SWISS-MODEL

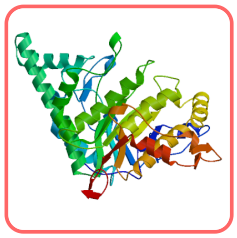
A359

Created: Jan. 8, 2025, 3:57 p.m. at 15:57

Templates Models

Order by: GMQE

Model 01



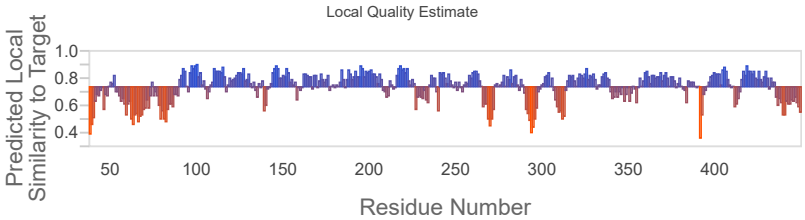
Display files

Oligo-State
Monomer

GMQE
0.63

QMEANDisCo Global:
0.74 ± 0.05

QMEANDisCo Local



QMEAN Z-Scores

Template

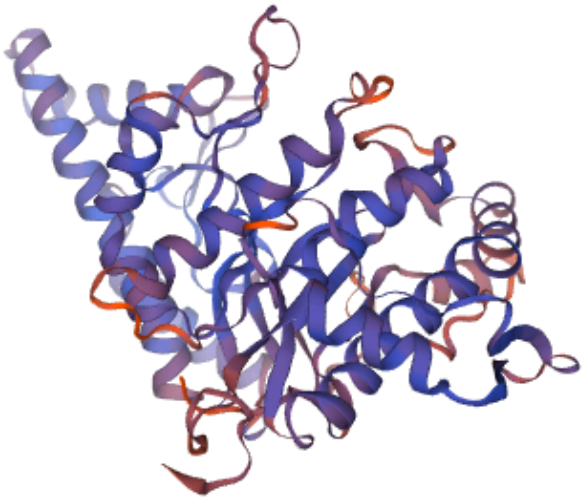
template_upload.1.A Polypeptide

Seq Identity
40.24%

Coverage

Model-Template Alignment

Petitioner Merck, Ex. 1073, p. 1



Cartoon

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SWISS-MODEL

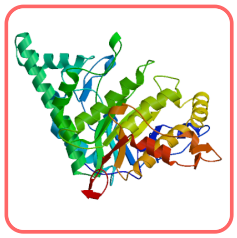
A359

Created: Jan. 8, 2025, 3:57 p.m. at 15:57

Templates Models

Order by: GMQE

Model 01



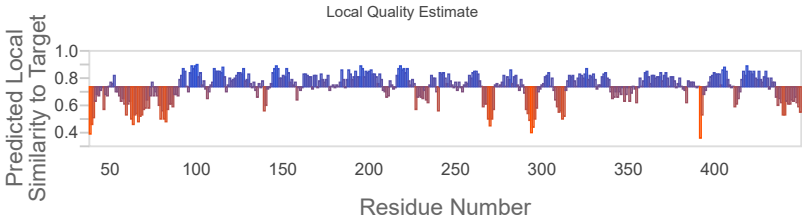
Display files

Oligo-State
Monomer

GMQE
0.63

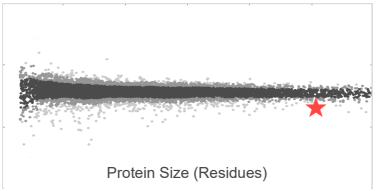
QMEANDisCo Global:
0.74 ± 0.05

QMEANDisCo Local



QMEAN Z-Scores

QMEAN	-2.99
Cβ	-0.37
All Atom	-0.76
solvation	0.35
torsion	-3.20



Template

template_upload.1.A Polypeptide

Seq Identity
40.24%

Coverage

Biounit Oligo State	Monomer
QSQE	0.00
Method	Unknown

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Seq Similarity	0.40
Coverage	0.81
Range	38-450

Model-Template Alignment

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template_upload.1.A -------SFRGPLLPNRPFTTVWNANTQWC  24

                Model_01 LGKFDEPLDMSLFSFIGSPRINATGQGVTI  90
template_upload.1.A LERHGVDVDVSVFDVVANPGQTFRGPDMTI  54

                Model_01 FYVDRLGYYPYIDSITGVTVNGGIPQKISL 120
template_upload.1.A FYSSQLGTYPYYTPT-GEPVFGGLPQNASL  83

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

                Model_01 WRPTWARNWKPKDVYKNRSIELVQQQNVQL 179
template_upload.1.A WRPRWAFNWDTKDIYRQRSRALVQAQHPDW 143

                Model_01 SLTEATEKAKQEFEKAGKDFLVETIKLGKL 209
template_upload.1.A PAPQVEAVAQDQFQGAARAWMAGTLQLGRA 173

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template_upload.1.A LRPRGLWGFYGFPDCYNYDFLSPNYTGQCP 203

                Model_01 NVEIKRNDDLSWLWNESTALYPSIYLNTQQ 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 PVLPYVQIFYDTT-NHFLPLDELEHSLGES 291

                Model_01 VALGASGIVIWGTLSIMRSMKSCLLLDNYM 358
template_upload.1.A AAQGAAGVVLWVSWENTRTKESCQAIKEYM 321

                Model_01 ATILNPYIINVTLAAKMCSQVLCQEQGVCI 388
template_upload.1.A DTTLGPFILNVTSGALLCSQALCSGHGRCV 351

                Model_01 RKNWNSSDYLHLNPDNFAIQLEK-GGKFTV 417
template_upload.1.A RRTSHPKALLLLNPASFSIQLTPGGGPLSL 381

                Model_01 RGKPTLEDLEQFSEKFYCSCYSTLSCKEKA 447
template_upload.1.A RGALSLEDQAQMAVEFKCRCYPGWQAPWCE 411

                Model_01 DVKDTDAVDVCIADGVCIDAFLKPPMETEE 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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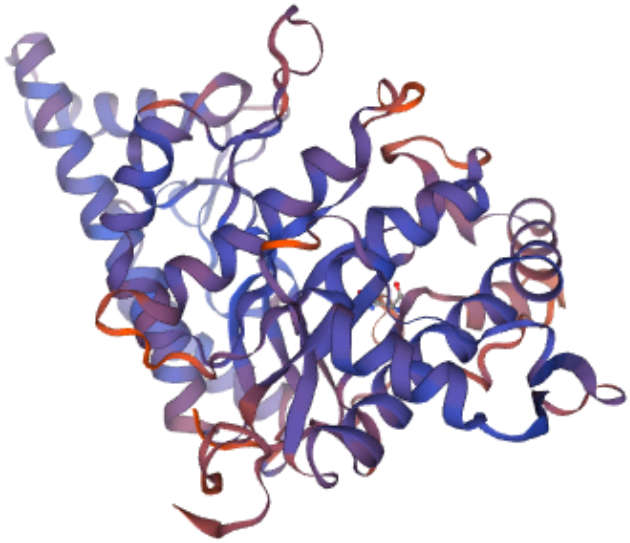

Cartoon

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