

Beamline Handbook

Version 3 – 02.11.2021

BL14.2

Symptom	Check	Fix	2. Check
The GROB robot arm freezes over an open lid during the attempt to mount or unmount a sample <u>OR</u> the robot arm moves back to its <i>safe</i> position and the lid remains open.	Has the “Transfer phase” of the goniometer been reached?	<p>If the transfer phase has been reached: Show SC-details -> write down robot message (e.g. Error code 1005) -> Acknowledge error -> Safe (wait until the robot arm has moved back)-> Close the lid</p> <p>If the transfer phase has not been reached (Error code 1005), press “Transfer Phase”</p>	<p>Try again.</p> <p><i>Note: You may also check the error code table provided for more information (only for on-site user)</i></p>
The sample has not been mounted (“error loading”) Error 1002.	Did the robot take the sample out of the puck?	<p>Show SC-details -> write down Robot message -> Acknowledge error -> Try to mount the same sample again.</p> <p><i>It is important to wait 3 minutes for the vial in the Dewar to refill, <u>OR</u> to mount another sample first.</i></p>	<p>Does the robot mount the sample on the second trial? If not, replace the sample vial with one of our “red-dot” vials. Measure the length of your vial at RT. If it is shorter than 37.9 mm (SPINE standard) do not use the vial again.</p>
The sample is not unmounted.	Check Error code in SC details. Do you read Error code 1003?	<p>1) Show SC details -> write down Robot message -> Acknowledge error -> Try to unmount the sample again.</p> <p>2) unmount manually (only for on-site users).</p> <p><i>Note: When you unmount your sample manually, remember to release smart magnet using the silver button on the goniometer.</i></p> <p>→ in SC-Details click “manual unmount”</p>	<p>Mount a new sample and continue as before.</p>

		<i>Note: when doing that, you need to be absolutely sure that there is no sample on the goniometer! Better check once again.</i>	
Data collection stopped in the middle of a data set. No more images are being written. The detector cover stays open.		Wait for the goniometer to finish its rotation, then press the button “Stop”, then record a single image. <i>Note: please do not press the “Stop” button, while the goniometer is still rotating.</i>	Once the single image has been recorded and written successfully and the detector cover has been closed after data collection, you should be able to resume normal operation.
The data collection or sample characterization has been added to a queue and started by “Collect Queue”, but no images are being recorded.	Does the queue say “waiting for input”?	Click “continue”.	Is the data being collected now? If yes, proceed normally. If not, delete all previous commands from the queue and try again.
The system is stuck during a phase change, for example during changing samples or after starting a data collection, before images are being recorded,	Are the buttons for the different phases in the right hand panel under “active phase” all greyed out and did you center using a zoom level other than 3?	The zoom motor is stuck; open a terminal and type “stop_zoom”.	If this happened during a sample change, follow the steps described under “The GROB robot arm freezes over an open lid”. If this happened during the start of data collection, image collection should now proceed as normally.
The zoom level of the on-axis microscope is frozen.	Have you selected zoom level 1 or 8?	There are three ways to resolve this issue: 1. Click on “Centering phase” once again, 2. Open a terminal window and type the command “stop_zoom” 3. Click on “Beam location phase”, then on “Centering phase” again.	Can the zoom level be changed now? If yes, the problem is fixed.
You observe artefacts on the diffraction images, e.g. circles or half circles.	Are these artefacts also visible on test images without sample present?	Open a terminal and type “home_motors”	Try collecting further test images.

<p>Diffraction images are either completely white or completely black.</p>	<p><u>Note:</u> remote users can check option 1-3 at https://www-csr.bessy.de/webopi/ws?opi=BL-Stat-MX.opi</p> <p>1) Check on the panel if the experimental hutch beam shutter is open?</p> <p>2) Check on the panel if the Main Beam shutter is open?</p> <p>3) Check on the panel if the beam shutters are unlocked? (see Status BESSY II)</p> <p>4) Did you optimize the beam?</p>	<p>1) Beam shutters unlocked and Main Beam shutter open: open experimental hutch beam shutter (remote users: speak to your local contact / MX service for shutter re-opening).</p> <p>2) Beam shutters unlocked and main beam shutter closed: open Main Beam shutter, wait 5-10 minutes, then open Experimental Hutch Beam shutter (remote users: speak to your local contact / MX service for shutter re-opening). Then check by clicking on "Beam location".</p> <p>3) If the beam shutters are locked, watch the messages on the info terminal (remote users: speak to your local contact / MX service for shutter re-opening)..</p> <p>4) If no, optimize the beam intensity from the right panel of <i>MXCuBE</i> ("<i>optimize intensity</i>") and check by clicking on "Beam location".</p>	<p>Take a test image and look for the beam stop shadow and/or diffraction. Open the image in <i>adxv</i> and check the total number of counts on the image.</p>
<p>The detector did not move to the resolution or to the detector distance that was set for the data collection.</p>	<p>Did you check the maximum resolution and/or the detector distance limits that are available on this beamline?</p> <p><i>Note: The maximum resolution depends on the selected energy.</i></p>	<p>Move your mouse over the "Set to" field at the resolution panel and you get an info box of the limits available for the beamline at this wavelength → Set the resolution according to these limits. Alternatively, open a terminal and type "bragg3", select the beamline an energy in the applet that will open and check the resolution limits displayed.</p>	<p>Try collecting data again.</p>
<p>Problems with backing up data, e.g. drive not mounted, backup not running or too slow.</p>	<p>Did you check that the format of your hard drive is suitable for our beamlines? (NTFS)</p>	<p>Reformat your hard drive, e.g. on your laptop.</p>	<p>Try mounting your hard drive again and starting the backup.</p> <p><i>Note: only disks formatted as NTFS are supported.</i></p> <p>If you do not have a suitable disk and you cannot reformat, ask your local contact for a HZB-MX disk on a loan basis.</p>

Forgot the backup command?	Connect your hard drive connected to the computer named SAVE2.	Run the following command from SAVE2: px-dbs <data> <hard drive> 5, e.g. <i>px-dbs /142dat/pxrdat/px12345/20200303/ /media/myHardDrive/ 5</i>	
A diffraction plan has been accidentally added to the queue.		Uncheck the "Characterisation" button when setting up the queue for collecting test images. <i>Note: this needs to be done after every restart of MXCuBE</i>	