pipedream reference card
most useful options

Brief help message	**pipedream**
Print autoPROC|BUSTER|rhofit help	pipedream **-h process|refine|rhofit**
Simple run, starting from unprocessed images	pipedream **-imagedir dir -xyzin pdbfile -hklref mtzfile -d outputdir**
Simple run, starting from specified scan of images	pipedream **-imagescan <idN>,<dirN>,<templateN>,<fromN>,<toN>** -xyzin pdbfile -hklref mtzfile -d outputdir
Simple run starting from pre-processed mtz file	pipedream **-hklin mtzfile** -xyzin pdbfile -hklref mtzfile -d outputdir
No reference mtz file input	pipedream -hklin mtzfile -xyzin pdbfile **-nofreeref** -d outputdir
Explicitly define direct beam position for autoPROC	pipedream -imagedir dir **-beam "153.2 158.4"** -xyzin pdbfile -hklref mtzfile -d outputdir
Test all transformation possibilities of direct beam position in autoPROC	pipedream -imagedir dir **-beaminit** -xyzin pdbfile -hklref mtzfile -d outputdir
Use autoPROC macro in processing ('process -M list')	pipedream -imagedir dir **-mproc macroname** -xyzin pdbfile -hklref mtzfile -d outputdir
Specify chains or groups of chains to be treated as separate bodies in the limited MR step	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile **-chains "AB C D"** -d outputdir
Use "quick" refinement protocol	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile **-quick** -d outputdir
Use BUSTER macro in refinement ('refine -M list')	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile **-mrefine macroname** -d outputdir
Define restraint dictionaries for ligands present in the reference structure	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile **-l dict1,dict2,dict3...** -d outputdir
Run rhofit to fit a single ligand	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile **-rhofit dict** -d outputdir
Run rhofit to fit a cocktail of ligands	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile **-rhofit dict1,dict2,dict3...** -d outputdir
Define number of "binding sites" for rhofit to fit to	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile -rhofit dict **-xclusters <n>** -d outputdir
Post-refine best rhofit solution – default protocol	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile -rhofit dict **-postref** -d outputdir
Post-refine best rhofit solution – quick protocol	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile -rhofit dict **-postquick** -d outputdir
Reference mtz file DOES NOT contain FreeR flags	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile **-nofreeref** -d outputdir
Retain water structure present in the input model	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile **-keepwater** -d outputdir

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Restrict number of "processors" that pipedream process can use	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile **-nthreads <n>** -d outputdir
Run with pre-processed mtz file and multiple input models. Automatically determine differences between input models	pipedream -hklin mtzfile **-xyzin pdbfile1,pdbfile2,pdbfile3** -hklref mtzfile1 -d outputdir
As above, but specify list of residues to use for comparison from input file	pipedream -hklin mtzfile -xyzin pdbfile1,pdbfile2,pdbfile3 -hklref mtzfile1 **-seqin1 residues.list** -d outputdir
As above, but specify list of residues to use for comparison on command line	pipedream -hklin mtzfile -xyzin pdbfile1,pdbfile2,pdbfile3 -hklref mtzfile1 **-seqin2 "ALA A 23,GLY A 24,THR A 25"** -d outputdir
Use anisotropically scaled output from Staraniso as input to to all subsequent refinement steps	pipedream -imagedir <dir> -xyzin pdbfile -hklref mtzfile **-useaniso**
Run SideAide (PDB_REDO) to refit incorrectly modelled sidechains by rotamer search	pipedream -hklin mtzfile -xyzin pdbfile **-remediate** -d outputdir
In addition, allow SideAide to rebuild stubbed residues	pipedream -hklin mtzfile -xyzin pdbfile **-remediate -sidechainrebuild** -d outputdir
In addition to SideAide, also run pepflip to check for and correct peptide bond flips	pipedream -hklin mtzfile -xyzin pdbfile **-remediate -runpepflip** -d outputdir