RSXS sample alignment

Use following steps for the initial sample alignment after loading a new sample:

1. Move tth to 105° and th to 90° (**uan 105 90**). Use one of the absorption edges to adjust the sample position y and z.

   a. Typical beamline setting: Horizontal variable aperture gap (**vah**) = **4.0 mm** and exit slit gap (**ES**) = **25 μm**, and detector height (**detz**) = **40 mm**.

   b. Move x-ray energy to the absorption edge of your sample (**moveE**).

   c. (Optional) Set EPU polarization to linear vertical (**setEPU polar lvn**).

   d. Align y (**lup y**). Move to center (**umv y**).

   e. Align z (**lup z**). Move to center (**umv z**).

   f. If no clear TEY or FY signal, lower the detector height down to 0 (**umv detz 0**), and repeat Steps 1d and 1e.

2. Move detz back to 40 mm (**umv detz 40**) for the photodiode detector on the scattering plane.

3. IMPORTANT: Verify the MCP, Channeltron, and SDD will not be in the direct beam. Direct beam will permanently damage the MCP, Channeltron and SDD detector. Replacing them is very expensive. Only photodiode can be used to align tth with direct beam.

4. Move tth and th to 0° (**uan 0 0**) for direct beam measurement.

5. Move x back by 1-2 mm (**umvr x -2**). Note the intensity of photodiode for the direct beam (ct) by looking at **PicoAm2** counter.

   The intensity shall be 10-20μA depending on the xray energy between 400-800 eV.

6. Align tth (**lup tth**). Move tth to centre (**umv tth**). Set tth to 0° (**set tth 0**).

7. Align x (**lup x**). Move x to centre (**umv x**). No need to set x!

8. Verify the intensity of the **PicoAm2** counter (**ct**). The intensity shall be about half of the direct beam value (see Step 5). Otherwise, the x needs to be adjusted until half of the direct beam intensity.

The x, y, and z of the sample are aligned at the centre of goniometer rotation and tth is aligned with respect to direct beam.

The next steps are to align th, chi, and phi with either (A) specular reflection (look at "**RSXS specular reflectivity alignment**") or (B) diffraction peaks (look at "**RSXS diffraction alignment**).