

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
VAL 584 CG2	LIG 0 H	0.800	2.080
THR 591 CG2	GLN 570 NE2	0.652	2.868
GLN 570 CD	THR 591 CG2	0.635	2.945
GLN 570 OE1	THR 591 CG2	0.606	2.754