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DNMT3b : FGIGDIIWVKIKGFSWPEAMVSVKATSKRQAMPG-----MRWVCFEGDGKFSEISADKLVALGLFSQHFNLATFNKL----- : 302
WHSC1  : YNVGDLVWSKVSQYPWWEPCMV SADPLLHSYTKLKGQKKSARQYHVQFFGDAPERAWIFEKSLVAFEGEGQFEKLCQESAKQA-- : 301
HDGF   : YKCGDLVFAKMKGYPHWPARIDEMPEAAVKSTAN-----KYQVFFFGTHTETAFLGPKDIFPYEESKEKFGKPNKR----- : 79
SPBC215.07 : YKFGMRVLTKMSGFPPWPSMVTESKMTSVARKSKPKRAGTFYFPVIFEPNKEYLWTGSDSLTPLTSEAISQFLEKPKPKTASLI : 207
AtATM  : FLVGNLIVVMTKYKKWVEGEVVDKADAKESFMVRSIGQ--SHLVSWEASSKLPFKESFEQVLNQRND----- : 172
HUA2   : WKVGDIVLAKVKGFPAWPAVVDEPEKWGHSADSK-----KVTVHFEGTQQIAFCNHGDIWESFTEEKKQSLLTRRHAKG---- : 90

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DNMT3b : VSYRKAM YHTLEKARVRA----- : 320
WHSC1  : PTKAEKIKLLKPISGKLRA----- : 320
HDGF   : KGFSEGLWEIENNPTVKA----- : 97
SPBC215.07 : KAYKMAQSTPDLDSLVSVP----- : 226
AtATM  : NGFFDAIQKAMSLLSNSL----- : 190
HUA2   : SDEVRAVKEITESYEKLLKQDDQ- : 112

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**Supplementary Fig S2** | Sequence alignment of some PWWP domain containing proteins, including Dnmt3b (DNA cytosine 5-methyltransferase 3B, *Mus musculus*, gi 51556223), WHSC1 (*Homo sapiens*, gi 30354464), HDGF (hepatoma derived growth factor, *Homo sapiens*, gi 598956), SPBC215.07 (*Schizosaccharomyces pombe*, gi 19113476), AtATM (*Arabidopsis thaliana*, gi 11357182) and HUA2 (putative transcription factor, *Arabidopsis thaliana*, gi 30695719). Boxed are the three regions of similarity in the PWWP proteins. Alignment performed using ClustalX, with manual adjustment.