Sup. Figure S1. MUSCLE alignment of *P. tetraurelia* Ptiwi proteins with selected Argonaute proteins from other eukaryotes. Piwi, Ago, and Wago proteins are shaded in pink, blue, and green, respectively. The PAZ, MID and PIWI domains are indicated by coloured bars on top of the alignment, according to their annotation in other eukaryotic proteins (the PAZ domain in yellow, the MID domain in blue and the PIWI domain in red). Highly conserved residues are highlighted in these bars. At, *A. thaliana*; Dm, *D. melanogaster*; Ce, *C. elegans*; Mm, *M. musculus*; Pt, *P. tetraurelia*; Sp, *S. pombe*; Tt, *T. thermophila*.
Accession numbers :

gene	accession	gene	accession	gene	accession
Ce-ZK757.3a	CAA82389	PTIWI02	PTETG3700002001	At-AGO2	NP_174413
Ce-T22B3.2b	CAA92619	PTIWI03	GSPATG00001395001	At-AGO3	NP_174414
Ce-T23D8.7	CAB03400	PTIWI04COR	PTETPS1700010001	At-AGO4	NP_565633
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Ce-ALG-2a	AAB66187	PTIWI06	GSPATG00002500001	At-AGO6	NP_180853
Ce-ERGO-1	NP_503362	PTIWI07	PTETG2500007001	At-AGO7	NP_177103
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Ce-C04F12.1	NP_492573	PTIWI12	GSPATG00001709001	Mm-AGO2	NP_694818
Ce-SAGO-1	NP_504610	PTIWI13	PTETG4800007001	Mm-AGO3	NP_700451
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Ce-PPW-2	AAF60414	Tt-4505902	XP_001015193	Dm-AGO1A	NP_725341
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Ce-F55A12.1	AAB54129	Tt-TWI8	ABI15747	Dm-PIWI	NP_476875
Ce-R04A9.2	AAA83284	Tt-TWI9	ABW36050	Dm-AUB	NP_476734
Ce-Y49F6A.1	AAF60724	Tt-TWI10	ABP68415	Dm-AGO3	ABO27430
Ce-C16C10.3	CAA86741	Tt-TWI11	ABW36051	Sp-AGO1	NP_587782
Ce-T22H9.3	AAC69228	Tt-TWI12	ABP68417		
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Mm-MIWI2       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Mm-MILI        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Dm-PIWI        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Dm-AUB         1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
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Ce-PRG-2       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
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PTIWI15        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI03        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI09        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI01        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI06        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI10        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI11        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI1        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI12       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI07        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI8        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI9        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI7        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI2        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-4505902     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI10       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI02        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI05        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI04cor     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI08        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI14        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
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At-AGO10       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
At-AGO7        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
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Ce-ALG-2a      1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-T23D8.7     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-ZK757.3a    1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-T22B3.2b    1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
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Ce-RDE-1       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-R04A9.2     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-C16C10.3    1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-T22H9.3     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-Y49F6A.1    1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-C04F12.1    1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
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Ce-R06C7.1     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-F55A12.1    1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-PPW-2       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-F58G1.1     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-C06A1.4     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-SAGO-2      1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-PPW-1a      1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-SAGO-1      1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
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Mm-MIWI2       1 -------------------------------------------------MSGRARVRARGITTGHSAREVGRSSRDLMVTSA------------------------------------------------------------------------------
Mm-MILI        1 -----------------------------MDPVRPLFRGPTPVHPSQCVRMPGCWPQAPRPLEPAWGRAGPAGRGLVFRKPEDSSPPLQPVQKDSVGLVSMFRGMGLDTAFRPPSKREVPPLGRGVLGRGLSANMVRKDREEPRSSLPDPSVLAAGDSKL
Dm-PIWI        1 ----------------------------------------------------------MADDQGRGRRRPLNEDDSSTSRGS------------------------------------------------------------------------------
Dm-AUB         1 -------------------------------------------------------MNLPPNPVIARGRGRGRKPNNVEANRG------------------------------------------------------------------------------
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Ce-PRG-2       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI11       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI12        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI15        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI03        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI09        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI01        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI06        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI10        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI11        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI1        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI12       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI07        1 ----------------------------------------MNIEKSSQKHTTSSNSSRSSSKLRSRSRSNSQRRDRKTEKTE------------------------------------------------------------------------------
Tt-TWI8        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI9        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI7        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI2        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-4505902     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI10       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI02        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI05        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI04cor     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI08        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI14        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI13        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Sp-AGO1        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
At-AGO5        1 --------------------MSNRGGGGHGGASRGRGGGRRSDQRQDQSSGQVAWPGLQQSYGGRGGSVSAGRGRGNVGRGE-----------------------------------------------------------------------NTGDLTA
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At-AGO10       1 ---------------------------------------MPIRQMKDSSETHLVIKTQPLKHHNPKTVQNGKIPPPSPSPVT----------------------------------------------------------------VTTPATVTQSQASS
At-AGO7        1 ---------------------------------------------MEEKTHHHHHSTNKHIPSSKSRTPLLHKPYHHHVQTN---------------------------------------------------------------PPPFLLHPSSHQNLN
At-AGO2        1 --------------MERGGYRGGRGDGRGRGGRGYGGGGGGGEQGRDRGYGGGEQGRGRGSERGGGNRGQGRGEQQDFRSQS----------------------------------------------------------------QRGPPPGHGGRGTT
At-AGO3       21 DRGRGYSGRGDGRGRGGDGDRGYSGRGDGHGRGGGGDRGRGYSGRGDGRGRGGGGDRGRGYSGRGDGHGRGGGGDRGRGYSGRGRGFVQDRDGGWVNPGQSSGGHVRGRGTQLQQPPPQEVPPSSSQAQVSQGVAPGDVGQGGVGDVGRDGVGDVGRDGV
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At-AGO4        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
At-AGO8        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
At-AGO9        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Mm-AGO2        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Mm-AGO1        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Mm-AGO4        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Mm-AGO3        1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Dm-AGO1A       1 ----------------------------------MSTERELAPGGPAQLHPHTLPLTFPDLQMTSTVGIIGKVYESQWTPSP-----------------------------------------------------------------TRPQSPSQAQTSF
Ce-ALG-1       1 ------------------------------------------MSGGPQYLPGVMNSTIQQQPQSATSSFLPSGPISSTSTSS---------------------------------------------------QVVPTSGATQQPPFPSAQAAASTALQN
Ce-ALG-2a      1 ------------------------------------------------MFPLPVHNGPRLGKLSIFEMPGDSLTSSSFMPDG------------------------------------------------------------------------------
Ce-T23D8.7     1 ---------------------------------------------MEDQWLLSAIYDDDLVEKLKVRSSTSSRSTSINVPSL------------------------------------------------------------------------------
Ce-ZK757.3a    1 ---------------------------------------------MSRRNATSFVDNNTLTSSGISGSGSMSPPITSRPASG------------------------------------------------------------------------------
Ce-T22B3.2b    1 ---------------------------------------------MSRRNATNFVDNNTLTSSGISGSGSLSPPITSRPASG------------------------------------------------------------------------------
Dm-AGO2B     161 PGQQQGGHQQGRQGQEGGYQQRPSGQQQGGHQQGRQGQEGGYQQRPPGQQQGGHQQGRQGQEGGYQQRPSGQQQGGHQQGRQGQEGGYQQRPPGQQQGGHQQGRQGQEGGYQQRPPGQQQGGHEQGRQGQEGGYQQRPSGQQQGGHQQGRQGQEGGYQQR
Ce-ERGO-1      1 ----------------------------MSYNNGGGGGGGGYRNDRDDRYHNNDRQNYRSSDQGRSGYNDDRRDNRYDDRRG---------------------------------------------SNNDRGCYDQHDRRGSSNDDRRGYRGYNQGGGG
Ce-RDE-1       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-R04A9.2     1 ----------------------------------------------------MDLLDKVMGEMGSKPGSTAKKPATSASSTP------------------------------------------------------------------------------
Ce-C16C10.3    1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-T22H9.3     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-Y49F6A.1    1 ----------------------------------------------------------------MSNQEPYRIPKRTASDPN------------------------------------------------------------------------------
Ce-C04F12.1    1 -------------------------------------------------MPSKKNKKAAAAERSATLSASASQQVAKDEQSA------------------------------------------------------------------------------
Ce-CSR-1a      1 ----------------MQSDNVGRGRGSRGGSRGGSGRGRGRGGYGDSYRPDLETRETHVTYQGKVKYEGGDRHDFNYEKTP----------------------------------------------------------TGSYRGSHRDGQEGSRGNRG
Ce-R06C7.1     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-F55A12.1    1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-PPW-2       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-F58G1.1     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-C06A1.4     1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-SAGO-2      1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Ce-PPW-1a      1 ----------------------------------------------------------MESRVIFESKCSLRKPIFNLKRVS------------------------------------------------------------------------------
Ce-SAGO-1      1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
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Dm-AGO3       45 LLSSHNIETDLITTLQHVNISVGRGRARLIDTLKTDDHTSNQFITSESKENITKKTKGPESEAIASENGLFFPDLIY----------------------------GSKGSS-------------------------------------------------
Mm-MIWI       31 ---------GYIPPRPQQSPTEGDLVGRGRQRGMVVGATSKSQELQISAGFQELSLAERGGRRRDFHDLGVNTRQNL--------------------DHVKESKTGSSGII-------------------------------------------------
Mm-MIWI2      34 ----------------SPGDSEAGGGTSVISQPYELGVSSGDGGRTFMERRGKGRQDFEELGVCTREKLTHVKDCKT----------------------------GSSGIP-------------------------------------------------
Mm-MILI      132 AEASVGWSRMLGRGSSEVSLLPLGRAASSIGRGMDKPPSAFGLTARDPPRLPQPPALSPTSLHSADPPPVLTMERKE---------------------KELLVKQGSKGTP-------------------------------------------------
Dm-PIWI       25 ------------GDGPRVKVFRGSSSGDPRADPRIEASRERRALEEAPRREGGPTERKPWGDQYDYLNTRPAELVSK---------------------------KGTDGVP-------------------------------------------------
Dm-AUB        28 ----FAPSLGQKSDPSHSEGNQASGGNGGGGDAQVGPSIEKSSLSAVQMHKSEGDPRGSVRGRRLITDLVYSRPPGM------------------------TSKKGVVGTH-------------------------------------------------
Ce-PRG-1       1 ------------------MASGSGRGRGRGSGSNNSGGKDQKYLGTIQPD------------------LFIRQQGQS--------------------------KTGSSGQP-------------------------------------------------
Ce-PRG-2       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
Tt-TWI11       1 ----------------------------------------------------------------------MSFNDNS-----------------------------------------------------------------------------------
PTIWI12        1 -------------------------------------------------------------------MHQQDKQFKT-----------------------------------------------------------------------------------
PTIWI15        1 -------------------------------------------------------------------MQQQDQQFKT-----------------------------------------------------------------------------------
PTIWI03        1 ----------------------------------------------------------------------MNQRTQE-----------------------------------------------------------------------------------
PTIWI09        1 -----------------------------------------------------------------------------------------------------------MFQN-------------------------------------------------
PTIWI01        1 -----------------------------------------------------------------------------------------------------------MFQN-------------------------------------------------
PTIWI06        1 ----------------------------------------------------------------------------------------------------------MIERG-------------------------------------------------
PTIWI10        1 ----------------------------------------------------------------------------------------------------------MIERG-------------------------------------------------
PTIWI11        1 ----------------------------------------------------------------------------------------------------------MIERG-------------------------------------------------
Tt-TWI1        1 --------------------------------------MSNKGLVQNNPR--------------------------------------------------------------------------------------------------------------
Tt-TWI12       1 ----------------------------------------------------------------------------------------------------------------------------------------------------------------
PTIWI07       43 -------------STDDKQGSDQNVKIESNIPQTARGKRQLTYIKDLPKR------------------PPKCPNYPQ------------------------------QFRE-------------------------------------------------
Tt-TWI8        1 ----------------------MDQGSLRGESEQGSSSQQKEQKLQLARR------------------PKLDYNQQS--------------------------------KS-------------------------------------------------
Tt-TWI9        1 ------------------------------------------MNLVLSKR------------------PQKSSSQEL----------------------------QKICKV-------------------------------------------------
Tt-TWI7        1 ------------------------------------------MITQLPKR------------------PNKSSSSTI----------------------------AKISNN-------------------------------------------------
Tt-TWI2        1 ------------------------------------------MLQQLPKR------------------PPKSSAQDI----------------------------SKICKN-------------------------------------------------
Tt-4505902     1 ------------------------------------------MLQQLPSR------------------PPISSTQEI----------------------------SQICKN-------------------------------------------------
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PTIWI05        1 ------------------------------------MQQKTNTICQLPLR------------------PQRRANLDK------------------------------DFRI-------------------------------------------------
PTIWI04cor     1 ------------------------------------MQQQSNTICQLPKR------------------PQRGENLNK------------------------------DYRM-------------------------------------------------
PTIWI08        1 ----------------------------------------MQKISDLPKR------------------PARSQRLEQ------------------------------ISRR-------------------------------------------------
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PTIWI13        1 --------------------------------MQQTNLKICDKISQLVNR------------------PKRSEQVNK------------------------------ICRP-------------------------------------------------
Sp-AGO1        1 --------------------------------------MSYKPSSEIALR------------------------PGY----------------------------GGLGKQ-------------------------------------------------
At-AGO5       70 TQVPVASAVSGGRGRGNIGDPTFSVASSSKTVSVASSSKEESKNTEVSETMSNLQITSTETKPEMTSLPPASSKAVT---------------------FPVRPGRGTLGKK-------------------------------------------------
At-AGO1       97 YGGGRGGGPSSGPPQRQSVPELHQATSPTYQAVSSQPTLSEVSPTQVPEPTVLAQQFEQLSVEQGAPSQAIQPIPSS----------------SKAFKFPMRPGKGQSGKR-------------------------------------------------
At-AGO10      58 PSPPSKNRSRRRNRGGRKSDQGDVCMRPSSRPRKPPPPSQTTSSAVSVATAGEIVAVNHQMQMGVRKNSNFAPRPGF----------------------------GTLGTK-------------------------------------------------
At-AGO7       53 LVASNLPSSYYYYYYCYFYSQFHNSLPPPPPPHLLPLSPPLPPLLPLPPPHSMTRFHKSLPVSQVVERKQQHQQKKKIQVSNNKVSGSIAIEEAALVVAKRPDFGGQDGSV-------------------------------------------------
At-AGO2       83 QFQQPRPQVAPQPSQAPASYAGSVGGVAGRGAWGRKPQVPSDSASPSTSTTVVSEPVRVAEVMNLKPSVQVATSDRK------------------EPMKRPDRGGVVAVRR-------------------------------------------------
At-AGO3      181 GDVGQGGVGDVGQVGVGDVGQGGVGDVGQGGVGDVGRDGVGDVGRDGVGDVGRGGVGDRGQSQSGLSSGHFGRGTQLQQPQPQAVSQSSSQGQVSQSFATGGVGLGAWARKPQLFSDSTVLPSSSSSNVVASHTASGSQVMTPKPSSSDKKEPVKRPDKG
At-AGO6        1 ---------------------METSSSLPLSPISIEPEQPSHRDYDITTR------------------------RGV----------------------------GTTGNP-------------------------------------------------
At-AGO4        1 -----------------MDSTNGNGADLESANGANGSGVTEALPPPPPVIPPNVEPVRVKTELAEKKGPVRVPMARK--------------------------GFGTRGQK-------------------------------------------------
At-AGO8        1 ----------------------MDTTLPPPQHMEREPLKSKSSLLPMTRR-----------------------------------------------------GNGSKGQK-------------------------------------------------
At-AGO9        1 ----------------MDSDEPNGSGLPPPPPFVPANLVPEVEPVKKNIL------------------LPMARPRGS----------------------------GSKGQK-------------------------------------------------
Mm-AGO2        1 ---------------------MYSGAGPVLASPAPTTSPIPGYAFKPPPR------------------------PDF----------------------------GTTGRT-------------------------------------------------
Mm-AGO1        1 ------------------------MEAGPSGAAAGAYLPPLQQVFQAPRR------------------------PGI----------------------------GTVGKP-------------------------------------------------
Mm-AGO4        1 --------------------------------MEALGPGPPASLFQPPRR------------------------PGL----------------------------GTVGKP-------------------------------------------------
Mm-AGO3        1 -------------------------------MEIGSAGPIGAQPLFIVPR-----------------------RPGY----------------------------GTMGKP-------------------------------------------------
Dm-AGO1A      62 DTLTSPPAPGSSVNPTAVTSPSAQNVAAGGATVAGAAATAAQVASALGATTGSVTPAIATATPATQPDMPVFTCPRR-------------------------PNLGREGRP-------------------------------------------------
Ce-ALG-1      68 DLEEIFNSPPTQPQTFSDVPQRQAGSLAPGVPIGNTSVSIGEPANTLGGGLPGGAPGQLPGGNQSGIQFQCPRRPNH----------------------------GVEGRS-------------------------------------------------
Ce-ALG-2a     35 -----------------GAETSSSSQLGGSAHGAIGTKPDAGVQFQCPVR------------------PNHGVEGRS-----------------------------------------------------------------------------------
Ce-T23D8.7    38 ----------------ENEFLSSSSGSRVSDDLYLHPIEENREPFKLIGK------------------PLPSTTGRF-----------------------------------------------------------------------------------
Ce-ZK757.3a   38 --------------QASPLTSNGSLSPPQYADDQGSVSYNLDSPRDLSPL--------LLSELACLNMREVVARPGL----------------------------GTIGRQ-------------------------------------------------
Ce-T22B3.2b   38 ----------------QASPLSSNGSLSPPVDDQGSVSYNSDSPRDLSPL--------LLSELACLNMREVVARPGL----------------------------GTIGRK-------------------------------------------------
Dm-AGO2B     321 PSGQQQGGHQQGRQGQEGGYQQRPSGQQQGGHQQGRQGQEGGYQQRPPGQQPNQTQSQGQYQSRGPPQQQQAAPLPL------------------PPQPAGSIKRGTIGKP-------------------------------------------------
Ce-ERGO-1     88 YQQQYSQDARYGSNQRNDNYGNNRGSHGGANMYSQNGGNRGGGGGRVGGGRTAAGMSNPGDLVGGADQPIHSVSKKS----------LRHNAQEFAVRPKTMVQDKGLGQK-------------------------------------------------
Ce-RDE-1       1 ------------------------MSSNFPELEKGFYRHSLDPEMKWLAR------------------PTGKCDGKF------------------------------YEKK-------------------------------------------------
Ce-R04A9.2    31 -----------RTNVWGTAKKPSSQQQPPKPLFTTPGSQQGSLGGRIPKR---------EHTDRTGPDPKRKPLGGL-----------------------SVPDSFNNFGT-------------------------------------------------
Ce-C16C10.3    1 ---------------MADLLDKIMGSSSSNRIPKRDNRMNQDKDEPTSKR-----------SAPMFSTPKSTTPIGR--------------------------DSFATMDT-------------------------------------------------
Ce-T22H9.3     1 --------------MPTTVQNPSPTGFLPQIPFRIPKRTRRSSEVDVPAT--------------KRPAPPLTSSTSL-----------------------PTRDSFSIIET-------------------------------------------------
Ce-Y49F6A.1   19 ---------------------QSGSQGSCVRPNQEGNVKKEESVNSAPRR--------------MFTLPSSSSTSGA--------------------------QVFNPIGK-------------------------------------------------
Ce-C04F12.1   34 ----------------PVVPTPELSRVSVSSNPPTPSAIEKPVPLPVPSK------------------PLFEYEPPA------------------------QLEALAKNKP-------------------------------------------------
Ce-CSR-1a     87 SFRGGRGGYDRRRDDEESKAENRFGGYNRGANGGNYRGRTGGSGRGGSTQTTTVDPKYNGLILENSAEPKLKGLNSD----------------------------MNQKQN-------------------------------------------------
Ce-R06C7.1     1 ---------MSPHPPQPHPPMPPMPPVTAPPGAMTPMPPVPADAQKLHQSTGNDACIKRLQQLNVEDGAKMYMKPTE---------------------------PGKMGRP-------------------------------------------------
Ce-F55A12.1    1 ----------------------MSPHPPQPHPPMPPMPPVTAPPGTMPPM------------------PPVPADAQK---------------------------LHQITGN-------------------------------------------------
Ce-PPW-2       1 -MPATPVPPVTMPPVPPVGFPPVTAPPGLHPPPPVPPVPVPTLPVTSEHKTAHDACIKRLEQLEIPPDPKIYPSPTE---------------------------PGTFGSV-------------------------------------------------
Ce-F58G1.1     1 ------------MPALPPVYTPSGAPSSVHAPPAVPPVPVPTQPLRSEYQTSNDACIKRLEELNIAPAAKLYPTPTE---------------------------PGKCGVE-------------------------------------------------
Ce-C06A1.4     1 ------------MPALPSVYTPSGAPSSVHAPPAVPPVPVPTQPLRSEYQTSNDACIKRLEELNIAPAAKLYPAPTE---------------------------PGKCGVE-------------------------------------------------
Ce-SAGO-2      1 -------------------------MEKQLKAMSVSDKPAAPAAQKLGTA------------------PLAAKKTRN----------------------------EEWGTK-------------------------------------------------
Ce-PPW-1a     25 -----------------------RTMEKQLEAMFVSDRPAAPAAQKLGTA------------------PLAAKKTRN----------------------------VERGTK-------------------------------------------------
Ce-SAGO-1      1 -----------------------MSNITQVTSSMASASLSNKAPLPVGHQ------------------PLAEKKPKE---------------------------VNQEGTP-------------------------------------------------
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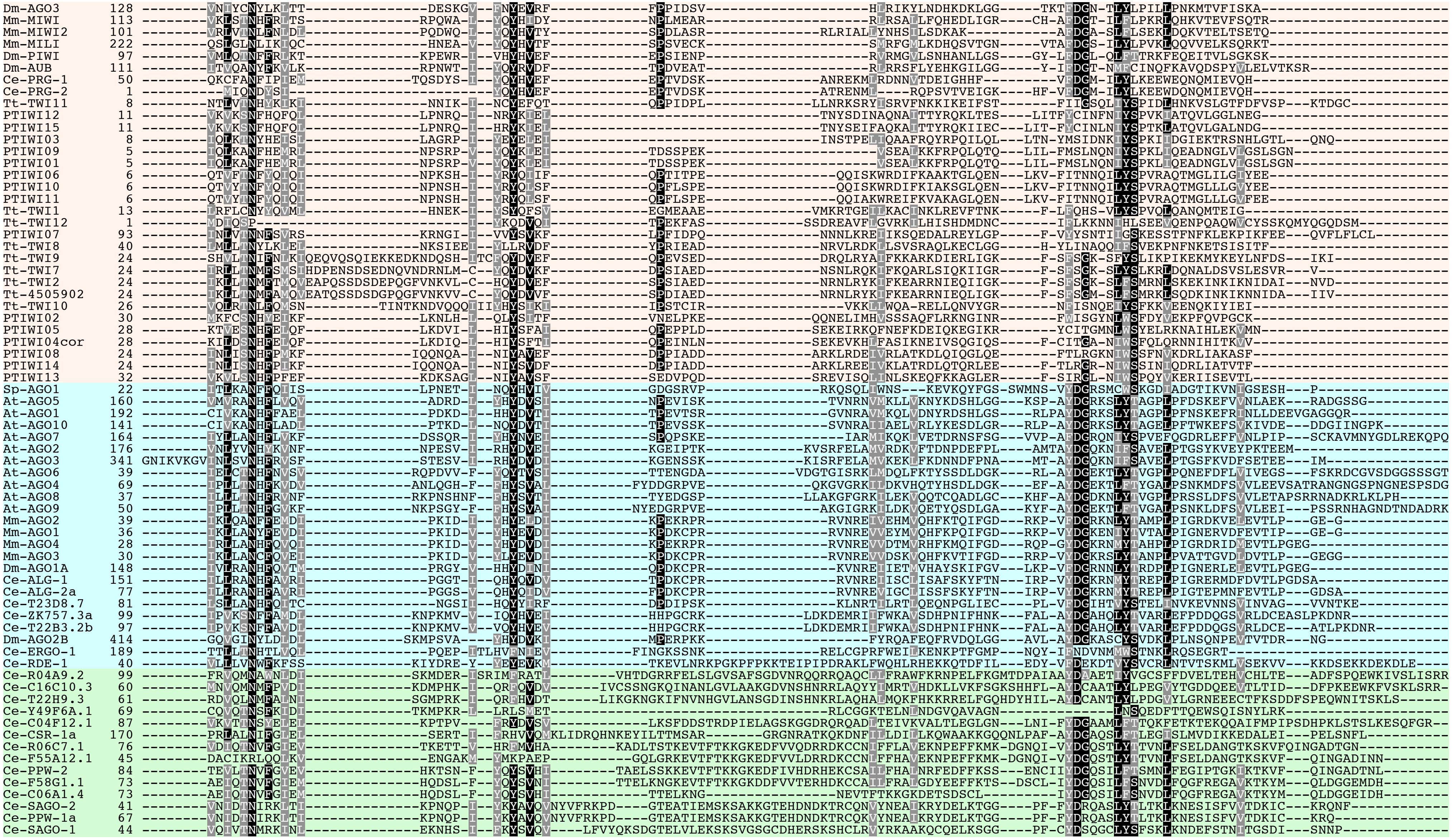

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Mm-MIWI2     101 --------VRLVTNLFNLDL--------------PQDWQ-L--YQYHVTY------------SPDLASR--------------RLRIALLYNHSILSDKAK-----------AFDGA-SLFLSEKLDQKVTELTSETQ----------------------
Mm-MILI      222 --------QSLGLNLIKIQC---------------HNEA-V--YQYHVTF------------SPSVECK--------------------SMRFGMLKDHQSVTGN-----VTAFDGS-ILYLPVKLQQVVELKSQRKT----------------------
Dm-PIWI       97 --------VMLQTNFFRLKT--------------KPEWR-I--VHYHVEF------------EPSIENP--------------------RVRMGVLSNHANLLGS----GY-LFDGL-QLFTTRKFEQEITVLSGKSK----------------------
Dm-AUB       111 --------ITVQANYFKVLK--------------RPNWT-I--YQYRVDF------------TPDVEAT--------------------RLRRSFLYEHKGILGG-----Y-IFDGT-NMFCINQFKAVQDSPYVLELVTKSR-----------------
Ce-PRG-1      50 --------QKCFANFIPIEM-------------TQSDYS-I--YQYHVEF------------EPTVDSK--------------ANREKMLRDNNVTDEIGHHF---------VFDGM-ILYLKEEWEQNQMIEVQH------------------------
Ce-PRG-2       1 ----------MIQNDYSI-------------------------YQYHVEF------------EPTVDSK--------------ATRENML----RQPSVTVEIGK----HF-VFDGM-ILYLKEEWDQNQMIEVQH------------------------
Tt-TWI11       8 --------NTLVTNHYKIKI---------------NNIK-I--NCYEFQT------------QPPIDPL-------------LLNRKSRYISRVFNKKIKEIFST-------FIIGSQLIYSPIDLHNKVSLGTFDFVSP---KTDGC------------
PTIWI12       11 --------VKVKSNFHQFQL--------------LPNRQ-I--NRYKIEL---------------------------------TNYSDINAQNAITTYRQKLTES----LITFYCINFNIYSPVKIATQVLGGLNEG-----------------------
PTIWI15       11 --------VKVKSNFHQFQL--------------LPNRQ-I--HRYKIEL---------------------------------TNYSEIFAQKAITTYRQKIIEC---LIT-FYCINLNIYSPTKLATQVLGALNDG-----------------------
PTIWI03        8 --------IQLKTNYHEISL--------------LAGRP-I--YEYELEI---------------------------------INSTPELIQAAFRQYRPQILQL---LTN-YMSIDNKIYSPKIIDGIEKTRSNHLGTL---QNQ--------------
PTIWI09        5 --------IQLKANFHEMRL--------------NPSRP-V--YQYKLEI------------TDSSPEK---------------------VSEALKKFRPQLQTQ---LIL-FMSLNQNIYSPKLIQEADNGLVLGSLSGN-------------------
PTIWI01        5 --------IQLKANFHEMRL--------------NPSRP-V--YQYKLEI------------TDSSPEK---------------------VSEALKKFRPQLQTQ---LIL-FMSLNQNIYSPKLIQEADNGLVLGSLSGN-------------------
PTIWI06        6 --------QTVFTNFYQIQI--------------NPKSH-I--YRYQIIF------------QPTITPE----------------QQISKWRDIFKAAKTGLQEN---LKV-FITNNQILYSPVRAQTMGLILGIYEE----------------------
PTIWI10        6 --------QTVYTNFYQIQI--------------NPNSH-I--YRYQLSF------------QPFLSPE----------------QQISKWRDIFKIAKSGLQEN---LKV-FITNNQILYSPVRAQTMGLLLGVYEE----------------------
PTIWI11        6 --------QTVYTNFYQIQI--------------NPNSH-I--YRYQLSF------------QPFLSPE----------------QQIAKWREIFKVAKAGLQEN---LKV-FITNNQILYSPVRAQTMGLLLGVFEE----------------------
Tt-TWI1       13 --------LRFLCNYYQVML---------------HNEK-I--YSYQFSV------------EGMEAAE-------------VMKRTGEILKACINKLREVFTNK-----F-LFQHS-VLYSPVQLQANQMTEIG-------------------------
Tt-TWI12       1 --------MDIQSP--------------------------I--YKQDVQI------------TPEKFAS------------SSDREAVFLGVRKILHISHDMDNC-------IFLKKNNIHLSEEVQENPQAQWVCYSSKQMYQGQDSM-----------
PTIWI07       93 --------INLVTNNFSVRS--------------KRNGI-I--VVYSVKF------------LPFIDPQ--------------NNNLKREIIKSQEDALREYLGP-----F-VYYSNTIIGSKESSTFNFKLEKPIKFEE---QVFLFLCL---------
Tt-TWI8       40 --------LMLLTNYLKLEL--------------NKSIEEI--YLLRVDF------------YPRIEAD--------------NRVLRDKLLSVSRAQLKECLGG-----H-YLINAQQIFSVEKPNFNKETSISITF----------------------
Tt-TWI9       24 --------SHVLTNIFNLKIQEQVQSQIEKKEDKNDQSH-ITCFQYDVEF------------QPEVSED--------------DRQLRYAIFKKARKDIERLIGK-----F-SFSGK-SFYSLIKPIKEKMYKEYLNFDS---IKI--------------
Tt-TWI7       24 --------IRLLTNMFSMSIHDPENSDSEDNQVNDRNLM-C--YQYDVKF------------DPSIAED--------------NSNLRQKIFKQARLSIQKIIGR-----F-SFSGK-SLYSLKRLDQNALDSVSLESVR---V----------------
Tt-TWI2       24 --------IKLLTNMFTMQVEAPQSSDSDEPQGFVNKVL-C--HQYDVEF------------SPSIAED--------------NRNLRYKIFKEARRNIEQIIGK-----F-SFSGK-SLFSMRNLSKEKINKIKNIDAI---NVD--------------
Tt-4505902    24 --------IKLLTNMFAMQVEATQSSDSDGPQGFVNKVV-C--YQYDVVF------------SPDIAED--------------NRNLRYKIFKEARRNIEQLIGK-----F-SFSGM-SLFSMRKLSQDKINKIKNNIDA---IIV--------------
Tt-TWI10      26 --------VQLRTNLFQMSN---------TINTKNDVQQQIIIYHYSIKI------------IPSTCIR-----------------VKKLLWQA-RELLQNVYGR-------NFISNQEIYSFKKVEENQKIYIEI------------------------
PTIWI02       30 --------MKFCSNHYEIKF--------------LKNLH-L--QLYSITF------------VNELPKE-------------QQNELIMHVSSSAQFLRKNGINR-------FWISGYNLWSFDYVEKPFQVPGCK------------------------
PTIWI05       28 --------KTVESNHFELQF--------------LKDVI-L--HIYSFAI------------QPEPPLD-------------SEKEIRKQFNEFKDEIQKEGIKR-------YCITGMNLWSYELRKNAIHLEKVMN-----------------------
PTIWI04cor    28 --------KILDSNHFELQF--------------LKDIQ-L--HIYSFTI------------QPEINLN-------------SEKEVKHLFASIKNEIVSQGIQS-----F-CITGA-NIWSFQLQRNNIHITKVV------------------------
PTIWI08       24 --------INLISNHFPMKF-------------IQQNQA-I--NIYAVEF------------DPPIADD-------------ARKLRDEIVRLATKDLQIQGLQE-------FTLRGKNIWSSFNVKDRLIAKASF------------------------
PTIWI14       24 --------INLISNHFPIKF-------------IQQNQA-I--NIYSVDF------------DPPIADD-------------ARKLREEIVKLATRDLQTQRLEE-----F-TLRGR-NIWSSINIQDRLIATVTF------------------------
PTIWI13       32 --------VKVLSNHFPFEF--------------KDKSAGL--NIYAVSF------------SEDVPQD-------------SREVISQLINLSKEQFKKAGLER-----F-SIRGL-NIWSPQYVKERIISEVTL------------------------
Sp-AGO1       22 --------ITLKANFFQIIS--------------LPNET-I--NQYHVIV------------GDGSRVP--------------RKQSQLIWNS---KEVKQYFGS-SWMNS-VYDGRSMCWSKGDIADGTIKVNIGSESH---P----------------
At-AGO5      160 --------VMVRANHFLVQV---------------ADRD-L--YHYDVSI------------NPEVISK---------------TVNRNVMKLLVKNYKDSHLGG---KSP-AYDGRKSLYTAGPLPFDSKEFVVNLAEK---RADGSSG----------
At-AGO1      192 --------CIVKANHFFAEL---------------PDKD-L--HHYDVTI------------TPEVTSR---------------GVNRAVMKQLVDNYRDSHLGS----RLPAYDGRKSLYTAGPLPFNSKEFRINLLDEEVGAGGQR------------
At-AGO10     141 --------CIVKANHFLADL---------------PTKD-L--NQYDVTI------------TPEVSSK---------------SVNRAIIAELVRLYKESDLGR---RLP-AYDGRKSLYTAGELPFTWKEFSVKIVDE---DDGIINGPK--------
At-AGO7      164 --------IYLLANHFLVKF--------------DSSQR-I--YHYNVEI------------SPQPSKE-----------------IARMIKQKLVETDRNSFSG---VVP-AFDGRQNIYSPVEFQGDRLEFFVNLPIP---SCKAVMNYGDLREKQPQ
At-AGO2      176 --------VNLYVNHYKVNF--------------NPESV-I--RHYDVEI------------KGEIPTK------------KVSRFELAMVRDKVFTDNPDEFPL----AMTAYDGQKNIFSAVELPTGSYKVEYPKTEEM-------------------
At-AGO3      341 GNIKVKGVINLSVNHFRVSF--------------STESV-I--RHYDVDI------------KGENSSK------------KISRFELAMVKEKLFKDNNDFPNA----MT-AYDGQKNIFSAVELPTGSFKVDFSETEE---IM---------------
At-AGO6       39 --------IELCTNHFNVSV-------------RQPDVV-F--YQYTVSI------------TTENGDA-----------VDGTGISRKLMDQLFKTYSSDLDGK----RL-AYDGEKTLYTVGPLPQNEFDFLVIVEGS---FSKRDCGVSDGGSSGT
At-AGO4       69 --------IPLLTNHFKVDV-------------ANLQGH-F--FHYSVAL----------FYDDGRPVE-------------QKGVGRKILDKVHQTYHSDLDGK----EF-AYDGEKTLFTYGALPSNKMDFSVVLEEVSATRANGNGSPNGNESPSDG
At-AGO8       37 --------ILLLTNHFRVNF-------------RKPNSHNF--FHYSVTI------------TYEDGSP------------LLAKGFGRKILEKVQQTCQADLGC---KHF-AYDGDKNLYTVGPLPRSSLDFSVVLETAPSRRNADKRLKLPH------
At-AGO9       50 --------IPLLTNHFGVKF-------------NKPSGY-F--FHYSVAI----------NYEDGRPVE--------------AKGIGRKILDKVQETYQSDLGA---KYF-AYDGEKTLFTVGALPSNKLDFSVVLEEI---PSSRNHAGNDTNDADRK
Mm-AGO2       39 --------IKLQANFFEMDI---------------PKID-I--YHYELDI------------KPEKRPR---------------RVNREIVEHMVQHFKTQIFGD---RKP-VFDGRKNLYTAMPLPIGRDKVELEVTLP---GE-G-------------
Mm-AGO1       36 --------IKLLANYFEVDI---------------PKID-V--YHYEVDI------------KPDKCPR---------------RVNREVVEYMVQHFKPQIFGD---RKP-VYDGKENIYTVTALPIGNERVDFEVTIP---GE-G-------------
Mm-AGO4       28 --------IRLLANHFQVQI---------------PKID-V--YHYDVDI------------KPEKRPR---------------RVNREVVDTMVRHFKMQIFGD---RQP-GYDGKRNMYTAHPLPIGRDRIDMEVTLPGEG-----------------
Mm-AGO3       30 --------IKLLANCFQVEI---------------PKID-V--YLYEVDI------------KPDKCPR---------------RVNREVVDSKVQHFKVTIFGD---RRP-VYDGKRSLYTANPLPVATTGVDLDVTLP---GEGG-------------
Dm-AGO1A     148 --------IVLRANHFQVTM---------------PRGY-V--HHYDINI------------QPDKCPR----------------KVNREIIETMVHAYSKIFGV---LKP-VFDGRNNLYTRDPLPIGNERLELEVTLPGEG-----------------
Ce-ALG-1     151 --------ILLRANHFAVRI---------------PGGT-I--QHYQVDV------------TPDKCPR----------------RVNREIISCLISAFSKYFTN---IRP-VYDGKRNMYTREPLPIGRERMDFDVTLPGDSA----------------
Ce-ALG-2a     77 --------ILLRANHFAVRI---------------PGGS-V--QHYQIDV------------FPDKCPR----------------RVNREVIGCLISSFSKYFTN---IRP-VYDGKRNMYTREPLPIGTEPMNFEVTLP---GDSA-------------
Ce-T23D8.7    81 --------LSLLANHFQITC----------------NGSII--HQYYIRF------------DPDIPSK----------------KLNRTILRTLQEQNPGLIEC----PL-VFDGIHTVYSTELINVKEVNNSVINVAG---VVNTKE-----------
Ce-ZK757.3a   99 --------IPVKSNFFAMDL-------------KNPKMV-V--IQYHVEI------------HHPGCRK------------LDKDEMRIIFWKAVSDHPNIFHNK---FAL-AYDGAHQLYTVARLEFPDDQGSVRLDCEASLPKDNR------------
Ce-T22B3.2b   97 --------IPVKSNFFAVDL-------------KNPKMV-V--VQYHVEV------------HHPGCRK------------LDKDEMRIIFWKAVSDHPNIFHNK---FAL-AYDGAHQLYTVARLEFPDDQGSVRLDCE---ATLPKDNR---------
Dm-AGO2B     414 --------GQVGINYLDLDL------------SKMPSVA----YHYDVKI------------MPERPKK--------------------FYRQAFEQFRVDQLGG---AVL-AYDGKASCYSVDKLPLNSQNPEVTVTDR---NG---------------
Ce-ERGO-1    189 --------TTLLTNHTLVQL---------------PQEP-ITLHVFNIEV----------FINGKSSNK--------------RELCGPRFWEILKENKPTFGMP---NQY-IFNDVNMMWSTNKLRQSEGRT---------------------------
Ce-RDE-1      40 --------VLLLVNWFKFSS-------------KIYDRE-Y--YEYEVKM------------TKEVLNRKPGKPFPKKTEIPIPDRAKLFWQHLRHEKKQTDFIL---EDY-VFDEKDTVYSVCRLNTVTSKMLVSEKVV---KKDSEKKDEKDLE----
Ce-R04A9.2    99 --------FRVQMNAWNLDI-------------SKMDER-ISRIMFRATL--------VHTDGRRFELSLGVSAFSGDVNRQQRRAQACLLFRAWFKRNPELFKGMTDPAIAAYDAAETIYVGCSFFDVELTEHVCHLTE---ADFSPQEWKIVSLISRR
Ce-C16C10.3   60 --------MNVQMNMFPVDI-------------KDMPHK-I--QRFQVDV------IVCSSNGKQINANLGVLAAKGDVNSHNRRLAQYYIMRTVHDKLLVKFSGKSHHFL-AYDCAATLYLPEGVYTGDDQEEVTLTID---DFPKEEWKFVSKLSRR-
Ce-T22H9.3    61 --------RDVQLNMFALNI-------------SGMPRK-I--QRFHVDT------LIKGKNGKIFNVNHGVLANSGDINSHNKRLAQHALMQKFHKKRRELFGQHDYHIL-AYDCANTLYLPDGVYLGRNEEECTFKSDDFSPEQWNITSKLS------
Ce-Y49F6A.1   69 --------CQVQTNSFKIDI-------------TKMPKR-L--LRLSMET----------------------------------RLCGGKTELNLNDGVQAVAGN--------------LNSQEDFTTQEWSQISNYLRK--------------------
Ce-C04F12.1   87 --------VKVTTNSYELEL--------------KPTPV----FRYDVSV------------LKSFDDSTRDPIELAGSKGGDRQRQADLTEIVKVALTLEGLGN---LNI-FYDGAAMLFTTQKFETKTEKQQAIFMPIPSDHPKLSTSLKESQFGR--
Ce-CSR-1a    170 --------PRLALNIFGLEL---------------SERT-I--FRHVVQMKLIDRQHNKEYILTTMSAR-------GRGNRATKQKDNFILLDILLKQWAAKKGQQNLPAF-AYDGAQSLFTLEGISLMVDIKKEDALEI---PELSNFL----------
Ce-R06C7.1    76 --------VDIQTNVFGIEV--------------TKETT-V--HRFMVHA--------KADLTSTKEVTFTKKGKEDFVVQDRRDKCCNIFFLAVEKNPEFFKMK-DGNQI-VYDGQSTLYTTVNLFSELDANGTKSKVFQINGADTGN-----------
Ce-F55A12.1   45 --------DACIKRLQQLKV---------------ENGAKM--YMKPAEP----------GQLGRKEVTFTKKGKEDFVVLDRRDKCCNLFFHAVEKNPEFFKMK-DGNQI-VYDGQSTLYTTVNLFSELDANGTKSKVF---QINGADINN--------
Ce-PPW-2      84 --------TEVLTNVFGVEV--------------HKTSN-F--YQYSVHI--------TAELSSKKEVTFTKKGKEDFIVHDRHEKCSAILFHALNRFEDFFKSS---ENCIIYDGQSILFTSMNLFEGIPTGKIKTKVF---QINGADTNL--------
Ce-F58G1.1    73 --------AEIQTNVFGIEM--------------HQDSL-F--YQYSVNI--------TTELKNGKEVTFTKKGKDDFVVTERHDKCCAILFRALGDYEEFFKTS--DSCL-IYDGQSILFSNVDLFQGFREGAVKTKYM---QLDGGEMDH--------
Ce-C06A1.4    73 --------AEIQTNVFGIEM--------------HQDSL-F--YQYSVHI------------TTELKNG----------------NEVTFTKKGKDETSDSCL---------IYDGQSILFSNVDLFQGFREGAVKTKYM---QLDGGEIDH--------
Ce-SAGO-2     41 --------VNIDTNIRKLTI--------------KPNQP-I--YKYAVQVNYVFRKPD----GTEATIEMSKSAKKGTEHDNDKTRCQNVYNEAIKRYDELKTGG----PF-FYDRQASLYTLTKLKNESISFVVTDKIC---KRQNF------------
Ce-PPW-1a     67 --------VNIDTNIRKLTI--------------KPNQP-I--YKYAVQVNYVFRKPD----GTEATIEMSKSAKKGTEHDNDKTRCQKVYNEAIKRYDELKTGG----PF-FYDRQASLYTLTKLKNESISFVVTDKIC---KRQ--------------
Ce-SAGO-1     44 --------VQIVTNMRKINL--------------EKNHS-I--FKYSVQV----LFVYQKSDGTELVLEKSKSVGSGCDHERSKSHCLRVYRKAAKQCQELKSGG----PF-CYDSQGCLYSFSKLKNDEFSTNITGSDI---SNNP-------------
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Dm-AGO3       202 ---------EDVELQIRILYK--------------KKEEM--------------RNCTQLYNILFDRVM----KVLNY--VKFDR---KQFDPS------------RPK------------------IIPLAKLEVWPGYVTAV-D-------EYKGGLM
Mm-MIWI       188 ---------NGEHVRITITLT------------NELPPTS--------------PTCLQFYNIIFRRLL----KIMNL--QQIGR---NYYNPS------------DPI------------------DIPNHRLVIWPGFTTSI-L-------QYENNIM
Mm-MIWI2      176 ---------RGETIKITLTLT------------SKLFPNS--------------PVCIQFFNVIFRKIL----KNLSM--YQIGR---NFYKPS------------EPV------------------EIPQYKLSLWPGFAISV-S-------HFESKLL
Mm-MILI       296 ---------DDAEISIKIQLT------------KILEPCS--------------DLCIPFYNVVFRRVM----KLLDM--KLVGR---NFYDPT------------SAM------------------VLQQHRLQIWPGYAASI-R-------RTDGGLF
Dm-PIWI       172 ---------LDIEYKISIKFV------------GFISCAE--------------PRFLQVLNLILRRSM----KGLNL--ELVGR---NLFDPR------------AKI------------------EIREFKMELWPGYETSI-R-------QHEKDIL
Dm-AUB        190 ---------AGENIEIKIKAV-----------GSVQSTD---------------AEQFQVLNLILRRAM----EGLDL--KLVSR---YYYDPQ------------AKI------------------NLENFRMQLWPGYQTSI-R-------QHENDIL
Ce-PRG-1      126 ---------PIDRSLICIRFK--------QTNRFLVDD----------------PQTINIFNTIIRRSF----DALQL--TQLGR---NYFNWG------------DSR------------------AVPDYNMSILPGYETAI-R-------MYEENFM
Ce-PRG-2       66 ---------PNDNSLICIRFK--------KTNRFLVDD----------------PQTINIFNTIIRRSF----DAMKL--TQIGR---NYFDWD-----------------------------------------NSRALRKEL-R--------------
Tt-TWI11       95 ---------ESFTQELEVFLV----KKKDIVGQQLEEEN---------------KELQNILGQLMRNFQ---NNTKGF--QQLGA--TKRFAMN-------------VI------------------KNISNGLEAVLGVETFF-KF------SPQTGFQ
PTIWI12        86 ---------NEVQNVVTLKYI-----------ESIDNG----------------TKLQQILAKIVKQII---STQQGM--VQIGR--DKLFWPK------------KSH------------------SFHEHKFEIWEGVQ------------IVQKQFG
PTIWI15        86 ---------EEIQNVASLKLV------------ESVDGG---------------PKLQQILARIVKQIM---STQQGM--VQIGK--DKLFWPK------------KSH------------------SFHDYKFEIWEGVQ------------IVQKQFG
PTIWI03        89 ---------EEAEQIVSIKFI------------NRLSENH--------------ISKNQIIARLIKQVV---RNQFQM--VSIGKTGSKLFWNS------------KTI------------------KQQENNLEIWPGVECIY-Q-------PSAFQNF
PTIWI09        84 ---------ETNQDTATLKLV-----------GKIENK----------------ADLNIIISRLFKQVI---RSQLQM--VSVGNKGQKLFWSS------------RAQ------------------QFKDQNLEIWPGVECIF-R-------PGEGGAQ
PTIWI01        84 ---------ETNQDTATLKLV-----------GKIENK----------------ADLNIIISRLFKQVI---RSQMQM--VSVGNKGQKLFWSS------------RAQ------------------QFKDQNLEIWPGVECIF-R-------PGEGGAQ
PTIWI06        87 ---------EGTSYTISIEEK------------AVLKPGE--------------PEYTGLIGRFFKMLL----KQQKL--LQIGR---KYFNTK------------NLI------------------NFDQFGLKVLPGVTCSL---------IKQEELG
PTIWI10        87 ---------EGTSYSISIEEK------------AVLKPGE--------------PEYTGLIGRFFKMLL----KQQKL--LQIGR---KYFNTK------------NLI------------------NFDQFGLKVLPGVSCSLIKQ------EEQGKYY
PTIWI11        87 ---------EGTSHSISIEEK------------AVLKPGE--------------PEYTGLIGRFFKMLL----KQQKL--LQIGR---KYFNTK------------NLI------------------NFDQFGLKVLPGVSCSLIKQ------EEQGKYY
Tt-TWI1        90 ---------TVDTKTVSLKLL-----------GEANNE----------------REVQNIFGRLIKTVF----AKIKL--NKLGR---KYFDPA------------SRK------------------EYNEYDLAVFSGYESSLEK-------YSFNQKL
Tt-TWI12       83 ---------SVLGYQVSIKQI------QQNGSPAFITTN---------------KERQLVLNYIAREIF----SKLNY--HQYQK---GFFNPI-----DPPNAALSKD------------------KTVVYQTYSWNGLRPKA-I-------EFRGKVY
PTIWI07       184 ---------NSYDYYLEIKKV------KVINMQDLENPNPIEA-----------DKPLMFFNYLIKDFF----KNLKY--QEHGK-TRKFHDIS------------RRQ------------------PIPETELSVIPGFAVNF-Q-------TNEQGFS
Tt-TWI8       122 ---------QKTDYQVNLKIT------KVFRLEDLNNENQRKS-----------QFPLLFFNVMVKNIL----KGLNF--FEFGK-NTKYFEPS----------AEYHS------------------KIEGTNLIVYKGWNTPF-E-------NCSDGLL
Tt-TWI9       125 ---------GEQSYSMRIKFV-K--QIEVQNDETVDQFSN--------------NQINQILNITFKDIL----REENF--IEIGK-NSKFYKEN-----DIKERQITLK------------------NGYDIQFQIYKGITFQI-Y-------QTLEKYQ
Tt-TWI7       121 ---------DDQTYSLSLTFT-KLFEVNEESAQNKDKTTPNYKKG---------NKVTQVLNVILKNII----DQEGF--KQIGR-NSQFFDLQ------SRADVVIKN------------------QNNTSTLEVYKGITFKV-S-------PTQQGLY
Tt-TWI2       123 ----------GQKFSILLRFT-KTFEVNDESAQNLDKTSPNFKKG---------NQVTQLLNIILKSIM----RDEKF--QEIGK-NSKFYNVN-----SRNEIVIKGR------------------DGNTSALEAYKGFTFNV-T-------PTQDKLY
Tt-4505902    123 ---------DKQKYSIHLVFT-KSFEVNDESAQNLDKTSPNFKKG---------NQVTQLLNIILKSIM----RDEKF--LEIGK-NSKFYEVN-----SKSDIIIKSR------------------EGSTSGLEAYKGFTFNV-T-------PTQDKIY
Tt-TWI10      108 ---------ENIIYCLKIFYR-REIELNLTESNQINQNKTLQKKIS--------SLAIQSISAIYKSVY-----------KQFQK---DILKQT---------------------------------GLAKNDCKQLDHYNFQC---------FFREQIN
PTIWI02       109 ---------QLSNINLLIKHV------KTYNLTQNLDLIPH-------------ESLKQAMNAILSQIY----QERNL--KQIFR-KGQFFDKD--------------K------------------IEKINDVQILQGFTSVL-Q-------MGQSSPL
PTIWI05       108 ---------KEKKMILDIKYV---KTINLKEMAQFDDQSSI-------------NVTKQAINAILKQLY----ESRNMK-ELFGK--GKFYESK---------MNEEKN------------------LQKNYNIGYMKGFRSAF-C-------SGQSSPL
PTIWI04cor    107 ---------DETKLIVDIKYV-K--TINLKDLTQYNDQQSI-------------NISKQAINAILKQIH-EKRNMKEF--FGKGK----FYESV----------MNCNQ------------------KFQEFQIAYLKGFRNVY-C-------PGQNTPL
PTIWI08       104 ---------QELEYVVIAQHK------KEYTLSDLSETTT--------------NPVTQSINVAVKRSL----KEMGM--IEIGR-QSKFYDPK----------NIECN------------------RINEHGLKVWRGVKTSF-Q-------FYQGMPF
PTIWI14       104 ---------QGQEYRVLVEHK------KEYTLQDLSETTV--------------NPVTQSINVAVKRSL----REMGM--IEIGR-QSKFYDPR----------DIDCN------------------RINEHGLKVWRGVKTSF-Q-------MYQGKPY
PTIWI13       112 ---------DGKKHCVYLNFT-KAIDFQYLEGDNQDPALM--------------QPLQQAVNVQVKKAL----KDMGL--RELNR-LSQFFDPK----------SIDAN------------------PVKGFPLKVWLGYKTSL-K-------LTSTKPQ
Sp-AGO1       107 ---------REIEFSIQKSSK-----INLHTLSQFVNSKYSSDPQV--------LSSIMFLDLLLKKKP-----SETL--FGFMH---SFFTGE-------------NG------------------VSLGGGVEAWKGFYQSI-R-------PNQGFMS
At-AGO5       250 ---------KDRPFKVAVKNV---TSTDLYQLQQFLDRKQREAP----------YDTIQVLDVVLRDKP-----SNDY--VSVGR---SFFHTS------LGKDARDGR------------------GELGDGIEYWRGYFQSL-R-------LTQMGLS
At-AGO1       283 ---------REREFKVVIKLV---ARADLHHLGMFLEGKQSDAP----------QEALQVLDIVLRELP---TSRIRY--IPVGR---SFYSPD-----------IGKK------------------QSLGDGLESWRGFYQSI-R-------PTQMGLS
At-AGO10      233 ---------RERSYKVAIKFV---ARANMHHLGEFLAGKRADCP----------QEAVQILDIVLRELS-----VKRF--CPVGR---SFFSPD-----------IKTP------------------QRLGEGLESWCGFYQSI-R-------PTQMGLS
At-AGO7       263 KK-------IEKLFRVNMKLV------SKFDGKEQRKEGEDWAPLP--------PEYIHALDVILRENP-----MEKC--TSIGR---SFYSSS-----------MGGS------------------KEIGGGAVGLRGFFQSL-R-------HTQQGLA
At-AGO2       264 ---------RGRSYTFTIKQV---NVLKLGDLKEYMTGRSSFNP----------RDVLQGMDVVMKEHP-----SKCM--ITVGK---SFFTRE-----------TEPD------------------EDFRFGVIAAKGYRHTL-K-------PTAQGLS
At-AGO3       437 ---------RGRSYTFIIKQV---KELKLLDLQAYIDGRSTFIP----------RDVLQGMDVVMKEHP-----SKRM--ITVGK---RFFSTR-------------LE------------------IDFGYGVGAAKGFHHTL-K-------PTVQGLS
At-AGO6       144 CKRSKRSF-LPRSYKVQIHYA-AEIPLKTVLGTQRGAYTPDKSA----------QDALRVLDIVLRQQA----AERGC--LLVRQ---AFFHSD------------GHP------------------MKVGGGVIGIRGLHSSF-R-------PTHGGLS
At-AGO4       177 DRKRLRRPNRSKNFRVEISYA---AKIPLQALANAMRGQESENS----------QEAIRVLDIILRQHA----ARQGC--LLVRQ---SFFHND-----------PTNC------------------EPVGGNILGCRGFHSSF-R-------TTQGGMS
At-AGO8       140 ---------QSKKFNVAILFA--PPEIPMEAIANALQGKKTKHL----------LDAIRVMDCILSQNA----ARQGC--LLVRQ---SFFHND-----------AKYF------------------ANIGEGVDCCKGFHSSF-R-------TTQGGLS
At-AGO9       155 RSRRPN---QTKKFMVEISYA---AKIPMQAIASALQGKETENL----------QDALRVLDIILRQSA----ARQGC--LLVRQ---SFFHND-----------VKNF------------------VPIGGGVSGCRGFHSSF-R-------TTQGGLS
Mm-AGO2       125 ---------KDRILKVSIKWV---SCVSLQALHDALSGRLPSVP----------FETIQALDVVMRHLP-----SMRY--TPVGR---SFFTAS-----------EGCS------------------NPLGGGREVWFGFHQSV-R-------PSLWKMM
Mm-AGO1       122 ---------KDRIFKVSIKWL---AIVSWRMLHEALVSGQIPVP----------LESVQALDVAMRHLA-----SMRY--TPVGR---SFFSPP-----------EGYY------------------HPLGGGREVWFGFHQSV-R-------PAMWKMM
Mm-AGO4       114 ---------KDQTFKVSVQWV---SVASLQLLLEALAGHLNEVP----------DDSVQALDVITRHLP-----SMRY--TPVGR---SFFSPP-----------EGYY------------------HPLGGGREVWFGFHQSV-R-------PAMWNMM
Mm-AGO3       117 ---------KDRPFKVSVKFV---SRVSWHLLHEALAGGTLPEPLELDKPVS--TNPVHAVDVVLRHLP-----SMKY--TPVGR---SFFSAP-----------EGYD------------------HPLGGGREVWFGFHQSV-R-------PAMWKMM
Dm-AGO1A      233 ---------KDRIFRVTIKWQ---AQVSLFNLEEALEGRTRQIP----------YDAILALDVVMRHLP-----SMTY--TPVGR---SFFSSP-----------EGYY------------------HPLGGGREVWFGFHQSV-R-------PSQWKMM
Ce-ALG-1      237 ---------VERQFSVSLKWV---GQVSLSTLEDAMEGRVRQVP----------FEAVQAMDVILRHLP-----SLKY--TPVGR---SFFSPPVPNASGVMAGSCPPQASGAVAGGAHSAGQYHAESKLGGGREVWFGFHQSV-R-------PSQWKMM
Ce-ALG-2a     163 ---------VERKFSVTMKWI---GQVCLSALDDAMEGRVRQVP----------HEAVQSIDVILRHLP-----SLKY--TPVGR---SFFTPP---GVMKPGMQMHQE------------------SKLGGGREVWFGFHQSV-R-------PSQWKMM
Ce-T23D8.7    168 ---------SPNLFKLYLTHV-DSFLLDTKIITGNQDQNQK-------------LRMMHAIDTVFRQTS-----TGNF--HAVLQ---SFFSIAQNSAIEPSHGLGWGT------------------VNLGVGREVCYGFYQNV-V-------ETFDTLT
Ce-ZK757.3a   195 ---------DRTRCAISIQNVGPVLLEMQRTRTNNLDERV--------------LTPIQILDIICRQSL-----TCPL--LKNSA---NFYTWK--SSCYRIPTAAGQA------------------LDLEGGKEMWTGFFSSAHI-------ASNYRPL
Ce-T22B3.2b   193 ---------DRTRCAISIQNVGPVLLEMQRTRTNNLDERV--------------LTPIQILDIICRQSL-----TCPL--LKNSA---NFYTWK--SSCYRIPTAAGQA------------------LDLEGGKEMWTGFFSSA-HI------ASNYRPL
Dm-AGO2B      496 ---------RTLRYTIEIKET-GDSTIDLKSLTTYMNDRIFDKP----------MRAMQCVEVVLASPC-----HNKA--IRVGR---SFFKMS----------DPNNR------------------HELDDGYEALVGLYQAF---------MLGDRPF
Ce-ERGO-1     270 ---------NNRRMNFVWKYV-----KQIKFGGNIEDEETM-------------QLLSTLIDAIATQRARLPLAPPKY--TVFKRLTYLICEEA----YEPELPDVSLC------------------HKLRIGTDARVGVSIAI-RT------NLRAGIT
Ce-RDE-1      153 ---------KKILYTMILTYR-KKFHLNFSRENPEKDEEANRSYKFLKNVMTQKVRYAPFVNEEIKVQF---AKNFVYDNNSILRVPESFHDPN----------RFEQS------------------LEVAPRIEAWFGIYIGIKE-------LFDGEPV
Ce-R04A9.2    226 ---------SGSTFEIRIKTN---PPIYTRGPNALTLENR--------------SELTRIIEAITDQCL----HNEKF--LLYSS---GTFPTK-----------GGDI------------------ASPDEVTLIKSGFVKTT-KI------VDRDGVP
Ce-C16C10.3   185 ---------KDDSYLVVLKPA---GFVYTQGEVAQEEANR--------------MELTRIIEIVTSQKL----NNEDY--LQFGN---ATFPRL-----------SPPH------------------SEPDAISEIRSGFAKVS-R-------LSQNGGG
Ce-T22H9.3    184 ---------RKKDYTYVMKIR-PSGFIYTSGEEASEVANR--------------MELTRCVEIVTSQKL----NNSDY--CQFGN---DTFSFR-----------AQPV------------------SEPDATSEIRSGFAKVS-RIV-----EGRNGKN
Ce-Y49F6A.1   137 ---------KNAEFKVKISPN-G--FVYTNGPNSLSDANR--------------QELPRLVEIATSEVL----NTPEY--LQFGN---QTYAVN-----------EPAV------------------SSPDALSEIRSGFDKSV-RLV-----DGENGST
Ce-C04F12.1   203 ---------ASGKFHVSIELNSKQSELNTIDLLNERLDSAA-------------CPVTQMAQIALSAEA----KQNGFIILDGGH---ELFDQK-----------NTRR------------------TIGKDGVEDMDGVAASI-KMA-----QGNKKTG
Ce-CSR-1a     283 ---------KDSISFLSGDLE-ISCEPDLEKPSFVQTELNEWSD----------PRFYAYLDIVTSQSA---IRSERY--LSQSK---GLYVHT-----------QSLE------------------ELRVKWAVAAKGIHKGC-RI------VGANGPL
Ce-R06C7.1    190 ---------DDLKTLPCISLEIYAPRDNSITLSSENLGKRTADQNIEVNN----REYTQFLELALNQHCVRETNRFGC--FEHGK---VYFLNA-----TEEGFDQRDC------------------VDVGDGKQLYPGLKKTI-QFIEGPYGRGQNNPS
Ce-F55A12.1   157 ---------DDLKTLPCISLE-IYAPRNNSITLSAENLSKRTADQNIEVNN---REYTQFLELALNQHCVRETKRFGC--FEHGK---VYFLNA-----TEEGFDQRDC------------------VDVGDGKQLYPGLKKAI-QFIEGPYGRGQNNPS
Ce-PPW-2      197 ---------KDLMVLPCIKLE-VFPTKNPVVNFSLEDIGRRTSDSNIESVN---MAYKQILDLAMSQYA--IRETSKCVVFEHGK---MFFINP-----LQEGYAPCDI------------------VEVGDGKQMKPGLKKTL-QFIEGPYGRNQNNPS
Ce-F58G1.1    186 ---------KDLKSLPCIKLE-VFPTKNPAVKFTREAVARRATDSNLDSVS---LAYQQILELALTQPC--LRNTARYVVFDHGK---MFFIDP-----LGEGFEKCDV------------------VDVGDGKQVVPGLKKTI-NFIEGPYGRGRSNPS
Ce-C06A1.4    160 ---------KDLKSLPCIKLE-VFPTKNPAVKFTREDVARRASDSNLDSVS---LAYQQILELALTQPC--IRNTARYVVFDHGK---MFFIDP-----LGEGFEKSDV------------------VDVGDGKQVVPGLKKTI-NFIEGPYGRGRSNPS
Ce-SAGO-2     152 ---------KEAQFVLK-KVD-QSFQSTSNDVIKTTNSCPANAD----------KTLLEAMNIIVSGPA---FENKNV--ITVGACVHYLIDPT--------GVDVAYK------------------EYPEGQLYSGVGVSKSV-KTLE----GTDKKVP
Ce-PPW-1a     176 ---------NFKEAQFVLKKVDQSFQSTSNDVIRTTNSCPANAD----------KTLLEAMNIIVSGPA---FENKNV--ITVGACVHYLIDPT--------VVDVAYK------------------EYAEGQLYSGVGASKSV-KTLE----GTDKKVP
Ce-SAGO-1     154 ---------KFLRVEFKLAKVQESFQTTTNDVAKSVNCRPALQE----------KTILEAMNQIVSTAP---INHPNV--LTIGNCVHYLYDDT---------NIDIRS------------------ITGEGGKSSAVGASKSV-RTL-----EGTGKTP
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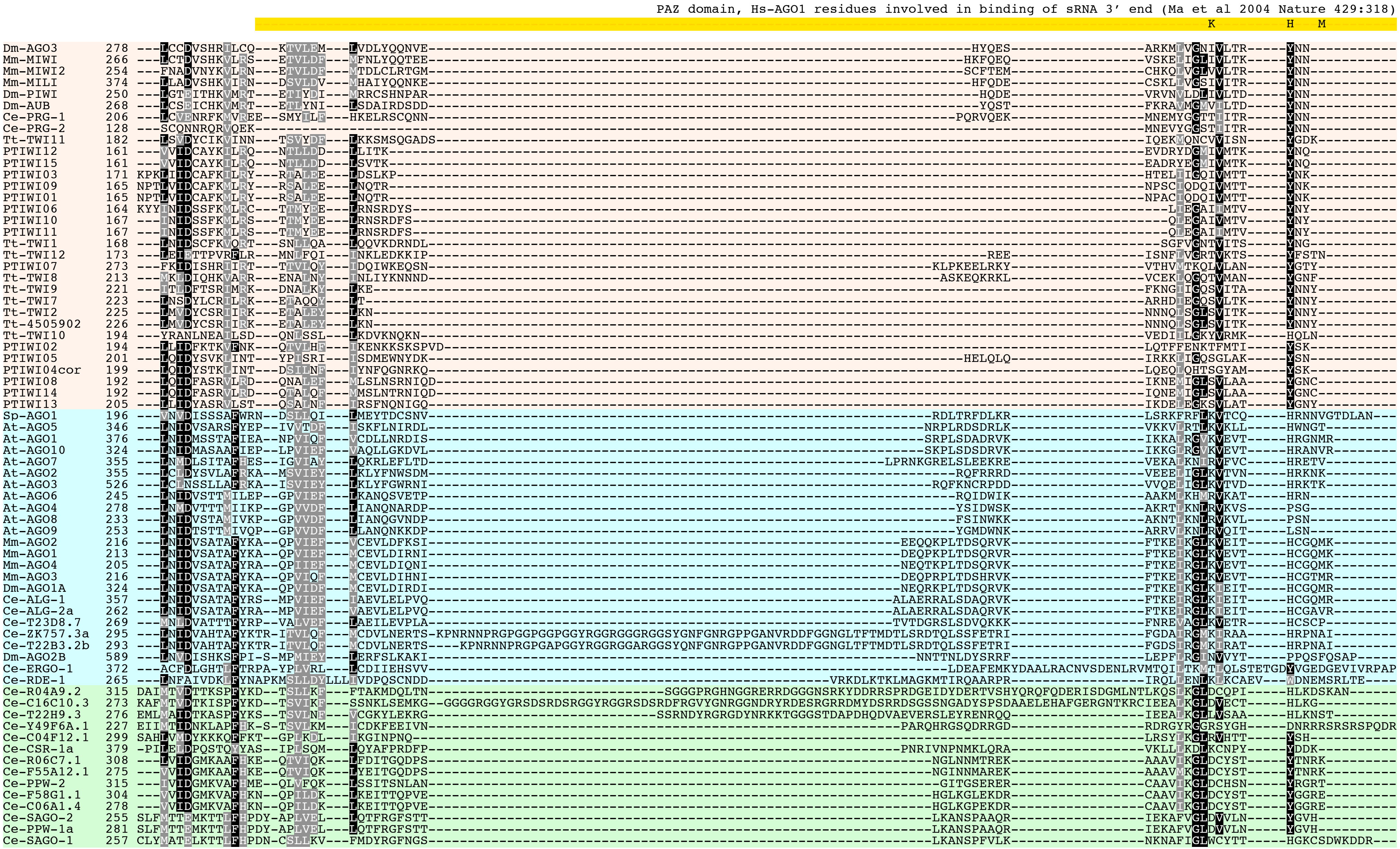

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                                                                                                   PAZ domain, Hs-AGO1 residues involved in binding of sRNA 3’ end (Ma et al 2004 Nature 429:318)
                                                                                                                                                              K         H   M
Dm-AGO3     278 ---LCCDVSHRILCQ---KTVLEM---LVDLYQQNVE---------------------------------------------------------------------HYQES-----------------ARKMLVGNIVLTR-----YNN-----------
Mm-MIWI     266 ---LCTDVSHKVLRS---ETVLDF---MFNLYQQTEE--------------------------------------------------------------------HKFQEQ-----------------VSKELIGLIVLTK-----YNN-----------
Mm-MIWI2    254 ---FNADVNYKVLRN---ETVLDF---MTDLCLRTGM--------------------------------------------------------------------SCFTEM-----------------CHKQLVGLVVLTR-----YNN-----------
Mm-MILI     374 ---LLADVSHKVIRN---DSVLDV---MHAIYQQNKE---------------------------------------------------------------------HFQDE-----------------CSKLLVGSIVITR-----YNN-----------
Dm-PIWI     250 ---LGTEITHKVMRT---ETIYDI---MRRCSHNPAR----------------------------------------------------------------------HQDE-----------------VRVNVLDLIVLTD-----YNN-----------
Dm-AUB      268 ---LCSEICHKVMRT---ETLYNI---LSDAIRDSDD----------------------------------------------------------------------YQST-----------------FKRAVMGMVILTD-----YNN-----------
Ce-PRG-1    206 ---LCVENRFKMVREE--SMYILF---HKELRSCQNN-------------------------------------------------------------------PQRVQEK-----------------MNEMYGGTTIITR-----YNN-----------
Ce-PRG-2    128 ---SCQNNRQRVQEK-----------------------------------------------------------------------------------------------------------------MNEVYGGSTIITR-----YNN-----------
Tt-TWI11    182 ---LSVDYCIKVINN---TSVYDF---LKKSMSQGADS------------------------------------------------------------------------------------------IQEKMQNCVVISN-----YGDK----------
PTIWI12     161 ---VVIDCAYKILRQ---NTLLDD---LLITK------------------------------------------------------------------------------------------------EVDRYDGMIVMTK-----YNQ-----------
PTIWI15     161 ---VVIDCAYKILRQ---NTLLDD---LSVTK------------------------------------------------------------------------------------------------EADRYEGMIVMTK-----YNQ-----------
PTIWI03     171 KPKLIIDCAFKILRY---RTALEE---LDSLKP-----------------------------------------------------------------------------------------------HTELIIGQIVMTT-----YNK-----------
PTIWI09     165 NPTLVIDCAFKMLRY---RSALEE---LNQTR------------------------------------------------------------------------------------------------NPSCIQDQIVMTT-----YNK-----------
PTIWI01     165 NPTLVIDCAFKMLRY---RSALEE---LNQTR------------------------------------------------------------------------------------------------NPACIQDQIVMTT-----YNK-----------
PTIWI06     164 KYYINIDSSFKMLRC---TTMYEE---LRNSRDYS------------------------------------------------------------------------------------------------LIEGAIIMTV-----YNY-----------
PTIWI10     167 ---INIDSSFKMLRS---TTMYEE---LRNSRDFS------------------------------------------------------------------------------------------------QLEGAIVMTV-----YNY-----------
PTIWI11     167 ---INIDSSFKMLRS---TTMYEE---LRNSRDFS------------------------------------------------------------------------------------------------QLEGAIIMTV-----YNY-----------
Tt-TWI1     168 ---LNIDSCFKVQRT---SNLLQA---LQQVKDRNDL---------------------------------------------------------------------------------------------SGFVGNTVITS-----YNG-----------
Tt-TWI12    173 ---LEIETTPVRFLR---MNLFQI---INKLEDKKIP-----------------------------------------------------------------------REE-----------------ISNFLVGRTVKTS-----YFSTN---------
PTIWI07     273 ---FKIDISHRIIRT---TTVLQY---IDQIWKEQSN----------------------------------------------------------------KLPKEELRKY-----------------VTHVMTKQLVLAN-----YGTY----------
Tt-TWI8     213 ---MKLDIQHKVARR---ENALNY---INLIYKNNND-----------------------------------------------------------------ASKEQKRKL-----------------VCEKLQGQTVMAN-----YGNF----------
Tt-TWI9     221 ---ITLDFTSRIMRK---DNALKY---LKE--------------------------------------------------------------------------------------------------FKNGIIGQSVITA-----YNNY----------
Tt-TWI7     223 ---LNSDYLCRILRK---ETAQQY---LT---------------------------------------------------------------------------------------------------ARHDIEGQSVLTK-----YNNY----------
Tt-TWI2     225 ---LMVDYCSRIIRK---ETALEY---LKN--------------------------------------------------------------------------------------------------NNNQLSGLSVITK-----YNNY----------
Tt-4505902  226 ---LMVDYCSRIIRK---ETALEY---LKN--------------------------------------------------------------------------------------------------NNNQLSGLSVITK-----YNNY----------
Tt-TWI10    194 ---YRANLNEAILSD---QNLSSL---LKDVKNQKN--------------------------------------------------------------------------------------------VEDIILGKYVRMK-----HQLN----------
PTIWI02     194 ---LLIDFKTKVFNK---QTVLHF---IKENKKSKSPVD-----------------------------------------------------------------------------------------LQTFFENKTFMTI-----YSK-----------
PTIWI05     201 ---LQIDYSVKLINT---YPISRI---ISDMEWNYDK--------------------------------------------------------------------HELQLQ-----------------IRKKLIGQSGLAK-----YSN-----------
PTIWI04cor  199 ---LQIDYSTKLINT---DSILNF---IYNFQGNRKQ-------------------------------------------------------------------------------------------LQEQLQHTSGYAM-----YSK-----------
PTIWI08     192 ---LQIDFASRVLRD---QNALEF---MLSLNSRNIQD------------------------------------------------------------------------------------------IKNEMIGLSVLAA-----YGNC----------
PTIWI14     192 ---LQIDFASRVLRD---QTALQF---MMSLNTRNIQD------------------------------------------------------------------------------------------IQNEMIGLSVLAA-----YGNC----------
PTIWI13     205 ---LLIDYASRVLST---QSALNF---IRSFNQNIGQ-------------------------------------------------------------------------------------------IKDELEGKSVLAT-----YGNY----------
Sp-AGO1     196 ---VNVDISSSAFWRN--DSLLQI---LMEYTDCSNV----------------------------------------------------------------RDLTRFDLKR-----------------LSRKFRFLKVTCQ-----HRNNVGTDLAN---
At-AGO5     346 ---LNIDVSARSFYEP--IVVTDF---ISKFLNIRDL---------------------------------------------------------------NRPLRDSDRLK-----------------VKKVLRTLKVKLL-----HWNGT---------
At-AGO1     376 ---LNIDMSSTAFIEA--NPVIQF---VCDLLNRDIS---------------------------------------------------------------SRPLSDADRVK-----------------IKKALRGVKVEVT-----HRGNMR--------
At-AGO10    324 ---LNIDMASAAFIEP--LPVIEF---VAQLLGKDVL---------------------------------------------------------------SKPLSDSDRVK-----------------IKKGLRGVKVEVT-----HRANVR--------
At-AGO7     355 ---LNMDLSITAFHES--IGVIAY---LQKRLEFLTD----------------------------------------------------------LPRNKGRELSLEEKRE-----------------VEKALKNIRVFVC-----HRETV---------
At-AGO2     355 ---LCLDYSVLAFRKA--MSVIEY---LKLYFNWSDM-------------------------------------------------------------------RQFRRRD-----------------VEEELIGLKVTVN-----HRKNK---------
At-AGO3     526 ---LCLNSSLLAFRKA--ISVIEY---LKLYFGWRNI----------------------------------------------------------------RQFKNCRPDD-----------------VVQELIGLKVTVD-----HRKTK---------
At-AGO6     245 ---LNIDVSTTMILEP--GPVIEF---LKANQSVETP-------------------------------------------------------------------RQIDWIK-----------------AAKMLKHMRVKAT-----HRN-----------
At-AGO4     278 ---LNMDVTTTMIIKP--GPVVDF---LIANQNARDP-------------------------------------------------------------------YSIDWSK-----------------AKRTLKNLRVKVS-----PSG-----------
At-AGO8     233 ---LNIDVSTAMIVKP--GPVVDF---LIANQGVNDP-------------------------------------------------------------------FSINWKK-----------------AKNTLKNLRVKVL-----PSN-----------
At-AGO9     253 ---LNIDTSTTMIVQP--GPVVDF---LLANQNKKDP-------------------------------------------------------------------YGMDWNK-----------------ARRVLKNLRVQIT-----LSN-----------
Mm-AGO2     216 ---LNIDVSATAFYKA--QPVIEF---VCEVLDFKSI------------------------------------------------------------EEQQKPLTDSQRVK-----------------FTKEIKGLKVEIT-----HCGQMK--------
Mm-AGO1     213 ---LNIDVSATAFYKA--QPVIEF---MCEVLDIRNI------------------------------------------------------------DEQPKPLTDSQRVR-----------------FTKEIKGLKVEVT-----HCGQMK--------
Mm-AGO4     205 ---LNIDVSATAFYRA--QPIIEF---MCEVLDIQNI------------------------------------------------------------NEQTKPLTDSQRVK-----------------FTKEIRGLKVEVT-----HCGQMK--------
Mm-AGO3     216 ---LNIDVSATAFYKA--QPVIQF---MCEVLDIHNI------------------------------------------------------------DEQPRPLTDSHRVK-----------------FTKEIKGLKVEVT-----HCGTMR--------
Dm-AGO1A    324 ---LNIDVSATAFYKA--QPVIDF---MCEVLDIRDI------------------------------------------------------------NEQRKPLTDSQRVK-----------------FTKEIKGLKIEIT-----HCGQMR--------
Ce-ALG-1    357 ---LNIDVSATAFYRS--MPVIEF---IAEVLELPVQ-----------------------------------------------------------ALAERRALSDAQRVK-----------------FTKEIRGLKIEIT-----HCGQMR--------
Ce-ALG-2a   262 ---LNIDVSATAFYRA--MPVIEF---VAEVLELPVQ-----------------------------------------------------------ALAERRALSDAQRVK-----------------FTKEIRGLKIEIT-----HCGAVR--------
Ce-T23D8.7  269 ---MNLDVATTTFYRP--VALVEF---LAEILEVPLA-----------------------------------------------------------TVTDGRSLSDVQKKK-----------------FNREVAGLKVETR-----HCSCP---------
Ce-ZK757.3a 295 ---LNIDVAHTAFYKTR-ITVLQF---MCDVLNERTS-KPNRNNPRGPGGPGGPGGYRGGRGGGRGGSYGNFGNRGPPGANVRDDFGGNGLTFTMDTLSRDTQLSSFETRI-----------------FGDAIRGMKIRAA-----HRPNAI--------
Ce-T22B3.2b 293 ---LNIDVAHTAFYKTR-ITVLQF---MCDVLNERTS----KPNRNNPRGPGAPGGYRGGRGGARGGSYQNFGNRGPPGANVRDDFGGNGLTFTMDTLSRDTQLSSFETRI-----------------FGDSIRGMKIRAT-----HRPNAI--------
Dm-AGO2B    589 ---LNVDISHKSFPI-S-MPMIEY---LERFSLKAKI--------------------------------------------------------------NNTTNLDYSRRF-----------------LEPFLRGINVVYT-----PPQSFQSAP-----
Ce-ERGO-1   372 ---ACFDLGHTLFTRPA-YPLVRL---LCDIIEHSVV------------------------------------------------------------------LDEAFEMKYDAALRACNVSDENLRVMTQILTKMTLQLSTETGDYVGEDGEVIVRPAP
Ce-RDE-1    265 ---LNFAIVDKLFYNAPKMSLLDYLLLIVDPQSCNDD---------------------------------------------------VRKDLKTKLMAGKMTIRQAARPR-----------------IRQLLENLKLKCAEV---WDNEMSRLTE----
Ce-R04A9.2  315 DAIMTVDTTKSPFYKD--TSLLKF---FTAKMDQLTN------------------------------SGGGPRGHNGGRERRDGGGNSRKYDDRRSPRDGEIDYDERTVSHYQRQFQDERISDGMLNTLKQSLKGLDCQPI-----HLKDSKAN------
Ce-C16C10.3 273 KAFMTVDTKISPFYKD--TSVIKF---SSNKLSEMKG--GGGGRGGYGRSDSRDSRGGYRGGRSDSRDFRGVYGNRGGNDRYRDESRGRRDMYDSRRDSGSSNGADYSPSDAAELEHAFGERGNTKRCIEEALKGLDVECT-----HLKG----------
Ce-T22H9.3  276 EMLMAIDTKASPFYKS--TSVLNF---VCGKYLEKRG-----------------------------SSRNDYRGRGDYNRKKTGGGSTDAPDHQDVAEVERSLEYRENRQQ-----------------IEEALKGLLVSAA-----HLKNST--------
Ce-Y49F6A.1 227 EIIMTIDNKLAPFHK-S-TSVLKM---ICDKFEEIVN------------------------------------------------------------PARQHRGSQDRRGD-----------------RDRGYRGGRSYGH-----DNRRRSRSRSPQDR
Ce-C04F12.1 299 SAHLVMDYKKKQFFKT--GPLKDL---IKGINPNQ---------------------------------------------------------------------------------------------LRSYLKGLRVHTT-----YSH-----------
Ce-CSR-1a   379 -PILELDPQSTQYYAS--IPLSQM---LQYAFPRDFP------------------------------------------------------------PNRIVNPNMKLQRA-----------------VKLLLKDLKCNPY-----YDDK----------
Ce-R06C7.1  308 ---LVIDGMKAAFHKE--QTVIQK---LFDITGQDPS----------------------------------------------------------------NGLNNMTREK-----------------AAAVIKGLDCYST-----YTNRK---------
Ce-F55A12.1 275 ---VVIDGMKAAFHKE--QTVIQK---LYEITGQDPS----------------------------------------------------------------NGINNMAREK-----------------AAAVMKGLDCYST-----YTNRK---------
Ce-PPW-2    315 ---IVIDGMKVAFHME--QLVFQK---LSSITSNLAN-----------------------------------------------------------------GITGSERER-----------------CAAVIKGLDCHSN-----YRGRT---------
Ce-F58G1.1  304 ---VVIDGMKVAFHKN--QPILDK---LKEITTQPVE----------------------------------------------------------------HGLKGLEKDR-----------------CAAVIKGLDCYST-----YGGRE---------
Ce-C06A1.4  278 ---VVIDGMKVAFHKN--QPILDK---LKEITTQPVE----------------------------------------------------------------HGLKGPEKDR-----------------CAAVIKGLDCYST-----YGGRE---------
Ce-SAGO-2   255 SLFMTTEMKTTLFHPDY-APLVEL---LQTFRGFSTT----------------------------------------------------------------LKANSPAAQR-----------------IEKAFVGLDVVLN-----YGVH----------
Ce-PPW-1a   281 SLFMTTEMKTTLFHPDY-APLVEL---LQTFRGFSTT----------------------------------------------------------------LKANSPAAQR-----------------IEKAFVGLDVVLN-----YGVH----------
Ce-SAGO-1   257 CLYMATELKTTLFHPDN-CSLLKV---FMDYRGFNGS----------------------------------------------------------------LKANSPFVLK-----------------NKNAFIGLWCYTT-----HGKCSDWKDDR---
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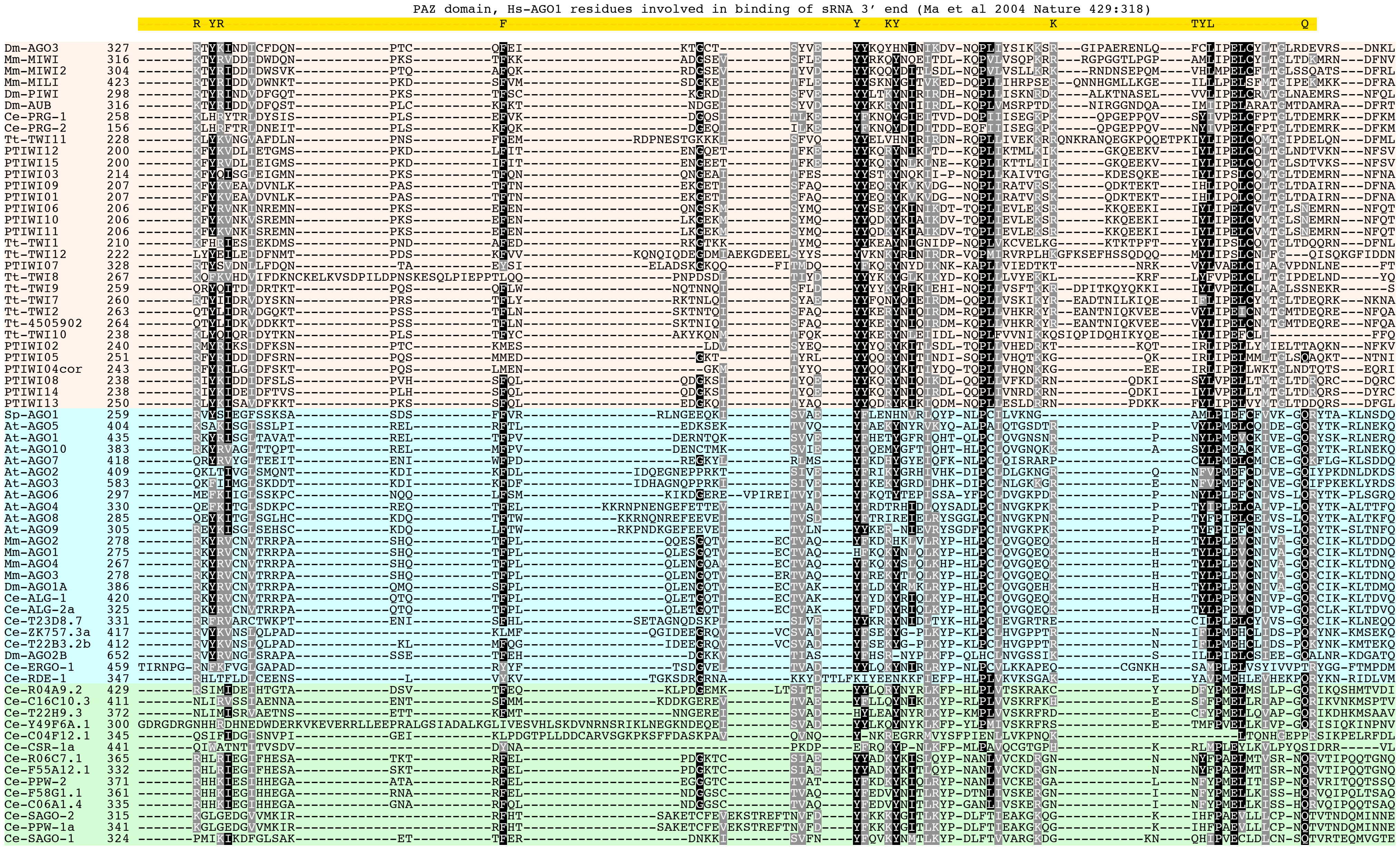

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                                                        PAZ domain, Hs-AGO1 residues involved in binding of sRNA 3’ end (Ma et al 2004 Nature 429:318)
                          R YR                                    F                                            Y   KY                   K                 TYL           Q

Dm-AGO3       327 -------RTYKINDICFDQN------------PTC----------QFEI--------------------KTGCT---------SYVE----YYKQYHNINIKDV-NQPLIYSIKKSR---GIPAERENLQ----FCLIPELCYLTGLRDEVRS---DNKL
Mm-MIWI       316 -------KTYRVDDIDWDQN------------PKS----------TFKK--------------------ADGSEV--------SFLE----YYRKQYNQEITDL-KQPVLVSQPKRR---RGPGGTLPGP----AMLIPELCYLTGLTDKMRN---DFNV
Mm-MIWI2      304 -------KTYRIDDIDWSVK------------PTQ----------AFQK--------------------RDGSEV--------TYVD----YYKQQYDITLSDL-NQPVLVSLLKRK----RNDNSEPQM----VHLMPELCFLTGLSSQATS---DFRL
Mm-MILI       423 -------RTYRIDDVDWNKT------------PKD----------SFVM--------------------SDGKEI--------TFLE----YYSKNYGITVKED-DQPLLIHRPSER--QNNHGMLLKGE----ILLLPELSFMTGIPEKMKK---DFRA
Dm-PIWI       298 -------RTYRINDVDFGQT------------PKS----------TFSC---------------------KGRDI--------SFVE----YYLTKYNIRIRDH-NQPLLISKNRDK----ALKTNASEL----VVLIPELCRVTGLNAEMRS---NFQL
Dm-AUB        316 -------KTYRIDDVDFQST------------PLC----------KFKT---------------------NDGEI--------SYVD----YYKKRYNIIIRDL-KQPLVMSRPTDK----NIRGGNDQA----IMIIPELARATGMTDAMRA---DFRT
Ce-PRG-1      258 -------KLHRYTRLDYSIS------------PLS----------EFVK---------------------DGQSI--------TLKE----YFKNQYGIEITVD-DQPIIISEGKPK-----QPGEPPQV----SYIVPELCFPTGLTDEMRK---DFKM
Ce-PRG-2      156 -------KLHRFTRLDNEIT------------PLS----------KFQK---------------------DGEQI--------ILKE----YFKNQYDIDITDD-EQFIIISEGKPK-----QPGEPPQV----NYIVPELCFPTGLTDEMRK---DFKM
Tt-TWI11      228 -------KLYKVNGVAFDLN------------PNS----------FFEM--------------RDPNESTGKKKI--------SFVQ----YYELVHNIRIRDN-RQPLLIVEKKRRQNKRANQEGKPQQETPKIYLIPELCQMTGIPDELQN---DFML
PTIWI12       200 -------KFYKVDLIETGMS------------PKD----------LFIT--------------------ENGQET--------TFKE----YYKQRYNIKLTD--KQPLIKTMLKIK------GKQEEKV----IYLIPELCQLTGLNDTVKN---NFSV
PTIWI15       200 -------KFYRVDLIEIGMS------------PKD----------IFIT--------------------ENGEET--------TFKE----YYKQRYNLKLNE--KQPLIKTTLKIK------GKQEEKV----IYLIPELCQLTGLSDTVKS---NFSV
PTIWI03       214 -------KFYQISGLEIGMN------------PKS----------TFQN--------------------QNGEAI--------TFES----YYSTKYNQKII-P-NQPLLKAIVTGK-------KDESQKE----IYLIPSLCQMTGLTDEMRN---NFNA
PTIWI09       207 -------KFYKVEAVDVNLK------------PAS----------TFTN--------------------EKGETI--------SFAQ----YYEQRYKVKVDG--NQPLIRATVRSK------QDKTEKT----IHLIPQLCQLTGLTDAIRN---DFNA
PTIWI01       207 -------KFYKVEAVDVNLK------------PAS----------TFTN--------------------EKGETI--------SFAQ----YYEQRYKVKVDG--NQPLIRATVRSK------QDKTEKT----IHLIPQLCQLTGLTDAIRN---DFNA
PTIWI06       206 -------KFYRVNKINREMN------------PKS----------EFEN--------------------QNGSKM--------SYMQ----YYSEKYKINIKDT-TQPLIEVLEKSR------KKQEEKI----IYLIPELCVLTGLSNEMRN---NFQT
PTIWI10       206 -------KFYKVNKVSREMN------------PKS----------EFEN--------------------LKGEKM--------SYMQ----YYQDKYKIAIKDV-TQPLIEVLEKSR------KKQEEKI----IYLIPELCVMTGLSNEMRN---NFQT
PTIWI11       206 -------KFYKVNKISREMN------------PKS----------EFEN--------------------LKGEKM--------SYMQ----YYQDKYKIAIKDV-TQPLIEVLEKSR------KKQEEKI----IYLIPELCVMTGLSNEMRN---NFQT
Tt-TWI1       210 -------KFHRIESIEKDMS------------PND----------AFED--------------------RKGTKK--------TYMQ----YYKEAYNIGNIDP-NQPLVKCVELKG------KTKTPFT----YYLIPSLCQVTGLTDQQRN---DFNL
Tt-TWI12      222 -------LYYEILEIDFNMT------------PDS----------KFVV--------------KQNQIQDEGDMIAEKGDEELSYYS----YVKNKYRINIRDR-VQPMIRVRPLHKGFKSEFHSSQDQQ----MYLIPSLCNLFG---QISQKGFIDDN
PTIWI07       328 -------RTYSVDNLLFDQN-------------TA----------EYSI----------------ELADSKGKQQ------FITMDQ----YFKQRYNYDIKNK-KAPLLVIEDTKT----------NRK----VYLVAELCIMAGVPDNLNE-----FT
Tt-TWI8       267 -------KQFKVHDVIFDKNCKELKVSDPILDPNSKESQLPIEPPTLQQ-------------------PNPDSDL--------TIYD----YYYKKYGLKIKYD-KQPLLLVYEKKL----------KRF----LYFVPELCLLTGIPDELND-----YQ
Tt-TWI9       259 -------QRYQITDLDRTKT------------PQS----------QFLW-------------------NQTNNQI--------SFLD----YYYYKYRIKIEHI-NQPLLVSFTKKR--DPITKQYQKKI----IYLVPELCLMAGLSSNEKR------S
Tt-TWI7       260 -------RTYIIDRVDYSKN------------PRS----------TFLY-------------------RKTNLQI--------SYAE----YYFQNYQIEIRDM-QQPLLVSKIKYR--EADTNILKIQE----IFLIPELCYMTGLTDEQRK---NKNA
Tt-TWI2       263 -------QTYLIDRVDGQKT------------PSS----------TFLN-------------------SKTNTQI--------SFAQ----YYKERYNIQIRDM-RQPLLVHKRKYR--EANTNIQKVEE----VYLIPEICNMTGMTDEQRE---NFQA
Tt-4505902    264 -------QTYLIDKVDDKKT------------PSS----------TFLN-------------------SKTNIQI--------SFAQ----YYKERYNIQIRDM-KQPLLVHKRKYR--EANTNIQKVEE----VYLIPELCNMTGMTDEQRE---NFQA
Tt-TWI10      238 -------KLYQIQRIDYTKN------------PLS----------TFYC-------------------AKYKQNM--------TFQK----YYKERYNLEIIDL-NQPLFVVNIKKQSIQPIDQHIKYQE----IYLIPEFCLI-------------FFQ
PTIWI02       240 -------RMYRIKSIDFKSN------------PTC----------KMES-----------------------LDV--------SYEQ----YYYQRYKITLSDL-TQPLLVHEDRKT----------KQT----IRLIPELLYMIELTTAQKN---NFKV
PTIWI05       251 -------RFYRIDDIDFSRN------------PQS----------MMED----------------------GKT---------TYRL----YYQQRYNITINDI-SQPLLVHQTKKG-----------QK----IRLIPELMMLTGLSQAQKT---NTNI
PTIWI04cor    243 -------RFYRILGIDFSKT------------PQS----------LMEN-----------------------GKM--------TYYQ----YYQQKYKITIYDQ-TQPLLVHQNKKG-----------EE----IRLIPELLWKTGLNDTQTS---EQRI
PTIWI08       238 -------RIYKIDDIDFSLS------------PVH----------SFQL--------------------QDGKSI--------TYQE----YYKQRYNIQIKDL-QQPLLVFKDKRN---------QDKI----SYLVPELLTMTGLTDRQRC---DQRC
PTIWI14       238 -------RIYKIDEIDFTVS------------PLH----------SFQL--------------------QDGKSI--------TYQE----YYKQRYNIQIRDL-QQPLIVNRDKRN---------QDKI----IYLVPELLTMTGLTDRQRS---DYRC
PTIWI13       250 -------RLYKISAVDFKKT------------PKS----------SFQL--------------------EDGKQI--------TYAQ----YYQDRYKIKIQDM-NQPLLESLDRRN---------PDKK----FYLIPELVYMTGLTDDQRS---DFGL
Sp-AGO1       259 -------RVYSIEGFSSKSA------------SDS----------FFVR-----------------RLNGEEQKI--------SVAE----YFLENHNVRLQYP-NLPCILVKNG-------------------AMLPIEFCFVVK-GQRYTA-KLNSDQ
At-AGO5       404 -------KSAKISGISSLPI------------REL----------RFTL--------------------EDKSEK--------TVVQ----YFAEKYNYRVKYQ-ALPAIQTGSDTR------------P----VYLPMELCQIDE-GQRYTK-RLNEKQ
At-AGO1       435 -------RKYRISGLTAVAT------------REL----------TFPV-------------------DERNTQK--------SVVE----YFHETYGFRIQHT-QLPCLQVGNSNR------------P----NYLPMEVCKIVE-GQRYSK-RLNERQ
At-AGO10      383 -------RKYRVAGLTTQPT------------REL----------MFPV-------------------DENCTMK--------SVIE----YFQEMYGFTIQHT-HLPCLQVGNQKK------------A----SYLPMEACKIVE-GQRYTK-RLNEKQ
At-AGO7       418 -------QRYRVYGLTEEIT------------ENI----------WFPD--------------------REGKYL--------RLMS----YFKDHYGYEIQFK-NLPCLQISRARP-----------------CYLPMELCMICE-GQKFLG-KLSDDQ
At-AGO2       409 -------QKLTIVGLSMQNT------------KDI----------KFDL--------------IDQEGNEPPRKT--------SIVE----YFRIKYGRHIVHK-DIPCLDLGKNGR------------Q----NFVPMEFCDLVE-GQIYPKDNLDKDS
At-AGO3       583 -------QKFIIMGLSKDDT------------KDI----------KFDF--------------IDHAGNQPPRKI--------SIVE----YFKEKYGRDIDHK-DIPCLNLGKKGR------------E----NFVPMEFCNLVE-GQIFPKEKLYRDS
At-AGO6       297 -------MEFKIIGLSSKPC------------NQQ----------LFSM------------------KIKDGERE--VPIREITVYD----YFKQTYTEPISSA-YFPCLDVGKPDR------------P----NYLPLEFCNLVS-LQRYTK-PLSGRQ
At-AGO4       330 -------QEFKITGLSDKPC------------REQ----------TFEL----------KKRNPNENGEFETTEV--------TVAD----YFRDTRHIDLQYSADLPCINVGKPKR------------P----TYIPLELCALVP-LQRYTK-ALTTFQ
At-AGO8       285 -------QEYKITGLSGLHC------------KDQ----------TFTW------------KKRNQNREFEEVEI--------TVSD----YFTRIREIELRYSGGLPCINVGKPNR------------P----TYFPIELCELVS-LQRYTK-ALTKFQ
At-AGO9       305 -------REYKISGLSEHSC------------KDQ----------LFTW------------RKPNDKGEFEEVEI--------TVLN----YYKER-NIEVRYSGDFPCINVGKPKR------------P----TYFPIEFCNLVS-LQRYTK-SLTNFQ
Mm-AGO2       278 -------RKYRVCNVTRRPA------------SHQ----------TFPL------------------QQESGQTV------ECTVAQ----YFKDRHKLVLRYP-HLPCLQVGQEQK------------H----TYLPLEVCNIVA-GQRCIK-KLTDDQ
Mm-AGO1       275 -------RKYRVCNVTRRPA------------SHQ----------TFPL------------------QLESGQTV------ECTVAQ----HFKQKYNLQLKYP-HLPCLQVGQEQK------------H----TYLPLEVCNIVA-GQRCIK-KLTDNQ
Mm-AGO4       267 -------RKYRVCNVTRRPA------------SHQ----------TFPL------------------QLENGQAM------ECTVAQ----YFKQKYSLQLKHP-HLPCLQVGQEQK------------H----TYLPLEVCNIVA-GQRCIK-KLTDNQ
Mm-AGO3       278 -------RKYRVCNVTRRPA------------SHQ----------TFPL------------------QLENGQTV------ERTVAQ----YFREKYTLQLKYP-HLPCLQVGQEQK------------H----TYLPLEVCNIVA-GQRCIK-KLTDNQ
Dm-AGO1A      386 -------RKYRVCNVTRRPA------------QMQ----------SFPL------------------QLENGQTV------ECTVAK----YFLDKYRMKLRYP-HLPCLQVGQEHK------------H----TYLPLEVCNIVA-GQRCIK-KLTDMQ
Ce-ALG-1      420 -------RKYRVCNVTRRPA------------QTQ----------TFPL------------------QLETGQTI------ECTVAK----YFYDKYRIQLKYP-HLPCLQVGQEQK------------H----TYLPPEVCNIVP-GQRCIK-KLTDVQ
Ce-ALG-2a     325 -------RKYRVCNVTRRPA------------QTQ----------TFPL------------------QLETGQTI------ECTVAK----YFFDKYRIQLKYP-HLPCLQVGQEQK------------H----TYLPPEVCDIVP-GQRCLK-KLTDVQ
Ce-T23D8.7    331 -------RRFRVARCTWKPT------------ENI----------SFHL--------------SETAGNQDSKPL--------SLVE----YYKRRYNIDLTYK-HLPCIEVGRTRE-----------------CILPLELCYVVS-GQRCIK-KLNEQQ
Ce-ZK757.3a   417 -------RVYKVNSLQLPAD-------------------------KLMF----------------QGIDEEGRQV------VCSVAD----YFSEKYG-PLKYP-KLPCLHVGPPTR------------N----IFLPMEHCLIDS-PQKYNK-KMSEKQ
Ce-T22B3.2b   412 -------RVYKVNSLQLPAD-------------KL----------MFQG------------------IDEEGRQV------VCSVAD----YFSEKYG-PLKYP-KLPCLHVGPPTR------------N----IFLPMEHCLIDS-PQKYNK-KMTEKQ
Dm-AGO2B      652 -------RVYRVNGLSRAPA------------SSE----------TFEH---------------------DGKKV--------TIAS----YFHSR-NYPLKFP-QLHCLNVGSSIK------------S----ILLPIELCSIEE-GQALNR-KDGATQ
Ce-ERGO-1     459 TIRNPG-RNFKFVGLGAPAD-------------------------RYYF-------------------TSDGVEL--------TVAD----YYLQKYNIRLRYP-NLPCVLKKAPEQ--------CGNKH----SAMPLELVSYIVVPTRYGG-FTMPDM
Ce-RDE-1      347 -------RHLTFLDLCEENS--------------L----------VYKV----------------TGKSDRGRNA--------KKYDTTLFKIYEENKKFIEFP-HLPLVKVKSGAK------------E----YAVPMEHLEVHEKPQRYKN-RIDLVM
Ce-R04A9.2    429 -------RSIMIDEIHTGTA------------DSV----------TFEQ------------------KLPDGEMK------LTSITE----YYLQRYNYRLKFP-HLPLVTSKRAKC------------Y----DFYPMELMSILP-GQRIKQSHMTVDI
Ce-C16C10.3   411 -------NLIRVSSIAENNA------------ENT----------SFMM-----------------KDDKGEREV--------TVAE----YFLLQYNIKLKYP-RLPLVVSKRFKH------------E----SFFPMELLRIAP-GQRIKVNKMSPTV
Ce-T22H9.3    372 -------NLIMISRVAETNS------------ETT----------KFMT-------------------NNGEREI--------SVAD----HYLEAYNYRLKYP-KMPLVVSKRFRD------------E----CFYPMELLQVAP-GQRIKDHKMSAAV
Ce-Y49F6A.1   300 GDRGDRGNHHRDHNEDWDERKVKEVERRLLEEPRALGSIADALKGLIVESVHLSKDVNRNSRIKLNEGKNDEQEI--------SVAD----YYLKQYNYKLKFP-YLPMIVSKRFRS------------E----TMFPVELLKIVP-GQKISIQKINPNV
Ce-C04F12.1   345 -------QSIFIDGISNVPI------------GEI----------KLPDGTPLLDDCARVSGKPKSFFDASKPAV--------QVNQ----Y-NKREGRRMVYSFPIENLLVKPNQK-----------------------LTQNHGEPPRSIKPELRFDL
Ce-CSR-1a     441 -------QIWATNTITVSDV-------------------------DYNA----------------------------------PKDP----EFRQKYP-NLKFP-MLPAVQCGTGPH------------K----RLMPLEYLKVLPYQSIDRR-----VL
Ce-R06C7.1    365 -------RHLRIEGIFHESA------------TKT----------RFEL--------------------PDGKTC--------SIAE----YYADKYKISLQYP-NANLVVCKDRGN------------N----NYFPAELMTVSR-NQRVTIPQQTGNQ
Ce-F55A12.1   332 -------RHLRIEGIFHESA------------SKT----------RFEL--------------------PDGKTC--------SIAE----YYADKYKITLQYP-NANLVVCKDRGN------------N----NYFPAELMTISR-NQRVTIPQQTGNQ
Ce-PPW-2      371 -------RHHKIESIHHEGA------------ATA----------RFEL--------------------EGGGTC--------TVAT----YFKDKYKIQLRYP-NANLIVCKERGA------------L----NFYPMELITISP-NQRVRITQQTSSQ
Ce-F58G1.1    361 -------RHHKIEGIHHEGA------------RNA----------RFEL--------------------NDGGSC--------TVAQ----YFEDVYNITLRYP-DTNLIVSKERGN------------I----NFYPMELLKISS-HQRVQIPQLTSAQ
Ce-C06A1.4    335 -------RHHKIEGIHHEGA------------GNA----------RFQL--------------------NDGGSC--------TVAQ----YFEDVYNITLRYP-GANLIVSKERGN------------I----NFYPMELLKISS-HQRVQIPQQTSAQ
Ce-SAGO-2     315 -------KGLGEDGVVMKIR-------------------------RFHT-----------------SAKETCFEVEKSTREFTNVFD----YFKKKYGITLKYP-DLFTIEAKGKQG------------K----IHFPAEVLLLCP-NQTVTNDQMINNE
Ce-PPW-1a     341 -------KGLGEDGVVMKIR-------------------------RFHT-----------------SAKETCFEVEKSTREFTNVFD----YFKKKYGITLKYP-DLFTIEAKGKQG------------K----IHFPAEVLLLCP-NQTVTNDQMINNE
Ce-SAGO-1     324 -------PMIKIKDFGLSAK-------------ET----------TFER---------------------DNKKI--------SVFN----YFQVKYNMTLKYP-DLFTVVARGKDG-----------KN----QHIPVECLDLCN-SQTVRTEQMVGTE
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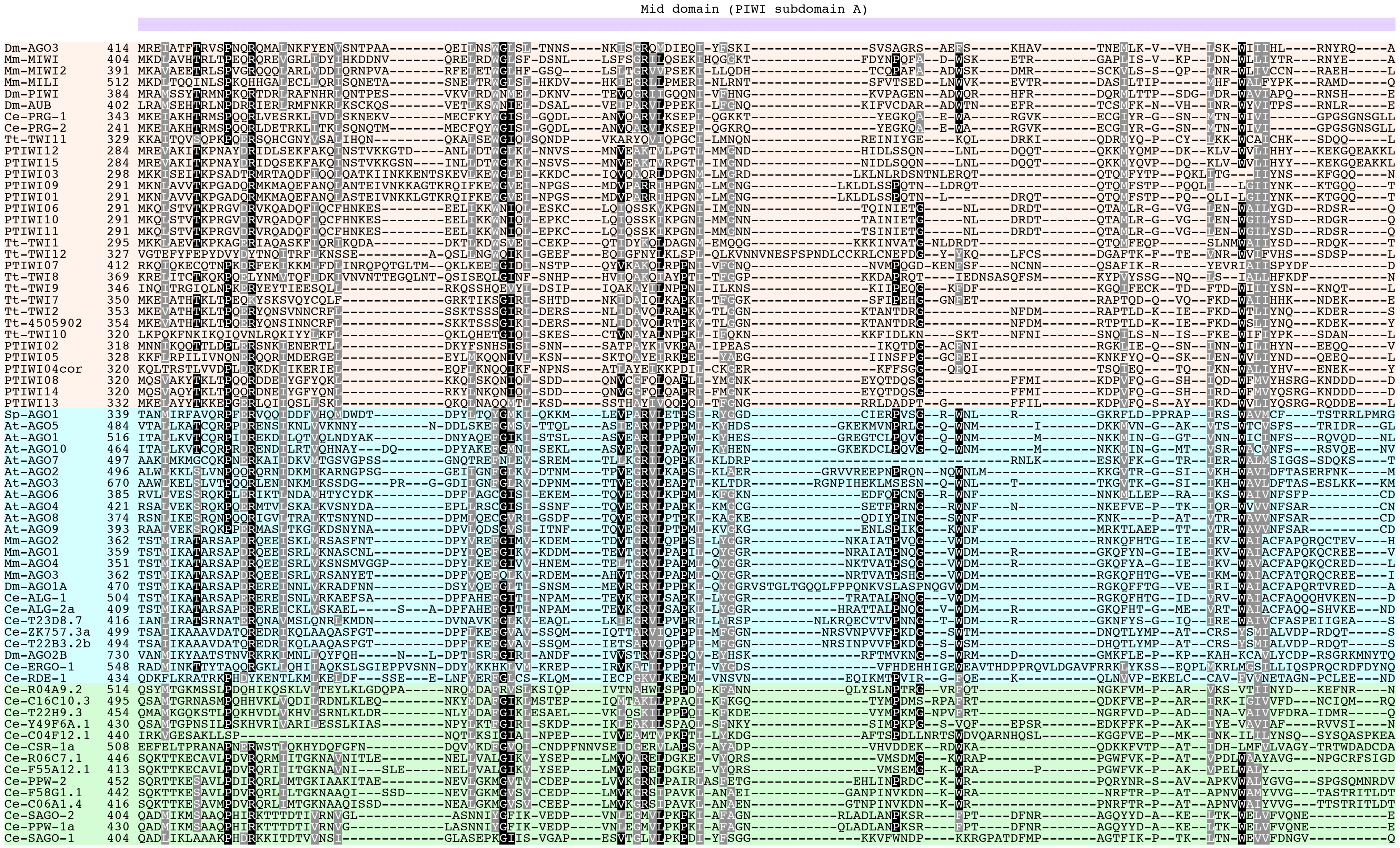

Mid domain (PIWI subdomain A)

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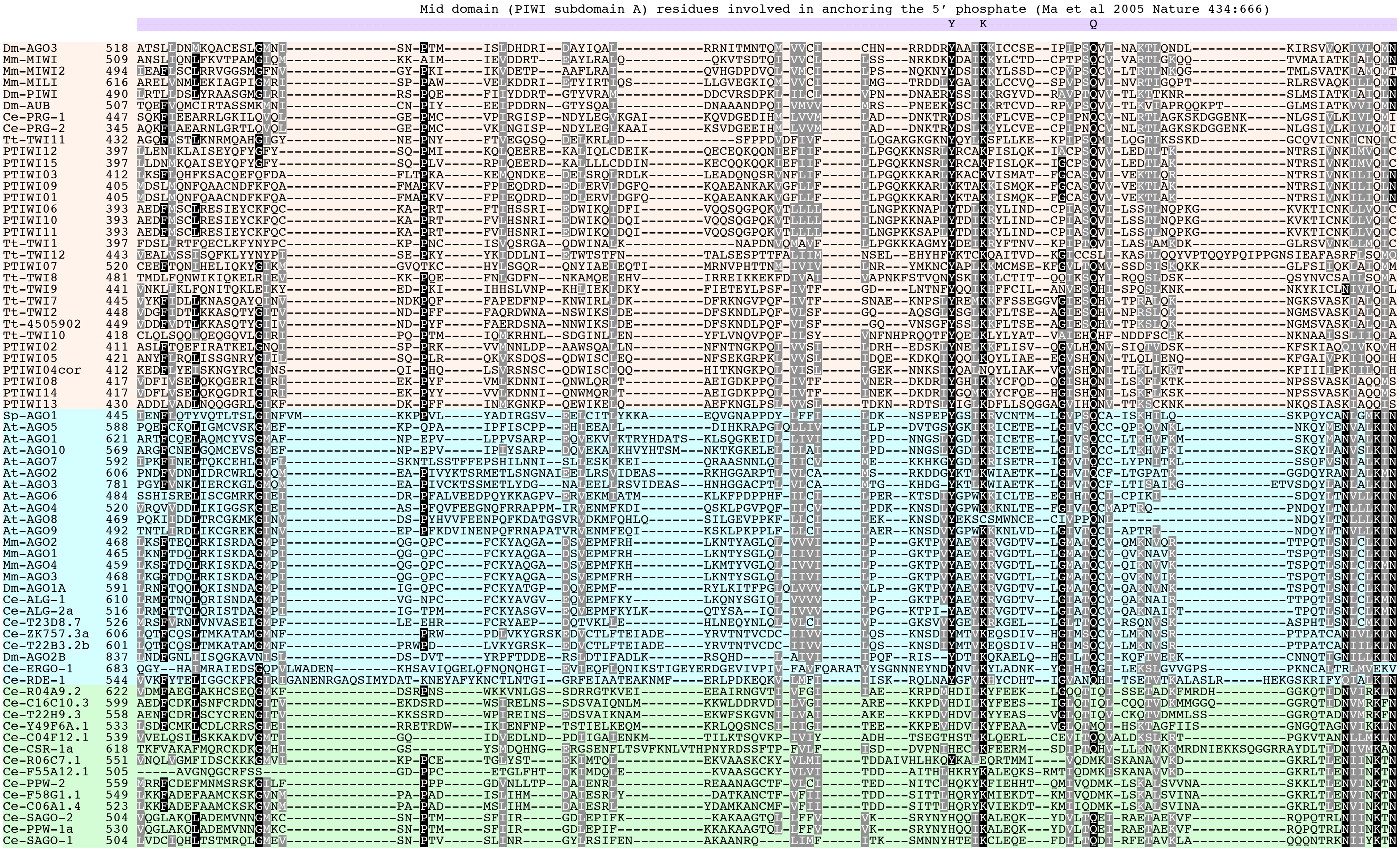
Dm-AGO3      414 MREIATFTRVSPNQRQMALNKFYENVSNTPAA-------QEILNSWGLSL-TNNS----NKISGRQMDIEQI-YFSKI---------------SVSAGRS--AEFS-----KHAV-------TNEMLK-V--VH--LSK-WIIIHL----RNYRQ----A
Mm-MIWI      404 MKDLAVHTRLTPEQRQREVGRLIDYIHKDDNV-------QRELRDWGLSF-DSNL----LSFSGRILQSEKIHQGGKT--------------FDYNPQFA--D-WSK----ETR--------GAPLIS-V--KP--LDN-WLLIYTR---RNYE-----A
Mm-MIWI2     391 MKAVAEETRLSPVGRQQQLARLVDDIQRNPVA-------RFELETWGLHF-GSQ-----LSLTGRVVPSEKI-LLQDH---------------TCQPAFA--ADWSK----DMR--------SCKVLS-S--QP--LNR-WLIVCCN---RAEH-----L
Mm-MILI      512 MKDLTQQINLSPKQHHGALECLLQRISQNETA-------SNELTRWGLSL-HKDV----HKIEGRLLPMERI-NLRNT---------------SFVTSED--LNWVK----EVTR-------DASILTIP------MHF-WALFYPK---RAMD-----Q
Dm-PIWI      384 MRAMSSYTRMNPKQRTDRLRAFNHRLQNTPES-------VKVLRDWNMEL-DKNV----TEVQGRIIGQQNI-VFHNG---------------KVPAGEN--ADWQR----HFR--------DQRMLTTP--SDG-LDR-WAVIAPQ---RNSH-----E
Dm-AUB       402 LRAMSEHTRLNPDRRIERLRMFNKRLKSCKQS-------VETLKSWNIEL-DSAL----VEIPARVLPPEKI-LFGNQ--------------KIFVCDAR--ADWTN----EFR--------TCSMFK-N--VH--INR-WYVITPS---RNLR-----E
Ce-PRG-1     343 MKEIAKHTRMSPQQRLVESRKLIVDLSKNEKV-------MECFKYWGISL-GQDL----ANVQARVLKSEPL-QGKKT----------------YEGKQA--E-WA-----RGVK-------ECGIYR-G--SN--MTN-WIVI------GPGSGNSGLL
Ce-PRG-2     241 MKEIAKHTRMSPQQRLDETRKLITKLSQNQTM-------MECFQYWGISL-GQDL----ANVQARVLKSEPL-QGKRQ----------------YEGKQA--E-WA-----RGVK-------ECGIYR-G--SN--MTN-WIVI------GPGSGNSGLL
Tt-TWI11     329 KKAITQVSQPKPQERSQHCGNYVSALIHQN---------QKALSEWGIQLSQNDP----VKARYQVIQPGCI-LMNQN--------------REINIYGE----KQL----DRKI-------QDRMYQ-P--CY--LKK-WCAICHK---SDQQ-----L
PTIWI12      284 MREVAKITKPNAYDRIDLSEKFAKQINSTVKKGTD----ANLLDTWGLKL-NNVS----MNVEAKTVLPGTL-MMGND--------------HIDLSSQN----LNL----DQQT-------QKKMYQMP--DK--KLV-WVLIHHY---KEKGQEAKKL
PTIWI15      284 MREVAKITKPNAYDRIDQSEKFAKQINSTVKKGSN----INLLDTWGLKL-NSVS----MNVEAKTVRPGTL-IMGND--------------NIDLSQQN----LNL----DQQT-------QKKMYQVP--DQ--KLV-WVLIHYY---KEKGQEAKKL
PTIWI03      298 MKKISEITKPSADTRMRTAQDFIQQLQATKIINKKENTSKEVLKEWGLEI-KKDC----IQVQAQRLDPGNM-LMGRD-------------LKLNLRDSNTNLERQT---------------QTQMFYTP--PQKLITG---IIYNS---KFGQQ----N
PTIWI09      291 MKNLAVVTKPGADQRMKMAQEFANQLANTEIVNKKAGTKRQIFKEWGVEI-NPGS----MDVPARRIHPGNM-LMGNG-----------LKLDLSSPQTN--LDRQT---------------QTQMFSTP--PQQLI---LGIIYNK---KTGQQ----T
PTIWI01      291 MKNLAVVTKPGADQRMKMAQEFANQLASTEIVNKKLGTKRQIFKEWGVEI-NPGS----MDVPARRIHPGNM-LMGNG-----------LKLDLSSPQTN--L--------DRQT-------QTQMFSTP--PQ--QLI-LGIIYNK---KTGQQ----T
PTIWI06      291 MKQLSTVTKPRGVDRVKQADQFIQCFHNKES--------EELIKKWNIQL-ESKC----LQIQSSKVKPGNI-IMGNN--------------TQINIETG-----NL----DRDT-------QTAMLR-G--VG--LEN-WAILYGD---RDSR-----Q
PTIWI10      291 MKQLSTVTKPRGVDRVRQADQFIQCFHNKES--------EELIKKWNIQL-EPKC----LQIQSSKIKPGNI-MMGNN--------------TAINIETG-----NL----DRDT-------QTAMLR-G--VG--LEN-WGILYSD---RDGR-----Q
PTIWI11      291 MKQLSTVTKPRGVDRVRQADQFIQCFHNKES--------EELIKKWNIQL-EPKC----LQIQSSKIKPGNI-MMGNN--------------TSINIETG-----NL----DRDT-------QTAMLR-G--VG--LEN-WGILYSD---RDSR-----Q
Tt-TWI1      295 MKKLAEVTKPKAGERIAQASKFIQRIKQDA---------DKTLKDWSVEI-CEKP----QTIDYKQLDAGNM-EMQQG-------------KKKINVATG-NLDRDT---------------QTQMFEQP------SLNMWAIIYSD---RDQK-----T
Tt-TWI12     327 VGTEFYFEPYDVYDYTNQITRFLKNSSE---------A-QSLLNGWQIKI-GEEF----EQIGFNYLKLSPL-QLKVNNVNESFSPNDLCCKRLCNEFDG--Y-YKQ----LFCS-------DGAFTK-F--TE--VNR-WVIFVHS---SDSP-----L
PTIWI07      412 RKQIQKECQTNPKDRFEKIKKMLFDLINRQPQTGLTM--QKLKEEFGIDI-NSTP----QYVKAKQLRPPNI-VFGNQ---------------NVMPQGD-KENFSF----NCNN-------QSAFIK-R------YEVRIAIISPYDF----------D
Tt-TWI8      369 KRELITCTKQKPQELYNMVTQFIDKIVNVNTTEGQLNT-QSISEQLGINF-SNHP----HVIQAKQIAYPTI-TFGGP--------------KKDAPRQT----IEDNSASQFSM-------KYPVYSSG--NQ--LS--IALLHFKDF----------N
Tt-TWI9      346 INQITRGIQLNPKERYEYTIEESQLL-------------RKQSSHQEVYI-DSIP----IQAKAYILNPPNI-ILKNS---------------KIIPEQG---KFDF---------------KGQIFECK--TD--FTD-WIIIYSN---KNQT-----L
Tt-TWI7      350 MKEIATHTKLTPEQKYSKSVQYCQLF-------------GRKTIKSGIRI-SHTD----NKIDAIQLKAPKI-TFGK----------------SFIPEHG--GNFET---------------RAPTQD-Q--VQ--FKD-WAIIHHK---NDEK-----E
Tt-TWI2      353 MKEVATHTKLTPQERYQNSVNNCRFL-------------SSKTSSSGIRI-DERS----NLIDAVQLRAPKV-TLGGN--------------KTANTDRG-----------NFDM-------RAPTLD-K--IE--FKD-WTLIYNQ---KDER-----S
Tt-4505902   354 MKEVATHTKLTPQERYQNSINNCRFL-------------SKKTSSSGIKI-DERS----NLIDAVQLRTPKV-TLGGN--------------KTANTDRG-----------NFDM-------RTPTLD-K--IE--FKD-WSLIYNQ---KDEK-----Y
Tt-TWI10     320 LKPQKFNKIKQIQVNLRQKIYYLKFL-------------QKLQHETGIQI-SKES----CTVNAYALNPPKL-IFQKN--------------KKFIDLKN----SKT----NFNI-------SNQILS-N--IS--FKE-WIFIYPK---SDAN-----L
PTIWI02      318 MNNIKQQTTLDPLERSNKIENERTLL-------------DKYFSNHSISI-SNN-----SATPAYKIVKPAL-IPEAS----------------IKQTDG--ACFNI---------------RGKLIE-Q--SN--INN-WILIHYN---EEQQ-----V
PTIWI05      328 KKFLRPILIVNQNERQQRIMDERGEL-------------EYLMKQQNIVL-KSN-----SKTQAYEIRKPEI--YAEG---------------IINSFPG--GCFEI---------------KNKFYQ-Q--SK--LEN-WVLIYND---QEEQ-----L
PTIWI04cor   320 KQLTRSTLVVDPLDRKDKIIKERIEL-------------EQFLKNQQIKF-NPNS----ATLAYEIKKPDIL-CKGER----------------KFFSGG---QFQI---------------TSQIEQ----TQ--LKN-WALIYHV---ENEK-----Y
PTIWI08      320 MQSVAKYTKLTPQQRDDEIYGFYQKL-------------KKQLSKQNIQL-SDD-----QNVCGFQLQAPLI-YMGNK--------------EYQTDQSG-----------FFMI-------KDPVFQ-G--SH--IQD-WFMVYHSRG-KNDDD----D
PTIWI14      320 MQSVAQYTKLTPQQRDNEIYGFYQNL-------------RKYLNKQNIQL-SDD-----QNVGGFQLQAPRI-FMGNK--------------EYQTDQSG-----------FFMI-------KDPVFQ-G--SH--IRD-WFMVYQSRG-KNDDD----D
PTIWI13      332 MKELAYYTKKEPGERLQIIQSLLSKL-------------QKQLNAQQMTL-KSD-----SSTHAYIVQQPQL-TFGNG--------------RRLDADPT--G--------FFIL-------KDPVFQ-S--AY--IKD-WVLIYQSRG-RQDDE----L
Sp-AGO1      339 TANMIRFAVQRPFERVQQIDDFVHQMDWDT---------DPYLTQYGMKI-QKKM----LEVPARVLETPSI-RYGGD--------------CIERPVSG--R-WNL----R----------GKRFLD-PPRAP--IRS-WAVMCF----TSTRRLPMRG
At-AGO5      484 VTALLKATCQRPPDRENSIKNLVVKNNY---------N-DDLSKEFGMSV-TTQL----ASIEARVLPPPML-KYHDS-----------GKEKMVNPRLG--Q-WNM-------I-------DKKMVN-G--AK--VTS-WTCVSFS---TRIDR---GL
At-AGO1      516 ITALLKVTCQRPIDREKDILQTVQLNDYAK---------DNYAQEFGIKI-STSL----ASVEARILPPPWL-KYHES-----------GREGTCLPQVG--Q-WNM-------M-------NKKMIN-G--GT--VNN-WICINFS---RQVQD---NL
At-AGO10     464 ITALLKVTCQRPRDRENDILRTVQHNAY---DQ------DPYAKEFGMNI-SEKL----ASVEARILPAPWL-KYHEN-----------GKEKDCLPQVG--Q-WNM-------M-------NKKMIN-G--MT--VSR-WACVNFS---RSVQE---NV
At-AGO7      497 AAKIMKMGCQKPNERKAIIDKVMTGSVGPSS--------GNQTREFNLEV-SREM----TLLKGRILQPPKL-KLDRP---------------------------------RNLK-------ESKVFK-G--TR--IER-WALMSIGGS-SDQKS----T
At-AGO2      496 ALWLKKLSLVNPQQRQRNIDKMIKARNGPSG--------GEIIGNFGLKV-DTNM----TPVEGRVLKAPSL-KLAER---------GRVVREEPNPRQN--NQWNLM--------------KKGVTR-G--SI--VKH-WAVLDFTASERFNK-----M
At-AGO3      670 AAWLKELSLVTPQQRLENINKMIKSSDG----PR---G-GDIIGNFGLRV-DPNM----TTVEGRVLEAPTL-KLTDR--------RGNPIHEKLMSESN--Q-WNL----T----------TKGVTK-G--SI--IKH-WAVLDFTAS-ESLKK---KM
At-AGO6      385 RVLLVESSRQKPLERIKTLNDAMHTYCYDK---------DPFLAGCGISI-EKEM----TQVEGRVLKPPML-KFGKN--------------EDFQPCNG--R-WNF---------------NNKMLLEP--RA--IKS-WAIVNFSFP---------CD
At-AGO4      421 RSALVEKSRQKPQERMTVLSKALKVSNYDA---------EPLLRSCGISI-SSNF----TQVEGRVLPAPKL-KMGCG--------------SETFPRNG---RWNF----N----------NKEFVE-P--TK--IQR-WVVVNFSAR---------CN
At-AGO8      374 RSNLIKESRQNPQQRIGVLTRALKTSNYND---------DPMLQECGVRI-GSDF----TQVEGRVLPTPKL-KAGKE--------------QDIYPING---SWNF---------------KNK----P--AT--VTR-WAVVNFSAR---------CD
At-AGO9      393 RAALVEKSRQKPPERMASLTKGLKDSNYNA---------DPVLQDSGVSI-ITNF----TQVEGRILPTPML-KVGKG--------------ENLSPIKG---KWNF---------------MRKTLAEP--TT--VTR-WAVVNFSAR---------CD
Mm-AGO2      362 TSTMIRATARSAPDRQEEISKLMRSASFNT---------DPYVREFGIMV-KDEM----TDVTGRVLQPPSI-LYGGR------------NKAIATPVQG---VWDM---------------RNKQFHTG--IE--IKV-WAIACFAPQRQCTEV----H
Mm-AGO1      359 TSTMIKATARSAPDRQEEISRLMKNASCNL---------DPYIQEFGIKV-KDDM----TEVTGRVLPAPIL-QYGGR------------NRAIATPNQG---VWDM----R----------GKQFYN-G--IE--IKV-WAIACFAPQKQCREE----V
Mm-AGO4      351 TSTMIKATARSAPDRQEEISRLVKSNSMVGGP-------DPYLKEFGIVV-HNEM----TELTGRVLPAPML-QYGGR------------NKTVATPSQG---VWDM----R----------GKQFYA-G--IE--IKV-WAVACFAPQKQCRED----L
Mm-AGO3      362 TSTMIKATARSAPDRQEEISRLVRSANYET---------DPFVQEFQLKV-RDEM----AHVTGRVLPAPML-QYGGR------------NRTVATPSHG---VWDM---------------RGKQFHTG--VE--IKM-WAIACFATQRQCREE----I
Dm-AGO1A     470 TSTMIKATARSAPDREREINNLVKRADFNN---------DSYVQEFGLTI-SNSM----MEVRGRVLPPPKL-QYGGRVSTGLTGQQLFPPQNKVSLASPNQGVWDM---------------RGKQFFTG--VE--IRI-WAIACFAPQRTVRED----A
Ce-ALG-1     504 TSTMIKATARSAPEREREISNLVRKAEFSA---------DPFAHEFGITI-NPAM----TEVKGRVLSAPKL-LYGGR------------TRATALPNQG---VWDM---------------RGKQFHTG--ID--VRV-WAIACFAQQQHVKEN----D
Ce-ALG-2a    409 TSTMIKATARSAPEREREICKLVSKAEL-----S---A-DPFAHEFGITI-NPAM----TEVKGRVLSAPKL-LYGGR-----------HRATTALPNQG--V-WDM----R----------GKQFHT-G--ME--VRT-WAIACFAQQ-SHVKE---ND
Ce-T23D8.7   416 IANLIRATSRNATERQNAVMSLQNRLKMDN---------DVNAVKFGLKV-EAQL----LKIEGRVLPVPRL-LYRSP--------NLKRQECVTVPNNG--T-WDM----R----------GKNFYS-G--IQ--IRE-WAIVCFASPEIIGEA----S
Ce-ZK757.3a  499 TSAIIKAAAVDATQREDRIKQLAAQASFGT---------DPFLKEFGVAV-SSQM----IQTTARVIQPPPI-MFGGN---------NRSVNPVVFPKDG---SWTM---------------DNQTLYMP--AT--CRS-YSMIALVDP-RDQT-----S
Ce-T22B3.2b  494 TSAIIKAAAVDATQREDRIKQLAAQASFGT---------DPFLKEFGVAV-SSQM----IETSARVIQPPPI-MFGGN---------NRSINPVVFPKDG--S-WSM---------------DHQTLYMP--AT--CRS-YSMIALVDP-RDQT-----S
Dm-AGO2B     730 VANMIKYAATSTNVRKRKIMNLLQYFQH-----N---L-DPTISRFGIRI-ANDF----IVVSTRVLSPPQV-EYHSK--------------RFTMVKNG--S-WRM----D----------GMKFLE-P--KP--KAH-KCAVLYCDP-RSGRKMNYTQ
Ce-ERGO-1    548 RADMINKTTYTAQQRGKLLQHIIAQKSLSGIEPPVSNN-DDYMKKHKLVM-KREP----IRVKATILPPPTL-VYGDS----------------VFHDEHHIGEWEAVTHDPPRQVLDGAVFRRKLYKSS--EQPLMKRLMGSILLIQSPRQCRDFDYNQ
Ce-RDE-1     434 QDKFLKRATRKPHDYKENTLKMLKELDF---SSE---E-LNFVERFGLCS-KLQM----IECPGKVLKEPML-VNSVN------------EQIKMTPVIR--G-FQE----K----------QLNVVP-EKELC--CAV-FVVNETAGN-PCLEE---ND
Ce-R04A9.2   514 QSYMTGKMSSLPDQHIKQSKLVLTEYLKLGDQPA-----NRQMDAFRVSLKSIQP----IVTNAHWLSPPDM-KFANN------------QLYSLNPTRG--VRFQT---------------NGKFVM-P--AR--VKS-VTIINYD---KEFNR----N
Ce-C16C10.3  495 QSAMTGRNASMPQHHVKLVQDILRDNLKLEQ--------NKYMDAFGIKLMSTEP----IQMTAKLLPPAQI-KFKGQ---------------TYMPDMS-RPAFRT---------------QDKFVE-P--AR--IRK-IGIVVFD---NCIQM---RQ
Ce-T22H9.3   454 QMAMKGQKSTLPQKHVDLVKHVLSRNLKLDR--------NLYMDAFGIKLESAEL----VKLQSKILPPPQI-KFKDE---------------VYMPKMG-NPVFRT---------------NGRFVD-P--AD--INA-VAIVVFDRA-IDMR-----Q
Ce-Y49F6A.1  430 QSAMTGPNSILPSKHVRIVARILESSLKIAS--------NPYLKTFGIRI-SKDP----IKLEAKILSPAQL-SFNKY---------------SIMPKPG--S-VQF----EPSR-------EDKFFK-P--AK--IYE-VAVIAF----RVVSI----N
Ce-C04F12.1  440 IRKVGESAKLLSP--------------------------NQTLKSIGIAI-NPEP----IVVEAMTVPKPTI-LYKDG--------------AFTSPDLLNRTSWDVQARNHQSL-------KGGFVE-P--MK--INK-ILILYNSQ--SYSQASPKEA
Ce-CSR-1a    508 EEFELTPRANAPNERWSTLQKHYDQFGFN----------DQVMKDFGVQI-CNDPFNNVSEIDGERVLAPSV-AYADP---------------VHVDDEK--RDWKA---------------QDKKFVTP--AT--IDH-LMFVLVAGY-TRTWDADCDA
Ce-R06C7.1   446 SQKTTKECAVLPDVRQRMIITGKNAVNITLE--------NELLVALGIKV-YSEP----LMVQARELDGKEL-VYQRS----------------VMSDMG---KWRAP--------------PGWFVK-P--AT--VPDLWAAYAVG---NPGCRFSIGD
Ce-F55A12.1  413 SQKTTKECAVLPDVRQRIIITGKNAVNI---SLE-----NELLVALGIKV-YSEP----LMVEARELDGKEL-VYQRS----------------VMSEMG--K-WRA-------P-------PGWFVK-P--AK--VPELWALY----------------
Ce-PPW-2     452 SQRTTKESAVLPDIRQRLIMTGKIAAKITAE--------NEVLGKMGVTV-CDEP----LVVKGRNLPAIRLASFETG-------------EHLINPRDC--K-WR----------------PQRYNR-S--AV--APKVWALYGVG---SPGSQMNRDV
Ce-F58G1.1   442 SQKTTKESAVLPDVRQRLILTGKNAAQI---SSD-----NEVLGKMGVSV-CEDP----LMVKGRSIPAVKL-ANAEI------------GANPINVKDN--K-WRA----------------NRFTR-P--AT--APNVWAMYVVG---TASTRITLDT
Ce-C06A1.4   416 SQKTTKESAVMPDVRQRLIMTGKNAAQISSD--------NEALGKMGVSV-CEEP----LMVKGRSIPAVKL-ANAEN------------GTNPINVKDN--K-WR----------------PNRFTR-P--AT--APNVWAIYVVG---TTSTRITLDT
Ce-SAGO-2    404 QADMIKMSAAQPHIRKTTTDTIVRNVGL------------ASNNIYGFIK-VEDP----VNLEGMVLPKPKI-AFAGN-----------RLADLANPKSR----FPT----DFNR-------AGQYYD-A--KE--LTK-WELVFVQNE----------E
Ce-PPW-1a    430 QADMIKMSAAQPHIRKTTTDTIVRNVG------------LASNNIYGFIK-VEDP----VNLEGMVLPKPKI-AFAGN-----------QLADLANPKSR----FPT----DFNR-------AGQYYD-A--KE--LTK-WELVFVQNE----------E
Ce-SAGO-1    404 QADLIKLAAAKPHDRKKITDTVVNSI-------------GLASEPKGIIS-VGAP----ESVTGLVLPKPDI-YFSGG--------------KKVFWNDP----KKRGPATDFMP-------AGTFIK-P--TK--LTN-WEVVFDNGV----------Q
```



```
                                                      Mid domain (PIWI subdomain A) residues involved in anchoring the 5′ phosphate (Ma et al 2005 Nature 434:666)
                                                                                                                        Y   K             Q
Dm-AGO3      518 ATSLLDNMKQACESLGMNI--------------SN-PTM-----ISLDHDRI--DAYIQAL-----------RRNITMNTQM-VVCI-----CHN---RRDDRYAAIKKICCSE--IPIPSQVI-NAKTLQNDL-------------KIRSVVQKIVLQMN
Mm-MIWI      509 ANSLIQNLFKVTPAMGIQM--------------KK-AIM-----IEVDDRT---EAYLRALQ-----------QKVTSDTQI-VVCL-----LSS---NRKDKYDAIKKYLCTD--CPTPSQCV-VARTLGKQQ-------------TVMAIATKIALQMN
Mm-MIWI2     494 IEAFLSCLRRVGGSMGFNV--------------GY-PKI-----IKVDETP---AAFLRAI-----------QVHGDPDVQL-VMCI-----LPS---NQKNYYDSIKKYLSSD--CPVPSQCV-LTRTLNKQG-------------TMLSVATKIAMQMT
Mm-MILI      616 ARELVNMLEKIAGPIGMRI--------------SP-PAW-----VELKDDRI--ETYIRTIQS---------LLGVEGKIQM-VVCI-----IMG---TRDDLYGAIKKLCCVQ--SPVPSQVI-NVRTIGQPT-------------RLRSVAQKILLQMN
Dm-PIWI      490 LRTLLDSLYRAASGMGLRI--------------RS-PQE-----FIIYDDRT--GTYVRAM-----------DDCVRSDPKL-ILCL-----VPN---DNAERYSSIKKRGYVD--RAVPTQVV-TLKTTKNR--------------SLMSIATKIAIQLN
Dm-AUB       507 TQEFVQMCIRTASSMKMNI--------------CN-PIY-----EEIPDDRN--GTYSQAI-----------DNAAANDPQI-VMVV-----MRS---PNEEKYSCIKKRTCVD--RPVPSQVV-TLKVIAPRQQKPT---------GLMSIATKVVIQMN
Ce-PRG-1     447 SQKFIEEARRLGKILQVQL--------------GE-PMC-----VPIRGISP--NDYLEGVKGAI-------KQVDGEDIHM-LVVM-----LAD---DNKTRYDSLKKFLCVE--CPIPNQCV-NLRTLAGKSKDGGENK------NLGSIVLKIVLQMI
Ce-PRG-2     345 AQKFIAEARNLGRTLQVQL--------------GE-PMC-----VKINGISP--NDYLEGLKAAI-------KSVDGEEIHM-LVVM-----LAD---DNKTRYDSLKKYLCVE--CPIPNQCV-NLRTLAGKSKDGGENK------NLGSIVLKIVLQMI
Tt-TWI11     432 AGQFMSTLKNRMQAHGIGY--------------NE-PNY-----FTVEGQSQ--DELKRLID--------------SFPPDVDFIVF-----ILQGAKGKGKNYQYLKSFLLKE--KPIPSQMI-LQGTIKSSKD------------GCQVICNKICNQIC
PTIWI12      397 LLENIKLAISEYQFYGFY---------------SQ-PMI-----KQLQEERE--KALIQLCDEIK-------QECEQKQQNIEFIIF-----LLPGQKKNSRLYRCAKFISLQK--IACPSQVV-LEDTLTK---------------NTRSIVNKIMVQIC
PTIWI15      397 LLDNMKQAISEYQFYGFY---------------SQ-PLV-----RPLQEERD--KALLLLCDDIN-------KECQQKQQKIEFIIF-----LLPGQKKNSRLYRCAKFISLQK--IGCPSQVV-LEDTLAK---------------NTRSIVNKIMVQIC
PTIWI03      412 LKSFLQHFKSACQEFQFDA--------------FLTPKA-----KEMQNDKE--DELSRQLRDLK-------LEADQNQSRVNFLIF-----LLPGQKKKARLYKACKVISMAT--FGCASQVI-VEKTLQR---------------NTRSIVNKILIQLN
PTIWI09      405 MDSLMQNFQAACNDFKFQA--------------FMAPKV-----FPIEQDRD--EDLERVLDGFQ-------KQAEANKAKVGFLLF-----LLPGQKKKARLYKTAKKISMQK--FGCASQVV-VEKTLAK---------------NTRSIVNKILIQLN
PTIWI01      405 MDSLMQNFQAACNDFKFQA--------------FMAPKV-----FPIEQDRD--EDLERVLDGFQ-------KQAEANKAKVGFLLF-----LLPGQKKKARLYKTAKKISMQK--FGCASQVV-VEKTLAK---------------NTRSIVNKILIQLN
PTIWI06      393 AEDFMSCLRESIEYCKFQC--------------KA-PRT-----FTIHSSRI--EDWIKQIDFI--------VQQSQGPQKVTLLLL-----ILNGPKKNAPLYTDLKRYLIND--CPIASQVI-LSSTLNQPKG------------KVKTICNKLLVQIC
PTIWI10      393 AEDFMSCLRESIEYCKFQC--------------KA-PRT-----FVLHSNRI--EDWIKQIDQI--------VQQSQGPQKVTLLLL-----ILNGPKKNAPLYTDIKRYLIND--CPIASQVI-LSSTLNQPKG------------KVKTICNKLLVQIC
PTIWI11      393 AEDFMSCLRESIEYCKFQC--------------KA-PRT-----FVLHSNRI--EDWIKQIDQI--------VQQSQGPQKVTLLLL-----ILNGPKKSAPLYTDIKRYLIND--CPIASQVI-LSSTLNQPKG------------KVKTICNKLLVQIC
Tt-TWI1      397 FDSLLRTFQECLKFYNYPC--------------KP-PNC-----ISVQSRGA--QDWINALK--------------NAPDNVQMAVF-----LLPGKKKAGMYYDEIKRYFTNV--KPIPTQVI-LASTAMKDK-------------GLRSVVNKLLMQIC
Tt-TWI12     443 VEALVSSISQFKLYYNYPI--------------SE-PKY-----YKIDDLNI--ETWTSTFN----------TALSESPTTFALIIM-----NSEL--EHYHFYKTCKQAITVD--KGICCSLI-KASTLQQYVPTQQYPQIPPGNSIEAFASRFLSQMQ
PTIWI07      520 CEEFTQNIHELIQKYGIKM--------------GVQTKC-----HYLSGQR---QNYIAEIEQTI-------MRNVPHTTNM-IVIV-----LNR---YMKNCYAPLKKMCMSE-KFGVLTQMV-SSDSISKQKK------------GLFSIIQKLAIQMM
Tt-TWI8      481 TMDLFQNWIKIQKELRIEV--------------KK-PQE-----FNLGDFN---NKAMQEIEHV--------IRREIKKEKFDIVAI-----VAPNKFSTVQNYSKIKKLCTIT--QQIKSQYI-RQQSLDSK--------------QSYNVCSAILSQMA
Tt-TWI9      441 VNKLLKLFQNITQKLEIKY--------------ED-PKI-----IHHSLVNP--KHLIEKLDKY---------FIETEYLPSF-IVTF-----GD----LNTNFYQQIKHFFCIL--ANVESQHI-SPQSLKNK--------------NKYKICLNIVLQIL
Tt-TWI7      445 VYKFIDLLKNASQAYQINV--------------NDKPQF-----FAPEDFNP--KNWIRLLDK---------DFRKNGVPQF-IVTF-----SNAE--KNPSLYREMKKFFSSEGGVGIESQHV-TPRALQK---------------NGKSVASKIALQIA
Tt-TWI2      448 VDGFIDTLKKASQTYGITV--------------ND-PFF-----FAQRDWNA--NSWIKSLDE---------DFSKNDLPQF-VLSF-----GQ----AQSGLYSGLKKFLTSE--AGIESQHV-NPRSLQK---------------NGMSVASKIALQIA
Tt-4505902   449 VDDFVDTLKKASQTYGIIV--------------ND-PYF-----FAERDSNA--NNWIKSLDE---------DFSKNDLPQF-VLSF------GQ---VNSGFYSSLKKFLTSE--AGIESQHV-TPKSLQK---------------NGMSVASKIALQIA
Tt-TWI10     418 CLQLSQQIQEQGQVLGIRI--------------PQ-PTM-----IQMKRHNL--SDGINLLEN---------YFLVNQVPQF-ILSY-----VNFNHPRQQTFYQELKLYLYAT--VAIEHQHF-NDDFSCHK--------------NKNAAISSLIIQIA
PTIWI02      411 ASLFTQEFIRATKELGNQI--------------SP-PRK-----VVMNNLDP--AAWSQALLN---------NFNTNGKPQI-VVSI-----LDRH--EDSKLYNELKKFLISV--QGVLHQNV-SIQTVDSK--------------KFSKIAQQIVKQVH
PTIWI05      421 ANYFLRQLISSGNRYGLIL--------------SQ-PLR-----QKVKSDQS--QDWISCLEQ---------NFSEKGRPKL-VVSL-----IDQE--KDKQIYQQLKQYLIAE--EGVSHQNV-TLQLIENQ--------------KFGAIVPKIIQQIH
PTIWI04cor   412 KEDFLYEISKNGYRCGLNS--------------QI-PHQ-----LSVRSNSC--QDWISCLQQ---------HITKNGKPQL-VISL-----LGEK--NNKSIYQALNQYLIAK--VGVSHQNI-TLKLIKKT--------------KFIIIIPKIILQIH
PTIWI08      417 VDFIVSELQKQGERIGIRI--------------EK-PYF-----VMLKDNNI--QNWLQRLT----------AEIGDKPPQL-IVTF-----VNER--DKDRIYGHIKKYCFQD--QGISHQNI-LSKFLKTK--------------NPSSVASKIAQQMS
PTIWI14      417 VDFLVSELQKQGDRIGIRI--------------EK-PYY-----VVLKDNNI--QNWMQRLT----------AEIGDKPPQL-IVTF-----INEK--DKDRIYGQMKKYCFQE--HGISHQNI-LSKFLKSK--------------NPSSVASKIAQQMS
PTIWI13      430 ADDLVADLNQQGGRLGIKF--------------DK-PFF-----INMKGNKP--QEWIKELQ----------AEFKNGLPSL-VVSL-----TDKN--RDTSLYIGLKDFLLSQGGAGVIHQNV-TTKSCKNK--------------NKQSIASKIAQQIS
Sp-AGO1      445 IENFLQTYVQTLTSLGINFVM------------KKPPVL-----YADIRGSV--EELCITLYKKA-------EQVGNAPPDY-LFFI-----LDK---NSPEPYGSIKRVCNTM--LGVPSQCA-ISKHILQ---------------SKPQYCANLGMKIN
At-AGO5      588 PQEFCKQLIGMCVSKGMEF--------------KP-QPA-----IPFISCPP--EHIEEALL-----------DIHKRAPGLQLLIV-----ILP---DVTGSYGKIKRICETE--LGIVSQCC-QPRQVNKL---------------NKQYMENVALKIN
At-AGO1      621 ARTFCQELAQMCYVSGMAF--------------NP-EPV-----LPPVSARP--EQVEKVLKTRYHDATS--KLSQGKEIDL-LIVI-----LPD---NNGSLYGDLKRICETE--LGIVSQCC-LTKHVFKM---------------SKQYMANVALKIN
At-AGO10     569 ARGFCNELGQMCEVSGMEF--------------NP-EPV-----IPIYSARP--DQVEKALKHVYHTSM---NKTKGKELEL-LLAI-----LPD---NNGSLYGDLKRICETE--LGLISQCC-LTKHVFKI---------------SKQYLANVSLKIN
At-AGO7      592 IPKFINELTQKCEHLGVFL--------------SKNTLSSTFFEPSHILNNI--SLLESKLKEI--------QRAASNNLQL-IICV-----ME----KKHKGYGDLKRISETR--IGVVTQCC-LYPNITKL---------------SSQFVSNLALKIN
At-AGO2      606 PNDFVDNLIDRCWRLGMQM--------------EA-PIVYKTSRMETLSNGNAIEELLRSVIDEAS------RKHGGARPTL-VLCA-----MS----RKDDGYKTLKWIAETK--LGLVTQCF-LTGPATK---------------GGDQYRANLALKMN
At-AGO3      781 PGYFVNKLIERCKGLGMQM--------------EA-PIVCKTSSMETLYDG---NALEELLRSVIDEAS---HNHGGACPTL-VLCA-----MTG---KHDG-YKTLKWIAETK--LGLVTQCF-LTISAIKG------------ETVSDQYLANLALKIN
At-AGO6      484 SSHISRELISCGMRKGIEI--------------DR-PFALVEEDPQYKKAGPV-ERVEKMIATM--------KLKFPDPPHF-ILCI-----LPER--KTSDIYGPWKKICLTE--EGIHTQCI-CPIKI------------------SDQYLTNVLLKIN
At-AGO4      520 VRQVVDDLIKIGGSKGIEI--------------AS-PFQVFEEGNQFRRAPPM-IRVENMFKDI--------QSKLPGVPQF-ILCV-----LPDK--KNSDLYGPWKKKNLTE--FGIVTQCMAPTRQ------------------PNDQYLTNLLLKIN
At-AGO8      469 PQKIIDDLTRCGKMKGINV--------------DS-PYHVVFEENPQFKDATGSVRVDKMFQHLQ-------SILGEVPPKF-LLCI-----LEK---KNSDVYEKSCSMWNCE--CIVPPQNL------------------------NDQYLTNLLLKIN
At-AGO9      492 TNTLIRDLIKCGREKGINV--------------EP-PFKDVINENPQFRNAPATVRVENMFEQI--------KSKLPKPPLF-LLCI-----LAER--KNSDVYGPWKKKNLVD--LGIVTQCI-APTRL------------------NDQYLTNVLLKIN
Mm-AGO2      468 LKSFTEQLRKISRDAGMPI--------------QG-QPC-----FCKYAQGA--DSVEPMFRH---------LKNTYAGLQL-VVVI-----LP----GKTPVYAEVKRVGDTV--LGMATQCV-QMKNVQR---------------TTPQTLSNLCLKIN
Mm-AGO1      465 LKNFTDQLRKISKDAGMPI--------------QG-QPC-----FCKYAQGA--DSVEPMFRH---------LKNTYSGLQL-IIVI-----LP----GKTPVYAEVKRVGDTL--LGMATQCV-QVKNAVK---------------TSPQTLSNLCLKIN
Mm-AGO4      459 LKSFTDQLRKISKDAGMPI--------------QG-QPC-----FCKYAQGA--DSVEPMFKH---------LKMTYVGLQL-IVVI-----LP----GKTPVYAEVKRVGDTL--LGMATQCV-QIKNVVK---------------TSPQTLSNLCLKMN
Mm-AGO3      468 LKGFTDQLRKISKDAGMPI--------------QG-QPC-----FCKYAQGA--DSVEPMFRH---------LKNTYSGLQL-IIVI-----LP----GKTPVYAEVKRVGDTL--LGMATQCV-QVKNVIK---------------TSPQTLSNLCLKIN
Dm-AGO1A     591 LRNFTQQLQKISNDAGMPI--------------IG-QPC-----FCKYATGP--DQVEPMF-----------RYLKITFPGLQLVVV-----VLP---GKTPVYAEVKRVGDTV--LGMATQCV-QAKNVNK---------------TSPQTLSNLCLKIN
Ce-ALG-1     610 LRMFTNQLQRISNDAGMPI--------------VG-NPC-----FCKYAVGV--EQVEPMFKY---------LKQNYSGIQL-VVVV-----LP----GKTPVYAEVKRVGDTV--LGIATQCV-QAKNAIR---------------TTPQTLSNLCLKMN
Ce-ALG-2a    516 LRMFTTQLQRISTDAGMPI--------------IG-TPM-----FCKYASGV--EQVEPMFKYLK-------QTYSA--IQL-IVVV-----LPG---KTPI-YAEVKRVGDTV--LGIATQCV-QAKNAIRT---------------TPQTLSNLCLKMN
Ce-T23D8.7   526 MRSFVRNLVNVASEIGMPF--------------LE-EHR-----FCRYAEP---DQTVKLLE----------HLNEQYNLQL-VLCI-----VP----GKSVVYGELKRKGEL---LGLTTQCV-RSQNVSK---------------ASPHTLSNLCMKIN
Ce-ZK757.3a  606 LQTFCQSLTMKATAMGMNF-----------------PRW-----PDLVKYGRSKEDVCTLFTEIADE-----YRVTNTVCDC-IIVV-----LQS---KNSDIYMTVKEQSDIV--HGIMSQCV-LMKNVSR---------------PTPATCANIVLKLN
Ce-T22B3.2b  601 LQTFCQSLTMKATAMGMNF--------------PRWPD------LVKYGRSK--EDVCTLFTEIADE-----YRVTNTVCDC-IIVV-----LQS---KNSDIYMTVKEQSDIV--HGIMSQCV-LMKNVSR---------------PTPATCANIILKLN
Dm-AGO2B     837 LNDFGNLIISQGKAVNISL--------------DS-DVT-----YRPFTDDE--RSLDTIFADLK-------RSQHD----L-AIVI-----IPQF--RIS--YDTIKQKAELQ--HGILTQCI-KQFTVERK--------------CNNQTIGNILLKIN
Ce-ERGO-1    683 QGY--HAIMRAIEDSGQPVLWADEN--------KHSAVIQGELQFNQNQHGI--EVIEQFLQNIKSTIGEYERDGEVIVPIV-FAVFQARATVYSGNNNEYNDYNVLKYLADNK--YGIHTQGI-LEKSLGVVGPS-----------PKNCALTRLMVEKV
Ce-RDE-1     544 VVKFYTELIGGCKFRGIRIGANENRGAQSIMYDAT-KNEYAFYKNCTLNTGI--GRFEIAATEAKNMF----ERLPDKEQKV-LMFI-----IISK--RQLNAYGFVKHYCDHT--IGVANQHI-TSETVTKALASLR------HEKGSKRIFYQIALKIN
Ce-R04A9.2   622 VDMFAEGLAKHCSEQGMKF--------------DSRPNS-----WKKVNLGS--SDRRGTKVEI--------EEAIRNGVTI-VFGI-----IAE---KRPDMHDILKYFEEK---LGQQTIQI-SSETADKFMRDH----------GGKQTIDNVIRKLN
Ce-C16C10.3  599 AEDFCDKLSNFCRDNGITV--------------EKDSRD-----WSIRELNS--SDSVAIQNLM--------KKWLDDRVDI-LVGI-----ARE---KKPDVHDILKYFEES---IGLQTIQL-CQQTVDKMMGGQ----------GGRQTIDNVMRKFN
Ce-T22H9.3   558 AENFCDRLSCYCRENGITV--------------KKSSRD-----WPIREINS--EDSVAIKNAM--------EKWFSKGVNI-LVAI-----AKE---KKPDVHDVLKYYEAS---VGLQTIQV-CKQTVDMMLSS-----------GGRQTADNVMRKFN
Ce-Y49F6A.1  533 LSDFCMKLCDLCRRSGLEI--------------RRETRDW----IKIENFNP--TSTIELKEQM--------KRLQQSNCSI-IIGI-----TEE---KKPEVHDVLKYFEAA---VGLQTMQI-HSKTAGFIIS------------GNGQTAGNVIKKLN
Ce-C04F12.1  539 VVELQSILSKKAKDVGMTI--------------GQ---------IDVEDLND--PDIIGAIENKM-------TILKTSQVKP-IVIY-----ADH---TSEGTHSTLKLQERL---CEVITQQVALDKSLKRT--------------PGKVTANNLLMKLN
Ce-CSR-1a    618 TKFVAKAFMQRCKDKGMHI--------------GS---------YSMDQHNG--ERGSENFLTSVFKNLVTHPNYRDSSFTP-FVLF-----ISD---DVPNIHECLKFEERM---SDIPTQHV-LLKNVKKMRDNIEKKSQGGRRAYDLTLDNIVMKAN
Ce-R06C7.1   551 VNQLVGMFIDSCKKKGMVI--------------KP-PCE-----TGLYST----EKIMTQL-----------EKVAASKCKY-VLMI-----TDDAIVHLHKQYKALEQRTMMI----VQDMKISKANAVVKD--------------GKRLTLENIINKTN
Ce-F55A12.1  505 -----AVGNQGCRFSS-----------------GD-PPC------ETGLFHT--DKIMDQLE-----------KVAASGCKY-VLVI-----TDD---AITHLHKRYKALEQKS-RMTIQDMKISKANAVVKD--------------GKRLTLENIINKTN
Ce-PPW-2     559 MRRFCDEFMNMSRSKGILF-----------------PPP-----GDVNLLTP--DAIENRL-----------REAANAGCTF-VLCI-----TED---NITCLHQKYKFIEHHT--QMIVQDMK-LSKALSVVNA------------SKKLTLENVINKTN
Ce-F58G1.1   549 LKKFADEFAAMCKSKGVNM--------------PA-PAD-----ISLIHM----DAIESRLY-----------DATKANCTF-VFII-----TDD---SITTLHQRYKMIEKDT--KMIVQDMK-LSKALSVINA------------GKRLTLENVINKTN
Ce-C06A1.4   523 LKKFADEFAAMCKSKGVNM--------------PA-PAD-----MSLIHM----DAIESRL-----------YDAMKANCMF-VFII-----TDD---SITTLHQRYKVIEKDT--KMIIQDMK-LSKALSVINA------------GKRLTLENVINKTN
Ce-SAGO-2    504 VQGLAKQLADEMVNNGMKC--------------SN-PTM-----SFIIR-----GDLEPIFK-----------KAKAAGTQL-LFFV-----VK----SRYNYHQQIKALEQK---YDVLTQEI-RAETAEKVF-------------RQPQTRLNIINKTN
Ce-PPW-1a    530 VQGLAKQLADEMVNNGMKC--------------SN-PTM-----SFIIR-----GDLEPIF-----------KKAKAAGTQL-LFFV-----VK----SRYNYHQQIKALEQK---YDVLTQEI-RAETAEKVF-------------RQPQTRLNIINKTN
Ce-SAGO-1    504 LVDCIQHLTSTMRQLGMEV--------------SN-PTV-----SLINR-----GYLRSIFEN---------AKAANRQ----LIMF-----ITK---SMNNYHTEIKCLEQE---FDLLTQDI-RFETAVKLA-------------QQQNTRKNIIYKTN
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PIWI domain (PIWI subdomain B) residues involved in slicer activity

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                  K                                       D                                                                                                              D
Dm-AGO3      621 CKLGGSLWTVKIPFK-------------------NVMICGIDSYHDPSNRGN------------SVAAFVASINSSYS-QWYSKAVVQTKREEI----------VNG--L-------------SASFEIALKM-Y--RKRNGKLPTNIIIYRDGIGDGQL
Mm-MIWI      611 CKMGGELWRVDMPLK-------------------LAMIVGIDCYHDTTAGRR------------SIAGFVASINEGMT-RWFSRCVFQDRGQEL----------VDG--L-------------KVCLQAALRA-W--SGCNEYMPSRVIVYRDGVGDGQL
Mm-MIWI2     596 CKLGGELWSVEIPLK-------------------SLMVVGIDICRDALNKNV------------VVVGFVASINSRIT-RWFSRCVLQRTAADI----------ADC--L-------------KVCMTGALNR-W--YRHNHDLPARIVVYRDGVGNGQL
Mm-MILI      721 CKLGGELWGVDIPLK-------------------QLMVIGMDVYHDPSRGMR------------SVVGFVASINLTLT-KWYSRVVFQMPHQEI----------VDS--L-------------KLCLVGSLKK-Y--YEVNHCLPEKIVVYRDGVSDGQL
Dm-PIWI      592 CKLGYTPWMIELPLS-------------------GLMTIGFDIAKSTRDRKR------------AYGALIASMDLQQNSTYFSTVTECSAFDVL----------ANT--L-------------WPMIAKALRQ-Y--QHEHRKLPSRIVFYRDGVSSGSL
Dm-AUB       614 AKLMGAPWQVVIPLH-------------------GLMTVGFDVCHSPKNKNK------------SYGAFVATMDQKESFRYFSTVNEHIKGQEL----------SEQ--M-------------SVNMACALRS-Y--QEQHRSLPERILFFRDGVGDGQL
Ce-PRG-1     561 CKTGGALWKVNIPLK-------------------NTMIVGYDLYHDSTLKGK------------TVGACVSTTSNDFT-QFYSQTRPHENPTQL----------GNN--L-------------THFVRKALKQ-YY-DSNDQTLPSRLILYRDGAGDGQI
Ce-PRG-2     459 CKTGGALWKVNIPLK-------------------STMIVGYDLYHDSTLKGK------------TVGACVSTTSNDFT-QFYSQTRPHENPTQL----------GNN--L-------------THFVRKSLKQ-YY-DNNDKTLPSRLILYRDGAGDGQI
Tt-TWI11     537 IKVGGIPYIIKDLPFSNL----------------PTMLVGIDYIRKE--------------NQKSVYSFVASVDSTFC-KFFSGAQLLDAQDQN----------NKF--V-------------DKLLQASLTQ-F--KQKNGILPQRVIIYRQ-AANNIL
PTIWI12      505 AKLGGVPWAIDKLPKLFQQQ--------------HTMICAAECYDRIHQIKH--------------LAFCSTVDKNMT-KYHSQILKGADYK------------GDN--L-------------KKCLIAAMQV-Y--KEKNTAFPQIVIIYRDGVSDGQI
PTIWI15      505 AKLGGVPWAIDKLPKLFQQQ--------------HTMICAAECYDRLHQIKH--------------LAFCSTVDKNMT-KYHSQILKGADYK------------GDN--L-------------KKSLITAMEV-Y--KEKNNVFPQIIIIYRDGVSDGQI
PTIWI03      522 AKIGGTPWALDGMPDMFTNQ--------------PTMICGVDIFTKAGRKSQ--------------LAFCSTINRQFS-RYYSQVITSGEFCSH---------------L-------------QLCLKAALLA-F--KQELSVYPKNVIIYRDGVGDGQQ
PTIWI09      515 AKVGGTPWAIDSLPLTFQNQ--------------PTMICGTDCFVKSGRKNQ--------------LAFCSTVDRNLS-RYYSQVVTSGEFSQH---------------L-------------QSVFKASLLA-F--KEQNGIFPKLVIIYRDGVGDGQQ
PTIWI01      515 AKVGGTPWAIDSLPTTFQNQ--------------PTMICGTDCFVKSGRKNQ--------------LAFCSTVDRNLS-RYYSQVVTSGEFSQH---------------L-------------QQVFKASLLA-F--KEQNGIFPKLIIIYRDGVGDGQQ
PTIWI06      504 AKVGGTPWGISDLPFTDQ----------------PTMICGMDVYHSTAKGRK------------SMLSFVSTEDEFFS-KYMTQSIEMDSGVEF----------SFS--L-------------CPILVKSLES-FT-SDNRTPLPSRIIIFRDGVSNSQA
PTIWI10      504 AKVGGTPWGVSELPFTDQ----------------PTMICGMDVYHSTGKAKK------------SMLSFVSTEDEFFS-KYMTQSIEMETGVEF----------SFS--L-------------CPVLVKSLQS-FC-GDRNGPLPSRIIIFRDGVSNSQA
PTIWI11      504 AKVGGTPWGVSELPFTDQ----------------PTMICGMDVYHSTGKAKK------------SMLSFVSTEDEFFS-KYMTQSVEMETGVEF----------SFS--L-------------CPVLVKSLQS-FC-GDRNGPLPSRIIIFRDGVSNSQA
Tt-TWI1      501 AKTGGVPWVMDNLPFQNL----------------PTMVVGMDVFHNTPGKKE------------SIFGFVSTVDRNFS-KYYSHSHVLPTGQEI----------TPF--L-------------QQVYEQALKE-F--KDSNGVYPQQIIIFRDGVGEGQF
Tt-TWI12     561 AKLGESPWLMQELPYNQN----------------PCTMIGFSVLRQRNARKI-------------IVAGAASINKQYS-KYLPDYRVISEVSTK----IKEDGTLEIVELSEQEINNSITNSMKDILQGFLSQ-F--ATTHKINPTWVIIIRDGI----F
PTIWI07      629 DKVGNCLWTVQLPQKWPD----------------NIMIVSVIIEKGK------------------FAGMLSSLDKTYS-RYYSQMSTKIVEKCL----------IKD--I-------------GDMMKQSFLQ-F--KQENGCFPQKIIYFRDGLSEESI
Tt-TWI8      589 AKCGTTLWVVNPPNGIPD----------------NTMIIGTSVQKVFINGQP-----------QFVIGFVASQDKNVS-RFYSRATFQKLNKDN----------IEK--I-------------STFIVDAIKQ-Y--FVQNKFVPENIIYLRENIADQGI
Tt-TWI9      545 QKTGNQIWNVEMPMQITSQTI-------------NTMIVGIETSRNIIKGKQ-------------IIAVVCSINRNFS-RYLSQVYFREKGCKQ----------LHQ--L-------------QKIIKDGILI-Y--QQIVKKLPKQIIIYKQGQGDDLK
Tt-TWI7      552 SKLGKRIWSVETPVGINQ----------------NTMIVGIETSMKKIRNQQ-------------VIGVVASINKDFN-KFYSQVDFRNGNDIK----------LPT--L-------------SKIISSAIEA-Y--SKNTKTVPEEIIIYRQGLGEGQI
Tt-TWI2      550 SKLGRRIWQVETPTGIDK----------------NTMIIGIETSMKKIKQQQ-------------VVGVVASIDKDFT-KYFSDVEIRKDNDTT----------LPT--L-------------SKIVTKAIQA-Y--VKNTKSVPAEVIVYRQGLGEGQI
Tt-4505902   551 SKLGRRIWQVETPRGIDK----------------NTMIIGIETSMKKVKQQQ-------------VVGVVASIDKDFT-KYFSDVEIRKDNDTT----------LPT--L-------------SKIVTKAIQA-Y--VKNTKSVPAEVIVYRQGLGEGQI
Tt-TWI10     525 SKLGYPLWQTHIPNQIFN----------------KTMIIAIAVEQKTLHLNK---------Q-QQMIAVVTTISKDFT-QMHSEIFFNEIQNGP----------ISI--L-------------SKIILSSIKN-Y--VLNTKQLPDQIIIYRQGL----I
PTIWI02      516 SKIGKQLWNIQKITEISE----------------KIMIIGIDVYHKTLANNK------------SCVGFNAQFGQQSE-KHFTKTIIVEKGKEL----------NKG--V-------------GQLLNLSLQQ-Y--QKQNKQYPDTIVIFRDGVGNSQI
PTIWI05      526 SKLGNQTWNIQKIQEISD----------------NIMIVGIDVYHKTVLGLD------------SCVGFNAQFGQQGY-ANFTKTIIVRKGKEI----------NKD--V-------------AMLLEQSLEE-Y--QNYNKKLPDTIIIFRDGVGTSQI
PTIWI04cor   517 SKLRNSSWMISKMKEISD----------------EIMIIGIDVYHKTEKKIN------------SCVGFNAQFGQQGD-TNFTKTIIVDQGKEI----------NKD--I-------------ANLLEQSLEE-YQ-ENQNYKLPETIVIFRDGVGNSQI
PTIWI08      521 MKLGNPLWAIPKPNGISD----------------KTMVVGIDIYHKLLTNRK------------SCMGFVAYLESECL-NTFAKPIIMREGQEM----------SQE--V-------------GRVIVEAISA-YFERNGRKYLPDTIIVFRDGVGNAQI
PTIWI14      521 MKLGNPLWAIPKPNGISD----------------KTMVIGIDIYHKLLTNRR------------SCMGFVAYLESECL-NTFARPIIMKEGQEM----------CHE--V-------------GRITVEAISA-YFERNGKKYLPDTIIVFRDGVGNAQI
PTIWI13      536 VKLGNPLWVIPKVKGISE----------------KIMIIGMDIYHKLVTGKQ------------SCMGFVAHFDLECK-TSFSKTIIMKSGQEF----------NQA--V-------------GQTFKEALQA-YFLHYGKKQLPDTILVYRDGVGDSQI
Sp-AGO1      553 VKVGGINCSLIPKSNPLGNV--------------PTLILGGDVYHPGVGATG-----------VSIASIVASVDLNGC-KYTAVSRSQPRHQEV----------IEG--M-------------KDIVVYLLQG-F--RAMTKQQPQRIIYFRDGTSEGQF
At-AGO5      690 VKTGGRNTVLNDAIRRNIPLITDR----------PTIIMGADVTHPQPGEDS----------SPSIAAVVASMDWPEINKYRGLVSAQAHREEI----------IQD--LYKLVQDPQRGLVHSGLIREHFIA-F--RRATGQIPQRIIFYRDGVSEGQF
At-AGO1      731 VKVGGRNTVLVDALSRRIPLVSDR----------PTIIFGADVTHPHPGEDS----------SPSIAAVVASQDWPEITKYAGLVCAQAHRQEL----------IQD--LFKEWKDPQKGVVTGGMIKELLIA-F--RRSTGHKPLRIIFYRDGVSEGQF
At-AGO10     678 VKMGGRNTVLVDAISCRIPLVSDI----------PTIIFGADVTHPENGEES----------SPSIAAVVASQDWPEVTKYAGLVCAQAHRQEL----------IQD--LYKTWQDPVRGTVSGGMIRDLLIS-F--RKATGQKPLRIIFYRDGVSEGQF
At-AGO7      701 AKIGGSMTELYNSIPSHIPRLLRPDE--------PVIFMGADVTHPHPFDDC----------SPSVAAVVGSINWPEANRYVSRMRSQTHRQEI----------IQD--L-------------DLMVKELLDD-F--YKAVKKLPNRIIFFRDGVSETQF
At-AGO2      718 AKVGGSNVELMDTFSFFKKED-------------EVMFIGADVNHPAARDKM----------SPSIVAVVGTLNWPEANRYAARVIAQPHRKEE----------IQG--F-------------GDACLELVKA-H--VQATGKRPNKIVIFRDGVSDAQF
At-AGO3      896 AKVGGTNVELVDNIFSFFKKED------------KVMFIGADVNHPAAHDNM----------SPSIVAVVGTLNWPEANRYAARVKAQSHRKEE----------IQG--F-------------GETCWELIEA-H--SQAPEKRPNKIVIFRDGVSDGQF
At-AGO6      592 SKLGGINSLLGIEYSYNIPLINKI----------PTLILGMDVSHGPPGRAD---------V-PSVAAVVGSKCWPLISRYRAAVRTQSPRLEM----------IDS--LFQPIENTEKGD--NGIMNELFVE-FY-RTSRARKPKQIIIFRDGVSESQF
At-AGO4      629 AKLGGLNSMLSVERTPAFTVISKV----------PTIILGMDVSHGSPGQSD---------V-PSIAAVVSSREWPLISKYRASVRTQPSKAEM----------IES--LVKKNGTED-----DGIIKELLVD-FY-TSSNKRKPEHIIIFRDGVSESQF
At-AGO8      573 AKLGGLNSVLDMELSGTMPLVMRV----------PTIIIGMDVSHGSPGQSD---------HIPSIAAVVSSREWPLISKYRACVRTQSPKVEM----------IDS--LFKPVSDKDD----QGIMRELLLD-F--HSSSGKKPNHIIIFRDGVSESQF
At-AGO9      601 AKLGGLNSLLAMERSPAMPKVTQV----------PTIIVGMDVSHGSPGQSD---------I-PSIAAVVSSRQWPLISKYKACVRTQSRKMEM----------IDN--LFKPVNGKD-----EGMFRELLLD-FY-YSSENRKPEHIIIFRDGVSESQF
Mm-AGO2      570 VKLGGVNNILLPQGRPPVFQQ-------------PVIFLGADVTHPPAGDGK----------KPSIAAVVGSMDAHPN-RYCATVRVQQHRQEI----------IQD--L-------------AAMVRELLIQ-F--YKSTRFKPTRIIFYRDGVSEGQF
Mm-AGO1      567 VKLGGINNILVPHQRSAVFQQ-------------PVIFLGADVTHPPAGDGK----------KPSITAVVGSMDAHPS-RYCATVRVQRPRQEI----------IED--L-------------SYMVRELLIQ-F--YKSTRFKPTRIIFYRDGVPEGQL
Mm-AGO4      561 AKLGGINNVPVPHQRPSVFQQ-------------PVIFLGADVTHPPAGDGK----------KPSIAAVVGSMDGHPS-RYCATVWVQTSRQEIAQELLYSQEVVQD--L-------------TSMARELLIQ-F--YKSTRFKPTRIIYYRGGVSEGQM
Mm-AGO3      570 VKLGGINNILVPHQRPSVFQQ-------------PVIFLGADVTHPPAGDGK----------KPSIAAVVGSMDAHPS-RYCATVRVQRPRQEI----------IQD--L-------------ASMVRELLIQ-F--YKSTRFKPTRIIFYRDGVSEGQF
Dm-AGO1A     693 VKLGGINSILVPSIRPKVFNE-------------PVIFLGADVTHPPAGDNK---------K-PSIAAVVGSMDAHPS-RYAATVRVQQHRQEI----------IQE--L-------------SSMVRELLIM-FY-KSTGGYKPHRIILYRDGVSEGQF
Ce-ALG-1     712 VKLGGVNSILLPNVRPRIFNE-------------PVIFFGCDITHPPAGDSR----------KPSIAAVVGSMDAHPS-RYAATVRVQQHRQEI----------ISD--L-------------TYMVRELLVQ-F--YRNTRFKPARIVVYRDGVSEGQF
Ce-ALG-2a    618 VKLGGVNSILLPNVRPRIFNE-------------PVIFLGCDITHPAAGDTR----------KPSIAAVVGSMDAHPS-RYAATVRVQQHRQEI----------ITD--L-------------TYMVRELLVQ-F--YRNTRFKPARIVVYRDGVSEGQL
Ce-T23D8.7   625 SKLGGINVILSSPPQSLNSE--------------PVLFIGCHLTRSSLASSSDSTSSIAHCD-SSIACLVGSMDGHPT-QFSPIFRTQPRHQRT----------IVD--M-------------CEMTREAIIN-F--RKSTGFKPHKIIIYRAGIADVTV
Ce-ZK757.3a  713 MKMGGINSRIVADKITNKYLVDQ-----------PTMVVGIDVTHPTQAEMR--------MNMPSVAAIVANVDLLPQ-SYGANVKVQKKCRES----------VVY--L-------------LDAIRERIIT-F--YRHTKQKPARIIVYRDGVSEGQF
Ce-T22B3.2b  708 MKMGGINSRIVADQITNKYLVDQ-----------PTMVVGIDVTHPTQAEMR--------MNMPSVAAIVANVDLLPQ-SYGANVKVQKKCRES----------VVY--L-------------LDAIRERIIT-F--YRHTKQKPARIIVYRDGVSEGQF
Dm-AGO2B     938 SKLNGINHKIKDDPRLPMMK--------------NTMYIGADVTHPSPDQRE---------I-PSVVGVAASHDPYGA-SYNMQYRLQRGALEE----------IED--M-------------FSITLEHLRV-Y--KEYRNAYPDHIIYYRDGVSDGQF
Ce-ERGO-1    817 LGKVGTTHRKLERGGAHKTWTIFTDPAK------PTLVLGIDVSHPSTRDRE----TGNVLQKMSAATVVGNIDLDVT-EFRASSRIQDTGVEC----------LID--F-------------SKEIDERIGE-F--IDHTGKRPAHIVVYRDGLSEGDF
Ce-RDE-1     681 AKLGGINQELDWSEIAEISPEEKERRKTMP----LTMYVGIDVTHPTSYSGI----------DYSIAAVVASINPGGT-IYRNMIVTQEECRPGERAVAHGRERTDI--L-------------EAKFVKLLRE-FA-ENNDNRAPAHIVVYRDGVSDSEM
Ce-R04A9.2   731 PKCGGTNFLIDVPESVGHRVVCNNSAEMRAKLYAKTQFIGFEMSHTGARTRFDIQKVMFDGD-PTVVGVAYSLKHSA--QLGGFSYFQESRLHK----------LTN--L-------------QEKMQICLNA-Y--EQSSSYLPETVVVYRVGSGEGDY
Ce-C16C10.3  708 LKCGGTNFFVEIPNAVRGKAVCSNNETLRKKLLEHVQFIGFEISHGASRTLF-DRSRSQMDGEPSVVGVSYSLTNST--QLGGFTYLQTQKEYK----------LQK--L-------------DEFFPKCVRS-Y--KEHSKTLPTRIVIYRVGAGEGNF
Ce-T22H9.3   666 LKCGGTNFFVQIPRSVNGRTVCADAHLLNEKLFERVQFIGFDISHGASRTLF-DRSTGKMDGEVSIVGVSYSLSHST--HLGGFAYMQTQKEYK----------LQK--L-------------DEVFPKCVDS-Y--RNHTGRLPSKIVIYRIGAGEGDF
Ce-Y49F6A.1  641 LKCGGINYIVEVPQSFNRTVVCSNNSFVQKKLFDGTQFIGFEMTHGAARTLF-DKSNGTFDGEPTIVGCAYSLQKAT--DLGGFNWFQEQNEYR----------LKN--L-------------GTHIPKCLQY-Y--KESSGSLPEKIVIYRTGAGEGDF
Ce-C04F12.1  642 LKYGGVNHKVRVDNSISHLWGDTS----------NTLIISYDVCHSSGKVYK----KDEICDEPSCVGFGFNGTACPE-AFIGDFHYQLPRHEQ----------VDEHLL-------------KLRARFMLNH-Y--ITSRKKYPQQVVILRDGVSEGQH
Ce-CSR-1a    740 IKCGGLNYTADIPRDLACWNEV------------STFVIGMDVAHPDRNAAR--------EGNPSTVGLSCNSAENPY-SFIGDFLYTDPRREA----------IQDEIL-------------RKFTDQSVRN-F---AEIRGFPKKVIIFRDGVSFGEE
Ce-R06C7.1   653 VKLGGLNYTVSDAKKSMTD---------------EQLIIGVGVSAPPAGTKY--MMDNKGHLNPQIIGFASNAVANH--EFVGDFVLAPSGQDT----------MAS--I-------------EDVLQNSIDL-F--EKNRKALPKRIIIYRSGASEGSH
Ce-F55A12.1  600 LKLGGLNYTVSDSKKSMTD---------------EQLIIGVGVSAPPAGTKF--MMDNKGHLNPQIIGFASNAVANH--EFVGDFVLAPSTQDT----------MAS--I-------------EDVLQNSIDL-F--ESSRKTLPKRIIIYRSGASEGSH
Ce-PPW-2     661 VKLGGSNYVYLDTKNFLQ----------------EHLIIGVGISSPPPGTKY--IMESRGILNPTIVGFAYNGNGKQ--EFSGDFVLNAAGQET----------IAP--I-------------EDIVSYSIKG-YK-KFHDGKAPKRITIYRSGSSEGNH
Ce-F58G1.1   651 VKLGGSNYVFVDAKKQLD----------------SHLIIGVGISAPPAGTKY--AMENKGVLNPNVIGYAYNAQHNQ--EFSGDFVLNSASQDT----------LAP--I-------------EDIVMHSLNE-YQ-KFHDGGLPRRVIVYRTGTSEGNH
Ce-C06A1.4   625 VKLRGSNYVFVDVKKQLD----------------SHLIIGVGISAPPAGTKY--AMENKGVLNPNVIGYAYNAQHNQ--EFSGDFMLNSASQDT----------LAP--I-------------EDIVMHSLSE-YQ-RFHNGGLPRRVIIYRTETSEGNH
Ce-SAGO-2    602 MKLGGLNYAIGSEAFNKP----------------NRLIVGFVTSQRVGGNPD----------YPISVGFAANMLKHHQ-KFAGGYVYVHRDRDV---------------F-------------GSIIKDTLLTIFKTCTEQRGRPDDILLYFNGVSEGQF
Ce-PPW-1a    628 MKLGGLNYAIGSEAFNKP----------------NRLIVGFVTSQRVGGNPD----------YPISVGFAANMLKHHQ-KFAGGYVYVHRDRDV---------------F-------------GSIIKDTLLAIFKTCTEQRGRPDDILLYFNGVSEGQF
Ce-SAGO-1    602 MKLGGLNYELRSGVFSNS----------------KRLIIGFETSQRGGLGDA-----------PIAIGFAANMMSHSQ-QFAGGYMFVKKSADN-----------YGPVI-------------PEILLTILKQ-AK-ANRPNDRPDELLIYFSGVSEGQH
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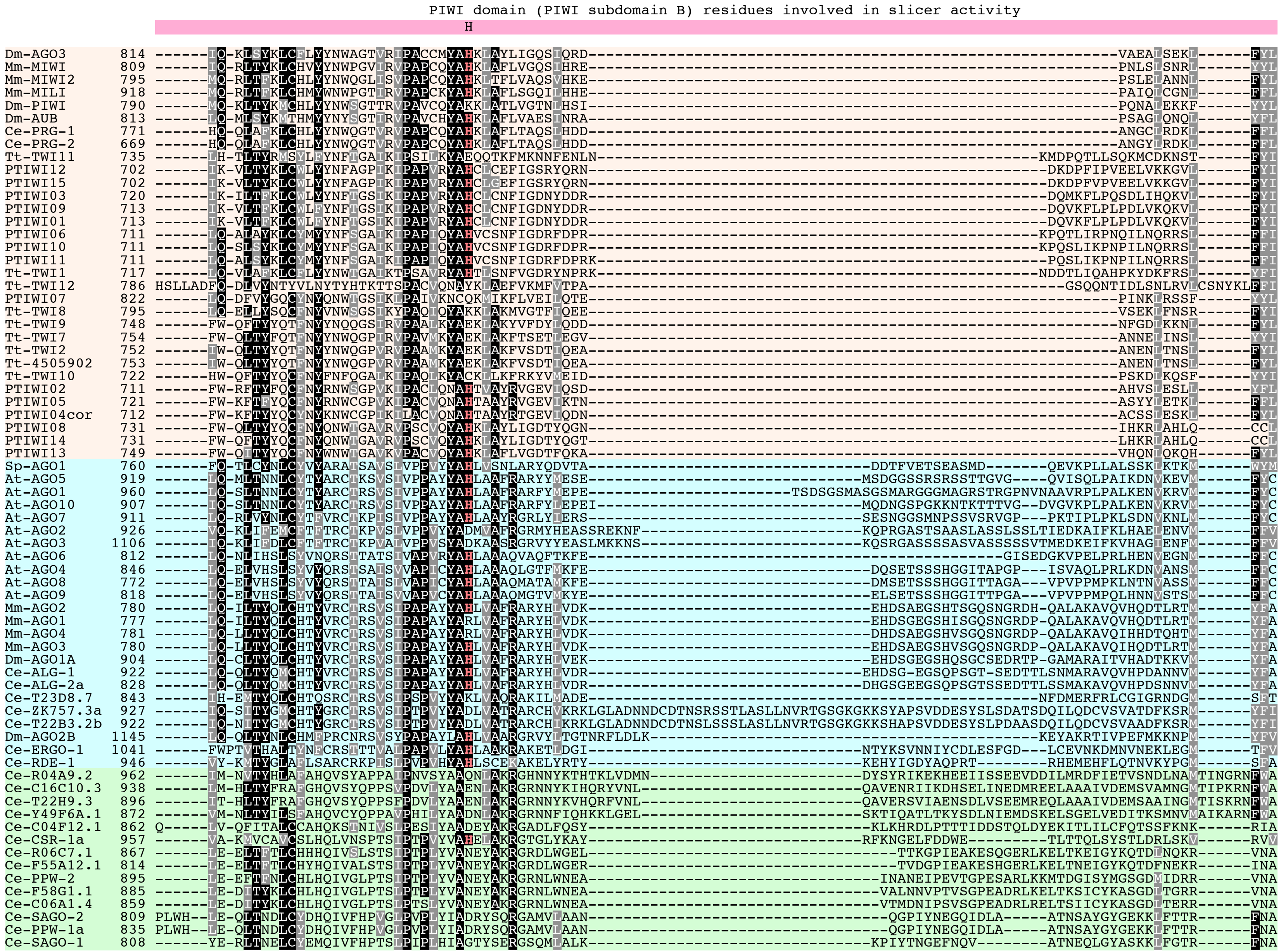
PIWI domain (PIWI subdomain B)



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                                                 PIWI domain (PIWI subdomain B) residues involved in slicer activity
                                                     H

Dm-AGO3        814 ------IQ-KLSYKLCFLYYNWAGTVRIPACCMYAHKLAYLIGQSIQRD------------------------------------------------------------VAEALSEKL------FYL
Mm-MIWI        809 ------IQ-RLTYKLCHVYYNWPGVIRVPAPCQYAHKLAFLVGQSIHRE------------------------------------------------------------PNLSLSNRL------YYL
Mm-MIWI2       795 ------MQ-RLTFKLCHLYYNWQGLISVPAPCQYAHKLTFLVAQSVHKE------------------------------------------------------------PSLELANNL------FYL
Mm-MILI        918 ------MQ-RLTFKLCHMYWNWPGTIRVPAPCKYAHKLAFLSGQILHHE------------------------------------------------------------PAIQLCGNL------FFL
Dm-PIWI        790 ------MQ-KLTYKMCHLYYNWSGTTRVPAVCQYAKKLATLVGTNLHSI------------------------------------------------------------PQNALEKKF------YYL
Dm-AUB         813 ------LQ-MLSYKMTHMYYNYSGTIRVPAVCHYAHKLAFLVAESINRA------------------------------------------------------------PSAGLQNQL------YFL
Ce-PRG-1       771 ------HQ-QLAFKLCHLYYNWQGTVRVPAPCQYAHKLAFLTAQSLHDD------------------------------------------------------------ANGCLRDKL------FFL
Ce-PRG-2       669 ------HQ-QLAFKLCHLYYNWQGTVRVPAPCQYAHKLAFLTAQSLHDD------------------------------------------------------------ANGYLRDKL------FFL
Tt-TWI11       735 ------LH-TLTYRMSYLFYNFTGAIKIPSILKYAEQQTKFMKNNFENLN--------------------------------------------------KMDPQTLLSQKMCDKNST------FYI
PTIWI12        702 ------IK-VLTYKLCWLYYNFAGPIKIPAPVRYAHCLCEFIGSRYQRN----------------------------------------------------DKDPFIPVEELVKKGVL------FYI
PTIWI15        702 ------IK-VLTYKLCWLYYNFAGPIKIPAPVRYAHCLGEFIGSRYQRN----------------------------------------------------DKDPFVPVEELVKKGVL------FYI
PTIWI03        720 ------IK-ILTFKLCWLYYNFTGSIKIPAPVRYAHCLCNFIGDNYDDR----------------------------------------------------DQMKFLPQSDLIHQKVL------FYI
PTIWI09        713 ------IK-VLTFKLCWLFYNFTGSIKIPAPVRYAHCLCNFIGDNYDDR----------------------------------------------------DQVKFLPLPDLVKQKVL------FYI
PTIWI01        713 ------IK-VLTFKLCWLFYNFTGSIKIPAPVRYAHCLCNFIGDNYDDR----------------------------------------------------DQVKFLPLPDLVKQKVL------FYI
PTIWI06        711 ------LQ-ALAYKLCYMYYNFSGAIKIPAPIQYAHVCSNFIGDRFDPR---------------------------------------------------KPQTLIRPNQILNQRRSL------FFI
PTIWI10        711 ------LQ-SLSYKLCYMYYNFSGAIKIPAPIQYAHVCSNFIGDRFDPR---------------------------------------------------KPQSLIKPNPILNQRRSL------FFI
PTIWI11        711 ------LQ-ALSYKLCYMYYNFSGAIKIPAPIQYAHVCSNFIGDRFDPRK---------------------------------------------------PQSLIKPNPILNQRRSL------FFI
Tt-TWI1        717 ------LQ-VLAFKLCFLYYNWTGAIKTPSAVRYAHTLSNFVGDRYNPRK--------------------------------------------------NDDTLIQAHPKYDKFRSL------YFI
Tt-TWI12       786 HSLLADFQ-DLVYNTYVLNYTYHTKTTSPACVQNAYKLAEFVKMFVTPA------------------------------------------------------GSQQNTIDLSNLRVLCSNYKLFFI
PTIWI07        822 ------LQ-DFVYGQCYNYQNWTGSIKLPAIVKNCQKMIKFLVEILQTE------------------------------------------------------------PINKLRSSF------YYL
Tt-TWI8        795 ------LQ-ELLYSQCFNYVNWSGSIKYPAQIQYAKKLAKMVGTFIQEE------------------------------------------------------------VSEKLFNSR------FYI
Tt-TWI9        748 ------FW-QFTYYQTFNYYNQQGSIRVPAALKYAEKLAKYVFDYLQDD------------------------------------------------------------NFGDLKKNL------FYL
Tt-TWI7        754 ------FW-QLTYFQTFNYYNWQGPIRVPAVMKYAEKLAKFTSETLEGV------------------------------------------------------------ANNELINSL------YYI
Tt-TWI2        752 ------IW-QLTYYQTFNYYNWQGPVRVPAAMKYAEKLAKFVSDTIQEA------------------------------------------------------------ANENLTNSL------FYL
Tt-4505902     753 ------IW-QLTYYQTFNYYNWQGPVRVPAAMKYAEKLAKFVSDTIQEA------------------------------------------------------------ANENLTNSL------FYL
Tt-TWI10       722 ------HW-QFTYYQCFNYFNFQGALKIPAQLKYACKLLKFRKYVMEID------------------------------------------------------------PSKDLKQSF------YYI
PTIWI02        711 ------FW-RFTYFQCFNYRNWSGPVKIPACLQNAHTVAYRVGEVIQSD------------------------------------------------------------AHVSLESLL------YFL
PTIWI05        721 ------FW-KFTFYQCFNYRNWCGPVKIPACVQNAHTAAYRVGEVIKTN------------------------------------------------------------ASYYLETKL------FFL
PTIWI04cor     712 ------FW-KFTYYQCYNYKNWCGPIKILACVQNAHTAAYRTGEVIQDN------------------------------------------------------------ACSSLESKL------FYL
PTIWI08        731 ------FW-QLTYYQCFNYQNWTGAVRVPSCVQYAHKLAYLIGDTYQGN------------------------------------------------------------IHKRLAHLQ------CCL
PTIWI14        731 ------FW-QFTYYQCFNYQNWTGAVRVPSCVQYAHKLAYLIGDTYQGT------------------------------------------------------------LHKRLAHLQ------CCL
PTIWI13        749 ------FW-QITYYQCFNYWNWTGAVKVPACVQYAHKLAFLVGDTFQKA------------------------------------------------------------VHQNLQKQH------FYL
Sp-AGO1        760 ------FQ-TLCYNLCYVYARATSAVSLVPPVYYAHLVSNLARYQDVTA--------------------------------DDTFVETSEASMD-------QEVKPLLALSSKLKTKM------WYM
At-AGO5        919 ------LQ-MLTNNLCYTYARCTKSVSIVPPAYYAHLAAFRARYYMESE-------------------------------MSDGGSSRSRSSTTGVG----QVISQLPAIKDNVKEVM------FYC
At-AGO1        960 ------LQ-SLTNNLCYTYARCTRSVSIVPPAYYAHLAAFRARFYMEPE-----------------------TSDSGSMASGSMARGGGMAGRSTRGPNVNAAVRPLPALKENVKRVM------FYC
At-AGO10       907 ------IQ-SLTNNLCYTYARCTRSVSIVPPAYYAHLAAFRARFYLEPEI------------------------------MQDNGSPGKKNTKTTTVG--DVGVKPLPALKENVKRVM------FYC
At-AGO7        911 ------LQ-RLVYNLCYTFVRCTKPISIVPPAYYAHLAAYRGRLYIERS-------------------------------SESNGGSMNPSSVSRVGP---PKTIPLPKLSDNVKNLM------FYC
At-AGO2        926 ------VQ-KLIFEMCFTFTRCTKPVSLVPPVYYADMVAFRGRMYHEASSREKNF-------------------------KQPRGASTSAASLASSLSSLTIEDKAIFKLHAELENVM------FFV
At-AGO3       1106 ------IQ-KLIFDLCFTFTRCTKPVALVPPVSYADKAASRGRVYYEASLMKKNS-------------------------KQSRGASSSSASVASSSSSVTMEDKEIFKVHAGIENFM------FFV
At-AGO6        812 ------LQ-NLIHSLSYVNQRSTTATSIVAPVRYAHLAAAQVAQFTKFE-----------------------------------------------GISEDGKVPELPRLHENVEGNM------FFC
At-AGO4        846 ------LQ-ELVHSLSYVYQRSTSAISVVAPICYAHLAAAQLGTFMKFE--------------------------------DQSETSSSHGGITAPGP---ISVAQLPRLKDNVANSM------FFC
At-AGO8        772 ------LQ-ELVHSLSYVYQRSTTAISLVAPICYAHLAAAQMATAMKFE--------------------------------DMSETSSSHGGITTAGA---VPVPPMPKLNTNVASSM------FFC
At-AGO9        818 ------LQ-ELVHSLSYVYQRSTTAISVVAPVCYAHLAAAQMGTVMKYE--------------------------------ELSETSSSHGGITTPGA---VPVPPMPQLHNNVSTSM------FFC
Mm-AGO2        780 ------LQ-ILTYQLCHTYVRCTRSVSIPAPAYYAHLVAFRARYHLVDK--------------------------------EHDSAEGSHTSGQSNGRDH-QALAKAVQVHQDTLRTM------YFA
Mm-AGO1        777 ------LQ-ILTYQLCHTYVRCTRSVSIPAPAYYARLVAFRARYHLVDK--------------------------------EHDSGEGSHISGQSNGRDP-QALAKAVQVHQDTLRTM------YFA
Mm-AGO4        781 ------LQ-LLTYQLCHTYVRCTRSVSIPAPAYYARLVAFRARYHLVDK--------------------------------DHDSAEGSHVSGQSNGRDP-QALAKAVQIHHDTQHTM------YFA
Mm-AGO3        780 ------LQ-LLTYQLCHTYVRCTRSVSIPAPAYYAHLVAFRARYHLVDK--------------------------------EHDSAEGSHVSGQSNGRDP-QALAKAVQIHQDTLRTM------YFA
Dm-AGO1A       904 ------LQ-CLTYQLCHTYVRCTRSVSIPAPAYYAHLVAFRARYHLVEK--------------------------------EHDSGEGSHQSGCSEDRTP-GAMARAITVHADTKKVM------YFA
Ce-ALG-1       922 ------LQ-QLTYQMCHTYVRCTRSVSIPAPAYYAHLVAFRARYHLVDR-------------------------------EHDSG-EGSQPSGT-SEDTTLSNMARAVQVHPDANNVM------YFA
Ce-ALG-2a      828 ------LQ-QLTYQMCHTYVRCTRSVSIPAPAYYAHLVAFRARYHLVDR-------------------------------DHGSGEEGSQPSGTSSEDTTLSSMAKAVQVHPDSNNVM------YFA
Ce-T23D8.7     843 ------IH-EMTYQLCHTQSRCTRSVSIPSPVYYAKLVAQRAKILMADE---------------------------------------------------NFDMERFRLCGIGRNDGM------SFT
Ce-ZK757.3a    927 ------IQ-SITYGMCHTYGRCTRSVSIPTPVYYADLVATRARCHVKRKLGLADNNDCDTNSRSSTLASLLNVRTGSGKGKKSYAPSVDDESYSLSDATSDQILQDCVSVATDFKSRM------YFI
Ce-T22B3.2b    922 ------IQ-NITYGMCHTYGRCTRSVSIPTPVYYADLVATRARCHIKRKLGLADNNDCDTNSLSSSLASLLNVRTGSGKGKKSHAPSVDDESYSLPDAASDQILQDCVSVAADFKSRM------YFI
Dm-AGO2B      1145 ------LQ-QLTYNLCHMFPRCNRSVSYPAPAYLAHLVAARGRVYLTGTNRFLDLK--------------------------------------------KEYAKRTIVPEFMKKNPM------YFV
Ce-ERGO-1     1041 ------FWPTVTHALTYNFCRSTTTVALPAPVLYAHLAAKRAKETLDGI-------------------------------NTYKSVNNIYCDLESFGD---LCEVNKDMNVNEKLEGM------TFV
Ce-RDE-1       946 ------VY-KMTYGLAFLSARCRKPISLPVPVHYAHLSCEKAKELYRTY-------------------------------KEHYIGDYAQPRT--------RHEMEHFLQTNVKYPGM------SFA
Ce-R04A9.2     962 ------IM-NVTYHLAFAHQVSYAPPAIPNVSYAAQNLAKRGHNNYKTHTKLVDMN------------------------DYSYRIKEKHEEIISSEEVDDILMRDFIETVSNDLNAMTINGRNFWA
Ce-C16C10.3    938 ------LM-HLTYFRAFGHQVSYQPPSVPDVLYAAENLAKRGRNNYKIHQRYVNL-------------------------QAVENRIIKDHSELINEDMREELAAAIVDEMSVAMNGMTIPKRNFWA
Ce-T22H9.3     896 ------IT-HLTYFRAFGHQVSYQPPSFPDVLYAAENLAKRGRNNYKVHQRFVNL-------------------------QAVERSVIAENSDLVSEEMREQLAAAIVDEMSAAINGMTISKRNFWA
Ce-Y49F6A.1    872 ------VM-NLTYILSFAHQVCYQPPAVPHILYAADNLAKRGRNNFIQHKKLGEL-------------------------SKTIQATLTKYSDLNIEMDSKELSGELVEDITKSMNVMAIKARNFWA
Ce-C04F12.1    862 Q-----LV-QFITALCCAHQKSTNIVSLPESIYAADEYAKRGADLFQSY--------------------------------KLKHRDLPTTTIDDSTQLDYEKITLILCFQTSSFKNK------RIA
Ce-CSR-1a      957 ------VA-KMVCAVCSLHQLVNSPTSIPTPVYVAHELAKRGTGLYKAY-------------------------------RFKNGELFDDWE---------TLTTQLSYSTLDRLSKV------RVV
Ce-R06C7.1     867 ------LE-ELTFTLCHHHQIVSLSTSIPTPLYVANEYAKRGRDLWGEL-----------------------------------TTKGPIEAKESQGERLKELTKEIGYKQTDLNQKR------VNA
Ce-F55A12.1    814 ------LE-ELTFTLCHYHQIVALSTSIPTPLYVANEYAKRGRDLWGER-----------------------------------TVDGPIEAKESHGERLKELTNEIGYKQTDFNEKR------INA
Ce-PPW-2       895 ------LE-EFTFNLCHLHQIVGLPTSIPTPLYVANEYAKRGRNLWNEA---------------------------------INANEIPEVTGPESARLKKMTDGISYMGSGDMIDRR------VNA
Ce-F58G1.1     885 ------LE-DITYKLCHLHQIVGLPTSLPTPLYVANEYAKRGRNLWNEA---------------------------------VALNNVPTVSGPEADRLKELTKSICYKASGDLTGRR------VNA
Ce-C06A1.4     859 ------LE-DITYKLCHLHQIVGLPTSLPTSLYVANEYAKRGRNLWNEA---------------------------------VTMDNIPSVSGPEADRLRELTSIICYKASGDLTERR------VNA
Ce-SAGO-2      809 PLWH--LE-QLTNDLCYDHQIVFHPVGLPVPLYIADRYSQRGAMVLAAN----------------------------------QGPIYNEGQIDLA-----ATNSAYGYGEKKLFTTR------FNA
Ce-PPW-1a      835 PLWH--LE-QLTNDLCYDHQIVFHPVGLPVPLYIADRYSQRGAMVLAAN----------------------------------QGPIYNEGQIDLA-----ATNSAYGYGEKKLFTTR------FNA
Ce-SAGO-1      808 ------YE-RLTNELCYEMQIVFHPTSLPIPLHIAGTYSERGSQMLALK--------------------------------KPIYTNGEFNQV--------ATNEQLGYASKKLFGTR------FNA
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