

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

2 contacts

atom1	atom2	overlap	distance
ILE 260 CD1	LYS 257 CG	0.823	2.937
ILE 256 CD1	LEU 211 CD2	0.779	2.981