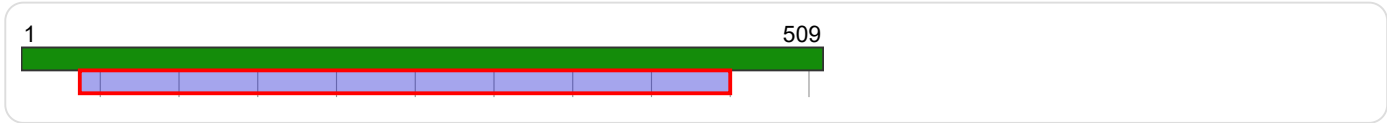


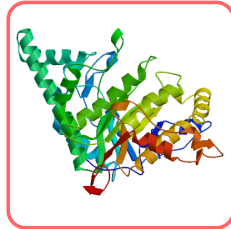



Templates Models

Order by: GMQE 



Model 01



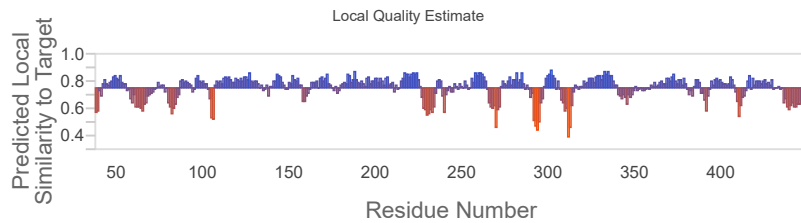
Display files 

Oligo-State ⓘ
Monomer

GMQE ⓘ
0.69

QMEANDisCo Global: ⓘ
0.75 ± 0.05

QMEANDisCo Local



QMEAN Z-Scores

Template

template_upload.1.A Polypeptide

Seq Identity
40.24%

Coverage

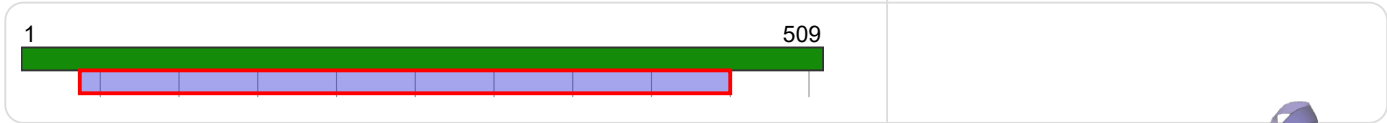

Model-Template Alignment



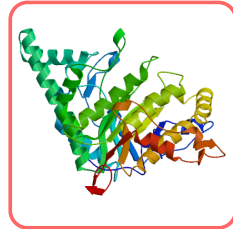


Templates Models

Order by: **GMQE** ▼



Model 01



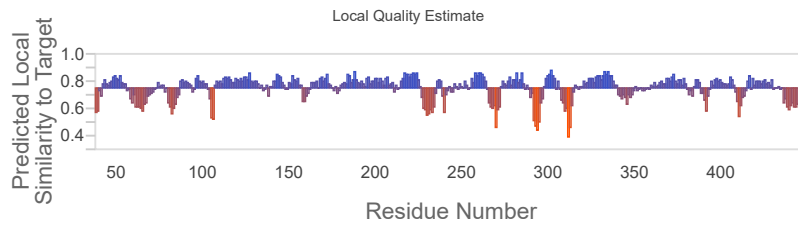
Display files ▼

Oligo-State ⓘ
Monomer

GMQE ⓘ
0.69

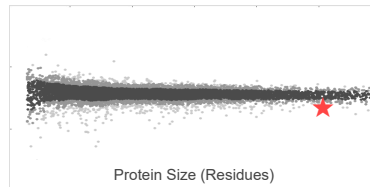
QMEANDisCo Global: ⓘ
0.75 ± 0.05

QMEANDisCo Local



QMEAN Z-Scores

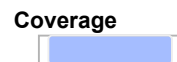
QMEAN		-2.83
Cβ		-0.17
All Atom		-0.79
solvation		0.38
torsion		-3.07



Template

template_upload.1.A Polypeptide

Seq Identity
40.24%



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 LERHGVDDVDVSVFDDVANPGQTFRGPDMTI 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 WRPTWARNWPKPKDVYKNRSIELVQQQNVQL 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 NVEIKRNDLSWLWNESTALYPSIYLNTQQ 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 VALGASGIVIWGTLSIMRSMKSCLELDNYM 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 RGALSLEDQAQMAVEFKRCRCYPGWQAPWCE 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 --

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