

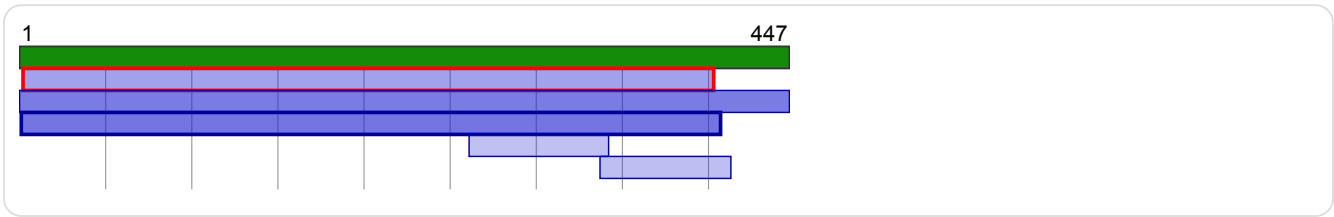
Untitled Project

Created: today at 01:53

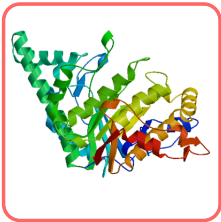
Summary Templates 44 Models 5 Project Data ▾

Model Results ⓘ

Order by: GMQE ▾



Model 05



Structure Assessment

Compare ☐

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Oligo-State
Monomer

GMQE
0.70

QMEANDisCo Global:
0.75 ± 0.05

QMEANDisCo Local
QMEAN Z-Scores

Template
2pe4.1.A Hyaluronidase-1

Seq Identity
43.07%
Coverage

Model-Template Alignment

Model_05 LNFRAPPVTPNVPFLWAWNPSEFCLGKFDEPLDM

2pe4.1.A --FRGP-LLPNRPFTTVWVANTQWCLERHGVVDVDV

Model_05 SLFSELTGSPRINATGQGVITIFYVDRLGYYPIYDSI

2pe4.1.A SVFDVVANPGQTFRGPDMTIFYSSQLGTYPYY-TP

Model_05 TGVTVNGGIPQKISLQDHLDKAKKDITFYMPV-DN

2pe4.1.A TGEIPVFGGLPQNASLIAHLARTEQDILAAIPAPDF

Model_05 LGMAVIDWEEWRPTWARNWKPKDVYKNRSIELVQQ

2pe4.1.A SGLAVIDWEAWRPRWAFNWDTKDIYRQRSRALVQA

Model_05 QNVQLSLTEATEKAKQEFEEKAGKDFLVETIKLGKL

2pe4.1.A QHPDWPAPQVEAVAQDQFQGAARAWMAGTLQLGRA

Model_05 LRPNHLWGYYLFPDCYNHHYKKPGYNGSCFNVEIK

2pe4.1.A LRPRGLWGFYGFPCYNDFLSPNYTGQCPSGIRA

Model_05 RNDPLSWLWNESTALYPSIYLNTIQQSPVAATLYV

2pe4.1.A QNDQLGWLWGQSRALYPSIYMPAVLEGTKSOMYV

Model_05 RNRVREAIRVSKIPDAKSPLPVFAYTRIVFTDQVL

2pe4.1.A QHRVAEAFRVA-VAAGDPNLPVLPYVQI-FYDTTN

Model_05 KFLSQDELVYTFGETVALGASGIVTWGTLSTIMRSM

2pe4.1.A HFLPLDELEHSLGESAAQGAAGVVLWVSWENTRTK

Model_05 KSCLLLLKNYMETIILNPYIINVTLAAKMCSQVLCQE

2pe4.1.A ESCQAIKEYMDTTLGPFILNVTSGALLCSQALCSG

Model_05 QGVCIRKNWNSSDYHLNPDNFAIQLE-KGGKFTV

2pe4.1.A HGRCVVRTSHPKALLLLNPASTSIQLTPGGGPLSL

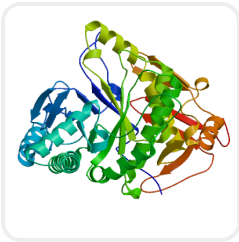
Model_05 RGKPTLEDLEQFSEKIFYCSCYSTLSCKEKADV KDT

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

Model_05 DAVDVCIADGVCIDAF LKPPMETEEPQIFY

2pe4.1.A -----

Model 01



Structure Assessment

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Oligo-State ⓘ
Monomer

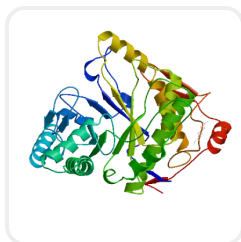
GMQE ⓘ
0.94

Template
P38568.1.A Hyaluronidase PH-20
AlphaFold DB model of HYALP_MACFA (gene: SPAM1, organism: Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey))

Seq Identity
89.26%
Coverage

Model-Template Alignment

Model 02


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Oligo-State

Monomer

GMQE

0.89

QMEANDisCo Global:

0.93 ± 0.05

Ligands

1 x NAG

QMEANDisCo Local**QMEAN Z-Scores****Template**

9jub.1.A Hyaluronidase PH-20

Cryo-EM structure of human hyaluronidase PH-20

Seq Identity

99.75%

Coverage**Model-Template Alignment**

Model 03


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Oligo-State

Monomer

(matching prediction)

GMQE

0.05

QMEANDisCo Global:

0.43 ± 0.10

QMEANDisCo Local**QMEAN Z-Scores****Template**

3iwp.3.A Copper homeostasis protein cutC homolog

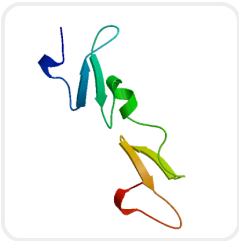
Crystal structure of human copper homeostasis protein CutC

Seq Identity

20.27%

Coverage**Model-Template Alignment**

Model 04



Structure Assessment

Compare ☐

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Oligo-State ⓘ

Monomer

GMQE ⓘ

0.05

QMEANDisCo Global: ⓘ

0.35 ± 0.11

QMEANDisCo Local

QMEAN Z-Scores

Template

9cli.1.D Coagulation factor X

Cryo-EM model derived from localized reconstruction of human adenovirus (Ad5)-hexon-FX complex at 3.6Å resolution

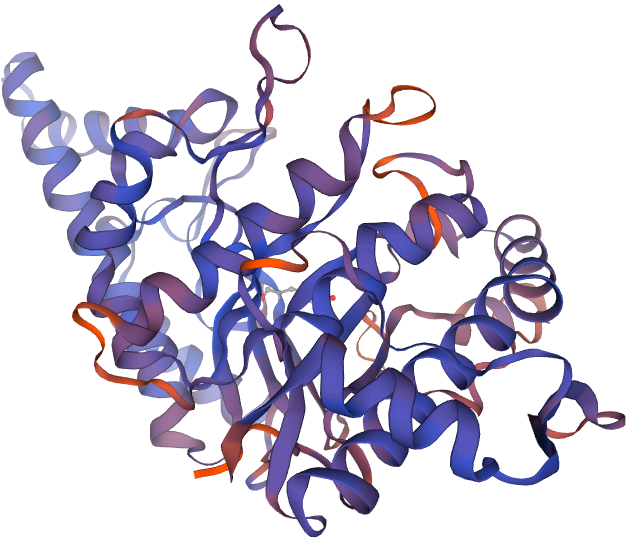
Seq Identity

18.06%

Coverage



Model-Template Alignment



  Cartoon ▲  ▲  ▲ 