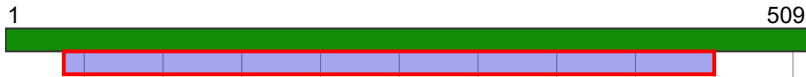


N359

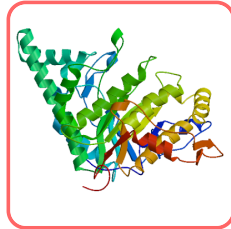
Created: Jan. 8, 2025, 3:21 p.m. at 15:21

Templates Models

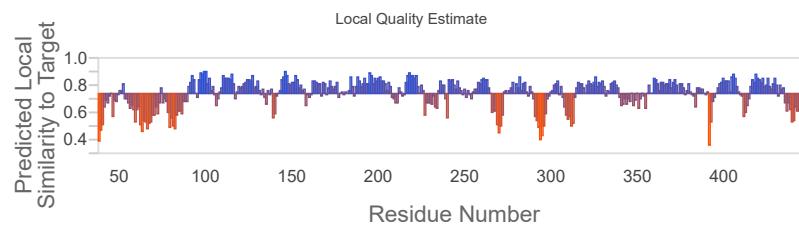
Order by: GMQE



Model 01

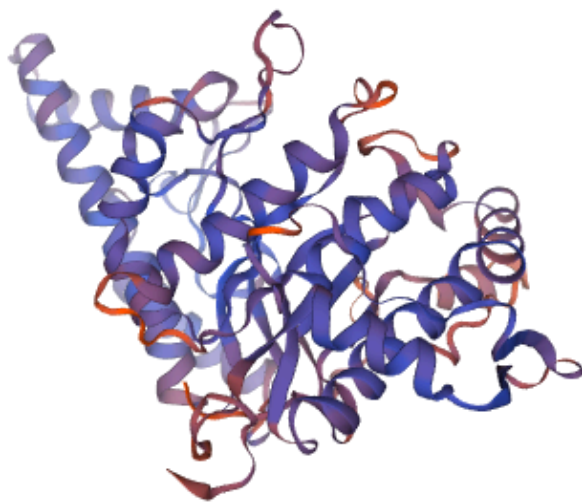


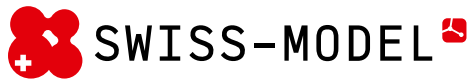
Display files

Oligo-State ⓘ
Monomer**GMQE** ⓘ
0.63**QMEANDisCo Global:** ⓘ
0.74 ± 0.05**QMEANDisCo Local** ^**QMEAN Z-Scores** v**Template** v

template_upload.1.A Polypeptide

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



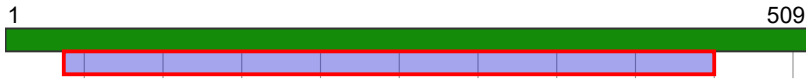


N359

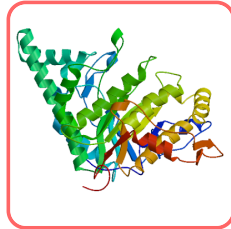
Created: Jan. 8, 2025, 3:21 p.m. at 15:21

Templates Models

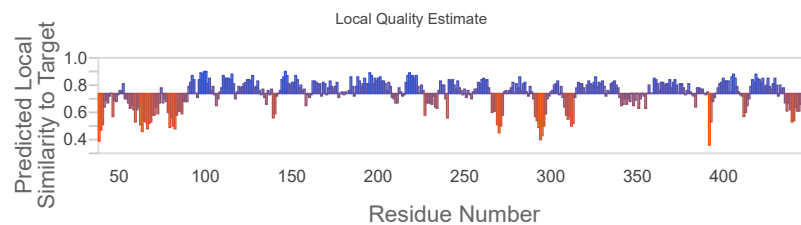
Order by: GMQE



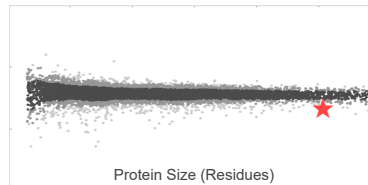
Model 01



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%**Coverage**

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 -----SFRGPLLPNRPFTTVWNANTQWC 24

Model_01 LGKFDDEPLDMSLFSFDGSPRINATGQGVTI 90
 template_upload.1.A LERHGVDDVDVSVDVAVANPGQTFRGPDMTI 54

Model_01 FYVDRLGYYPYIDSITGVTYNGGIPQKISL 120
 template_upload.1.A FYSSQLGTYPPYPTT-GEPPVFGGLPQNASL 83

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

Model_01 WRPTWARNWPKPDVYKNRSIELVQQQNVQL 179
 template_upload.1.A WRPRWAFNWDTKDIYRQRSRALVQAQHPDW 143

Model_01 SLTEATEKAKQEFKAGKDFLVETIKLGKL 209
 template_upload.1.A PAPQVEAVAQDQFQGAARAWMAGTLQLGRA 173

Model_01 LRPNHLWGYLFPDCYNHHYKKPGYNGSCF 239
 template_upload.1.A LRPRGLWGFYGFPCYNYDFLSPNYTGQCP 203

Model_01 NVEIKRNDLSWLWNESTALYPSIYLNTQQ 269
 template_upload.1.A SGIRAQNDQLGWLWQSRALYPSIYMPAVL 233

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

Model_01 PVFAYTRIVFTDQVLKFLSQDELVYTFGET 328
 template_upload.1.A PVLPPYVQIEYDNTT-NHPLPDELEHSLGES 291

Model_01 VALGASGIVIWGTLSIMRSMKSCLLLDNYM 358
 template_upload.1.A AAQGAAGVVLWVSWENTRTKESCQAIKEYM 321

Model_01 NTILNPYIINVTLAAKMCSQVLCQEQQVCI 388
 template_upload.1.A DTTLGPFILNVTSGALLCSQALCSGHGRCV 351

Model_01 BKNWNSSDYHLNPDNFAIQDEK-GGKFTV 417
 template_upload.1.A BRTSHPKALLLNPAFSIQTPGGGPLSL 381

Model_01 RGKPTLEDLEQFSEKFYCSCYSTLSCKEKA 447
 template_upload.1.A RGALSLEDQAQMAVEFKCRCPYGNQAPWCE 411

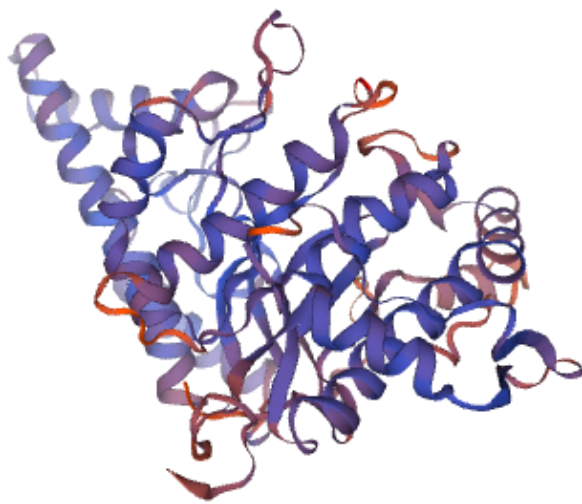
Model_01 DVKDTDAVDVCIADGVCIDAFLLKPPMETEE 477
 template_upload.1.A RKS----- 414

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

Model_01 SL 509
 template_upload.1.A --

GLN 268 A

Confidence: 0.61



Cartoon ▲

