

View Protocols SPA

- ▶ Preprocess
- ▶ Filter
- ▶ Mask

## 2D

- ▶ Align
- ▶ Classify

## 3D

- ▶ Initial volume
- ▶ Preprocess
- ▶ Classify
- ▶ Refine
- ▶ Analysis
- ▶ Reconstruct

## Tools

## Model Building

- ▶ xmipp3 - extract unit cell
- ▶ chimera - rigid fit
- ▶ scipion - model from template
- ▶ powerfit - powerfit
- ▶ ccp4 - coot refinement
- ▶ **ccp4 - refrac**
- ▶ phenix - emringer
- ▶ phenix - real space refine
- ▶ phenix - molprobit



## Protocol: ccp4 - refrac

Cite Help

## Run

Run name **ccp4 - refrac HBA\_HUMAN**

Comment

Run mode

☒ Continue ☐ Restart

Host

localhost

Use queue?

☐ Yes ☒ No

Wait for

Expert Level

☐ Normal ☒ Advanced

Input

Input

Input Volume **xmipp3 - extract unit cell symC2 off**Input PDBx/mmCIF file **phenix - real space refine HBA\_HUM**

Max. Resolution (Å):

3.2

Min. Resolution (Å):

200.0

Generate masked volume

☒ Yes ☐ No

SFCALC mapradius:

3.0

SFCALC mradius:

3.0

Number of refinement iterations:

30

Matrix refinement weight:

0.0

B Factor:

40.0

Close

Save

Execute

018 Protocols | Data

Refresh

emringer (copy) finished

ccp4

p

Analyze Results

/px)

lume=False)

lume=True)