

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
GLN 900 CG	GLN 748 2HE2	0.795	2.085
TYR 908 HN	PRO 906 C	0.773	1.927
GLN 900 CB	GLN 748 2HE2	0.736	2.144
GLN 900 CB	GLN 748 NE2	0.638	2.867