

Suppl. Fig. 3

CLUSTAL O(1.2.4) multiple sequence alignment

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Hs_HIWI      ETVLDFMFNFYHQTEEHKFQEQVSKELIGLVVLTKYNNKTYRVD DIDWDQNP KSTFKKAD
Dm_PIWI      ETIYDIMRRC SHNP--ARHQDEV RVNVLDLIVLTDYNNRTYRINDVDFGQTPKSTFS-CK
Eh_Ago2-1    -----QFMENKGVEQIKFEFKPMSLFNSLTKKLVKIDSIDFSKTPLHTFKLKD
Eh_Ago2-2    -----YLDSIRSKDQDTIKKEFQPMVLYNSQTKRLEKID DIDFGKNPSFSFTRKD
Eh_Ago2-3    -----LEESKEYSYDEIAIKFRPSWYYNEVSKQLEWIDEVKMNVTPDSQKFFWG
              :      : :  :.      ..  :::  :::. . . *
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Hs_HIWI      GSEVSFLEYYRKQYNQEIT-DLKQPVLVSQP KRRRGPG-GTLP GPAMLIPELCYLTG
Dm_PIWI      GRDISFVEYYLT KYNIRIR-DHNQPLLISKNRDKA-LK-TNASELVVLIPELCRVTG
Eh_Ago2-1    GKEISFIDYYKSKYGVIIK-NTEQPLL VQNNPFFNENN--NSNEFSYFIPEFMYMTG
Eh_Ago2-2    GSSVSIAEYYKQRYQIEIR-DMDQPLL VQKKIEKDSEGKEVEKQPCYFVP-----
Eh_Ago2-3    DQEVSVSQYYMQRYGGAVHFDPNQFLMVQKQRKFG-----RIEYAYYVPQLMHRV-
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