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**B** **Protocol Run: ChimeraSubtractionMaps** finished Cite Help

**Protocol: chimeraX - map subtraction**

**Run**

Run name **chimerax - map subtraction** edit Comment edit

Run mode ☒ Continue ☐ Restart ? Host **localhost**

Use queue? ☐ Yes ☒ No edit ?

Wait for edit ?

Expert Level ☐ Normal ☒ Advanced

Input Help

**Input**

Input 3D Map **pwem - import volumes HEMOGLOBIN.outputVolume** search trash eye ?

Select the operation to perform ☒ Subtraction ☐ Mask ?

Subtraction/Mask of ☒ 3D map ☐ atomic structure ?

Map to subtract (subtrahend) search trash eye ?

Other atomic structures

Object	Info
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Filter to apply to the differential map ☒ Gaussian ☐ Fourier Transform ?

Gaussian filter width **1.5** edit ?

Close Save Execute

**C**

Select the operation to perform ☐ Subtraction ☒ Mask

Contour level (subtrahend) **0.001**

**D**

**Input**

Input 3D Map **pwem - import volumes HEMOGLOBIN.outputVolume** search trash eye ?

Select the operation to perform ☒ Subtraction ☐ Mask ?

Subtraction/Mask of ☐ 3D map ☒ atomic structure ?

Map resolution (A): **3.2** edit ?

Atomic structure **phenix - real space refine whole.outputPdb** search trash eye ?

Select a specific chain? ☒ Yes ☐ No ?

Chain of the atomic structure **{"model": 0, "chain": "A", "residues": 142}**

Remove residues from the atomic structure? ☒ Yes ☐ No ?

Chain **{"model": 0, "chain": "A", "residues": 142}** edit ?

First residue to remove **{"residue": 22, "ALA"}** edit ?

Last residue to remove **{"residue": 28, "GLU"}** edit ?

Apply symmetry to the atomic structure: ☒ Yes ☐ No ?

Symmetry **1222r (1222r)** edit ?

Range of distance **100** edit ?

Other atomic structures

Object	Info
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Map fraction around the atomic structure? ☒ Yes ☐ No ?

Atom radius (Angstroms) **15** edit ?

Filter to apply to the differential map ☒ Gaussian ☐ Fourier Transform ?

Gaussian filter width **1.5** edit ?

Close Save Execute