

S1. Multiple Alignments used for pylogenetic analyses

Dicer proteins (without Drosha)

Tc-Dicer1 1 PREYQVELLDLSAKKFNITIVCSSASSAKAFITIKLLQEFSSHKMRVPHG----KQALFVLDG
Dm-Dicer1 1 PRDFQVELLATAYERNITICLGHRSSEKFIALKLLQELSRARRRHGR----VSVYLSCEV
Ce-Dicer1 1 PRDYQVELLDKATKKNTIVQLGTGSGKTFIAVILLKEYGVQIFAPLDQGGKRAFFVVEKV
Tc-Dicer2 1 PRNYQVNLMEIAIRENTIITYLPTGSGKTFIAIMVLKQLCAPILRPYSDGGKISVILVNSV
Dm-Dicer2 1 PRGYQLRLVDHLTKSNGIVYLLPTGSGKTFVAILVLKRESQDFDKPIESGGKRALFMCNTV

Tc-Dicer1 57 PNVPIMTSHVKLLTDLIVTSDIKEESIHKASNVIVITAEVCVLLCKKNFVHLDSEYALIVID
Dm-Dicer1 57 GTSTEPCSIYTMILTHLIDLRVWQEQCWTDYHVSILRPEGFLYLLLETRELLSSVELIVLE
Ce-Dicer1 61 NLVEQQAIHIEVHTSEFKVGVHGGQTFMKRHHVWVITAOCLLDLIRHAYLKIETDMCVLIFD
Tc-Dicer2 61 ALVDQHGKYVRDHATFSVGTYYTGEMQFNKYQVVMITSOIMVNLINNRIFIDLGVNLMIFD
Dm-Dicer2 61 ELARQQAMAVRRCITNEKVGFFVGEQELKKNQVVLVGTAVFLDMVVTQTYVALSSLSVVIID

Tc-Dicer1 117 CLYGGQ-QSLVREIMARYQAIQAPRPRILGLTAGLIGSEMOPDRLEAEILQRLEKLLSSSV
Dm-Dicer1 117 DCHDSA-VYQRIRPLFENHIMPAPRPRILGLAGPLHSAGCELQQLSAMLATLEQSVLCQI
Ce-Dicer1 121 ECHHALGSQLPYSIMVDYKLLKKVPRVLGLTASLIKAKVAPEKLMEQKKLESAMDSVI
Tc-Dicer2 121 ECHHGVEDQPMRQIMKHEHSCDK-PRVLGLTATLLNCKLSKVMDEIRSLVETFHASKV
Dm-Dicer2 121 ECHHGTGHHPFREFMRLTIANQTLPRVGLTGVLLKGNELTNVATKLELEITYRGTV

Tc-Dicer1 176 DTSSIELTLIRLSRPRERIDPKEQPLSFFDDELEILLDDLGPSADRAAYGMLIKIEKIK
Dm-Dicer1 176 ETASDIVTVLRYCSRPEHYIDPKVDPLNVINSLLVVLEHMGPWCTQRAAHHFYQCNEKIK
Ce-Dicer1 181 ETASDLVSLISKYGAAPYEVVDFRPIKDSIKTTRAVFRQLGPWAAWRTAQVWEKELKIK
Tc-Dicer2 180 ATVEGLDVVVGYSTNPQELFDVLKSLRNLIISDLMIHIEMLGAFGGHIACVAHMIQIERIK
Dm-Dicer2 180 SDTKEMENVMLYATKPTVM-KKSFVKQLFNDFLYQMKYGIYAASIAIISLIVEFDIKR

Tc-Dicer1 236 VKVPYERHYLLICVASSVLVSIRALCELEFQDYVFRFSTPKVLRFLQVLLQFKPLCALVF
Dm-Dicer1 236 VKTPHERHYLLYCHVSTALIQLYSLCEHAFHRHIERYS SPKVRRLIQTLRCFKPLCALIY
Ce-Dicer1 241 SQVLPDKTLRFLNMAKTSMTITIKRLEPEMKKILRPYVPOVIRLFEILETENPLSALIF
Tc-Dicer2 240 KHCQNHQLEIVLNYVMTIMGTIKLLEETMAGYIRKFSDDKVLKVFEILDEYKTLCCLVF
Dm-Dicer2 239 RQAETLSVKLMHRTALTICEKIRHLLVQKIQDMIMNFSIPKVQRELMSLKVSFAICCLVF

Tc-Dicer1 296 VKNRYKAEALFALLCVMSKSDSEYVWVSVSFSVKNKIADPVREPREAES EHKRQEEVLRKY
Dm-Dicer1 296 CNONHTARVLFELLAETSRDPDLKFLRCQYTTDRVADPTEPKAELEHRRQEEVLRKF
Ce-Dicer1 301 VDRYIAYSLLMMRHIKSWEPKFKFVNPDYVVG-ASGRNLASSDSQGLHKRQTEVLRRF
Tc-Dicer2 300 TKRRFTAKVLLHHLLDKASQVDPKEYHIKSNFVVGKNNPYNDFRENLYITKKNREVLNRF
Dm-Dicer2 299 VERRYTKCKLYGLLLNYIQSTPELRLVITPOFMVG--RNNISPDFESVLERKWKQSAIQQF

Tc-Dicer1 356 RSHECNIMIAATSALEQGCPLPKCNLVIRFDLIPQSEHSYIHSKARARANEAHFLLANNEV
Dm-Dicer1 356 RMHDCNVLIQTSVLEEGIDVPCNLVVRWDPPPTTYRSYVQCKGRARAAAPAYHVIIVASTT
Ce-Dicer1 360 HRNEINCLIAATSVLEEGVDVKQCNLVIKFDRPLDMRSYVQSKGRARRAGSRVITVE--E
Tc-Dicer2 360 VSKEINVLVSSNVLEEGVDIPKCTLVIKFDSYRSYIQSKGRARHIKSLMYTIVETDV
Dm-Dicer2 357 RDGNANLMICS SVLEEGIDVQACNHVIFILDVVKTFNMYVQSKGRARTTEAKFVLF TAKER

Tc-Dicer1 416 SDFVRYCAKLPSDTFTTRITTEIWHEEKVENGSIRLPINSPVKKTVTSPPMINTLLARRAAA
Dm-Dicer1 416 KDLVKYCARLPSDTFTKLTALWRCTRNERATIRLPINSPLKHDI VGLPMPQTQTLAARRLAA
Ce-Dicer1 418 KDTAAYCSKLPSDIFTRIVPHNQIIPIEENELLLPINSPIKHAIVLKPMPNKKTAQMAVA
Tc-Dicer2 420 AKYDRYCSNLSADKYTTYAPEWYVE--EDSVIFLPMVCPLIDPIVGPYMHNNKDAKRAAA
Dm-Dicer2 417 EKTIRYQQTIPIDAFGFVIPWFHVLQEDERSINMPVNCMLRDTIYSDPMDNVKTAKISAA

Tc-Dicer1 476 FMICQLLHKAGELDDNLQPIGKEDPRPGTTKRRQYKYKVVADAILDCHPIIGQPTYFYKI
Dm-Dicer1 476 IQACVELHRI GELDDQLQPIGKEEPRPGTTKRRQYKYKRIASEFCDCRPVAGAPCYLYFI

Ce-Dicer1 478 LEACRQLHLEGELEDDNLLPKGREAAKVGSSKRRQLYDKKIARATNESFVEADKCEFTIYAF
Tc-Dicer2 478 LVACIKLHQCGELDDNLLPWKKQ--DAGNKKKKRLHDKETIAPSVKSAIQPD-RVLYLHTTI
Dm-Dicer2 477 FKACKVLYSLGELNERFVPKTLTKTVNKADKSKDRTYKTECPLEFYDALPRVGEICYAYEII

Tc-Dicer1 536 VMKLTCPLEPEEQNTRGRKIYPPEDSPQGFGLITSKEIPKISAFPIFTRSGEVSVLDLQICCS
Dm-Dicer1 536 QLTLCQPIPEEQNTRGRKIYPPEDAQQGFGLITTKRIPKISAFSIFTRSGEVKVSLELAK
Ce-Dicer1 538 ELERFREAEELTLNPKRRKFEDEFNYEYCFGLLSAKEIPKIPFPVFLROGNMKVRLIVAP
Tc-Dicer2 535 NINPOYKRSDDLKN-AVTLYDLYKTPLKFGLLSPKPIPDLCCKEPLFDSNGTLEIETRNNV
Dm-Dicer2 537 FLEPQFESCEYTEHMYLNIQTERN----YAILLRNKLPRIAEMLIFSNOGKLVVRVANAP

Tc-Dicer1 596 Q-LIVTENQICKIREFLNYTFTSVLRLQKYLTLFNPDA SANSYLVPTIIDCAT--TTVDW
Dm-Dicer1 596 ERVILTSEQIVCINGFLNYTFTNVLRLQKFLMLFDPDSTENCVFIIVPTVKA PAGGKHIDW
Ce-Dicer1 598 KKTIVTAAQLQELQLFHNYLFTQVQLQMKCTGNLEFDNAPLNTLIVPLNKRKDDMSYTIM
Tc-Dicer2 594 REVEFAANEMKEMREFHFVFNLDLLEILKEFLIFDNTGMNSEMLIVVPVQDRCGDVCVDF
Dm-Dicer2 593 LEVLIQNSQLELLHQFHGMVFRDILKIWHPPFVLDRRSKENSYLVVPLILCAGEQKCFDW

Tc-Dicer1 653 DFIDLIIYANLTVLPEIIPPEVRKSYEFDPKRYRDVMPWYRNQDQPFYVAEICSNLNPA
Dm-Dicer1 656 QFLELIQANGNTMPRAVPDEERQAQFFDPQRFQDAVMPWYRNQDQPFYVAEICPHLSPL
Ce-Dicer1 658 KYVSEVVANMENMPRI PKDEVRRQYKFNADYKDAIVMPWYRNLEQPYVAEILPEWRPS
Tc-Dicer2 654 RVTRDNKNLKNKLEPAATERIN--LNVTEETYLHKIVSPWYRS--PPYVVTKVCPDKSAL
Dm-Dicer2 653 ELMTNFRRLPQSHGSNVQREQQ-PAPRPEDTEGKIVTQWYANYDKPMLVTKVHRELTP

Tc-Dicer1 713 SDFPGSDYATFEEYYLRKYSIQIQNKSQHLLDVDHTSARLNFLTFRYVNRKGVALPTISSE
Dm-Dicer1 716 SCFPGDNRYRTFKHYLVKYGLTIQNTSQPLLDVDHTSARLNFLTFRYVNRKGVALPTISSE
Ce-Dicer1 718 SKFPDTHETTFNEYFVKKYKLEIYDQNSLLDVDFTSTRLNLLQPRIQNPFRSRTVSNS
Tc-Dicer2 710 SRFPNHEYPNFVSYSEKHSLSILDPSQPLLVKGLSERLNAFKPRGAGGKRKKEKMYEE
Dm-Dicer2 712 SYMENQDQKTYEFTMSKYGNRIQDGVVHKDKFMI EVRDLTEQLTFYVHNRGKFNAKSKAK

Tc-Dicer1 773 QKQILVPELCAIHPFSASLWRKAVCLPCILYRINALLLADQIRRTVALEINLKGKIELDS-
Dm-Dicer1 776 QKQILVPELCTVHPFPASLWRTAVCLPCILYRINGLLADDIRKQVSADLGLGRQQIEDE
Ce-Dicer1 778 QRQILVPELMDIHPISATLWNVIAALPSIFYRVNQLLLTDELRETILVKAFGKEKTKLDD
Tc-Dicer2 770 LEEYLIPELVIKQEFPSCLWIQARFLPSIILSRAYLILKLQQLQVDIARGIGAKAEYIKDC
Dm-Dicer2 772 MKVILLIPELCFNFNFGDLWLKLIIFLPSILNRMVFLHAEALRKRFRNTYLNHLLLPFNGT

Tc-Dicer1 832 EFKWPPPLNFGWSLADVILKSKDEEKKKQEKIEPVGSPNVLLQAL TMSNANDGINLERLE
Dm-Dicer1 836 DFEWPMPLDFGWSLSEVILKKSRESKQKESIKDDTIGPSPSIILOAL TMSNANDGINLERLE
Ce-Dicer1 838 NVEWNSLAYATEYEEKQTIIVKKIQQLRDLNOKSGVSPCLLITALTTSNAADGMSLERFE
Tc-Dicer2 830 PPLELNLHLLHYEPNDPQLTQESDKSTPIIDNCISPNLCQIYQALTAABANDIVNLERLE
Dm-Dicer2 832 DYMPPRPLEIDYSIKRNVDP LGNVIPTEDIIEPKSPAEQGEFLAATASSAADVFDMERLE

Tc-Dicer1 892 TIGDSFLKYAITNYLYSKYENVHEGKLSHLRSKQVSNLNLNLYRLGRRKGLGEYMIATKFDP
Dm-Dicer1 896 TIGDSFLKYAITTYLYITYENVHEGKLSHLRSKQVANLNLNLYRLGRRKRLGEYMIATKFEF
Ce-Dicer1 898 TIGDSFLKFATTDYLYHTLLDQHEGKLSFARSKEVSNONLYRLGKKLGTIPQLIVANKFDA
Tc-Dicer2 890 TIGDSFLKFVASLYIFKFPPTYNEGKSTTLKGLKLVSNKNLYYLGVRRKNLGGI LKNSDLSF
Dm-Dicer2 892 IIGDSFLKLSATLYLASKYSDWNEGTLIEVSKSLVSNRNLLFCLIDADIPKTIINTIQETP

Tc-Dicer1 952 HDNWLPPCFYVVPKELIEEIPYNLVITQHSIPDKSIADDCVEALIGAYLIECGPRGALLFMAWL
Dm-Dicer1 956 HDNWLPPCYVVPKELIEKIPYNLVISQHSIPDKSIADDCVEALIGAYLIECGPRGALLFMAWL
Ce-Dicer1 958 HDSWLPPCYIPTCDFKALPYNLLTQQHISDKSIADAVEALIGVHLLTLGPNPTLKVMMNWM
Tc-Dicer2 950 SDWVPPCFCTIPQTI SKNMCNFNLNKQYVGDKSIADSV EALIGAYFLSGGTOGGIKFMEMI
Dm-Dicer2 952 RYTWLPPGISLPHNVLAEVNFCVGLVTIPNKVIADTLEALLGVIIVKNYGLQHAFAKMLEYF

Tc-Dicer1 1012 GIRVLPPEEELDMLLDGYDQFERHIGYKFRDRSYLLQALTHASFSPNTITDCYQRLEFLG
Dm-Dicer1 1016 GVRVLPATEELDQLLSGFEFEESLGYKFRDRSYLLQAMTHASYIPNRIITDCYQRLEFLG
Ce-Dicer1 1018 GLKVIQNFLNNLWQQFQFOTQLEEKIGYRFKERAYLVQAETHASYINNRVTGICYQRLEFLG
Tc-Dicer2 1009 GILPLSTKTVDVDFHMPQWREIEQRLGYTFTNRAFLQALTHSSYSPNRIITLSYERLEFLG
Dm-Dicer2 1012 KICRADNTTEIDGFLINHYYLEKNLGYTFKDRRYLLQALTHPSYPTNRIITGSYQELEFLG

Tc-Dicer1 1072 DAVLDYLITRHLIEDTRMHSFGALDRLSALVNNTIFASLAVRNGFHRVFRNLSPSLNEV
Dm-Dicer1 1076 DAVLDYLITRHLIEDPRQHSFGALDRLSALVNNTIFASLAVRHGFHKKFRRHLSPLNDV
Ce-Dicer1 1078 DAVLDYMITRYLFEDSRQYSPGVLTDLRSALVNNTIFASLAVKFEFFQKHFTIAMCPGLYHM
Tc-Dicer2 1069 DAVLDFLITCYIFEHCGHLEPGQVTDLRSALVNNTIFASLAVVRCGFHKELEMMNSNLQGH
Dm-Dicer2 1072 DAILDFELISAYIFENNTKMNPGALDRLSALVNNTIACIVRHRHLHFFILAEAKLSEI

Tc-Dicer1 1132 VEKfVRLQEDSGHTIVDEILYLVVET--EEVEDVEVPKALGDVFEVAGAIIFLDSGMSLDA
Dm-Dicer1 1136 IDRfVRIQQENGHCTISEEYILLSEEECDDAEDVEVPKALGDVFESTAGAIIFLDSNMSLDV
Ce-Dicer1 1138 IEKfVKLCSEDTNFNAEMYMVMTTEEIIQBEDIEVPKAMGDI FESVAGAIYLDGRNLDV
Tc-Dicer2 1129 IDKfADYLASKNYVIDDEVLLLEEDENIAEYVDVPKVLGDI FEALAGAIYLDNKNLKT
Dm-Dicer2 1132 ISKfVNFQESQGHRTVNYVRILLLEADNMSTNVDPKALGDVLEALIAAVYLDRC-DLQR

Tc-Dicer1 1190 VVKVYYNMMKSEIEQFSNKPVPKSPIRELELEPETAKFGKPEKLADGRVRVTVVEVFGVF
Dm-Dicer1 1196 VWHVYSNMMSPETIEQFSNSVPKSPIRELELEPETAKFGKPEKLADGRVRVTVDFVGTTF
Ce-Dicer1 1198 TWQVIHFHMRGTIELCCANPPRSPIRELMEFEQSKVRFKMERILESGKVRVTVVEVVMRF
Tc-Dicer2 1189 VWRVYFKIIVREIDLFSKNVPKNVIRRLYECHTVYPPQFSK--ALEVGNQKTMVDFMGRV
Dm-Dicer2 1191 TWEVIFENLFEPELQEFTRKVPINHIRQLVEHKKHAKPVFSSP--IVEGETVMVVSCTCMEKV

Tc-Dicer1 1250 KGI GRNYRIAKCTAAKCALKNLKK
Dm-Dicer1 1256 RGI GRNYRIAKCTAAKCALRQLKK
Ce-Dicer1 1258 TGMGRNYRIAKATAAKRALKYLHQ
Tc-Dicer2 1247 HGFGTNKLIAKRAAAKIALRALKL
Dm-Dicer2 1249 YGFGSNKDQAKLSAAKHALQQLSK

Dicer proteins (with Drosha)

Tc-Dicer1 1 HPGSPNVLLQAL TMSNANDG TNLERLETIGDSFLKVAITNYLYSKYENVHEGKLSHLRS
Dm-Dicer1 1 HPGSPSII LQAL TMSNANDG TNLERLETIGDSFLKVAITTYLYITYENVHEGKLSHLRS
Tc-Dicer2 1 NQSPNLCQIYQAL TAAEBANDIVNLERLETIGDSFLKVASLYIFKFPPTYNEGKSTTLKG
Dm-Dicer2 1 ITPAEQGEFLAAITASSAADVFDMERLEILGDSFLKLSATLYLASKYSDWNEGTLTEVKS
Ce-Dicer1 1 GLGVSPCLLLTALTTSNAADGMSLERFETIGDSFLKEATTDYLYHTLLDQHEGKLSFARS
Tc-Drosha 1 RAFTDRSVGYTNLTIG-----SNQRLEFLGDTIVLQLIASEYLYKYFPEHHEGHSLLRS
Dm-Drosha 1 RAFTDRSIGFTHLTIG-----SNQRLEFLGDTIVLQLICSEYLYRHFPEHHEGHSLLRS

Tc-Dicer1 61 KQVSNLNLYRLGRRKGLG EYMIATKFTQHSIPDKSIADDCVEALIGAYLIECGPRGALLFM
Dm-Dicer1 61 KQVANLNLYRLGRRKRLG EYMIATKFSQHSIPDKSIADDCVEALIGAYLIECGPRGALLFM
Tc-Dicer2 61 KLVSNKNLYYLGVRRKNGEYI LKNSDLNKQYVGDKSIADSV EALIGAYFLSGGTOGGIKFM
Dm-Dicer2 61 KLVSNRNLLFCLIDADIPKTLNTIQFGLVTIPNKVIADTLEALLGVIIVKNYGLQHAFAKML
Ce-Dicer1 61 KEVSNONLYRLGKKLGLI PQLIVANKFTQQHSIDKSIADAVEALIGVHLLTLGPNPTLKVMM
Tc-Drosha 55 SLVNNRTQAVVCDDLGM SNYAVYNNP-KAEIKTKDRADLLEAFI GALYVDQGEFCEVEFC
Dm-Drosha 55 SLVNNRTQAVVCDDLGM PKYAVYANP-KADIKTKDRADLLEAFI GALYVDKGLLYCEQFC

Tc-Dicer1	121	AWLGI	RVLPQLEDGR	DRSYLLQAL	THASFS	PNRITLDCY	QRLE
Dm-Dicer1	121	AWLG	RVLPITRQL	DRSYLLQAM	THASYT	PNRITLDCY	QRLE
Tc-Dicer2	121	EWIG	LPLSEIQ	IRTNRAL	LQAL	THSSYSP	NRITLSYERLE
Dm-Dicer2	121	EYFK	ICRADIDK	PLKDRRY	LQAL	THPSYPT	NRITGSYQELE
Ce-Dicer1	121	NWMG	LKVIQK	DQKSKER	AYLVQA	FTHASYI	NNRV
Tc-Drosha	114	QVTL	FPRLQDF	IMNQD	WNDPKS	KLQQCCL	LR
Dm-Drosha	114	HVCL	FPRLQL	FIMNQD	WNDPKS	KLQQCCL	LR

dsRBM proteins

Dm_R2D2	1	KS	AVSALQ	EF	CARTQ	INLPT	YSFI	PG	EDG	----	GY	VCKV	EILEI	----	EAL	GN	GR	SK	RD																																						
Tc_R2D2	1	KTP	AMV	LQ	EFTM	KR	GFSP	PEYI	LV	MS	KT	GT	HENE	E	HY	KV	NVAN	----	CGL	GF	GR	SK	QV																																		
Tc_C3PO	1	KTP	IS	LQ	EL	MA	ARGI	SL	PV	YIE	EEG	----	FG	T	SF	K	CT	V	K	AG	GV	----	AC	GY	G	T	SK	KN																													
Dm_Loqs	1	KTP	V	S	I	LQ	EL	S	R	R	G	-	I	T	P	G	Y	E	L	V	Q	I	E	G	A	I	H	E	P	T	F	R	F	V	S	F	K	D	-	D	T	P	F	T	A	M	G	A	G	R	S	K	K	E			
Tc_Loqs	1	KTP	V	S	V	LQ	EL	S	R	R	G	-	A	T	P	K	Y	E	L	V	Q	I	E	G	A	I	H	E	P	I	F	R	Y	R	V	F	I	N	N	----	D	L	V	A	T	G	T	GR	S	K	K	D					
Dm_Pasha	1	K	S	F	V	C	I	L	H	E	Y	M	Q	H	A	L	K	T	Q	P	T	Y	E	F	K	E	L	Q	N	A	A	T	P	Y	S	A	T	V	S	V	N	N	L	K	Y	----	G	T	G	Y	G	T	S	K	K	Q	
Tc_Pasha	1	K	S	Y	V	C	I	L	H	E	Y	M	Q	H	A	L	K	K	Q	P	T	Y	K	F	T	E	L	E	N	A	A	T	P	Y	A	A	T	V	S	I	N	D	M	Q	Y	----	C	V	G	Y	G	T	S	K	K	Q	
Hs_TRBP2	1	K	T	P	I	S	L	Q	E	Y	G	T	R	I	G	-	K	T	P	V	Y	D	L	K	A	E	G	A	H	Q	P	N	F	T	F	R	V	T	V	G	D	T	----	S	C	T	G	Q	G	P	S	K	K	A			
Hs_PACT	1	K	T	P	I	Q	V	L	H	E	Y	G	M	K	T	K	-	N	I	P	V	Y	E	C	E	R	S	D	V	Q	I	H	V	P	T	F	T	F	R	V	T	V	G	D	I	----	T	C	T	G	E	G	T	S	K	K	L
Hs_DGCR8	1	K	S	E	V	C	I	L	H	E	Y	M	Q	R	V	L	K	V	R	P	V	Y	N	F	F	E	C	E	N	P	S	E	P	F	G	A	S	V	T	I	D	G	V	T	Y	----	G	S	G	T	A	S	S	K	K	L	

Dm_R2D2	52	A	K	H	L	A	A	S	N	I	L	L	R	D	Y	C	V	R	R	E	M	P	L	P	C	I	E	V	V	Q	S	G	T	P	S	A	P	E	F	V	A	C	S	V	A	S	I	V	R	Y	G	K	S	D	K	K	D	A			
Tc_R2D2	56	A	K	H	N	A	A	S	K	A	L	L	K	D	M	C	E	F	K	L	P	Y	P	E	F	K	E	I	S	D	V	G	P	P	H	C	R	E	F	T	Y	E	C	C	I	A	S	I	T	Q	A	T	A	N	T	K	K	Q	A		
Tc_C3PO	51	A	K	H	E	S	A	K	N	A	L	L	N	E	Y	A	A	S	R	-	-	Y	G	A	K	Y	P	S	Y	D	F	L	T	V	S	V	D	G	E	F	F	F	K	C	S	F	A	N	E	S	I	G	E	G	M	N	K	K	D	A	
Dm_Loqs	59	A	K	H	A	A	A	R	A	L	L	Q	E	M	C	M	Q	R	R	W	P	P	P	S	Y	E	T	E	T	E	V	G	L	P	H	E	R	L	F	T	I	A	C	S	I	L	N	Y	R	E	M	G	K	G	S	K	K	I	A		
Tc_Loqs	56	A	K	H	A	A	A	K	N	L	L	Q	E	M	C	M	S	R	R	W	P	P	P	S	Y	E	M	E	H	E	E	G	L	P	H	E	R	Q	F	T	I	A	C	Q	V	L	K	F	K	E	V	G	T	G	K	S	K	K	L	A	
Dm_Pasha	55	A	K	S	E	A	A	R	E	T	L	L	L	T	C	L	Q	R	N	Y	G	S	-	D	V	Q	I	S	Q	E	I	N	R	T	A	N	N	K	N	E	F	T	M	T	V	G	K	H	T	A	K	V	V	C	K	N	K	R	E	G	
Tc_Pasha	55	A	K	S	E	A	A	R	A	T	L	L	L	T	C	L	Q	R	N	F	G	I	N	D	L	Q	I	S	Y	Q	G	N	T	L	K	N	K	N	Q	F	T	M	T	V	G	K	H	T	A	T	V	V	C	K	N	K	R	D	G		
Hs_TRBP2	55	A	K	H	K	A	A	E	V	A	L	L	Q	E	L	V	V	Q	K	G	W	R	L	P	E	Y	T	V	T	Q	E	S	G	P	A	H	R	K	E	F	T	M	T	C	R	V	E	R	F	I	E	I	G	S	G	T	S	K	K	L	A
Hs_PACT	55	A	K	H	R	A	A	E	A	A	L	L	Q	E	L	A	I	H	H	G	W	R	L	P	E	Y	T	L	S	Q	E	G	G	P	A	H	K	R	E	Y	T	T	I	C	R	L	E	S	F	M	E	T	G	K	G	A	S	K	K	Q	A
Hs_DGCR8	55	A	K	N	K	A	A	R	A	T	L	L	H	E	C	L	K	R	N	H	G	M	G	L	T	S	I	K	F	E	V	V	P	G	K	N	Q	K	S	E	Y	V	M	A	C	G	K	H	T	V	R	G	W	C	K	N	K	R	V	G	

Dm_R2D2	112	R	Q	R	A	A	I	E	M	L	A	L	I
Tc_R2D2	116	K	Q	L	A	A	R	E	M	L	E	K	I
Tc_C3PO	109	K	Q	D	S	A	R	K	M	L	E	L	V
Dm_Loqs	119	K	R	L	A	A	H	R	M	W	M	R	L
Tc_Loqs	116	K	R	M	A	A	H	K	M	W	Q	A	L
Dm_Pasha	114	K	Q	L	A	S	Q	A	I	L	Q	I	L
Tc_Pasha	115	K	Q	R	A	S	Q	A	I	L	Q	A	L
Hs_TRBP2	115	K	R	N	A	A	A	K	M	L	L	R	V
Hs_PACT	115	K	R	N	A	A	E	K	F	L	A	K	F
Hs_DGCR8	115	K	Q	L	A	S	Q	K	I	L	Q	L	L

Argonaute proteins

Sp-Ago	1	D	Y	I	F	F	I	L	D	K	N	S	P	E	P	Y	G	S	I	K	R	V	C	N	T	M	L	G	V	P	S	Q	C	A	I	S	K	H	I	L	----	Q	S	K	P	Q	Y	C	A	N	I	G	M		
Tc-Ago2a	1	D	L	I	V	V	V	P	N	S	G	P	Q	-	Y	S	L	V	Q	A	A	E	L	N	V	G	C	L	T	Q	C	I	K	E	R	T	I	A	----	K	L	N	P	Q	L	I	A	N	I	L	L				
Tc-Ago2b	1	D	L	I	V	V	V	P	N	S	G	P	Q	-	Y	S	F	V	Q	A	A	E	L	N	V	G	C	L	T	Q	C	I	K	E	R	T	I	G	----	R	L	N	P	Q	T	V	G	N	I	L	L				
Tc-Ago1	1	Q	L	V	V	V	V	I	P	G	K	T	P	V	-	Y	A	E	V	K	R	V	G	D	T	V	L	G	M	A	T	Q	C	V	Q	A	K	N	V	N	----	K	T	S	P	Q	T	L	S	N	I	C	L		
Tc-Ago3	1	M	V	A	F	I	C	P	T	L	R	A	D	R	Y	S	I	I	K	K	M	C	C	V	N	I	P	V	A	S	Q	V	I	L	S	K	T	L	S	----	N	P	Q	K	V	R	T	I	H	K	I	A	M		
Tc-Piwi	1	T	M	I	V	I	L	P	N	N	S	T	E	R	Y	S	A	I	K	K	K	C	Y	V	D	R	G	I	P	T	Q	M	F	V	A	R	N	L	T	----	S	K	G	V	M	S	A	T	K	V	A	I			
Dm-Ago2	1	D	L	A	I	V	I	P	Q	F	R	I	S	-	Y	D	T	I	K	Q	A	E	L	Q	H	G	I	L	T	Q	C	I	K	Q	F	T	V	E	R	----	K	C	N	N	Q	T	I	G	N	I	L	L			
Dm-Ago3	1	Q	M	V	V	C	I	C	H	N	R	R	D	D	R	Y	A	A	I	K	K	I	C	C	S	E	I	P	I	P	S	Q	V	I	N	A	K	T	L	Q	----	N	D	L	K	I	R	S	V	V	Q	K	I	V	L

Dm-Piwi 1 KLIIICLVENDNAERYSSIKKRGYVDRAPTQVVTLLKTK-----KPYSLMSIATKIAI
Dm-Aub 1 QIVMVVMRSPNEEKYSCIKKRRCVDRPVPSQVVTLLKVIAPRQQ---KPTGLMSIATKVVI
Dm-Ago1 1 QLVVVVVLPGKTPV-YAEVKRVGDTVLTGMATQCVQAKNVN-----KTSPQTLISNLCL
Ce-Alg1 1 TLVVVVVLPGKTPV-YAEVKRVGDTVLTGIATQCVQAKNAI-----RTTPQTLISNLCL
Ce-Alg2 1 QLIVVVVLPGKTPI-YAEVKRVGDTVLTGIATQCVQAKNAI-----RTTPQTLISNLCL
Ce-Prg1 1 HMLVVMLADDNKTRYDSLKKFLCVECPTPNOCVNLRTLAGKSKDGGENKNLGSIVLKIIVL
Ce-Prg2 1 HMLVVMLADDNKTRYDSLKKYL CVECPTPNOCVNLRTLAGKSKDGGENKNLGSIVLKIIVL
Ce-RDE1 1 VLMFIIISKRQLNAYGFVKHYCDHTIGVANQHTTSETVTKALASLRHEKGSKRIFYQIAL
Ce-Ergo 1 RATVYSGNNNEYNDYNVLYKYLADNKYGIHTQGLEKSLGVVGPS-PKNCALTRLMVEKVL
Ce-PPW1 1 TQLIFFVVKSRNYHQQLKALEQKYDVTQEIIRAETAEK-----VFRQPQTRLNIIN
Ce-PPW2 1 TFLVLCITEDNITCLHQKYKFIHHTQMIVQDMKLSKALSVVN-----ASKKLTLENNVIN

Sp-Ago 52 KINVKVGGINCSLIP-KSNPLGNVP-TLILGGDVYHPGVGATG-VSTASIVASVD-LNGC
Tc-Ago2a 51 KINSKLNGTNHILS--SRLPIMSRP-CIIMGADVTHPPGDAKDVPSVAAVTASHD-PNAF
Tc-Ago2b 51 KINSKMNGTNHRLSPNSRPLIMKRP-CIIMGADVTHPPSPDARDIPSVAAVTASHD-PNAF
Tc-Ago1 51 KINVKLGGINSILVPSIRPKIFNEP-VIFLIGADVTHPPAGDNKKPSIAAVVGSMD-AHPS
Tc-Ago3 54 QITCKLGGTLWSVKIPVSG-----WMVCGIDVYHGA--NNQ--SVCCGFVASIN-GSMT
Tc-Piwi 53 QMNCKLGGAPWCVPPIPLSG-----LMVVGVDVCRDT--VNKKKSEAGIVGSLD-KNIS
Dm-Ago2 52 KINSKLNGINHKIKDDPRLPMMKN--TMYIGADVTHPPSPDQREIPSVVGVAAASHD-PYGA
Dm-Ago3 54 QMNCKLGGSLWTVKIPFKN-----VMVCGIDSYHDP--SNRGNVAAAFVASIN-SSYS
Dm-Piwi 54 QLNCKLGYTPWMEELPLSG-----LMTIGFDIAKST--RDRKRAYCALIASMDLQONS
Dm-Aub 58 QMNAKLMGAPWQVVIPLHG-----LMTVGFVDVCHSP--KNKNKSYGAFVATMDQKESF
Dm-Ago1 51 KINVKLGGINSILVPSIRPKVFNEP-VIFLIGADVTHPPAGDNKKPSIAAVVGSMD-AHPS
Ce-Alg1 51 KMNVKLGGVNSILLPNVRPRIFNEP-VIFFGCDITHPPAGDSRKPSSIAAVVGSMD-AHPS
Ce-Alg2 51 KMNVKLGGVNSILLPNVRPRIFNEP-VIFLIGCDITHPPAAGDTRKPSIAAVVGSMD-AHPS
Ce-Prg1 61 QMICKTGGALWKNIPLKN-----TMIVGYDLYHDS--TLKGKTVGACVSTTS-NDFT
Ce-Prg2 61 QMICKTGGALWKNIPLKS-----TMIVGYDLYHDS--TLKGKTVGACVSTTS-NDFT
Ce-RDE1 61 KINAKLGGINQEISPEEKERRKTMPLTMYVGVGDVTHPTSYSGIDYSIAAVVASINPGGTI
Ce-Ergo 60 GKVGTGAHKTWTIFTDPKAP-----TLVLGIDVSHPSTRDRETMSAATVVGNIID-LDVT
Ce-PPW1 53 KTNMKLGGLNVAIGSEAFNKPN----RLIVGFVTSQRVGGNPDYPI SVCFANMLKHHQK
Ce-PPW2 55 KTNVKLGGSNVYLDTKNFLQ----EHLIIIGVGLSSPPPGTKYILNPTIVGFAYN-GNGK

Sp-Ago 108 KYTAVSRSQPRHQEVEIEGMKDIVVYLLQGFAMTK-QQPQRIIYFRDGTSEGQFLSVIND
Tc-Ago2a 107 QYNICWRLQPPKVELIEDLICAITVEQLMFFYRKTR-HKPETIVFFERDGVSEGQFAEVRRA
Tc-Ago2b 109 QYNICWRLQPPKVELIEDLCNITVEQLKFFYQKTG-FKPESIVFFERDGVSEGQFKQVQRA
Tc-Ago1 109 RYAATVRVQOHRQELIQEISSMVRELLIMFYKSTGGYKPHRIIYRDGVSEGQFLQLLQH
Tc-Ago3 102 KYFSKAMFQD--GELIGDYFKMPFRQMLQAAKDRE-GAFPSKVIVFRDGVGDGQLEHCRKY
Tc-Piwi 103 RFYNICCEHKMEEELSDNFAAA VLLCKQYKEQN-GHYPERILYRDGVGEGQLPFVVEH
Dm-Ago2 109 SYNMQYRLQRGALLETEDMFSITLEHLRVYKEYRN-AYPDHIIYRDGVSDGQFPKIKNE
Dm-Ago3 104 QWYSKAVVQTKREELVNGLSASFEIALKMYRKRN-GKLPNTIYRDGIGDGLYTCNLNY
Dm-Piwi 105 TYFSTVTECSAFDVLANTLWPMIAKALROYQHEH-RKLPSRIVFYRDGVSSGSLKQLFEF
Dm-Aub 109 RYFSTVNEHIKGOELSEQLSVNMALCALRSYQEQH-RSLPERILFFERDGVGDGQLYQVVNS
Dm-Ago1 109 RYAATVRVQOHRQELIQEISSMVRELLIMFYKSTGGYKPHRIIYRDGVSEGQFPFVQLQ
Ce-Alg1 109 RYAATVRVQOHRQELISDLTYMVRELLVQFYRNTR-FKPARIVVYRDGVSEGQFFNVLQY
Ce-Alg2 109 RYAATVRVQOHRQELITDLYMVRELLVQFYRNTR-FKPARIVVYRDGVSEGQLFNVLQY
Ce-Prg1 111 QFYSQTRPHENPTQLGNNLTHFVRKALKQYDSDNDQTLPSRLIYRDGAGDGQIPYIKNT
Ce-Prg2 111 QFYSQTRPHENPTQLGNNLTHFVRKSLKQYDNDNDKTLPSRLIYRDGAGDGQIPYIKNT
Ce-RDE1 121 YRNMIVTQEECRERTDILEAKFVKLLREFAENNDNRAPAHIVVYRDGVSDSEMLRVSHD
Ce-Ergo 113 EFRASSRIQDTGVECLIDFSKEDERIGEIDHT-GKRPAAHIVVYRDGISEGDFQKYLFE
Ce-PPW1 109 FAGGYVYVHRDLDVFGSITKDTLLAIFKTCTEQR--GRPDDILLYFNGVSEGQFSMINEE
Ce-PPW2 110 QEFSGD-VLNAAQETIAPIEDIVSYSIKGYKKFHDGKAPKRITLYRSGSSEGNGHGPLISY

Sp-Ago 167 ELSQIKKACHSISP-----KYNPKILVCTTQKRHHAREFIKNKSDG--DRNGNPLPGTI
Tc-Ago2a 166 ELSAIHQACKKLQRE-----GYEPRITFLVQKRHHTRIFPTNPRDSE-DRNNNV PAGTC
Tc-Ago2b 168 EIAAIQKACKMLQKD-----DYEPKITFLVQKRHHTRIFPTNPRDSE-DKNNNV PAGTC
Tc-Ago1 169 ELTAIREACIKLES-----DYKPGITFLVQKRHHTRIFCADKKEQS-GKSGNIPAGTT
Tc-Ago3 159 EITQIQEVIKELNIE-----TTITFVQKRINTRIFRTVNETN----FENPPSGTV
Tc-Piwi 162 EVANIKRKLQEEIYINGEVK-----MAFVVVSKRINTRIFTEKD-----NPPPGTV

Dm-Ago2 168 EIRCIKQACDKVG-----CKPKICCVIVVKRHHTRFFPSGDVTTS-NKFNNVDPGTV
Dm-Ago3 163 EIPQFEMVCGNR-----IKISYIVVOKRINTRIFSGS-GIH----LENPLPGTV
Dm-Piwi 164 EMKDIIEKLLKTEYARVQLSP---PQLAYIVVTRSMNTRFFLNGQ-----NPPPGTI
Dm-Aub 168 EVNTLKDRLDEIYKSAGKQEG--CRMTFFIIVSKRINSRYFTGHR-----NPVPGTV
Dm-Ago1 169 ELTAIREACIKLEP-----EYRPGITFIVVQKRHHTRIFCAEKKEQS-GKSGNIPAGTT
Ce-Alg1 168 ELRAIREACMMLEP-----GYQPGITFIAVQKRHHTRIFAVDKKDQV-GKAYNIPPGTT
Ce-Alg2 168 ELRAIREACVMLES-----GYQPGITFIAVQKRHHTRIFAADKADQV-GKAFNIPPGTT
Ce-Prg1 171 EVKLVRDACDAVTDKAAEELSQEIKLAFIIVTKRVNMRIILKQGLDN----AINPQPGTV
Ce-Prg2 171 EVKLVRDACDAVTDKAAEELSQEIKLAFIIVTKRVNMRIILKQSSKS----AINPQPGTV
Ce-RDE1 181 EIRSLKSEVKQFMSERDGEDPE-PKYTFIIVLQKRHNTRILRRMEKESKETGIVNPPSSGTT
Ce-Ergo 172 ERVCIIEERCLKIDTSFQP-----SITYIVVTKRHHTRIFLEDPSQGYESQGYNVLPGLT
Ce-PPW1 167 FSARVKEACMAFQKEGTP--PFRPHITIIASSKAHNERLYKSDKGR-----IVNLEPGTV
Ce-PPW2 169 EMPLARVAMRNFSF-----DTQLLYIVVSKHEHTYRFFFKKESSAPPKPWELNIGPGLT

Sp-Ago 219 IEKHVTHPYQYDFYLISSHPSIQGVSVPVHYTVLHDEIQMPDQFQTLQYNLCYVYARATS
Tc-Ago2a 220 VDTHITNPMQDFYLVSHASIQGVAKPTKYCTLWDDNNMSNDDIEELTYYLCHMFTRCNR
Tc-Ago2b 222 VDTHITNPRMDFYLVSHASIQGVAKPTKYCTLWDDNNMNDDIEELTYHLCHMFTRCNR
Tc-Ago1 222 VDVGITHPTEEDFYLCSHQGIQGTSRPSHYHVLWDDSHIDSDELQCLTYQLCHTYVRCTR
Tc-Ago3 207 VDNMVTFRQFYDFFLVPPQSVROGTVNPTHYVVLVDEGNIKPDHLQRLAYKLCIYYNWSG
Tc-Piwi 208 VDDVITLPERYDFYIVSQCVROGTVAPTISYNVIEDSMGLPPEKLYLTYYKLTHTMYNWSG
Dm-Ago2 219 VDRITVHPNEMQDFMVSHQAIQGTAKPTRYNVIENTGNLIDIDLLQCLTYNLCHEMFPFCNR
Dm-Ago3 207 VDQHITKSNMYDFFLVSQLVROGTVTPHYVVLRDDCNYPDIIQKLSYKLCFLYYNWAG
Dm-Piwi 212 VDDVITLPERYDFYLVSQQVROGTVSPTSYNVLYSSMGLSPEKMKOKLYKMCHEYYNWSG
Dm-Aub 217 VDDVITLPERYDFYLVSQAVRIQGTVSPTSYNVISDNMGINADKLOMLS YKMTHTMYNWSG
Dm-Ago1 222 VDVGITHPTEEDFYLCSHQGIQGTSRPSHYHVLWDDNHFDSEDELQCLTYQLCHTYVRCTR
Ce-Alg1 221 VDVGITHPTEEDFYLCSHAGIQGTSRPSHYHVLWDDNNTADELQCLTYQMCHTYVRCTR
Ce-Alg2 221 VDVGITHPTEEDFYLCSHAGIQGTSRPSHYHVLWDDNNTADELQCLTYQMCHTYVRCTR
Ce-Prg1 227 VDTTVTRPERMDFYLVPPQFVNQGTVPVSYNLIHDDTDLGPDKHQQLAFKLCIYYNWQG
Ce-Prg2 227 VDTTVTRPERMDFYLVPPQFVNQGTVPVSYNLIHDDTDLGPDKHQQLAFKLCIYYNWQG
Ce-RDE1 240 VDKLIVSKYKEDDFFLASHHGVLGTSRPGHYTVMYDDKGMSEQDEVYKMTYGLAFLSARCRK
Ce-Ergo 226 IEDAVITNKYYDFFLSTQIGNEGCFRPTHYYVVLHDTWTGKPDFWPTVTHALTYNECRSIT
Ce-PPW1 220 VDHTIVSNVYTEWYHASAVAROGTATKFTLIFTTKAGQAEPLHLEQLTNDLCYDHOIVFH
Ce-PPW2 221 VDYGVITNPACKQFFLNSHMTIQGSAKTPLYTVLADDRNIGMSALEEFTENLCHLHQIVGL

Sp-Ago 279 AVSIVPPEVYYAHLVSNLARYQDV
Tc-Ago2a 280 SVSYPAPTYAHLAAARAKVYVE
Tc-Ago2b 282 SVSYPAPTYAHLAAARAKVYIE
Tc-Ago1 282 SVSIPAPAYYAHLVAFRARYHLV
Tc-Ago3 267 TIRVPAPCLYAHKLAIVGQYIK
Tc-Piwi 268 TVRVPAPCQYAHKLAFMVSQYIH
Dm-Ago2 279 SVSYPAPAYLAHLVAARGRVYLT
Dm-Ago3 267 TVRVPACCMYAHKLAYLIGOSIQ
Dm-Piwi 272 TTRVPAVCQYAKKLATLVGTNLH
Dm-Aub 277 TIRVPAVCHYAHKLAFLVAESIN
Dm-Ago1 282 SVSIPAPAYYAHLVAFRARYHLV
Ce-Alg1 281 SVSIPAPAYYAHLVAFRARYHLV
Ce-Alg2 281 SVSIPAPAYYAHLVAFRARYHLV
Ce-Prg1 287 TVRVPAPCQYAHKLAFLTAQSLH
Ce-Prg2 287 TVRVPAPCQYAHKLAFLTAQSLH
Ce-RDE1 300 PISLPVPVHYAHLSCCKAKELYR
Ce-Ergo 286 TVALPAPVLYAHLAAKRAKETLD
Ce-PPW1 280 PVGLPVELYIADRYSQRCAMVLA
Ce-PPW2 281 PTSIPTELYVANEYAKRGRNLWN

RdRP families

Branchiostoma 1 WRCALSRGYKVS DRTASALHQIAD TELKHVYVARKVWVTPITQMLELKLKPEPIVENRVVREY
Schizosachara 1 PDYKHRCSLINDKENLKKLSKERAKKFLSSIHKKLYVTPITTRIVEDSIEAGNRVIRNF

Neurospora 1 EDVRYQLEVCI SQGRARLILEYVADEYAHCAWVRRVTITPTRIYESTPCVEPTNRVLRQW
Aspergillus 1 FSVRYQLEVCI SNGQATKLEHVATQKRYCCYIRSARVTPSTVYYETPMSDMSNRIIRHY
Coccidioides 1 FTLKFKIAKLVWNGNLEYPSPDTHESDVNNVVKVHRAQVTPSGTYLYGPNIETKNRVLRQY
Arabidopsis 1 FEILFKINTLVQNAACLEKLFHLECCYEGLVVYMYRVQVTPARVYFSGPEVNVSNRVLRHY
Nicotiana 1 YKILFKISSLIQHGALEKLYLKECCYDGLVYVRRVWVTPCKVYFCGPEVNVSNRVLRNY
Hordeum 1 YEILFKINHLVQNGALEKMSYLKKTCLNGLVYVYRVQITPAKVYFYGPEINVSNRVLRNY
Solanum 1 YKILFKISSLVQHGALEKLYLKECCYDGLVYVRRVWVTPCKVYFCGPEVNVSNRVLRNY
Ce-egol 1 FAITYLLECLLSRGGLEDLVHMDGRKRGYQVRVKLIIFTPTRVLYVAPETLMGNRVLRRY
Ce-RRF1 1 FSITYLLECLLSRGALEDLVHMDGRKRGYQVRVKLIIFTPTRVLYVAPETLMGNRVLRRY
Ce-RRF3 1 FRANYALQALITRGTLEQLLNAFDERRQNCVSAKVIIVTPSRILLMAPEVMMVNRVVRRE
Dyctiostelium 1 YESSLEINCFIQGGIITSLISKRTKFINFTMIRDVFTTPSRITFIQPTLQORSCRVRKF
Tetrahymena 1 FNLISYSILTLISHNGIQYYYNQKKEINRKVIATRVRVSIITPSGLIYNLKELELSNRVLRIF

Branchiostoma 61 G--VDNFI RVAERDEDFSKLAVTSRVKDVLERGIRIGERHFVKYLGSSNSQMRHGCWMYA
Schizosachara 61 KDFANRFMRVQITDEYYKQKILYSRIQQILTYGIKVGNOIYEFLLAFGNSQLREHGAYFFA
Neurospora 61 KHAQDYFIRIQFTDEVLEGRILEFLRVYRVLEKGVAMGPWHKFLAFGNSQIREAGAFMFC
Aspergillus 61 IEYADRFLRVRFTEKLLGRIVFTRVKRALANGIVIGDRRYEFLLAFGNSQIREHGAYFFA
Coccidioides 61 NDHINNFLRVSEFVDETDGDPVYFHERFKGVILKQGIKIGGCHFSFLGFSHSSLSRSQTCWVFA
Arabidopsis 61 SKYINNFLRVSEFVDEDELEKVRLYDRISVLRDGIIVIGDKKFEFLAFSSSQLRENSAWMFA
Nicotiana 61 SEDINNFLRVSEFVDEEWEKIHIIYERILSTLRNGFIIGDKRFEFLAFSSSQLRDNSVWMFA
Hordeum 61 AADLDNFLRISFVDEDECEKLRVLRVLSVLSNGITIGDKHFDLAFSSSQLRDNSAWMFA
Solanum 61 SEDIDNFLRVSEFVDEEWEKLYIYERILSTLRKGFVIGDKKIEFLAFSSSQLRDNSVWMFA
Ce-egol 61 DHGTRVLRITFRDDNOKMRLEKTVNQYLKNGITVAGRNFGLGSSNSQMRDNGAYFME
Ce-RRF1 61 DKDTRVLRITFRDDNNKMRLEKTVNQYLKNGITVAGRNFGLGSSNSQMRDNGAYFMM
Ce-RRF3 61 G--PDYALRCVFRDDNLGRILAVTEGYLTLKNGIQVADRVYSEFLGWSNSQMRDQGCYLYA
Dyctiostelium 61 G--SSNFIMVKIVNESLEPLIQHENRIKPILEGGILVGGKIYSYACNSNSQLREYSSWVFS
Tetrahymena 61 QDSTDSEIRGTIQDDSLNAK---RYFRQKLSFKVLNWEIINFGWSASQLRNSSSWFFH

Branchiostoma 119 AVDTTSTSDIRGWMGDLSEHCVAITYVSRLGQFFSSSRNAT-HTFSDGIGKISVPLAKKV
Schizosachara 121 SGSDLNAKQIREWMGDFSEINSVSKYAARMGQCFSTTKEINNHCFTDGVGMASLSVIRRL
Neurospora 121 EQSNLTGDMRAWMGRFSSHIVLAKYAARLGQCFSTTRLVDGFCFTDGVGKISPLLAKIV
Aspergillus 121 PLPNLTAANIRAWMGHFDIRNVAKHAARLGQCFSTTRAIINGYRFSDGVGRISKFLAQMV
Coccidioides 121 PFTRFDAQSI IQGIGSFSHIYSPAKLAARIGQTFSETQTSNGRVFSDGVGTFSPRILLYKI
Arabidopsis 121 PIDRITAAHIRAWMGDFDHIRNVAKYAARLGQSFSSSRETTRYVFSFDGIGKISAEFARKV
Nicotiana 121 SRPGLIANDIRTWMGDFRQIRNVAKYAARLGQSFSSSRETTRYVFSFDGIGKISADFAHRV
Hordeum 121 SRPGLSASDIREWMCNERNIRNVAKYAARLGQSFSSSRETTRYVFSFDGIGTISADFADEV
Solanum 121 SRPGLIANDIRTWMGDFSQIKNVAKYAARLGQSFSSSRETTRYVFSFDGIGKISADFAFRV
Ce-egol 121 KYSNPKIQAAARKNLGRFETIDNIPKMMARLGQCFIQSRLSDEYTFSDGVGMMSYRFAQMV
Ce-RRF1 121 RFTKPKIDEVRFQIGRFSEIENVPKLMARLGQCFIQSRLTSEYTFSDGVGMMSYQFAQEV
Ce-RRF3 121 PRVTGTVEDIRVWMGDFRDAISVPKMMSRMGQCFIQAOPTNKYCFSDGCGRISIKLATHI
Dyctiostelium 119 NQI---THTVKIWSG-IEHVDNVRKIFRCLGLMFSTTIPTNTHVFTEGCGEIGPELAKHL
Tetrahymena 118 ETEVLKKQDVITRIGDFSGINPPAKKSARIGQCFSSSTPYKKKVFIDGIGTISQDLIRKI

Branchiostoma 178 PSAFQIRYAGCKGVLAQDPTLRIQIRGSMKKFETLEVTSGRIMMGTMDETGKLOYGQVFI
Schizosachara 181 PSAFQFRMGGYKGVLSLAPPTLVFPRFSQDKFKKVSVPKAYLLGVADETGTLKGHYDDA
Neurospora 181 PSAYQFRMGCKGVLVTFDVEVHIRKSQEKFVRLNVEKSAFVLGCVDETGTLKGHMKVIT
Aspergillus 181 PSVFQFRLGGCKGILTVSPQAEVHIRKSQAKFTKITIDKACVFCMDETGTLKGYFHEK
Coccidioides 181 PTVFQIRFAGAKGMVSLDTRLQIRLRESMVKFSRIRVPEAVTLYGIMDETGYLEGELFC
Arabidopsis 181 PSAFQIRYGGYKGVVAVDPNKSLSRKSMSKFERIFISGGRSMMGCLDETRTLEYQGVV
Nicotiana 181 PSSFQIRYGGYKGVVAVDPYKSLSRKSMLKYERIFIPNGRTMMGCLDESRTLEYQGVV
Hordeum 181 PSAFQIRYGGYKGVVAIDPYSKLSRKSMSKFORIFVPKGRAMMGCLDETRTLKYQGVFI
Solanum 181 PSAFQIRYGGYKGVVAVDPYKSLSRKSMSKYEERIFIPNGRAMMGCLDESRTLEYQGVV
Ce-egol 181 PSCFQFRERGMKGVISIEPLLNCMFRPSQIKFIQIPIPCGRSMLGVVDETGRLQYQVFI
Ce-RRF1 181 PSCFQIRFRGNKGVIAIEPFLKCLFRPSQIKFQQIPIPSGRSMLGVVDETGRLQYQVFI
Ce-RRF3 179 PACFQVRFKGFKGIILVIDPTIKVIFRKSQQKFGKIFLPPGRSMYGVVDETGRLQYQVFI
Dyctiostelium 175 TCAYQVRIIGGNKGMVWVNNQAGTYIRPSMVKFNHIEIKDSRMLLGVCDPTNSLPPNTVFI
Tetrahymena 178 MCALQVRYGGAKGVLTIDYKSTIQIRESMIKYNKIFLKK SARLMGVIDEYNVLEQDEVEA

Branchiostoma 238 QYSVVHQGVTVTKNPYFHPGDMRKFTAQVAVDVPVPELRHMVDCIVFVPSRGPRPHPEMSGSDL
Schizosachara 241 VLSRVIVGLCTVARNPSLHPGDVVRVCKAVRCDELMHLKNVIVFPTTGDRSIPAMCSGGDL
Neurospora 241 EDWRVITGTCVVGRRNPSLHPGDIRVVEAVDVPALRHLRQVVFVPLTGDTRDVPMSCSGGDL
Aspergillus 241 IPDEVITQGMCLARNPSLHSGDIRVVKAVDVPALRHLQDVVVLVPLTGDTRDIASMCSGGDL
Coccidioides 241 TELILVRDQVIVTRAPALHPGDVQYAKAVDVPPLRSLHNCVIFSOHGFRDLPSMISGGDL
Arabidopsis 241 QYSEFIIITGFPVVAKNPCLHPGDVRLQAVNVPALNHMVDCVVFVQKGLRPHPNCECSGSDL
Nicotiana 241 QYSEFIIKGNVVVAKNPCLHPGDIRVLRVAVDVPALHMHMVDCVVFVQKGLRPHPNCECSGSDL
Hordeum 241 QASSVVTGKVIIVAKNPCLHPGDIRLILQAVHSPVLLGHMVNCVVFVQKGLRPHPNCECSGSDL
Solanum 241 QYTFILKGNVVVAKNPCLHPGDIRVLRVAVDVPALHMHMVDCVVFVQKGLRPHPNCECSGSDL
Ce-ego1 241 QYTVQVLTGTVLLTKNPCLVAGDVRIFEAVDIPVPELHMHMVDCVVFVQKGLRPHPNCECSGSDL
Ce-RRF1 241 QYTEIVTGTVLLTKNPCLVPGDVRIFEAVDIPVPELHMHMVDCVVFVQKGLRPHPNCECSGSDL
Ce-RRF3 239 QYSILKTKGKVLITKNPCHVPGDVRVFDVAVWQPALAHLVDVVFVQKGLRPHPNCECSGSDL
Dyctiostelium 235 QLEKVIIEGLVMVTKNPCTHPGDVRYLKAVDNL-LRHLRNVIVFVSTKGDVVPNFKEISGSDL
Tetrahymena 238 YISFQVEGDVIVVKNPCLHPGDIRKLRKAVTLEPFKKLRNLIIFVQKGLRPHPNCECSGSDL

Branchiostoma 298 DGDYFVITWREGLILPRENRPAMDFTAQKRVLHRPVQESDMIEFFAAYIGSNQLGLIANA
Schizosachara 301 DGDEYTVIWDQRLIPKIVNYPLESSEPKKIDFLEIGKPLIDSVKEFFVNYIKYDLSGLIISNA
Neurospora 301 DGDDFVFIWDFELIPKERSHPMISEPIGKELATEPTVNNLIITFFVLYMKYNNLPIIAHA
Aspergillus 301 DGDDYVVIWDDLIIPKDWFRPPMNYTTNARDLDRDVTVDVDEITSFFVLYMKNDCLPTIAHA
Coccidioides 301 DGDLYNVIIYDERLMPPCTYPP-ANYPKVEKLLDREVVRDDIIDFFVTFMQDQLGRIATI
Arabidopsis 301 DGDYFVFCWDFDLIPPRQVQSMYTPAPTQILDHVDVTEEEVEEYFANYIVNDSLGLIANA
Nicotiana 301 DGDYFVFCWDFDLIPPRQVQSMYTPAPTQILDHVDVTEEEVEEYFTNYIINDSLGLIANA
Hordeum 301 DGDYFVFCWDFDLIPTRMVAFPMYTPAPTQILDHVDVTEEEVEEYFTNYIVNDSLGLIANA
Solanum 301 DGDYFVFCWDDMIIPPRQVQSMYTPAPTQILDHVDVTEEEVEEYFTNYIVNDSLGLIISNA
Ce-ego1 301 DGDEYSIIWDQQLLLDKNEDPYDFTSEKKASFKEDEIDDLMREFYVVKYIKLDSVGOISNS
Ce-RRF1 301 DGDEYSVVIWDQQLLLERNEEPPDFAVEKKVPYDREKLDVLMREFYVTKYIKLDSVGOISNS
Ce-RRF3 299 DGDEYSIIWDQQLLDYNEEA-MVFPSSAAEEDKEPTTDDMVEFFLRYLQODSIGRMSHA
Dyctiostelium 294 DGDRYFFCYDKSLIGNRSKSEYLGDETVNNDKKNNDPFALSSMYSTNVERQELGKMYNS
Tetrahymena 298 DGDYFVFCWDFDLIPPRQVQSMYTPAPTQILDHVDVTEEEVEEYFTNYIVNDSLGLIISNA

Branchiostoma 358 HLIVHADKEDQGIIFSQKCIDLAQLHSDAVDAPKTGELKGDLPPEVYPDFMMSKDKPOYSER
Schizosachara 361 WKAWADNNPEGIFGNVCLLELAEMHASKAVDFAKSGKMQAKYHPKRYPDFMOKTKTRSESET
Neurospora 361 HLAATADAEVGVKSPKCLELASHMSAVDVKVTGFEFPRRLDPKTPHFMKRNRYTHSVT
Aspergillus 361 HLAWADRLDNGVDEEKIRLAQLHSDAVDYNKNGHMTRNLEPKLWPHFMKKEKVKYKSGK
Coccidioides 360 HQAIADQRPACTLDQDCLLAEHLHSAVAVDFSKSGLTRIPKRPYYPDFMAPSRIKIASIE
Arabidopsis 361 HTAFADKEPLKAFSDPCIEELAKKFSSTAVDFPKTGVIPOHLYVKEYPDFMEKPKDKPTYSKN
Nicotiana 361 HVVEADRDPDAMSDPCKQLAQLFSTIAVDFPKTGVIPOHLYVKEYPDFMEKPKDKPTYSEK
Hordeum 361 HVVEADRQSLKAESTQCIKLAELFSTIAVDYPKTGVIPOHLYVKEYPDFMEKPKDKPTYSEG
Solanum 361 HVVEADRDPDAMSDPCKKLAELCSIAVDFPKTGVIPOHLYVKEYPDFMMDKPKDKPTYSER
Ce-ego1 361 HLHNSDQYGLNAR--VCMDLAKKNCQAVDFTKSGEMIPPERAERVDPYHMGNHTPMYSR
Ce-RRF1 361 HLHNSDQYGLNSR--VCMDLAKKNCQAVDFTKSGEVIPPENPERIPDFHMGNHTPMYSR
Ce-RRF3 358 HLAYA--DLHGLFHENCHATAALKCAVAVDFPKSGPSSFEQCEMTDPYMMSGGKPMYSTR
Dyctiostelium 354 HLAIS--DLFGANHEFSTQLSKECFKEDYPKTGVIPOHLYVKEYPDFMEKPKDKPTYSKN
Tetrahymena 358 HLVEADKSPLYAEDPKCLKLAELHQAQAVDYAKTGVIPOHLYVKEYPDFMEKPKDKPTYSKN

Branchiostoma 418 IIGRLFRKQELVREGFDSYIEDAQQLNINNMMSIMSLYGITSEGEVVSQCILKVKQ
Schizosachara 421 AVGKIFRYAARKLPRFKTEYLNVAEEVKKHYDNDLRSIMAREDISTEYEVYTAFILFKDD
Neurospora 421 ALGKLYDMVVRKCRALRGTAKARRIKSQYDTAMRRVMCQLEIATEFEVWVAFVMSKPR
Aspergillus 421 IIGQLYDAVERIP--VAEDLYQFARDMCKDYDIALRRIMAQHEIKTEFEVWVSTFVLSHAN
Coccidioides 420 VVEEEQYLAEDINEQELNVAARNASKLRRDNTLLNATWDYVASETEGFQWDHLVEDGRK
Arabidopsis 421 VIGKLFREVKEMEVDGHEEYVDEAFYQKANYDFKLGNLMDYYGKTEAEIISGGIMRMSK
Nicotiana 421 VIGKLFQKVKNMIVDGFEDYIDEAFYKSEYDNKLGNLMDYYGKTEAEIISGGIMKASK
Hordeum 421 VIGKLYREIKKLIIVDGYQDYITEAVWFKEEYDFKLGNLMEHYGINSEAEIISGCILKMAK
Solanum 421 VIGKLFREVKEMEVDGHEEYVDEAFYKSEYDNKLGNLMDYYGKTEAEIISGGIMKTSK
Ce-ego1 419 LCGKLFREFKAIKIDGYTEYMASAKNDLARYNAQLRSMMENYGIKTEGEVVSQCIVDMRN
Ce-RRF1 419 LCGKLFREFQAFVVTGFEYRYSQAQQLSSYNGQLRSIMENYGIKTEGEVVSQCIVDMRN
Ce-RRF3 416 LCGKLFREVKEMEVDGHEEYVDEAFYKSEYDNKLGNLMDYYGKTEAEIISGGIMKTSK

Dyctiostelium 412 IMGKMYDQIDQNLVDDYEIYINSAKILYSQYKLVHSLIRHYSAESEEESIMIGFI DQGF I
Tetrahymena 418 IIGILYRQVKDENKTYLEQEIDFAIEANNQWNIEINNLKQFFGAQNEFEIYTCNFSKLIK

Branchiostoma 478 RLKNERFEVAEYVTLWRKTRAEFFKQFDVLKASAWYMVVYSDSPKLLSFPWVYDVLAS
Schizosachara 481 LVNEYGLREEVSFLLKKKYTOEYLEKCALNSAVAATYDVTYDQTEVLI SFPYLFSSRLCQ
Neurospora 481 VYKIQDNVGRESSALKQHFKDQCKKEAGLSFVVSAMYRVTYEETMPLV SFPWLFWDKIGE
Aspergillus 479 MYKFHEEIGMLSSSIREGFKRECYDKVGGAPLALAMYRI THEEQPLI SFPWIFPRVLGQ
Coccidioides 480 VYEDKLR EIMQQYTPWKSSLTEVEVVMGNSNSKQSRRDKEASQSTPLSAQLEPLFGTHYMRS
Arabidopsis 481 SKRRDAESI GRAVRALRKETLSLENASEE SAKASAWYHVYH SRDHFISFAWCVYDKLVR
Nicotiana 481 TRRKDAEAI GVAVRCLRKEARAWFKRRSD LAKASAWYHVYHHRDHFISFPWCVYDQLIQ
Hordeum 481 NKKSDADAIRLAVKSLRKEARSWFSEMGSVAKASAWYHVYHPRPHLISFPWCVYDKLIL
Solanum 481 TRRKDAEAI SIAVRALRKEARTWFKRHNDLPKASAWYHVYHPRDHFISFPWCVYDQLIQ
Ce-ego1 479 RKDQDDMSFFNTNQMIETKLTNLFKKYREEGNTEAF SRYGRDSENKKSFAWLAYDVI AK
Ce-RRF1 479 RKDQDDMSFYNTNQMIETKMTSLVCKFRETVKCTLLPNAYDNGEVRKLSFAWLAYDVI AK
Ce-RRF3 476 LERDDYSFYHTDKKIYAVFRAKFFEEFEGGKNTRLKCTKAMHEKRCIGQSLPWWAIDALCD
Dyctiostelium 472 SSKDIKGEKNDYKIQQTFENEELKEFGEEKKVS AWYHVAYSDNKKKDTLFPVYESRLMI
Tetrahymena 478 VKKMSAEIVQORIAIKNRFELLEFKNLDEKIRATLWYIICYLRKDSLIGQTF TFLSQQKY

Branchiostoma 538 LKKI
Schizosachara 541 LSRK
Neurospora 541 LARA
Aspergillus 539 IATG
Coccidioides 540 IVDR
Arabidopsis 541 IKKT
Nicotiana 541 IKKA
Hordeum 541 IKQK
Solanum 541 IKKE
Ce-ego1 539 VKQD
Ce-RRF1 539 VKET
Ce-RRF3 536 LRRQ
Dyctiostelium 532 VKEL
Tetrahymena 538 FGET

Eri-1-like nucleases

Ce_eril 1 DYLLAIDFECTCVEI IY---DYPHEIIE LPAVLI DVREMKIIS--EFFTYVRPVRNPKLS
Ce_M02B7.2 1 DYLLVLD FEATCQDNWKGMPHPVQEIIEFPVVLSTADWSEIR--RFHOYIKPTEFPRLT
Hs_3hExo 1 DYLCIIDFEATCEEIGNPP--EFVHEIIEFPVLLNTHLEIED--TFQOYVRPEINTQLS
Hs_NP542394 1 DYLLVIDFESTCWNDGKHH-HS-QEIIIEFPVLLNLTSTGQIDS--EFQAYVQPEHPHLS
Hs_Pint1 1 HYFLVIDFEATC-DKQP---IHPQEIIEFPVLLKLNRTMEIES--TFHMYVQPVVHPQLT
Tc_Snp 1 DYLLVLD FEATCWSNGDPR-KNPAEIIIEFPVVLVDVKNAKIIA--EFQOYVMPVENPKLS
Dm_Snp 1 SYVIANDFEATCWEKQAPPEWREAEIIEFPVVLNLTGKIEA--EFHOYILPFE SPRLS
Urchin_1 1 DYLCVIDVFEATCQEIINPV--DYIHEIIEFPVLLNLTQIVN--TFDAFCCKPVINPQLS
Urchin_2 1 SYLLVIDFESTCWKDKKN---TSQEIIEFPVLLNLTGQIES--EFQOYVMPDEHPVLS
Urchin_3 1 DYFLVIDFEATCLDNER---IEPQEVIEFPVLLKVS GKTFFETA--TFHOYVEPQVH-GVG

Ce_eril 56 EFCMQFTKIAQETVDAAPYFREALQRLYTWMRKFN-----LIGQKN
Ce_M02B7.2 59 SFCTSLTRIIQEMVDEKPKLPEVLSEFDSWLKEDS-----RLK-Q
Hs_3hExo 57 DFCISLTGITQDQVDRADTFPQVLLKVIDWMLKE-----LIGTKY
Hs_NP542394 57 EFCMELTGIKQAQVDEGVPLKICLSQFCKWVHKIQQQKNIIFATGISEP-----SASEV
Hs_Pint1 55 PFCTELTGIIQAMVDGQPSLQQVLEFVDEWMAKEG-----LLDPN
Tc_Snp 58 DFCTELTGIIQHQVDNCPVLPQACLLLSRWVAEKMSLYDMDFPNGESQ-----AT
Dm_Snp 59 ACTELTGIIQKTVDSGMPILRTAVMFEWLRNEMRARNLTLPKMNS-----NIL
Urchin_1 57 KFCSQLTNIISQKMVDKADFPVLEKAEERWVRQKG-----LIGSKH
Urchin_2 56 DFCTELTGIIQEQVNGVPLFICLNKFTSWLKKIESEKNLAYNRS-TD-----DTR
Urchin_3 55 EFCRTLGTITPDMVKGQPTFADTLKLEHVWMEKEG-----LVDPE

Ce_eril 96 SREAFVTDGPHDMWKFMOFQCLLSNIRMPHMFR-SEINIKKTFKEKENGL--IKGNKGSG
 Ce_M02B7.2 98 GNEAFVTCGDWDLKVALPSEAKFKNIEIPEYFN-QWINVVKAYAEHTN-----HFAK-G
 Hs_3hExo 97 K-YSLTLDGSDWMSKFLNIQCQLSRLKYPPFAK-KWINIRKSYGNFYK-----VPRSQTK
 Hs_NP542394 111 KLCAFVTWSDWDLGVCLYEYCKRQQLKPVFLN-SWIDIRATYKLFYR-----RKPK-G
 Hs_Pint1 95 VKSIFVTCGDWDLKVMPLPGCQYLGIPVADYFK-QWINLKKAYSFAMG-----CWPKN
 Tc_Snp 108 KTCAFATWSDWDLGTCLRKECIRKNIKRIEKMYR-KWIDIRALEFKRYIR-----RPFY-G
 Dm_Snp 110 GNCAFVTWTDWDFGICLAKECSRKGIKRPAYFN-QWIDVRAIYRSWYK-----YRPC-N
 Urchin_1 97 S-FALATDCSLDMDIYLKLOCLVSEIPYPOYAK-EWVNIISKVEANLYK-----TKR--LP
 Urchin_2 106 KLCTFVTWSDWDLVCLRYECQRKQIYKPSALN-HWIDARAVYRNEYQ-----RKPK-G
 Urchin_3 95 VKEIFVTCGDWDLKTMFSPQCAHFELPYHSYFR-RWINIKKAFATVTS-----HYPK-G

Ce_eril 153 IENMLERLDLSEVGNKHSGLDDATNIAATAIQMMKLK
 Ce_M02B7.2 150 MTQQLLAIYKLOHQGRLLHSGTDDVANICEIVRCLGRDG
 Hs_3hExo 150 LTIMLEKLGMDYDGRPHCGLDDSKNIARIAVRMIQDG
 Hs_NP542394 163 LSGALQEVGIEFFSGREHSGLDDSRNTALLAWKMIRDG
 Hs_Pint1 148 LLDMMNKGLSLQHGIRPHSGIDDCKNIANIMKTLAYRG
 Tc_Snp 160 IAGALAEGLITEEGTEHCGLHDARNTARLVGKMVDKG
 Dm_Snp 162 FTDALSHVGLAFEGKAHSGIDDAKNLALMCKMVRDG
 Urchin_1 148 IRLAML DSTGLAFIIGQPHRGIDDARNIARVALQLIEDG
 Urchin_2 158 LSGALQEVGIEFFAGROHSGLDDAKNTAILVWFRMIQDG
 Urchin_3 147 MMQMLERLNIIPHVGRHHSGLDDCRNIANILQALALKR

Sid-1-related proteins

Tc_A 1 YLWHILSIAIFYSIPVVMQLVITYQRVVNR---TGDQDMCYYNFLCANPAFGLSDFNHIIFS
 Tc_B 1 YLWQILNVGLFYIIPVILQLVMTLQSFILIQ---TGDFDLCYYNFLCANPLWIIISDFNHVFS
 Tc_C 1 YLYNVLTVALFYGLPVIQLVVTYQALNE---TGQDLCYYNFLCAHPLGVISDFNHVFS
 Ce_sid1 1 LHGOMLQYPVAIILPVLMTHTAIEFHKWTSTMANRDEMCFHNNHACARPLGELRAWNNIIT
 Ce_tag130 1 YKIALAIIIGIFYNITVLLQLIISKAGSLRQ---SGDLDECTENFOCARPLWYFVAFNNVVS
 Ce_Y37H2C1 1 KYENFLFFQLFGSILPALTTIFQNRILQKAN--KTNLDTCYLNYRCSLNVIGFNSFNMSMTS
 Am_sid1 1 YLYYLIITVALFYTLPAVQLLITYQHVLHV---TGNQDMCYYNFLCAHFFQALSDFNHVFS
 Hs_sidT1 1 YFWNIITIAVFYALPVIQLVITYQTVVNV---TGNQDLCYYNFLCAHPLGVLSAFNNIILS
 Hs_sidT2 1 YFWNIATIAVFYALPVMQLVITYQTVVNV---TGNQDLCYYNFLCAHPLGNLSAFNNIILS
 Bm_3022 1 YFWGALTLAVVYALPVMQLLITYQRMVFQ---TGDQDLCYYNFLCAHPLGLTSLDFNHVFS
 Bm_3026 1 YLWIVLTVSVFYTLPVLQLVMTYQRLINQ---SGNQDLCYFNFFCAHPLMMLSDFNHVFS
 Bm_2839 1 YLHTLYTVAVFYALPVLQFVAAEQVMLNI---SGSLDMCYYNFLCAHPAGGLSDFNHVFS

Tc_A 58 NVGYLIVGILFLGLVVLHROTKIPNSST-----GIPVHYGVYAMGIALIEGILSA
 Tc_B 58 NIGYILMGIVFSINVFYRHFYSPPLTT-----GVFANYGVYAMGAALIMEGVLSG
 Tc_C 58 NSGYVLLGLLFLGITYRREITHKDLNFER-----QYGIPOHYGMFYAMGVALIMEGVLSG
 Ce_sid1 61 NIGYTLYGAFIVLSICORRRHEYSHV-----FGTYECTLLDVTIGVFMVLQSIASA
 Ce_tag130 58 NCGYMYFGTLIIVMNYCRERSFRRLFVAVQPTLAERYGLPOHSGLMTAIGLAVIMEGISSA
 Ce_Y37H2C1 59 ASSLAVLGIINLIVFRKQIFRYEIPRFPT----SRGIQORDAPKIVCLLGLVALGVYSA
 Am_sid1 58 NIGYIMLGFLFLFLTSFREHNEFDKEKNK-----CYGIPOHYGLFYAMGTALIMEGITLSG
 Hs_sidT1 58 NIGHVLLGFLFLIVLFRDILHRRALEAKDIFAVEYGIKHFGLFYAMGTALMMEGVLSA
 Hs_sidT2 58 NIGYILLGFLFLIILQREINENRALLRNDLCALECGIPKHFGLFYAMGTALMMEGILSA
 Bm_3022 58 NVGYVLLGAVFAGQVRFQVKSFRORPE-----NLGIPOHYGLLYSMGLALSMEGILSA
 Bm_3026 58 NIGYVLLGALFLLQVWRQRIMRNEPEEKK----QKGIPOHFGLLYAMGVALISEGFLSA
 Bm_2839 58 NIGYILLGALFMIQLQRKRNRKRAPR-HE----EYGIPIAHYGLLSSIGAAMMVVALISA

Tc_A 109 CYHICPSQSNYQFDTSFMYVMAVLCMIKLYQNRHPDVNATAYATFTVLGMAIFLAMIGIL
 Tc_B 109 CYHICPNETNFQFDTSFMYVMIVLCLVLYQNRHPDVPTAYTTFSTILGATILCGTIGIV
 Tc_C 113 SYHVCNNTANFQFDSFMYVMAVLCMKLYQNRHPDINATAYATFGVLAVAILLGMIGIL
 Ce_sid1 113 TYHICPSDVAFQFDTPCIVQVICGLLMVVRQVFRHESPSF-AYINILLVGVVSLN-----
 Ce_tag130 118 TYHVCNPNINIQFDTALMYVIGMLGKIKLWVSLRHPDMVVSAYHAFGFLGVFLMAAAGVY
 Ce_Y37H2C1 115 ILNNCQCKSMLOFYDYTIILWVQYSALILWVYSKRHG-MFVVDSLSRLLIKIVFSICSTIGFT
 Am_sid1 113 SYHVCNPNRSNFQFDSFMYIITVLCMIKLYQNRHPDINARASVTFAMLAFLIFINLMGVL

Hs_sidT1 118 CYHVCNPYSNFRFDTSFMYMIAGLCMIKLYQTRHPDINASAYSAYASEFAVVIMVTVIGVV
Hs_sidT2 118 CYHVCNPYTNFQFDTSFMYMIAGLCMIKLYQKRHPDINASAYSAYACLAVIFFSVIGVV
Bm_3022 111 CYHLCPNKMNQFQDSFMYVIAVLTIKLYQNRHSDIIPSAHSTFMTLAVIMTIGLFGIL
Bm_3026 114 AYHVCNPNSMNFQFDTSFMYVTSALCMVKTYQSRHPDINARAHATFGVLALITIFIGLVGVL
Bm_2839 113 SYHVCNPNSLNFQFDTAfMYVLAVLCMVKTYQSRHPDINARAHATFGVLAVFTIALVWVGVL

Tc_A 169 NG-SLTVWIVFVVI--YSLLCAYISFKIYFISFVFDGFKQLKQSLKSSNKV-----EAIA
Tc_B 169 FK-APPVFIIVFVTIAYLVLLIYASLNIYHFGTARNFLR--RCCLRNSEVP-----RPIQ
Tc_C 173 EG--NLYFWIVFTIIYLLSCFYLSIQIYYMGCKLDAGIAMRVWRICVYEFWSGPLNVIK
Ce_sid1 166 -----FLISAFSKTSYVRFIIAVIHVIVVGSICLAKERSLGSEK-----
Ce_tag130 178 VH--NMIFWALFSLIYIASMLLVSLIEFYFKGIWTLNLRERNSIRLSWVSS--RHLSCVV
Ce_Y37H2C1 174 GYFAYKYFYERPSGLQSHQWICTPLSSQOK-VLEDDKNVKRRPLN-----
Am_sid1 173 NG--SIYFWILFTIITHLLTCLFMTIQIYYMGRWKFRALITRVLQVILYS--SGIRYLF
Hs_sidT1 178 FGKNDVWFVWVIFSATHVLASLALSTOIYYMGRFKIDLGITFRRAAMVFYTD---CIQQCSR
Hs_sidT2 178 FGKGNATFWIVFSLIHLIATLLSTOIYYMGRWKLDSGIFRRILHVLVYTD---CIRQCSG
Bm_3022 171 HP--SAGFAASFTLLHLGACLVLTIKIYYAGREKMDRRVILRAYAHVAARG----WRSLL
Bm_3026 174 NA--NVYFWVAFTALHLLTCFFITFQIYYLGRKLDMGWVRAASRGAALR-----
Bm_2839 173 GG--GPLFWSVFTVLIHVFTFLLLSIRIYYVGOERLEKSSIAVAARGLRAR-----

Tc_A 221 PIRKSRFALLVIANIINYAMLIITGLCLYN-TGVTDFGTFLLLGILMGNSVLYAVFYTGMKL
Tc_B 220 SPNTHRWLWLLLAITVNIILYGLGLILFYHTKTIDFATFILQILAGNAFLYTVVYTCMKI
Tc_C 231 PTHKARMCLLIANLCNWGMAFWG---VYKHQ-KDFALELLAIFMGNTILYFSFYIVMKI
Ce_sid1 205 --LKTREFFIMAFSMGNFAIVMY-----LTLSAFHNLQIATYCFIINCIMYLMYYGCMKV
Ce_tag130 234 PAKKAREFVILLNLNIAATAVVYVY----LEAHPKDELSELLIPFIGNLFIYIYYILMKM
Ce_Y37H2C1 218 --SKMSYVFISIGYALICSVTEFL-----HSGISVHSATYFSAKQOLVIYLFYIIOKI
Am_sid1 228 PIYIGREFMLVIANIWNIALAVIG---NIYQE-KNFATFLLAILMSNLILYTTTFYIIMKI
Hs_sidT1 235 PIYMDRMVLLVVGNLVNWSEALEG---LIYRP-RDFASYMLGIFICNLLLYLAFYIIMKI
Hs_sidT2 235 PIYVDRMVLLVMGNVINWSLAAYG---LIMRP-NDFASYLLAIGICNLLLYLAFYIIMKI
Bm_3022 225 PAHPYRAGLLGLANLANWLAGYS---VYSHHNTDLARQLLAILMGNAIYTMFYVMVKL
Bm_3026 222 ---PSRGLMLLLANLINWGLAGYG---VAQHS-RDFASHLLLVLMTNLFLYTLFYIVMKL
Bm_2839 221 PLYTPRLVMLLIANAANWGFATYG---LLTHA-GDIATHLLNVLLCNTLLYIVFYVLMKL

Tc_A 280 VN-----GERICFEALYGLIATAAWATAAVYFLDNAT--LWIVTPAESRQWNOECI
Tc_B 280 KCTSVRECTCSEKICAQALYGFALVTVWVLAGVFFTEAS--KWIESPAQSRQLNKQCI
Tc_C 287 IN-----KERVNKLSEFFISLSVICAISAMYFFLNKSI--SWSRTPAQSRQFNQECK
Ce_sid1 258 LH-----SERITSKAKICGALSLLAWAVAGFFFFQDDT--DWTRSAASRALNKPCI
Ce_tag130 290 IY-----REKIPKRALALFAAVISWTCAGILFNORVS--DWSKMPAISRELNKPCI
Ce_Y37H2C1 270 RFEWSS----FTFSYTIRCIFLIVFLVLFQTLNRYFANFASPFNFYESPALSRELNSECI
Am_sid1 284 CH-----KERILLQPCIYIVLSIVFWAAALYFFINKTI--SWELTSAQSRHYNKPCI
Hs_sidT1 291 RS-----SEKVLVPVLCFIVATAVMWAAALYFFFQNLNLS--SWEGTPAESREKNRCCI
Hs_sidT2 291 RS-----GERIKLIPLLICVCTSVVWGFALFFFOGLS--TWQKTPAESREHNRDCI
Bm_3022 282 VN-----RERILARTWMYCIIAHVAWFLALRLEFLDSKT--KWSETPAQSRQHNAPCS
Bm_3026 275 LH-----RETTITCYTWVIVLTIYSSWAGSSYFYLDQNT--NWALSPAQSRERNAACS
Bm_2839 277 LH-----GERIRWYSWCFLAAAAACWVPALYFFFTSGST--DWSATPARSRHRNHECR

Tc_A 330 VMSFYDKHDVWHLLSAPALYLTFMFLLSLDDDL
Tc_B 338 FADFYDSRDWHEFFSSIALYFTFMYLICIDDDL
Tc_C 337 LLRFYDFHDIWHELSAIGMFFTFMVLLTLDDDL
Ce_sid1 308 LLGFFGSHDIWHIFGALAGLFTFIFVSFVDDDL
Ce_tag130 340 FLNFYDNHDIWHLSSAFALFFSFTAINVIDDDL
Ce_Y37H2C1 326 IPG-IDWNNVRHYNAVITCSEFFILLLDYIDINI
Am_sid1 334 LLHFEDSHDIWHELSALAMFFSFMVLLTLDDDL
Hs_sidT1 341 LLDFFDDHDIWHELSATALFFSFLVLLTLDDDL
Hs_sidT2 341 LLDFFDDHDIWHELSSTAMFGSFLVLLTLDDDL
Bm_3022 332 SLSFYDTHDLWHGVSAALFLSFNMLLTMDDAL
Bm_3026 325 VLRLFDAHDAWHAMSAVAMFLSFNMYLTLDDGL
Bm_2839 327 VLQFYDSDHDIWHMLSAALYFTFNVMLTWDDGL