

Structure Assessment

DeepView-Project-Swiss-Model-LcOamb-Transmembrane-Antagonist-2; Model 01;

Project Data ▼



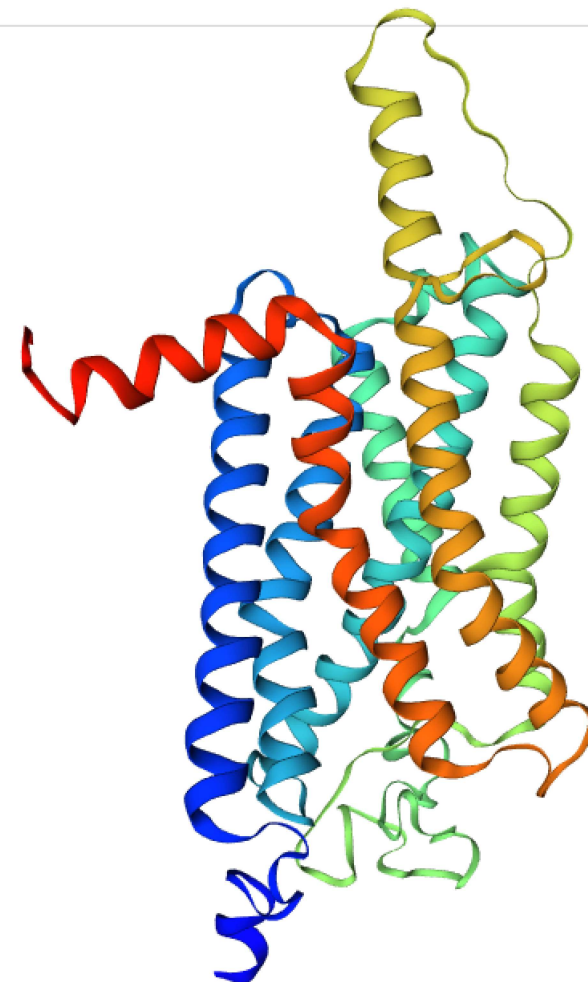
Created: Fri 6th Aug, 17:03;

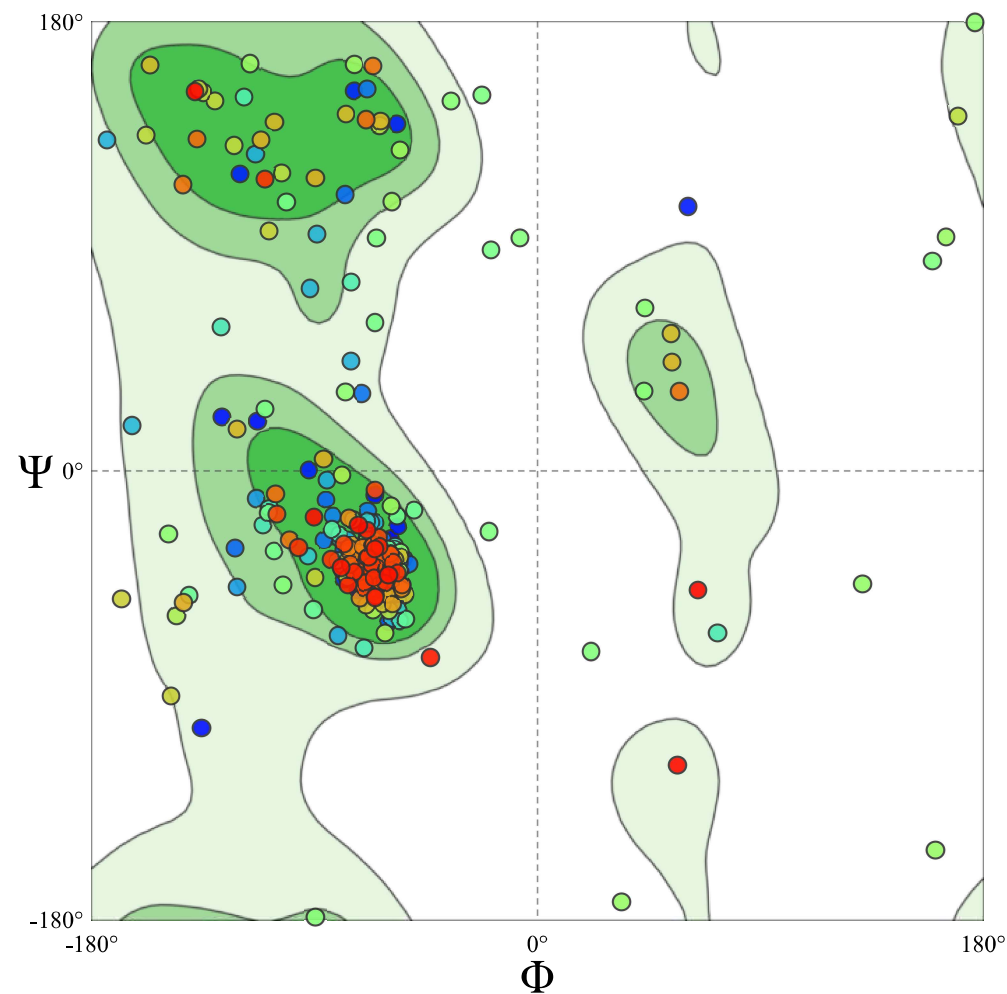
Ramachandran Plots



Help

Examples ▼





General

Glycine

Proline

Pre-Proline

Chain A ▼

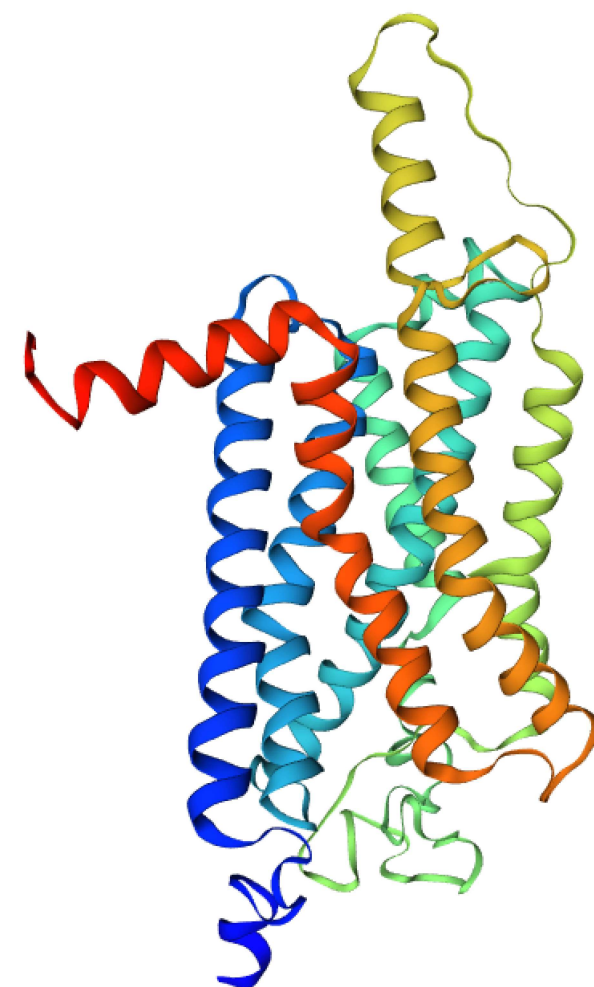


MolProbity Results

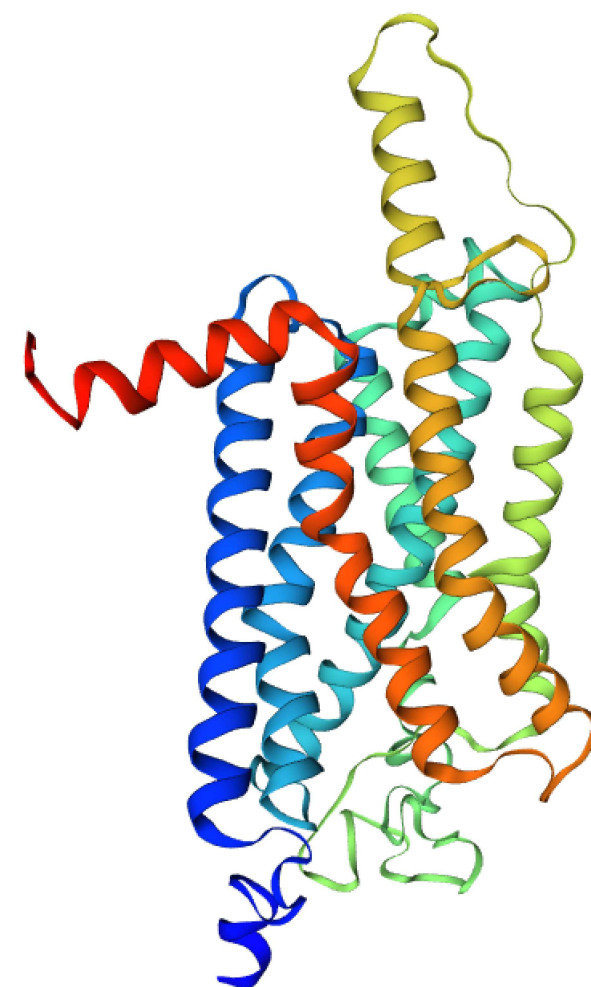


MolProbity
Score

3.58



<input type="checkbox"/>	Clash Score	68.89	(A227 ARG-A252 VAL), (A170 TYR-A171 THR), (A188 PRO-A190 CYS), (A169 THR-A176 THR), (A246 ARG-A250 PHE), (A167 GLN-A168 PRO), (A188 PRO-A189 PRO), (A169 THR-A184 ALA), (A233 THR-A240 PHE), (A169 THR-A188 PRO), (A236 ILE-
	Ramachandran Favoured	86.65%	
<input type="checkbox"/>	Ramachandran Outliers	6.23%	A167 GLN, A52 ARG, A329 ARG, A165 MET, A189 PRO, A226 TYR, A237 ASN, A12 SER, A153 PHE, A180 MET, A175 TYR, A236 ILE, A194 CYS, A170 TYR, A193 LYS, A171 THR, A172 ARG, A174 ASN, A192 TRP, A166 ILE, A190 CYS
<input type="checkbox"/>	Rotamer Outliers	7.00%	A5 GLU, A293 ILE, A195 GLU, A157 VAL, A230 VAL, A88 PHE, A110 ASN, A221 PHE, A315 ILE, A71 LEU, A67 LEU, A2 ASN, A177 LEU, A33 LEU, A152 CYS, A62 LEU, A324 ARG, A223 TRP, A69 VAL, A169 THR, A50 LYS
<input type="checkbox"/>	C-Beta Deviations	16	A252 VAL, A169 THR, A188 PRO, A174 ASN, A227 ARG, A259 THR, A166 ILE, A253 LYS, A254 ARG, A236 ILE, A213 ILE, A193 LYS, A228 ALA, A237 ASN, A257 VAL, A183 TYR
<input type="checkbox"/>	Bad Bonds	13 / 2813	A188 PRO, A227 ARG, A169 THR, A145 TRP, A183 TYR, A251 GLN-A252 VAL, A321 HIS, A291 HIS, A254 ARG-A255 PHE, A176 THR
<input type="checkbox"/>	Bad Angles	68 / 3836	A169 THR, A252 VAL, A188 PRO, A236 ILE, A176 THR, A257 VAL, A227 ARG, (A254 ARG-A255 PHE), A254 ARG, A230 VAL, (A170 TYR-A171 THR), (A236 ILE-A237 ASN), (A259 THR-A260 LYS), (A174 ASN-A175 TYR), A174 ASN, A168 PRO,
<input type="checkbox"/>	Cis Non-Proline	3 / 321	(A170 TYR-A171 THR), (A174 ASN-A175 TYR), (A183 TYR-A184 ALA)



<input type="checkbox"/> Cis Prolines	2 / 17	(A185 THR-A186 PRO), (A188 PRO-A189 PRO)
<input type="checkbox"/> Twisted Non-Proline	6 / 321	(A159 TRP-A160 LYS), (A165 MET-A166 ILE), (A172 ARG-A173 GLY), (A179 SER-A180 MET), (A259 THR-A260 LYS), (A337 THR-A338 ARG)
<input type="checkbox"/> Twisted Prolines	2 / 17	(A154 PRO-A155 PRO), (A186 PRO-A187 PRO)

Results obtained using MolProbity version 4.4

Quality Estimate

QMEANDisCo Global: 0.55 ± 0.05

QMEANDisCo Local

Local Quality Estimate

Predicted Local Similarity to Target

QMEAN Z-Scores

QMEAN

Cβ

All Atom

solvation

torsion

-9.27

-6.24

-3.96

-1.65

-7.62

Comparison with Non-redundant Set of PDB Structures

ormalized QMEAN4

Protein Size (Residues)

<https://swissmodel.expasy.org/assess/HrUkCE/01>

4/7

Residue Quality



QMEAN	39
Chain:A MNETECDNLIKSVKW-TEPSNLISLAILEFINVLVIGGNL	
project_template_0.1.A MNESECASLLASVQW-TDPTNLVSLAVLAFINVLVIVGNC	39
QMEAN	
Chain:A LVIAAVFCSNKLRSVTNFFIVNLAVADLLVGLAVLPFSAT	79
project_template_0.1.A LVIAAVLCSHKLRSVTNFFIVSLAVADLLVGLAVLPFSAT	79
QMEAN	
Chain:A WEVFKVWIFGDVWCRIWLAVDVWMCTASILNLCAISLDRY	119
project_template_0.1.A WEVFKVWIFGDVWCRIWLAVDVWMCTASILNLCAISLDRY	119
QMEAN	
Chain:A VAVTRPVTYPSIMSTKKAKSLIAGIWVLSFVICFPPLVGW	159
project_template_0.1.A VAVTRPVTYPSIMSTRRAKSLIAGLWVLSFVICFPPLVGW	159
QMEAN	
Chain:A KDQKPMIQPTYTRGNYTLYSMSSYATPPPPCPWKCELTND	199
project_template_0.1.A KEQKVKENVYYQYGNYTLVSVTPSPAPPLPCPWTCELTND	199
QMEAN	
Chain:A RGYVLYSALGSFYIPMFVMLFFYWRIYRAAVRTT--RAIN	237
project_template_0.1.A AGYVVYSALGSFYIPMFVMLFFYWRIYRAAVRTK--KLGK	237

