

All Projects

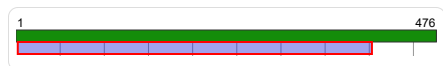
Untitled Project

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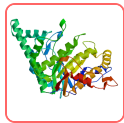
Summary Templates 34 Models 1 Project Data

Model Results

Order by: GMQE



Model 01



Structure Assessment

Compare

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Oligo-State	GMQE	QMEANDisCo Global:
Monomer	0.65	0.73 ± 0.05

QMEANDisCo Local ▼
QMEAN Z-Scores ▼

Template ▼
 2pe4.1.A Hyaluronidase-1 Seq Identity
43.83%
Coverage

Model-Template Alignment

```

Mode1_01 L NFRAPPIIPNMPFLWAWAPSEFC LGK DDEPLDM
2pe4.1.A --FRGP-LIPNPPFTVWVA NTQWCLERHGVDVDV
Mode1_01 SLFSLPGSPRINVTGQAVTIPYVDBLGYPPYD SI
2pe4.1.A SVFDVW ANPGQTFRGPDMITIPYSS LGTYPVY TP
Mode1_01 TGVIVNGGIPQWISLQDHLDKAKKDI LEYMPV-DN
2pe4.1.A TGEDVYFGGLQNASL LAHLARTEQDILAAIPAPDF
Mode1_01 LGMAVFDWEWRPTWARNNWKPKDVYKNRSTELVQQ
2pe4.1.A SGLAVFDWEAWRPRWAPNWDTKDIYRQRSRALVQA
Mode1_01 QNVQLNTEATEKAKQEFKAGKDFHVFETIKLQKL
2pe4.1.A QHPDWPA PQVEAVAQQDFQGAARAWMAGTLQLQRA
Mode1_01 ERPNHLEWGYLFPDCYNHHYKPGYNGSCFVYVYIK
2pe4.1.A ERPRGELWGFYGFDCYNDFLSPNYTGQCPSSGTRA
Mode1_01 RNDLSLWLNHSTALYPSIYLNIQQSPVAATLYV
2pe4.1.A QNDQLGWELWGSRALYPSIYMPAVLEGTGKSSQMYV
Mode1_01 RRRVREAIRVSKLRDAKSPLPVFAVRIVETDQVL
2pe4.1.A QHRVAEAFRVA-V AAGDPNLPVLPYVQI-FYDTTN
Mode1_01 KFLSQBELVYTFGETVALGSGIVLIGSSLSMRSM
2pe4.1.A HFLPLDELEHSLGESAAQGAAGVVLHVSWENTRTK
Mode1_01 KSCCLLDNYMDFLNPYIINVFLAAKMCSQVLCQE
2pe4.1.A ESCQAIKEYMDFLGPFI LNVTSGALLCSQALCSG
Mode1_01 QGVCIKDWNSDYLHLNPDNFAIQLEKGGKKT V
2pe4.1.A HGRRCVRRISHPKALLLNPA SFSIQLTPGGGPLSL
Mode1_01 RQKPTCEDLEQFSEKFYCSQYSLSCKEKADVKDT
2pe4.1.A RGALSLEDQAQMAVEFKRCY-----
Mode1_01 DAVDVC IADGVCIDAF LKPPMETEESQIFYNASPS
2pe4.1.A -----
Mode1_01 T L S A T M F I W R L E V W D Q G I S R M G F F
2pe4.1.A -----
  
```



Cartoon

