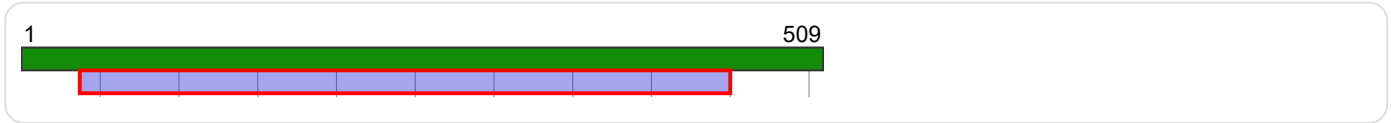
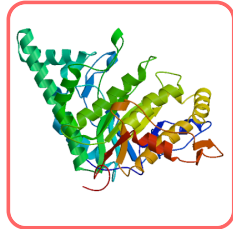


Templates Models

Order by: GMQE



Model 01



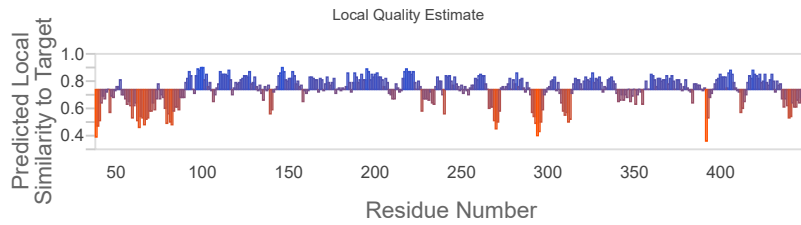
Display files

Oligo-State
Monomer

GMQE
0.63

QMEANDisCo Global:
0.74 ± 0.05

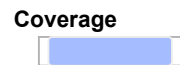
QMEANDisCo Local



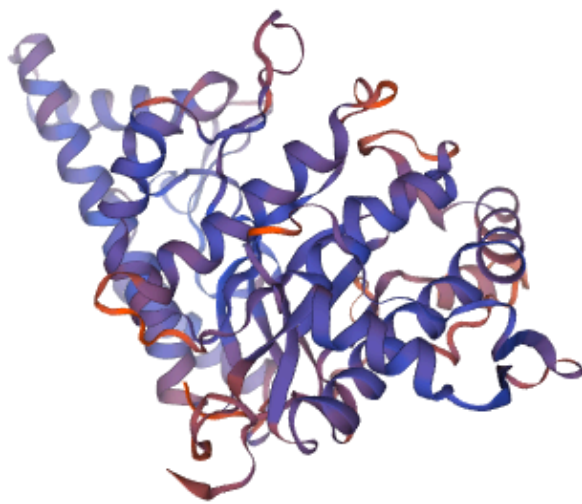
QMEAN Z-Scores

Template
template_upload.1.A Polypeptide

Seq Identity
40.24%

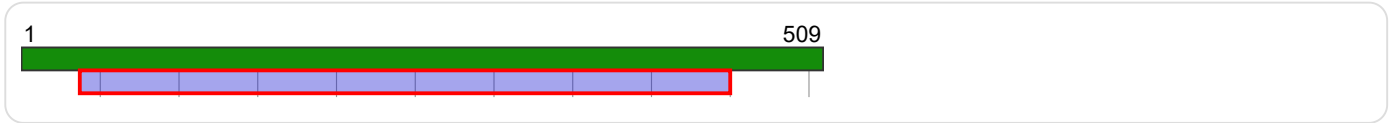


Model-Template Alignment

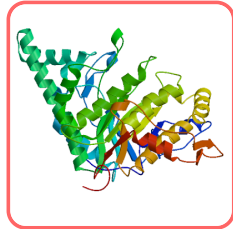


Templates Models

Order by: GMQE



Model 01



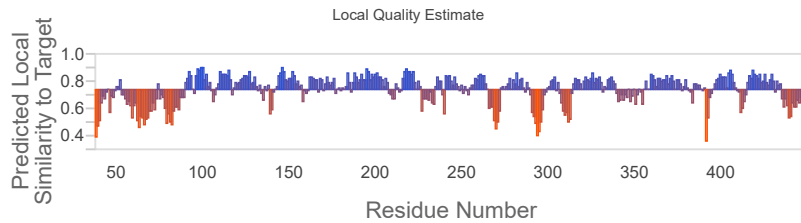
Display files

Oligo-State Monomer

GMQE 0.63

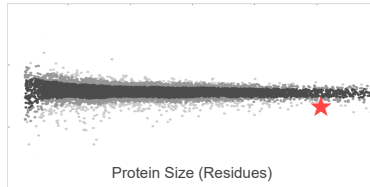
QMEANDisCo Global: 0.74 ± 0.05

QMEANDisCo Local



QMEAN Z-Scores

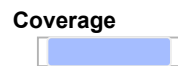
QMEAN	██████████	-2.85
Cβ	██████████	-0.40
All Atom	██████████	-0.81
solvation	██████████	0.40
torsion	██████████	-3.06



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 PCCLTLNFRAPPVDPNVPFLWAWNAPSEFC 60
template_upload.1.A -----SFRGPLLPNRPFITTVWVANTQWC 24

Model_01 LGKFDDEPLDMSLFSFDIGSPRINATGQGVTI 90
template_upload.1.A LERHGVDVDVSVFDVVANPGQTFRGPDMTI 54

Model_01 FYVDRLGYYPYIDSITGVTVNGGIPQKISL 120
template_upload.1.A FYSSQLGTYPYTPT-GEPIVFGGLPQNASL 83

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

Model_01 WRPTWARINWKPKDVYKNRSIELVQQQNVQL 179
template_upload.1.A WRPRWAFNWDTKDIYRQRSRALVQAQHPDW 143

Model_01 SLTEATEKAKQEFEKAGKDFLVETIKLGKL 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 SGIRAQNDQLGWLWQSRALYPSIYMPAVL 233

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

Model_01 PVFAYTRIVFTDQVLKFLSQDELVYTFGET 328
template_upload.1.A PVLPIYVQIIFYDIT-NHPLLDELEHSLGES 291

Model_01 VALGASGIVIWGTLSIMRSMKSCLLLDNYM 358
template_upload.1.A AAQGAAGVVLVSWENTRTKESCQAIKEYM 321

Model_01 NTILNPYIINVTLAAKMCSQVLCQEQGVCI 388
template_upload.1.A DTTLGPFILNVTSGALLCSQALCSGHGRCV 351

Model_01 RKNWNSSDYHLHNPDNFAIQDEK-GGKFTV 417
template_upload.1.A RRTSHPKALLLNPFASFSIQITPGGGPLSL 381

Model_01 RGKPTLEDLEQFSEKFCYSCYSTLSCKEKA 447
template_upload.1.A RGALSLEDQAQMAVEFKCRCPYGNQAPWCE 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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GLN 268 A
Confidence: 0.61

