

QMEAN

[CAMEO evaluation](#) [Help](#) [Examples ▾](#)[Untitled \(created 2024-06-25T17:44:35\)](#) [CNGC \(created 2024-06-25T17:08:07\)](#)

Untitled Project

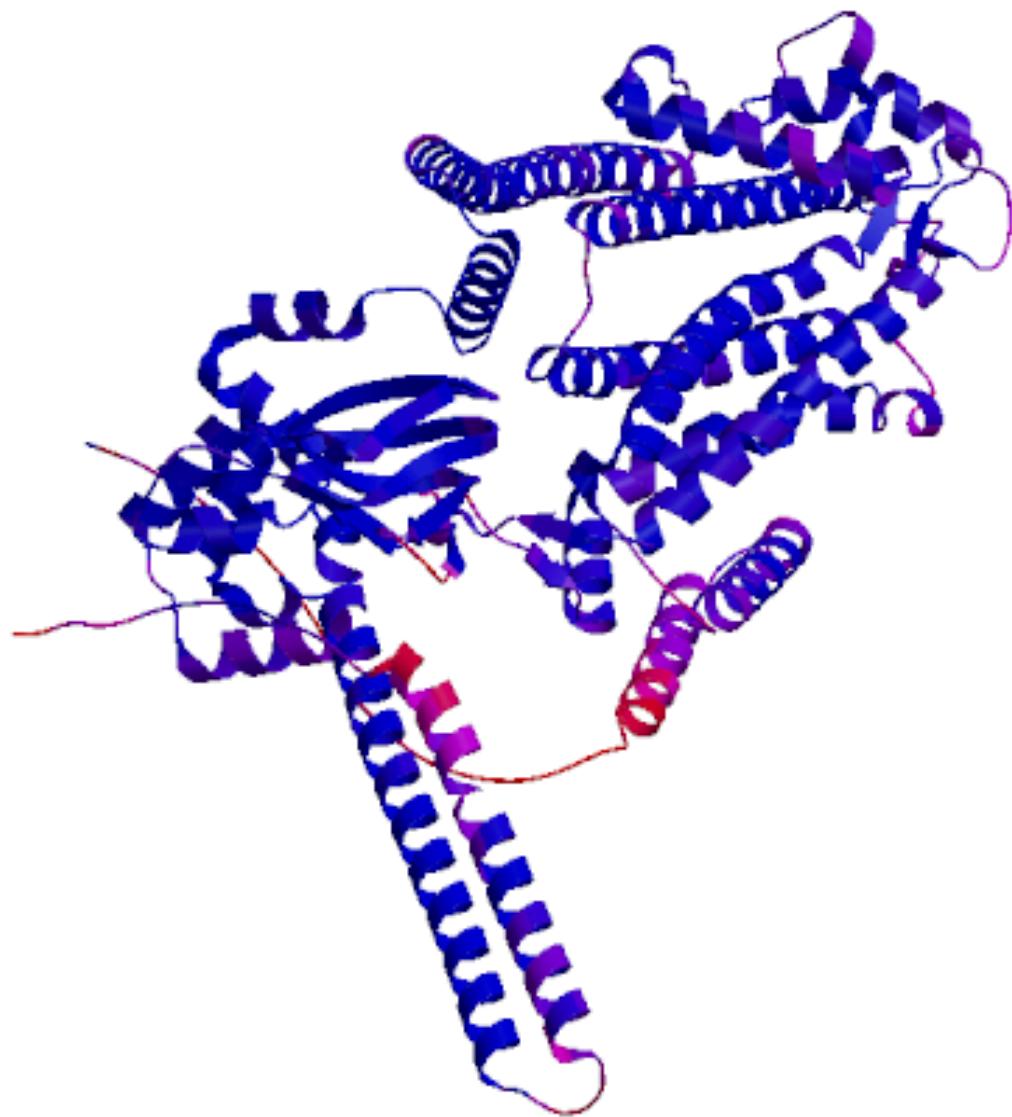
(Created: an hour ago) [Project Archive](#) [Delete](#)

Total model count : 16.

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

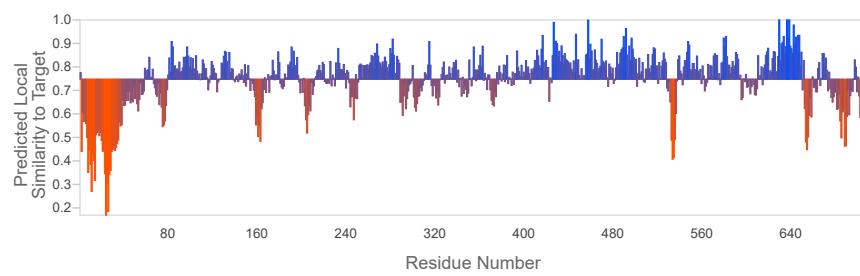
Quality for IntFOLD701.pdb

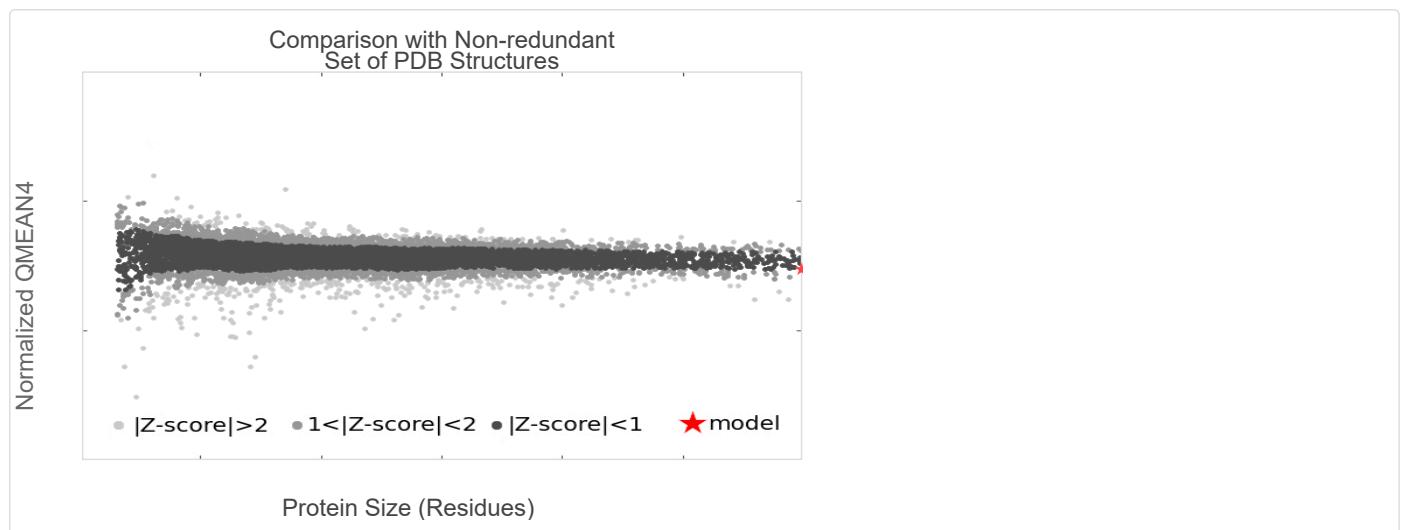
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Local Quality Estimate



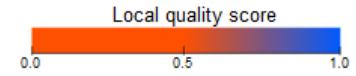


QMEAN4 Value: -0.77 ⓘ

Δ During preprocessing, 1278 atoms were removed .

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

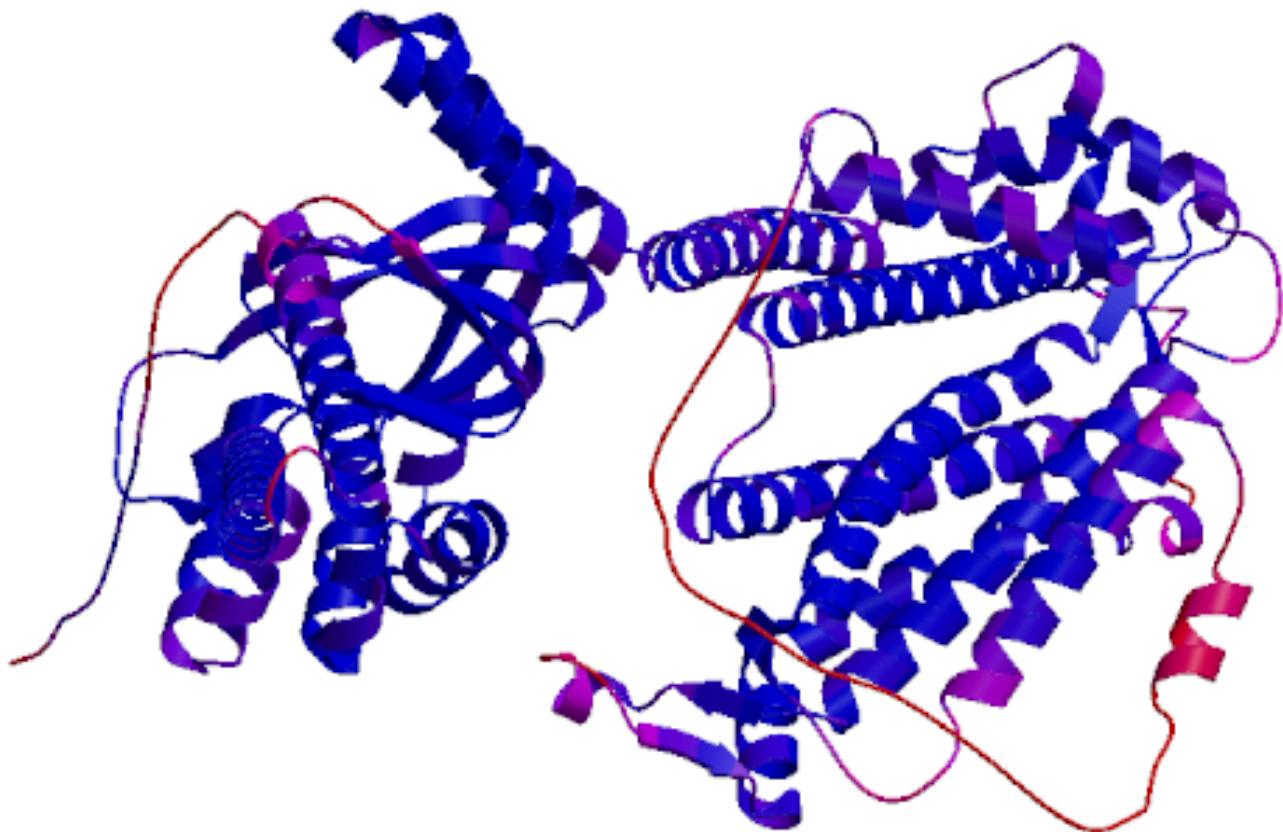
⌚ Sequence colored by local quality:



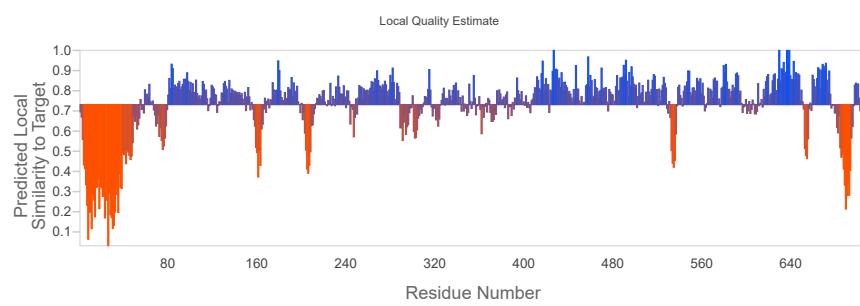
```
A: MNHQRQEKFVRFQDWNSSEKSSEGPNFPYKDGAHRGRFGVFSNELHKSLESGSGRIKSIIHALSSCLSLLVKSLGSEKKMLDPQGPFLQKWNKIFVL 95
A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRISITDIFYLFHIVLQFRTGFIAPSSRVFGRGVLVEDAWEIAKRYLSSYFLIDILAVL 190
A: PLPQVAILIVIPKLRGAKSLNTKTLLKFVVFQYIPRLLRVYPLYKEVTRTSGILTETAWAGAAFNLLYMLASHVLGAFWYLFSTIERESTCWQR 285
A: ACGNNTSACHHSSLYCDDDHNTFIKLLNDSCPPIETPNTTLFDGIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSLGLQNLETSTYVWEICFAVF 380
A: ISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPPEHLRERIRRYEQQYWQETRGVDEETLILNLPKDLRRDIKRHLCLALLM 475
A: RVPFMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMELFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFCGEELLTWALDPHPSNNLPISTR 570
A: TVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRWTAAACFIQAAWRRHCRKKLEESLCEEENRLQDALARGGGSSPSLGATIYA 665
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708
```

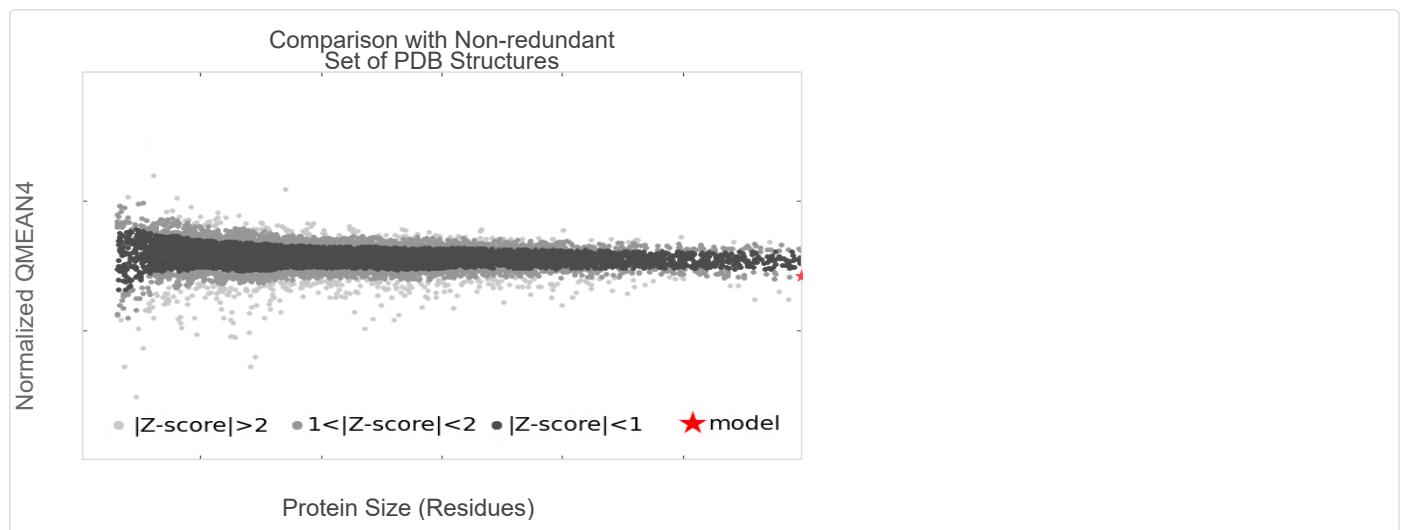
Quality for CNGC6AlphaFold.pdb

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QMEAN4 Value: -1.56 ⓘ

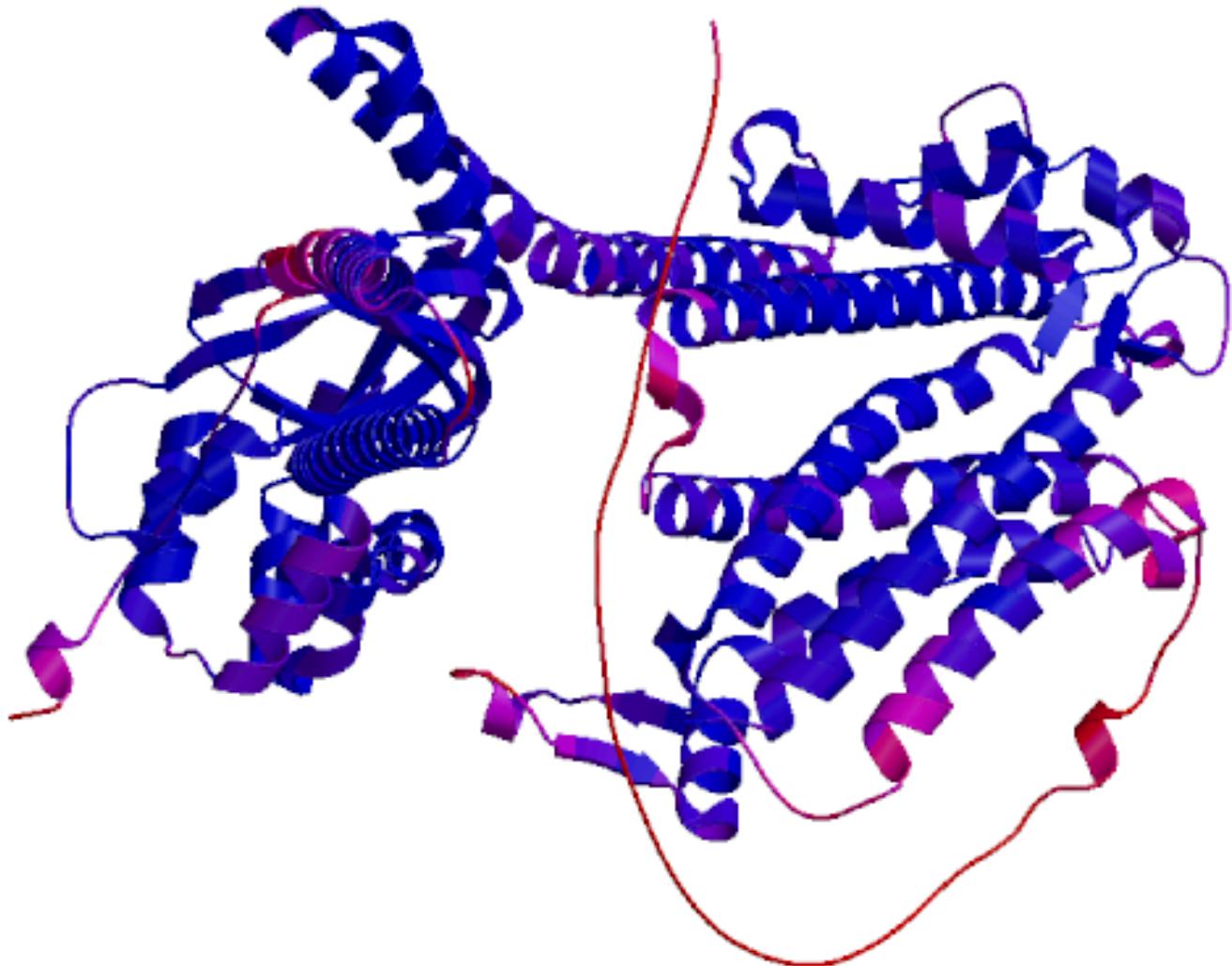
⌚ Sequence colored by local quality:



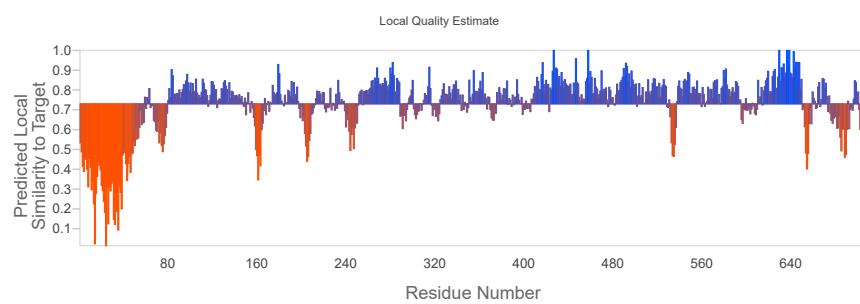
```
A: MNHRQEKFVRFQDWNSEKSEGSSEGPNFPYKDGGAHGRGRFGVFSNELHKSLESGSGRIKSIIHALSSCLSCLLVKSLGSEKKMLDPQGPFLQKWNKIFV 95
A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRSSITDIFYLFHIVLQFRTGFIAPSSRVFGRGVLDWEIAKRYLSSYFLIDILAVL 190
A: PLPQVAILIVIPKLRGAKSLNTKTLLKFVVFFQYIPRLLRVYPLYKEVTRTSGILTEAWAGAAFNLLYMLASHVLGAFWYLFISIERESTCWQR 285
A: ACGNTSACHHSSLYCDDDHNTFIKLLNDSCPPIETPNTTLFDGIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSSLGQNLETSTYVWEICFAVF 380
A: ISIAGLVLFLSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPPEHLRERIRRYEQYKWQETRGVDEETLILNLPKDLRRDIKRHLCALLM 475
A: RVPMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMLFIMRGKLLTVTTNGGRTFFFNSDYLKAGDFCGEELLTWALDPHPSSNNLPISTR 570
A: TVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRWTAAACFIQAAWRHCRKKLEESLCEEENRLQDALARGGGSSPSLGA 665
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708
```

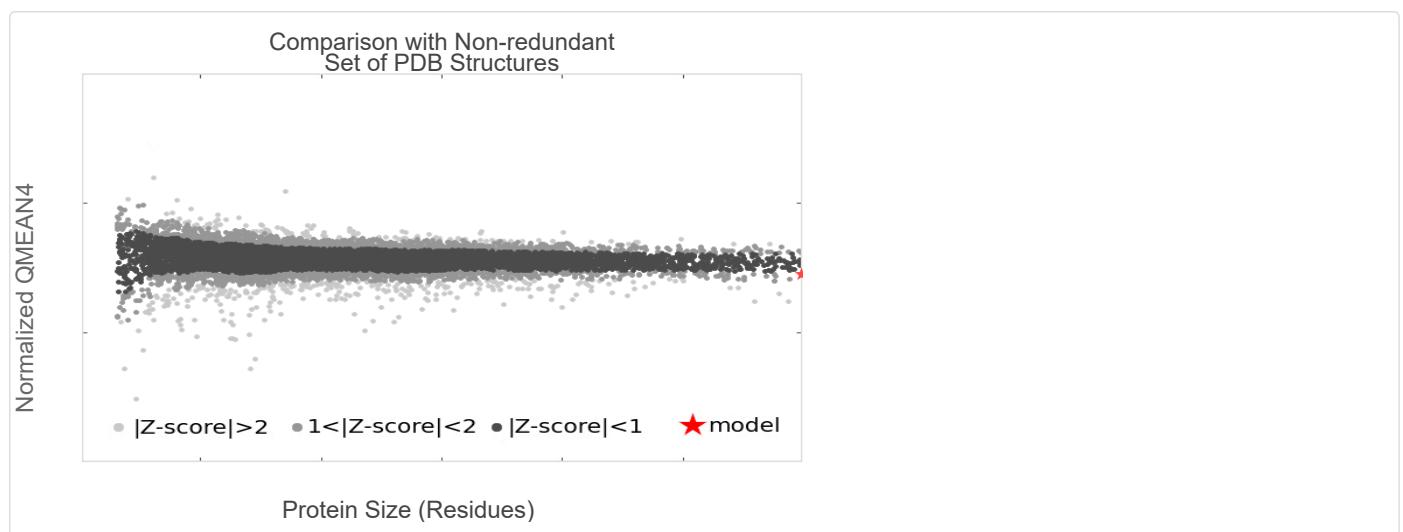
Quality for IntFOLD703.pdb

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Compare





QMEAN4 Value: -1.07 ⓘ

⚠ During preprocessing, 1278 atoms were removed .

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

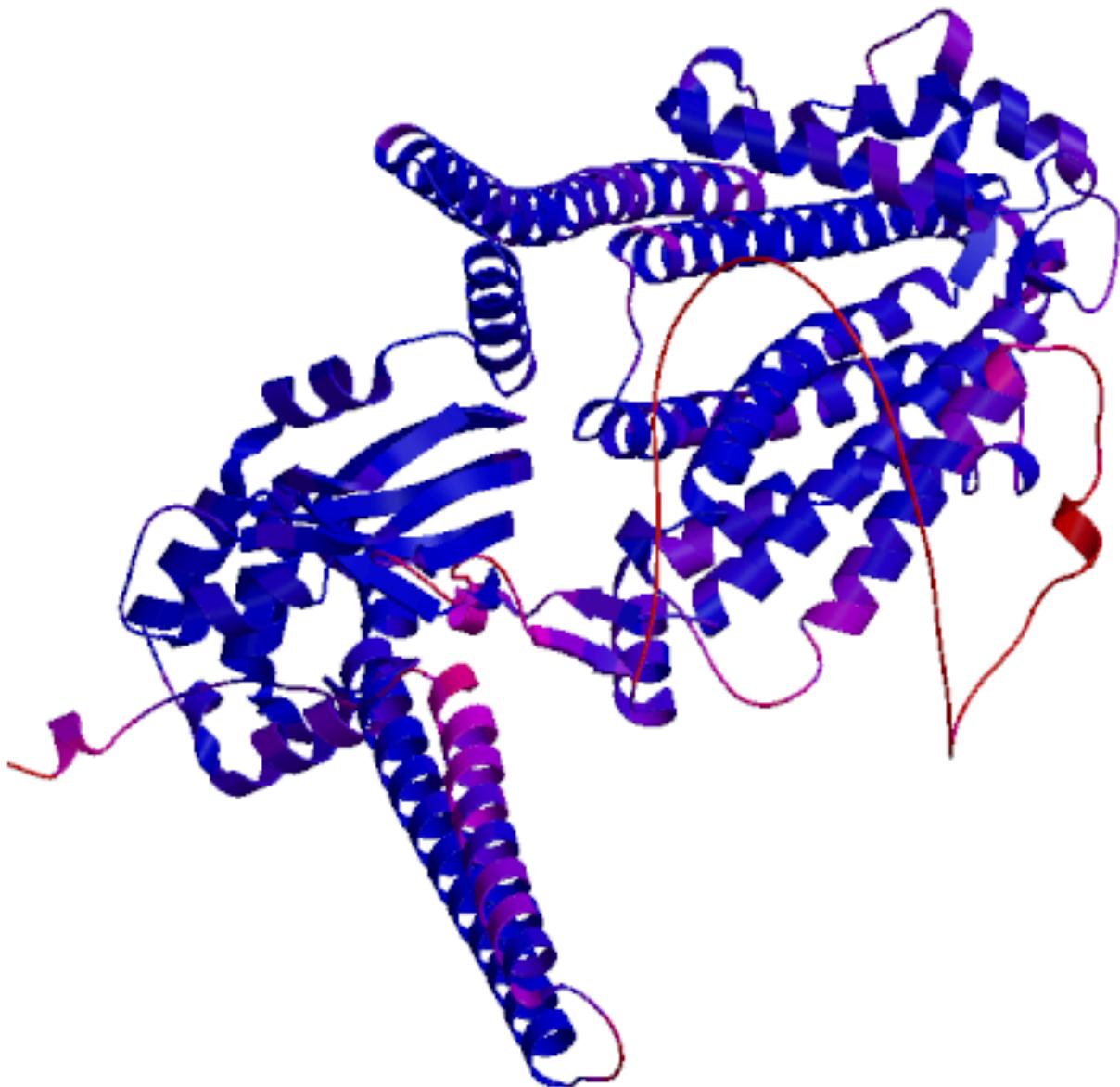
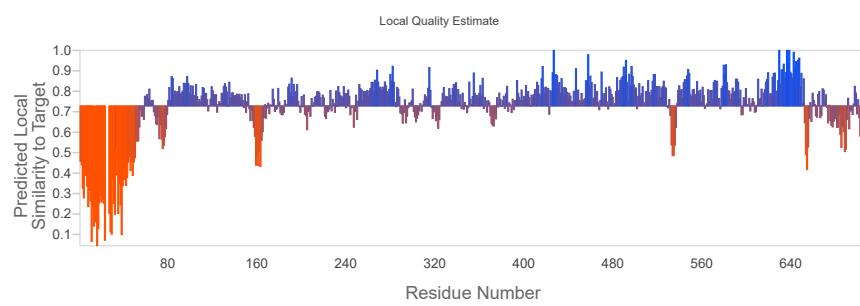
⌚ Sequence colored by local quality:

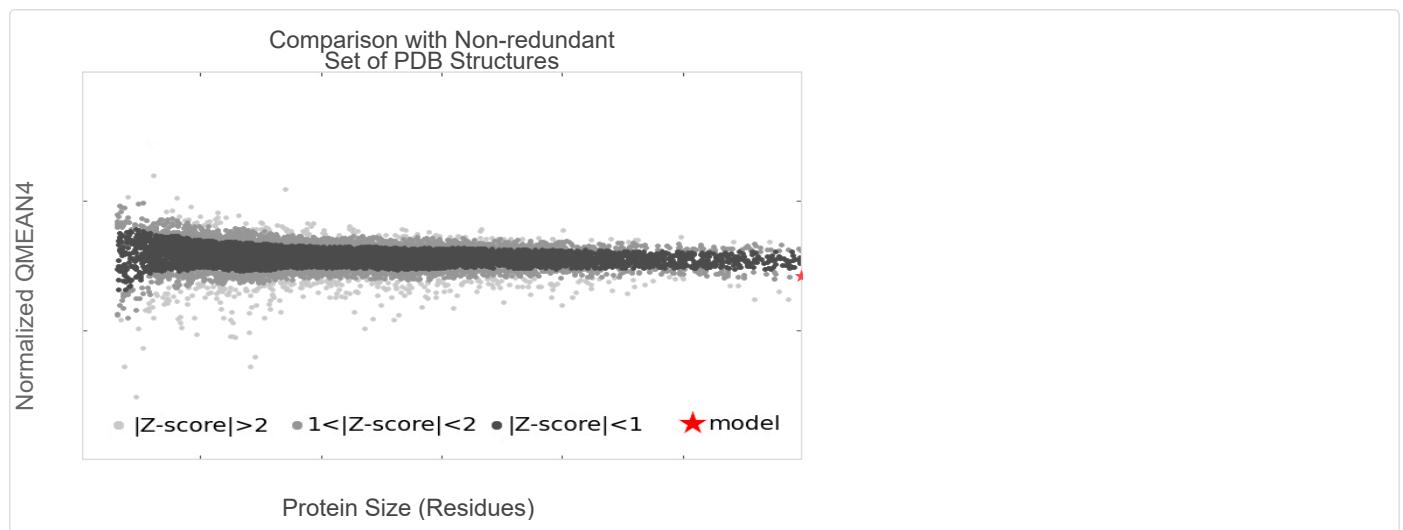


A:	MNHRQEKFVRFQDWNSSEKSSEGNGFPYKDGAHRGRFGVFSNELHKSLESGSGRIKSIIHALSSCLSLLVKSLGSEKKMLDPQGPFLQKWNKIFVL	95
A:	SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRISITDIFYLFHIVLQFRTGFIAPSSRVFGRGVLVEDAWEIAKRYLSSYFLIDILAVL	190
A:	PLPQVAILIVIPKLRGAKSLNTKTLKVFVFFQYIPRLLRVYPLYKEVTRTSGILTETAWAGAAFNLLYMLASHVLGAFWYLFSTIERESTCWQR	285
A:	ACGNTSACHHSSLYCDDDHNTFIKLNDSCPPIETPNTTLFDGIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSLGQNLETSTYVWEICFAVF	380
A:	ISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPPEHLRERIRRYEQQYWQETRGVDEETLILNLPKDLRRDIKRHLCLALLM	475
A:	RVPMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMELFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFCGEELLTWALDPHPSNNLPISTR	570
A:	TVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRWTWAACFIQAAWRRHCRKKLEESLCEEENRLQDALARGGGSSPSLGA	665
A:	SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK	708

Quality for IntFOLD702.pdb

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 Compare

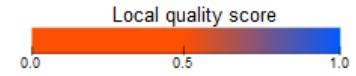


QMEAN4 Value: -1.60 ⓘ

⚠ 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: MNHQRQEKFVRFQDWNSSEKSSEGNGFPYKDGAHRGRFGVFSNELHKSLESGSGRIKSIIHALSSCLSLLVKSLGSEKKMLDPQGPFLQKWNKIFVL 95
A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRISITDIFYLFHIVLQFRTGFIAPSSRVFGRGVLVEDAWEIAKRYLSSYFLIDILAVL 190
A: PLPQVAILIVIPKLRGAKSLNTKTLLKFVVFQYIPRLLRVYPLYKEVTRTSGILTETAWAGAAFNLLYMLASHVLGAFWYLFSTIERESTCWQR 285
A: ACGNNTSACHHSSLYCDDDHNTFIKLNDSCPPIETPNTTLFDGIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSLGLQNLETSTYVWEICFAVF 380
A: ISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPPEHLRERIRRYEQYKWQETRGVDEETLILNLPKDLRRDIKRHLCLALLM 475
A: RVPFMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMELFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFCGEELLTWALDPHPSNNLPISTR 570
A: TVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRWTWAACFIQAAWRRHCRKKLEESLCEEENRLQDALARGGGSSPSLGATIYA 665
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708
```

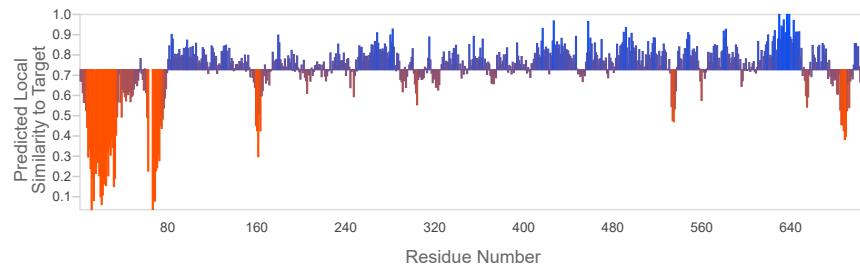
Quality for swissmodel02.pdb

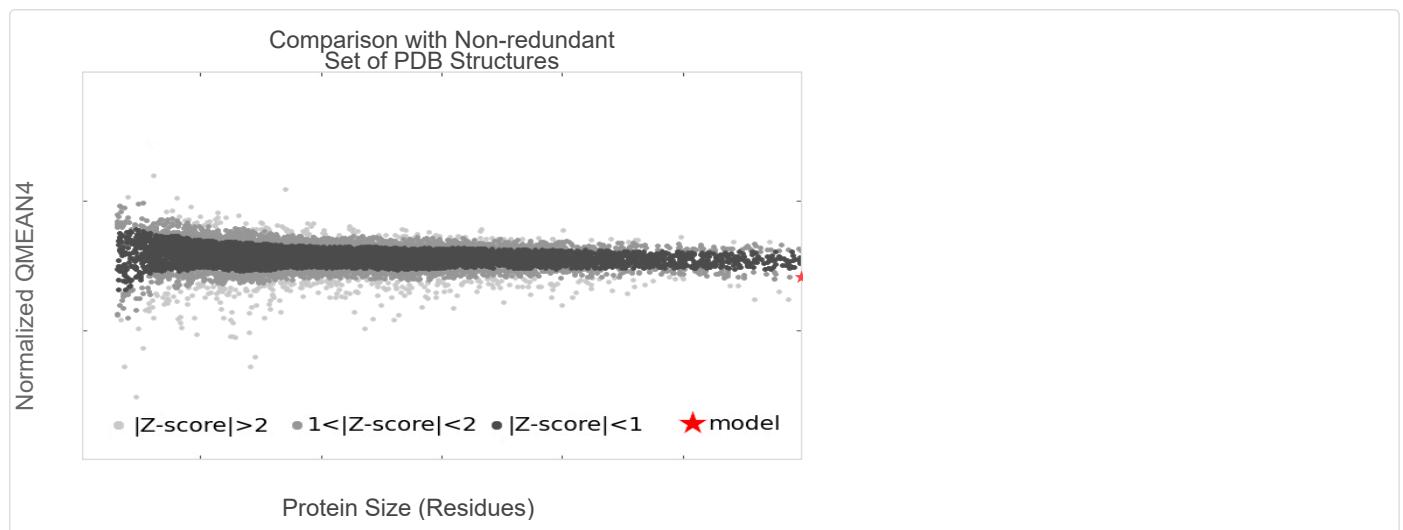
Downloads ▾



Compare

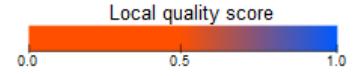
Local Quality Estimate





QMEAN4 Value: -1.72 ⓘ

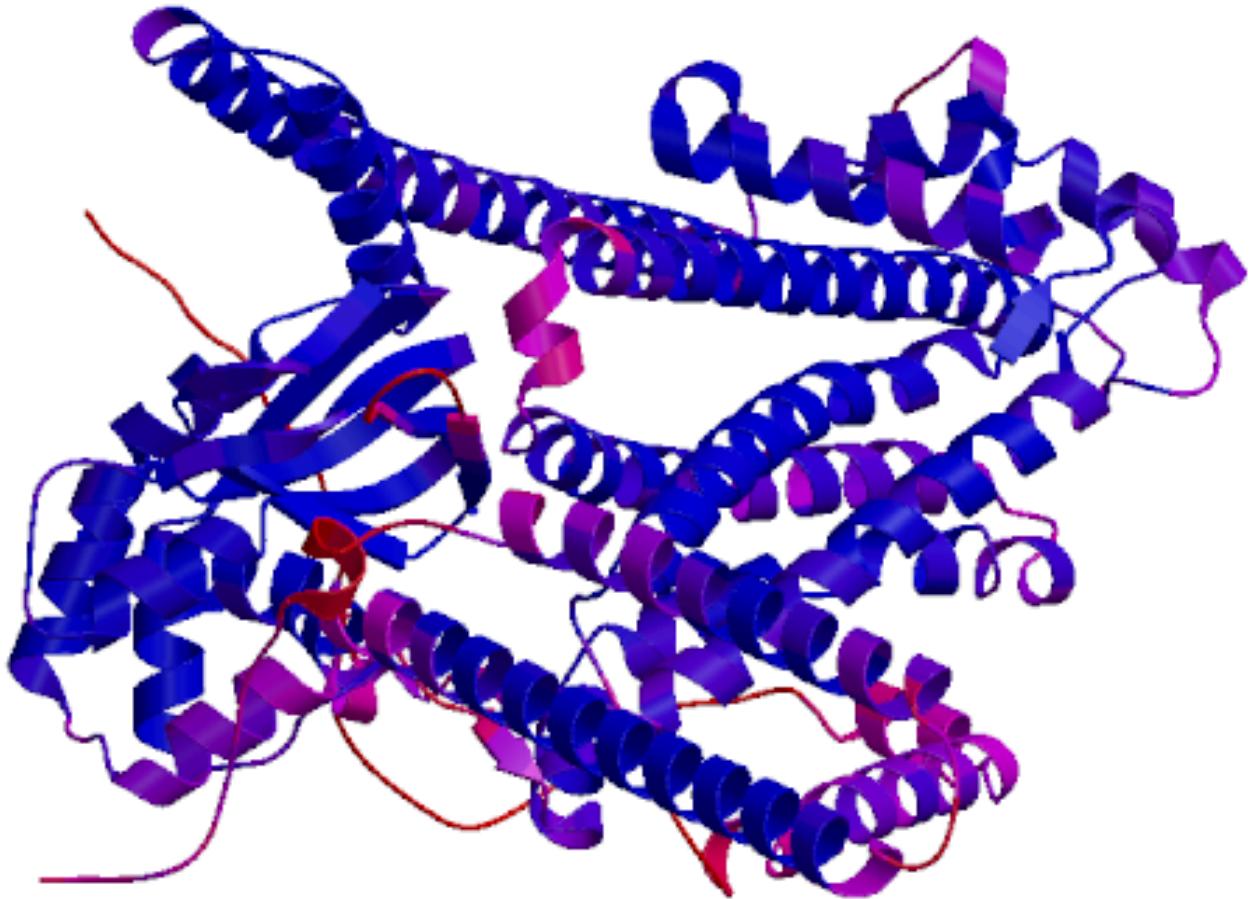
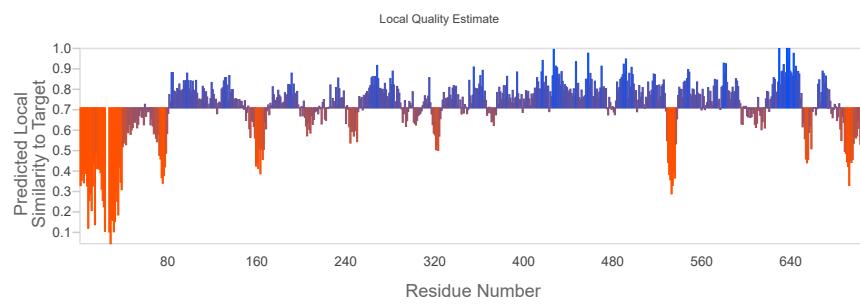
⌚ Sequence colored by local quality:

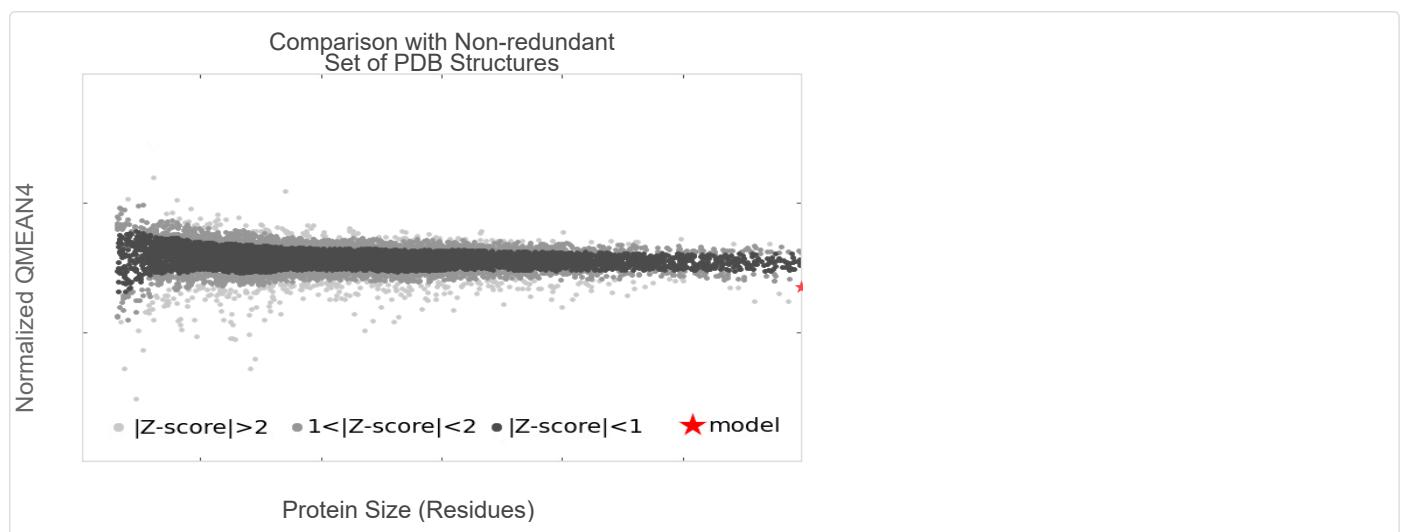


```
A: MNHRQEKFVRFQDWNSKSSEGPNFPYKDGAHRGRFGVFSNELHKSLESGSGRIKSIIHALSSCLSCLLVKSLGSEKKMLDPQGPFLQKWNKIFV 95
A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRSLTIDIFYLFHIVLQFRTGFIAPSSRVFGRGVLDWEIAKRYLSSYFLIDILAVL 190
A: PLPQVAILIVIPKLRGAKSLNTKTLLKFVVFFQYIPRLLRVYPLYKEVTRTSGILTEAWAGAAFNLLYMLASHVLGAFWYLFISIERESTCWQR 285
A: ACGNTSACHHSSLYCDDDHNTFIKLLNDSCPIETPNTTLFDGIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSSLGQNLETSTYVWEICFAVF 380
A: ISIAGLVLFLSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPHEHLRERIRRYEQYKWQETRGVDEETLILNLPKDLRRDIKRHLCALLM 475
A: RVPMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMLFIMRGKLLTVTTNGGRTFFFNSDYLKAGDFCGEELLTWALDPHPSSNNLPISTR 570
A: TVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRWTAAACFIQAAWRHCRKKLEESLCEEENRLQDALARGGGSSPSLGA 665
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708
```

Quality for ESMFold.pdb

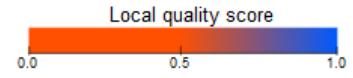
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 Compare



QMEAN4 Value: -2.53 ⓘ

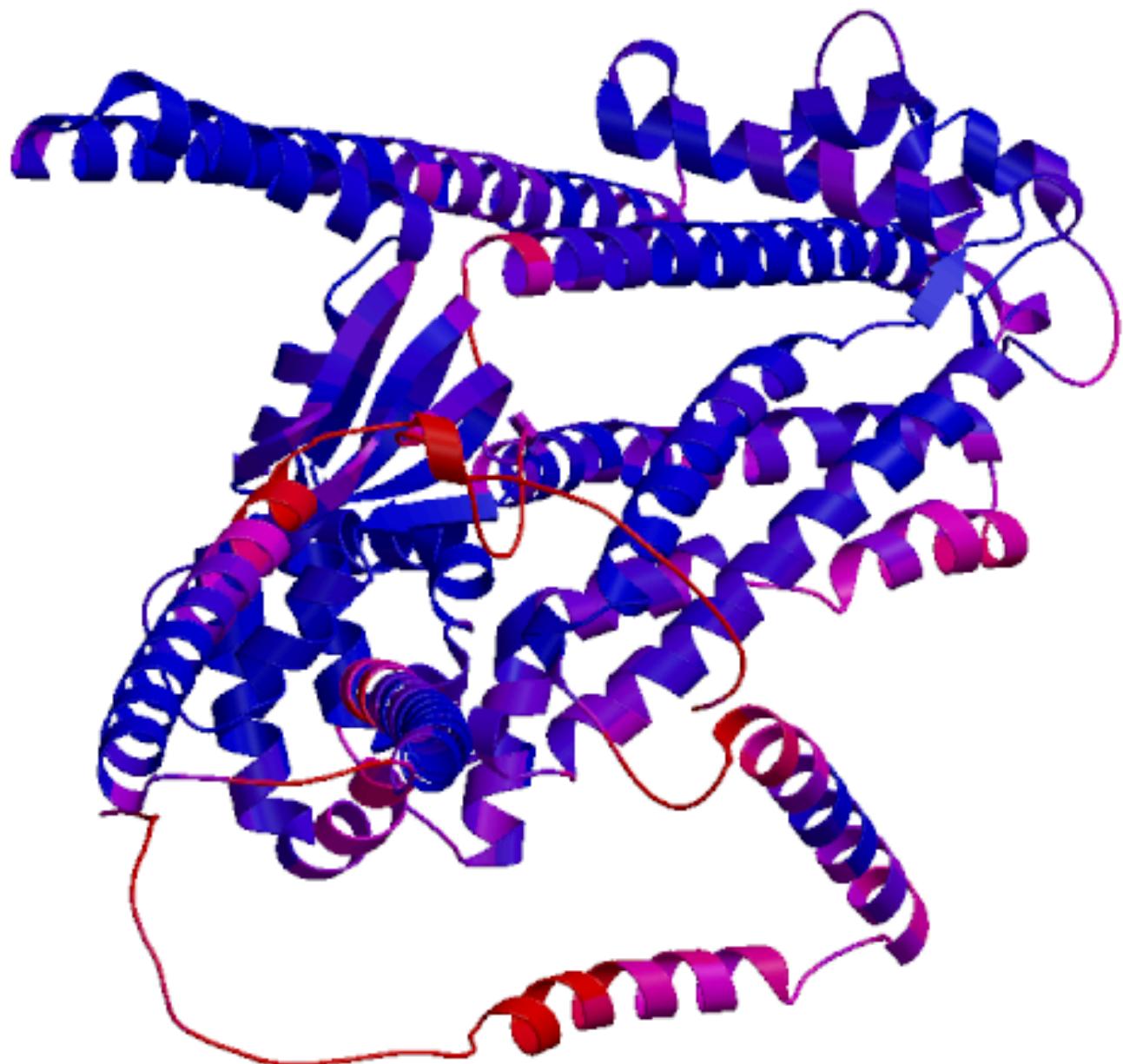
Sequence colored by local quality:



```
A: MNHRQEKFVRFQDWNSKSSEGPNFPYKDGGAHGRGRGVFSNELHKSLESGSGRIKSIIHALSSCLSCLLVKSLGSEKKMLDPQGPFLQKWNKIFV 95
A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRSSITDIFYLFHIVLQFRTGFIAPSSRVFGRGVLDWEIAKRYLSSYFLIDILAVL 190
A: PLPQVAILIVIPKLRGAKSLNTKTLLKFVVFFQYIPRLLRVYPLYKEVTRTSGILTEAWAGAAFNLLYMLASHVLGAFWYLFISIERESTCWQR 285
A: ACGNTSACHHSSLYCDDDHNTNFIKLLNDSCPPIETPNTTLFDGIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSSLGQNLETSTYVWEICFAVF 380
A: ISIAGLVLFLSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLIPEHLRERIRRYEQYKWQETRGVDEETLILNLPKDLRRDIKRHLCALLM 475
A: RVPMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMELFIMRGKLLTVTTNGGRTFFFNSDYLKAGDFCGEELLTWALDPHPSSNNLPISTR 570
A: TVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRWAACFIQAAWRHCRKKLEESLCEEENRLQDALARGGGSSPSLGATIYA 665
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708
```

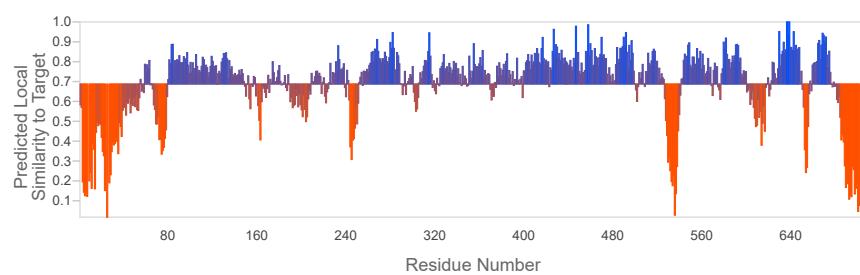
Quality for OmegaFold.pdb

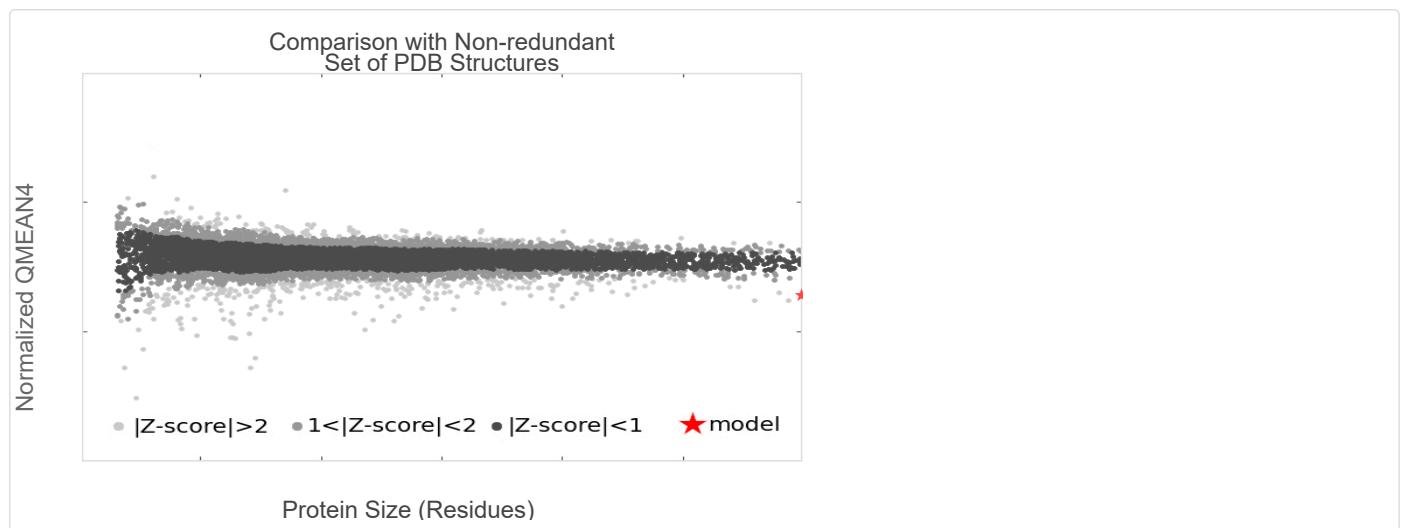
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Compare

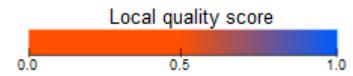
Local Quality Estimate





QMEAN4 Value: -3.56 ⓘ

⌚ Sequence colored by local quality:



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A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRSLTIDIFYLFHIVLQFRTGFIAPSSRVFGRGVLDWEIAKRYLSSYFLIDILAVL 190
A: PLPQVAILIVIPKLRGAKSLNTKTLLKFVVFQYIPRLLRVYPLYKEVTRTSGLTETAWAGAAFNLLYMLASHVLGAFWYLFISIERESTCWQR 285
A: ACGNTSACHHSSLYCDDDHNTNFIKLLNDSCPPIETPNTTLFDGIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSSLGQNLETSTYVWEICFAVF 380
A: ISIAGLVLFLSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPEHLRERIRRYEQYKWQETRGVDEETLILNLPKDLRRDIKRHLCALLM 475
A: RVPMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMELFIMRGKLLTVTTNGGRTFFFNSDYLKAGDFCGEELLTWALDPHPSSNNLPISTR 570
A: TVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRWTWAACFIQAAWRHCRKKLEESLCEEENRLQDALARGGGSSPSLGA 665
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708
```

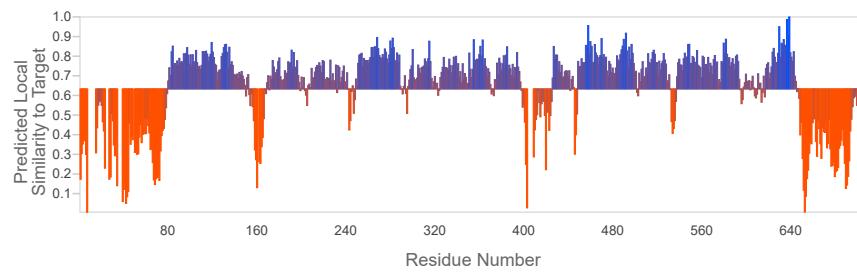
Quality for RoseTTAFold2.pdb

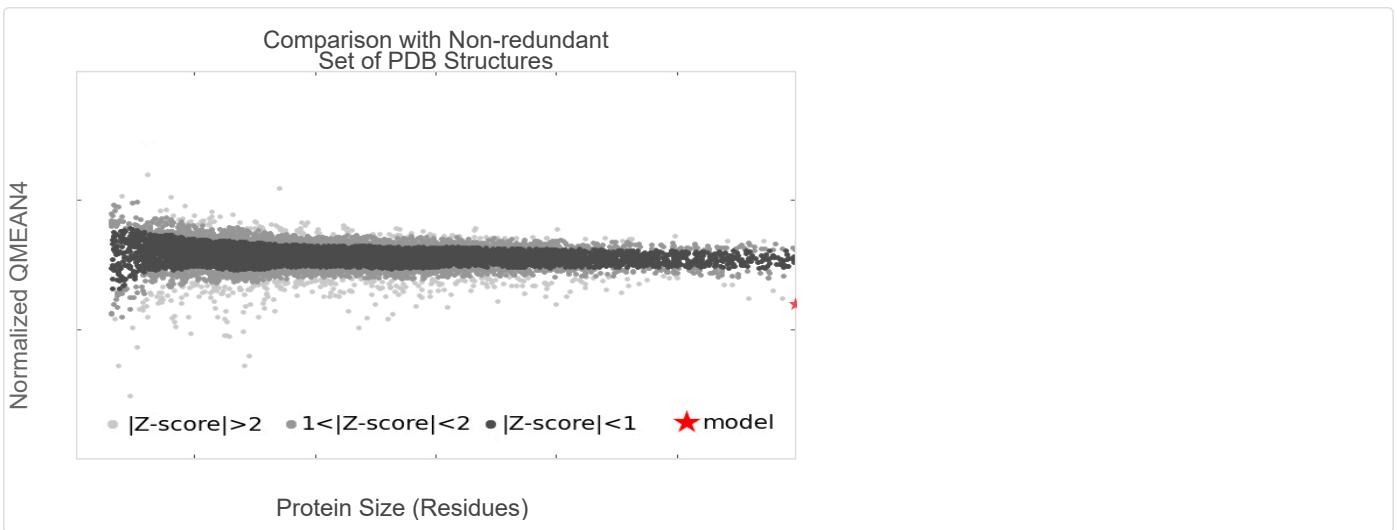
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Compare

Local Quality Estimate





QMEAN4 Value: -4.73 ⓘ

⚠ During preprocessing, 2074 atoms were removed .

```

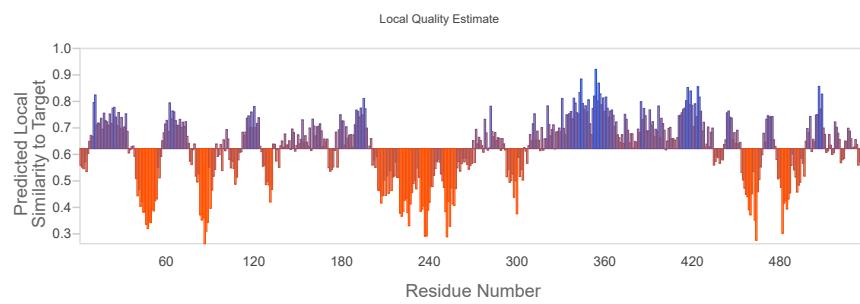
removing atoms with zero occupancy
--> removed 0 atoms with zero occupancy
removing hydrogen atoms
--> removed 1770 hydrogen atoms
residue A.GLU6 contains unknown atom A.GLU6.1HB --> removed
residue A.GLU6 contains unknown atom A.GLU6.2HB --> removed
  
```

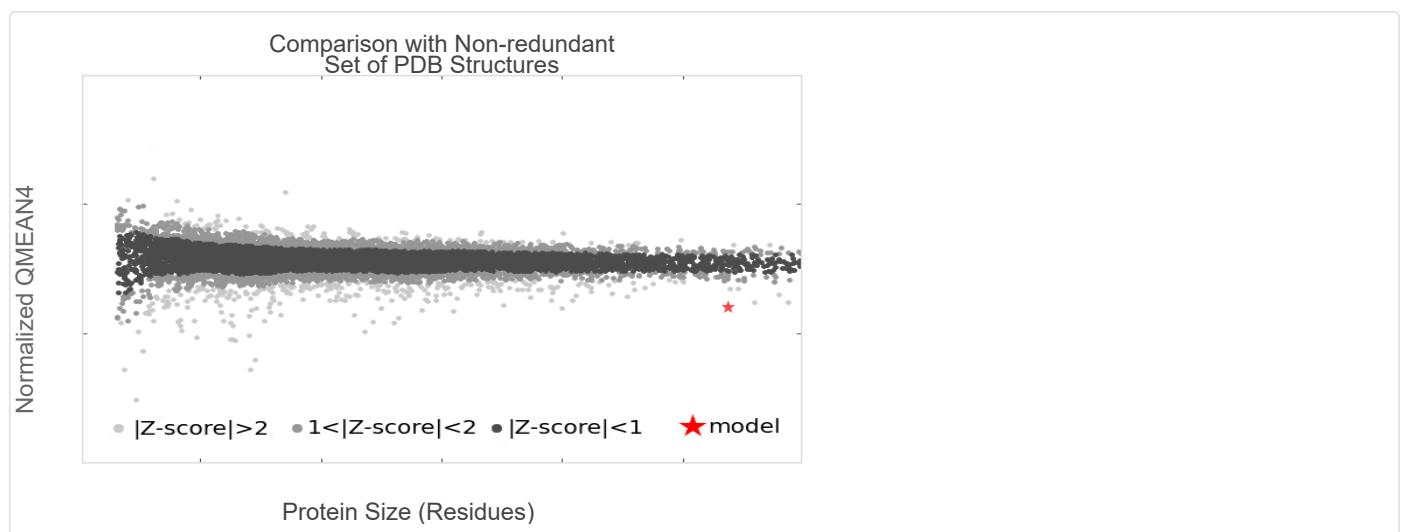
⌚ Sequence colored by local quality:

	Local quality score
A: MNHRQEKFVRFQDWNSSEKSSEGNFYKDGGAHRGRFGVFSNELHKSLESGSGRIKSIIHALSSCLSCLLVKSLGSEKKMLDPGPFLQKWNKIFV 95	0.0
A: SCVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLR SITDIFYLFHIVLQFRTGFIAPSSRVFGRGVLVEDAWEIAKRYLSSYFLIDILAVL 190	0.0
A: PLPQVAILIVIPKLRGAKSLNTKTLLKFVVFQYIPRLLRVYPLYKEVTRTSGILTEAWAGAAFNLMLYMLASHVLGAFWYLFSIERESTCWQR 285	0.0
A: ACGNTSACHHSSLYCDDDHNTFIKLLNDSCPIETPNTTLFDFFGIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSSLGQNLETSTYVWEICFAV 380	0.0
A: ISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPFHRLRERIRRYEQQWKQETRGVDEETLILNLPKDLRRDIKRHLCLALLM 475	0.0
A: RVPMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMELFIMRGKLLTVTTNGGRTFFFNSDYLKAGDFCGEELLTWALDPHPSNLPISTR 570	0.0
A: TVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRRHCRKKLEESLCEEENRLQDALARGGGSPSLGATIYA 665	0.0
A: SRFAANALRALRHNTAKKARMTDRISPILLQKPAEPDFTAEDK 708	1.0

Quality for modeller07.pdb

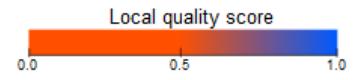
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 Compare



QMEAN4 Value: -4.86 ⓘ

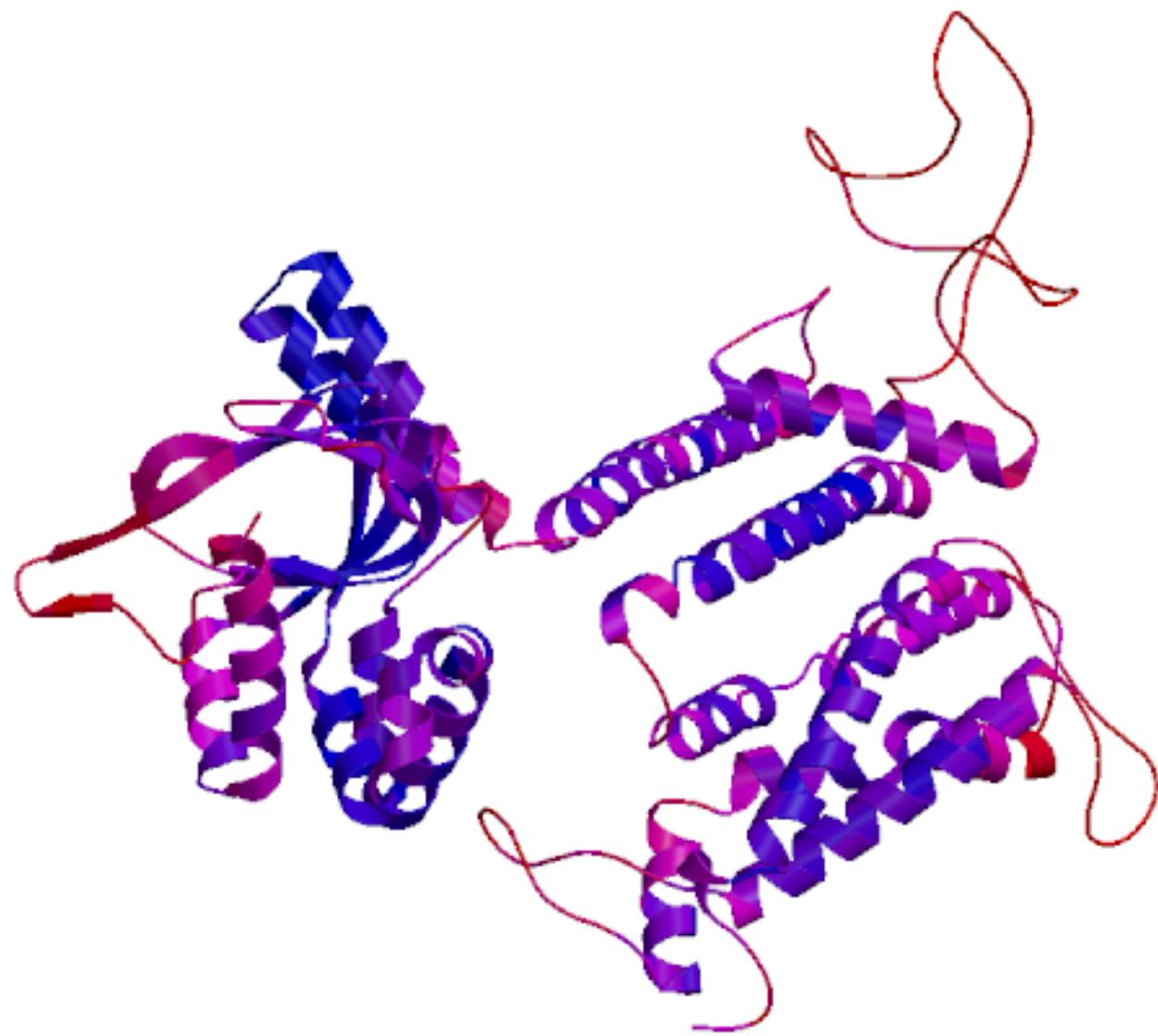
ⓘ Sequence colored by local quality:



```
X: SEKKMLDPQGPFLQKWNKIFVLSCLVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRSTITDIFYLFHIVLQFRTGFIAPSSRVFGRGVLV 95
X: DAWEIAKRYLSSYFLIDILAVLPLPQVAILIVIPKLRGAKSLNTKTLKVVFFQYIPRLLRVYPLYKEVTRTSGILTEAWAGAAFNLLYMLA 190
X: SHVLGAFWYLFSIERESTCWQRACGNTSACHHSSLYCDDDHNTFIKLLNDSCPPIETPNNTLFDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQN 285
X: LSSLGQNLETSTYVWEICFAVFISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPEHLRERIRRYEQQYKWQETRGVDETL 380
X: ILNLPKDLRRDIKRHLCALLMRVPMPFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMFLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFC 475
X: GEELITWALDPHPSNNLPISTRTVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQ 539
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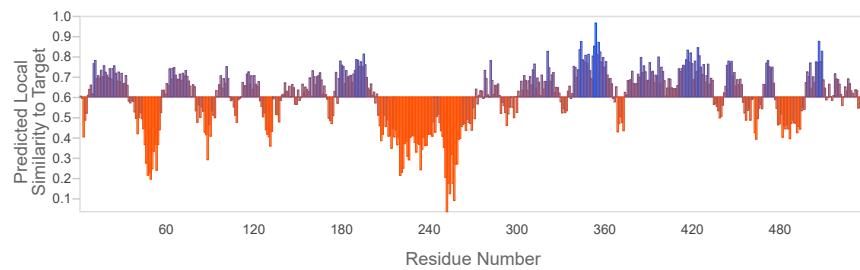
Quality for modeller02.pdb

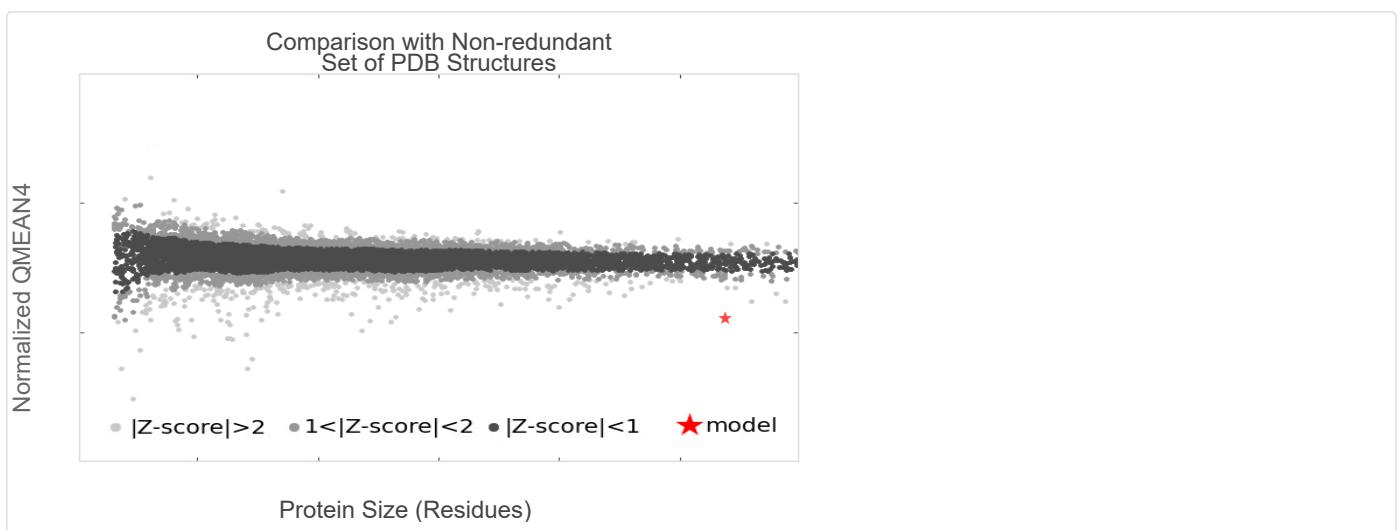
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Compare

Local Quality Estimate





QMEAN4 Value: -6.29 ⓘ

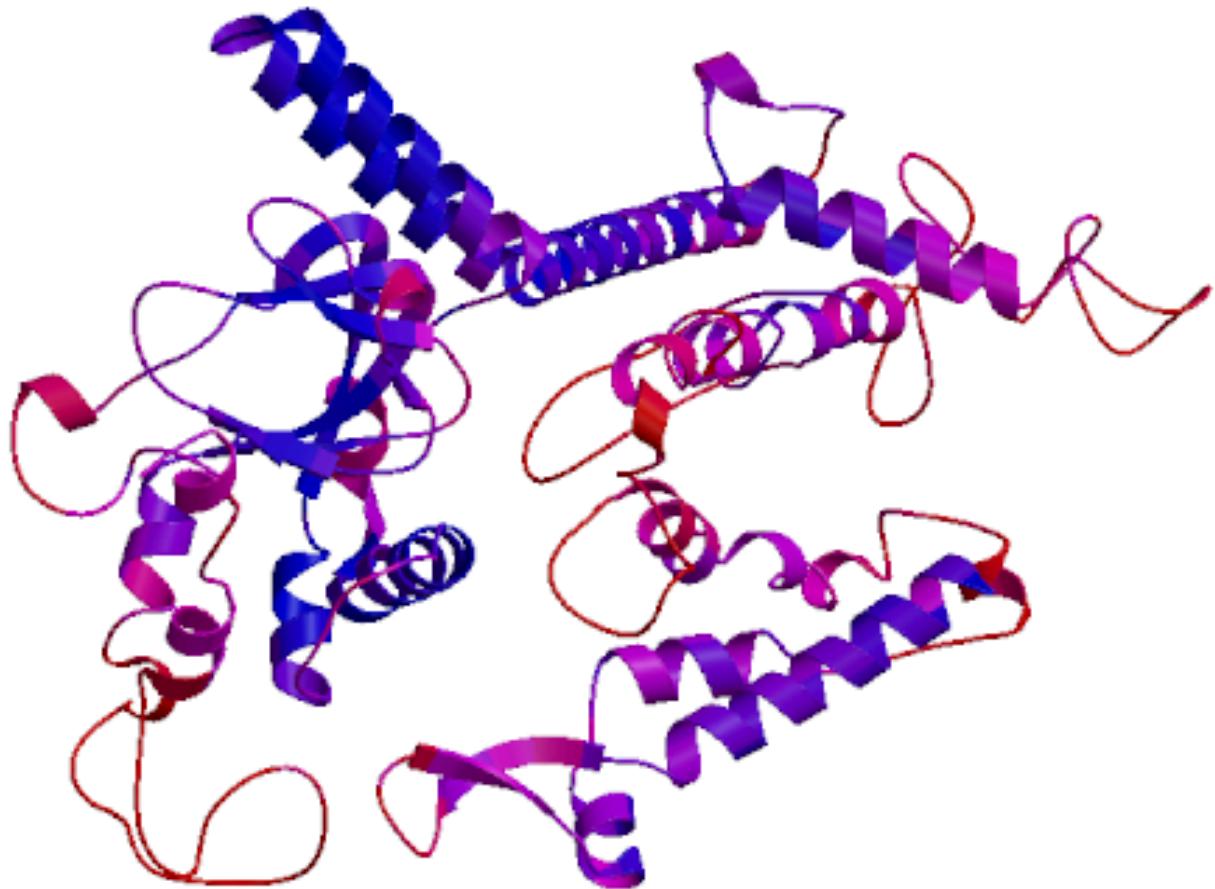
Sequence colored by local quality:



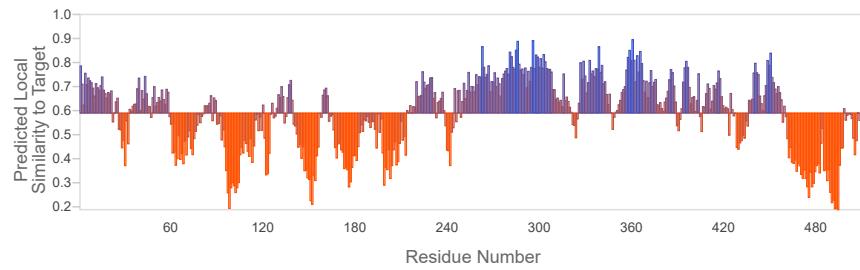
```
X: SEKKMLDPQGPFLQKWNKIFVLSCLVIAISLDPLFFYIPVIDNNNKCLHLDRKMEVTASVLRSTITDIFYLFHIVLQFRTGFIAPSSRVFGRGVLV 95
X: DAWEIAKRYLSSYFLIDILAVLPLPQVAILIVIPKLRGAKSLNTKTLKVVFFQYIPRLLRVYPLYKEVTRTSGILTEAWAGAAFNLLYMLA 190
X: SHVLGAFWYLFSIERESTCWQRACGNTSACHHSSLYCDDDHNTFIKLLNDSCPPIETPNNTLFDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQN 285
X: LSSLGQNLETSTYVWEICFAVFISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPEHLRERIRRYEQQYKWQETRGVDETL 380
X: ILNLPKDLRRDIKRHLCALLMRVPFMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFC 475
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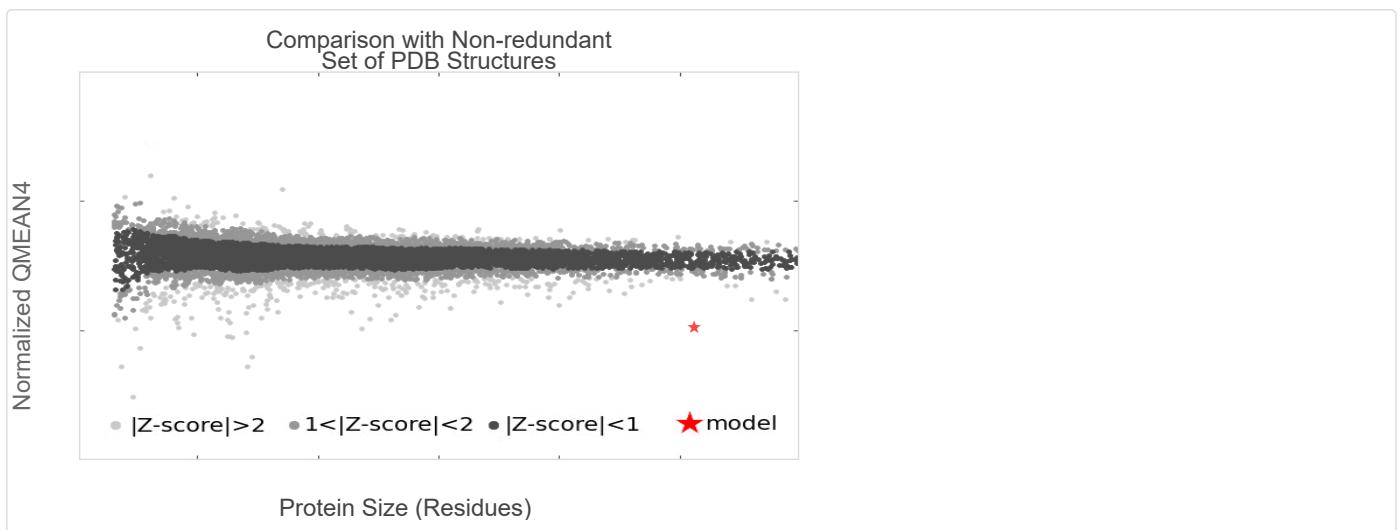
Quality for swissmodel01.pdb

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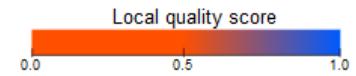
Local Quality Estimate





QMEAN4 Value: -8.30 ⓘ

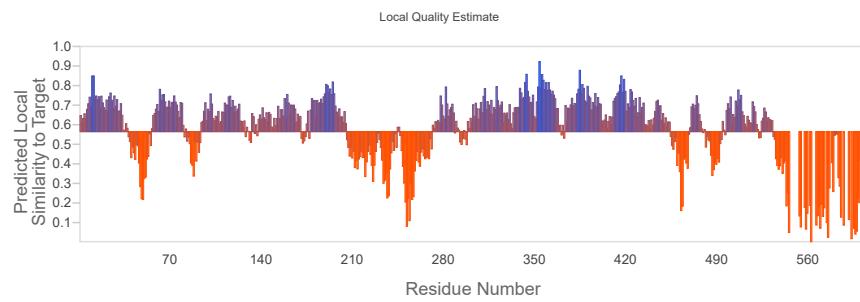
ⓘ Sequence colored by local quality:

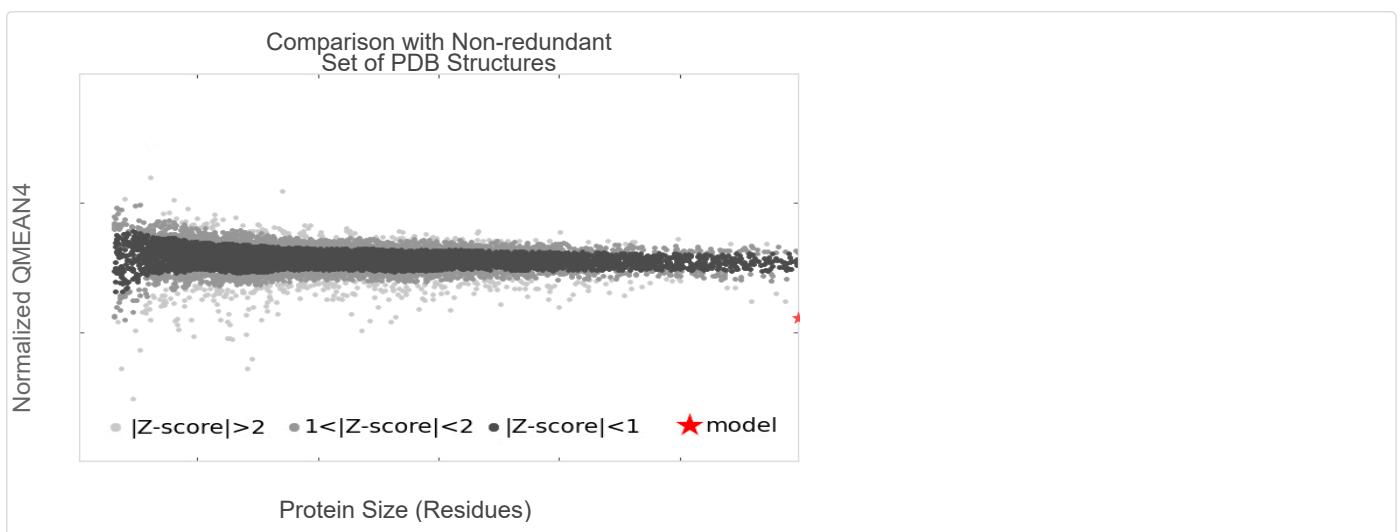


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B: VLRSITDIFYLFHIVLQFRGFIAPSSRVFGRGVLVEDAWEIAKRYLSSYFLIDILAVLPLPVAILIVIPKLRGAKSLNTKTLLKFVVFFQYIP 95
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B: TTLFDGFIFHDALNSGVVESMDFPQKFFYCFWWGLQNLSLGQNLETSTYVWEICFAVFISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRD 285
B: AEQWMMSHRLLPFHRLRERIRRYEQYKWQETRGVDEETLILNLPKDLRRDIKRHLCLALLMRVPMFEKMDEQLLDALCDRLRPVLYTENSFIVREGD 380
B: PVDEMILFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFCGEELLTWALDPHPSPNNLPISTRTVQALSEVEAFALVADDLKVASQFRRLHSKQLRHT 475
B: FRFYSQQWRTWAACFIQAAWRHCRKKLEESLCEEEENR 513
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Quality for modeller04.pdb

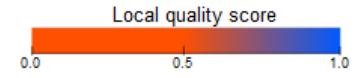
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 Compare



QMEAN4 Value: -6.02 ⓘ

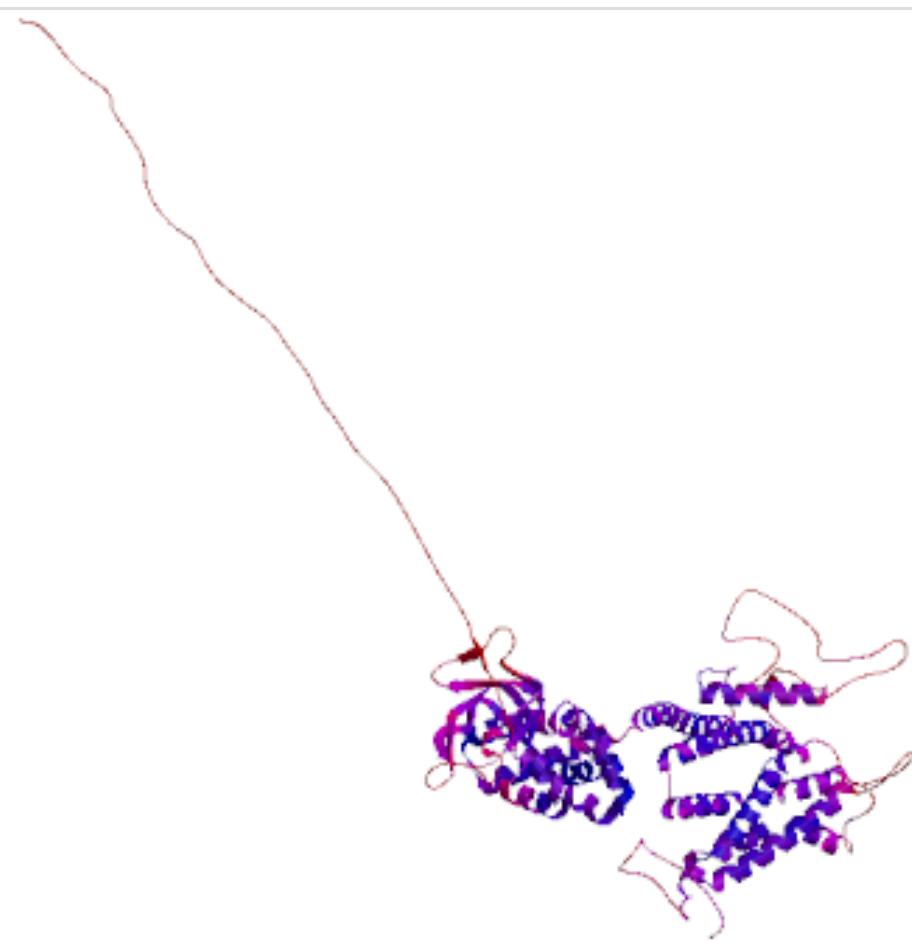
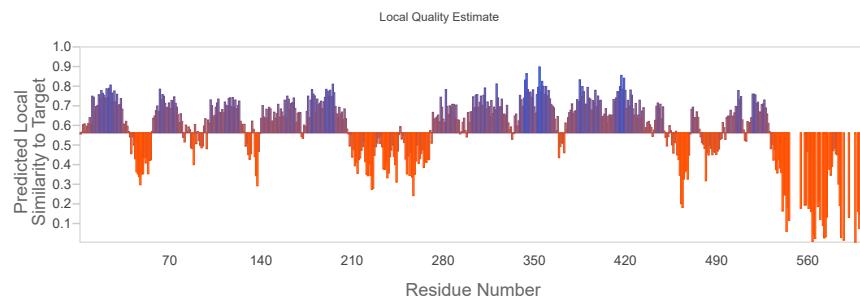
ⓘ Sequence colored by local quality:

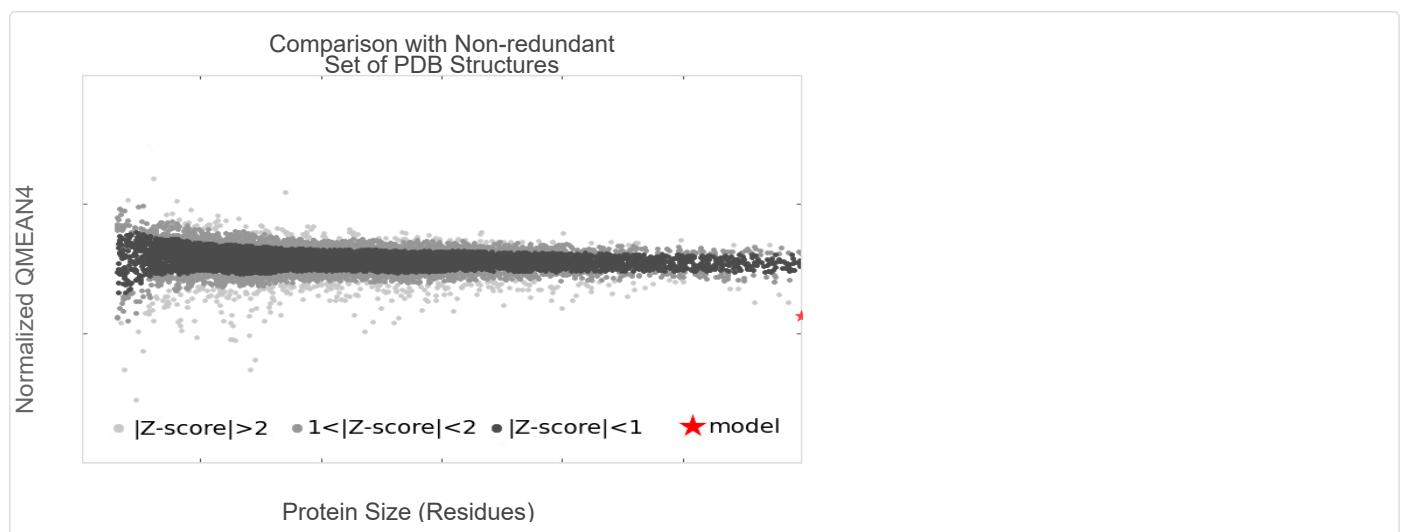


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X: DAWEIAKRYLSSYFLIDILAVLPLPQVAILIVIPKLRGAKSLNTKTLKVVFFQYIPRLLRVYPLYKEVTRTSGILTEATAWAGAAFNLLYMLA 190
X: SHVLGAFWYLFSIERESTCWQRACGNTSACHHSSLYCDDDHNTFIKLLNDSCPPIETPNNTLFDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQN 285
X: LSSLGQNLETSTYVWEICFAVFISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPHEHLRERIRRYEQQYKWQETRGVDETL 380
X: ILNLPKDLRRDIKRHLCALLMRVPFMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFC 475
X: GEELITWALDPHPSNNLPISTRTVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRHCRKLEESLCEEEN 570
X: RLQDALARGGGSSPSLGATIYASRFAANALRALRH 605
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Quality for modeller01.pdb

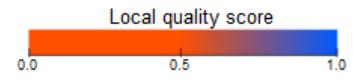
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 Compare



QMEAN4 Value: -5.60 ⓘ

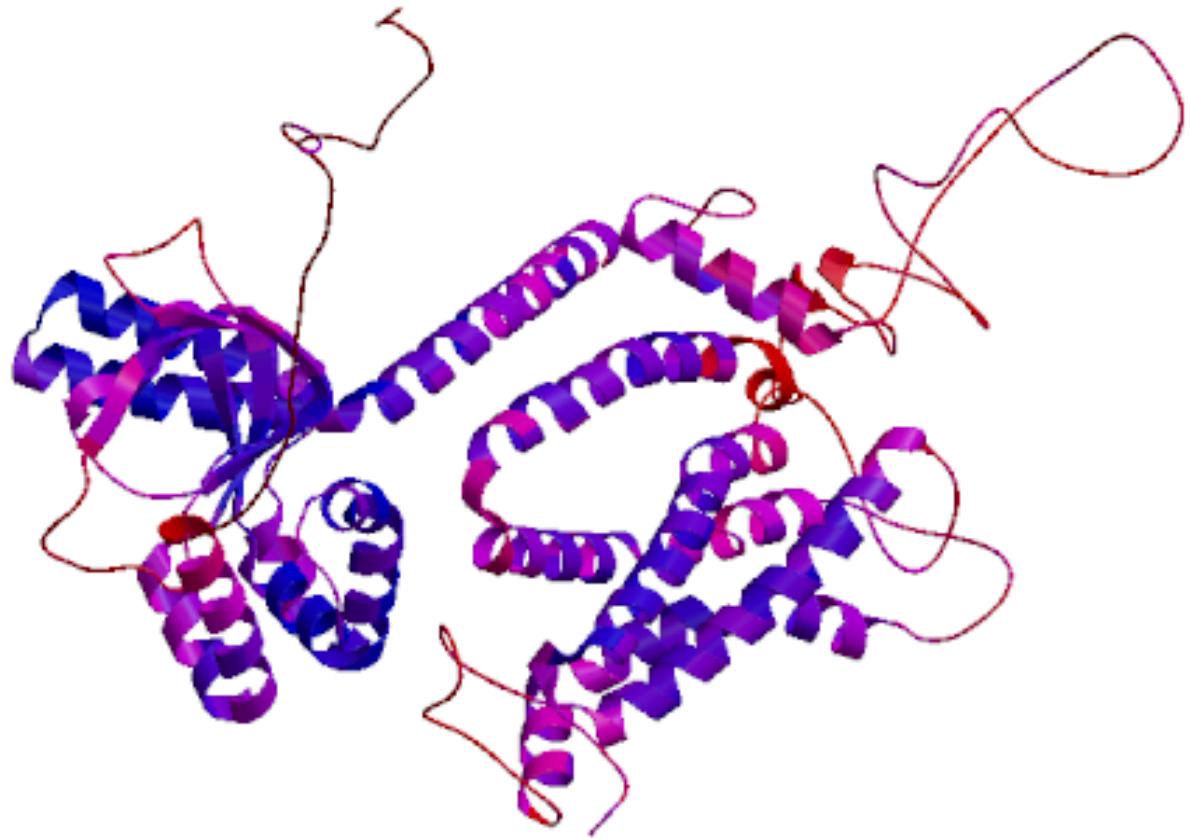
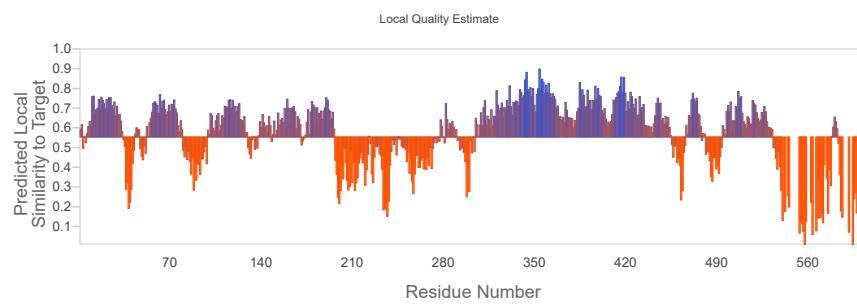
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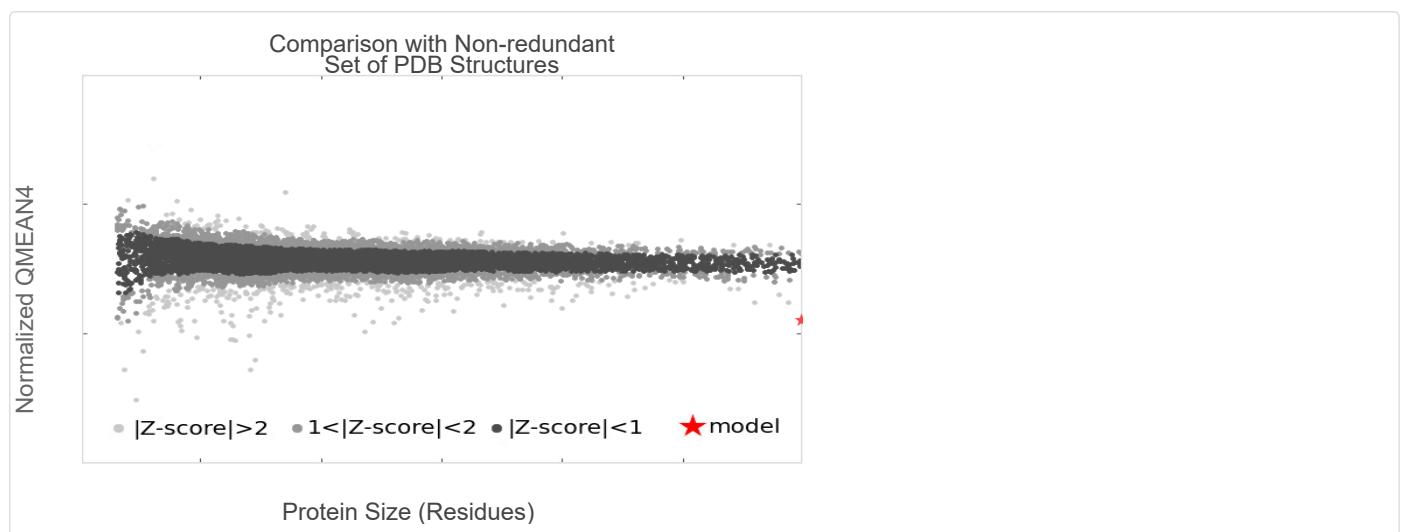


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X: SHVLGAFWYLFSIERESTCWQRACGNTSACHHSSLYCDDDHNTFIKLLNDSCPPIETPNNTLFDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQN 285
X: LSSLGQNLETSTYVWEICFAVFISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQQWMSSHRLLPHEHLRERIRRYEQQYKWQETRGVDETL 380
X: ILNLPKDLRRDIKRHLCALLMRVPFMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMFLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFC 475
X: GEELITWALDPHPSNNLPISTRTVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRHCRKLEESLCEEEN 570
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Quality for modeller06.pdb

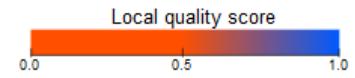
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 Compare



QMEAN4 Value: -6.05 ⓘ

ⓘ Sequence colored by local quality:



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X: SHVLGAFWYLFSIERESTCWQRACGNTSACHHSSLYCDDDHNTFIKLLNDSCPPIETPNNTLFDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQN 285
X: LSSLGQNLETSTYVWEICFAVFISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPPEHLRERIRRYEQQYKWQETRGVDETL 380
X: IILNLPKDLRRDIKRHLCALLMRVPMEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMFLFIMRGKLLTVTTNGGRTGFNSDYLKAGDFC 475
X: GEELITWALDPHPSNNLPISTRTVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRHCRKLEESLCEEEN 570
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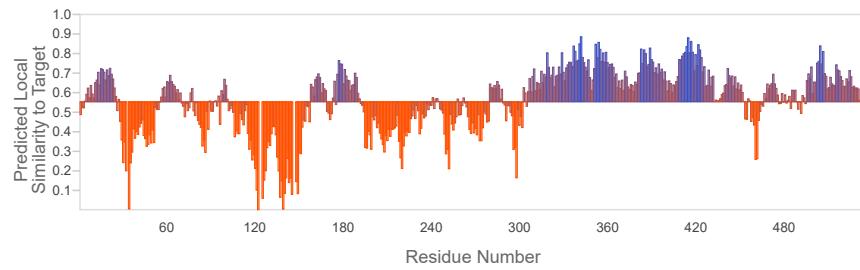
Quality for modeller03.pdb

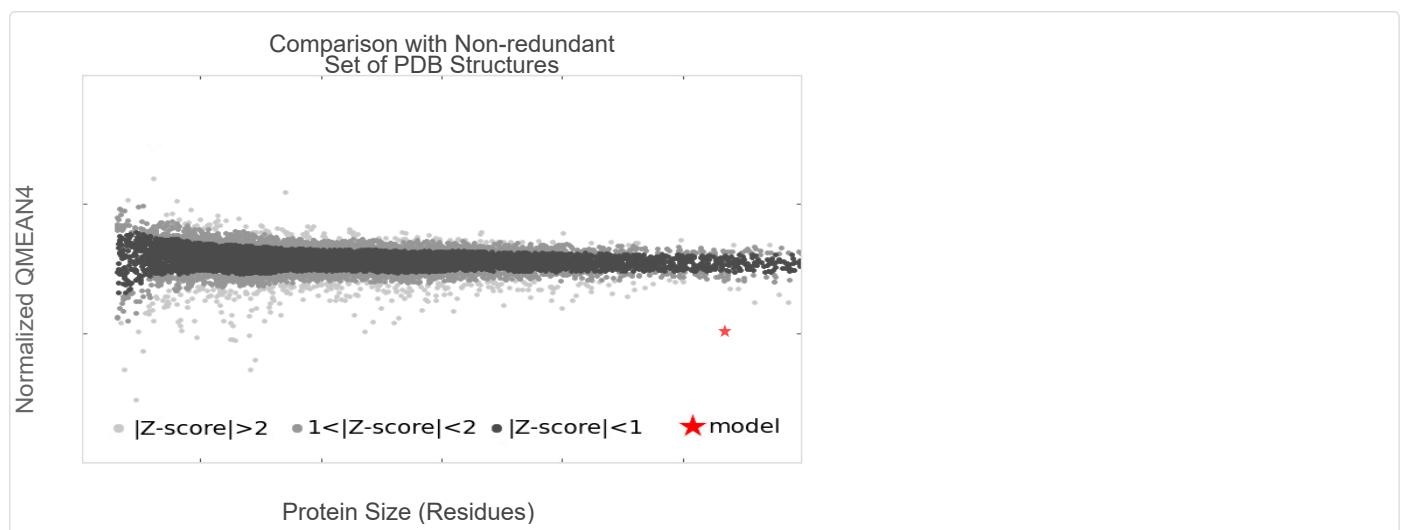
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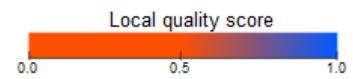
Local Quality Estimate





QMEAN4 Value: -7.69 ⓘ

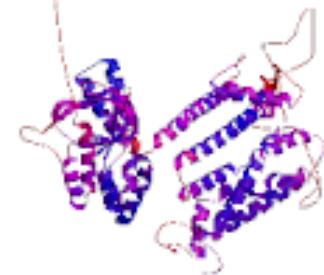
ⓘ Sequence colored by local quality:



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X: WEIAKRYLSSYFLIDILAVLPQVAILIVIPKLRGAKSLNTKTLLKFVVFFQYIPRLLRVYPLYKEVTRTSGILTETAWAGAAFNLLLYMLASH 190
X: VLGAFWYLFSLIERESTCWQRACGNTSACHSSLYCDDDHNTFIKLNDSCPIETPNNTLFDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQNL 285
X: SLGQNLETSTYVWEICFAVFISIAGLVLFSFLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSHRLLPHEHLRERIRRYEQQYKWQEYTRGVDEETLIL 380
X: NLPKDLRRDIKRHLCLALLMRVPMPFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMELFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFCGE 475
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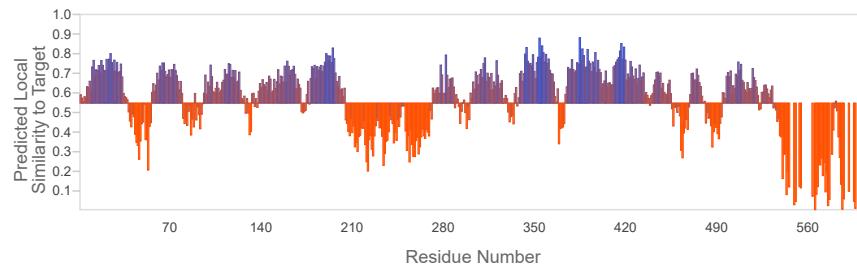
Quality for modeller05.pdb

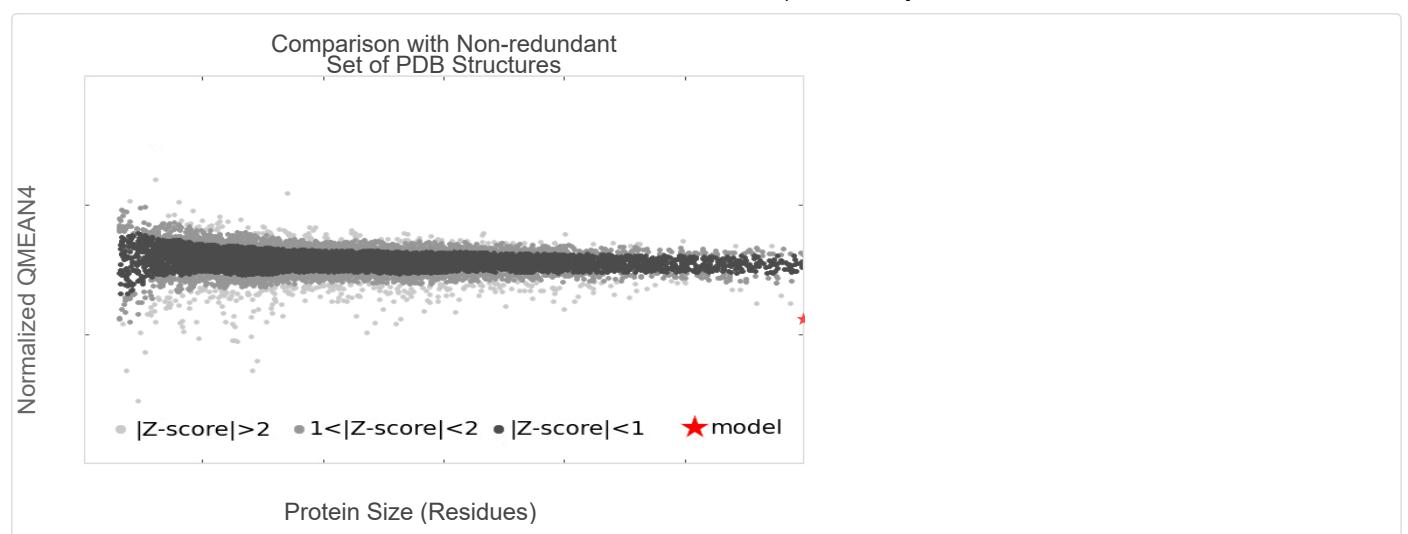
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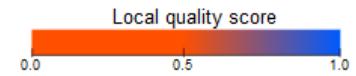
Local Quality Estimate





QMEAN4 Value: -5.93 ⓘ

⌚ Sequence colored by local quality:



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X: SHVLGAFWYLFSSIERESTCWQRACGNTSACHHSSLYCDDDHNTFIKLLNDSCPPIETPNNTLFDFGIFHDALNSGVVESMDFPQKFFYCFWWGLQN 285
X: LSSLGQNLETSTYVWEICFAVFISIAGLVLFSLIGNMQTYLQSTTLRLEEMRVKRRDAEQWMSSHRLLPEHLRERIRRYEQQYKWQETRGVDEETL 380
X: ILLNLPKDLRRDIKRHLCALLMRVPFMFEKMDEQLLDALCDRLRPVLYTENSFIVREGDPVDEMFLFIMRGKLLTVTTNGGRTGFFNSDYLKAGDFC 475
X: GEELITWALDPHPSNNLPISTRTVQALSEVEAFALVADDLKVASQFRRLHSKQLRHTFRFYSQQWRTWAACFIQAAWRHCRKLEESLCEEEN 570
X: RLQDALARGGGSSPSLGATIYASRFAANALRALRH 605
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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 10.1093/bioinformatics/btq662

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 10.1093/bioinformatics/btz828

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 10.1093/bioinformatics/btu457

