESRF							

```
Dear User,

Your parcel Dewar1 (Proposal: FX##, Session date: 10-05-2013, Shipment:  name date
Barcode: ESRF ###### ) has been received by the ESRF on 06/05/2013 at 11:31 AM (GMT+0200)
and will be dispatched to beamline ##

You can check its location at anytime via ISPyB.

Don't hesitate to contact us at mxind@esrf.fr.

Best regards

The MXpress team
```

3

1 Click here to open bottom tab
2 Follow your shipment transport status
3 E-mail received when your components arrive on-site

How to:
Describe the samples in your shipment
Procedure summary

This action requires steps 1 and 2 from the “How to ? : Track your shipment”

Option 1

On-line creation

- Fill in each puck of each dewar
- SAVE
- View all your samples in a list or per puck

Option 2

Excel upload

- Download your template filled with your protein acronyms
- Fill the template outside ISPyB
- Submit your .xls file

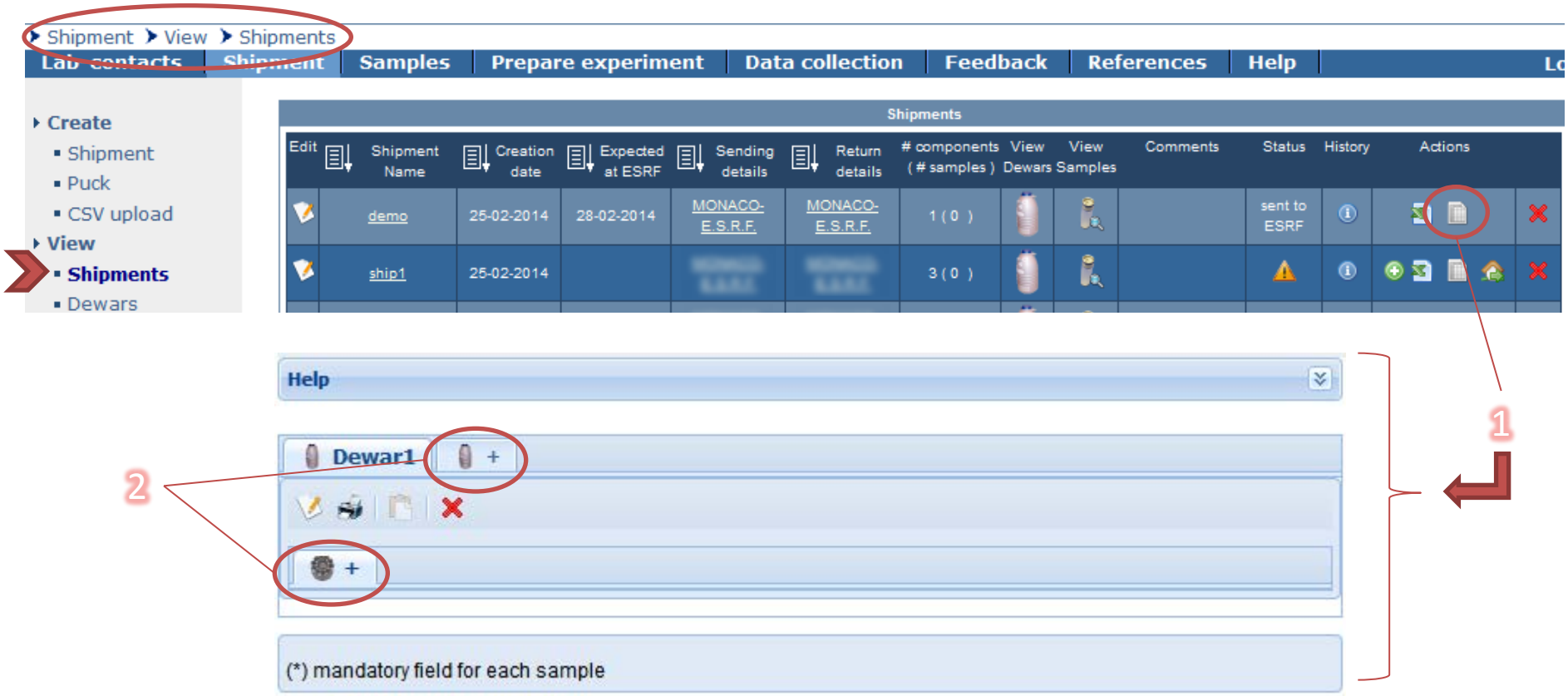
Option 3

CSV upload

- Prepare a file of the type on your computer
- Click on browse to select the file from your computer files
- Describe the field & text separator types
- Upload

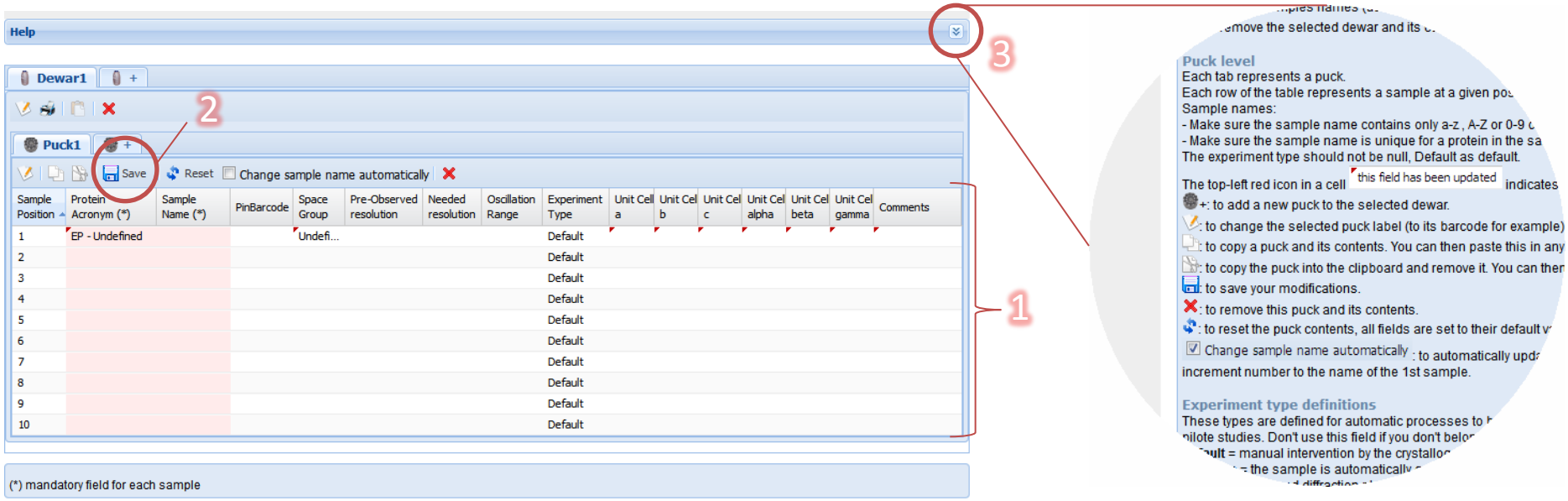
How to:
Describe the samples of your shipment
On-line creation(1/2)

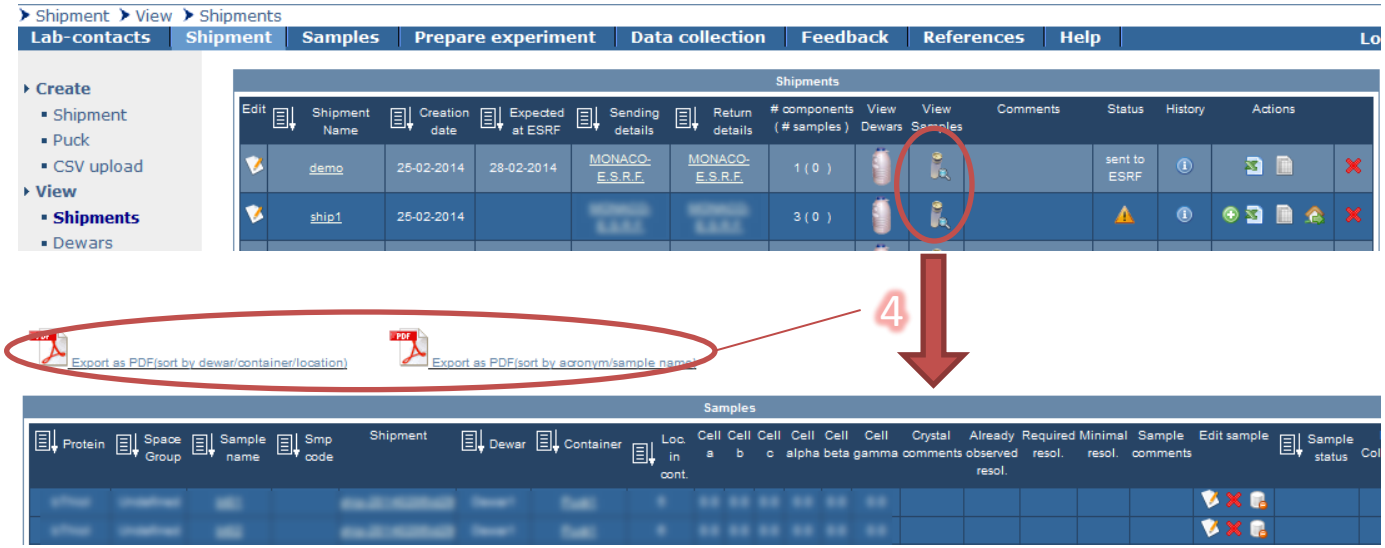
This action requires steps 1 and 2 from the “How to ? : Track your shipment”



1 You can directly access creation page via the View shipment page
2 Create the dewars and pucks you will need

How to:
Describe the samples of your shipment
On-line creation(2/2)



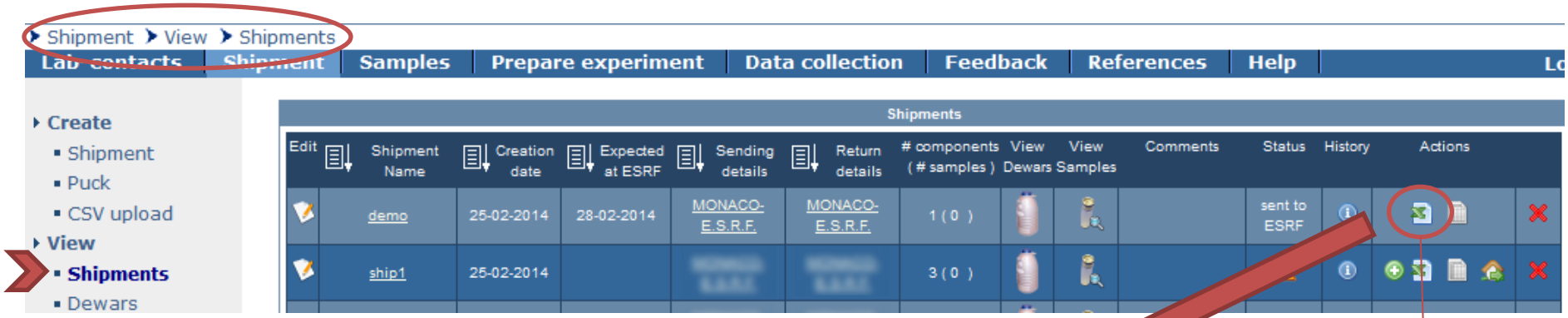


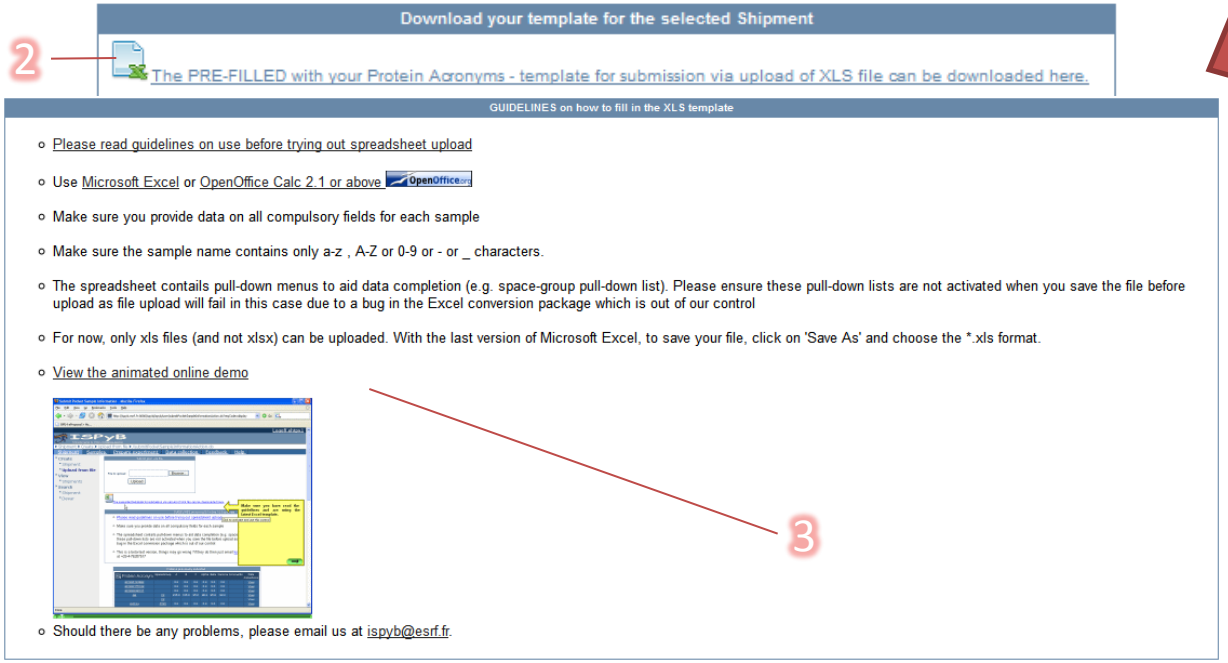
1 Fill in each puck of each dewar
2 SAVE (red corner = NOT saved)
3 Open help page if necessary

4 To view all your samples in a list or per puck and to export this list in pdf sorted by dewar/container/location or by acronym/sample name

How to:
Describe the samples of your shipment
Excel Upload (1/2)

This action requires steps 1 and 2 from the “How to ? : Track your shipment”





1 You can directly access the excel upload page via the View shipment page
2 Download your template filled with your protein acronyms
3 Use guidelines & videos at bottom of the page to fill the file

How to:
Describe the samples of your shipment
Excel Upload (2/2)

Shipment ➤ View ➤ Shipments

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help

- Create
  - Shipment
  - Puck
  - CSV upload
- View
  - **Shipments**
  - Dewars
- Search
  - Shipment
  - Dewar

Shipment

Name	demo
Creation date	25-02-2014
Status	sent to ESRF
	Back to this Shipment

Fill Shipment online

Download your template for the selected Shipment

The PRE-FILLED with your Protein Acronyms - template for submission via upload of XLS file can be downloaded here.

Submit your .xls file

The file must be a xls file (not xlsx).

File to upload: Browse... No file selected. (1)

Samples and Containers: Overwrite current shipment / Add to current shipment (2)

Upload (3)

Warning :

"Overwrite current shipment" will delete the previously existing samples and pucks for that shipment.

"Add to current shipment" will add new pucks and samples to that shipment. Be aware that if a puck already exists with the same name or barcode it will be overwritten.

Please correct your file and re-submit it.

View Samples in Shipping

- Cannot load file: [A-TIM + sampA1] is already exist
  unique. [A-TIM + sampA4] is already existing, and
  [A-TIM + sampA1] is already existing, and should b
  sampA4] is already existing, and should be uniqu
- Warning: the unit cell parameters are not filled for
  are not filled for the spaceGroup P2221 (A-TIM)!W
  P2221 (A315S)!Warning: the unit cell parameters (4)

Submit your .xls file :

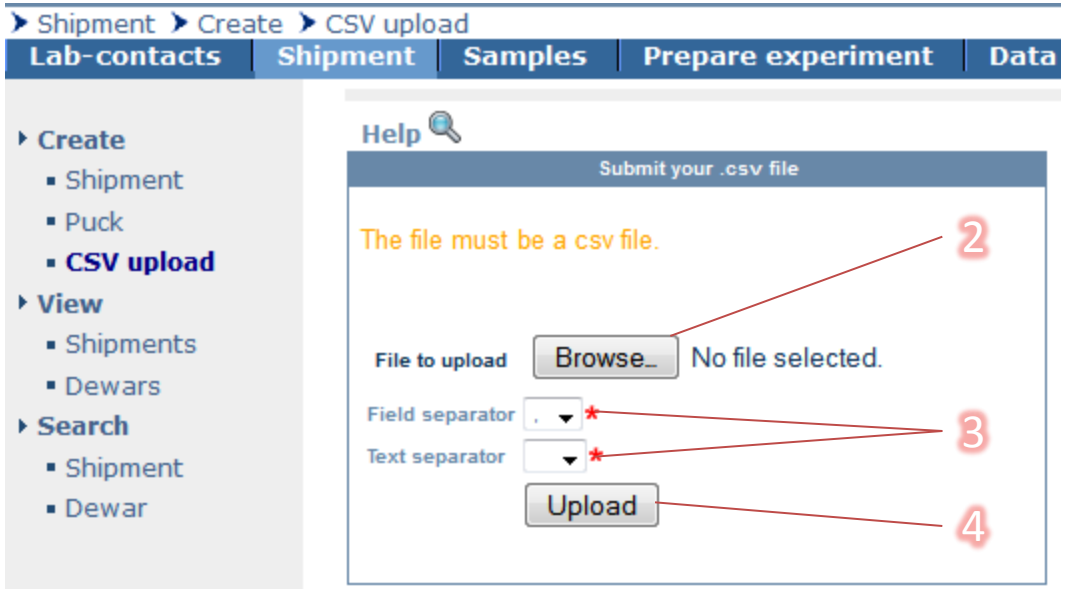
1 Click on “Browse” to select the file on your computer
2 Set the upload parameters: overwrite existing shipment content or add to current shipment
3 Upload
4 Example of error message that will appear if your file contains incorrect parameters

NOTE : Make sure the uploaded file is of .xls format and not .xlsx format

How to:
Describe the samples of your shipment
CSV Upload

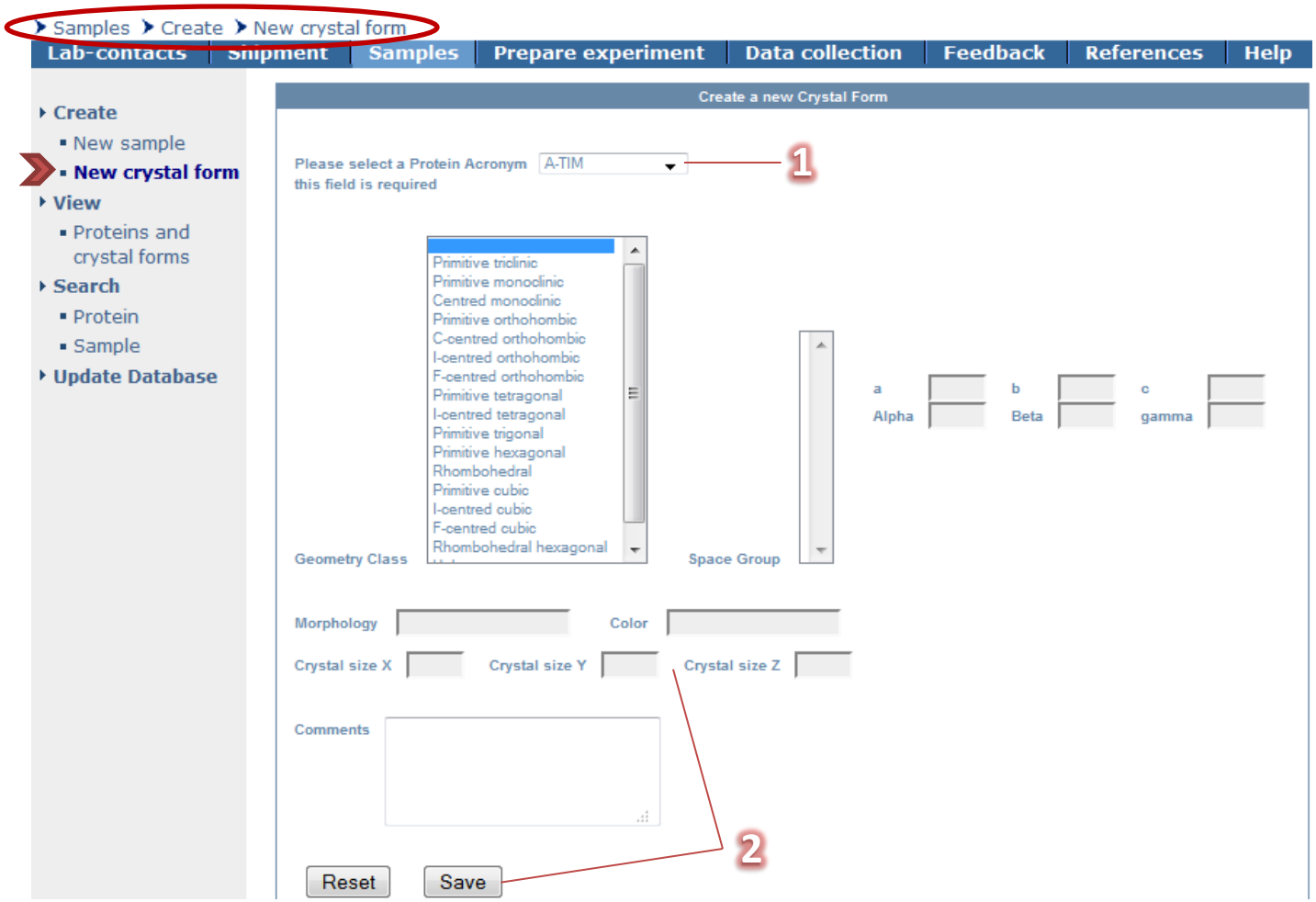
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
1	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample01	1		90	90	90	90	90	90
2	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample02	2		90	90	90	90	90	90
3	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample03	3		90	90	90	90	90	90
4	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample04	4		90	90	90	90	90	90
5	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample05	5		90	90	90	90	90	90
6	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample06	6		90	90	90	90	90	90
7	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	t2	thiolase	C222	0	sample07	7		90	90	90	90	90	90
8	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	CMY-10	beta-lactamase	P41212	0	sample08	8		90	90	90	90	90	90
9	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	CMY-10	beta-lactamase	P41212	0	sample09	9		90	90	90	90	90	90
10	mx	123	1	ship-20140214	Dewar1	Puck1	3	2.1	0.5	CMY-10	beta-lactamase	P41212	0	sample10	10		90	90	90	90	90	90
11	mx	123	1	ship-20140214	Dewar1	Puck2	3	2.1	0.5	t2	thiolase	C222	0	s01	1		90	90	90	90	90	90
12	mx	123	1	ship-20140214	Dewar1	Puck2	3	2.1	0.5	t2	thiolase	C222	0	s02	2		90	90	90	90	90	90
13	mx	123	1	ship-20140214	Dewar2	Puck3	3	2.1	0.5	t2	thiolase	C222	0	test01	1		90	90	90	90	90	90
14	mx	123	1	ship-20140214	Dewar2	Puck3	3	2.1	0.5	t2	thiolase	C222	0	test02	2		90	90	90	90	90	90

1



1 Prepare a file of this type on your computer
2 Select the file from your computer files
3 Describe the field & text separator types
4 Upload

How to:
Attach a new crystal form to a protein



Go to Samples -> Create -> New crystal form

1 Choose your protein acronym (from the list populated with your sample sheets)

2 Enter the parameters of your new crystal form and save

How to:
Upload a PDB file in view of automatic phasing (Dimple, autoMR, …)

Samples ▸ View ▸ Proteins and crystal forms

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help | Lo

- Create
  - New sample
  - New crystal form
- View
  - **Proteins and crystal forms**
- Search
  - Protein
  - Sample
- Update Database

Click on the acronym, or on the space group to see the samples attached to corresponding acronym, space group.

Proteins and Crystal Forms List

Protein Name	Protein Acronym	New Crystal Form	SpaceGroup	A	B	C	Alpha	Beta	Gamma	Comments	Edit	Delete	PDB File	Data Collections
test	test1			108.666	180.159	101.144	90.0	110.3	90.0				Upload	View
test			Undefined	32.016	33.281	48.002	77.97	70.54	61.28				Upload	View
Mnth	Mnth		R32	0.0	0.0	0.0	0.0	0.0	0.0				Upload	View
PA0688	PA0		P21	0.0	0.0	0.0	90.0	0.0	90.0				Upload	View

1

Samples ▸ View ▸ Proteins and crystal forms

Lab-contacts | Shipment | Samples | Prepare experi

- Create
  - New sample
  - New crystal form
- View
  - **Proteins and crystal forms**
- Search
  - Protein
  - Sample
- Update Database

Protein and Crystal Form

Acronym

Back to this protein

Space Group Undefined

Back to this crystal form

Uploaded Pdb

/data/pyapdb/mx415/4KMP.pdb

2

Submit your pdb file

Browse... No file selected.

Update the unit cell parameters

Upload File

3

Go to Samples -> View -> Proteins and crystal forms

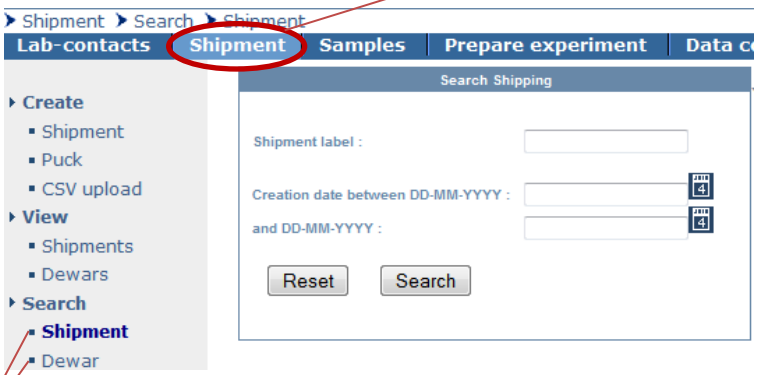
1 Click on "upload" (blue paper clip means that you already downloaded a PDB file for this protein/crystal)

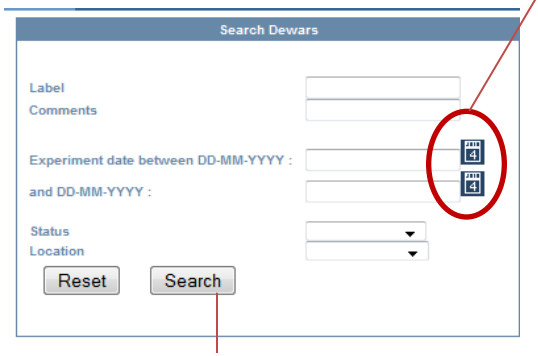
2 Previously uploaded PDB file. Delete by clicking on the red cross. NB: If no PDB file has been previously uploaded there will be no box here.

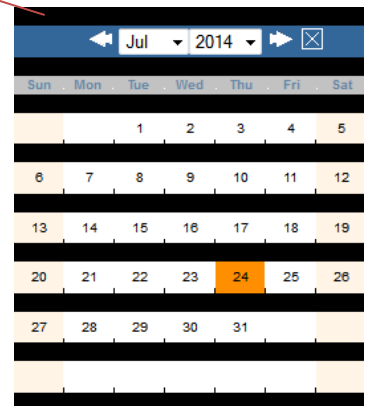
3 Browse to select your PDB file and upload it. You can choose to update the unit cell parameters according to the data from the PDB file or not

How to:
Search the database
Shipment/ Dewar and Data collection

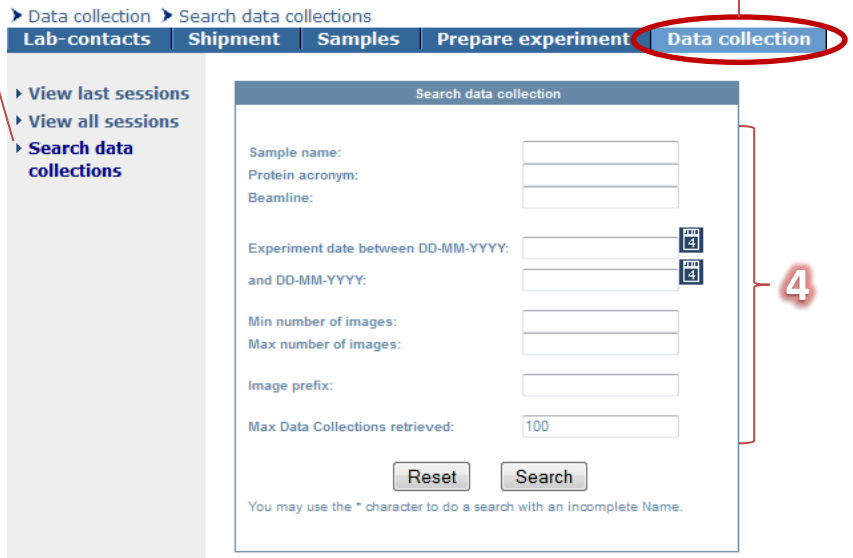
Shipment/ Dewar







Data collection



Go to Shipment (1) or Data collection (2)

3 Click on Search -> “Shipment” (or “Dewar” or “data collections”)

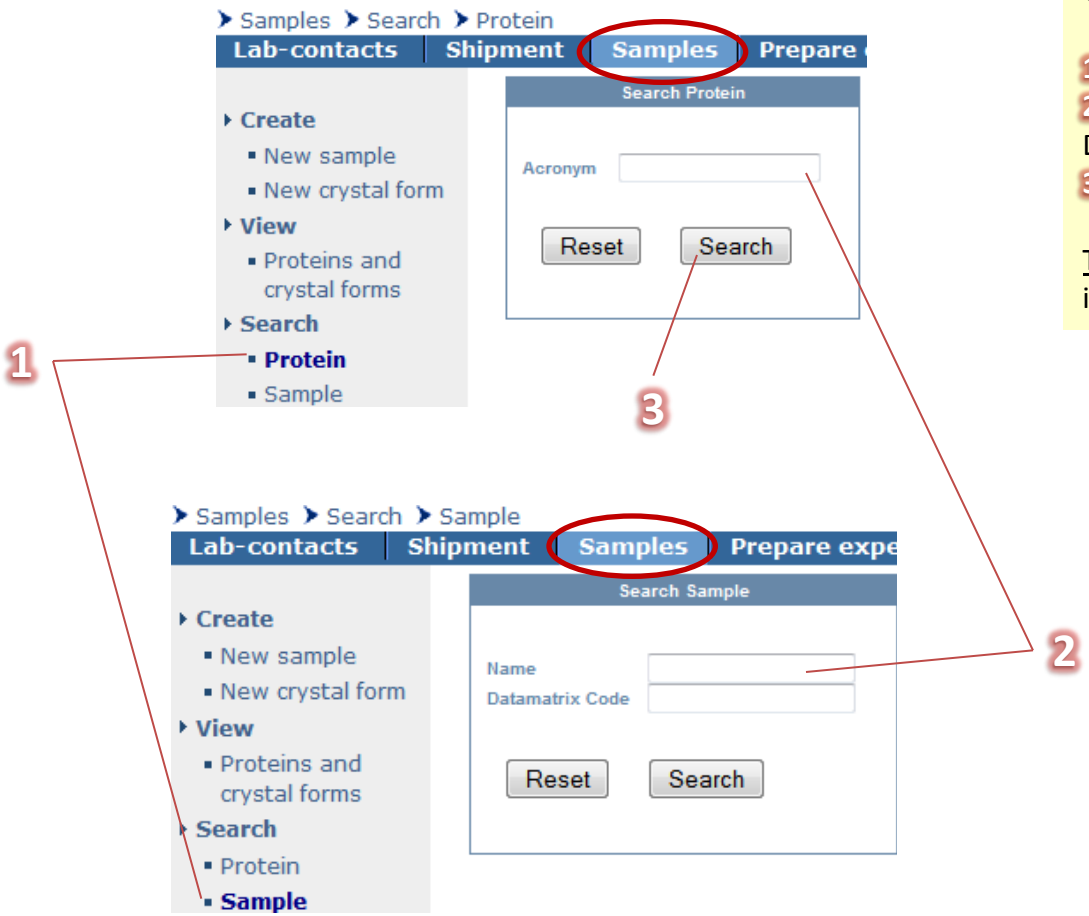
4 Fill in the parameters that you want to include in your search

5 If you want to search by date, click on the calendar icon and choose the date in the calendar

6 Click on “Search”

<u>Tip</u>: If you want to do a search with an incomplete name/label, use the * character

How to:
Search the database
Protein/sample

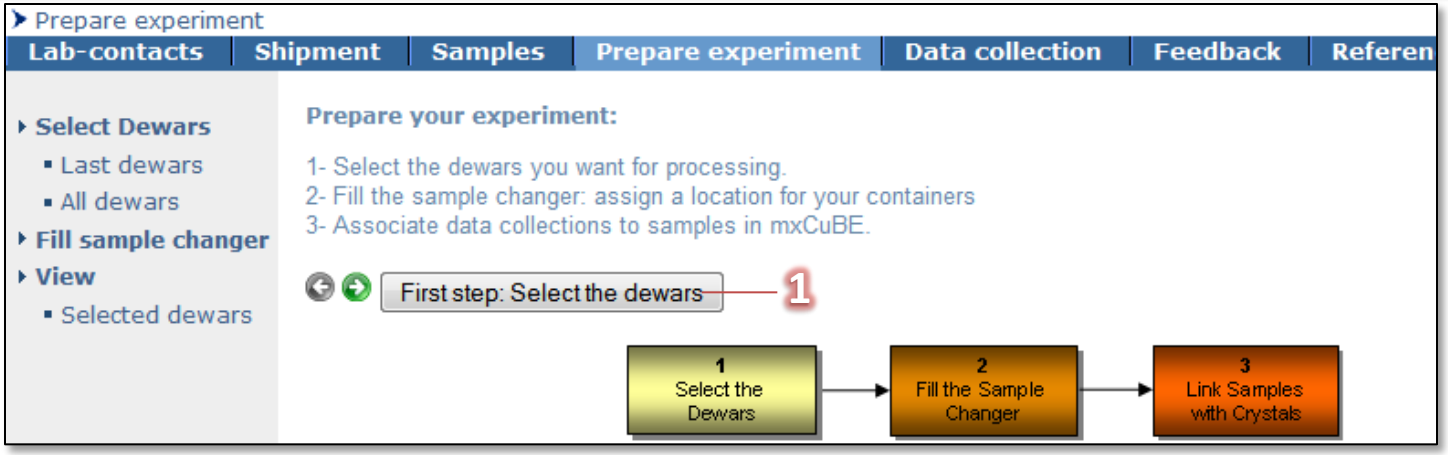


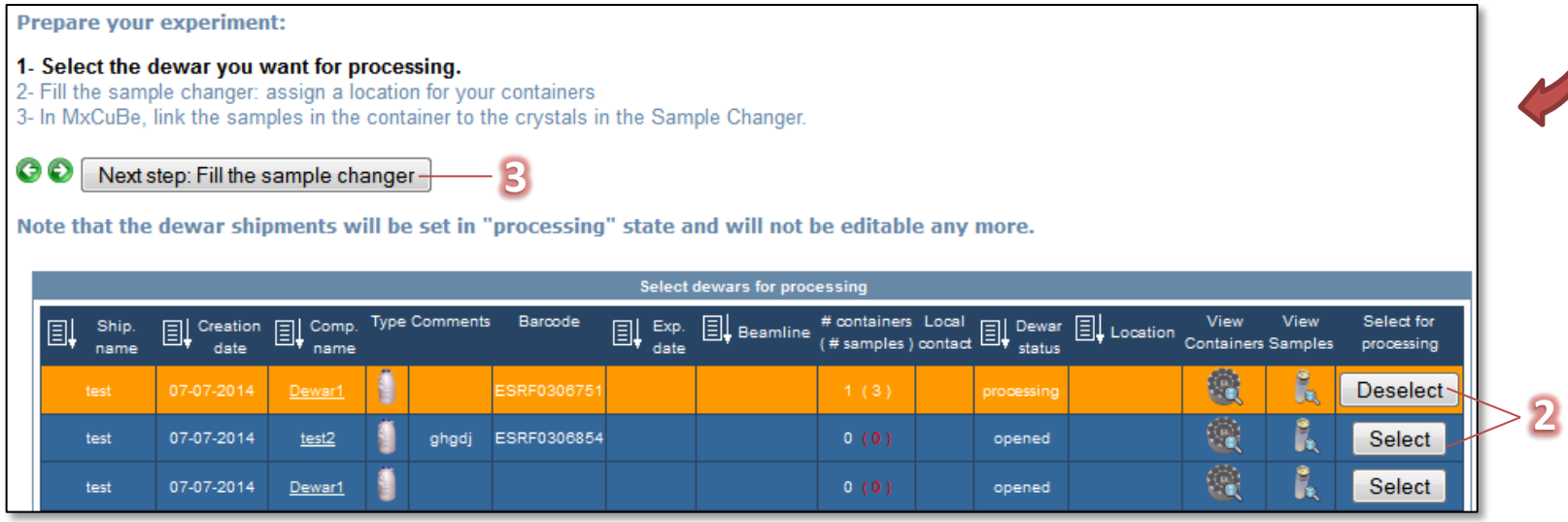
Go to Samples

1 Click on Search -> “Protein” (or “Sample)
2 Fill in the Protein Acronym, Sample name or Datamatrix Code
3 Click on “Search”

Tip: If you want to do a search with an incomplete name/label, use the * character

How to:
Populate your sample list in MXCuBE (sample changer content) with your samples described in ISPyB (1/2)



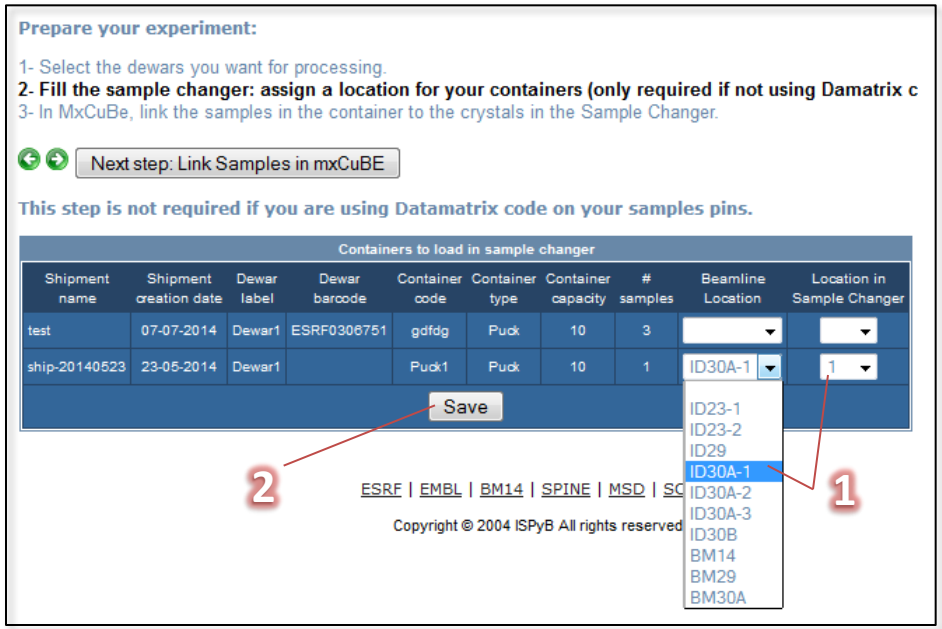


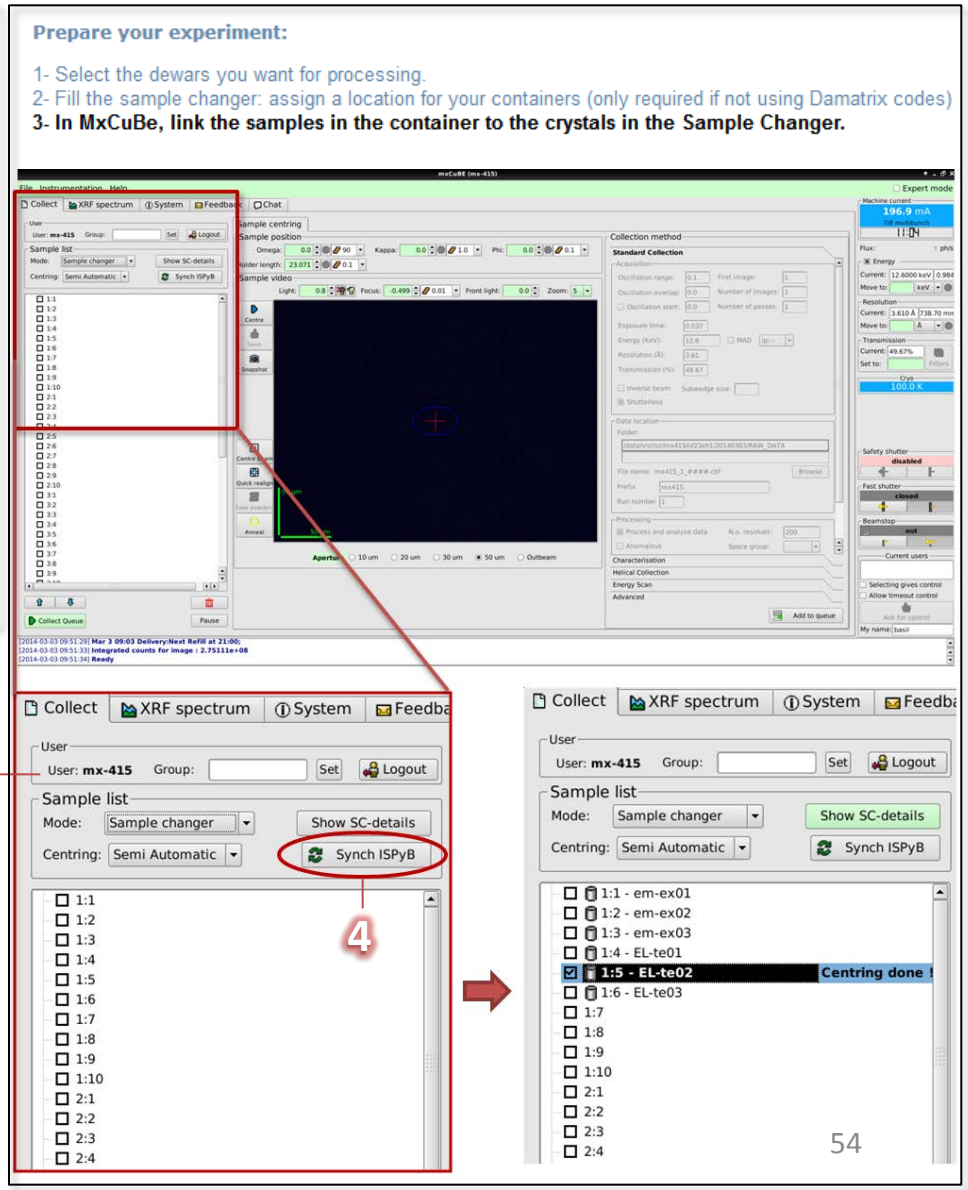
This action requires to have previously followed the "How to ? : Track your shipment-> Create a shipment"

Go to Prepare experiment

1 Click on "First step: Select the dewars"
2 Choose the dewar currently in use at the beamline
3 Click on "Next step: Fill the sample changer"

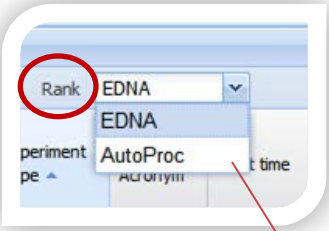
How to:
Populate your sample list in MXCuBE with your samples described in ISPyB (2/2)

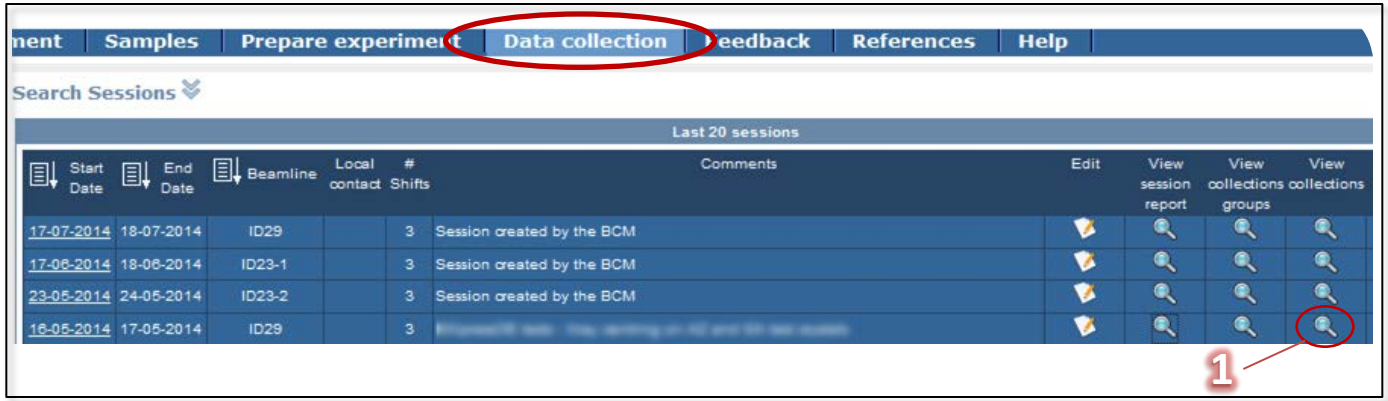


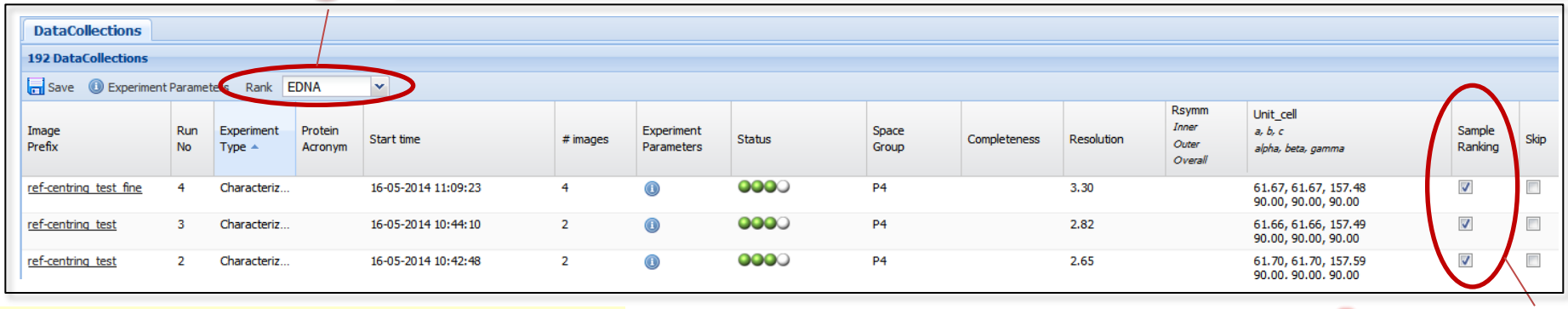


1 Choose the beamline and Sample changer location for each puck
2 Click on save
3 Log into mxCuBE
4 Click on "Synch ISPyB"

How to:
View all your processing results for a session & rank your samples







Go to Data collection

1 Click on “View collections”

2 Tick the “Sample Ranking” box of the samples that you want to rank

3 Select if you want to rank the results based on EDNA characterisation or autoprocessing results and click on “Rank”

4 View the ranking according to different parameters (clicking on the icon)

Tip: In the “view collection summary”, sort the results by experiment type

How to:
View your experiment parameters and results

Data collection

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help

- View last sessions
- View all sessions
- Search data collections

Search Sessions

Last 20 sessions

Start Date	End Date	Beamline	Local contact	# Shifts	Comments	Edit	View session report	View collections groups	View collections	SMIS A-Form
17-07-2014	18-07-2014	ID29		3	Session created by the BCM					
17-06-2014	18-06-2014	ID23-1		3	Session created by the BCM					
23-05-2014	24-05-2014	ID23-2		3	Session created by the BCM					
16-05-2014	17-05-2014	ID29		3	[illegible]					

1'

1

5

6

Session

Save Comments | View All Summary info | View All DataCollection | Expand All | Collapse All | Clear Grouping

Experimen Type	Acronym Sample na	Image Pre	Run#	Parameters	Results	Image Thumbnail	Crystal snapshot	Graph	Second Graph	Comments
Start time: 12:57:16 16-05-2014 (1 Item)										
MXPres...	CER-sam pA04	CER-samp	1	Nb tot images: 3817 Nb images: 3817 Exp. time: 0.04 s Phi range: 0.10 ° Flux: 1.69E11 ph/se Detector resolution: ... Transmission: 13.74 Wavelength: 0.976 Total expo time: 133...	MXPressE EDNA dp GrenADES fp GrenADES pp Space Group: P 41 21 2 Completeness:					

2

3

4

7

Experiment parameters | Beamline parameters | AutoProcessing

Autoprocessing Summary (click on an entry for more details)

Method	Point Group	Cell A	Cell B	Cell C	Cell Alpha	Cell Beta	Cell Gamma
Anomalous: OFF (Friedel pairs merged) (7 Items)							
EDNAproc	P 41 21 2	62.2	62.2	158.8	90	90	90
parallelproc	P 41 21 2	62.2	62.2	158.7	90	90	90
fastproc	P 4 2 2	62.2	62.2	158.7	90	90	90

Go to Data collection

1 Click on "View session report" or on experiment date (1')

2 View the summary of your experiment parameters

3 Summary of the autoprocessing status and best results (cf p.58)

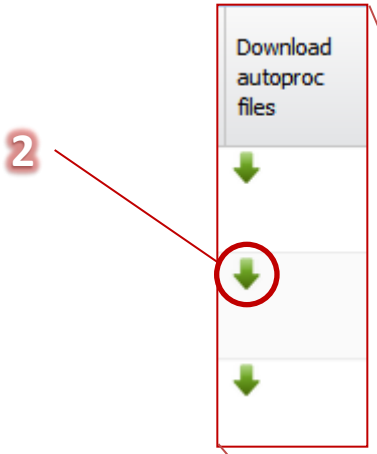
4 Summary snapshots and graphs for that experiment

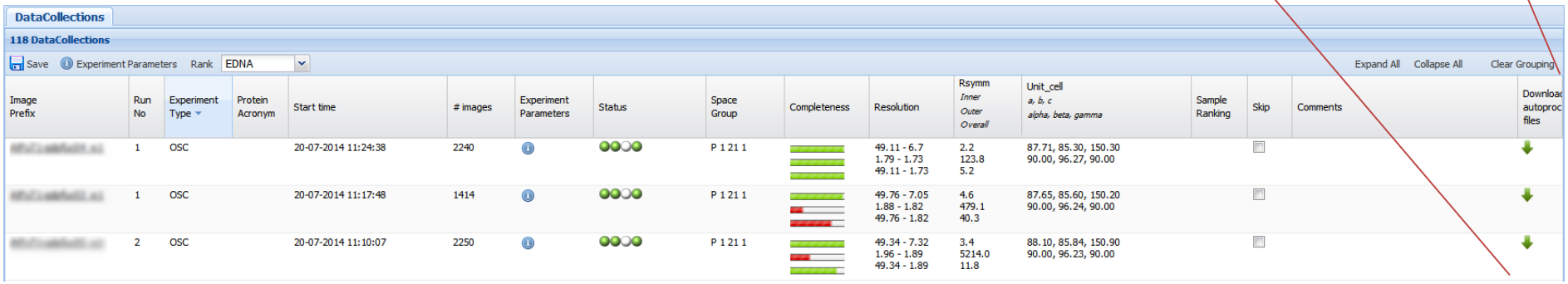
5 Note that, by default, only the last 20 groups are displayed. Click here to access to the whole summary

6 Go to All data collection and access the downloadable autoprocessing files

7 Click on the Image prefix to access to experiment or beamline parameters and autoprocessing results for that experiment

How to:
View/Download all autoprocessing files for one data collection

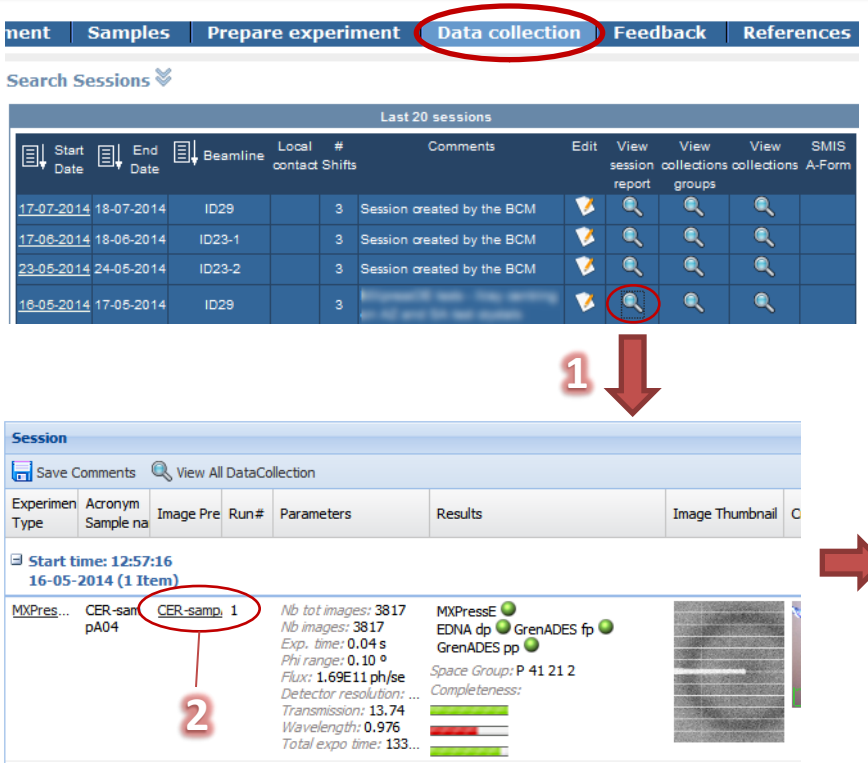


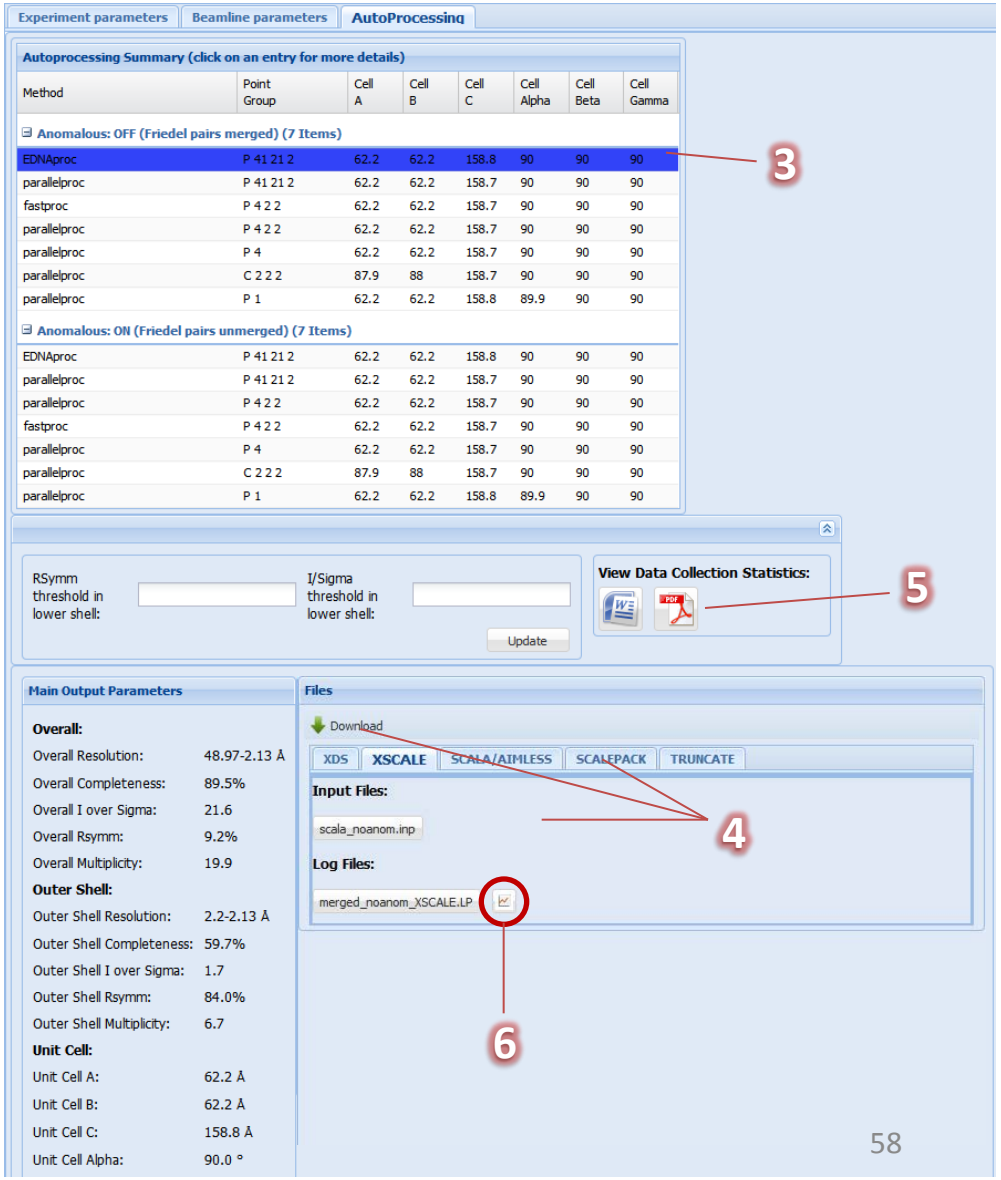


Go to Data collection

1 Click on “View collections”
2 Click on the green arrow to download all Autoprocessing files at once

How to:
View/Download specific autoprocessing results





Go to Data collection

1 Click on “View session report”
2 Click on the Image prefix then go to the AutoProcessing tab
3 Select the autoprocessing result you want to view in particular
4 Click on the file name to view a file or on the green arrow to download all the files for that autoprocessing at once
5 View the statistics report for this data collection
6 Click on the graph icon to view graph extracted from the corresponding log file

How to:
View your processing results -*EDNA characterisation*

Data collection

Lab-contacts | Shipment | Samples | Prepare experiment | Data collection | Feedback | References | Help

- View last sessions
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- Search data collections

Search Sessions

Last 20 sessions

Start Date	End Date	Beamline	Local contact	# Shifts	Comments	Edit	View session report	View collections groups	View collections	SMIS A-Form
17-07-2014	18-07-2014	ID29		3	Session created by the BCM					
17-06-2014	18-06-2014	ID23-1		3	Session created by the BCM					
23-05-2014	24-05-2014	ID23-2		3	Session created by the BCM					
16-05-2014	17-05-2014	ID29		3	[illegible]					

1

Session

Save Comments | View All DataCollection

Experiment Type	Acronym Sample name	Image Prefix	Run#	Parameters	Results
Start time: 11:09:23 16-05-2014 (1 Item)					
Characterization		ref-centring_test_fine	4	*Nb images:* 4 *Exp. time:* 0.20 s *Phi range:* 1.00 ° *Flux:* 3.63E11 ph/sec *Detector resolution:* 2.00 Å *Transmission:* 100.00 *Wavelength:* 0.976 Å *Total expo time:*	Indexing Strategy *Space Group:* P4 *Unit Cell:* *a, b, c:* 61.67, 61.67, 157.48 *α, β, γ:* 90.00, 90.00, 90.00 *Mosaicity:* 0.38 Å *Ranking Resolution:* 3.30 Å

2

Experiment parameters | Beamline parameters | Characterisation parameters | Characterisation results | AutoProcessing

Characterisation Results (EDNA log file)

Data collection info

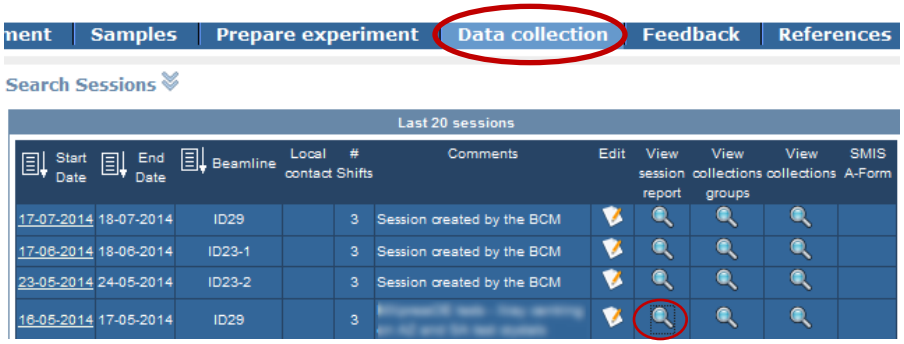
Data collection date	2014/May/16 11:09:35.889
Image prefix	ref-centring_test_fine_4

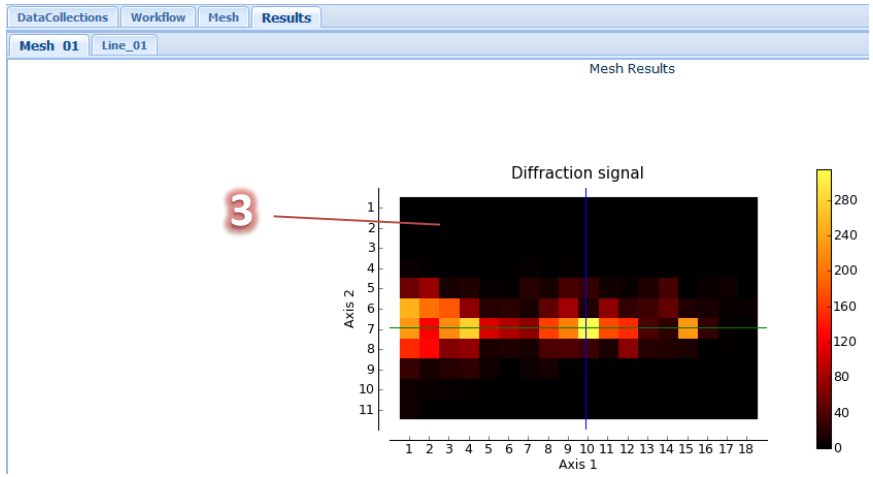
Go to Data collection

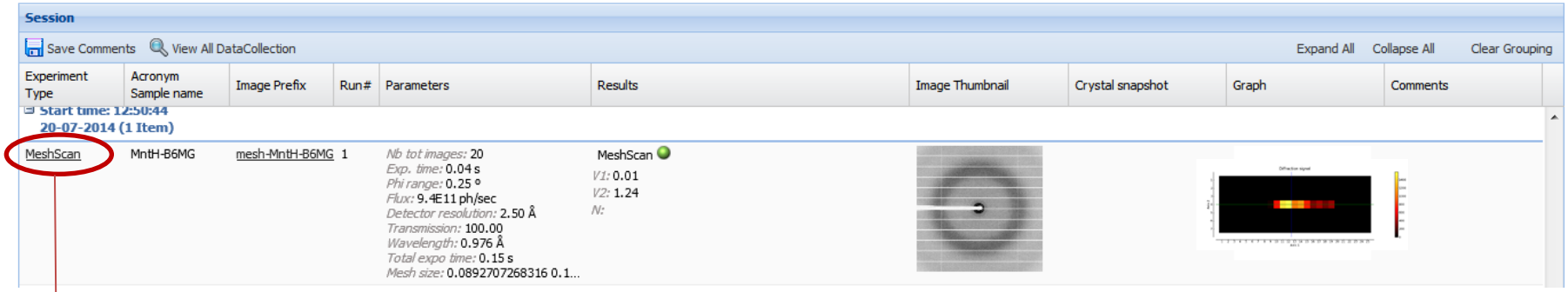
1 Click on "View session report"

2 Click on the Image prefix then go to the "Characterisation results" tab to obtain more details

How to:
View your Workflow results- *Mesh scan and X-ray centring*







Go to Data collection

1. Click on “View session report”
2. Click on the Experiment Type prefix then go to Mesh tab
3. View your mesh/line plots and results in the “results” tab

How to:
Extract reports

Data collection

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23-05-2014	24-05-2014	ID23-2		3	Session created by the BCM					
16-05-2014	17-05-2014	ID29		3	[illegible]					

1

Data collection

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Selected Session

Start Date 16-05-2014

BeamLine ID29 +33476882805

Back to this session

Back to sessions

Session Information

Local Contact:

Comments: MXpressOE [illegible]

Save

Session Statistics

Nb Collect:	179
Nb Test:	13
Nb Energy Scan:	0
Nb XRFSpectra:	0

Reports

General report:

Screening report:

MXPressO-MXPressE report:

2

Go to Data collection

1 Click on View session report

2 Click on the icon to download the report either in word or PDF format