

All Projects

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Summary Templates 41 Models 1 Project Data

Model Results

Order by: GMQE

1447

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 LNFRAPPVDPNPFLWANNAPSEFCLGKPDDEPLDM

2pe4.1.A --FRGP-LIPNPPFTITVWVANIQCLERHGVDDVDV

Model_01 SLFSEEGSPRINATGGQVITPYVDBLGYYPYDSDI

2pe4.1.A SVFDVYANPGQTFRGPDMITPYSSQLGTYPVY-TP

Model_01 TGVLYNGGITPQWISLQDHLDAKKKDITFVMPV-DN

2pe4.1.A TGEDVYFGGLQNASLIAHLARTEQDILAAIPAPDF

Model_01 LGMAVYDWEWRPTWARRNWKPKDVYKNRSIELVQQ

2pe4.1.A SGLAVYDWEAWRPWAFNWDTKDIYRQRSRALVQA

Model_01 QNVQLSFEATEKAKQFEKAGKDFLVETIKLGKL

2pe4.1.A QHPDWPAQVEAVAQDQFGGAARAWMAGTLQLERA

Model_01 LRPNHLMGYLLFPDCYNHHYKPGYNGSCFAYVYIK

2pe4.1.A LRPRLWGFYGFDPDCYNVDFLSPNYTGQCPSGTRA

Model_01 RNDLSWLNNESTALYPSIYLNIQSQSPVAATLYV

2pe4.1.A QNDQLGWEWGQSRALYPSIYMPAYLEGTGKSQMYV

Model_01 RNRVREAIRVSKLRDAKSPLPFAVIRIVETQVL

2pe4.1.A QHRVAEAFRVA-VAAGDPNLPYLPYVQI-FYDTTN

Model_01 KFLSQDELVYTFGETVALGASGIVLNGTASHMRSM

2pe4.1.A HFLPLDELEHSLGESAAQGAAGVVLWVSWENTRTK

Model_01 KSCLELDNYMETILNPYIINVFLAAKMSQVLCQE

2pe4.1.A ESCQAIKEYMDTTLGPFILNVTSGALLCSQALCSG

Model_01 QGVCIKNWNSSDYHLNPDNFAIQLEKGGKKTIV

2pe4.1.A HGRVCVRRISHPKALLLNPAFSISQILTPGGGPLSL

Model_01 RSKPTCEDLEQFSEKFYCSQYSTLSCKEKADV KDT

2pe4.1.A RGALSLEDQAQMAVEFKRCY-----

Model_01 DAVDVCIAIDGVCIDAFLLKPMMEETEPQIFY

2pe4.1.A -----

Cartoon

Halozyme EX2186
Merck v. Halozyme
PGR2025-00050

<https://swissmodel.expasy.org/interactive/pLkWYd/models/>

1/2

