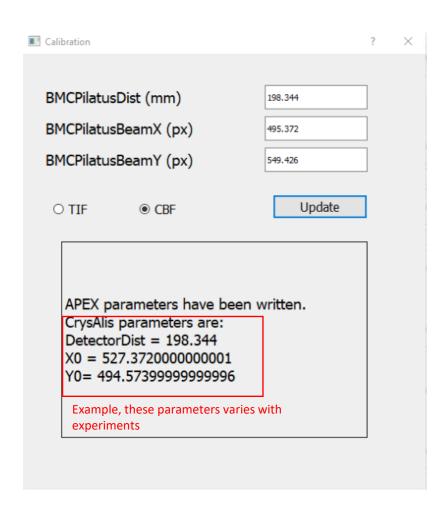
Notes on converting 13-BMC single crystal data to CrysalisPro

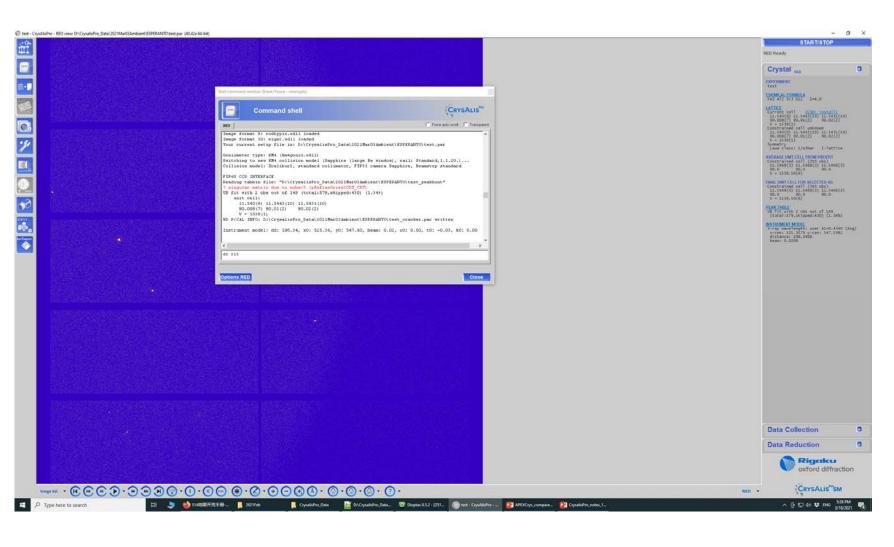
Dongzhou Zhang 2021/03/18

Information needed

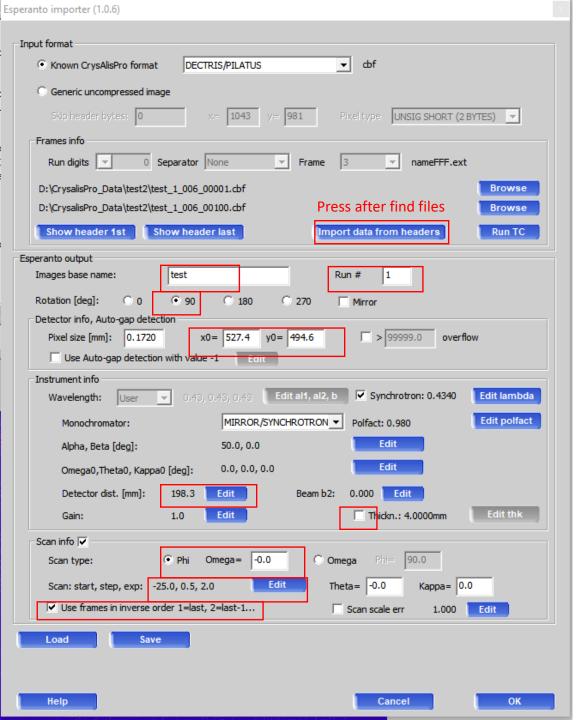


- CrysAlis parameters from "Calibration" panel of BMC_Xtal
- Total phi-scan range, step size and exposure time for the cbf image sequences
- Total phi-scan range e.g.: start from 66, end in 116, then total range is 50 degs.

Start CrysalisPro



 Select a random project, then go to command shell, type "dc rit" then enter



Del = 0, Nu = 0

X0 = Dioptas X0+32 pixel (for CrysalisPro square image pading)

Y0 = 1044 - Dioptas Y0

Use frames in inverse order

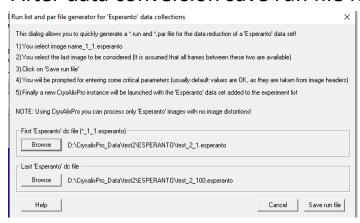
Start = -(phi-scan range)/2

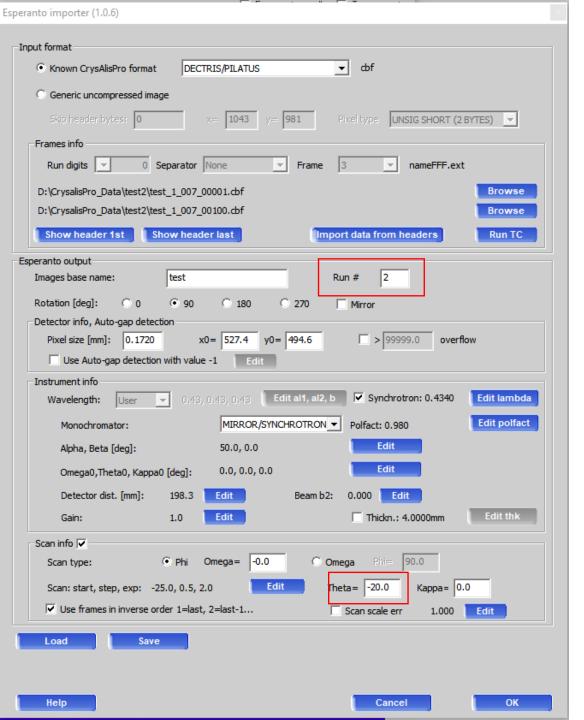
Uncheck "Thickn"

Remember to change your images base name, and Run#. For (del = 0, nu = 0), use them as Run#1.

If peak harvest still screw up, use "um i" command to update the detector info

After data conversion save run file for future use.





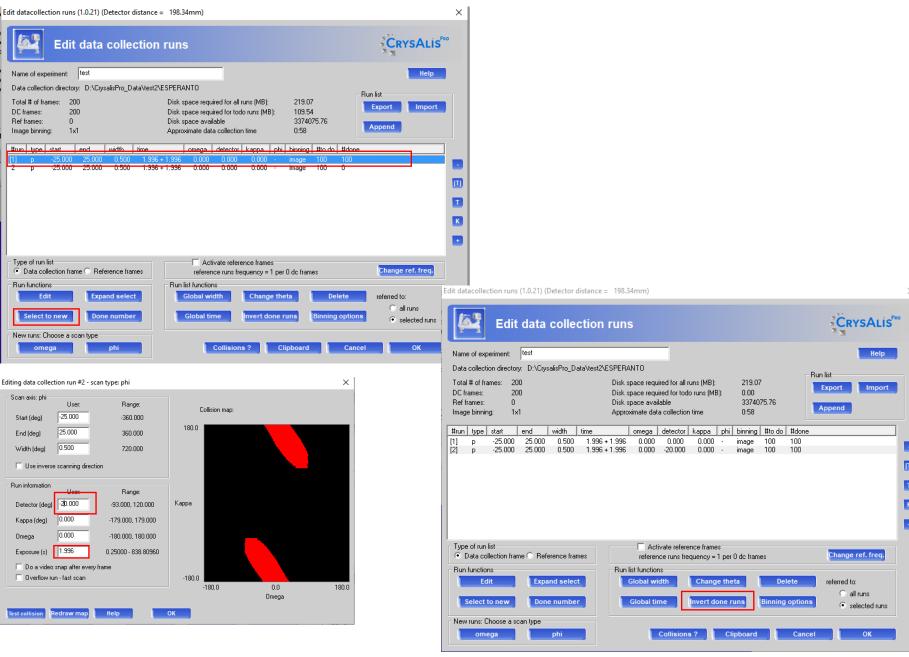
For data collected at non-zero del angle, Theta = - del, Other parameters should be the same as zero-del.

Remember to change the image base name and the run #

You don't need to save run file for the second detector position of the same pressure point.

Run list and par file generator for 'Esperanto' data collections	×
This dialog allows you to quickly generate a *.run and *.par file for the data reduction of a 'Esperanto' data set!	
1)You select image name_1_1.esperanto	
2) You select the last image to be considered (It is assumed that all frames between these two are available)	
3) Click on 'Save run file'	
4) You will be prompted for entering some critical parameters (usually default values are OK, as they are taken from image	headers)
5) Finally a new CrysAlisPro instance will be launched with the 'Esperanto' data set added to the experiment list	
NOTE: Using CrysAlisPro you can process only 'Esperanto' images with no image distortions!	
Browse D:\CrysalisPro_Data\test2\ESPERANTO\test_2_1.esperanto	
Last 'Esperanto' do file Browse D:\CrysalisPro_Data\test2\ESPERANTO\test_2_100.esperanto	
Help Cancel Save r	un file

Merge two detector positions



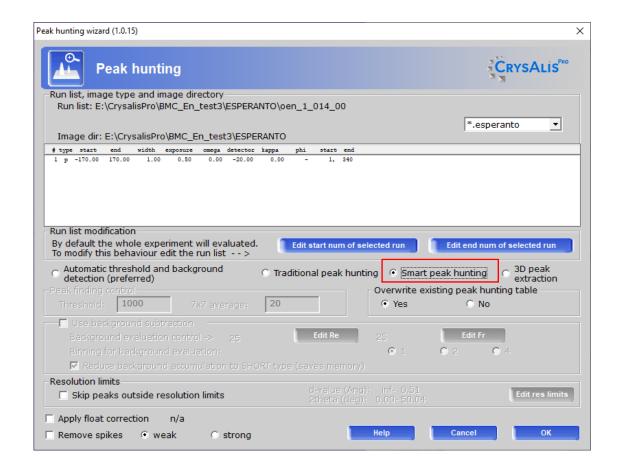
- Go to command shell, "dc editruns", highlight the experiment, then click "select to new"
- Edit the second run so that the detector angle and the exposure is correct
- Then highlight the second run and "invert done runs" so that "#done" is the same as "#to do"

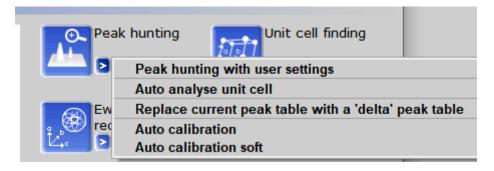
Peak hunting





- Now go to lattice wizard->peak hunting with user settings
- Usually use smart peak hunting.





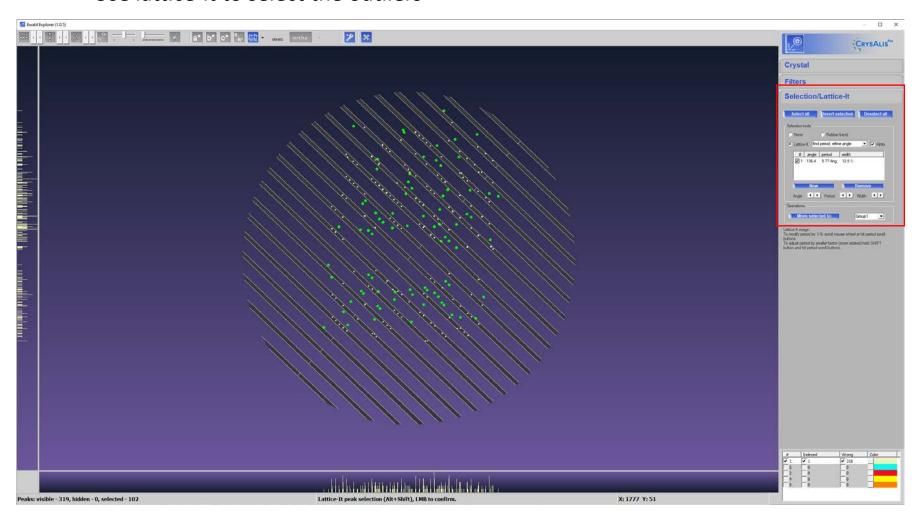
Play with other peak hunting settings if smart hunting doesn't give you enough peaks

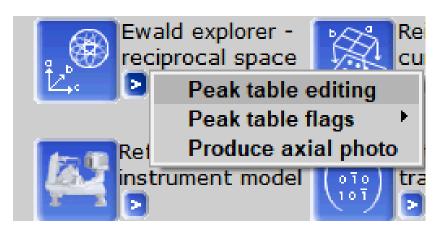
Find lattice

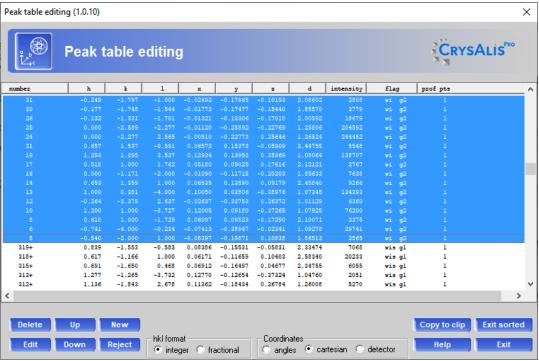
Go to Ewald explorer



Use lattice-it to select the outliers





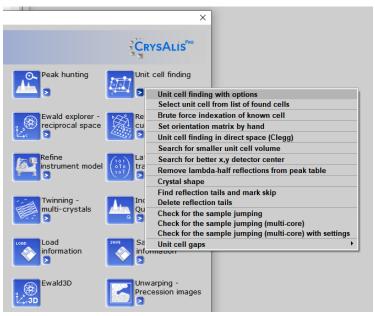


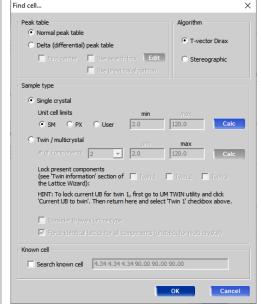
Move all outliers to g2

Go to Ewald explorer-> peak table editing

Remove all g2 peaks.

Find unit cell



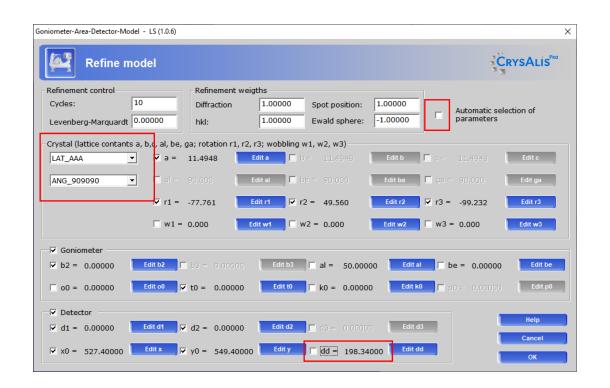


Select unit cell from list of found cells (1.0.1) % Indexed Cell Niggli Priority Vpr ٧r 100.000 5.75 5.76 5.76 89.94 90.00 89.44 190.78 190.78 3 10 100.000 12 11.53 11.52 11.49 90.56 90.00 90.06 381.57 1526.26 100.000 12 8.14 8.14 9.94 90.27 89.61 119.73 572.35 572.35 12 8.14 8.14 19.88 90.27 89.61 119.73 1144.70 1144.70 100.000 18 16.29 16.30 11.49 89.61 89.61 90.05 1526.33 3052.66 100,000 12.85 12.88 5.76 90.23 90.38 90.17 953.25 953.25 Cancel

- Go to unit cell finding, then unit cell finding with options
- Find unit cell automatically, or search known cell
- If the correct cell is not found, select the correct one from list of found cells.

Refine instrument model

- Uncheck automatic selection of parameters
- Select the correct lattice type
- Uncheck dd



Ready for integration

- Now you should have the correct unit cell.
- Next step please refer to integration and find space group manual by Dr Stella Chariton.

