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---MPSSSGPG--DTSSSAAREEDRDKGEEQEEPRGKEERQEPSTTARKVGRGPKRKRKHPVVESSGDTPKDPAVTSKSPSMAQDPCASELLPNGDLEKRSE 95
-----EGEEQEEBARAKEERQEPSTTARKVGRGPKRKRKHPVVESSDTPKDPVTSKSL SMAQDSSGSELYPNGDLEKRSE 74
---MPSSSGPG--DTSSSAAREEDRKEGEEQEEPRGKEERQEPSTTARKVGRGPKRKRKHPVVESSDTPKDPTVTSKSPSMAQDSSGSELLPNGDLEKRSE 95
---MPSSSGPG--DTSSISLEREDRKEGEEQEEPRGKEERQEPSTTARKVGRGPKRKRKHPVVESSDTPKDPVTSKSPSMAQDSSGSELLPNGDLEKRSE 95
---MPSSSGPG--DTSSSLEREDRKEGEEQEEPRGKEERQEPSTTARKVGRGPKRKRKHPVVESSDTPKDPVTSKSPSMAQDSSGSELLPNGDLEKRSE 95
---MPSSGATTVDNSSSLEREDRKEEELLESKKEERQDSTPMRKVGRGPKRKRKHPVVESSDTPKEVAPTSKAP SMAQDTCPSSELLPNGDVEKPSSE 97
-----MNSMEDTGEVESPEPKKDVITVPLLFPPMPPTPTTPMQ-----QQPFO 44

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PQPEEGSPAGGQKGGAPAEGEGAAETLPEASRAVENGCCCTPKDGRGAPAEVGC-----KEQKE-TNIESMKMEGSRGRLRGGI 171
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PQAQH----- 49

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→ PWWP domain ←

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PKS--TTESEYEDGRGFGINELVWGKLRGFSWWPGRVSWRMTLRSPA AEGTRVWTFWFGDGKFSVVCVEKLLPLSSFHNAFHQP YNKQPMYKKAIFEVLQ 196

VASSRAGKLFPA CPENDESDTAKAVEVQNKQMI EWALGGFQPSGPKGLEPPEEKNPYKEVYTD MW--VEPEAAAYAPPPAKKPKRS--TTEKPKVKEII 436
VASSRAGKLFVCHDSDES DTAKAVEVQNKQMI EWALGGFQPSGPKGLEPPEEKNPYKEVYTD MW--VEPEAAAYAPPPAKKPKRS--TAEKPKVKEII 471
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VASTRAGKTLFSLCPASDSDTSSKLVVDEENKMI EWAMSGFOPTGPKGLEPPEEKNPYKEVYTD MW--VEPEAAAYAPPPAKKPKRS--TAEKPKVKEII 288

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DERTRERLVYEVQRKCRNIEDICISCGSLNVTLEHPLF IGGMCQCNKCFLECAQYD DDGYQSYCTICCGGREVLMCGNNNCCRCFCVCEVDLLVGPGA 388

→ DNA Methylase domain

AQAAIKEDPWNCYMGHGKTYGLLRRREDWPSRLQMF FANNHDQEFDPKVPYPPVPAEKRRKPIRVLSLFDGIATGLLVKDLGLIQVDRIYASEVCEDSIT 636
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←
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