

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

15 contacts

atom1	atom2	overlap	distance
LIG 0 H	GLN 990 NE2	1.892	0.748
LIG 0 C	GLN 990 NE2	1.825	1.515
LIG 0 O	VAL 991 CG2	1.486	1.874
LIG 0 C	GLN 990 NE2	1.235	2.105
LIG 0 C	GLN 990 NE2	0.985	2.355
LIG 0 H	GLN 990 CD	0.942	1.758
LIG 0 C	PHE 303 CZ	0.930	2.530
LIG 0 C	GLN 990 CD	0.889	2.511
LIG 0 C	PHE 303 CZ	0.839	2.621
LIG 0 C	VAL 991 CG2	0.805	2.775
PHE 303 CE2	ILE 299 CD1	0.691	2.949
ILE 299 CG1	PHE 303 CE2	0.689	2.951
PHE 303 CE1	LIG 0 C	0.680	2.780
LIG 0 C	GLN 990 NE2	0.672	2.668
PHE 303 CD2	ILE 299 CG1	0.619	3.021