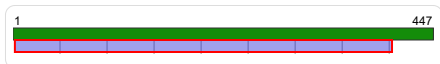
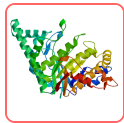


Model Results ?

Order by: GMQE ▼



Model 01



Structure Assessment

Compare ☐Download files 

Display files

**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

43.07%

Coverage

Model-Template Alignment

Model_01 LNFAPPVPPNPPLWAPAPSEFLCKGPDDEPLDM
2pe4.1.A --FRGP--LNPBPPTITVNAWQWCLERGDVDDV
Model_01 SLFSESPRNINATGGQVITLVDPGLVYPYDSI
2pe4.1.A SVFQVAPNPQGTFRGPDHTLPSYSSQLGTYPY--T
Model_01 TGVTVNGTQKQNTSLQDLHKAKKDITMYPV--V
2pe4.1.A TGEVTPVGGIQRASITLAHLARTQDTLAAIPAFD
Model_01 LGMAYVDWEWRNPWAPWNPCKDDVYKNSRELVLQ
2pe4.1.A SGLVAVDWEARNPRAWNPWTKDVIQRQSRALVQA
Model_01 QNVQLSETEATEKAKQFEKAGKDFVITETIKLQ
2pe4.1.A QHPNDPAQPEVAAGQDQFGAARWMAAGTLQGLRA
Model_01 LRPNHNGVYLPDPCNHHYKKGPGVNSCFNVEIK
2pe4.1.A LRPRLGNGVYFGDPCYNVDFPSNYPQCSGPGZRA
Model_01 RNRDPLSHNLSNATYPIYLVNQTSVPAAVETLV
2pe4.1.A QNDQLGWLWGSRALYPSIYMPAVLEGTGKSMYV
Model_01 RHRVRVATRVSKIPDAKSPLYFAKXRIVETDQVL
2pe4.1.A RHRVAVETRVFA--VAGGDPLNLPVPYQI--FYDTN
Model_01 KFLSDEFLVYVETGTVLGAAGSLGVITGTSNMRSM
2pe4.1.A HFLPLDEFLHSLGESAAQGAQGVLLWSWENRTFK
Model_01 KSCCLLBNYMETLNPYINNVITAAKMKSQVLCQ
2pe4.1.A ESCQAQKWMYDITLPGFLINVTSGALLCSACSG
Model_01 QGVCKIKWNSSDYHLHNPDNATGLE--KGGKRTV
2pe4.1.A HGRCKVTRSHPKALLNIPAFSTQLTPGGGFLSL
Model_01 RSKPCTLEDLEDFSEKPYCSY--SLTSCKEADKVDT
2pe4.1.A RGLSLSDQAQMAVEFKRCY--
Model_01 DAVDVCITADGVCIIDAFLLKPPMETEPEQIFY
2pe4.1.A

