Refinement	EIAV Gag∆MA spheres pH6 residues 143-359	EIAV Gag∆MA tubes ph6 residues 143-359	EIAV Gag∆MA tubes ph8 residues 143-359
Resolution of map (Å)	3.7	3.8	3.7
Number of CA-SP monomers	1	3	3
All-atom clash score	6.78	2.91	5.91
Favored rotamers	93.58%	91.27%	89.30%
Ramachandran outliers (number of residues)	0	0.31% (2)	0
Ramachandran favoured	93.95%	92.71%	91.94%
C-beta deviations	0	0	0
Rmsd (angles, degrees)	0.861	0.839	0.917
Rmsd (bonds, Å)	0.006	0.005	0.006