

MolProbity Ramachandran analysis

3d0h.H.pdb, model 1



Source: 3d0h.H.pdb, model 1
 Residue: 322 ASN
 Chain: B
 Conformer: 1
 MolProbity: 0.00
 Ramachandran: 0.00
 Clashscore: 0.00
 Density: 0.00
 B-factor: 0.00
 Occupancy: 1.00
 Displacement: 0.00
 ... (repeated for all residues) ...