

Allowed overlap: 0.6
H-bond overlap reduction: 0.4
Ignore contacts between atoms separated by 4 bonds or less
Detect intra-residue contacts also

5 contacts

atom1	atom2	overlap	distance
LEU 598 N	LEU 598 CA	1.885	1.635
LEU 598 N	LEU 598 HN	1.620	1.020
LEU 598 N	LEU 598 CB	0.901	2.619
THR 720 CG2	LEU 598 CG	0.822	2.938
THR 720 CG2	LEU 598 CB	0.710	3.050