

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

13 contacts

atom1	atom2	overlap	distance
LIG 0 C	GLN 990 NE2	1.229	2.111
LIG 0 H	GLN 990 NE2	1.152	1.488
LIG 0 O	GLN 990 OE1	0.993	1.967
LIG 0 C	GLN 990 OE1	0.827	2.353
LIG 0 N	GLN 990 NE2	0.768	2.497
LIG 0 C	VAL 991 CG2	0.723	2.857
PHE 303 CE2	ILE 299 CD1	0.691	2.949
ILE 299 CG1	PHE 303 CE2	0.689	2.951
LIG 0 H	ALA 987 CA	0.653	2.227
LIG 0 C	VAL 991 CG2	0.653	2.927
LIG 0 C	GLN 990 CD	0.640	2.760
ILE 299 CG1	PHE 303 CD2	0.619	3.021
ALA 987 CB	LIG 0 O	0.610	2.750