

Structure Assessment

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Untitled Project; Model 01;



PDB

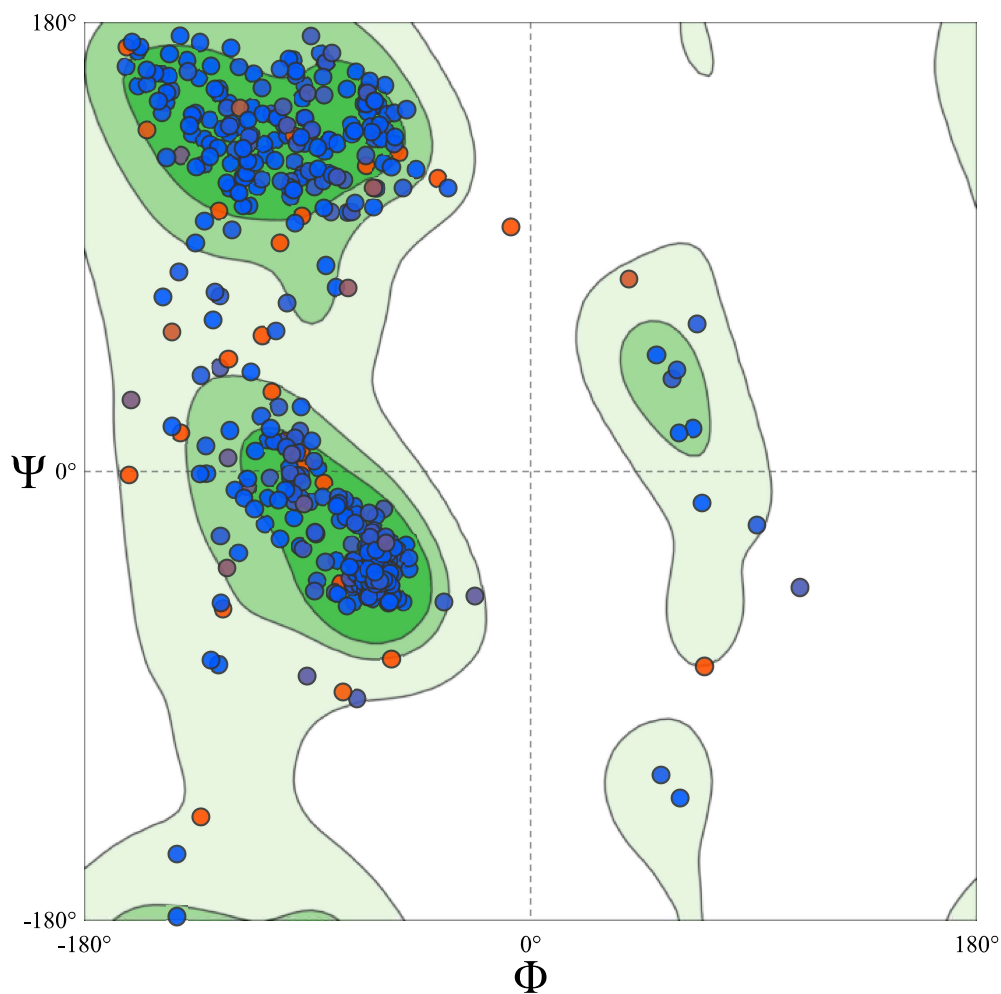


JSON



Created: Thu 24 Dec 2020, 14:35;

Ramachandran Plots



General

Glycine

Proline

Pre-Proline

Chain A ▾



MolProbity Results

MolProbity
Score

2.38



Clash Score

7.03

(A264 HIS-A661 ASP), (A273 ASN-A274 THR), (A273 ASN-A367 TRP)

Ramachandran
Favoured

92.40%



Ramachandran
Outliers

1.77%

A673 PRO, A287 GLY, A263 ASP, A274 THR, A266 ILE, A273 ASN, A486 LYS, A241 SER, A249 ARG, A561 TYR

24/12/2020

Structure Assessment

<input type="checkbox"/>	Rotamer Outliers	4.83%	A440 VAL, A393 VAL, A489 ASP, A687 LEU, A147 GLN, A539 LYS, A640 GLU, A163 ARG, A670 LYS, A484 LEU, A204 THR, A142 ASP, A565 GLN, A481 PRO, A646 LEU, A267 HIS, A369 THR, A447 VAL, A674 VAL, A450 LYS, A526 ARG, A587 LEU, A689 ARG	
<input type="checkbox"/>	C-Beta Deviations	4	A275 THR, A615 LEU, A342 VAL, A204 THR	
	Bad Bonds	0 / 4621		
<input type="checkbox"/>	Bad Angles	35 / 6290	A267 HIS, A689 ARG, (A480 ASP-A481 PRO), (A703 LEU-A704 PRO), (A328 SER-A329 PRO), (A171 ILE-A172 PRO), A535 ASN, (A626 GLN-A627 PRO), (A270 THR-A271 PRO), (A268 SER-A269 ALA), A357 ASN, (A274 THR-A275 THR), A616 HIS, (A560 GLY-A561 TYR), (A485 MET-A486 LYS), A264 HIS, A256 HIS, (A386 SER-A387 PRO), A247 HIS, (A578 CYS-A579 PRO), A561 TYR, A661 ASP,	<div><div></div></div>

Results obtained using MolProbity version 4.4



Residue Quality

QMEAN

40

Chain:A

MARFITSSSLSPSTTPSFASATASPAIASSLPRSKSTKAT

template_upload.1.A

QMEAN

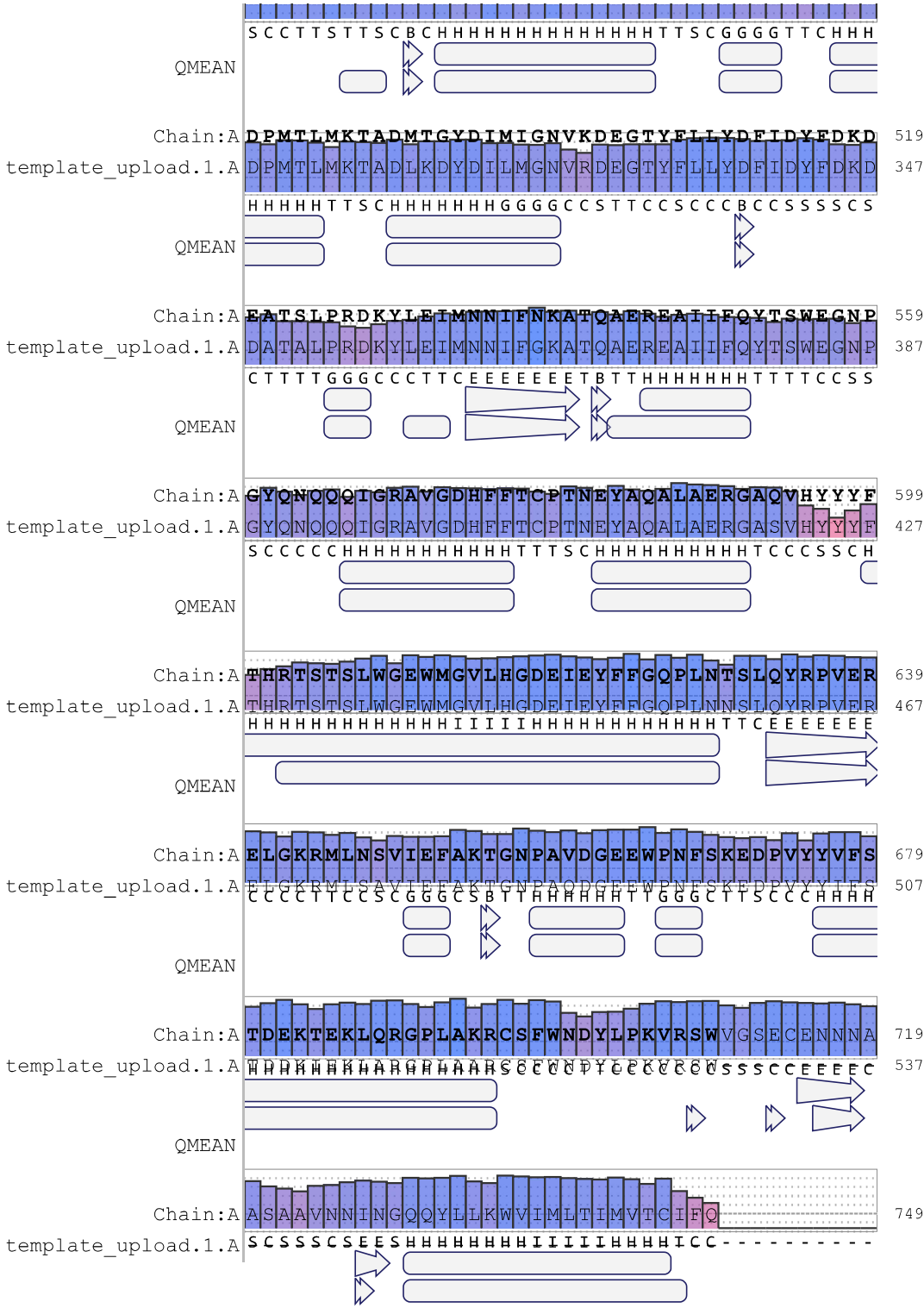
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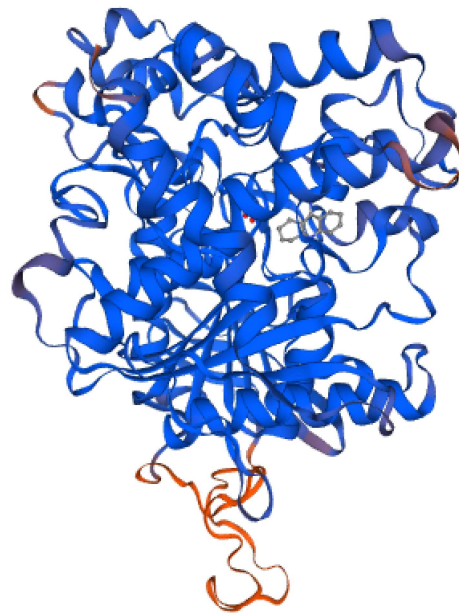
Chain:A

KARKTILSANSFKTSSLSSLSASSPSLSSSPSFFKSSS

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Cartoon ▲

