


View Protocols SPA

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Protocol: xmipp3 - extract particles
finished
[Cite](#)
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Run

Run name [✎](#)
 Comment [✎](#)

Run mode ☒ Continue ☐ Restart [?](#)
 Host

Parallel ☒ Threads ☐ MPI [?](#)
 Use queue? ☐ Yes ☒ No [✎](#) [?](#)

Wait for [?](#)

Expert Level ☒ Normal ☐ Advanced

Input Preprocess

Input

Input coordinates [🔍](#) [🗑️](#) [👁️](#) [?](#)

Micrographs source ☒ same as picking ☐ other [?](#)

CTF estimation [🔍](#) [🗑️](#) [?](#)

Downsampling factor [?](#)

Particle box size (px) [✎](#) [?](#)

Fill pixels outside borders ☐ Yes ☒ No [?](#)

✕ Close
💾 Save
⚙️ Execute

Protocols | Data

View: Tree [👤](#) [🔄 Refresh](#)

significant

xmipp3 - remove duplicates finished

xmipp3 - extract particles 2/3 size finished

[👁️ Analyze Results](#)

```

inputCoordinates (from xmipp3 - remove duplicates -> outputCoordinates) SetOfCoordinates (3356 items, 300 x 300)
ctfRelations (from xmipp3 - ctf consensus GCTF+CTFFind4+Xmipp -> outputCTF) (28 items)
▼ Output
  ➔ xmipp3 - extract particles 2/3 size -> outputParticles SetOfParticles (3215 items, 250 x 250, 0.74 Å/px)
  
```

SUMMARY

```

Micrographs source: same as picking
Particle box size: 250
Particles extracted: 3215
  
```