

MolProbity Ramachandran analysis

3d0h.H.pdb, model 1



Source: 3D0H.H.pdb, model 1
 Residue: A 289 PRO
 Psi: -170.0
 Phi: -150.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: A
 Residue: A 409 SER
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: A
 Residue: A 401 ASP
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: A
 Residue: A 91 LEU
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: A
 Residue: A 163 TRP
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: A
 Residue: B 338 ASN
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: B
 Residue: A 20 THR
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: A
 Residue: B 338 ASN
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: B
 Residue: E 370 SEI
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: E
 Residue: E 416 PHE
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: E
 Residue: F 416 PHE
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: F
 Residue: E 471 ALA
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: E
 Residue: A 614 ALA
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: A
 Residue: B 322 ASN
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: B
 Residue: 387 PHE
 Psi: -10.0
 Phi: -10.0
 B-factor: 10.0
 Occupancy: 1.00
 Conformation: TRANS
 Chain: 387