SETUP Pilatus	
A) In MEDM	
	1) In Surf_Main (work space IDC)
	Select the last one "User Pilatus"
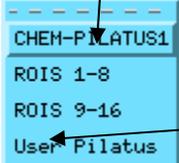
userPilatusROI_1.adl

Pilatus Detector CHEM-PILATUS1:

File

Full filename: /disk2/Data/lin/oct2008/pilatus/102308_SCAN-29_0000.ti

Collection

Acquire mode: Internal

Exposure time: 2.600000

XMax/Min   YMax/Min

65   108

59   96

iroi: 1062274

Acquire   Abort   Done   Unarmed

Detector

Threshold (eV): 8000

Shaping time/Gain: Medium/Medium
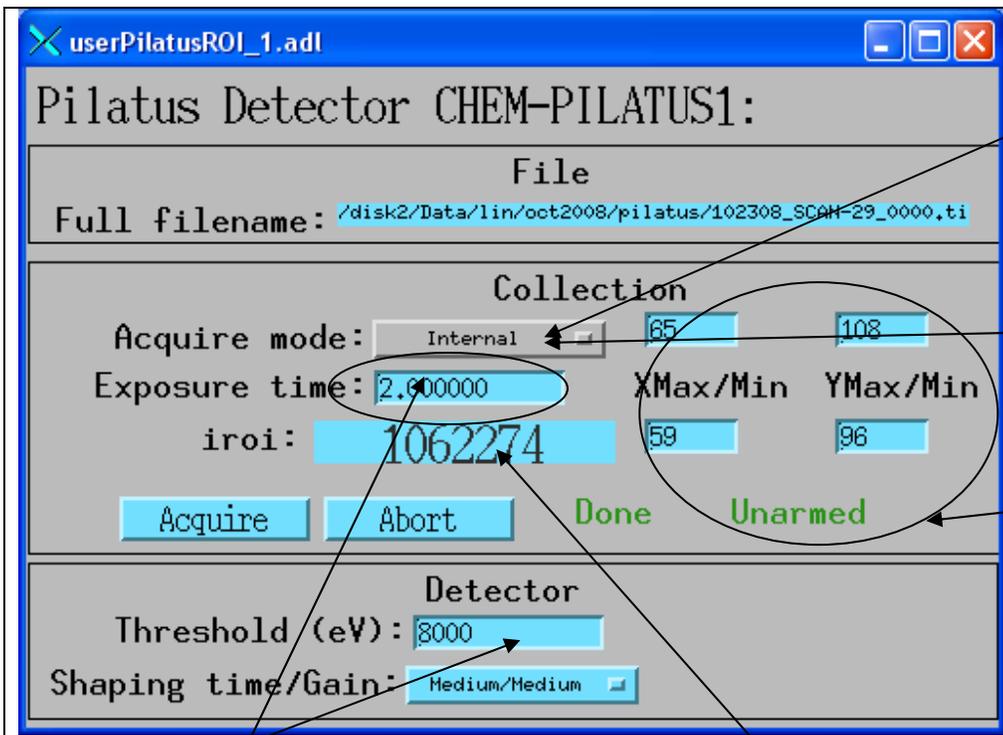
Two acquisition modes:
1) **Alignment**: for continuous counting. In this mode, choose "Exposure time" to be 1 sec.
(use to check alignment and/or counts)
2) **Internal**: for scans from SPEC (use this for data scans)

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ROI (region of interest)

Top left:**Xmax**
Bottom left: **Xmin**
Top right:Ymax
Bottom right:Ymin

ROI Range in use
Xmax/min=pdx ± 3
Ymax/min=pdy ± 6

Maximum range
X: 0 to 486
Y: 0 to 194

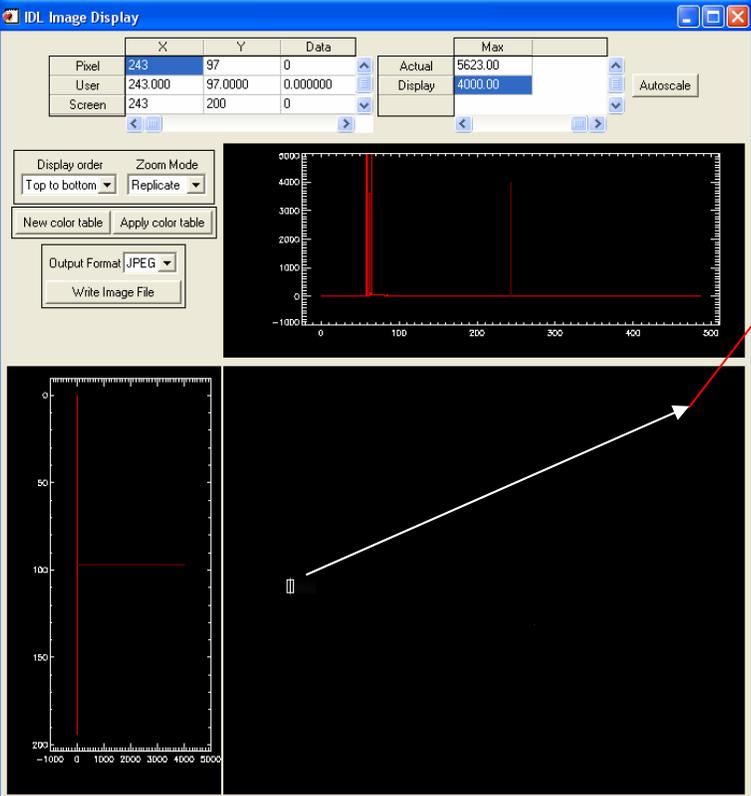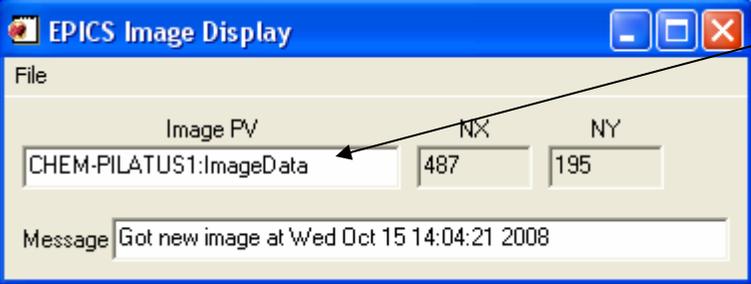Count rate for ROI
iroi (DET=iroi)

For alignment scans, select a small ROI around the direct beam

$$Max count
rate:<500,000/pixel/second

E threshold:
E dependent (eg. 10kev, choose 8000, 30keV, choose 20000)

$$$%%% *Note: the "Abort" key does not really work*—if your exposure time is set to 300, for example, you will have to wait 300s before you can continue to use the Pilatus.

In SPEC	
SURF> startpd	Start using Pilauts in SPEC scans
SURF>DET=iroi;plotselect iroi	
1) SURF> pilrun 1	Acquiremode:"**Internal**" Quick 1 sec count
2) SURF>lup dth 0 0 1 1	Acquiremode:"**Internal**" Snapshots at the same dth
3) SURF>ascan dth 0 1 20 1	Acquiremode:"**Internal**" GID scans
For conventional GID scans; choose "s4h 0.7 0.7" ;"s5h 0.7 0.7" With the 610mm flight tube	Angular resolution=0.12deg, the same as our Soller slits
SURF> stoppd	Stop generating Pilatus images in SPEC

Pilauts IDL display panel	
Open IDL program	Click IDL or see Mati for help
IDL>@pilatus	
	Reflected beam or direct beam should be in this box (ROI)
	This one should be "CHEM-PILATUS1:ImageData"

Check and input direct beam coordinate in Pilatus Pdx and pdy	Need to check this before any pinhole scans—if changed from XR
1) SURF>absclose; umk 0 0 0;abs 35; umvr sh -1 2) set absorber to 35 3) umvr sh -0.5 4) On "Pilatus Detector" MEDM panel, choose "Alignment" mode, and set the exposure to 1sec 5) click "Acquire"	Procedure to obtain **pdx and pdy**
| ```
IDL>scan_info,0,/new  ; if a new file; and select
the current spec file
IDL>pd_align
(IDL display::)
     Read file
Z:\spec\pilatus\Gentle\july08\pilatus\alignment.tif
     Created on Sun Jun 29 00:50:06 2008

     In SPEC enter:
              SURF> pdx =  62
              SURF> pdy = 103
``` | See Mati for help |
| **Enter those coordinates in SPEC**<br>```
     In SPEC enter:
              SURF> pdx = (the number from IDL)
              SURF> pdy = (the number from IDL)
``` | |

Data directory ***backup and copy your data to your external HD*** The data are NOT saved on our computer.	
Your spec files are in: \home\epics\spec\pilatus***GROUP\DATE***	
Your pilatus images are in \home\epics\spec\pilatus***GROUP\DATE***\pilatus	

For pinhole scans/snapshots, choose, "s4h 0.1 0.1' and "s5h 10 10" With the 610mm flight tube	Angular resolution=0.017deg
1. S4 slit blades are at 275mm from center. 2. For the short tube (200 mm) the S4-Pilatus distance is 275mm. 3. For the long tube (610 mm) the S4-Pilatus distance is 675mm. 4. Pilatus extends 76mm above beam. Calculations are for k = 5 Short tube: 200mm S4 = 0.24 mm → angular resolution of 0.05 deg (delta_Qxy ~ 0.004) S4 = 0.48 mm → angular resolution of 0.1 deg (delta_Qxy ~ 0.009) In either case the Qz range is ~ 0.69 with with resolution of 0.0016 at low Qz values (getting worse for higher Qz). Long tube:610mm The corresponding (same resolution) S4 values are 0.6 mm for 0.05 deg and 1.2mm for 0.1 deg. Qz range is ~ 0.40 with with resolution of 0.0009 at low Qz values (again, getting worse for higher Qz).	Qz range and Qxy resolution for the two flight tubes

Some "Do files" for SPEC scans	
Pd_ref.do usr/local/lib/spec.d/user_macros/scans) Pd_pin.mac (usr/local/lib/spec.d/user_macros/scans) Set_abs.mac (usr/local/lib/spec.d/user_macros/scans)	

This is the panel for the ***beamline staff*** to set up Pilatus

In SURF:

File name should be short.

pdx,pdy,pddist,pds4dist,pdorient

Align:
1)Dth scan S5 0.1 0.1
2)S4hscan to center S4 to S5
3)S4h and S5h linearization

Setup the data path (!!start SURF in this folder)

Use this format

Highlight ROIs :"YES"

Post Images => should be "YES"

Pilatus Detector CHEM-PILATUS1:

Camserver
To camserver: SetThreshold midG 20000,000000
From camserver: 15 OK LdCmndFile /tmp/setthreshold,cmd

Connect   Disconnect   asyn record

File
Path: /disk2/Data/
Base filename: 081208_SCAN-18_
Next file number: 178
Filename format: %s%s%4,4d.tif
Full filename: /disk2/Data/081208_SCAN-18_017?.tif
Auto increment: Yes

Detector
Threshold (eV): 20000
Shaping time/Gain: Medium/Medium

Data corrections
Bad pixel file:
Bad pixels: 0
Flat field file:
Flat field valid: No   Min. flat field: 100

ROIs/Images
ROI definitions: ROIs   Min. array update: 0,200
Clear ROIs: Clear ROIs   Highlight ROIs: Yes
Post images: Yes   Min. image update: 1,000

Collection
Acquire mode: Internal   Exposure period: 1,100000
Exposure time: 1,000000
Number of images: 1   Exposures/image: 1
Read TIFF timeout: 30,000
Status: Waiting for command
Acquire   Abort   Done   Unarmed   Scan

	When chemmat28 crashes	
	Start surf in the folder with the current data!!!	
1) SURF	Startup	To get the correct wavelength and geometry parameters
	Do params.dat	If g_l and energy have been saved
	Startpd	
	P pddist; p pds4dist; p pdorient; p pdx; p pdy	
2)Pilatus	Need to check the data path, base file name,	