

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

7 contacts

atom1	atom2	overlap	distance
ILE 260 CD1	LYS 257 CG	0.819	2.941
ARG 253 CA	ARG 253 1HH1	0.819	2.061
LEU 211 CD2	ILE 256 CD1	0.811	2.949
ARG 253 CA	ARG 253 NH1	0.642	2.863
ARG 253 O	LYS 257 CG	0.628	2.732
LYS 252 O	ILE 256 CG2	0.628	2.732
LYS 252 O	ILE 256 CB	0.625	2.735