

autoPROC reference card	
set up (probably already arranged by local IT)	
Set up for csh or tcsh	<code>source /some/where/autoPROC/installed/setup.csh</code>
Set up for bash, ksh, zsh, or sh	<code>. /some/where/autoPROC/installed/setup.sh</code>
autoPROC: most useful options	
Brief help message	<code>process -h</code>
Simple run (in directory containing images)	<code>process -d outputdir &gt; log</code> - or - <code>process -d outputdir   tee log</code>
Simple run (remote directory)	<code>process -d outputdir -I imagedir &gt; log</code>
Read image header information	<code>imginfo test_0123.img</code>
Check beam centre conventions	<code>beam8.sh &lt;beamX&gt; &lt;beamY&gt; &lt;sizeX&gt; &lt;sizeY&gt;</code>
Define direct beam transform	<code>process BeamCentreFrom="header:y,-x" -d outputdir &gt; log</code>
Let autoPROC determine most likely direct beam transform [1]	<code>process BeamCentreFrom="getbeam:init" -d outputdir &gt; log</code>
Define direct beam position [2]	<code>process beam="1556 1512" -d outputdir &gt; log</code>
Identify image scans	<code>find_images -d imagedir -l</code>
Identify HDF5/Eiger scans	<code>find_images -d imagedir -l -h5</code>
Manual sweep definition	<code>process -Id "test,/where/ever/images,test_###.cbf,1,90" -d outputdir &gt; log</code>
Manual sweep definition for HDF5/Eiger data	<code>process -Id "test,/where/ever,test_master.h5,1,900" -d outputdir &gt; log</code>
Define cell dimensions and symmetry [3]	<code>process cell="a b c al be ga" symm="P21" -d outputdir &gt; log</code>
Include "reference" file for symm, cell and test-set	<code>process -ref mtzfile -d outputdir &gt; log</code>
List available "macros" [4]	<code>process -M list</code>
Settings that might help difficult diffraction data [5]	<code>process -M LowResOrTricky -d outputdir &gt; log</code>
Process in "fast" mode [6]	<code>process -M fast -d outputdir &gt; log</code>
Restrict number of "processors"	<code>process -nthreads &lt;no&gt; -d outputdir &gt; log</code>
Restrict resolution range	<code>process -R 50.0 2.0 -d outputdir &gt; log</code>
List known multi-axis goniostats	<code>x_kappa -list</code>
Process multi sweep data collected with different goniostat/2-theta settings	<code>process KapparotSite="siteID" -d outputdir &gt; log</code>
Switch off detection/exclusion of ice-ring resolution ranges	<code>process XdsExcludeIceRingsAutomatically=no -d outputdir &gt; log</code>
Exclude all known ice-ring resolution ranges from the start	<code>process XdsExcludeIceRingsAutomatically=all -d outputdir &gt; log</code>
AIMLESS-only scaling path	<code>process -M ScalingA3 -d outputdir &gt; log</code>
XSCALE-only scaling path	<code>process -M ScalingX -d outputdir &gt; log</code>
Process Dectris/Eiger data (HDF5 format)	<code>process -h5 /where/ever/some_master.h5 -d outputdir &gt; log</code>

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results	
Progress summary	<b>summary.html</b> (in output directory: open with browser) standard output (might give more details about problems)
Reflection data, traditional (isotropic) analysis	<b>truncate-unique.mtz</b> truncate_<wavelength>-unique.mtz (multi-wvl data)
Reflection data, anisotropic (STARANISO) analysis	<b>staraniso_alldata-unique.mtz</b> staraniso_<wavelength>_alldata-unique.mtz
PDF reports	<b>report.pdf</b> <b>report_staraniso.pdf</b>
XML (ISPyB compatible)	autoPROC.xml autoPROC_staraniso.xml
helper programs and options	
Scaling module: help message	<b>aP_scale -h</b>
Simple scaling of data set with 360 batches/images	<b>aP_scale -mtz XDS_ASCII.mtz -P lyso test A -b 1-360 -id 01 &gt; log</b>
More detailed scaling of 'early' and 'late' batches	<b>aP_scale -mtz XDS_ASCII.mtz -P lyso test early -b 1-180 -P lyso test late -b 181-360 -id 02 &gt; log</b>
Allowing different high-resolution limit for decaying crystal ("chunking")	<b>aP_scale -mtz XDS_ASCII.mtz -P lyso test early -b 1-180,30 -P lyso test late -b 181-360,30 -id 03 &gt; log</b>
Use XSCALE for scaling	<b>aP_scale -hkl XDS_ASCII.HKL ...</b>
Compare indexing of datasets	<b>check_indexing mtzfile1 mtzfile2 ... mtzfileN</b>
Compare orientation matrices	<b>cmpmat 01/XPARM.XDS 02/XPARM.XDS P21</b>
Combine integrated intensities from several scans manually	<b>combine_files -f 01/XDS_ASCII.mtz -P lyso test lowres \ -f 02/XDS_ASCII.HKL -P lyso test highres \ -o low-high.mtz</b>
Calculate statistics on unmerged data	<b>mrfgana INTEGRATE.HKL</b> - or - <b>mrfgana XDS_ASCII.mtz</b>
further information	
autoPROC homepage	<a href="http://www.globalphasing.com/autoprocd/">http://www.globalphasing.com/autoprocd/</a>
autoPROC manual	<a href="#">\$autoPROC_home/docs/autoprocd/manual/autoPROC0.html</a> - or - <a href="http://www.globalphasing.com/autoprocd/manual/index.html">http://www.globalphasing.com/autoprocd/manual/index.html</a>
autoPROC wiki	<a href="http://www.globalphasing.com/autoprocd/wiki/">http://www.globalphasing.com/autoprocd/wiki/</a>
beamline information	<a href="http://www.globalphasing.com/autoprocd/wiki/index.cgi?BeamlineSettings">http://www.globalphasing.com/autoprocd/wiki/index.cgi?BeamlineSettings</a>

### Notes:

- [1] This should only be attempted as a last resort – see also [2].
- [2] <http://www.globalphasing.com/autoprocd/wiki/index.cgi?BeamlineSettings>
- [3] You could also only give the SG name (and let autoPROC decide on the most likely cell).
- [4] Using “show” instead of “list” gives details of each macro, ie. potential ideas for own macros.
- [5] Not all difficult crystals behave the same – please check diagnostics in summary.html carefully.
- [6] This involves various shortcuts that could impinge on data quality – use with care.