

View Protocols SPA

- ▼ Protocols SPA
 - ▶ Imports
 - ▶ Movies
 - ▼ Micrographs
 - ▶ CTF estimation
 - ▶ Preprocess
 - ▼ Particles
 - ▼ Picking
 - ▶ xmipp3 - particle boxsize
 - ▶ xmipp3 - manual-picking (step)
 - ▶ xmipp3 - auto-picking (step)
 - ▶ xmipp3 - deep consensus pick
 - ▶ xmipp3 - deep micrograph cl
 - ▶ xmipp3 - assign tiltpairs
 - ▶ xmipp3 - picking consensus
 - ▶ xmipp3 - pick noise
 - ▶ xmipp3 - remove duplicates
 - ▶ sphire - cruolo picking
 - ▶ sphire - cruolo training
 - ▶ relion - auto-picking
 - ▶ relion - auto-picking LoG
 - ▶ eautomatch - auto-picking
 - ▶ eman2 - boxer
 - ▶ eman2 - boxer auto
 - ▶ eman2 - sparx gaussian pick
 - ▶ cistem - find particles
 - ▶ Extract
 - ▶ Preprocess
 - ▶ Filter
 - ▶ Mask
 - ▼ 2D
 - ▶ Align
 - ▶ Classifu
 - ▼ 3D
 - ▶ Initial volume
 - ▶ Preprocess
 - ▶ Classifu
 - ▶ Refine
 - ▶ Postprocess
 - ▶ Analysis
 - ▶ Reconstruct
 - ▼ Tools

Protocol Run: XmippProtPickingRemoveDuplicates

mipp Protocol: xmipp3 - remove duplicates finished [Cite](#) [Help](#)

Run

Run name `xmipp3 - remove duplicates` [✎](#) Comment [✎](#)

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

Use queue? ☐ Yes ☒ No [✎](#) [?](#)

Wait for [?](#)

Input

Input coordinates `xmipp3 - center particles.outputCoordinates` [🔍](#) [🗑](#) [👁](#) [?](#)

Radius [✎](#) [?](#)

[✕](#) Close [💾](#) Save [⚙️](#) Execute

Summary | Parameters | Output Log

▼ Input
inputCoordinates (from xmipp3 - center particles -> outputCoordinates) | SetOfCoordinates (3491 items, 300 x 300)

▼ Output
xmipp3 - remove duplicates -> outputCoordinates | SetOfCoordinates (3356 items, 300 x 300)

SUMMARY

Radius = 100

Protocols | Data

View: Tree [👤](#) [🔄](#) Refresh

significant

xmipp3 - remove duplicates finished

xmipp3 - extract particles 2/3 size finished

[👁](#) Analyze Results