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 previous autoPROC run	pipedream **-autoprocdir dir** -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	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	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, followed by post-refinement of top solution	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile **-rhofit dict** -d outputdir
Run Rhofit to fit a cocktail of ligands followed by post-refinement	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
Fit ligand with Rhofit but do not run post-refinement	pipedream -hklin mtzfile -xyzin pdbfile -hklref mtzfile -rhofit dict **-nopostref** -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

pipedream reference card	
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