

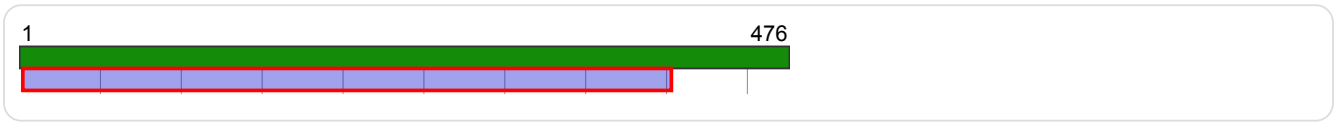
Untitled Project

Created: today at 06:33

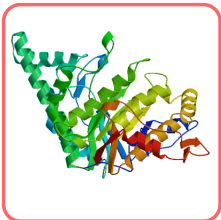
Summary Templates 37 Models 1 Project Data ▾

Model Results ⓘ

Order by: GMQE ▾



Model 01



Structure Assessment

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Oligo-State Monomer	GMQE 0.65	QMEANDisCo Global: 0.73 ± 0.05
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QMEANDisCo Local	▾
QMEAN Z-Scores	▾

Template 2pe4.1.A Hyaluronidase-1	Seq Identity 43.83% Coverage 	▾
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Model-Template Alignment	▴
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Model_01 LNFRAPPIIPNMPFLWAWNAPSEFCLGKFDEPLDM
 2pe4.1.A --FRGP-LLPNRPFTTVWVANTQWCLERHGVVDVDV

Model_01 SLFSLTGSPRINVTGQAVTIFYVDRLGYYPYIDSI
 2pe4.1.A SVFDVVANPGQTFRGPDMTIFYSSQLGTYPYY-TP

Model_01 TGVTVNGGIPQKISLQDHLDKAKKDILFYMPV-DN
 2pe4.1.A TGEIPVFGGLPQNASLIAHLARTEQDILAAIPAPDF

Model_01 LGMAVIDWEEWRPTWARNWKPKDVYKNRSIELVQQ
 2pe4.1.A SGLAVIDWEAWRPRWAFNWDTKDIYRQRSRALVQA

Model_01 QNVQLNLTEATEKAKQEFEEKAGKDFMVETIKLGKL
 2pe4.1.A QHPDWPAPQVEAVAQDQFQGAARAWMAGTLQLGRA

Model_01 LRPNHLWGYYLFPDCYNHHYKKPGYNGSCFNVEIK
 2pe4.1.A LRPRGLWGFYGFPCYNYDFLSPNYTGQCPSGIRA

Model_01 RNDLWSLWNESTALYPSIYL-NTQQSPVAATLYV
 2pe4.1.A QNDQLGWLWGQSRALYPSIYMPAVLEGTGKSQMYV

Model_01 RNRVREAIRVSKIPDAKSPLPVFVYARIVFTDQVL
 2pe4.1.A QHRVAEAFRVA-VAAGDPNLPVLPYVQI-FYDTTN

Model_01 KFLSQDELVYTFGETVALGASGIVTWGSLSIMRSM
 2pe4.1.A HFLPLDELEHSLGESAAQGAAGVVLWVSWENTRTK

Model_01 KSCLLLNKNYMETIILNPYIINVTLAAKMCSQVLCQE
 2pe4.1.A ESCQAIKEYMDTTLGPFILNVTSGALLCSQALCSG

Model_01 QGVCIRKDNSSDYHLNPDNFAIQLE-KGGKFTV
 2pe4.1.A HGRCVVRTSHPKALLLNPAFSTIQLTPGGGPLSL

Model_01 RGKPTLEDLEQFSEKFYCSCTLSCKEKADV KDT
 2pe4.1.A RGALSLEDQAQMAVEFKRCY-----

Model_01 DAVDVCIADGVCIDAF LKPPMETEESQIFYNASPS
 2pe4.1.A -----

Model_01 TLSATMFIWRLEVWDQGISRMGFF
 2pe4.1.A -----

