

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

3 contacts

atom1	atom2	overlap	distance
PRO 906 C	TYR 908 HN	0.830	1.870
GLN 900 CA	GLN 900 2HE2	0.670	2.210
GLN 748 NE2	GLN 900 CB	0.643	2.862