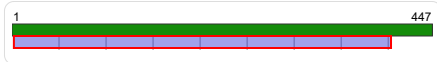
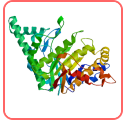


Model Results

Order by: GMQE 



Model 01



Structure Assessment

Compare ☐

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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

Model_01 LFRAPPVDPNPFFLHANNAPSEFLCKGPDPEPLDM
2pea.1.A---FRGP-LLPNPFITVVAHQWCLERHGVDVDD
Model_01 SLFSSEQSPSRINATGGKPTFVDDHLYGVPYD51
2pea.1.ASVFDVYANPGPTFRGPDMTIFVSSQLGTGYPTF--TD
Model_01 TGVTVPTGVTGQSTLDHLHAKKADKTFEYMPV--
2pea.1.ATGCVPTVGGIQRNASITLAHLAREQDILAAIPAPDF
Model_01 LGMAYVDWEERWPTWARNWKPDKVYKNRSLETVLQO
2pea.1.ASGLAVVDWEAWRNPWAPNWDKDIYRQSLRSLVQ
Model_01 QNVQLSELEATEKAKQEFKAGKDFVRSITLAKGL
2pea.1.AQHPDNPAPQVEAAVQDQFGAARWMAAGTLQLRGA
Model_01 LRPNHLLHGYTPDPCYNNHHYKPKGVNGSCFNVEIK
2pea.1.ALRPRGLHGYFGDPCYNYDFTLSPNYTGQCSGFGZRA
Model_01 RNDPLSHUNLSTNCTYPIYLNTQSPVAVALVTV
2pea.1.AQNDQLHGWGSRALYPSIYMPAYLEGTGKSMYV
Model_01 RNRVREIATRVSRIDAKSPILPFAIRIVKTDQVL
2pea.1.ARHVRAEAFRYA-VAAGDGNLPLVPYQI-KYDNTN
Model_01 KFLSDELYVYFTEGTVLAGSGVILVGTGTSKMRSM
2pea.1.AHFLPDELEHSLGESAQAAGVGLVWYSWENTRTK
Model_01 KSCLEENDDMETLNLNPTVINVTAAKMSQVSCQE
2pea.1.AESCCQAIKEYMDDTLGPFLLNVTSGALLCSQALCSG
Model_01 QGVCEVNNSSSDYVHLHNPDAFAGLE-KGGRKTV
2pea.1.AHGRCVVRTSHPKALLINPDSFISQILTPGGGFLSL
Model_01 RSKPTCELEGFSEKPYCESEVLTSCKEADVKDT
2pea.1.ARGALSLEDQAQMAVEFKRCY-----
Model_01 DAVDVCIDAGVCIADFALKPMTEPEQIF
2pea.1.A-----

