

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
GLY 691 CA	LYS 736 CG	0.824	2.936
LIG 1.het C	LYS 257 HZ1	0.662	2.038
ARG 253 CD	LYS 257 HZ2	0.623	2.257