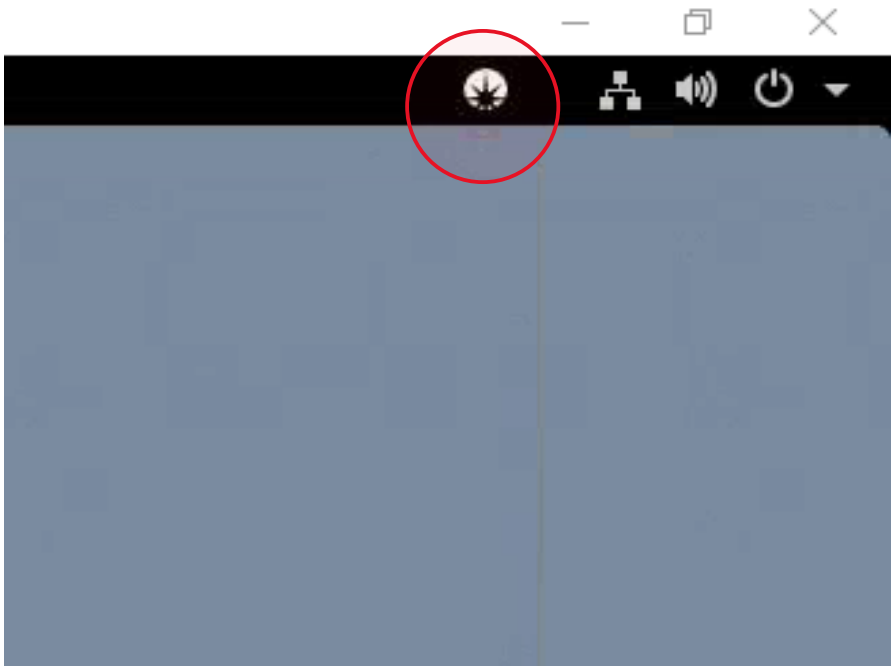
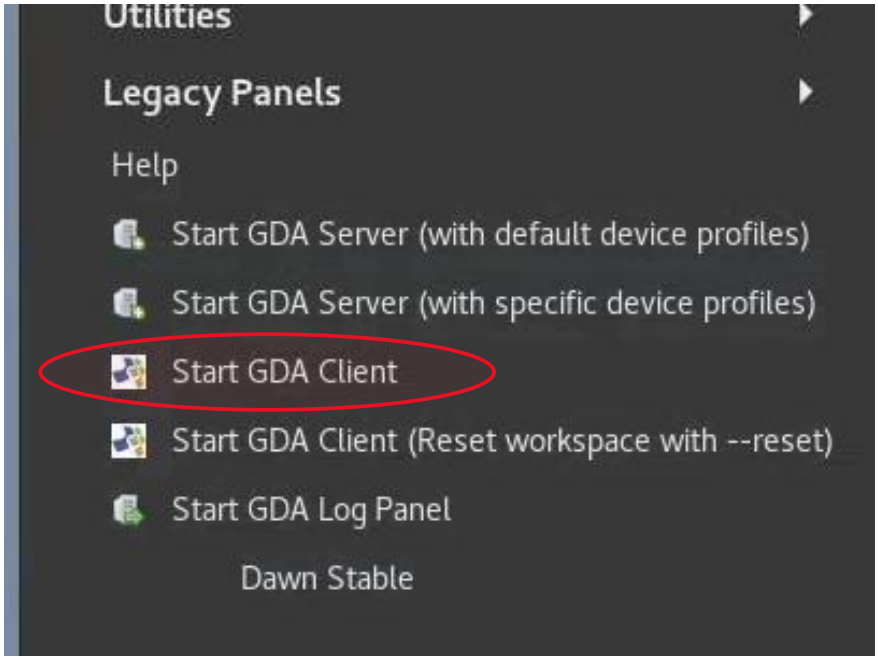
Open GDA

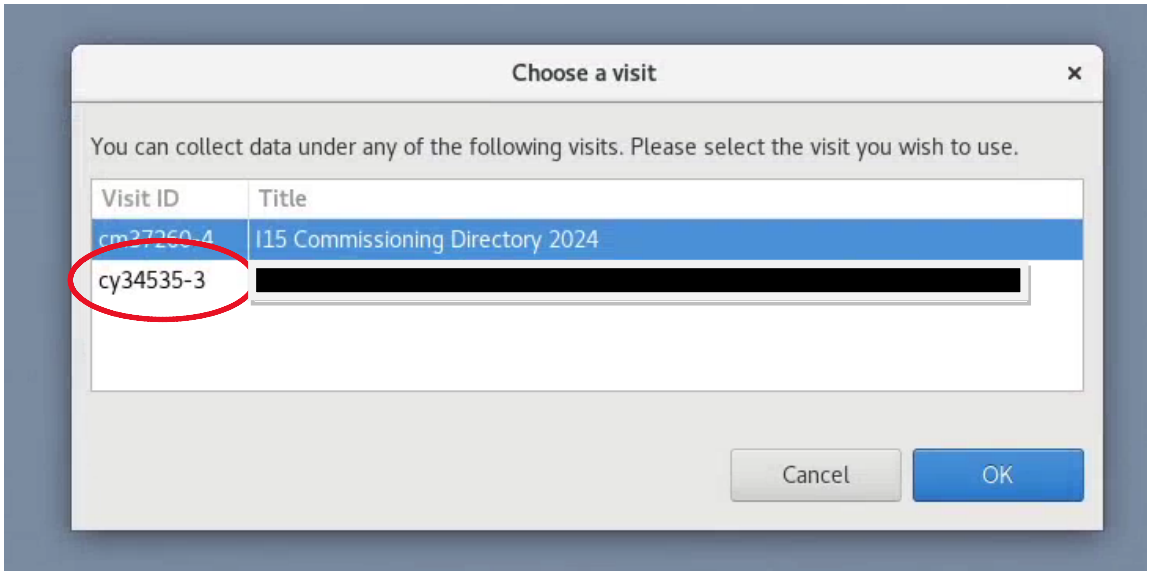
In the top-right corner of the desktop, click the Diamond icon, as highlighted in a red circle.



Select **Start GDA Client** from the resulting drop-down menu.

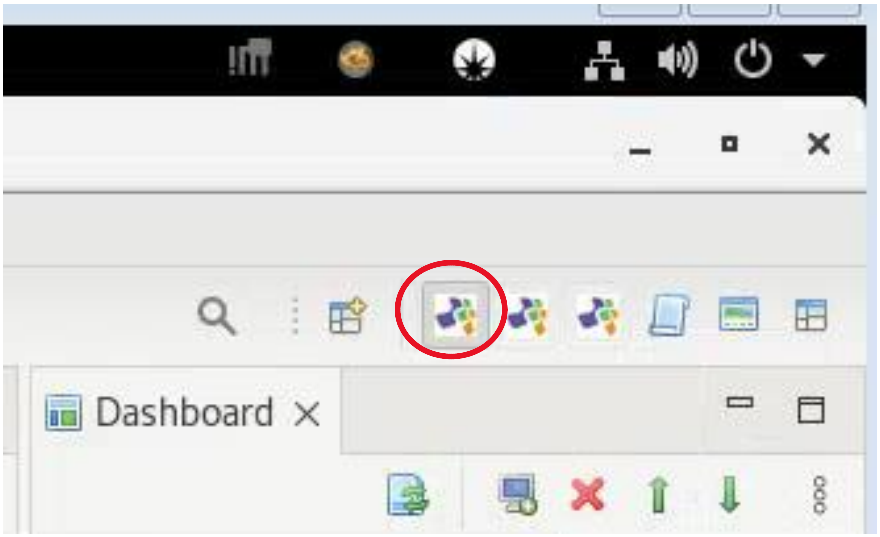


Select the appropriate proposal number if given a choice of visits, and click **ok**



*If the GDA crashed, close GDA. Then start GDA Server first by clicking **Start GDA Server** (with default device profiles), then **Start GDA Client**.

On **I15 Scan Perspective**, you can enter your commands at the bottom of the Jython Console.



General Beamline Controls Using GDA Commands

shopen #open the experimental hutch shutter

shclose #close the experimental hutch shutter

pos #moves a motor you specify to the demand position as you defined

pos <moto_name> # reports the current position of a motor

e.g. pos dx # reports the current position of the x motor on the sample stage

pos <motor_name> <motor_position>

e.g. pos dx 0.5 #moves the diffractometer sample stage along the x-axis to an absolute position of x = 0.5 mm

inc #moves the motor incrementally

e.g. inc dx 0.5 #move the sample stage along the x-axis by 0.5 mm (dx = current position + 0.5)

Alternatively, you can control motors via **Synoptic** (Please see Experiment Startup For Users)

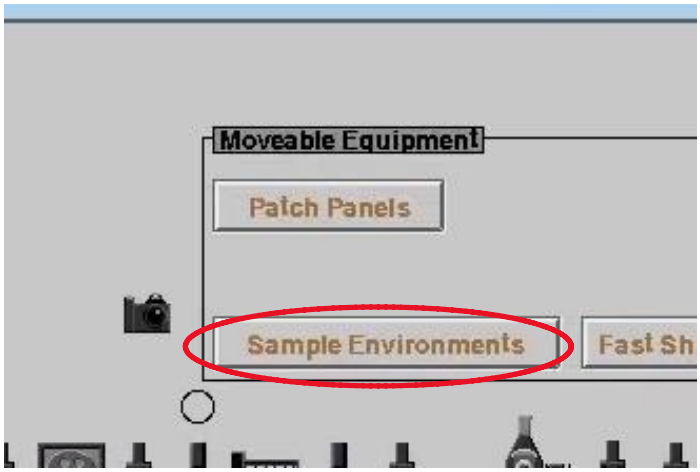
Optical Sample Alignment (For Standard DAC Experiment)

For initial sample alignment, it is recommended to perform the optical sample alignment with the experiment hutch door open.

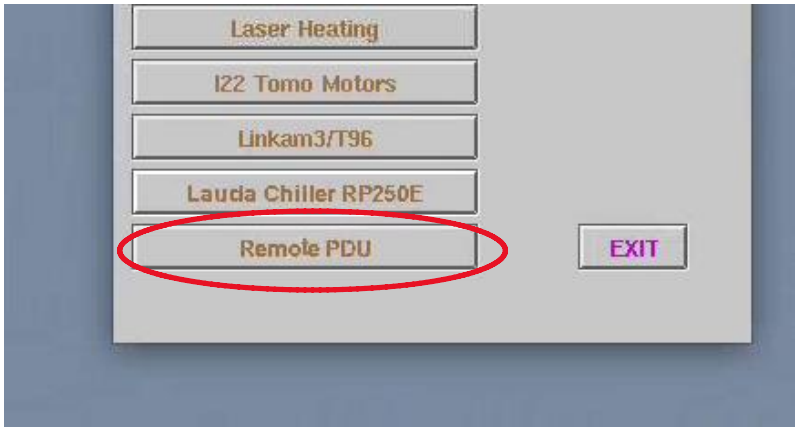
The focal point of the Superhead at the focus position (shdx = 0) aligns with the centre of rotation (shdy = shdz = 0). Thus, the optical alignment is to align your sample to this centre of rotation, by bringing sample to the focal point.

First, rotate the sample to face the Superhead, before moving the Superhead to the focus position. *For the first-time alignment, move it gradually to avoid any collision with the sample holder.* If needed, turn on the Superhead transmitted light (Synoptic – Sample Environment – Remote PDU).

To control the Superhead lights, click **Sample Environments** on the Synoptics.



Click on **Remote PDU.**



Then enter the hutch and use a piece of paper to locate the focal point. Use this as a guide to align your sample to the centre of rotation by adjusting sample positions (Figure 1).

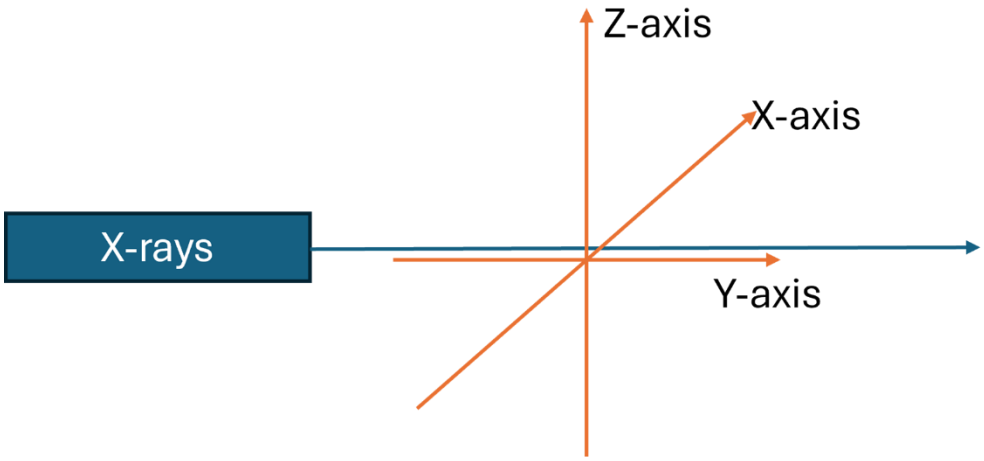


Figure 1. scheme of coordinating system of sample stage motors on the diffractometer.

For this process, it is recommended to adjust motors using the **Synoptic** panels. Alternatively, you also use **GDA commands**.

The name of the Superhead motor along x-axis: shdx

e.g. inc shdx 200 # move the superhead by 200 µm away from the sample stage, along x-axis

Names of sample stage motors along x-, y- and z- axes: dx, dy, dz

e.g. inc dz 0.1

pos dy 0.5

X-ray Sample Alignment (Synoptic)

Move the Superhead away (x = 200) and rotate the sample back to face X-ray (kPhi = 58). Then you can scan the sample with X-rays to further refine the alignment. To do this, you need to proceed with the **research process** and ensure the experimental hutch door is closed. During the X-ray alignment, diodes will be used to read X-rays. Due to the high

sensitivity of diodes to ambient light, please make sure that the lights in the experimental hutch are turned off.

Commands for starting alignment in GDA:

align #move in diodes and open the shutter

alignment along x- and z- axes

cscan dx 0.3 0.02 w 0.1 d3 (*centre scan, motor name, scan range, step size, wait, wait time, diode name*) # scan along the x-axis and move back to the starting position

you can adjust the **scan range** and **step size** accordingly.

If the peak centre calculated by GDA matches your reading, enter go peak. If not, enter pos dx *xx* (replacing *xx* with your readout position)

cscan dz 0.3 0.02 w 0.1 d3 # scan along the z-axis

> *note that the y-axis is along the X-ray direction, so please DO NOT scan dy. If you accidently start the scan, leave it to finish. Please DO NOT interrupt the scanning process, as motors would stop at a radon position.

Then align the centre of the cell to the **Centre of Rotation,** along the y-axis

centre(dkphi, 0.3, 0.02, 3, d3) (*motor name, scan range of dx, step size of dx, rotation angle of dkphi, diode name*)

you can adjust the **scan range, step size, and angle** accordingly.

> *When the alignment is done, it is recommended to record the coordinates for future alignment

Data Collection

Before starting the data collection,

ready #move diodes out and closes the shutter

Data collection without rotating the sample stage:

expose(10, “test_10s”) (*data collection time, file name*) # unit of data collection time: second

you can adjust the **time** and **file name** accordingly.

Data collection while rotating the sample stage:

exposeRock(10, 7, “test_10s_7deg”) (*data collection time, rotation range of dkphi, “file name”*) # unit of rotation angle: degree

you can adjust the **time, angle,** and **file name** accordingly.

Normally, the shutter will close automatically after data collections. If not, enter shclose to close the shutter before opening the hutch door.

*Alternatively, if you wish to use a beamline script, please contact your local contact for help.