

QMEAN

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CNGC

(Created: an hour ago) Project Archive

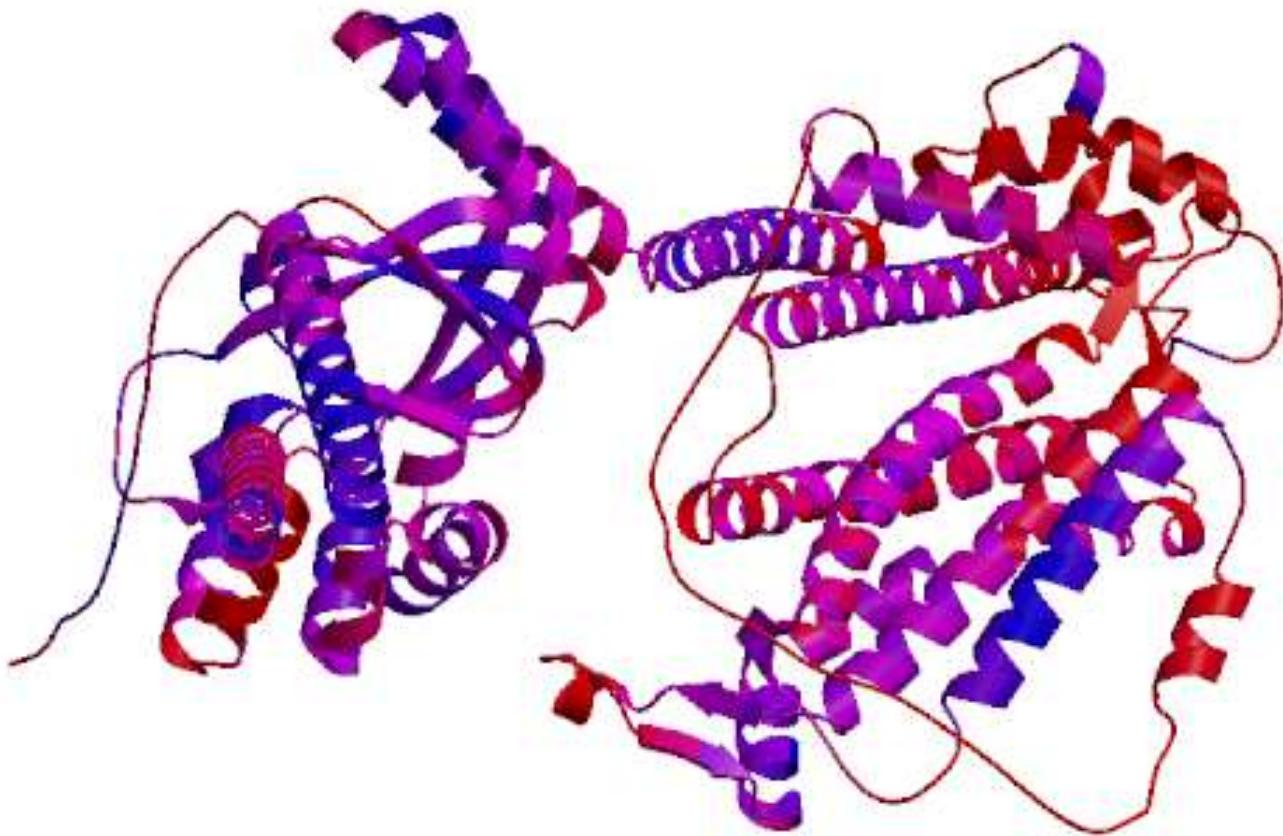
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Total model count : 17.

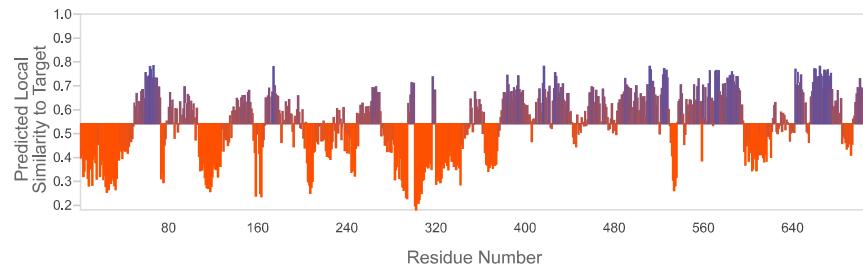
Uploaded Structure:	CNGC6AlphaFold.pdb ; CNGC6AlphaFold.pdb ; IntFOLD701.pdb ; IntFOLD702.pdb ; IntFOLD703.pdb ; ESMFold.pdb ; swissmodel02.pdb ; OmegaFold.pdb ; modeller07.pdb ; modeller02.pdb ; RoseTTAFold2.pdb ; modeller03.pdb ; modeller04.pdb ; modeller05.pdb ; modeller01.pdb ; modeller06.pdb ; swissmodel01.pdb
Method:	QMEANDisCo
QMEAN Version:	4.3.1
SMTL Version:	2024-06-20
SEQRES:	Not specified - sequence was extracted from coordinates.
Results:	JSON
Email:	camilo.tayac@ucaldas.edu.co

Quality for CNGC6AlphaFold.pdb

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Local Quality Estimate

**QMEANDisCo Global:** 0.54 ± 0.05 ⓘ

ⓘ Sequence colored by local quality:

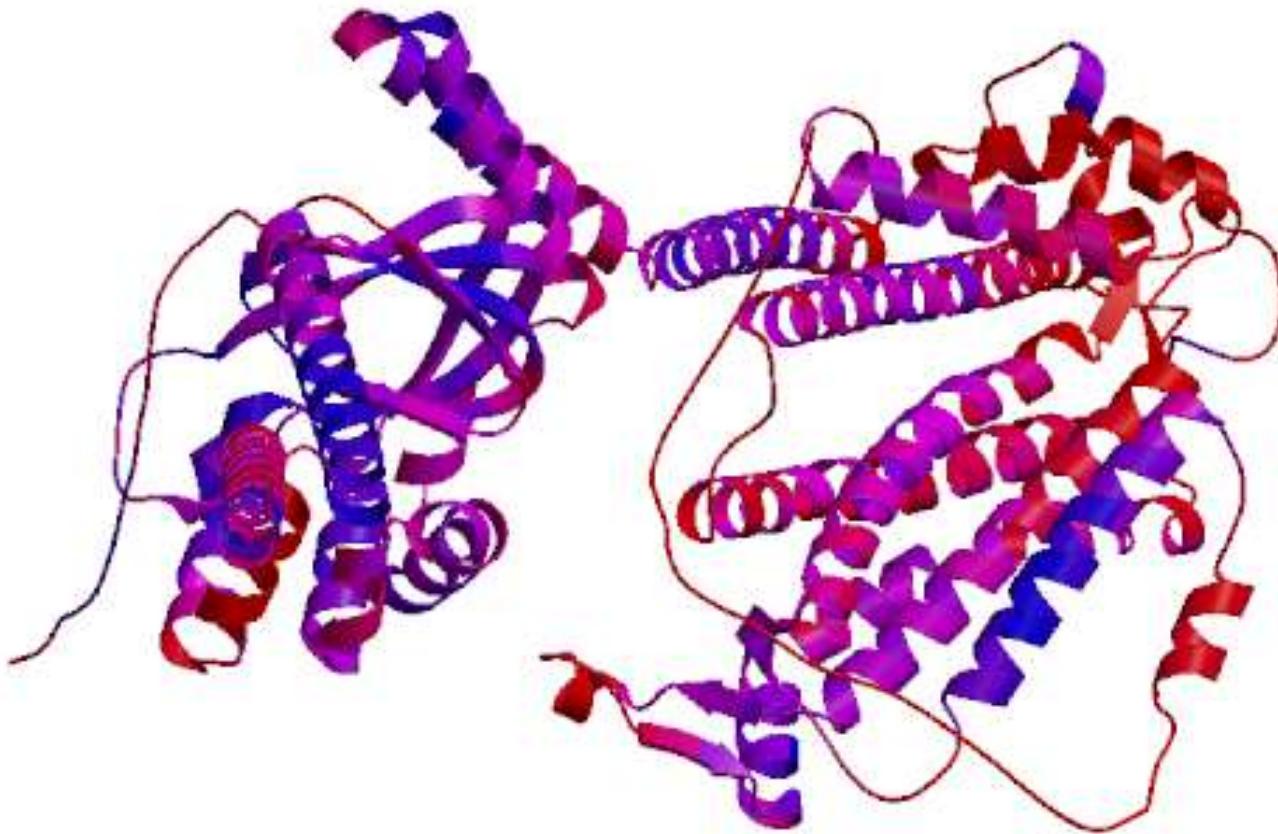


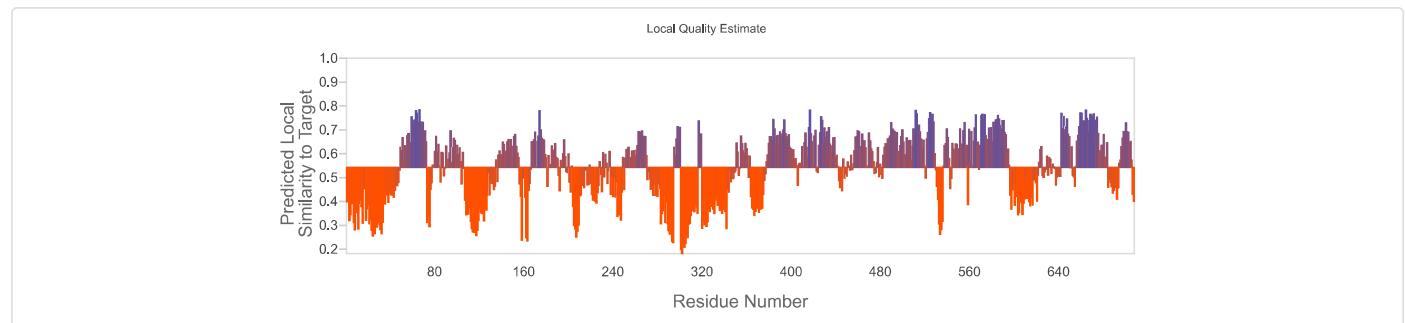
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A: MNHRQEKFVRFQDWNSEKSGEKNFPYKDGAHRRGRFGVFSNELHKSL  
A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLR  
A: PLPQVAILIVIPKLRGAKSLNTKTLKVVFFQYIPRLLRVYPLYKEV  
A: ACGNTSACHHSSLYCDDDHNTFKLNDSCPIETPNTLFDFGIFHD  
A: ISIAGLVLFSLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSH  
A: RVPMFEKMDQEQLDALCDRLRPVLYTENSFIVREGDPVDEM  
A: TVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQ  
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK
```

95
190
285
380
475
570
665
708

Quality for CNGC6AlphaFold.pdb

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QMEANDisCo Global: **0.54 ± 0.05** ⓘ

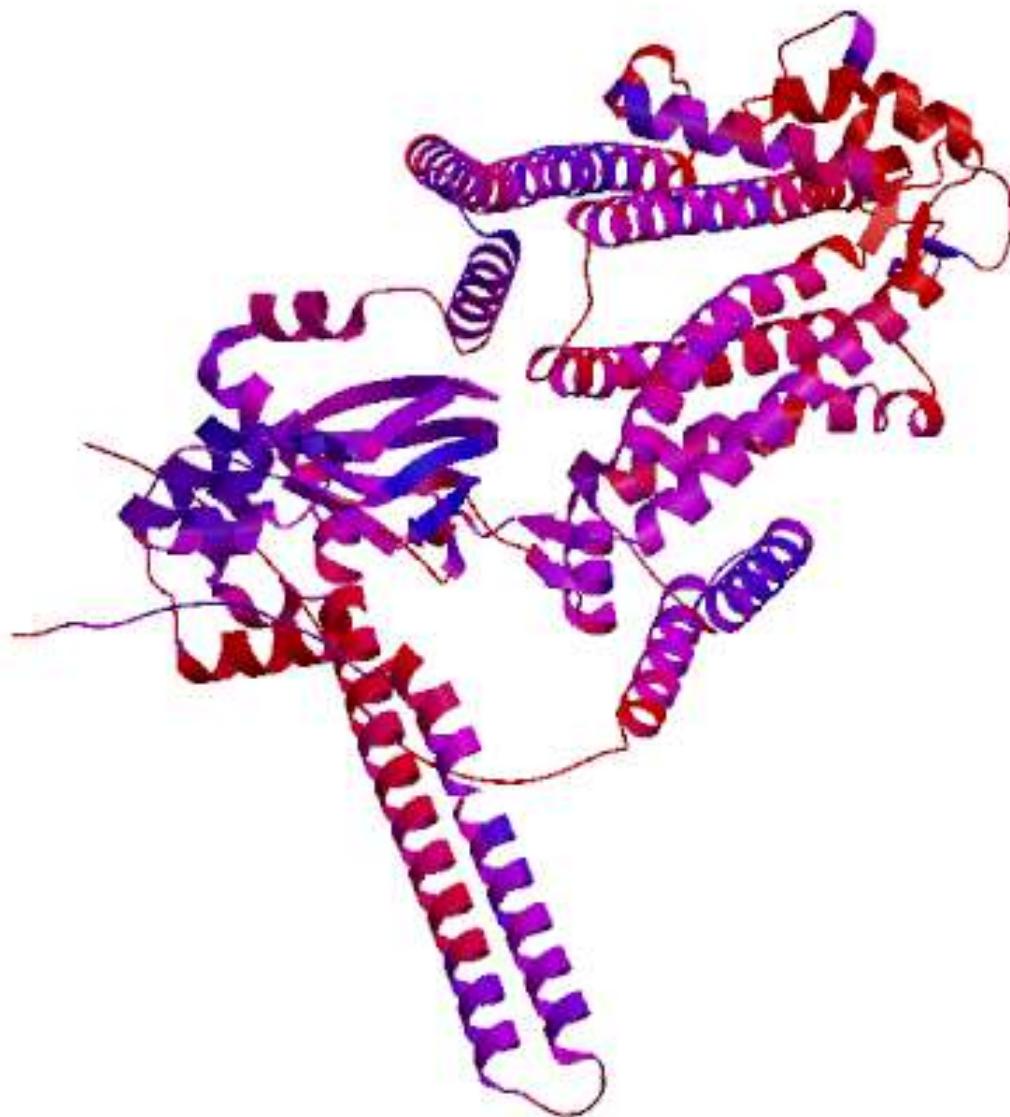
ⓘ Sequence colored by local quality:



```
A: MNHRQEKFVRFQDWNSEKSGNFPYKDGAHRRGRFGVFSNELHKSLESGSGRIKSIIHALSSCLSCLLVKSLGSEKKMFLDPQGPFLQKWNKIFVL 95
A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRISITDIEYLHFIVLQFRGFIAPSSRVFGRGVLVEDAWEIAKRYLSSYFLIDILAVL 190
A: PLPQVAILIVIPKLRGAKSLNTKTLLKFVVFFQYIPRLLRVYPLYKEVTRTSGILTETAWAGAAFNLLYMLASHVLGAFWYLFISTERESTCWQR 285
A: ACGNTSACHHSSLYCDDDHTNFIKLLNDSCPPIETPNTTLFDGFIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSSLGQNLETSTYVWEICFAVF 380
A: ISIAGLVLFLSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMMSHRLIPEHLRERIRRYEQQYKWQETRGVDEETLILNLPKDLRRDIKRHLCLALLM 475
A: RVPMEFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMLFIMRGKLLTVTTNGGRTFFFNSDYLKAGDFCGEELLTWALDPHPSSNNLPISTR 570
A: TVQALSEVEAFALVADDLKVFVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRHCRKKLEESLCEEENRLQDALARGGGSSPSLGATIYA 665
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708
```

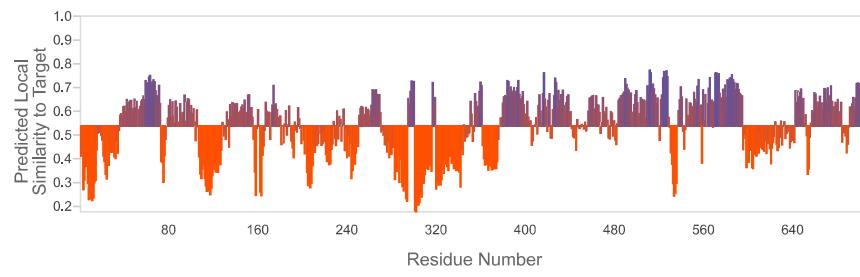
Quality for IntFOLD701.pdb

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Compare

Local Quality Estimate



QMEANDisCo Global: 0.54 ± 0.05 ⓘ

⚠ During preprocessing, 1278 atoms were removed .

```

removing atoms with zero occupancy
--> removed 0 atoms with zero occupancy
removing hydrogen atoms
--> removed 1278 hydrogen atoms

```

Sequence colored by local quality:



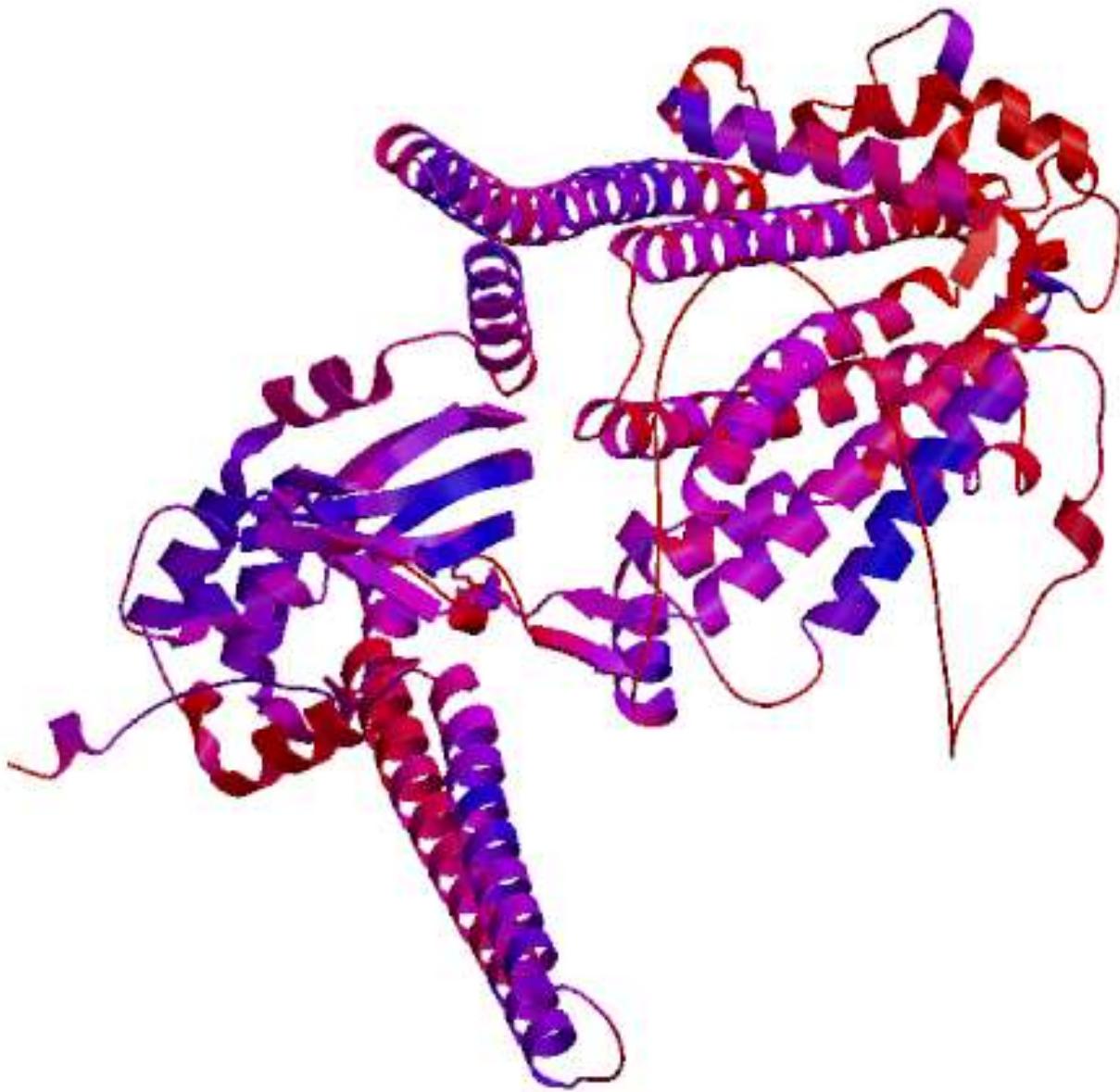
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A: MNHRQEKFVRFQDWNSEKSSEGNFPYKDGAHGRGRFGVFSNELHKSLIESGSGRIKSIIHALSSCLSCLLVKSLGSEKMLDPQGFFLQKWNKIFVLU 95
A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRISITDIFYLFHIVLQFRGFIAPSSRVFGRGVVLVEDAWEIAKRYLSSYFLIDILAVL 190
A: PLPQVAILIVIPKLRGAKSLNTKTLLKFVVFFQYIPRLLRVYPLYKEVTRTSGILTETAWAGAAFNLLYMLASHVLGAFWYLFISIERESTCWQR 285
A: ACGNTSACHHSSLYCDDDHTNFIKLLNDSCPPIETPNTTLFDGFIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSLGQNLETSTYVWEICFAVF 380
A: ISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPFHLRERIRRYEQYKWQETRGVDEETLILNLPKDLRRDIKRHLCLALLM 475
A: RVPMFEEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFCGEELLTWALDPHPSSNNLPISTR 570
A: TVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRRHCRKKLEESLCEEENRLQDALARGGGSSPSLGATIYA 665
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708

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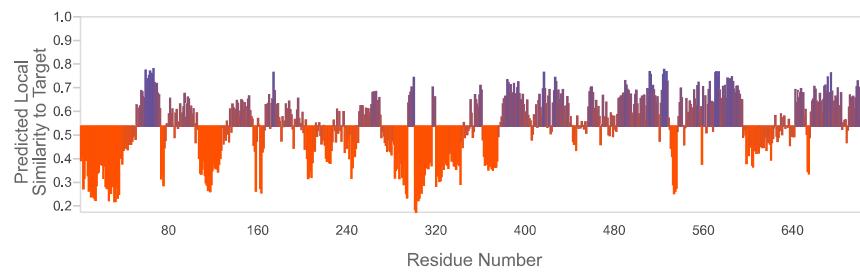
Quality for IntFOLD702.pdb

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Compare

Local Quality Estimate



QMEANDisCo Global: 0.54 ± 0.05 ⓘ

⚠ During preprocessing, 1278 atoms were removed .

```

removing atoms with zero occupancy
--> removed 0 atoms with zero occupancy
removing hydrogen atoms
--> removed 1278 hydrogen atoms

```

Sequence colored by local quality:



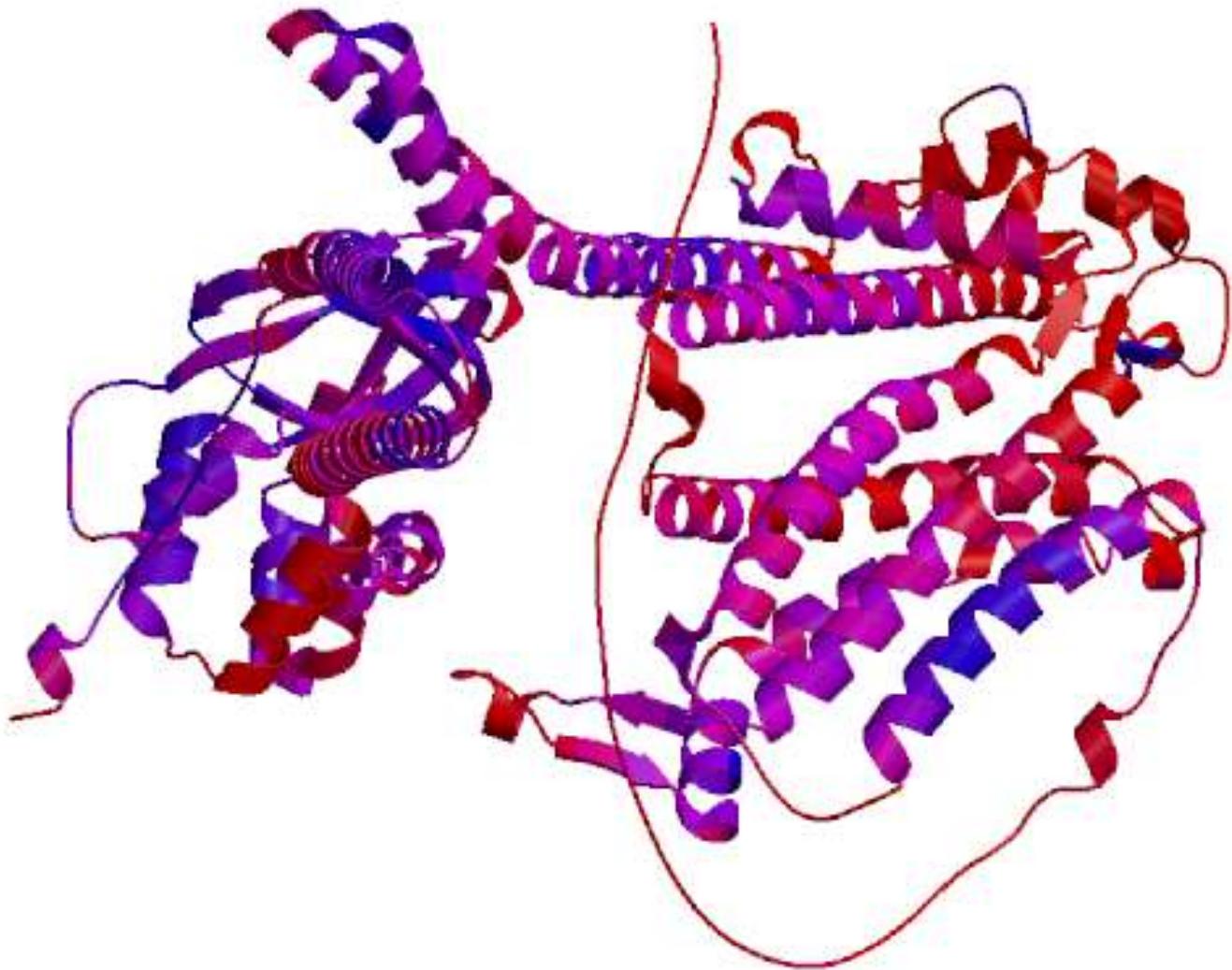
```

A: MNHRQEKFVRFQDWNSEKSSEGNFPYKDGAHGRGRFGVFSNELHKSLIESGSGRIKSIIHALSSCLSCLLVKSLGSEKMLDPQGFFLQKWNKIFVLU 95
A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRISITDIFYLFHIVLQFRGFIAPSSRVFGRGVVLVEDAWEIAKRYLSSYFLIDILAVL 190
A: PLPQVAILIVIPKLRGAKSLNTKTLLKFVVFFQYIPRLLRVYPLYKEVTRTSGILTETAWAGAAFNLLYMLASHVLGAFWYLFISIERESTCWQR 285
A: ACGNTSACHHSSLYCDDDHTNFIKLLNDSCPPIETPNTTLFDGIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSLGQNLETSTYVWEICFAVF 380
A: ISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPFHLRERIRRYEQYKWQETRGVDEETLILNLPKDLRRDIKRHLCLALLM 475
A: RVPMFEEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFCGEELLTWALDPHPSSNNLPISTR 570
A: TVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRRHCRKKLEESLCEEENRLQDALARGGGSSPSLGATIYA 665
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708

```

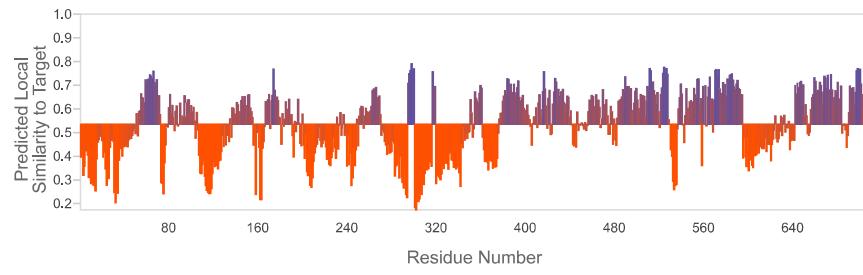
Quality for IntFOLD703.pdb

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Local Quality Estimate



QMEANDisCo Global: **0.53 ± 0.05** ⓘ

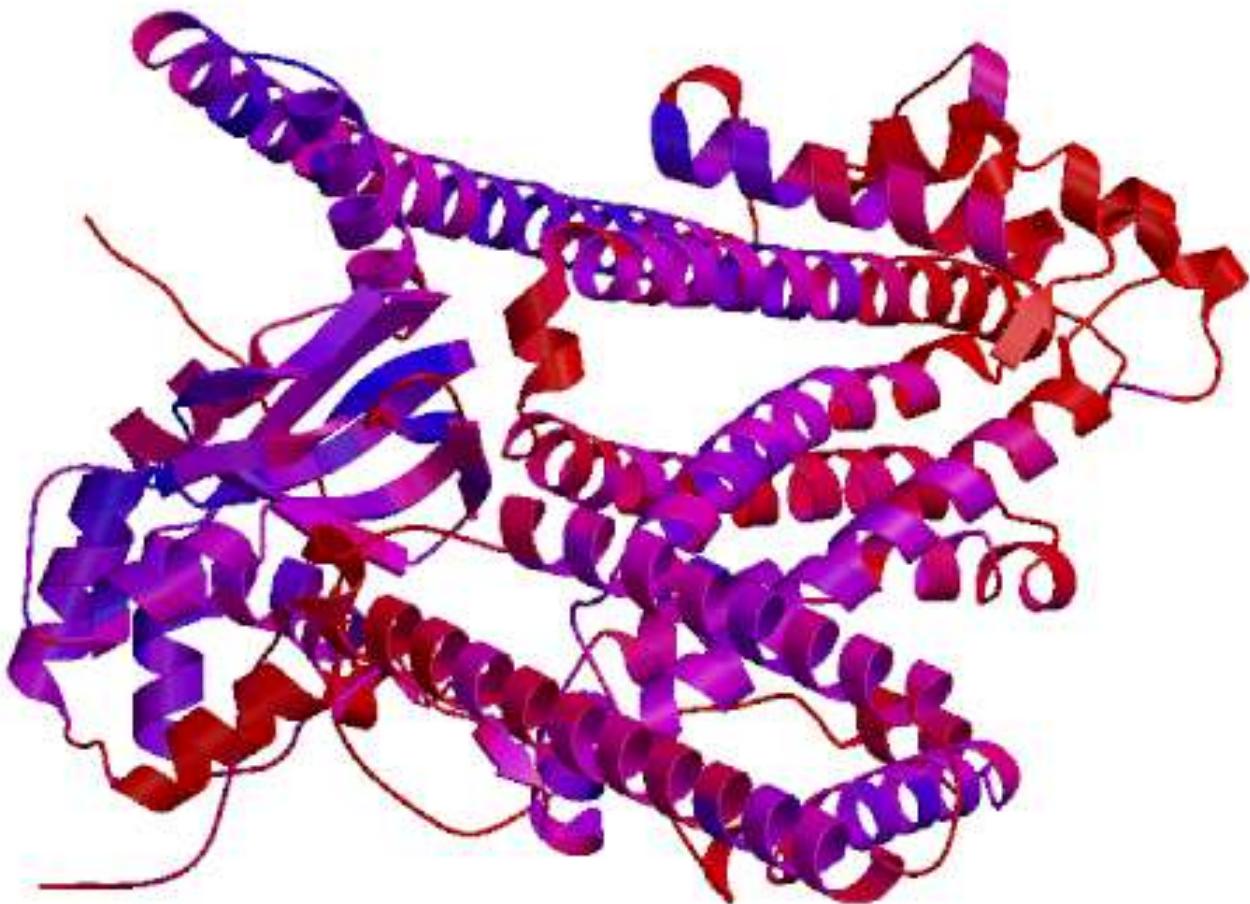
⚠ During preprocessing, 1278 atoms were removed .

```
removing atoms with zero occupancy  
--> removed 0 atoms with zero occupancy  
removing hydrogen atoms  
--> removed 1278 hydrogen atoms
```

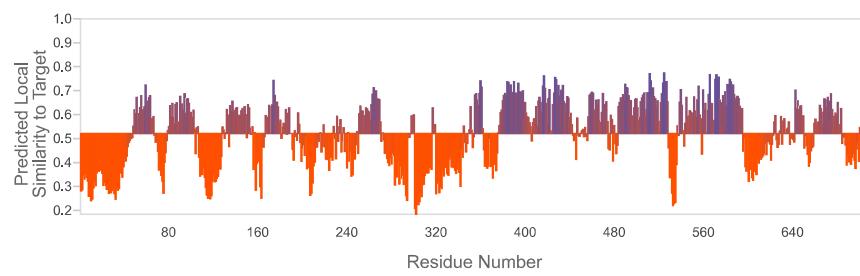
Sequence colored by local quality:

	Sequence	Length
A:	MNHRQEKFVRFQDWNSEKSEGNSFPYKDGAHGRGRFGVFSNELHKSLIESGSGRIKSIIHALSSCLSCLLVKSLGSEKMLDPQGFFLQKWNKIFV	95
A:	SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRISITDIFYLFHIVLQFRGFIAPSSRVFGRGVVLVEDAWEIAKRYLSSYFLIDILAVL	190
A:	PLPQVAILIVIPKLRGAKSLNTKTLLKFVVFFQYIPRLLRVYPLYKEVTRTSGILTETAWAGAAFNLLYMLASHVLGAFWYLFISIERESTCWQR	285
A:	ACGNTSACHHSSLYCDDDHNTFIKLLNDSCPPIETPNTTLFDGFIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSLGQNLETSTYVWEICFAVF	380
A:	ISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPFHLRERIRRYEQYKWQETRGVDEETLILNLPKDLRRDIKRHLCLALLM	475
A:	RVPMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFCGEELLTWALDPHPSSNNLPISTR	570
A:	TVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRRHCRKKLEESLCEEENRLQDALARGGGSSPSLGATIYA	665
A:	SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK	708

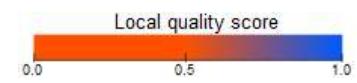
Quality for ESMFold.pdb[Downloads ▾](#)

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Local Quality Estimate

**QMEANDisCo Global:** **0.52 ± 0.05** ⓘ

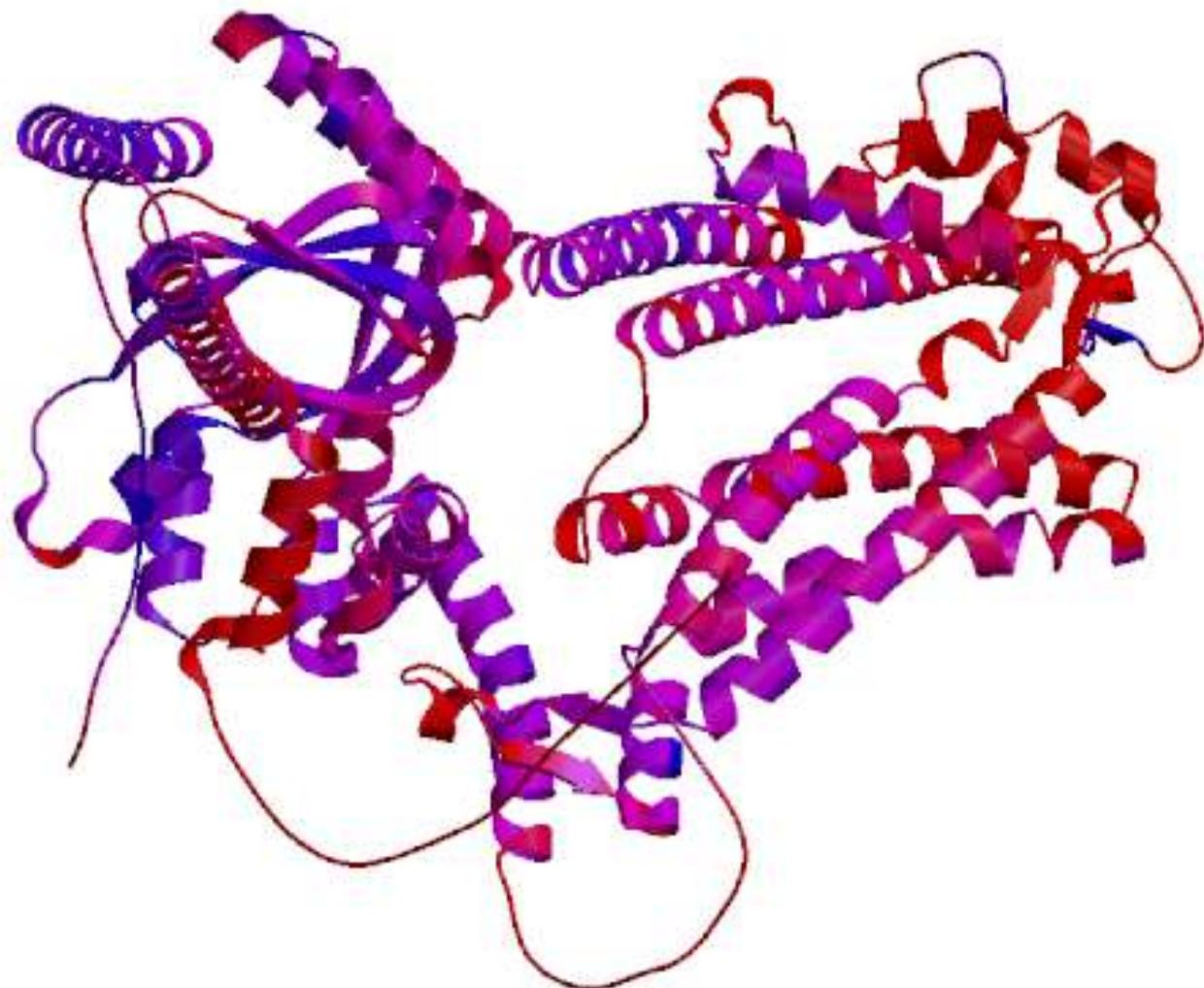
ⓘ Sequence colored by local quality:

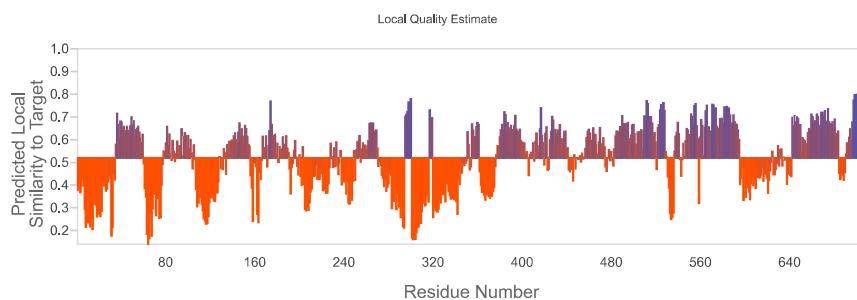


A: MNHRQEKFVRFQDWNSEKSGEFPYKDGGAHRRGFGVFSNELHKSLESGSGRIKSIIHALSSCLSCLLVKSLGSEKKMLDPQGPFLQKWNKIFV 95
A: A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLR SITDIFYLFHIVLQFRTGFIAPSSRVFGRGV LVEDANEIAKRYLSSYFLIDILAVL 190
A: PLPQVAILIVIPKL RGAKSLNTKTLK FVVFQYIPRLLRVYPLYKEVTRTSGILTETAWAGAAFNL LLYMLASHVLGAFWYLF SIERESTCWQR 285
A: ACGNTSACHHSSLYCDDDH TNIKLLNDSCPIETPNTLFDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSSLGQNLETSTYVWEICFAV 380
A: FVQALSEVEAFALVADDLK FVASQFRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRRHCRKKLEESLCEEENRLQDALARGGGSPSLGATIYA 665
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708

Quality for swissmodel02.pdb

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QMEANDisCo Global: **0.52 ± 0.05** ⓘ

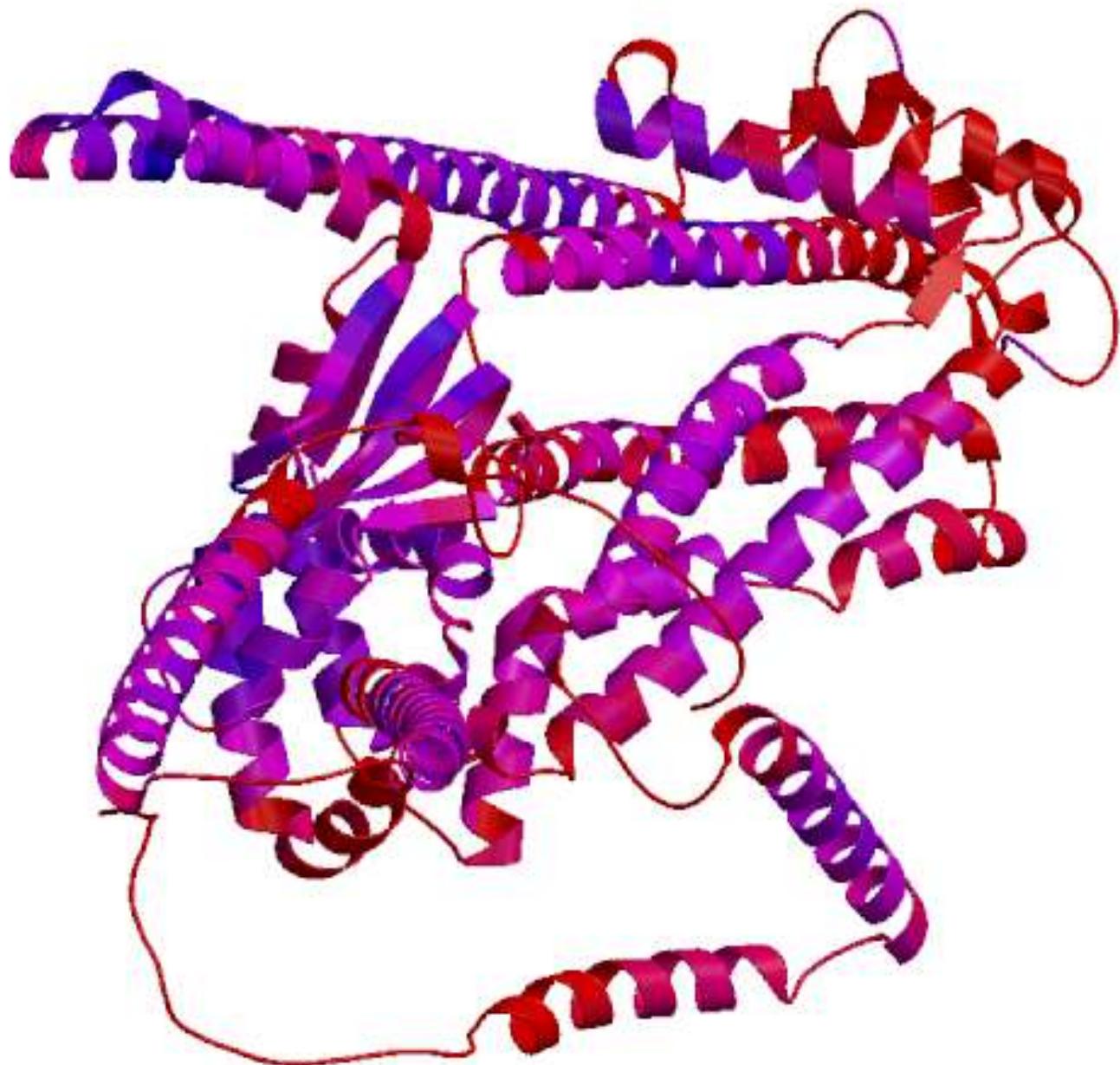
ⓘ Sequence colored by local quality:



```
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A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRISITDIEYLHFIVLQFRGFIAPSSRVFGRGVLVEDAWEIAKRYLSSYFLIDILAVL 190
A: PLPQVAILIVIPKLRLGAKSLNTKTLLKFVVFFQYIPRLLRVYPLYKEVTRTSGILTETAWAGAAFNLLYMLASHVLGAFWYLFISTERESTCWQR 285
A: ACGNTSACHHSSLYCDDDHTNFIFKLLNDSCPPIETPNTTLFDGFIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSSLGQNLETSTYVWEICFAVF 380
A: ISIAGLVLFLSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMMSHRLIPEHLRERIRRYEQYKWQETRGVDEETLILNLPKDLRRDIKRHLCLALLM 475
A: RVPMEFKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMFLFIMRGKLLTVTTNGGRTFFFNSDYLKAGDFCGEELLTWALDPHPSSNNLPISTR 570
A: TVQALSEVEAFALVADDLKVFVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRHCRKKLEESLCEEENRLQDALARGGGSSPSLGATIYA 665
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708
```

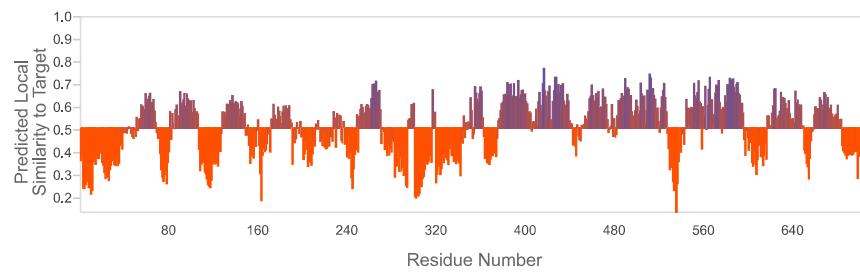
Quality for OmegaFold.pdb

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Compare

Local Quality Estimate



QMEANDisCo Global: 0.51 ± 0.05 ⓘ

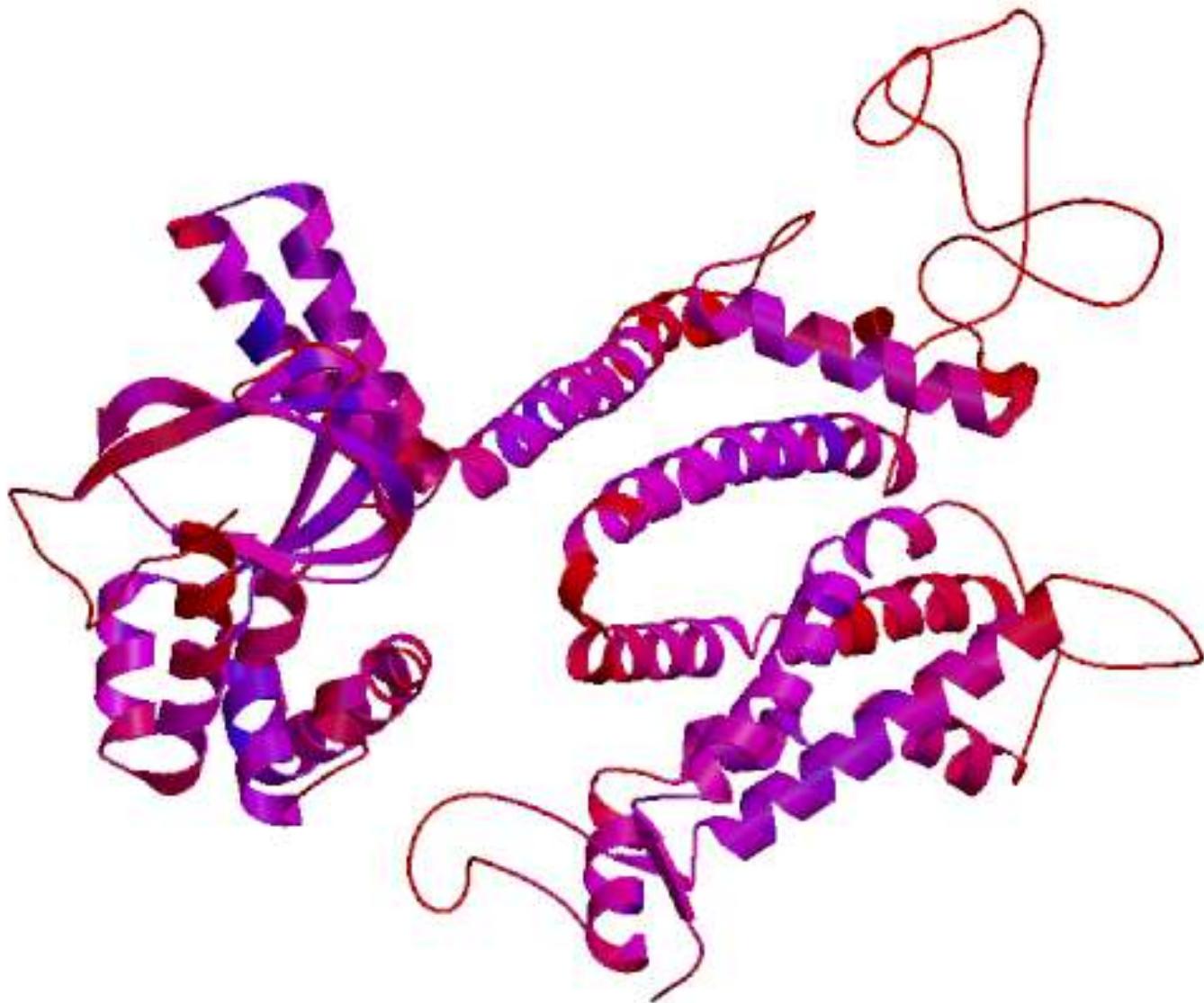
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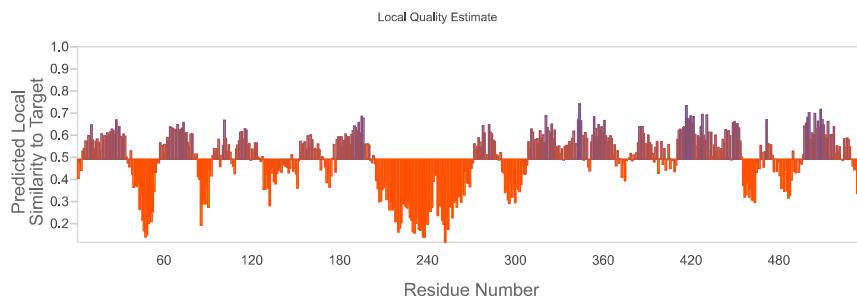


A: MNHRQEKFVRFQDWNSEKSSEGNFPYKDGGAHRRGRGVFSNELHKSLESGSGRIKSIIHALSSCLSCLLVKSLGSEKKMLDPQGPFLQKWNKIFVL 95
A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRSTITDIFYLFHVILQFRTGFIAPSSRVFGRGVLVEDAWEIAKRYLSSYFLIDILAVL 190
A: PLPQVAILIVIPKLRGAKSLNTKTLLKFVVFQYIPRLLRVYPLYKEVTRTSGILTETAWAGAAFNLLLYMLASHVLGAFWYLSIERESTCWQR 285
A: ACGNTSACHHSSLYCDDDHNTFIKLLNDSCPIETPNTLFDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSSLGQNLETSTYVWEICFAVF 380
A: ISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQQWMSSHRLLPHELRERIRRYEQYKWQETRGVDEETLILNLPKDLRRDIKRHLCLALLM 475
A: RVPMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMELFIMRGKILTVTTNGGRTGFFNSDYLKAGDFCGEELLTWALDPHPSNNLPISTR 570
A: TVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRHCRKKLEESLCEEENRLQDALARGGGSPSLGATIYA 665
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708

Quality for modeller07.pdb

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QMEANDisCo Global: **0.49 ± 0.05** ⓘ

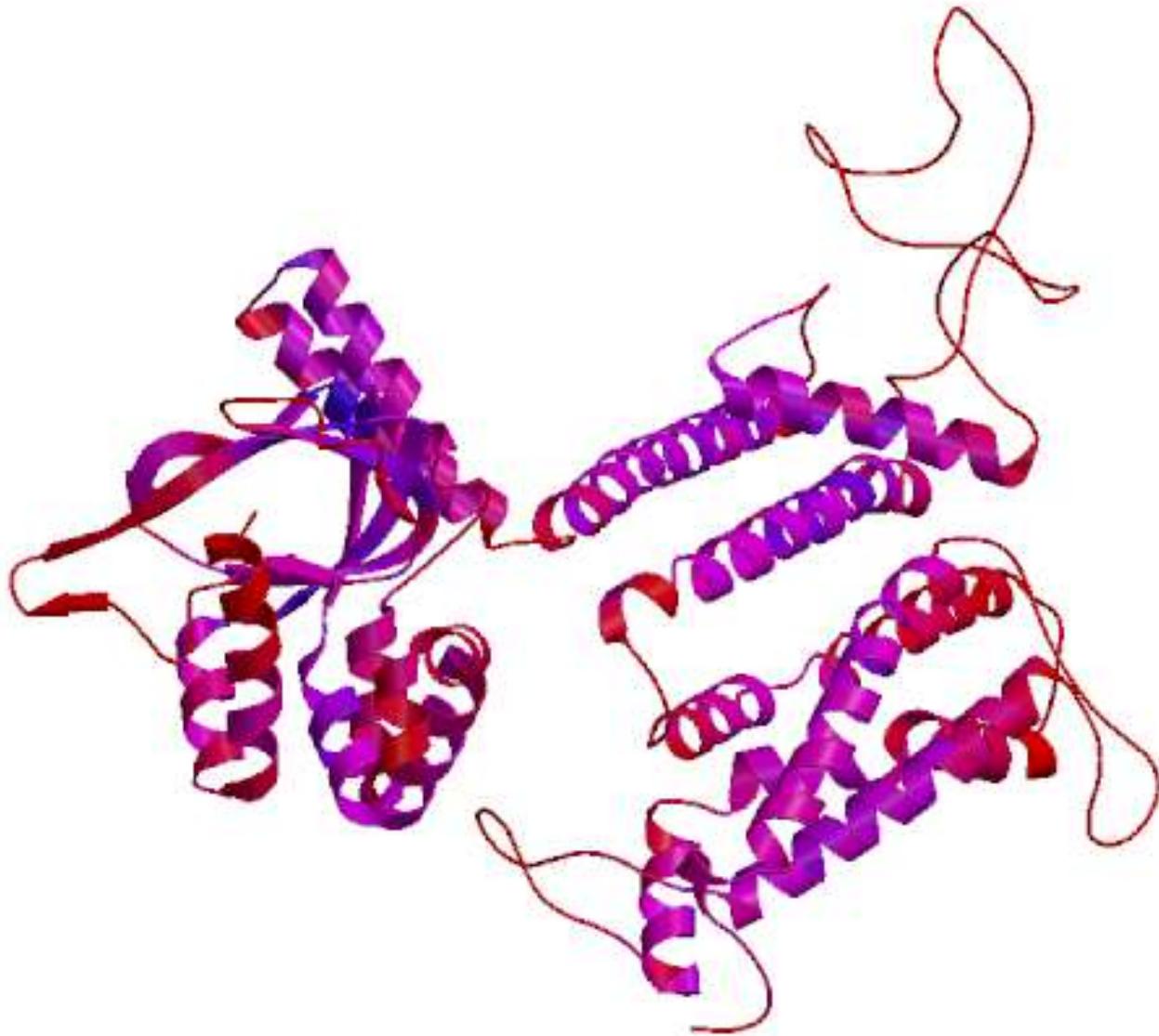
ⓘ Sequence colored by local quality:

ⓘ Local quality score

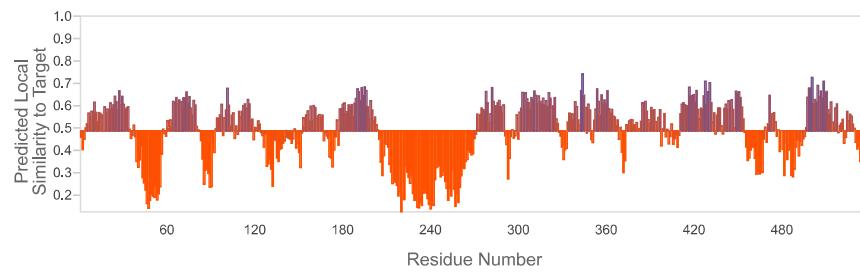
X: SEKKM	LDPLFFYIPVIDNNNKCLHLDRKMEVTASV	LRSITDIFYLFHIVLQFR	TGFIAPSSRVFG	RGVVLVE	95									
X: DAW	EIAKRYLSSYFLIDILAVLP	LPQVAILIVIPKL	RGA	SLNTK	TLLKFVV	VFFQYIPRLLRV	PLYKEVTR	TSGI	LTEA	WAGAA	FNLLY	MIA	190	
X: SHV	LGFWYLFSIERESTCWQRACGNTS	SACHHSSLYCDD	DHTNF	I	KLLNDSCPIE	TPN	TLLFDFG	GIFHDALNSGV	VE	SMDFPQK	FFYCFWW	GLQN	285	
X: LSS	LGQNLETSTYVWEICFAV	FISIAGLVLF	SFLIGNMQTYLQ	STTLR	LEEMRV	KRRDAEQ	QWM	SHRLLP	EHLRER	IRRYE	QYKWQ	ETRGV	DEETL	380
X: I	LNLPKDLRRDIKRHLCLALLMRV	PVMFEKMDEQ	LLDALCDRLRPVLY	TENS	FIVREGDPV	DEM	LFIMRGK	LLTV	TNGGRTG	FFNS	DY	LKAGDFC	475	
X: GEEL	LTWALDPHPSNNLP	ISTR	TVQALSE	VEAF	ALVADDLK	FVASQ	FRR	LHS	QLR	HTR	FR	YSQ	539	

Quality for modeller02.pdb

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Local Quality Estimate

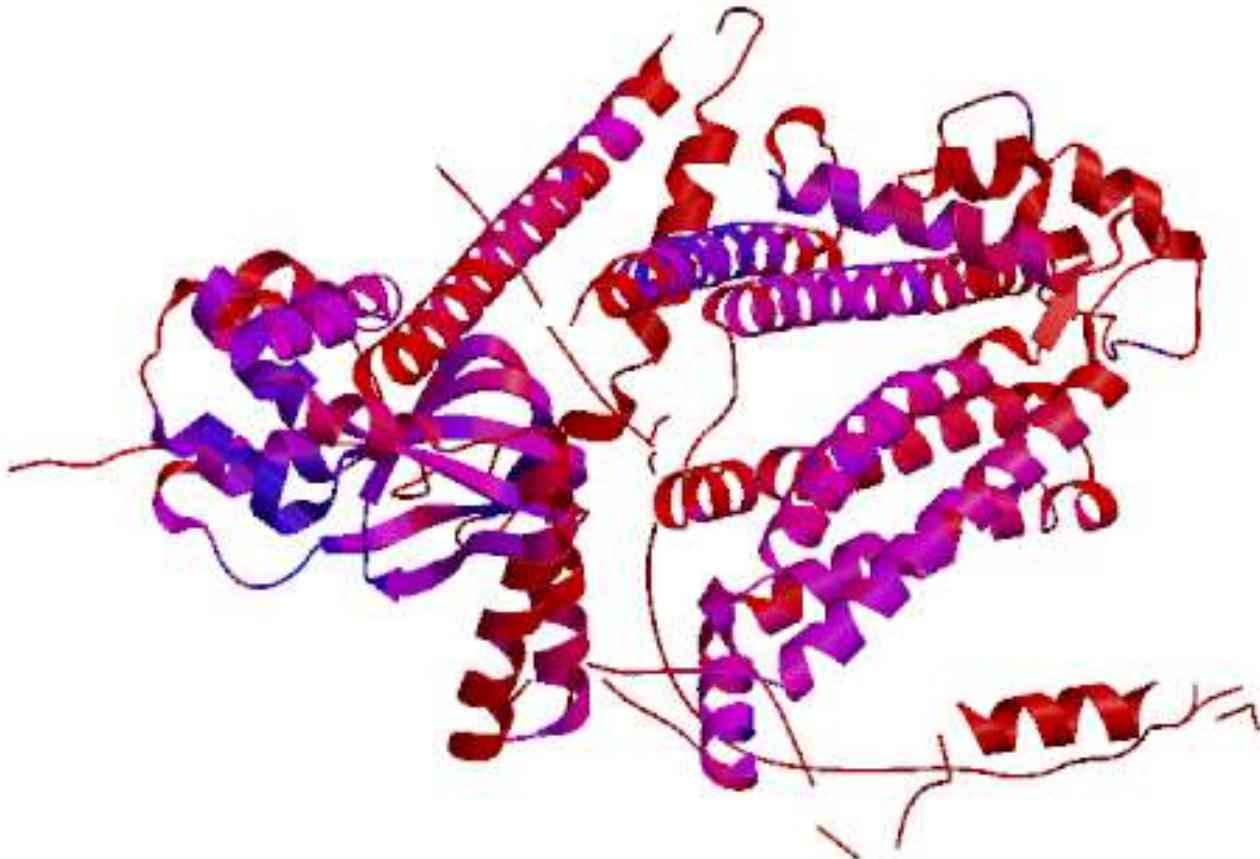
**QMEANDisCo Global:** **0.49 ± 0.05** ⓘ

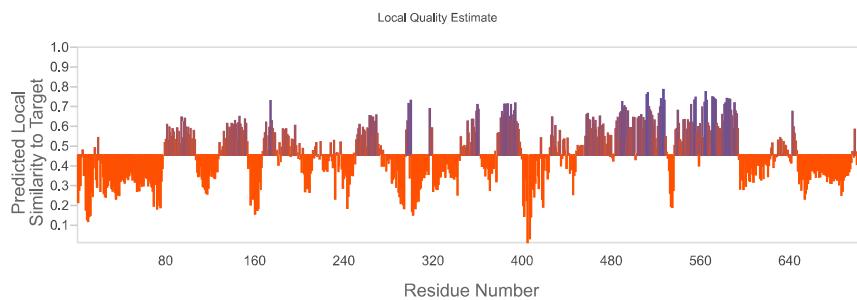
ⓘ Sequence colored by local quality:



```
X: SEKKMLDPQGPFLQKWNKIFVLSGVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRSLTIDIFYLFHIVLQFRTGFIAPSSRVFGRGVLVE 95
X: DAEWEIAKRYLSSYFLIDILAVLPLPQVAILIVIPKLRGAKSLNTKLLKFVVFQYIPRLLRVPLYKEVTRTSGILTETAWAGAAFNLLLYMLA 190
X: SHVLGAFWYLFSSIERESTCWQRACGNTSACHHSSLYCDDDHNTFIKLLNDSCPIETPNTTLDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQN 285
X: LSSLGQNLETSTYVWEICFAVFISTIAGLVLFSLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPHEHLRERIRRYEQQYKWQETRGVDEETL 380
X: ILNLPKDLRRDIKRHLCLALLMRVPMPFEKMDQLLDALCDRLRPVLYTENSFIVREGDPVDEMLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFC 475
X: GEEILLTWALDPHPSSNLPPISTRTVQALSEVEAFALVADDLKTFVASQFRRLHSKQLRHTFRFYSQ 539
```

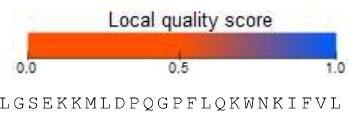
Quality for RoseTTAFold2.pdb

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**QMEANDisCo Global: 0.45 ± 0.05 ⓘ**

⚠ During preprocessing, 2074 atoms were removed .

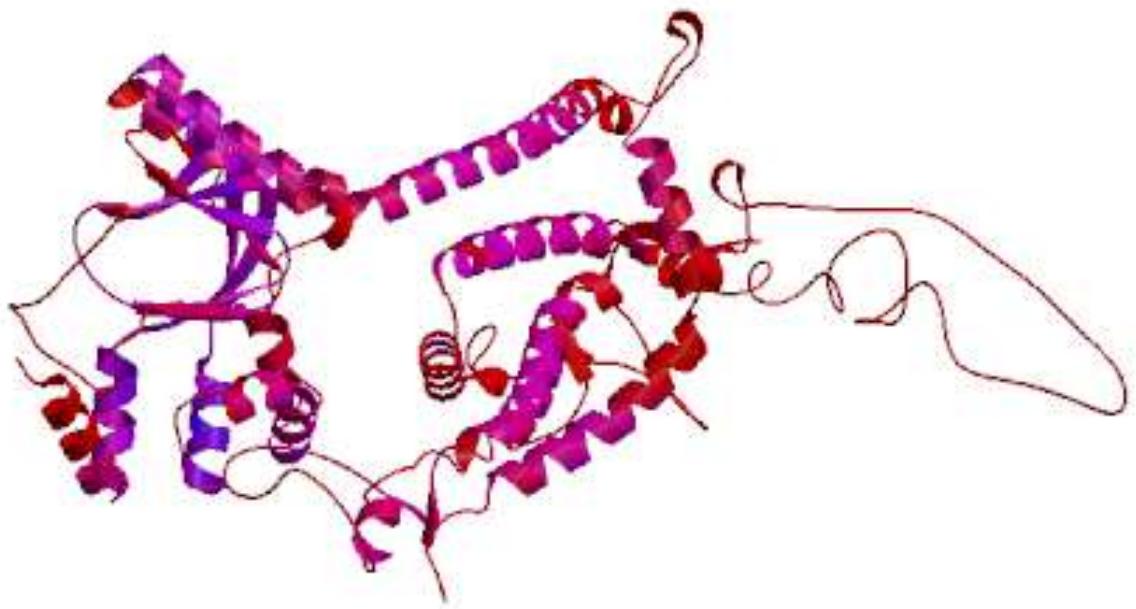
removing atoms with zero occupancy
--> removed 0 atoms with zero occupancy
removing hydrogen atoms
--> removed 1770 hydrogen atoms
residue A.GLU6 contains unknown atom A.GLU6.1HB --> removed
residue A.GLU6 contains unknown atom A.GLU6.2HB --> removed

 ⓘ Sequence colored by local quality:

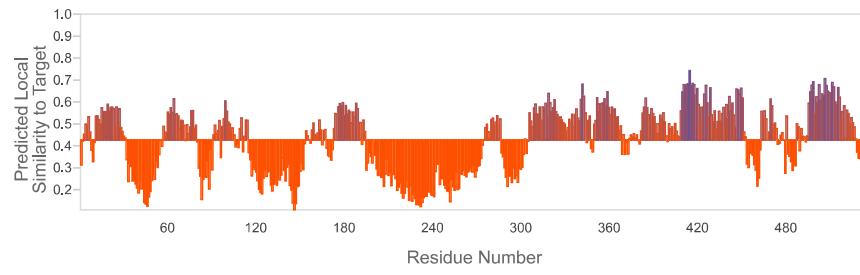
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A: MNHRQEKFVRFQDWNSEKSSEGNFPYKDGKAHRGRFGVFSNELHKSLESGSGRIKSIIHALSSCLSCLLVKSLGSEKKMLDLDPQGPFLQKWNKIFV 95
A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRISITDIFYLFHIVLQFRTGFIAPSSRVFGRGVLVEDAWEIAKRYLSSYFLIDILAVL 190
A: PLPQVAILIVIPKLRGAKSLNTKTLKFVVFFQYIPRLLRVYPLYKEVTRTSGILTETAWAGAAFNLLYMLASHVLGAFWYLFISTERESTCWQR 285
A: ACGNTSACHHSSLYCDDDHNTFIKLLNDSCPIETPNTTLFDFFGIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSSLGQNLETSTYVWEICFAVF 380
A: ISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMMSHRLLPHEHLRERIRRYEQQYWQETRGVDEETLILNLPKDLRRDIKRHLCLALLM 475
A: RVPMEFKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMELFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFCGEELLTWALDPHPSPNNLPISTR 570
A: TVQALSEVEAFALVADDLKVFVASQFRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRHCRKKLEESLCEEENRLQDALARGGGSSPSLGATIYA 665
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708
```

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Quality for modeller03.pdb

 Compare

Local Quality Estimate

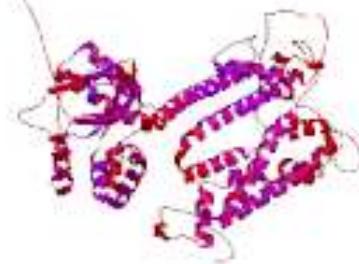
**QMEANDisCo Global: 0.43 ± 0.05** ⓘ

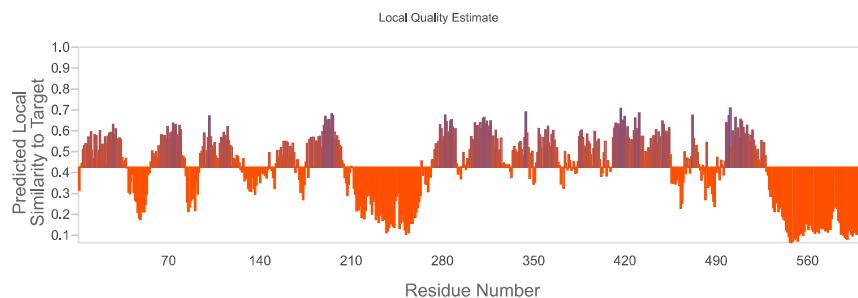
ⓘ Sequence colored by local quality:



```
X: KKMLDPQGPFLQKWNKIFVLSGVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLR  
SITDIFYLFHIVLQFRGFIAPSSRVFGRGVLVEDA 95  
X: WEIAKRYLSSYFLIDILAVLPQVAILIVIPKLRGAKSLNTKTLLKFVVFFQYIPRLLRVY  
PLYKEVTRTSGILTETAWAGAAFNLLLYMASH 190  
X: VLGAFWYLFSIERESTCWQRACGNTSACHSSLYCDDDHTNFIKLLNDSCPIETPNTTL  
FDGIFHDALNSGVVESMDFPQKFFYCFWWGLQNL 285  
X: SLGQNLETSTYVWEICFAVFISTAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAE  
QWMSHRLLPEHLRERIRRYEQYKWQETRGVDEETLIL 380  
X: NLPKDLRRDIKRHLCLALLMRVPMPFEKMDEQLLDALCDRLRPVLYTENSFIVREG  
DPVDEMLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFCGE 475  
X: ELLTWALDPHPSNLPISTRVQALSEVEAFALVADDLKFPVASQFRRLHSKQLRHTFRFYS  
536
```

Quality for modeller04.pdb

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QMEANDisCo Global: **0.42 ± 0.05** ⓘ

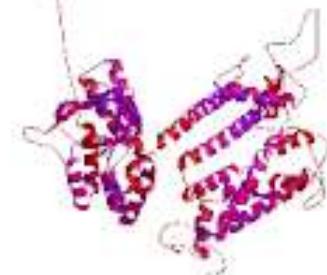
ⓘ Sequence colored by local quality:

ⓘ Local quality score

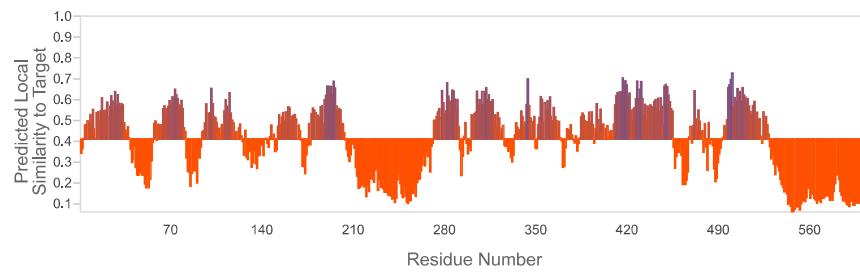
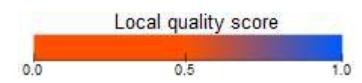
X: SEKKMILDQGPFLQKWNKIFVLSVCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVRLSITDIFYLFHVVLQFRTGFIAPSSRVFGRGVLVE 95
X: DAWEIAKRYLSSYFLIDILAVLPLPQVAILIVIPKLRGAKSLNTKTLLKFVVVFQYIPRLLRVYPLYKEVTRTSGILTEAWAGAAFNLLLYMLA 190
X: SHVLGAFWYLFSIERESTCWQRACGNTSACHHSSLYCDDDHNTFIKLLNDSCPIETPNNTLFDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQN 285
X: LSSLGQNLETSTYYWEICFAVFISIAGLVLFSLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPPEHLRERIRRYEQQYKWQETRGVDEETL 380
X: IILNLPKDLRRDIKRHLCALLMRVPFMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFC 475
X: GEELLTWALDPHPSSNNLPISTRTVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRHCRKKLEESLCEEEN 570
X: RLQDALARGGGSSPSLGATIYASRFAANALRALRH 605

Quality for modeller05.pdb

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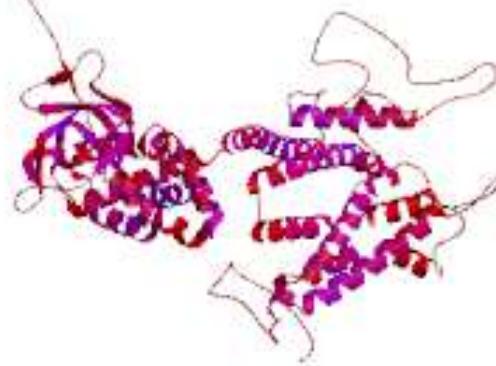
Local Quality Estimate

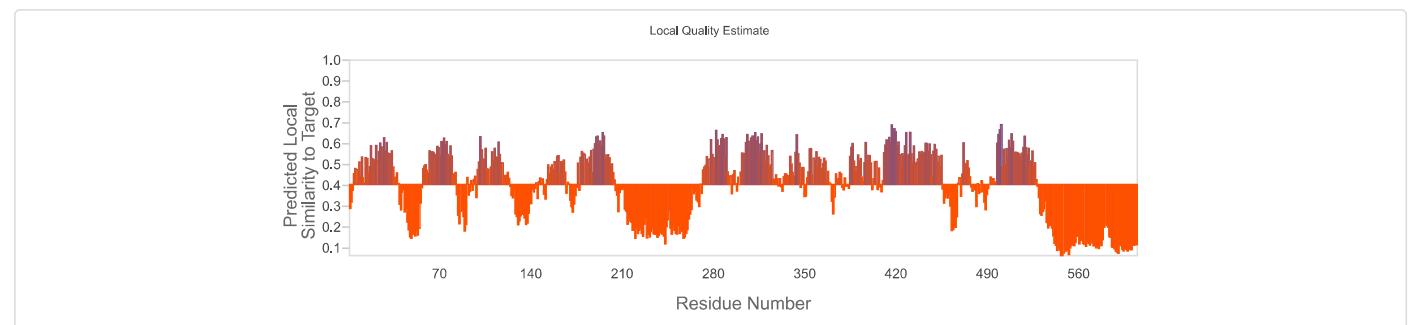
**QMEANDisCo Global:** **0.41 ± 0.05** ⓘ **ⓘ Sequence colored by local quality:**

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X: DAEWEIAKRYLSSYFLIDILAVLPLPQVAILIVIPKLRGAKSLNTKLLKFVVFQYIPRLLRVVPLYKEVTRTSGILTETAWAGAAFNLLLYMLA 190
X: SHVLGAFWYLFISIERESTCWQRACGNTSACHHSSLYCDDDHNTNFIKLLNDSCPIETPNTTLDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQN 285
X: LSSLGQNLETSTYVWEICFAVFISTIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPHEHLRERIRRYEQQYKWQETRGVDEETL 380
X: ILNLPKDLRRDIKRHLCLALLMRVPMEKMDQQLDALCDRLRPVLYTENSFIVREGDPVDEMLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFC 475
X: GEELLTWALDPHPSSNLPISTRTVQALSEVEAFALVADDLKTFVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRHHCRKLEESLCEEEN 570
X: RLQDALARGGGSSPSLGAATIYASRFAANALRALRH 605
```

Quality for modeller01.pdb

Downloads ▾

Compare



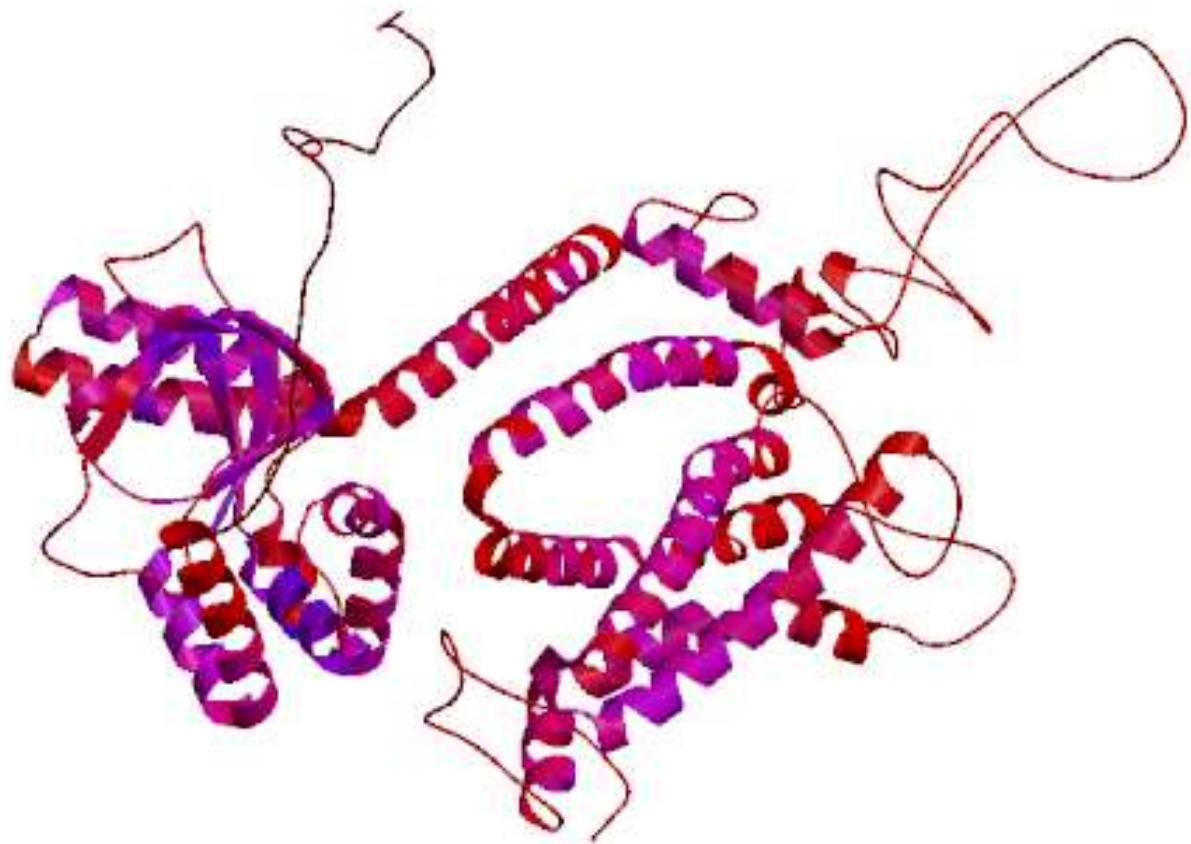
QMEANDisCo Global: **0.40** ± 0.05 ⓘ

ⓘ Sequence colored by local quality:

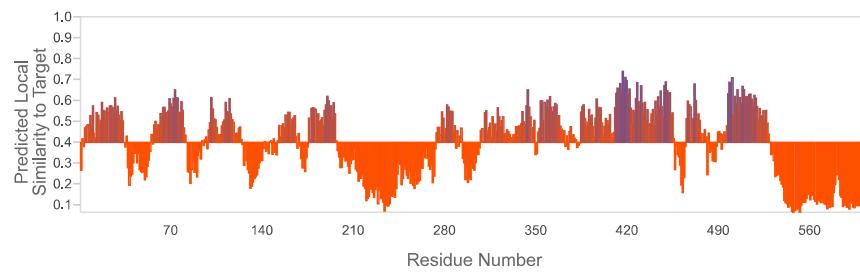
X: SEKKMLDPQGPFLQKWNKIFVLSVCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVRLSITDIFYLFHVVLQFRTGFIAPSSRVFGRGVLVE 95
 X: DAWEIAKRYLSSYFLIDILAVLPLPQVAILIVIPKLRGAKSLNTKTLKFWVVFFQYIPRLLRVYPLYKEVTRTSGILTEAWAGAAFNLLLYMIA 190
 X: SHVLGAFWYLFSIERESTCWQRACGNTSACHHSSLYCDDDHNTFIKLLNDSCPIETPNNTLFDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQN 285
 X: LSSLGQNLETSTYYWEICFAVFISIAGLVLFSLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPEHLRERIRRYEQQYKWQETRGVDEETL 380
 X: IILNLPKDLRRDIKRHLCALLMRVPFMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFC 475
 X: GEELLTWALDPHPSSNNLPISRTTVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRHCRKKLEESLCEEEN 570
 X: RLQDALARGGGSSPSLGATIYASRFAANALRALRH 605

Quality for modeller06.pdb

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Local Quality Estimate

**QMEANDisCo Global:** 0.40 ± 0.05 ⓘ

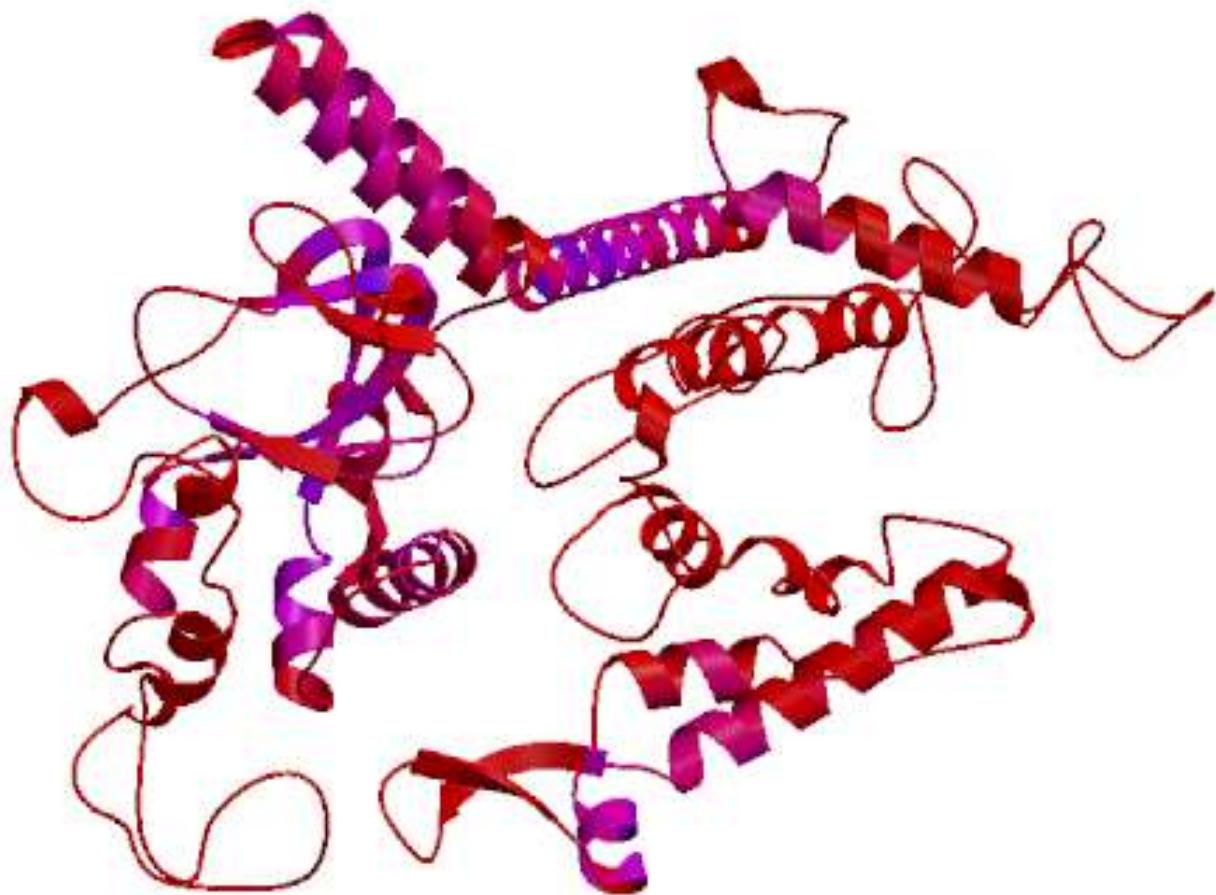
ⓘ Sequence colored by local quality:

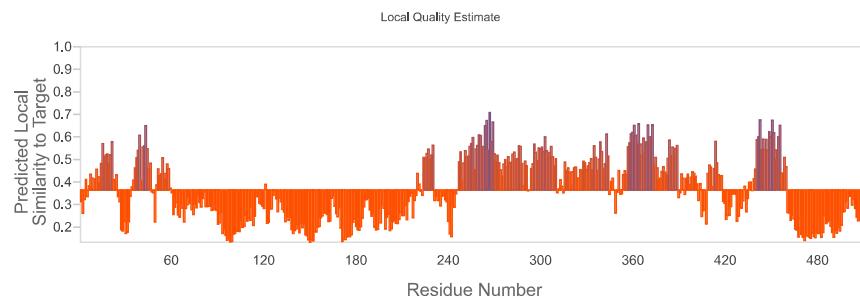


```
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X: DAEWEIAKRYLSSYFLIDILAVLPLPVQVAILIVIPKLRGAKSLNTKLLKFVVFQYIPRLLRVVPLYKEVTRTSGILTETAWAGAAFNLLLYMLA 190
X: SHVLGAFWYLFISIERESTCWQRACGNTSACHHSSLYCDDDHNTNFIKLLNDSCPIETPNTTLDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQN 285
X: LSSLGQNLETSTYVWEICFAVFISTIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPHEHLRERIRRYEQQYKWQETRGVDEETL 380
X: ILNLPKDLRRDIKRHLCLALLMRVPMEKMDQLLDALCDRLRPVLYTENSFIVREGDPVDEMLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFC 475
X: GEEILTWAQDPHSNNLPISTRTVQALSEVEAFALVADDLKTFVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRHRCKKLEESLCEEEN 570
X: RLQDALARGGGSSPSLGATIYASRFAANALRALRH 605
```

Quality for swissmodel01.pdb

Downloads ▾

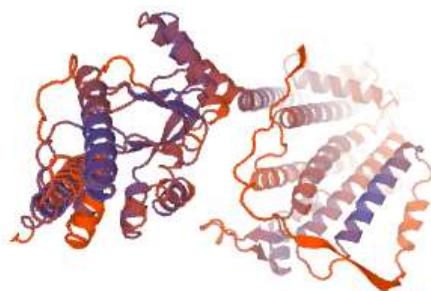
Compare



QMEANDisCo Global: **0.36 ± 0.05** ⓘ

ⓘ Sequence colored by local quality:

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 B: RLLRVYPLYKEVTRTSGILTETAWAGAAFNLLYMLASHVLGAFWYLFSIERESTCWQRACGNTSACHHSSLYCDDDHNFIKLLNDSCPIETPN 190
 B: TTLFDGFIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSSLGQNLETSTYVWEICFAVFISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRD 285
 B: AEQWMMSHRLLPKDIIRRDIKRHLCLALLMRVPMPFEKMDEQLLDALCDRLRPVLYTENSFIVREGD 380
 B: PVDEMILFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFCGEELLTWALDPHPSNLPISTRTVQALSEVEAFALVADDLKVASQFRRLHSKQLRHT 475
 B: FRFYSSQQWRTWAACFIQAAWRRHCRKKLEESLCEEENR 513



Toggle Selected PV

Reference for the QMEAN scoring function:

[1] Benkert P, Biasini M, Schwede T *Toward the estimation of the absolute quality of individual protein structure models.* Bioinformatics 27, 343-350. (2011)  21134891  10.1101/21134891

Reference for the QMEANDisCo scoring function:

[2] Studer G, Rempfer C, Waterhouse AM, Gumieny R, Haas J, Schwede T *QMEANDisCo - distance constraints applied on model quality estimation.* Bioinformatics 36, 1765-1771. (2020)  31697312  10.1101/31697312

Reference for the QMEANBrane scoring function:

[3] Studer G, Biasini M, Schwede T *Assessing the local structural quality of transmembrane protein models using statistical potentials (QMEANBrane).* Bioinformatics 30, i505-i511. (2014)  25161240  10.1101/25161240