

Protocol Run: ChimeraProtContacts

Protocol: chimera - contacts finished [Cite](#) [Help](#)

**Run**

Run name: chimera - contacts (whole mac) [✎](#) Comment: [✎](#)

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

Use queue? ☐ Yes ☒ No [?](#)

Wait for: [?](#)

Expert Level: ☒ Normal ☐ Advanced

**Input**

**Atomic Structure:** atomstructutils - operator (whole macromolecule).outputPdb [🔍](#) [🗑️](#) [👁️](#) [?](#)

Chain Labeling: {"A": "chainA", "A002": "HEM\_A", "B": "chainB", "B002": "HEM\_B", "C": "chainC", "C002": "HEM\_C", "D": "chainD", "D002": "HEM\_D"} [✎](#) [?](#)

Apply symmetry: ☐ Yes ☒ No [?](#)

**1** **4** **2**

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

**Entry Grid** [-](#) [□](#) [✕](#)

	<i>label</i>
<b>A</b>	chainA
<b>A002</b>	HEM_A
<b>B</b>	chainB
<b>B002</b>	HEM_B
<b>C</b>	chainC
<b>C002</b>	HEM_C
<b>D</b>	chainD
<b>D002</b>	HEM_D

**OK**

**3**