SCIPION v2.0 (2019-04-23) Diocletian   Example_10248_v2   Protocols | Data

View: Tree ▾ 🔗 ⟳ Refres

Protocol Run: XmippProtConvertToPseudoAtoms — ⊟ ☐ ⊗

🔴 **Protocol: xmipp3 - convert to pseudoatoms**   `finished` ⬀Cite ❓Help

Run

Run name xmipp3 - convert to pseudoato ✎   Comment [   ] ✎

Run mode   ◉ Continue   ○ Restart ❓   Host localhost ▾

Parallel Threads [4] ❓   Use queue? ○ Yes ◉ No ❓

Wait for [   ] ❓

Expert Level   ◉ Normal   ○ Advanced

Input

Input

Input structure xmipp3 - swarm consensus.outputVolume 🔍 🗑 👁

Mask mode none ▾ ❓

Pseudoatom radius (vox) [2.0] ❓

✖ Close   💾 Save   ⚙ Execute

View:

xmipp...

xmipp3 - convert to pseudoatoms
finished

atsas - convert PDB to SAXS curve
finished

👁 **Analyze Results**

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

⯆ Input
    inputStructure (from xmipp3 - swarm consensus -> outputVolume [output Volume (74 x 74 x 74, 1.98 Å/px)
⯆ Output
   ⮕xmipp3 - convert to pseudoatoms -> outputVolume   Volume (74 x 74 x 74, 1.98 Å/px)
   ⮕xmipp3 - convert to pseudoatoms -> outputPdb   AtomStruct (pseudoatoms=True, volume=True)