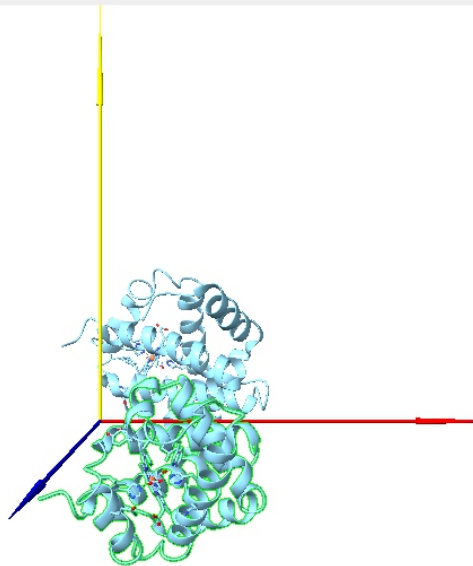




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Seqview [ID: aligned\_1.fasta]



1 11 21

Consensus m v L S p a D K t n v k a a W s K l g g H a g e y G A E A L

Conservation

1pbx\_0\_A - S L S D K D K A A V R A L W S K I G K S A D A I G N D A L

HBA\_HUMAN\_P69905 M V L S P A D K T N V K A A W G K V G A H A G E Y G A E A L

HBA\_TURTLE\_P83134 - M L T E D D K Q L I Q H V W E K V L E H Q E D F G A E A L

HBA\_TURKEY\_P81023 M V L S A A D K N N V K G I F T K I A G H A E E Y G A E T L

HBA\_RABBIT\_P01948 M V L S P A D K T N I K T A W E K I G S H G G E Y G A E A V

HBA\_HORSE\_P01958 M V L S A A D K T N V K A A W S K V G G H A G E Y G A E A L

31 41 51

Consensus E R M F l v y P t T K T Y F P H F - D l s H G S a Q I K a H

Conservation

1pbx\_0\_A S R M I V V Y P Q T K T Y F S H W P D V T P G S P H I K A H

HBA\_HUMAN\_P69905 E R M F L S F P T T K T Y F P H F - D L S H G S A Q V K G H

HBA\_TURTLE\_P83134 E R M F I V Y P S T K T Y F P H F - D L H H D S E Q I R H H

HBA\_TURKEY\_P81023 E R M F I T Y P P T K T Y F P H F - D L S H G S A Q I K G H

HBA\_RABBIT\_P01948 E R M F L G F P T T K T Y F P H F - D F T H G S E Q I K A H

HBA\_HORSE\_P01958 E R M F L G F P T T K T Y F P H F - D L S H G S A Q V K A H