

Structure Assessment

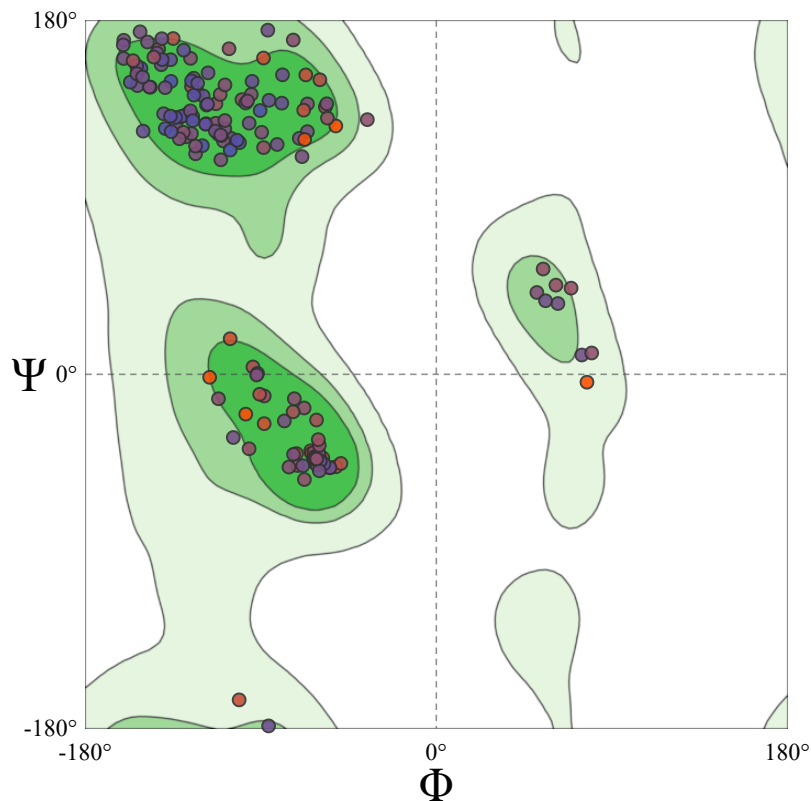
[Help](#)[Examples ▾](#)

MHC II Alpha Chain; Model 01;

[Project Data ▾](#)

Created: Fri 4th Feb, 02:53;

Ramachandran Plots

[General](#)[Glycine](#)[Proline](#)[Pre-Proline](#)[Chain A ▾](#)

MolProbity Results



MolProbity
Score 1.42

☐ Clash Score 3.71 (A66 TYR-A75 ASP)

Ramachandran 96.17%
Favoured

Ramachandran 0.00%
Outliers

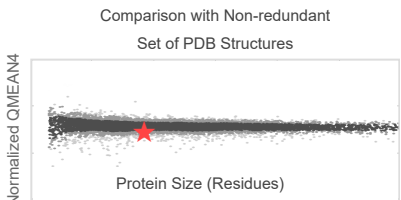
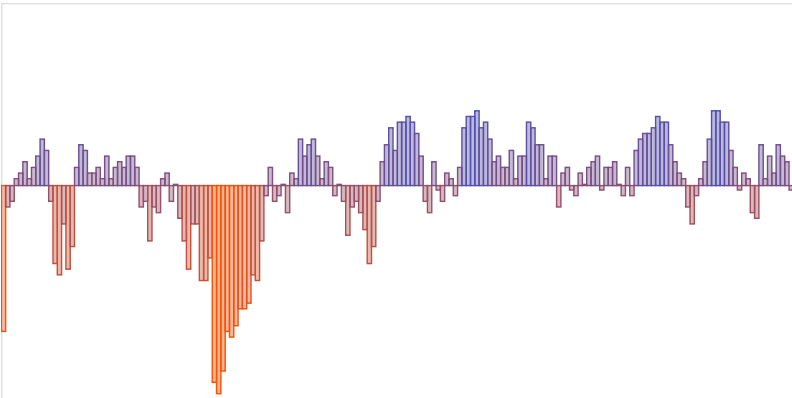
Rotamer Outliers	0.00%	
<input type="checkbox"/> C-Beta Deviations	3	A199 ALA, A173 GLN, A108 ASN
Bad Bonds	0 / 1565	
<input type="checkbox"/> Bad Angles	16 / 2136	A80 PHE, (A41 GLY-A42 THR), A110 PRO, A84 ASN, (A109 ASN-A110 PRO), A175 PHE, A29 HIS, A57 VAL, A197 HIS, (A37 CYS-A96 CYS), A94 ASN, A174 THR, (A184 THR-A185 PRO), (A143 TYR-A144 PRO), A75 ASP, A107 GLU
<input type="checkbox"/> Cis Non-Proline	1 / 170	(A41 GLY-A42 THR)
<input type="checkbox"/> Cis Prolines	1 / 14	(A143 TYR-A144 PRO)

Results obtained using MolProbity version 4.4

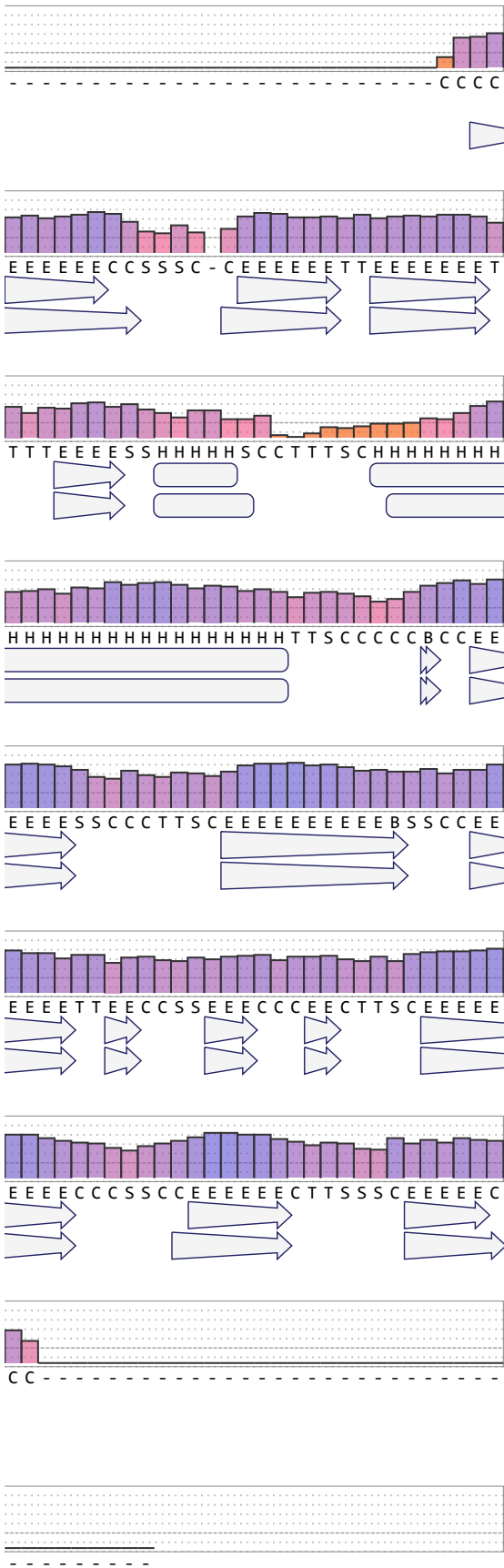
Quality Estimate



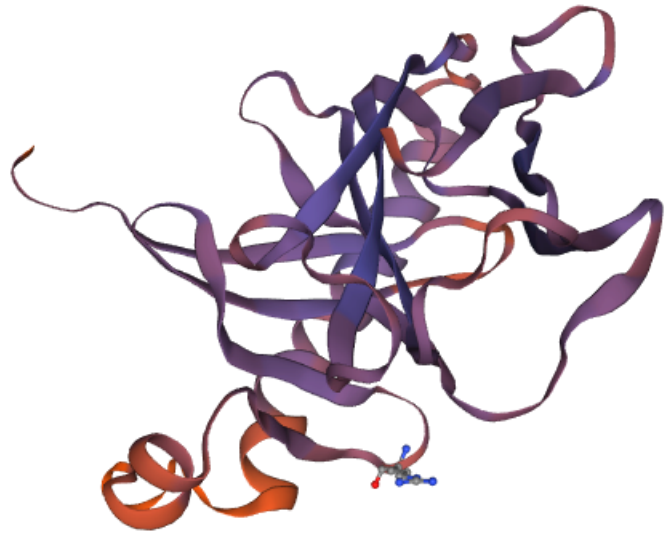
QMEANDisCo Global: 0.68 ± 0.06 ⓘ



Residue Quality



QMEAN		30
Chain:A	MKTCSSDMRRSALIIILMINSFCAFSQIPHE	
3wex.1.A	-----ADHV	6
QMEAN		
Chain:A	VVYVVGCFENGTEAVFEFDAEELLYVDF	59
3wex.1.A	STYAMFVQTHRPTGEFMFEFDEDEQFYVDL	36
QMEAN		
Chain:A	DRDEVVYTMPRFLTDDPSKLFENLNVFNNA	89
3wex.1.A	DKKETVWHLEEFGRAF---SFEAQ---GG	59
QMEAN		
Chain:A	KKNRNICLSIIKIYKLEENNPPEEMDPPES	119
3wex.1.A	LANIAILNNNLNTLIQRSNHTQAANDPPEV	89
QMEAN		
Chain:A	IILYPSEEVQLGVENSLICFVNHFYPPPIKV	149
3wex.1.A	TVFPKEPVVELGQPNTLICHIDRFFPPVLNV	119
QMEAN		
Chain:A	SWTRNGRLVSEGQSLSRYYPNNDQTFHQFT	179
3wex.1.A	TWLCNGEPVTEGVAESLFLPRTDYSFHKFH	149
QMEAN		
Chain:A	TLTFTPKEGDIYSCTVEHLALDRPKTRSWV	209
3wex.1.A	YLTfVPSAEDVYDCRVEHWGLDQPLLKHWE	179
QMEAN		
Chain:A	PDFSHPSLPGPGVYCGVGLTVGLLGVAVGTF	239
3wex.1.A	AQ-----	181
QMEAN		
Chain:A	LMVKGCRGQ	248
3wex.1.A	-----	



Cartoon ▲

