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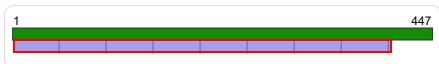
Untitled Project

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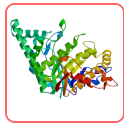
Summary Templates 45 Models 1 Project Data

Model Results

Order by: GMQE



Model 01



Structure Assessment

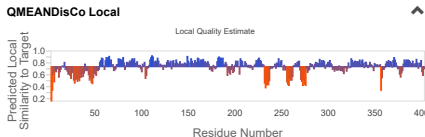
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Oligo-State Monomer

GMQE 0.69

QMEANDisCo Global: 0.74 ± 0.05



QMEAN Z-Scores

Template

Template	Seq Identity
2pe4.1.A Hyaluronidase-1	42.82%
	Coverage

Model-Template Alignment

```

Mode1_01 L NFRAPPVDPNPF L W A N A P S E F C L G K P D D E P L D M
2pe4.1.A - - F R G P - L P N D P F T I V W A N T Q W C L E R H G V D V D V
Mode1_01 S L F S E P G S P R I N A T G Q Q V I T P V D R L G Y Y P D S I
2pe4.1.A S V F D V A N P G T F R G P D M I T P Y S S L G T Y P V Y - T P
Mode1_01 T G V I N G G I P Q I S L Q D H L D K A K K D I T F M P V - D N
2pe4.1.A T G E P V F G G L E Q N A S L T A H L A R T E Q D I L A A I P A P D F
Mode1_01 L G M A V P D W E E W R P T W A R N W K P K D V Y K N R S I E L V Q Q
2pe4.1.A S G L A V P D W E A W R P R W A P N W T K D I Y R Q R S R A L V Q A
Mode1_01 Q N V Q L S T E A T E K A K O E F E K A G K D F L V E T I K L Q K L
2pe4.1.A Q H P D W P A P Q V E A V A Q D Q F G A A R A W M A G T L Q L Q R A
Mode1_01 R P N H L W G Y L P P D C Y N H H Y K K P G Y N G S C F N V E I K
2pe4.1.A E R P R G L W G F Y G F P D C Y N Y D F L S P N Y T G Q C P S G P R A
Mode1_01 R N D L S W L N E S T A L Y P S I Y L N I Q Q S P V A T L Y V
2pe4.1.A Q N D L G W L W G S R A L Y P S I Y M P V L E G T G K S Q M Y V
Mode1_01 R R R V E A I R V S K L R D A K S P L P F A Y R I V E T Q V L
2pe4.1.A Q H R V A E A F R V A - V A G D P N L P Y L P Y Q I - K Y D T T N
Mode1_01 K F L S Q D E L V Y T F G E T V A L G S G I V I N G T E S I M R S M
2pe4.1.A H F L P L D E L E H S L G E S A A Q G A A G V L W V S W E N T R T K
Mode1_01 K S C R L E D N Y M E T I L N P Y I I N V T L A A K M S Q V L C Q E
2pe4.1.A E S C Q A I K E Y M D T T L G P F I L N V T S G A L L C S Q A L C S G
Mode1_01 Q G V E I K N W N S S D Y L H L N P D N F A I Q L E - K G G K T V
2pe4.1.A H G R C V R R T S H P K A L L L N P A S F S I Q L T P G G G P L S L
Mode1_01 R G K P T C E D L E Q F S E N F Y C S Y S T L S C K E K A D V K D T
2pe4.1.A R G A L S L E D Q A Q M A V E F K R C Y - - - - -
Mode1_01 D A V D V C I A D G V C I D A F L K P P M E T E E P Q I F Y
2pe4.1.A - - - - -

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Halozyyme EX2193
 Merck v. Halozyyme
 PGR2025-00030

