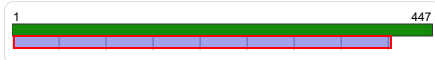
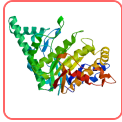


Model Results

Order by: GMQE 

Model 01



Structure Assessment

Compare ☐

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**Oligo-State
Monomer**

GMQE
0.69

QMEANDisCo Global:
0.73 ± 0.05

QMEANDisCo Local
QMEAN Z-Scores

Template
2pe4.1.A Hyaluronidase-1

Seq Identity

42.82%

Coverage

Model-Template Alignment

Model_01 LFRAPPVDPNPFFLHANNAPSEFCLGKDPDEPLDM
2pe4.1.A -FRGP-LPPNPFTITVANNQWCLERHGVDVDD
Model_01 SLFSESPSRINATGQGVITFVDBLGYVPYDSI
2pe4.1.A SVFDVYANPQGTFRGPDMTIFVSSQLGTGYPTF-T
Model_01 TGVTVNTPVSTQHLHLAKKADKTIEMPV-ND
2pe4.1.A TGEVPVFGGLQNASITDAHIREQDTILAAIPADF
Model_01 LGMAYVDWEERWPTWARNWKPDKVYKNRSTELVQQ
2pe4.1.A SOLVAVDWEANRPPWAPNWDKDIYRQSRALVQA
Model_01 QNVQLSLTEATEKAQKQFEKAGDITFETIKLGL
2pe4.1.A QHPNDPAPOQVEAAVQDQFGAARWMAAGTLQGRA
Model_01 LRPNHNGVYLPDCYVNHYYKPKPGVNGSCFNVEIK
2pe4.1.A LRPKRGHGLVFGPDYCNVDFPSNYPQCPGSGZRA
Model_01 RNDPDLHNSLSTNCTPYTLNTQSPVAETLTV
2pe4.1.A QNDQLWHLWGSRALYPSIYNPAVLEGTGKSNVY
Model_01 RHNRVREATIRVSLDAKSPILPFAKXIRIVETDYN
2pe4.1.A RHNRVAREFRVA-VAAGDNDPLVPYVQI-PYDTN
Model_01 KFLSDEQLVYFYGETVALGASGIVLNGTLESMRSM
2pe4.1.A HFLPLDELEHSLGESAAQAGVVLWWSWENRTRK
Model_01 KSCLELLDNMTETLNPVQINVTAAKMSQVLCQE
2pe4.1.A ESCQAIKEYMDDTLPGFLLNVTSGALACSCSG
Model_01 QGVCIKNNWSSDYHLNPNDAIGLE-KGGKRTV
2pe4.1.A HGRCVRRTHSPHKKLLINPAFSFJQLTPGGGFLSL
Model_01 RSKPTCELEDFSEKPYSLTSLSCKEADKVDPT
2pe4.1.A RGLSLSDQAQMAVEFKRCY-
Model_01 DAVDVCIDAGVCIIDAFLLPKPMETEEPIQFY
2pe4.1.A

