

All Projects

Untitled Project Created: today at 01:04

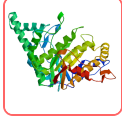
Summary Templates 37 Models 1 Project Data

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
	43.58%
	Coverage

Model-Template Alignment

```

Mode1_01 L NFRAPPIIPNMPFLWAWAPSEFC LGK DDEPLDM
2pe4.1.A --FRGP-LIPNPPFTVWVA NTQWCLERHGVDVDV
Mode1_01 SLFSLPGSPRINVTGQAVTIPYVDBLGYPPYD SI
2pe4.1.A SVFDVWV ANPGQTFRGPDMITIPYSSQLGTYPIY TP
Mode1_01 TGVIVNGGIPQWISLQDHLDKAKKDILEYMPV-DN
2pe4.1.A TGEDVYFGGLQNASL LAHLARTEQDILAAIPAPDF
Mode1_01 LGMAVFDWEWRPTWARNNWKPKDVYKNSIETLVQQ
2pe4.1.A SGLAVFDWEAWRPRWAPNWDTKDIYRQRSRALVQA
Mode1_01 QNVQLNTEATEKAKQEFKAGKDFHMETIKLQK L
2pe4.1.A QHPDWPA PQVEAVAQDFQGAARAWMAGTLQLERA
Mode1_01 ERPNHLEWQYLF PDCYNHHYKPGYNGSCFVYKIK
2pe4.1.A ERPRGELWGFYGF PDCYNDFLSPNYTGQCPSTRA
Mode1_01 RNDLSLWLNHSTALYPSIYLNIQQSPVAATLYV
2pe4.1.A QNDQLGWELWQSRA LYP SIYMPAVLEGTGKSQMYV
Mode1_01 RRRVREAIRVSKLRDAKSPLPVFAVRIVETQVL
2pe4.1.A QHRVAEAFRVA-V AAGDPNLPVLPYQI-FYDTTN
Mode1_01 KFLSQBELVYTFGETVALGASGIVLIGSLSIMRSM
2pe4.1.A HFLPLDELEHSLGESAAQGAAGVVLHVSWENTRTK
Mode1_01 KSCCLLDNYMRTILNPIYIINVFLAAKMCSQVLCQE
2pe4.1.A ESCQAIKEYMDTTLGPFILNVTSGALLCSQALCSG
Mode1_01 QGVCIKXDNWSSDYLLHLPDNFAIQLEKGGKKT V
2pe4.1.A HGRRCVRRISHPKALLLNPA SFSIQLTPGGGPLSL
Mode1_01 RSKPTCEDLEQFSEKIFYSQYSLSCKEKADV KDT
2pe4.1.A RGALSLEDQAQMAVEFKRCY-----
Mode1_01 DAVDVCIADGVCIDAF LKPPMETEESQIFYNASPS
2pe4.1.A -----
Mode1_01 TLSATMFIWRLEVWDQGISRMGFF
2pe4.1.A -----

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Cartoon ▼ 📷 ▶ ⏪ ⏩ 🔄

