

☰ All Projects

Untitled Project Created: today at 02:07

Summary

Templates

45

Models

1

Project Data ▾

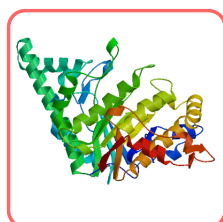
Model Results ⓘ

Order by:

GMQE



Model 01



Structure Assessment

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Oligo-State
Monomer

GMQE
0.69

QMEANDisCo Global:
0.74 ± 0.05

QMEANDisCo Local

QMEAN Z-Scores

Template

2pe4.1.A Hyaluronidase-1

Seq Identity

42.82%

Coverage



Model-Template Alignment

The image displays a sequence alignment between Model_01 and 2pe4.1.A. The alignment is presented in a table-like format with three columns: the model identifier, the amino acid sequence, and the residue number. Blue arrows indicate specific annotations or mutations between the two sequences. For example, arrows point from 'P' in Model_01 to 'L' in 2pe4.1.A at position 1, and from 'S' in Model_01 to 'Q' in 2pe4.1.A at position 10. Other arrows highlight conserved regions or specific substitutions throughout the alignment.

Model_01	LNFRAPPVTPNVPFLWAWNPSEFCLGKFDEPLDM	35
2pe4.1.A	--FRGP-LLPNRPFTTVWVANTQWCLERHGVVDVDV	34
Model_01	SLFSFETGSPRINATGQGVTIFYVDRLLGYYPYIDSI	70
2pe4.1.A	SVFDVVANPGQTFRGPDMTIFYSSQLGTYPYY-TP	68
Model_01	TGVTVNGGIPQKISLQDHLDKAKKDITFYMPV-DN	104
2pe4.1.A	TGEPVFGGLPQNASLIAHLARTEQDILAAIPAPDF	103
Model_01	LGMAYIDWEEWRPTWARNWKPKDVYKNRSIELVQQ	139
2pe4.1.A	SGLAVIDWEAWRPRWAFNWDTKDIYRQRSRALVQA	138
Model_01	QNVQLSLTEATEKAKQEFEEKAGKDFLVETIKLGKL	174
2pe4.1.A	QHPDWPAPQVEAVAQDQFQGAARAWMAGTLQLGRA	173
Model_01	LRPNHLWGYYLFPDCYNHHYKKPGYNGSCFNVEIK	209
2pe4.1.A	LRPRGLWGFYGFDPDCYNDFLSPNYTGQCPSGIRA	208
Model_01	RNDPLSWLWNESTALYPSIYL-NTQQSPVAATLYV	243
2pe4.1.A	QNDQLGWLWGQSRALYPSIYMPAVLEGTKSQMYV	243
Model_01	RNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVL	278
2pe4.1.A	QHRVAEAFRVA-VAAGDPNLPVLPYVQI-FYDTTN	276
Model_01	KFLSQDELVYTFGETVALGASGIVTWGTLSTMRSM	313
2pe4.1.A	HFLPLDELEHSLGESAAQGAAGVVLWVSWENTRTK	311
Model_01	KSCLLLNHYMETIILNPYIINVTLAAKMCSQVLCQE	348
2pe4.1.A	ESCQAIKEYMDTTLGPFILNVTSGALLCSQALCSG	346
Model_01	QGVCIKKNWNSSDYHLNPDNFAIQLE-KGGKFTV	382
2pe4.1.A	HGRCVVRTSHPKALLLNPAFSIQLTPGGGPLSL	381
Model_01	RGKPTLEDLEQFSEKFYCSYSTLSCKEKADV KDT	417
2pe4.1.A	RGALSLEDQAQMAVEFKRCY-----	402
Model_01	DAVDVCIADGVCIDAF LKPPMETEEPQIFY	447
2pe4.1.A	-----	

