





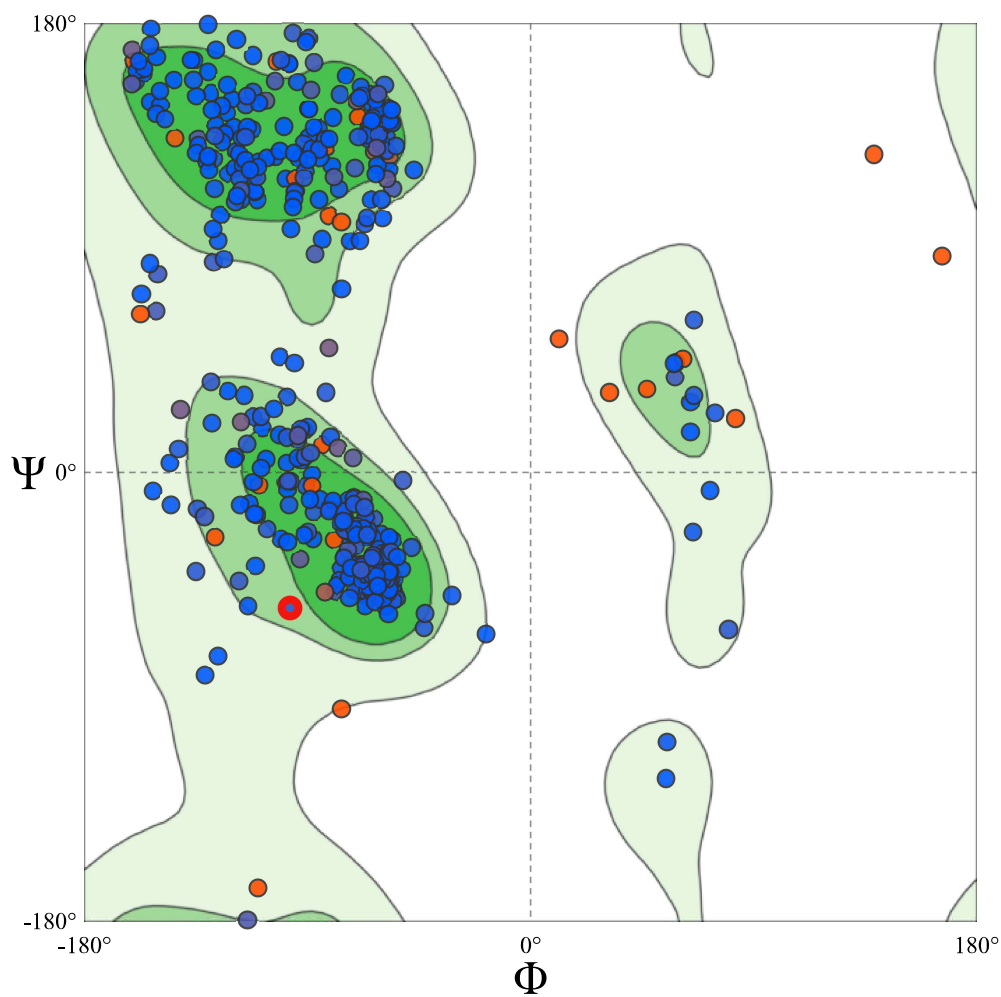
Structure Assessment

[Help](#)[Examples ▾](#)AChE; Model 01;    

PDB JSON

Created: Thu 24 Dec 2020, 14:01;

Ramachandran Plots



General

Glycine

Proline

Pre-Proline

Chain A ▾



MolProbity Results

MolProbity
Score

1.76

☐ Clash Score 3.08 (A154 ARG-A197 ASP), (A573 ASP-A695 ARG)Ramachandran
Favoured


90.62%

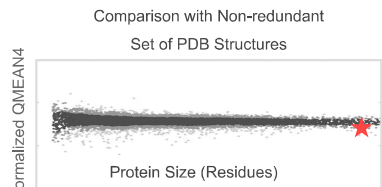
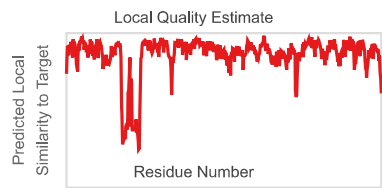
☐ Ramachandran
Outliers 1.77% A437 PRO, A269 ALA, A433 LEU, A673 PRO, A503 GLU, A263 ASP,
A251 ALA, A249 ARG, A272 GLN, A332 PRO

<input type="checkbox"/> Rotamer Outliers	1.47%	A640 GLU, A489 ASP, A260 THR, A163 ARG, A531 GLU, A610 GLU, A425 ASP
<input type="checkbox"/> C-Beta Deviations	9	A263 ASP, A267 HIS, A578 CYS, A429 ASN, A342 VAL, A251 ALA, A424 ASN, A709 TRP, A371 PHE
<input type="checkbox"/> Bad Bonds	3 / 4609	A306 ALA-A307 VAL, A306 ALA, A238 TRP
<input type="checkbox"/> Bad Angles	43 / 6273	A357 ASN, (A250 GLY-A251 ALA), A477 PHE, (A270 THR-A271 PRO), (A328 SER-A329 PRO), A302 ASP, (A578 CYS-A579 PRO), (A262 PRO-A263 ASP), (A333 GLY-A334 PHE), (A703 LEU-A704 PRO), A263 ASP, A238 TRP, A448 ASP, (A626 GLN-A627 PRO), A601 HIS, A489 ASP, (A271 PRO-A272 GLN), (A239 ALA-A240 PRO), (A502 ASP-A503 GLU), A163 ARG, A268 SER, A258 ALA,

Results obtained using MolProbity version 4.4

Quality Estimate

QMEAN		-1.40
C β		0.44
All Atom		-1.09
solvation		-0.29
torsion		-1.29



Residue Quality

QMEAN	40
Chain:A	MARFITSSSLSPSTTPSFASATASPAIASSLPRSKSTKAT
template_upload.1.A	-----
QMEAN	
Chain:A	KARKTILSANSFKTSSLSSLSASSPSLSSSPSFFKSSS 80
template_upload.1.A	-----

