

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
LEU 834 CD2	SER 803 HG	0.872	2.008
VAL 146 CG1	LEU 142 O	0.618	2.742