

Structure Assessment

Help

Examples ▾

salmon_MHCII_refined.pdb;

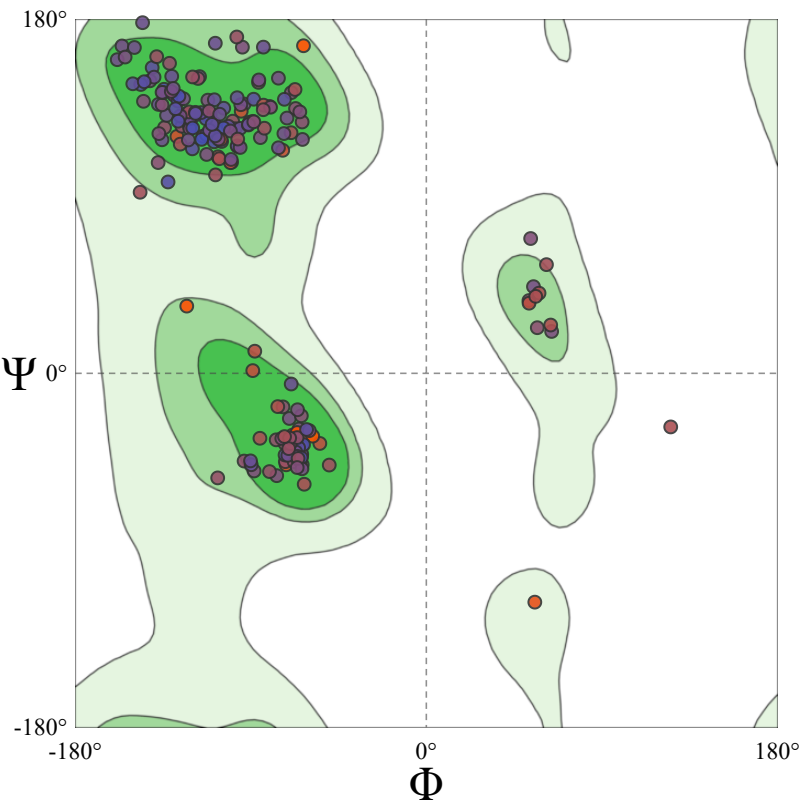
Project Data ▾

 ☐

Created: Fri 14th Jan, 23:57;

We do not predict the uploaded structure to have a transmembrane segment.

Ramachandran Plots



General

Glycine

Proline

Pre-Proline

All selected (2) ▾



MolProbity Results

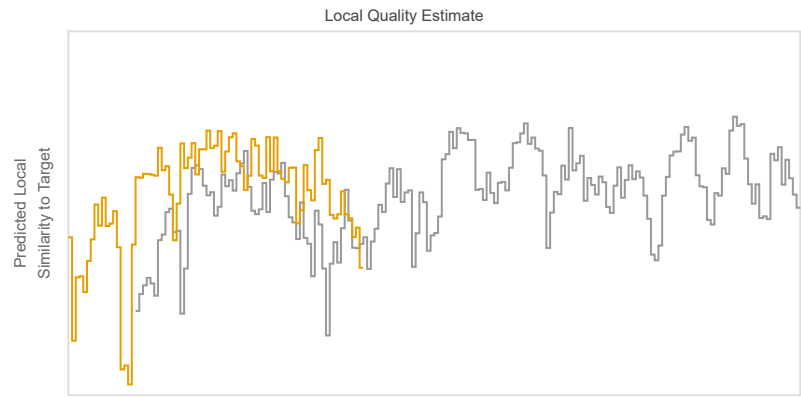
MolProbity Score	1.50	
<input type="checkbox"/> Clash Score	9.35	(B23 PHE-B75 CYS)
Ramachandran Favoured	98.43%	

<input type="checkbox"/>	Ramachandran Outliers	1.18%	A160 VAL, A73 TYR, A131 PRO
<input type="checkbox"/>	Rotamer Outliers	0.92%	A131 PRO, B81 ILE
<input type="checkbox"/>	C-Beta Deviations	9	A131 PRO, A160 VAL, A163 ASN, A122 LEU, A187 LEU, B44 TYR, A120 ASN, A155 TYR, A73 TYR
	Bad Bonds	0 / 2097	
<input type="checkbox"/>	Bad Angles	41 / 2857	B4 PHE, (A132 ALA-A133 PRO), B25 HIS, A131 PRO, A120 ASN, A122 LEU, (A159 ASP-A160 VAL), (A65 ASP-A66 PRO), (B79 ALA-B80 PRO), B5 TYR, A163 ASN, (A61 PRO-A62 PRO), B44 TYR, A77 VAL, B77 HIS, A47 TRP, A126 VAL, A187 LEU, A72 HIS, (A72 HIS-A73 TYR), A132 ALA, A155 TYR, A105 HIS, A22 HIS, A73 TYR, A125 HIS, B23 PHE, A63 PHE, (B2 GLY-B3 TYR), (A168 LEU-A169 PRO), A184 HIS, A164 GLN, A79 ASN, A156 PRO
<input type="checkbox"/>	Twisted Non-Proline	1 / 239	(A97 PRO-A98 GLU)

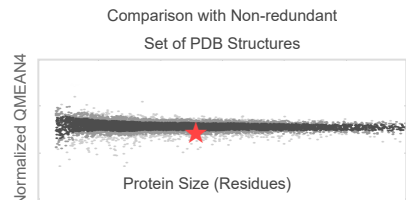
Results obtained using MolProbity version 4.4

Quality Estimate

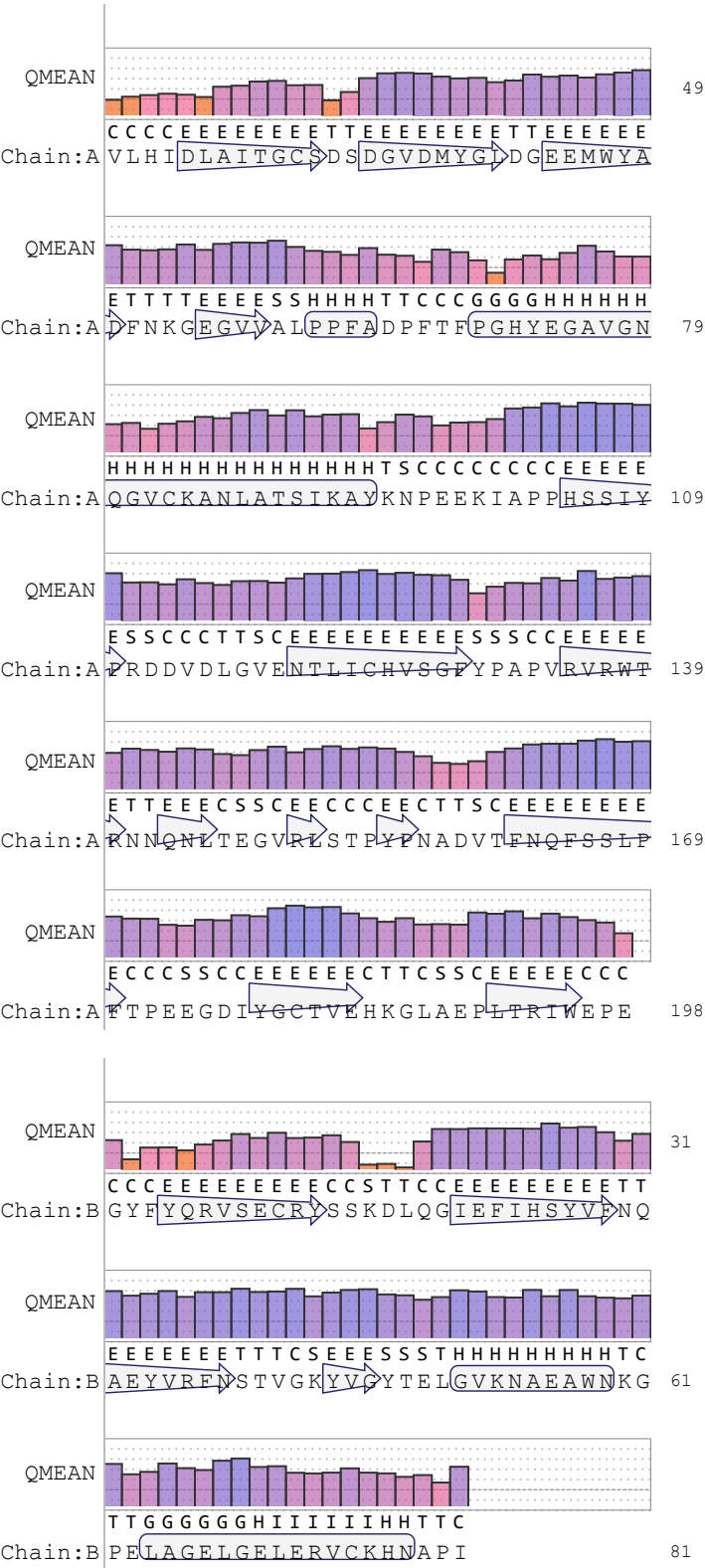
QMEANDisCo Global: 0.68 ± 0.05 ⓘ

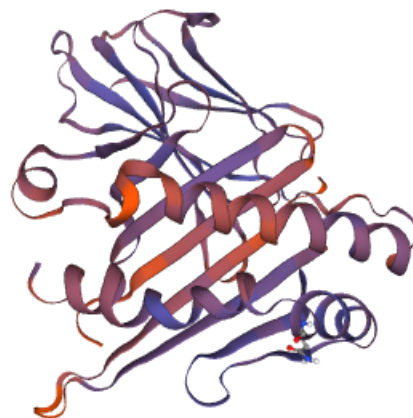


QMEAN Z-Scores		
QMEAN		-1.47
Cβ		-0.61
All Atom		-0.55
solvation		-0.48
torsion		-1.27



Residue Quality





Cartoon ▲

