

A

Protocol Viewer: ChimeraProtContactsViewer

Protocol: chimera - Contacts Viewer

Display Results

3D Visualization

Interacting chains

Contacts between interacting chains

Swap chain columns in the summary of contacts Yes No

Distance to group residues (Number of residues) 4

Select two interacting chains and get the summary of contacts

0,HEM_A,A002:#0,chainA,A
#0,HEM_A,A002:#0,chainA,A
#0,HEM_B,B002:#0,chainB,B
#0,chainA,A:#0,chainB,B
#0,chainA,A:#1,chainA,A
#0,chainA,A:#1,chainB,B
#0,chainB,B:#1,chainB,B

Close

3

1
2
4**C**

RESULTS for: 50, #0, HEM_A, A002, #0, chainA, A

atoms, prot_1, model_1, chain_1, AA_1, prot_2, model_2, chain2, AA_2

1, HEM_A, #0, A002, Hem1, chainA, #0, A, Thr39

2, HEM_A, #0, A002, Hem1, chainA, #0, A, Phe43

2, HEM_A, #0, A002, Hem1, chainA, #0, A, His45

1, HEM_A, #0, A002, Hem1, chainA, #0, A, Phe46

2, HEM_A, #0, A002, Hem1, chainA, #0, A, His58

2, HEM_A, #0, A002, Hem1, chainA, #0, A, Lys61

1, HEM_A, #0, A002, Hem1, chainA, #0, A, Val62

2, HEM_A, #0, A002, Hem1, chainA, #0, A, Ala65

1, HEM_A, #0, A002, Hem1, chainA, #0, A, Leu66

3, HEM_A, #0, A002, Hem1, chainA, #0, A, Leu83

21, HEM_A, #0, A002, Hem1, chainA, #0, A, His87

4, HEM_A, #0, A002, Hem1, chainA, #0, A, Leu91

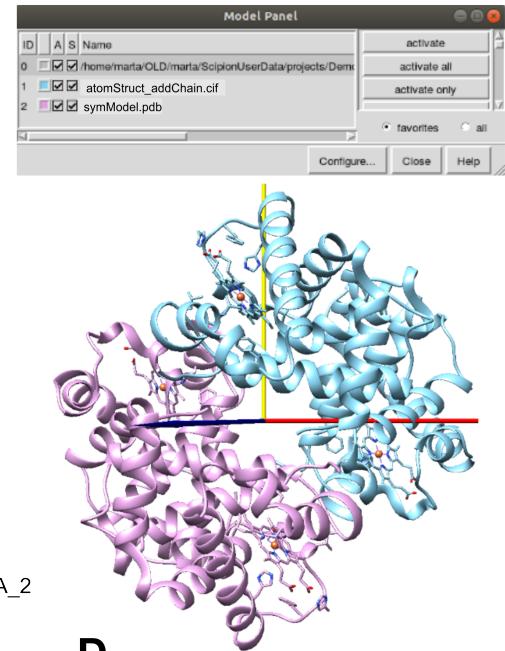
1, HEM_A, #0, A002, Hem1, chainA, #0, A, Val93

2, HEM_A, #0, A002, Hem1, chainA, #0, A, Asn97

2, HEM_A, #0, A002, Hem1, chainA, #0, A, Phe98

3, HEM_A, #0, A002, Hem1, chainA, #0, A, Leu101

>>> Hem1 ---- Thr39_Leu101?????

B**D**