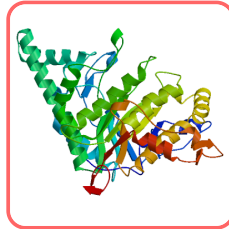


Templates Models

Order by: GMQE



Model 01



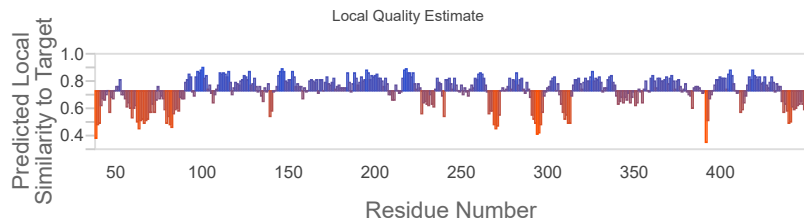
Display files

Oligo-State Monomer

GMQE 0.63

QMEANDisCo Global: 0.73 ± 0.05

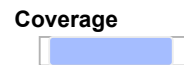
QMEANDisCo Local



QMEAN Z-Scores

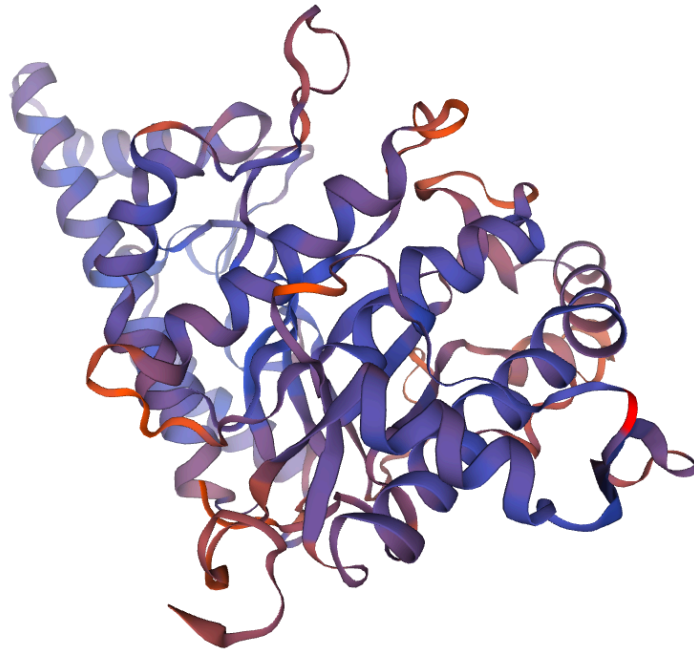
Template template_upload.1.A Polypeptide

Seq Identity 40.24%



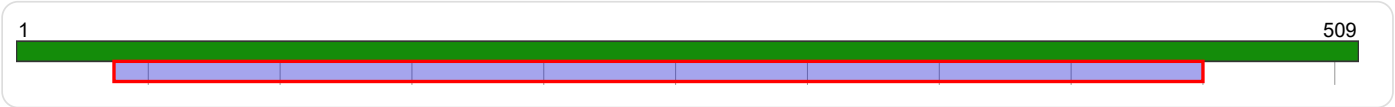
Model-Template Alignment

ASP 403 A
Confidence: 0.82

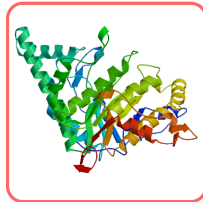


Templates Models

Order by: GMQE



Model 01



Display files

Oligo-State
Monomer

GMQE
0.63

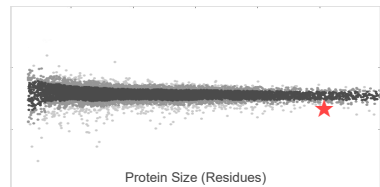
QMEANDisCo Global:
0.73 ± 0.05

QMEANDisCo Local



QMEAN Z-Scores

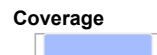
QMEAN	-2.81
C β	-0.11
All Atom	-0.73
solvation	0.41
torsion	-3.08



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 MGVLKFKKHIFRFSVKSSGVSQIVFTFLLLIPCLLTNFRAPPVDPNVPFLWAWMAPSEFCLGKFD 65
template_upload.1.A -----SFRGPLDPNRPFFTTVWVANTQWCLERHG 29

Model_01 EPLDMSLFSFDGSPRINATGQGVTFYVDRLGYYPYDSDITGVTYNGGIPQKISLQDHLDKAKKD 130
template_upload.1.A VDVDVSVDVYANPGQTFRGPDMTTFYSSQLGTYPYVTPT-GEVYFGGLPONASLIAHLARTFQD 93

Model_01 ITFYMPV-DNLGMAVTDWEWRPTWARBNWPKPDVYKNRSIELVQQQNVQLSLTEATEKAKQEFEK 194
template_upload.1.A ILAAIPAPDFSGLAVIDWEAWRPRWAFENWDTKDIYRQRSRALVQAQHPDWPAPQVEAVAQDQFQG 158

Model_01 AGKDFLVEITIKLGKLLRPNHLWGYLFPDCYNHYYKPGYNGSCFNVEIKRNDLSWLWNESTAL 259
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Model_01 YPI8IYLNMQQS-PVAATLYVRNRVREAIRVSKIPDAKSLPVEFAYTRIVFADQVLKFLSQDELVY 323
template_upload.1.A YPI8IYMPAVLEGTGKSQMYVQHRVAEAFRVAVAA-GDPNLPWLPYVQIFVDTT-NHFLPLDELEH 286

Model_01 TFGETVALGASGIVIVGTLTIMRSMKSCRLLDNYMETILNPYIINVTLAAKMCSQVLCQEQGVCF 388
template_upload.1.A SLGESAAQGAAGVVLWVSWENTRTKESCQAIKEYMDTTLGPFILNVTSGALLCSQALCSGHGRCV 351

Model_01 RKNWNSSDYHLNPDNFAIQLEK-GGKFTVRGKPTLEDLEQFSEKFCYSCYSTKSCKEKADYKDT 452
template_upload.1.A RRTSHPKALLLLNPASFSIQLTGGGGLSLRGALSLEDQAQMAVEFKRCYPGWQAPWCERKS-- 414

Model_01 DAVDVCIA DGVCIDAF LKPPMETE EPQIFYNASPSTLSATMFIVSILFLIISVVASL 509
template_upload.1.A -----

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