



View Protocols SPA

Protocols SPA

Imports

- import movies
- import micrographs
- import particles
- import volumes

more

Movies

Micrographs

Particles

2D

3D

- Initial volume
- Preprocess
- Classify
- Refine
- Postprocess

Analysis

- Heterogeneity
- Validation
- Resolution

more

- xmipp3 - subtract projection
- xmipp3 - convert to pseudoatoms
- atsas - convert PDB to SAXS curve

Reconstruct

Resolution

Protocol Run: AtsasProtConvertPdbToSAXS

Protocol: **atsas - convert PDB to SAXS curve** finished Cite Help

Run

Run name: **atsas - convert PDB to SAXS** Comment

Run mode: ☒ Continue ☐ Restart Host: localhost

Use queue? ☐ Yes ☒ No

Wait for

Expert Level: ☒ Normal ☐ Advanced

Input

Input structure: xmipp3 - convert to pseudoatoms.outputPdb

Experimental SAXS curve (optional)

Other parameters for Crysol

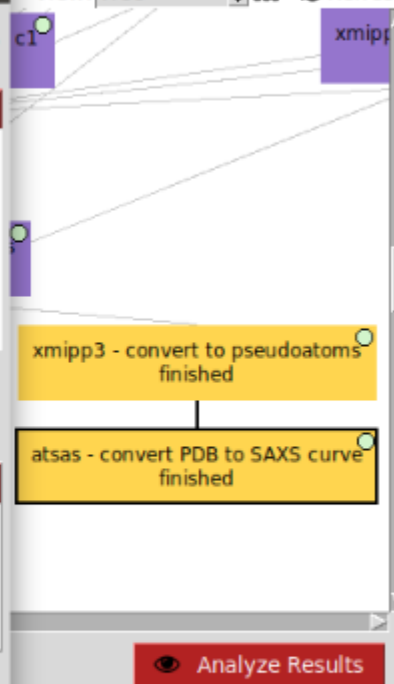
Close Save Execute

Input

inputStructure (from xmipp3 - convert to pseudoatoms -> outputPdb [out: AtomStruct (pseudoatoms=True, volume=True)])

Output

View: Tree Refresh



Analyze Results