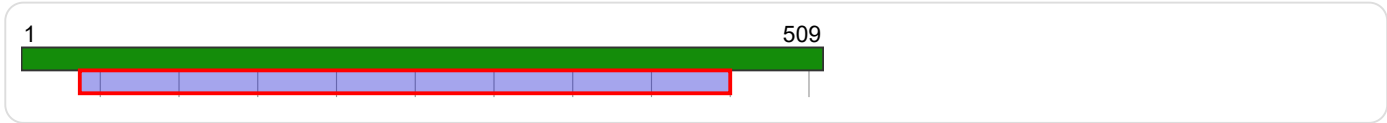


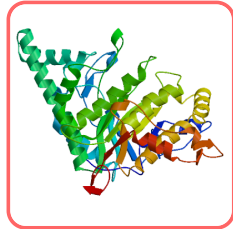


Templates Models

Order by: GMQE ▼



## Model 01



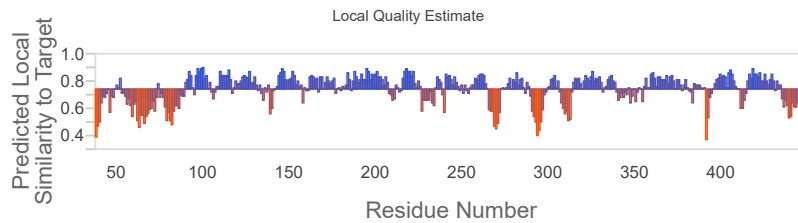
Display files

**Oligo-State** ⓘ  
Monomer

**GMQE** ⓘ  
0.64

**QMEANDisCo Global:** ⓘ  
0.74 ± 0.05

### QMEANDisCo Local ▲



### QMEAN Z-Scores ▼

#### Template ▼

template\_upload.1.A Polypeptide

**Seq Identity**  
40.49%

**Coverage**

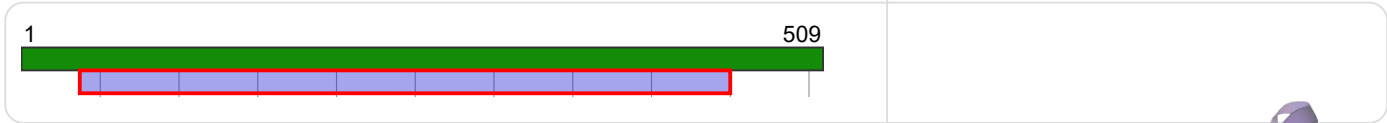
### Model-Template Alignment ▼



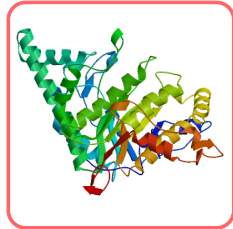


Templates Models

Order by: GMQE



## Model 01



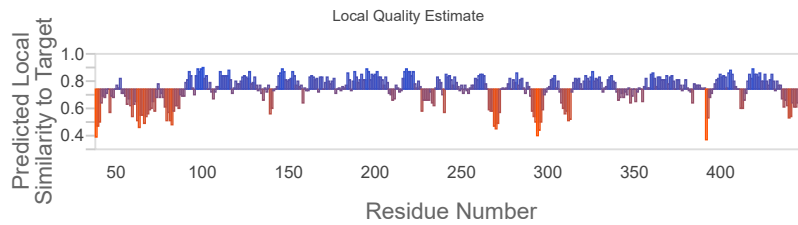
Display files

Oligo-State   
Monomer

GMQE   
0.64

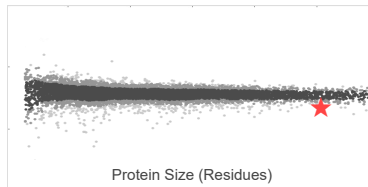
QMEANDisCo Global:   
0.74 ± 0.05

### QMEANDisCo Local



### QMEAN Z-Scores

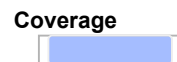
QMEAN		-2.79
Cβ		-0.07
All Atom		-0.68
solvation		0.36
torsion		-3.05



### Template

template\_upload.1.A Polypeptide

Seq Identity  
40.49%



Biounit Oligo State      Monomer  
 QSQE                      0.00  
 Method                    Unknown

**Seq Similarity** 0.40  
**Coverage** 0.81  
**Range** 38-450

**Model-Template Alignment**

```

Model_01 MGVLKFKHIFFRSFVKSSGVSQIVFTFLLI 30
template_upload.1.A -----

Model_01 PCCLTLNFRAPPVTPNYPFLWAWNAPSEFC 60
template_upload.1.A -----SFRGPLLPNRPFTTVWYANTQWC 24

Model_01 LGKFDDEPLDMSLFSFETGSPRINATGQGVTI 90
template_upload.1.A LERHGVDDVDVSVFDVYANPGQTFRGPDMTI 54

Model_01 FYVDRLGYYPIYDSITGVTVNGGIPQKISL 120
template_upload.1.A FYSSQLGTYPIYTPPT-GEPIVFGGLPQNASL 83

Model_01 QDHLDKAKKDITFYMPV-DNLGMAVTDWEE 149
template_upload.1.A IAHLARTEFDILAAIPAPDFSGLAVIDWEA 113

Model_01 WRPTWARNWPKPDVYKNRSIELVQQQNVQL 179
template_upload.1.A WRPRWAFNWDTKDIYRQRSRALVQAQHPDW 143

Model_01 SLTEATEKAKQEFKAGKDFLVETIKLGKL 209
template_upload.1.A PAPQVEAVAQDQFQGAARAWMAGTLQLGRA 173

Model_01 LRPNHLWGYLFPDCYNHHYKPGYNGSCF 239
template_upload.1.A LRPRGLWGFYGFPCYNYDFLSPNYTGQCP 203

Model_01 NVEIKRNDLSWLWNESTALYPSIYLNITQQ 269
template_upload.1.A SGIRAQNDQLGWLWGQSRALYPSIYMPAVL 233

Model_01 S-PVAATLYVRNRVREAIRVSKIPDAKSPL 298
template_upload.1.A EGTGKSQMYVQHRVAEAFRVAVAAGDPNL 262

Model_01 PVFAYIRIVFDQVLKELSDLELVYTFGET 328
template_upload.1.A PVLPIYVQIFDYDTT-NHFLPLDELEHSLGES 291

Model_01 VALGASGIVIWGTLSIMRSMKSCLELLKNYM 358
template_upload.1.A AAQGAAGVVLWVSWENTRTKESCQAIKEYM 321

Model_01 ETILNPYIINVTLAAKMCSQVLCQEQGVCI 388
template_upload.1.A DTTLGPFILNVTSGALLCSQALCSGHGRCV 351

Model_01 RKNWNSSDYHLNPDNFAIQLEK-GGKFTV 417
template_upload.1.A RRTSHPKALLLLNPASFISIQLTTPGGGPLSL 381

Model_01 RGKPTLEDLEQFSEKFYCSYSTLSCKEKA 447
template_upload.1.A RGALSLEDQAQMAVEFKCRCYPGWQAPWCE 411

Model_01 DVKDTDAVDVCIADGVCIDAF LKPPMETEE 477
template_upload.1.A RKS ----- 414

Model_01 PQIFYNASPSTLSATMFIVSILFLIISSVA 507
template_upload.1.A -----

Model_01 SL 509
template_upload.1.A --

```