

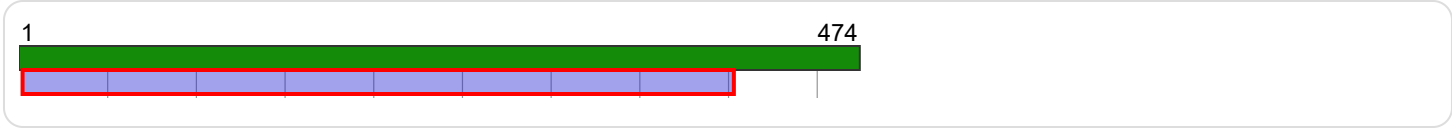
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# Untitled Project Created: today at 18:31

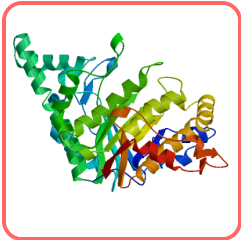
Summary    Templates 37    Models 1    Project Data ▼

## Model Results

Order by: GMQE ▼



### Model 01



Structure Assessment

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|                               |                     |                                          |
|-------------------------------|---------------------|------------------------------------------|
| <b>Oligo-State</b><br>Monomer | <b>GMQE</b><br>0.66 | <b>QMEANDisCo Global:</b><br>0.73 ± 0.05 |
|-------------------------------|---------------------|------------------------------------------|

|                         |   |
|-------------------------|---|
| <b>QMEANDisCo Local</b> | ▼ |
| <b>QMEAN Z-Scores</b>   | ▼ |

|                 |   |
|-----------------|---|
| <b>Template</b> | ▼ |
|-----------------|---|

|                          |                                                                                                                                          |
|--------------------------|------------------------------------------------------------------------------------------------------------------------------------------|
| 2pe4.1.A Hyaluronidase-1 | <b>Seq Identity</b><br>43.83%<br><b>Coverage</b><br> |
|--------------------------|------------------------------------------------------------------------------------------------------------------------------------------|

|                                 |   |
|---------------------------------|---|
| <b>Model-Template Alignment</b> | ▲ |
|---------------------------------|---|

Halozyyme EX2199  
Merck v. Halozyyme  
PGR2025-00033

Model\_01 L N F R A P P V I P N V P F L W A W N A P S E F C L G K F D E P L D M  
 2pe4.1.A - - F R G P - L L P N R P F T T V W N A N T Q W C L E R H G V D V D V

Model\_01 S L F S L T G S P R I N V T G Q G V T I F Y V D R L G Y Y P Y I D S I  
 2pe4.1.A S V F D V V A N P G Q T F R G P D M T I F Y S S Q L G T Y P Y Y - T P

Model\_01 T G V T V N G G I P Q K I S L Q D H L D K A K Q D I T E Y M P V - D N  
 2pe4.1.A T G E P V F G G L P Q N A S L I A H L A R T F Q D I L A A I P A P D F

Model\_01 L G M A V I 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 I D W E A W R P R W A F N W D T K D I Y R Q R S R A L V Q A

Model\_01 Q N V Q L S L A E A T E K A K Q E F E K A G K D F M V E T I K L G K L  
 2pe4.1.A Q H P D W P A P Q V E A V A Q D Q F Q G A A R A W M A G T L Q L G R A

Model\_01 L R P N H L W G Y Y L F 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 L 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 I R A

Model\_01 R N D D L S W L W N E S T A L Y P S I Y L N T Q Q S P V A A T L Y V  
 2pe4.1.A Q N D Q L G W L W G S R A L Y P S I Y M P A V L E G T G K S Q M Y V

Model\_01 R N R V R E A I R V S K I R D A K S P L P V F V Y A R I V E T D Q V L  
 2pe4.1.A Q H R V A E A F R V A - V A A G D P N L P V L P Y V Q I - F Y D T T N

Model\_01 K F L S R D E L V Y T L G E T V A L G A S G I V I N G S L S I V 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 V L W V S W E N T R T K

Model\_01 K S C L L L K N Y M E T I L N P Y I I N V T L A A K M C 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

Model\_01 Q G V C I R K D W N S S D Y L H L N P D N F A I Q L E - K G G K F 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

Model\_01 R G K P T P E D L E Q F S E K F Y C S C 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 C R C Y - - - - -

Model\_01 D A V D V C I A D G V C I D A F L K P P K E T E E S Q I F Y N A S P S  
 2pe4.1.A - - - - -

Model\_01 T L S A T M F I V S I L F L I I S S V V S L  
 2pe4.1.A - - - - -

