

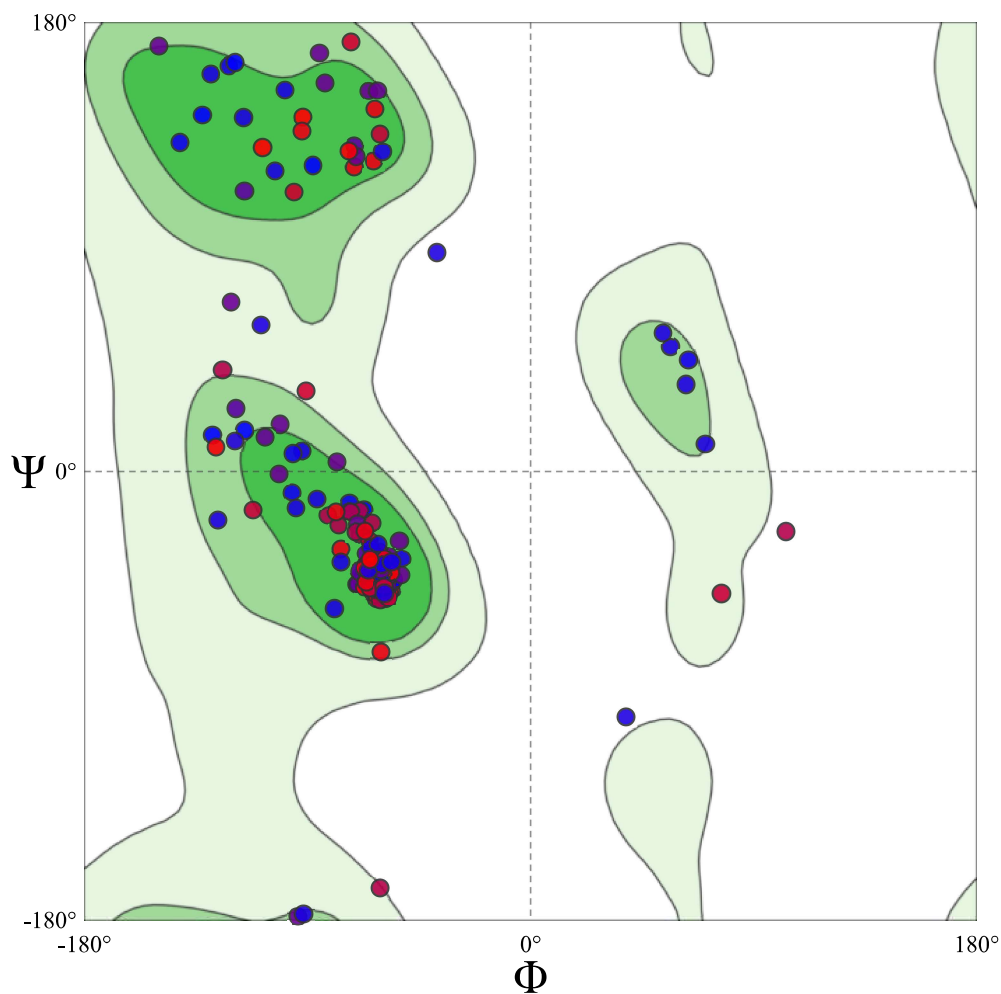
# Structure Assessment

[Help](#)[Examples ▾](#)Untitled Project; Model 01;    

PDB JSON

Created: Wed 30 Dec 2020, 15:52;

## Ramachandran Plots



General

Glycine

Proline

Pre-Proline

Chain A ▾




## MolProbity Results

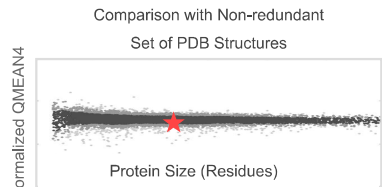
MolProbity  
Score 1.66☐ Clash Score 2.50 (A728 GLU-A769 HIS)Ramachandran 95.80%  
Favoured☐ Ramachandran 1.68% A618 ASP, A651 ALA, A799 MET, A620 ASN  
Outliers

|  |           |   |
|--|-----------|---|
| <input type="checkbox"/> Rotamer Outliers  | 2.73%     | A798 GLU, A676 MET, A611 LYS, A799 MET, A817 ILE, A800 CYS  |
| <input type="checkbox"/> C-Beta Deviations | 3         | A800 CYS, A585 SER, A685 ASP  |
| Bad Bonds                                  | 0 / 2004  |   |
| <input type="checkbox"/> Bad Angles        | 17 / 2710 | (A581 ILE-A582 PRO), A719 MET, A676 MET, (A616 SER-A617 PRO), (A655 ILE-A656 PRO), A621 GLU, A778 PHE, A769 HIS, A714 HIS, A800 CYS, A772 ASP, A682 HIS, A708 ASN, A630 HIS, A698 ASP, A609 ASP |

Results obtained using MolProbity version 4.4

Quality Estimate

|           |   |       |
|-----------|---|-------|
| QMEAN     |  | -0.41 |
| C $\beta$ |  | -0.14 |
| All Atom  |  | 1.22  |
| solvation |  | 1.77  |
| torsion   |  | -1.10 |



Residue Quality

|          |  |
|----------|--|
| QMEAN    | 50   |
| Chain:A  | MNLSPPMYRLNHAQGQKLPMAAEQQQQQSQQHPQQQQPTTTTPQTTPPTP     |
| 4oxt.1.A | -----  |
| QMEAN    |  |
| Chain:A  | TQSQQQIIIPSHILLQQQLDAASANTNSSNSNTTISNSHSITHHSNNEPV 100 |
| 4oxt.1.A | -----  |

|          |  |     |
|----------|--|-----|
| QMEAN    |  |     |
| Chain:A  | FLNNFTEQESNTPLALRQASNASSTSNSALLHTIHQHHSHTHQAPPTPPN         | 150 |
| 4ozt.1.A | -----  |     |
| QMEAN    |  |     |
| Chain:A  | HSRLIHSTAANNLVITNAAAAAALVAASAAAAAANQVDVLSSNSSVEENL         | 200 |
| 4ozt.1.A | -----  |     |
| QMEAN    |  |     |
| Chain:A  | KLLKTAIKSEPLPHDLNSASNSNHNHNNVNNLSSNKEDLISLAACSALA          | 250 |
| 4ozt.1.A | -----  |     |
| QMEAN    |  |     |
| Chain:A  | NVVIPASSANAVASSSTSVSSTMSSAKANVLKNVSTSALSNAITQVALAA         | 300 |
| 4ozt.1.A | -----  |     |
| QMEAN    |  |     |
| Chain:A  | GAGNGGSVSASGGVVSAAAGSVAGAGGSGGEALTSSNGSMVFVPSKRARM         | 350 |
| 4ozt.1.A | -----  |     |
| QMEAN    |  |     |
| Chain:A  | ELREEWISTPSPGSVPSTAPLSPSSASQNHMYGANMSNGYASPMSAGSYD         | 400 |
| 4ozt.1.A | -----  |     |
| QMEAN    |  |     |
| Chain:A  | PFSPNGKTGRDDLSPSSSLNGFSTSDASDVKKIKKGPAPRLQEELCLVCG         | 450 |
| 4ozt.1.A | -----  |     |
| QMEAN    |  |     |
| Chain:A  | DRASGYHYNALTCEGCKGFFRRSVTKNAVYCCKFGHACEMDMYMRKQCQE         | 500 |
| 4ozt.1.A | -----  |     |
| QMEAN    |  |     |
| Chain:A  | CRLKKCLAVGMRPECVVPENQCAMKRREKKAQKEKDKIQTSVCA TEIKKE        | 550 |
| 4ozt.1.A | -----  |     |
| QMEAN    |  |     |
| Chain:A  | ILDLMTCEPPSHPTCPLLPEDILAKQARN <b>IPPLSYNQ</b> LAVIYKLIWYQD | 600 |
| 4ozt.1.A | -----VKPISPEQEELIHRLVYFQN                                  | 20  |

