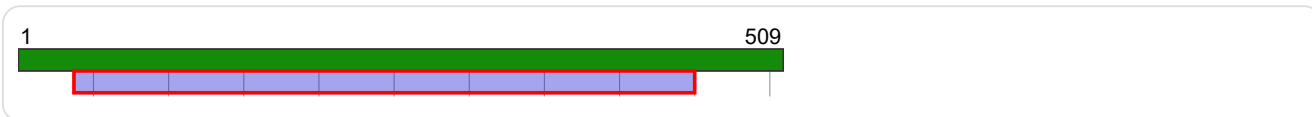
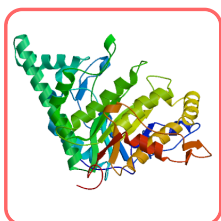



Templates Models

Order by: GMQE 





### Model 01



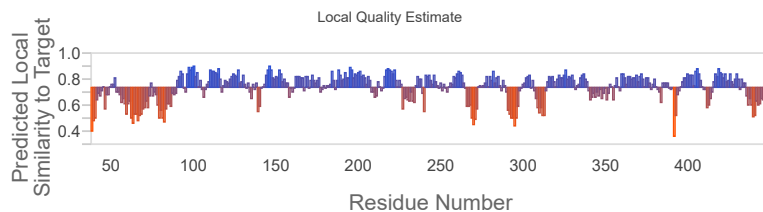
Display files 

**Oligo-State**   
Monomer

**GMQE**   
0.63

**QMEANDisCo Global:**   
0.74 ± 0.05

#### QMEANDisCo Local



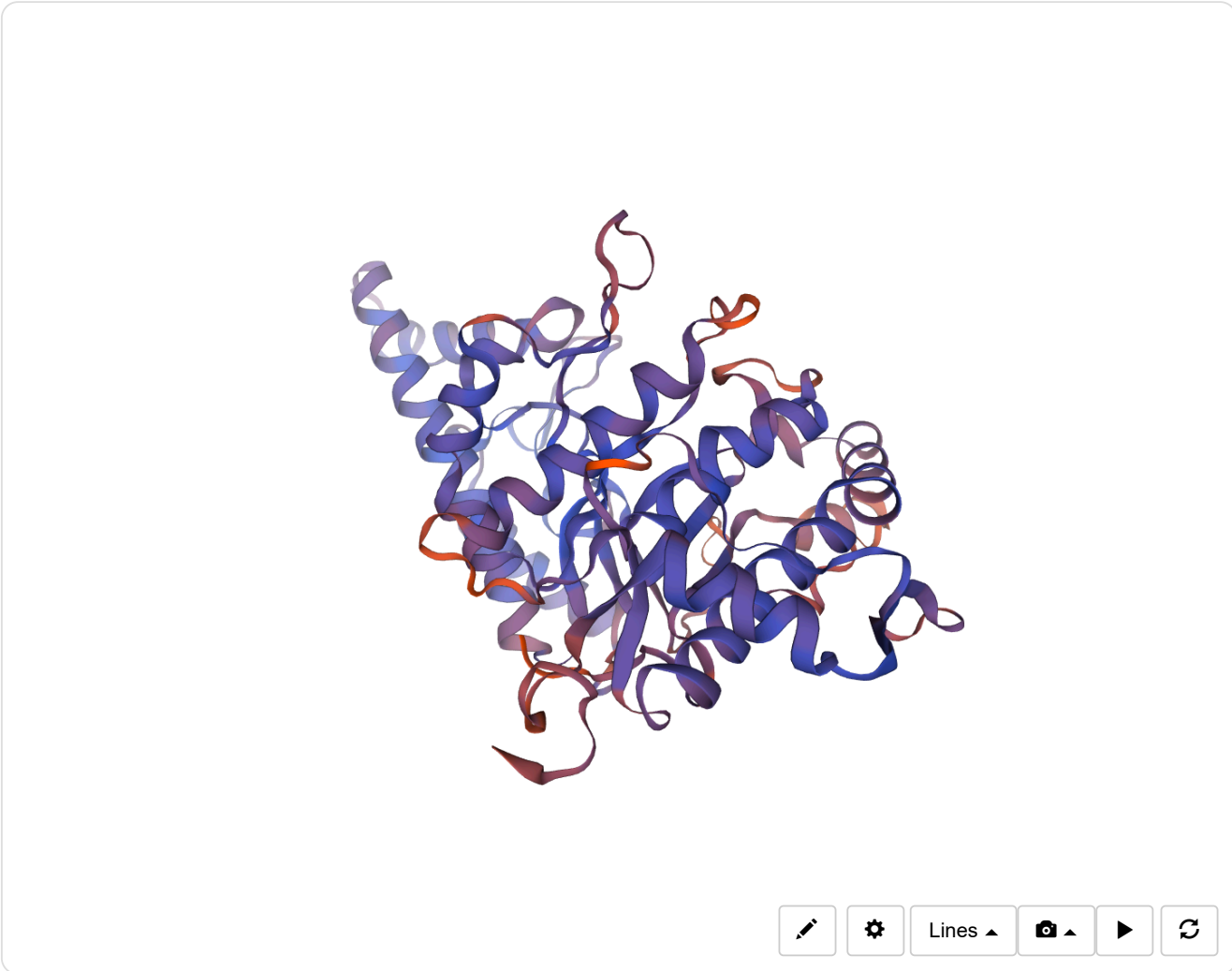
#### QMEAN Z-Scores

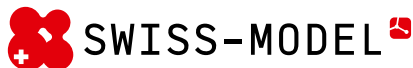
**Template**  
template\_upload.1.A Polypeptide

**Seq Identity**  
40.49%



#### Model-Template Alignment



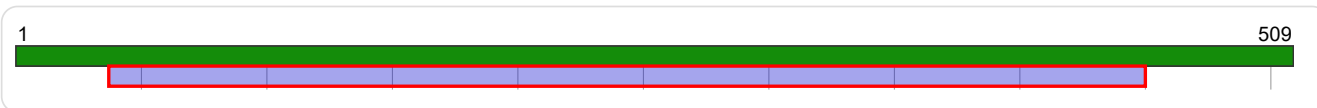


q352

Created: Dec. 4, 2024, 5:58 a.m. at 05:58

Templates Models

Order by: GMQE



Model 01



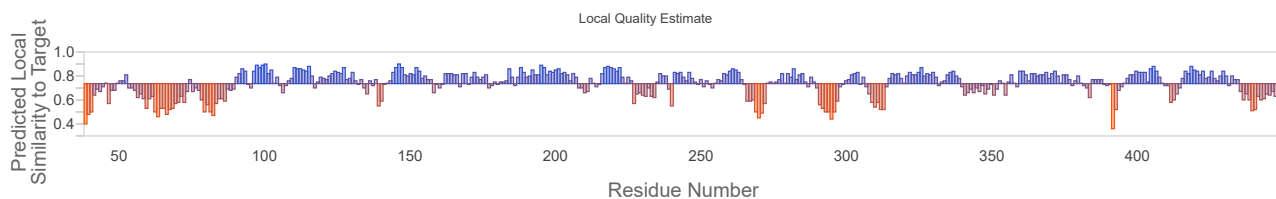
Display files

Oligo-State   
Monomer

GMQE   
0.63

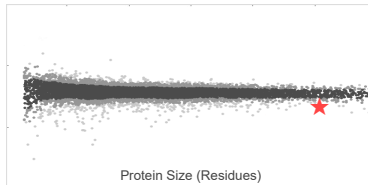
QMEANDisCo Global:   
0.74 ± 0.05

QMEANDisCo Local



QMEAN Z-Scores

QMEAN	-2.79
Cβ	-0.16
All Atom	-0.73
solvation	0.39
torsion	-3.04



Template

template\_upload.1.A Polypeptide

Seq Identity  
40.49%

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	MGVLFKFKHIFFRSFVKSSGVSQIVFTFLLLIPCLLTNFRAPPVDPNPPFLWAWVAPSEFCLGKFD	65
template_upload.1.A	-----SFRGPLDPNPPFTTVWVANTQWCLERHG	29
Model_01	EPLDMSLFSFGSPRINATGQGVTIFVDRLLGYYPYDSDITGVTVNGGIPOKISLQDHLDKAKKD	130
template_upload.1.A	VDVDVSVFDVAVANPGQTFRGPDMTIFYSQLGTYPYPTT-GERVFGGLPONASLIAHLARTFQD	93
Model_01	ITFYMPV-DNLGMAVTDWEWRPTWABNWKPKDVYKNSIELVQQQNVQLSLTEATEKAKQEFEK	194
template_upload.1.A	ILAAIPAPDFSGLAVIDWEAWRPRWAFNWDTKDIYRQRSRALVQAQHPDWPAPQVEAVAQDQFQG	158
Model_01	AGKDFELVETTKLGKLLRPNHLWGYLFPDCYNHYYKPGYNGSCFNVEIKRNDLSQLWNESTAL	259
template_upload.1.A	AARAWMAGTLQLGRALRPRGLWGFYGFPCYNYDFLSPNYTGQCPGSGIRAQNDQLGWLWGQSRAL	223
Model_01	YPSIYLNMQQS-PVAATLYVRNRVREAIRVSKIIPDAKSPLPVEAYTRIVFTDQVLKFLSQDELVY	323
template_upload.1.A	YPSIYMPAVLEGTGKSQMYVQHRVAEAEFVAVAA-GDPNLPWLPVYQIFVDTT-NHFLPLDELEH	286
Model_01	TFGETVALGASGIVTNGTLSIMRSMKSCQLLDNYMETILNPYIINVTLAAKMCISOVLCEQGVCI	388
template_upload.1.A	SLGESAAQGAAGVVLWVSWENTRTKESCQAIKEYMDTTLGPFILNVTSGALLCSQALCSGHGRCV	351
Model_01	RKNWNSSDYHLNPDNFAIQLEK-GGKFTVRGKPTLEDLEQFSEKFEYCSYSLSCKEKADYKDT	452
template_upload.1.A	RTSHPKALLLLNPASFSTQLTPGGGLSLRGLSLEDQAQMAVEFKCRCYPGWQAPWCERKS--	414
Model_01	DAVDVCIADGVCIDAFLLKPPMETEEPQIFYNASPSTLSATMFIVSILFLIISVVASL	509
template_upload.1.A	-----	

LEU 72 A  
Confidence: 0.58

