

# ISPyB manual

## Connection via SunSET

### Login in the SunSET

Please type your SUN set username and password to enter

Attention : Fields are case sensitive

Username: isabet

Password: \*\*\*\*\*

Don't have a SUN set login yet? Sign up for an account : [Click here](#)

Don't remember your SUN set username and/or password? : [Click here](#)

Don't have an Umbrella login yet? Sign up for an account : [Click here](#)

### Search for your project-1

Proposal Management

Proposal Application

Before experiment

After experiment

INFORMATION

- General Tab/ co-proposers: "Will attend the experiment?" Issue (09/18/2018)
  - Please be sure to have completed your proposal (click on "Check and save all" button)
  - Please duly complete all eventual missing fields
  - Click on "Save" button
  - Then at the end (before submission) go to "General" Tab
  - Answer the question for each coproposer
  - Click on "Save" button
  - Click on "Submit" button
- Proposal description template information (09/17/2018)
  - Please use the recommended fonts: Arial or Calibri or Symbol otherwise it may not be displayed in the proposal preview (Preview button) but this only a display issue. Your proposal description is duly stored in the SUN set.
- New release (07/23/2018)
  - All User Menu functionalities (Main Proposer / BAG coordinator and Participants) are now available in this version (See shortcuts below).
  - Proposal submission has been optimized (All tabs displayed at the first step, "Save" button at each step, ...).
  - Proposal descriptions and Experimental reports have to be uploaded as a PDF file.
  - 3 types of publications (Journal Article, Conference Proceedings and Thesis) can be added
  - BAG proposals can be visualized in ISPyB with confidentiality managed by team

### Search for your project-2

Enter your project number and then click on the magnifying loop

Enter search string here

Status:  Accepted

Proposal Type:  Block Allocation Group  Standard  Rapid Access  Next  Transnational Access\_EU  In House  Test  Training  Other Facilities

BAG proposal type is:  MX/BioSAXS  not MX/BioSAXS

Show proposals as:  Main Proposer  Coproposer  BAG Coordinator  Principal Investigator

Participants List Status:  Not Submitted  Submitted  Accepted  Declined

Beamline: [dropdown]

Total Nb of props: 0

Icons legend (Before Experiment)

- To view a proposal
- Participants declaration including guest house booking, subsidized participants appointments, samples selection, laboratory request for a session
- User declaration to print, to fill in, to sign and to give at your arrival at SOLEIL reception desk
- Team members to add or view (BAG: PX1, PX2A and SWING)
- Samples to view or to post declare, on accepted proposal
- To have information about Travel & Accommodation and download the "Travel and accommodation application form" and "SOLEIL Expenses Claim form"
- Proposal account password to view and to change it
- To access to ISPyB (BAG: PX1, PX2A and SWING)

Project appears at the bottom with the ISPyB icon  
Click on the Eye icon, a new tab window will be opened with ISPyB webpage

20140720

Status:  Accepted

Proposal Type:  Block Allocation Group  Standard  Rapid Access  Next  Transnational Access\_EU  In House  Test  Training  Other Facilities

BAG proposal type is:  MX/BioSAXS  not MX/BioSAXS

Show proposals as:  Main Proposer  Coproposer  BAG Coordinator  Principal Investigator

Participants List Status:  Not Submitted  Submitted  Accepted  Declined

Beamline: [dropdown]

Total Nb of props: 1

Icons legend (Before Experiment)

- To view a proposal
- Participants declaration including guest house booking, subsidized participants appointments, samples selection, laboratory request for a session
- User declaration to print, to fill in, to sign and to give at your arrival at SOLEIL reception desk
- Team members to add or view (BAG: PX1, PX2A and SWING)
- Samples to view or to post declare, on accepted proposal
- To have information about Travel & Accommodation and download the "Travel and accommodation application form" and "SOLEIL Expenses Claim form"
- Proposal account password to view and to change it
- To access to ISPyB (BAG: PX1, PX2A and SWING)

## Click GO on the right project

ISPyB  
International Synchrotron Protein Crystallography Database

Welcome

Select the proposal you want to work on :

Proposal	Title	Type	
mx20170871110...	BAG STRASBOURG-PALAISEAU-NANCY	MX	GO
mx20170871144...	BAG STRASBOURG-PALAISEAU-NANCY	MX	GO
mx20181360110...	Scientific Case for a BAG application for 2019-2021: submit...	MX	GO
mx20180857	Structure-function studies on metabolic enzymes for new the...	MX	GO
mx09110155	Commissioning PROXIMA 2: Test data collections on protein ...	MX	GO
mx20170718144...	Paris Rive Gauche BAG	MX	GO
mx20170746110...	Structural studies of protein of medical interests	MX	GO
mx20170871144...	BAG STRASBOURG-PALAISEAU-NANCY	MX	GO
mx20170720144...	Block Allocation Group Marseille	MX	GO
mx20170718110...	Paris Rive Gauche BAG	MX	GO

ESRF | EMBL | BM14 | SPINE | MSD | MAX IV | SOLEIL

## ISPyB Mainpage

ISPyB  
International Synchrotron Protein Crystallography Database

Welcome to User : mx20100023

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

Latest ISPyB News & Information

In case of problems when creating shipments/samples, [update ISPyB database](#) (this may take a few minutes).

**"Shipment" tab**  
Click on this tab to deal with the samples you are planning to send by courier. You will be able to define an electronic shipment, containing electronic dewars and containers. You will be able to enter the samples description based on the protein you have submitted through "samplesheets". You will be able to retrieve information about the shipments, dewars and containers already submitted.

**"Samples" tab**  
Click on this tab to deal with data concerning your proteins, crystals and samples. You will be able to create new samples for experiment: samples description will be based on the protein you have submitted through "samplesheets". You will be able to add/edit a new crystal form for your protein. You will be able to view the lists of your proteins, crystal forms, samples. You will be able to edit the diffraction plans linked to your samples.

**"Prepare experiment" tab**  
Click on this tab to prepare the list of samples you want to see during experiment. You will also need to fill the sample changer manually if you are not using pins with DM codes.

**"Data collection" tab**  
Click on this tab to deal with the data collection you perform on your samples. You will be able to retrieve information about a particular session. You will be able to retrieve information about a particular data collection. You will be able to retrieve information about a particular protein. You will be able to retrieve information about a particular sample.

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## 1- Create a shipment

ISPyB  
International Synchrotron Protein Crystallography Database

Shipment > Create > Shipment

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

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

New/Edit Shipment

Details

Creation date: Wed Apr 24 10:30:32 CEST 2019

Shipment label:

Number of dewars:

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

09-02-2010 Proxima1  
18-02-2010 Proxima1  
09-03-2015 Proxima1  
10-03-2015 Proxima1  
11-03-2015 Proxima1  
01-04-2015 Proxima1

Scientific Experiment:

Comments:

Shipment status: opened

Lab-contacts

Lab-Contact for sending:

Return address is identical as sending address (Y/N):

If No, Lab-Contact for Return:

Optional electronic details for return

These informations are request for all shipments.

Courier company for return (if SOLEIL, sends a dewar back):

Courier account:

Billing reference:

Average Customs value of a dewar (Euro):

1- Fill the \*box  
2- Then 'SAVE and EXIT' or 'SAVE'

## 2- Upload your Excel file (1) or add components by hand (2)

In the case of Excel upload, after uploading, all the messages should appear in Green. If you see Red messages, it means something went wrong, and you will have to correct your Excel file

ISPyB  
International Synchrotron Protein Crystallography Database

Shipment > Create > Shipment

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

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

Upload Shipment from Excel file

27-03-test successfully inserted into database.

Help

Dewar

1  
2

(\*) mandatory field for each sample.  
11 to 16 rows of the table are only used in case of unpucks.

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### 3- Prepare your experiment

1- Click on 'Prepare experiment' on the top menu

2- Click on First step : Select the dewars

Prepare your experiment:

- 1- Select the dewars you want for processing.
- 2- Fill the sample changer: assign a location for your containers
- 3- Associate data collections to samples in mxCuBE.

First step: Select the dewars

Linking Samples to Data Collection: how does it help my experiment?

Linking Samples of your Shipment (sample descriptions) with Crystals in the Sample changer (physical samples) will allow you to associate the description. Then, you will be able to make Sample Ranking or to make reports that can be processed by your LIMS.

3- Select the proper session (appear in orange background)

4- Then click on Next step : Fill the sample changer

Prepare your experiment:

- 1- Select the dewar you want for processing.
- 2- Fill the sample changer: assign a location for your containers
- 3- Associate data collections to samples in mxCuBE.
- 3- In MxCuBe, link the samples in the container to the crystals in the Sample Changer.

Note that the dewar shipments will be set in "processing" state and will not be editable any more.

Ship name	Creation date	Comp. name	Type	Comments	Barcode	Exp. date	Beamline	# containers (# samples)	Local contact	Dewar status	Location	View Containers	View Samples	Select for processing
27-03-test	24-04-2019	Dewar1			SOLEIL094	18-02-2010	PROXIMA1	0 (1)	THOMPSON A	opened				Select

1 results found in the last 60 days

5- Select the beamline and the puck location

6- Don't forget to SAVE (it takes some seconds)

7- Then click on Next step : Link Samples in MXCuBE

Prepare your experiment:

- 1- Select the dewars you want for processing.
- 2- Fill the sample changer: assign a location for your containers
- 3- Associate data collections to samples in mxCuBE.
- 3- In MxCuBe, link the samples in the container to the crystals in the Sample Changer.

Next step: Link Samples in mxCuBE

Shipment name	Shipment creation date	Dewar label	Dewar barcode	Container code	Container type	Container capacity	# samples	Beamline Location	Location in Sample Changer
24-Janv2017	24-01-2017	Dewar1	SOLEIL094	X00	Puck	16	16	PROXIMA1	2
Oct2015a	27-10-2015	DewarSOLEIL1		ILO-001	Puck	16	16		

Save

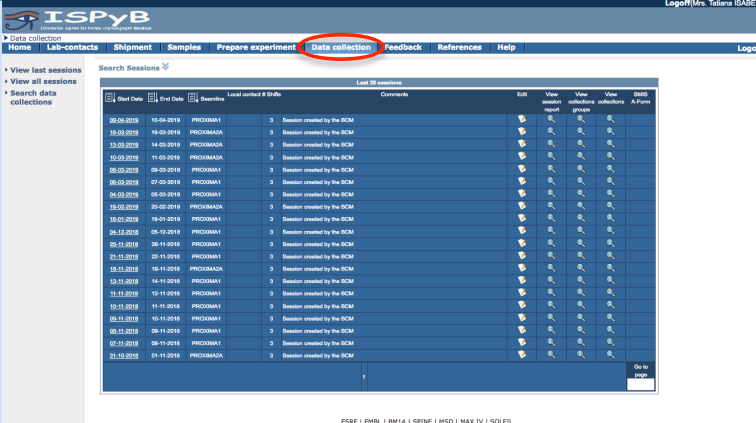
ESRF | EMBL | BM14 | SPINE | MSD | MAX-IV | SOLEIL

Final page : if you arrived here, it means that you can click on the ISPyB synchronisation button within MXCuBE

## 4- Data collection

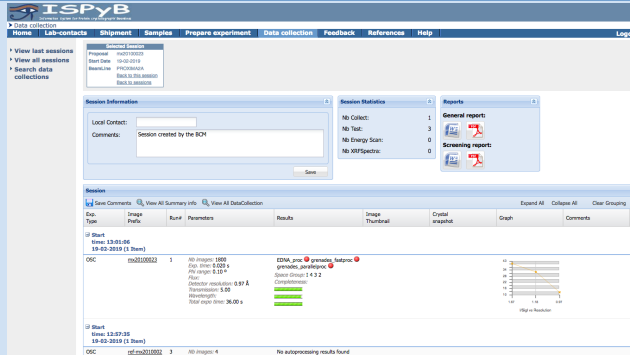
1- Click on Data collection on the top menu

2- Click on your session



The screenshot shows the ISPyB web interface. The top navigation bar includes 'Home', 'Lab-contacts', 'Shipment', 'Samples', 'Prepare experiment', 'Data collection' (highlighted with a red circle), 'Feedback', 'References', and 'Help'. Below the navigation bar, there are options to 'View last sessions', 'View all sessions', and 'Search data collections'. The main content area displays a table of sessions with columns for Start Date, End Date, Session ID, Local Contact #, and Comments. The table lists multiple sessions created by the BCM. At the bottom of the page, there are links for 'ESRF | EMBL | RMC | SIBNE | HSD | MAX-IV | SOLEIL'.

A list of data collection appears with results of autoproccessing

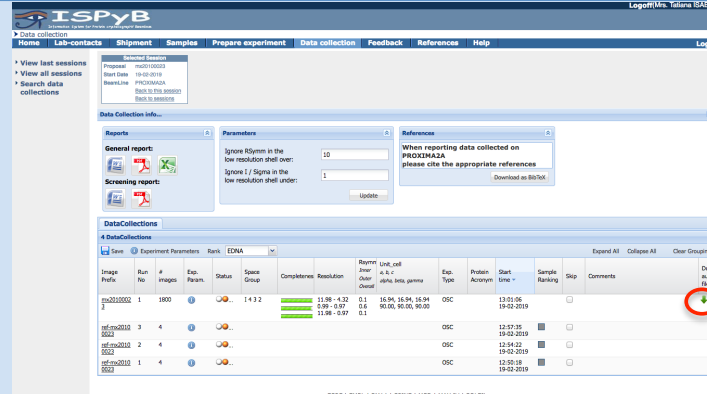


The screenshot shows the 'Data Collection Information' page in ISPyB. It displays session details for 'Session created by the BCM'. The 'Session Information' section includes 'Local Contact', 'Comments', and 'Session Status'. The 'General report' section shows 'No Collect', 'No Scan', and 'No Energy Scan'. The 'Screening report' section shows 'No XFSpectra'. Below this, there is a table of data collections with columns for 'Exp. Type', 'Run#', 'Parameters', 'Results', 'Image', 'Crystal', and 'Graph'. The table shows two data collections with their respective parameters and results.

If you click on **View All DataCollection**, a new display appears :

you can see results with a different graphical display in which you can download results (mtz file and logs)

If you click on a data collection, you will find more autoproccessing detailed results



The screenshot shows the 'Data Collection Information' page in ISPyB, similar to the previous one. The 'Data Collection info...' section is expanded, showing 'General report' and 'Screening report' options. Below this, there is a table of 'DataCollections' with columns for 'Image Prefix', 'Run #', 'Exp. Param.', 'Status', 'Space Group', 'Completeness', 'Resolution', 'RayTilt', 'Unit Cell', 'Indexing', 'Data Quality', 'Exp. Type', 'Protein Acronym', 'Start Date', 'Sample Ranking', 'Skip', and 'Comments'. A red circle highlights a download icon in the 'Download' column of the table.