

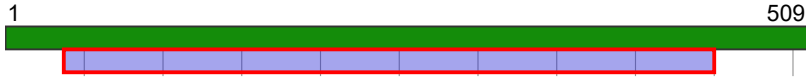


Templates

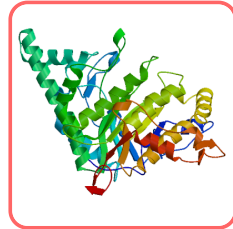
Models

Order by:

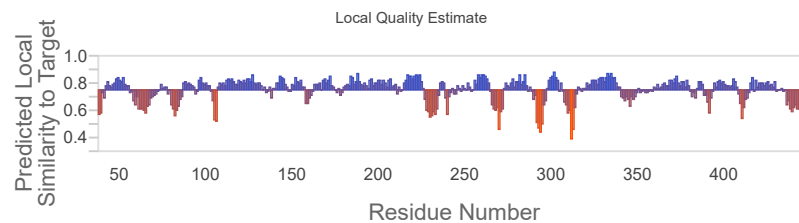
GMQE



Model 01

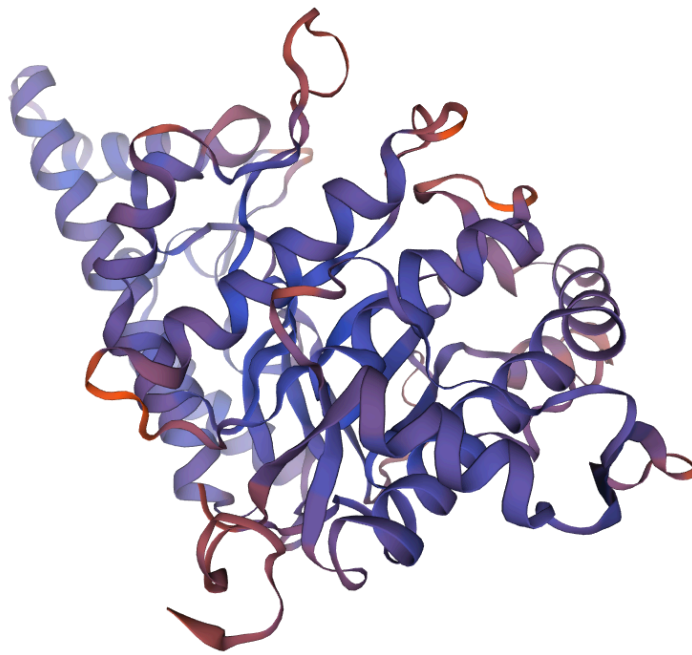


Display files ▼

Oligo-State ⓘ
Monomer**GMQE** ⓘ
0.69**QMEANDisCo Global:** ⓘ
0.75 ± 0.05**QMEANDisCo Local** ^**QMEAN Z-Scores** ▼**Template** ▼

template_upload.1.A Polypeptide

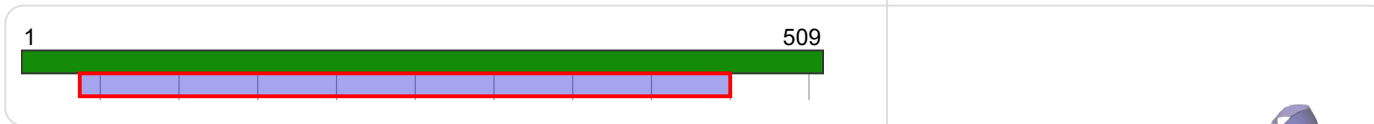
Seq Identity
40.24%**Coverage****Model-Template Alignment** ▼



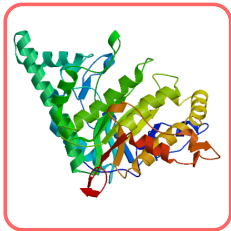
Templates Models

Order by:

GMQE



Model 01



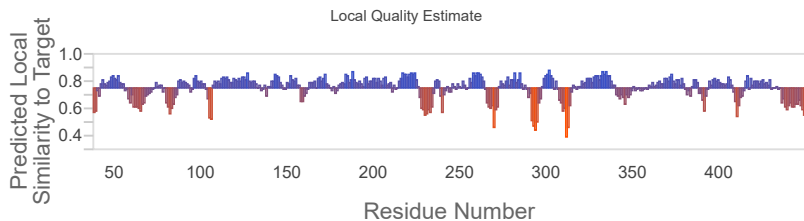
Display files

Oligo-State
Monomer

GMQE
0.69

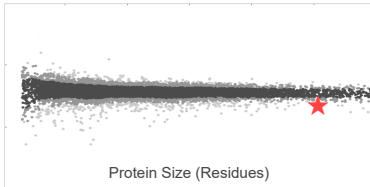
QMEANDisCo Global:
0.75 ± 0.05

QMEANDisCo Local



QMEAN Z-Scores

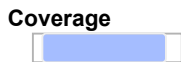
QMEAN		-2.83
Cβ		-0.17
All Atom		-0.79
solvation		0.38
torsion		-3.07



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 MGVLKFKHIFFRSFVKSSGVSQIVFTLLI 30
 template_upload.1.A -----
 Model_01 PCCLTLNFRAPPVTPNYPFLWAWNAPSEFC 60
 template_upload.1.A -----SFRGPLLPNRPFTTVWNANTQWC 24
 Model_01 LGKFDDEPLDMSLFSFETGSPRINATGQGVTI 90
 template_upload.1.A LERHGVDDVDVSVDVYANPGQTFRGPDMTI 54
 Model_01 FYVDRLGYYPIYIDSITGVTVNGGIPQKISL 120
 template_upload.1.A FYSSQLGTYPIYPTT-GEPIVFGGLPQNASL 83
 Model_01 QDHLDKAKKDITFYMPV-DNLGMAVTDWEE 149
 template_upload.1.A IAHLARTEQDILAAIPAPDFSGLAVIDWEA 113
 Model_01 WRPTWARNWKPKDVYKNRSIELVQQQNVQL 179
 template_upload.1.A WRPRWAFNWDTKDIYRQRSRALVQAQHPDW 143
 Model_01 SLTEATEKAKQEFEEKAGKDFLVETIKLGKL 209
 template_upload.1.A PAPQVEAVAQDQFQGAARAWMAGTLQLGRA 173
 Model_01 LRPNHLWGYYLFPDCYNHHYKKPGYNGSCF 239
 template_upload.1.A LRPRGLWGFYGFDCYNYDFLSPNYTGQCP 203
 Model_01 NVEIKRNDLSWLWNESTALYPSIYLNITQQ 269
 template_upload.1.A SGIRAQNDQLGWLWGQSRALYPSIYMPAVL 233
 Model_01 S-PVAATLYVRNRVREAIRVSKIPDAKSPL 298
 template_upload.1.A EGTGKSQMYVQHRVAEAFRVAVAA-GDPNL 262
 Model_01 PVFAYTRIVFTDQVLKFLSQDELVYTFGET 328
 template_upload.1.A PVLPPYQIFYDTT-NHFLPLDELEHSLGES 291
 Model_01 VALGASGIVIWGTLSIMRSMKSCLELDNYM 358
 template_upload.1.A AAQGAAGVVLWVSWENTRTKESCQAIKEYM 321
 Model_01 ETILNPYIINVTLAAKMCQVLCQEQGVCI 388
 template_upload.1.A DTTLGPFILNVTSGALLCSQALCSGHGRCV 351
 Model_01 RKNWNSSDYHLNPDNFAIQLEK-GGKFTV 417
 template_upload.1.A RRTSHPKALLLNPAFSIQLTTPGGGPLSL 381
 Model_01 RGKPTLEDLEQFSEKFYCSCYSTLSCKEKA 447
 template_upload.1.A RGALSLEDQAQMAVEFKRCYPGWQAPWCE 411
 Model_01 DVKDTDAVDVCIADGVCI DAFLKPPMETEE 477
 template_upload.1.A RKS ----- 414
 Model_01 PQIFYNASPSTLSATMFIVSILFLIISSVA 507
 template_upload.1.A -----
 Model_01 SL 509
 template_upload.1.A --