

Petromyzon marinus

C Score = 3990
 Length of alignment = 199
 Sequence *HsPOLR3G* : 1 - 223 (Sequence length = 223)
 Sequence *PmPOLR3GL* : 1 - 193 (Sequence length = 193)

*Hs*POLR3G MAGNKGGRGAAAYTFNIEAVGFSKGEKLPDVVLKPPPLFPDTDYKPVPLKTGEGEEYMLALKQ
 ||| .|||. . |||||. |||. ||| || |. ||||| .|.|. || || |. |||||
*Pm*POLR3GL MAG-RGRGRGQMTFNIEAIGFAKGEALPPPTLQPPPLFPPLLEYRPLPLLTGEETDYLLALKQ

*Hs*POLR3G ELRETMKRMPYFIETPEERQDIERYSKRYM-KVYKEE---WIPDWRRLPREM---MPR-NKC
 ||| .|| .||| |. |. ||||| |. | | |. |||| |||. . . |
*Pm*POLR3GL ELRGAMKNLPYFIKPAERKKDIERYSDKYQSKGPADNAIDWAPDWRLLPRELRIQVRKATKA

*Hs*POLR3G KKAGPKPKKAK-DAGKGTPLTNTEDVLKKMEELEKRGDGEKSDEENEEKEGSKEKSKEGDDD
 ||| |. |. .|||..| ||.. . ||| .|. | || ...
*Pm*POLR3GL KKA>VVK>TQVLKPEKSKKASESENLEMLKNLETLEQKEQQAPSDE-----DGAEKEKEEGEE

*Hs*POLR3G DDDDAAEQEEYDE
||..|
*Pm*POLR3GL AEEFVLDEEEEEE

Percentage ID = 44.72

D Score = 6200
 Length of alignment = 193
 Sequence *Hs*POLR3GL : 1 - 218 (Sequence length = 218)
 Sequence *Pm*POLR3GL : 1 - 193 (Sequence length = 193)

[illegible]

Percentage ID = 62.69

Figure S3 2