

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

4 contacts

atom1	atom2	overlap	distance
PHE 714 CD2	ILE 228 CG2	0.695	2.945
THR 721 HG1	ALA 226 CB	0.679	2.201
LEU 598 CD1	THR 597 C	0.641	2.939
THR 720 O	LEU 724 CD1	0.620	2.740