

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
LEU 834 CD2	SER 803 HG	0.872	2.008
LEU 800 CG	ASP 796 O	0.619	2.741
VAL 146 CG1	LEU 142 O	0.618	2.742
VAL 146 CG1	THR 143 O	0.617	2.743