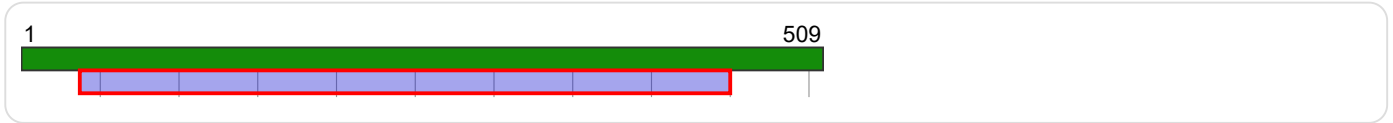
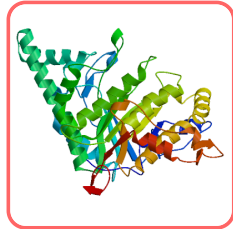



Templates Models

Order by: GMQE



Model 01



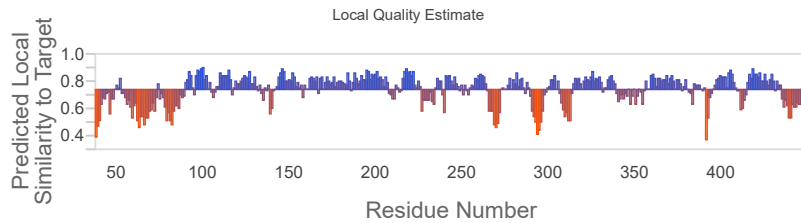
Display files 

Oligo-State ⓘ
Monomer

GMQE ⓘ
0.63

QMEANDisCo Global: ⓘ
0.74 ± 0.05


QMEANDisCo Local



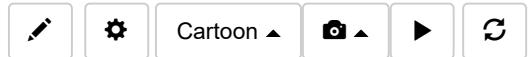
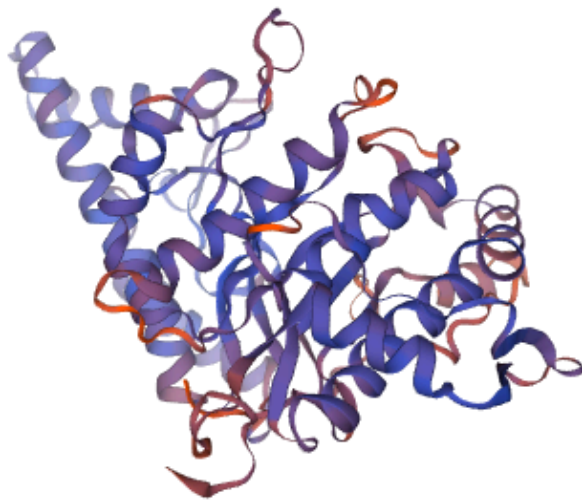
QMEAN Z-Scores

Template
template_upload.1.A Polypeptide

Seq Identity
40.49%

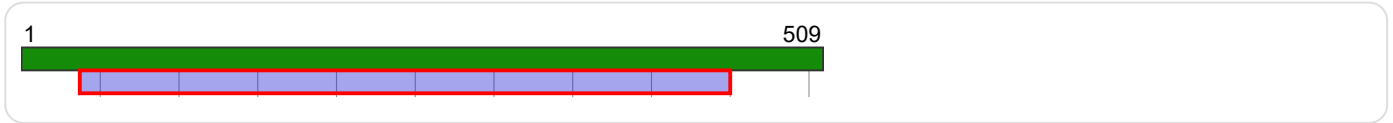
Coverage


Model-Template Alignment

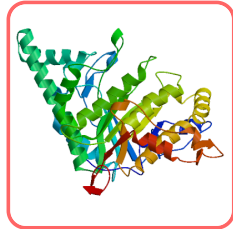


Templates Models

Order by: GMQE



Model 01



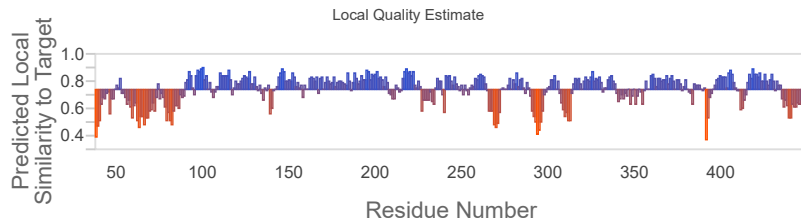
Display files

Oligo-State Monomer

GMQE 0.63

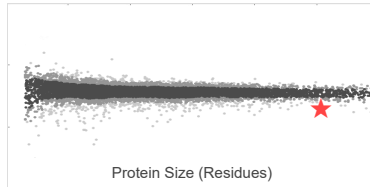
QMEANDisCo Global: 0.74 ± 0.05

QMEANDisCo Local



QMEAN Z-Scores

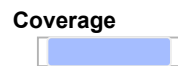
QMEAN	██████████	-3.20
Cβ	██████████	-0.29
All Atom	██████████	-0.76
solvation	██████████	0.33
torsion	██████████	-3.44



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

Model_01 LGKFDDEPLDMSLFSFDIGSPRINATGQGVTI 90
template_upload.1.A LERHGVDVDVSVFDDVANPGQTFRGPDMTI 54

Model_01 FYVDRLGYYPYIDSITGVTVNGGIPQKISL 120
template_upload.1.A FYSSQLGTYPYTPT-GEFVFGGLPQNASL 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 LRPNHLWGYLPPDCYNHHYKKPGYNGSCF 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-NHFLP(LDELEHSLGES 291

Model_01 VALGASGIVIWGTLSIMRSMKSCLLLDNYM 358
template_upload.1.A AAQGAAQVVLWVSWENTRTKESCQAIKEYM 321

Model_01 DTILNPYIINVTLAAKMCSQVLCQEQQVCI 388
template_upload.1.A DTTLGPFILNVTSGALLCSQALCSGHGRCV 351

Model_01 RKNWNSSDYHLHNPDNFAIQDEK-GGKFTV 417
template_upload.1.A RRTSHPKALLLNPAFSIQITPGGGPLSL 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 --

```

GLN 268 A
Confidence: 0.58

