

Suppl. Fig. 7

CLUSTAL O(1.2.4) multiple sequence alignment

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Hs_Hiwi      -----IVVCLLSSNRKDKYDAIKKYLCTDCPTPSQCVVARTLGKQQTVMA
Dm_Piwi      -----LILCLVPNDNAERYSSIKKRGYVDRAVPTQVVTLK-TTKNRSLSMS
Eh_Ago2-1    MIGLSLDDYFNEILNYKIVFVVILNDSLYEDIK-RKCFDKEIITQCIHPDTL-KKQNLFP
Eh_Ago2-2    -----NSSMVLAVSVTDSIYEQIK-KFCVDENVPTQCIKPNTL-RRQPPTP
Eh_Ago2-3    -----QIVFSVFDSIEQMVEIKEVFMIYGNIPQIIDLNERYYDDKKITN
              : : . ** *: : :

Hs_Hiwi      IATKIALQMNCKMGGELWRVDIPLKL--VMIVGIDCYHDMTAGRRSIAGFVASINEGMT-
Dm_Piwi      IATKIAIQLNCKLGYPWMIELPLSG--LMTIGEDIKSTRDRKRAYGALIASMDLQQNS
Eh_Ago2-1    IVSQITYQIQSKIGGIPWDVLTNNKFIKTMIIIGIAVT--PYDDNKECISLVSSMKYNSFA
Eh_Ago2-2    VIQMITLQMQSKMGGIPWKTEIDSSFADGMTVGI DVI--SAGKDREIVAIVSSVD-KDFT
Eh_Ago2-3    ----LCLRTGIKLGCSRMLKLDQNTSD--ICVIGITSR--EFFVNKTLITLCISKDENLN-
              : : ** . *: : * .

Hs_Hiwi      RW-FSRCIFQDRGQELVDGLKVCLQAALRAWNSCNEYMPSRIIVYFDGVGDGQLKTLVNY
Dm_Piwi      TY-FSTVTECSAFDVLANTLWPMIAKALRQYQHEHRKLPSRIVFYFDGVSSGSLKQLFEF
Eh_Ago2-1    TRKKYSAIETKSGNAGYNSQILIQKALDDWYKENLKYP SNI IYFKANK-TSLKIKEG
Eh_Ago2-2    VYKKSSVVEKKGLHTAGIHIGEFMKKALESYTEYNGSHPKKVI IYFGSANTGDLKNIQQG
Eh_Ago2-3    VFDTESYFVSDNWNHSGIGLEQILPKL-----EGRKLRIFVYFCGISDNLKAIKRFG
              . : * . . . . ** . : :

Hs_Hiwi      EYVQFLDCLKSIGR---GYNPRLTVIVVKKRVNTRFFAQSGGRLQNPLPGTVIDVEVTRP
Dm_Piwi      EVKDIIEKLTTEYARVQLSPPQLAYIVVTRSMNTRFFLNG----QNPPPGTIVDDVITLP
Eh_Ago2-1    ELNLLKQIINSK-----SISIKLLYFIVSCRNDIKVFSQNYQSYFNPQGTIICDTIFEH
Eh_Ago2-2    ELVEVKKAITEY-----DQSIQFIYITVNNKHDMKFFSKDGNNFINPLPGTVITQGVTKT
Eh_Ago2-3    EYEQFLKICKQSC---GEEVKVCFITTD-NISSAIAIEENGELKSTKEGTFVISPLVNK
              *: . . . :. : . . : . **.: :

Hs_Hiwi      EWYDFFIVSQAVRSGSVSPHYNVIYDMSG-LKPDHIQRLTYKLCCHIYYNWPGVIRVPAP
Dm_Piwi      ERYDFYLVSQQVRQGTVSPTSYNVLYSSMG-LSPEKMQLTYKMCHLYYNWSGTRVPAV
Eh_Ago2-1    DNFEFYLI SHIPIKGVVRPVL YTSLYNSTE-FTQQQIYQITFDLCHLHYSVLSSIYTPAH
Eh_Ago2-2    DVFQFYLVSHVPRKGLVKPSMYFVLENTIENLSQLSLYNFTYELTHLYFNGANSVCFPPT
Eh_Ago2-3    NVKGFILNA---KPEICKTLKYVVLYDNTG-LTLREIIQFTFDNCHLSQGMSTGKLPYC
              : * : : * : . . :. :. *: . . *

Hs_Hiwi      CQYAKKLAFLVGQSIH
Dm_Piwi      CQYAKKLATLVGTNLH
Eh_Ago2-1    LFEANELSHVLNKCQY
Eh_Ago2-2    LYQANKFCKMLNDCGY
Eh_Ago2-3    ANEAKHFQKRLYS---
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