

	660	670	680	690	700	710	720	730	740	750	760	770	780																																																																																																							
AtDCL4	GAI	CAAK	-----	IQLNSDHN	VQDE	---	PVGKNPKSK	ICDT	YL	SMAAEAL	SSGVA	-----	KD-----	EN----	ASD	---	L	S	L	A	A	K	E	P	L	F	S	R	L	V	Q	L	I	K	I	L	S	V	I	R	L																																																																											
MidDCL4	GAR	L	F	Y	L	L	L	K	A	I	D	S	L	S	G	D	P	S	V	R	N	E	L	I	E	A	E	G	N	S	M	D	D	T	C	-	R	Y	L	S	Q	A	A	E	V	F	A	S	A	F	T																																																																	
SIDCL4	GAL	CA	-----	SC	I	L	L	K	G	D	H	H	E	R	H	Q	M	V	E	A	E	V	N	A	S	D	D	S	L	C	D	R	Y	L	S	Q	V	D	T	V	F	T	S	G	C	A	-----	KD-----	GM----	NPD	---	A	L	M	E	V	I	K	E	P	Y	F	S	K	L	R	L	I	G	I	L	S	N	E	G	V																																								
SIDCL2d	LAF	K	S	C	E	-----	END	-----	F	L	S	-----	DDAC	V	R	D	I	C	L	G	A	S	T	I	F	S	A	H	I	P	-----	S	-----	S	-----	GP--	HWS	I	G	G	D	I	C	A	N	V	D	A	C	Y	L	S	S	K	V	N	C	L	E	S	L	L	E	Y	R	D																																																		
SIDCL2c	LAF	K	A	A	E	F	L	S	Q	E	T	D	-----	F	S	W	G	E	L	D	V	C	A	Q	T	I	V	R	D	I	S	S	D	A	S	K	V	F	S	A	C	I	P	-----	S	-----	GP--	HWS	I	G	G	D	I	C	A	N	T	D	A	C	Y	L	S	S	K	V	H	C	L	E	S	L	L	E	Y	R	N																																							
SIDCL2a	LAF	K	A	T	E	F	L	S	R	E	E	V	D	-----	F	L	S	W	G	E	L	D	V	C	A	Q	T	I	V	R	D	I	S	S	W	G	A	S	K	I	F	S	A	R	I	P	-----	S	-----	GP--	YWS	I	G	G	D	I	C	A	N	V	D	A	C	Y	L	S	S	K	V	A	T	C	L	E	S	L	L	E	Y	R	D																																			
SIDCL2b	LAF	K	A	A	E	F	L	S	F	E	E	N	D	-----	F	F	S	W	G	E	F	D	C	A	Q	T	I	V	R	D	I	S	S	L	G	A	S	K	I	F	S	A	R	I	P	-----	S	-----	GP--	HWS	I	G	G	D	I	C	A	N	A	D	A	C	Y	L	S	S	K	V	N	C	L	E	S	L	L	E	Y	R	D																																					
AtDCL2	LAK	Q	A	A	Q	S	L	S	A	S	Q	N	D	-----	S	F	L	W	G	E	L	N	M	F	S	V	A	L	V	K	K	I	C	S	D	A	S	Q	E	F	L	A	E	I	P	-----	Q	-----	GL--	NWS	V	A	N	-	I	N	G	N	A	E	A	C	L	L	I	T	V	Q	L	E	S	L	L	E	Y	S	S																																							
MidDCL2a	LAK	Q	A	A	Q	S	L	S	R	Y	E	N	D	-----	F	F	A	L	G	R	L	D	V	L	G	G	S	I	V	I	R	I	F	S	L	D	A	H	K	V	F	A	T	V	I	P	-----	S	-----	GP--	GWS	I	G	N	N	K	V	N	V	D	A	C	L	E	S	L	L	E	Y	S	S																																													
MidDCL2b	LAK	Q	A	A	R	S	L	S	R	Y	E	N	D	-----	F	F	A	W	G	H	L	D	V	L	G	G	S	I	V	K	R	I	S	S	D	A	H	K	V	F	A	T	V	I	P	-----	S	-----	GP--	GWS	I	G	N	N	K	V	N	V	D	T	C	L	E	S	L	L	E	Y	S	S																																														
SIDCL1	CAY	K	V	A	H	S	F	L	T	A	L	Q	N	-----	D	E	R	A	S	-----	Y	Q	L	D	V	K	F	Q	E	S	Y	L	D	K	V	S	I	L	Q	C	E	I	S	E	G	A	V	A	Q	S	N	L	N	A	-	E	T	H	K	G	D	N	P	S	D	R	P	D	E	M	E	E	G	E	L	L	E	S	H	V	V	S	V	G	E	H	V	D	V	I	L	G	A	A	V	A	D	C	K	V	I	P	E	V	Q	S	L	I	K	I	L	L	K	Y	Q	H
MidDCL1	CAY	K	V	A	Q	S	F	L	T	A	L	Q	N	-----	D	E	R	A	N	-----	Y	Q	L	D	V	K	F	Q	E	S	Y	L	S	K	V	S	I	L	Q	C	E	I	L	E	G	A	V	S	D	K	A	A	N	S	D	N	G	I	V	Q	D	S	T	Y	V	D	E	I	E	E	G	E	L	P	D	S	H	V	V	S	G	G	E	H	V	D	V	I	L	G	A	A	V	A	D	C	K	V	I	P	E	V	Q	S	L	I	K	I	L	L	R	Y	Q	H		
AtDCL1	CAY	K	V	G	Q	S	F	L	S	A	L	Q	S	-----	D	E	R	V	N	-----	F	Q	V	D	V	K	F	Q	E	S	Y	L	S	E	V	V	S	I	L	Q	C	E	I	L	E	G	A	A	A	E	K	V	A	A	E	-----	V	G	K	P	E	N	G	N	A	H	D	E	M	E	E	G	E	L	P	D	D	P	V	S	G	G	E	H	V	D	E	V	I	L	G	A	A	V	A	D	C	K	V	I	P	E	V	Q	S	L	I	K	I	L	L	K	Y	Q	H	
AtDCL3	CAH	L	A	A	E	V	C	L	E	K	I	S	D	-----	T	K	E	S	E	T	Y	K	E	C	S	M	V	C	K	E	I	L	E	D	I	L	S	T	I	G	V	Y	I	P	-----	QD	-----	QD	-----	DK	S	L	V	-----	D	I	Q	Q	N	H	L	S	A	M	I	S	C	H	V	S	P	K	E	I	F	H	L	I	D	S	F	R	G																																	
MidDCL3	CAY	E	A	V	K	V	C	L	E	N	V	P	K	-----	V	Q	D	E	C	E	I	Y	R	E	S	S	L	Q	C	K	Y	I	L	E	E	I	L	C	I	I	G	G	S	I	P	L	V	L	F	P	-----	S	H	P	T	G	-----	QD	-----	E	K	N	F	L	-----	D	F	G	F	D	Y	T	K	A	V	D	L	C	Y	I	S	P	E	H	E	I	Q	L	F	L	S	E	G	G																						
SIDCL3	CAY	E	A	V	K	I	C	L	E	N	V	P	N	-----	D	K	D	E	N	I	L	R	T	S	S	L	Q	H	R	Y	I	L	E	E	A	L	S	I	V	Q	E	S	M	P	-----	QD	-----	QD	-----	C	E	S	L	F	-----	D	V	G	Y	D	L	S	A	T	L	S	M	C	H	I	S	P	E	H	E	I	Q	L	F	L	S	E	G	G																																

SF2_C_dicer

	790	800	810	820	830	840	850	860	870	880	890	900	910																																																																																																								
AtDCL4	E	P	H	M	K	C	I	F	V	N	R	I	V	T	A	R	T	I	L	S	C	I	L	N	N	I	-	E	L	L	R	S	W	K	S	D	F	L	V	G	L	S	S	G	L	K	S	M	S	R	I	S	M	E	T	I	L	K	R	F	Q	S	K	E	L	N	L	L	V	A	T	K	V	G	E	E	G	L	D	I	Q	T	C	C	L	V	I	R	Y	D	L	P	E	T	V	S	F	I	Q	S	R	G	R	A	R	M	P	Q	S	E	I	A	F	L	V	-----	-----
MidDCL4	Q	P	N	M	K	C	I	F	V	N	R	I	V	T	A	R	T	I	L	S	C	I	L	N	N	I	-	K	F	L	A	Y	W	K	C	H	F	L	V	G	H	A	G	L	K	S	M	S	R	I	A	M	K	S	I	L	E	K	F	R	C	G	E	L	N	L	L	V	A	T	K	V	G	E	E	G	L	D	I	Q	T	C	C	L	V	I	R	F	D	L	P	E	T	V	S	F	I	Q	S	R	G	R	A	R	M	P	Q	S	E	I	A	F	L	V	-----	-----	
SIDCL4	Q	P	D	M	K	C	I	F	V	N	R	I	V	T	A	R	S	I	S	Y	I	L	Q	H	I	-	K	I	L	S	W	K	C	G	F	L	V	G	H	S	G	L	K	S	M	S	R	I	N	T	N	I	I	L	D	K	F	R	S	C	E	L	N	L	I	A	T	K	V	G	E	E	G	L	D	I	Q	T	C	C	L	V	I	R	F	D	L	P	E	T	V	A	S	F	I	Q	S	R	G	R	A	R	M	P	K	S	E	I	A	F	L	V	-----	-----			
SIDCL2d	R	K	D	L	R	C	I	F	V	E	R	I	T	A	I	V	L	R	S	I	L	N	E	I	-	F	L	E	R	S	G	W	R	T	E	T	T	G	R	I	T	T	F	-----	K	Q	N	K	I	V	E	E	F	R	K	G	L	V	N	I	V	A	T	S	I	L	E	E	G	L	D	V	R	S	C	N	L	V	I	R	F	D	P	S	T	I	V	C	S	F	I	Q	S	R	G	R	A	R	M	Q	N	S	D	F	I	L	M	V	-----	-----							
SIDCL2c	L	K	D	L	R	C	I	F	V	E	R	I	T	A	I	V	L	R	S	I	L	N	E	I	-	L	P	K	L	S	G	W	R	T	E	C	T	A	G	H	A	S	V	V	Q	S	S	R	I	Q	N	K	I	V	E	E	F	R	K	G	L	V	N	I	V	A	T	S	I	L	E	E	G	L	D	V	Q	S	C	N	L	V	I	R	F	D	P	S	A	T	I	V	C	S	F	I	Q	S	R	G	R	A	R	M	Q	N	S	D	F	I	L	M	V	-----	-----		
SIDCL2a	Q	K	D	L	R	C	I	F	V	E	R	I	T	A	I	V	L	R	S	I	L	N	E	I	-	L	P	E	L	C	G	W	R	T	E	T	A	G	H	I	S	V	V	Q	S	S	R	I	Q	N	K	I	V	E	E	F	R	K	G	L	V	N	I	V	A	T	S	I	L	E	E	G	L	D	V	Q	S	C	N	L	V	I	R	F	D	P	S	A	T	I	V	C	S	F	I	Q	S	R	G	R	A	R	M	Q	N	S	D	F	I	L	M	V	-----	-----			
SIDCL2b	Q	K	D	L	R	C	I	F	V	E	R	I	T	A	I	V	L	R	S	I	L	N	E	I	-	L	P	E	R	S	G	W	R	T	E	T	A	G	H	V	S	V	L	Q	S	S	R	I	Q	N	K	I	V	E	E	F	R	K	G	L	V	N	I	V	A	T	S	I	L	E	E	G	L	D	V	Q	S	C	N	L	V	I	R	F	D	P	S	A	T	I	V	C	S	F	I	Q	S	R	G	R	A	R	M	Q	N	S	D	F	I	L	M	V	-----	-----			
AtDCL2	L	E	N	I	R	C	I	F	V	D	R	V	I	T	A	I	V	L	E	S	I	L	A	E	I	-	L	P	N	C	N	W	K	T	K	Y	A	G	N	N	S	G	L	Q	N	Q	T	R	I	K	Q	N	E	I	V	E	D	F	R	R	G	L	V	N	I	V	A	T	S	I	L	E	E	G	L	D	V	Q	S	C	N	L	V	I	R	F	D	P	S	A	N	I	C	S	F	I	Q	S	R	G	R	A	R	M	Q	N	S	D	F	I	L	M	V	-----	-----		
MidDCL2a	L	Q	D	I	R	C	I	F	V	Q	R	V	I	T	A	I	V	L	E	A	L	N	E	I	-	L	P	G	Y	C	S	W	K	T	K	Y	A	G	N	N	S	G	L	Q	C	S	K	K	Q	N	E	I	V	E	E	F	R	C	G	L	V	N	I	V	A	T	S	I	L	E	E	G	L	D	V	Q	S	C	N																																						

	1,050	1,060	1,070	1,080	1,090	1,100	1,110	1,120	1,130	1,140	1,150	1,160	1,170
AtDCL4	S S L L P S T E A A K K	D A C L K A V H E L H N I G V L N D F L L P	D S K D E I E D E L S D D E F D N I K G E G C S R G	D L Y E M R V P V L F K Q K W D P S T S C V N	--L H S Y Y I M F V P	-----	HP A D R I Y K K F G F F M K S P I P						
MidDCL4	G K P Q S S I E A A K K	D A C L K A I E E L H K I G A L N D Y L L P	D E G N E I E E D G E L D S S D S D S C E G Q	-I L R C E R H E M L V P A L I K E S W S M S E N H V C	--L N S Y Y I Q F F P	-----	DP K D R I Y K D F G I F V K S P I P						
SIDCL4	S A P Q S S I E A A K K	D A C L R A C K S I H E L G A L T D Y L L P	D Q A D E D - K D L V P D F S D L E C C E G E	-D A R E E L H E M I V P A S I K E P W T E T D N P V C	--L N S Y Y I S F F P	-----	FP N D R V Y K K F G I F L K A P I P						
SIDCL2d	S V Q G K R - K I L K Q	L A C L E A C K Q L H R V G A L T D N L V P	D I V E E E T I N K E L E	---C K I ---K I V H Q - S L Y Y P S E F V S H C G	---N E S ---E A V Y Y C Y L V E L P H	-----	DS Y N D S Q L H G I I I I A V R T K I K						
SIDCL2c	T V Q G N S T K I L R Q	L A C L E A C K E L H R V G A L T D N L V P	D I V E E E A I N K E L E	---C Q I ---H T V E - S K Y F I P P E F V S H I G	---N E T ---E A V Y Y C Y L V E L Q H	-----	ET Y D D F Q L H G I I I I A V R T K I K						
SIDCL2a	S V Q G N S - K I S K Q	L A C L E A C K E L H R V G A L T D N L V P	D I M E E E T I N K E L E	---C Q I ---H T V E - L K Y F I P P E V S H C G	---N D S ---E A V Y Y C Y L V E L Q H	-----	D A C N D F Q L H G I I I I A V R T K I K						
SIDCL2b	S V Q G K R - K I L K Q	L A C L E A C K Q L H R V G A L T D N L V P	D I V E E E I I N K E L E	---C Q I ---Q T V E - S K Y F I P P E V S H C S	---N D S ---E A V Y Y C Y L V E M Q H	-----	AS Y N D F E L H G I I I I A V R T K I K						
AtDCL2	K A E A N N - K V L K Q	A V C L K A C I Q L H K V G A L S D H L V P	D M V V A E T V S Q K L E	---K I Q ---Y N T H Q - P C Y F I P P E V S Q F S	---A Q P ---E T T Y H F Y L I R M K P	-----	N S P R N F L H N D V L L G T R V L E I						
MidDCL2a	Q V R G H V - K T L K Q	T A C L E A C Q L H Q N G A L T D N L V P	D I V E E E T D A Q K S A	---N D P ---S N D H Q - P I Y F I P P E V N E Q A	---H I T ---K T M Y Q C Y L I E L K Q	-----	N F N Y D V P L H D I I I I A M R T E L E						
MidDCL2b	Q V Q G N V - K A L K Q	I A C L E A C K Q L H Q T G A L T G N L V P	D I V V E E A E A Q K S E	---N D P ---Y N D H Q - P I Y F I P P E V N E H A	---H I A ---K T M Y Q C Y L I E L K Q	-----	N F N Y D V P L H D I I I I A M R T E L E						
SIDCL1	G P V C S S M R L A Q Q	A A C L D A C K K L H Q M G A F T D M L L P	D K G S G V S E K V E Q D E E G D P I P G T	-S R H R E F Y P E G V A D I I R G D W I L S G K D P L V S S K F I	H L Y M Y A I K C V N I G P S K D P F L T D V S E F A I L F G N E I D								
MidDCL1	G P V C S S M R L A Q Q	A C Y N A V C L A A C K K L H E M G A F T D M L L P	D K G S G E Q Q E K V D Q N D E G D L P G T	-A R H R E F Y P E G V A D I I Q G E W I L S G R D G C S D S K M H L Y M Y A V K C V N S G I	S K D P F L T Q V S E F A V V F S N E I D								
AtDCL1	G P V C S S M R L A Q Q	A V C L A A C K K L H E M G A F T D M L L P	D K G S G Q D A E K A D Q D D E G E P V P G T	-A R H R E F Y P E G V A D V I K G E W V S S G K E V C S E K L H L Y M Y N V R C V D F G S	S K D P F L S E V S E F A I L F G N E I D								
AtDCL3	D P P S R N E Q L	---P P C K K R L	---D N N L Q S N G K E K V A S S K	---S K S S S A A G S - K R R K L H G T T C A N A I S G T W G E N	---I D G A T T Q A Y K F D F C C N I S G E	-----	V Y S S F S I L L E S T L A						
MidDCL3	G P P S R N K N L S K Q	L V C L E A C K K L H Q M G A L N D H L L P	D I E E P F S N L	---I V K N K P A G A T - T K R K L H G T N P I R A I S G S W G E K	---V D G V L H A Y K F D F S C N I A S E	-----	I Y S G F M F L T E S K I D						
SIDCL3	G P E C R S S Q L S R Q	L V C L D A C K K L H Q T G A L N D H L L P	D F N E K P P R G G S D	---V Q D R K L G A G T - T K L K L H G T A C I S A I S G S W G N D	---P N G E V Y Q V Y K M N F L C N I K E V	-----	K Y S S F I L L L Q S E I D						

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	1,310	1,320	1,330	1,340	1,350	1,360	1,370	1,380	1,390	1,400	1,410	1,420	1,430
AtDCL4	---P	---	---	---	S V L	---	V E D I F P P S G S H	L K L A N G C W N I	D D V K N S L V F T T Y S K Q F Y F V A D I C H G R N G F S P V	--K E	---	S S T K S H V E S I Y K	
MidDCL4	---P	---	---	---	P S S	---	M S T K K F P S D E Y L Q L D N G C W S I	---	S D V E N S L I F V R I K E S F Y F V S N I V R E K N G Y S L Y	--K N	---	S G T R N V E L V E	
SIDCL4	---S	---	---	---	V C T	---	S - N N M S K F E E Q I Q L A N G S K S V	---	H D M V N S L V Y V P C K D A F F I S D V V K D K N A Y S M Y	--K D	---	S - K N V E H Y Y D	
SIDCL2d	K H M D	---	---	---	W C S	---	T Q	---	G R R C S V N T I S E V V C S	---	---	E E S I T Y R E H Y R K	
SIDCL2c	K H M D	---	---	---	W C S	---	T Q	---	D R K R S V N T K T G V V C S	---	---	G E S I T Y R E H Y R K	
SIDCL2a	K H M D	---	---	---	W C S	---	T Q	---	G R K R S V S T K T G V I C S	---	---	G E P I T Y I E Y Y K K	
SIDCL2b	K H M D	---	---	---	W C S	---	T Q	---	D R K R S V N T K N G L V C S	---	---	G E S I T Y I E Y Y K K	
AtDCL2	K H E	---	---	---	N C S	---	T N	---	G A S R I I H T K D G L F C T	---	---	S G D Q I Y I E Y Y E E	
MidDCL2a	D H T	---	---	---	N C P	---	S E	---	G N A H F V E T K S G R F C I	---	---	G A V I T Y R E Y Y K K	
MidDCL2b	D H T	---	---	---	N C P	---	S E	---	G N A H F V E T K S G R F C T	---	---	G A V I T Y R E Y Y K K	
SIDCL1	N E R S L G G D R R E Y G F A K L R H G M A I G L K S H P T Y G V R G A I A H Y D L V Q A S G L V P N R S S L D	D V E V D L N K D K I M M A D C S L R A	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K
MidDCL1	N E R T L G G D R R E Y G F G K L R H G M A F G Q A C H P T Y G I R G A V A K Y D V V Q A S G L V P Y R D T M Q L Q - N V D I G K G K I I M A H S F T D A	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K
AtDCL1	N E R T L G G D R R E Y G F G K L R H N I V F G Q K S H P T Y G I R G A V A S F D V V R A S G L L P V R D A F E K E V E E D L S K G K I M M A D G C M V A	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K	E D I V G R I V T A A I S C K R F Y V D C I R S D M T A E N S F P R K E G Y L G P L E Y S S Y A A Y Y K K
AtDCL3	R D S D	---	G	---	N Q C	---	N T S S G Q E V L L D D K	---	M E E T N L I H F A N A S S D K	---	---	S G Y A T Y A E Y F N K	
MidDCL3	N H S N	---	G	---	Y E G	---	N L S P H R T D S S Q K E	---	C N I E D I I H F A N C S V D A	---	---	K D I K N R V V L A I I T E R I Y S T V E V V C N T S A E S P F D G T A - D G A P S V Y T I F T D Y F R K	
SIDCL3	E K S E	---	A	---	K R K	---	N S L V D R T A S F V E D	---	I D Q T D L I H F A N M S I S F	---	---	S K I M D M V V V A I I T E R I Y S V L E A V A N S S A E S P F E V D S - E A T V A P F S S F A D Y F R K	

PAZ

	1,440	1,450	1,460	1,470	1,480	1,490	1,500	1,510	1,520	1,530	1,540	1,550	1,560
AtDCL4	L	---	---	---	---	---	---	---	---	---	---	---	---
MidDCL4	R	---	---	---	---	---	---	---	---	---	---	---	---
SIDCL4	T	---	---	---	---	---	---	---	---	---	---	---	---
SIDCL2d	R	---	---	---	---	---	---	---	---	---	---	---	---
SIDCL2c	R	---	---	---	---	---	---	---	---	---	---	---	---
SIDCL2a	R	---	---	---	---	---	---	---	---	---	---	---	---
SIDCL2b	R	---	---	---	---	---	---	---	---	---	---	---	---
AtDCL2	R	---	---	---	---	---	---	---	---	---	---	---	---
MidDCL2a	K	---	---	---	---	---	---	---	---	---	---	---	---
MidDCL2b	K	---	---	---	---	---	---	---	---	---	---	---	---
SIDCL1	N	Q M L N C L Q G L G G S A P W L Y L N N K R L M	Y G V D L V Y K K Q P L I R G R G V S Y C K N L S P R F E H S E E H E G	---	E L E E A T D K T Y Y V F L P P E L C V H	---	P I P G S L V R G A Q R L P S I M R R I E S M L A V Q L K E M I G	---	---	---	---	---	
MidDCL1	K	---	---	---	---	---	---	---	---	---	---	---	---
AtDCL1	K	---	---	---	---	---	---	---	---	---	---	---	---
AtDCL3	K	---	---	---	---	---	---	---	---	---	---	---	---
MidDCL3	K	---	---	---	---	---	---	---	---	---	---	---	---
SIDCL3	K	---	---	---	---	---	---	---	---	---	---	---	---

PAZ

PAZ

1,570 1,580 1,590 1,600 1,610 1,620 1,630 1,640 1,650 1,660 1,670 1,680 1,690

AtDCL4 PEIAEVSCHRVLEALITEKCHERLSLERLHVLGDFAFLKHAVSRHLFLHDSLDLGEELTWRRSNVYNNSNLCRLAIKKNLQVYIRDQALDPTCHFAFGHPCRVTCDVEASK-----EVHSLN
MiDCL4 SAGAEISADRVLEALITEKCHERLSLERLHVLGDFAFLKHAVGRHLFLHDSLDLGEELTRRRSNVYNNSNLHKLATKSNLQVYIRDQALDPTCHFAFGHPCRVTCTEEAER-----KIHSRK
SiDCL4 PEGRELAIDHVLFAITENCHESLERLHVLGDFAFLKHAVGRHLFLHDSLDLGEELTRRRSNVYNNSNLYMVAIKKNLQVYIRDQALDPTCHFAFGHPCRVTCTCNQKTEK-----NIHGLC
SiDCL2d TQNVVPIPTAKILEAMITKNCLEKHLHSLHSLTLGDSFLKYAASIKLHKTYENDHOGLLTVKVKQTILSNATLCRLGCARKMPGFTIRNKPIFLKAWIIPGDNSSQVHN-----FD
SiDCL2c KLVNFIPTAMVLEAVITRKKLEKHLHSLHSLTLGDSFLKYAVSTQLEKTYENHHEGLLCVKKSKILSNAAALCKLGCARKIPGFTIRNEAFTLQAWIIPGDNSSQVHS-----FN
SiDCL2a TLDIFIPITIKVLEAVITTKKCLEKHLHSLHSLTLGDSFLKYAASIQLEKTYENHHEGLLTKKNTILSNDAALCKLGCARKIPGFTIRNEAFTLQAWIIPGDNSSQVHS-----FD
SiDCL2b TLVNFIPTATILEAMITKNCLEKHLHSLHSLTLGDSFLKYAASIKLHKTYENHHEGLLTVKVKQTILSNAAALCKLGCARKIPGFTIRNEAFTLQAWIIPGDNSSQVHS-----FD
AtDCL2 ----IPIIKVLEAVITTKKCEDEKHLHSLHSLTLGDSFLKYAVCQQLFQHCHTHHEGLLSTKKDGMISNVMICQFGCQKIKQGTIRDECEPKGWMVPCQSSAAYS-----LV
MiDCL2a ----MQ-----NVTIPTMKGFTIRTEPIFDPKSWIIPGDNSSGSYS-----LQ
MiDCL2b ----MQ-----NVTIPTMKGFTIRTEPIFDPKSWIIPGDNSSGSYP-----LQ
SiDCL1 ---YPIPALKILLEALIAASCQHTTCYERAHLLGDAYIKWVVSRYLFLKYPQKHHEGQLTRMRQOMYSNMLVYQYALNGLIQSYIQADREAPSRWAAPGVLPVYDEDLNEDETSIFDHEAENGTVAAKALA
MiDCL1 ---YPIPALSKILLEALIAASCQHTTCYERAHLLGDAYIKWVVSRYLFLKYPQKHHEGQLTRMRQOMYSNMLVYQYALNGLIQSYIQADREAPSRWAAPGVLPVYDEDLNEDETSIFDHEAENGTVAAKALA
AtDCL1 ---YPIPTSKILLEALIAASCQHTTCYERAHLLGDAYIKWVVSRYLFLKYPQKHHEGQLTRMRQOMYSNMLVYQYALNGLIQSYIQADREAPSRWAAPGVLPVYDEDLNEDETSIFDHEAENGTVAAKALA
AtDCL3 -DNFSLISTSLLEAVITLTCPESESMRLELHSLGDSVLKYAISCHEFLKYPDKDEGQLSGRRQVSLCNSTLHKFGTDRLKQGYIRDSAFDARRWAAPGQLSVFPVPCCEGVDTL-----VP----LD
MiDCL3 -SSLHPISSSLLEALITLRCCEKESMRLELHSLGDSVLKYAISCHEFLKYPDKDEGQLSGRRQVSLCNSTLHKFGTDRLKQGYIRDSAFDARRWAAPGQLSVFPVPCCEGVDTL-----VP----LE
SiDCL3 -GDLHPISSSLLEALITLRCNESESMRLELHSLGDSVLKYAVSCYLFLKYPKKHEGQLTNERSQLSNLHKLGTNHLKQGYIRDSAFDARRWAAPGQLSVLPVPCCEHGVETSQ-----VP----LD

RIBOc

1,700 1,710 1,720 1,730 1,740 1,750 1,760 1,770 1,780 1,790 1,800 1,810 1,820

AtDCL4 RDLGIL--ESNTGEIRCSKGHHWYKKTITADVVEALVGAFLVDSGFKCAVFLKWLIGVNVDFESLD--VQDACIASRRYLPLTTRNNLETEENQLDYKFLHKGLLVQAFIHPSSYNRH-GGGCYCRLEFLC
MiDCL4 KFRAAD--DANSAEIRCSKGHHWHKKTITADVVEALVGAFLVDSGFKCAVFLKWLIGVNVDFESLD--VTNACLASRSYLSLTHAMDLAALNFIQGYFLHKGLLVQAFIHPSSYNRH-GGGCYCRLEFLC
SiDCL4 --GSGT--DGIKTEVRCISKYHHWRKKTITADVVEALVGAFLVDSGFKCAVFLKWLIGVNVDFESLD--LKSICSAKSVFMPPLADEIDVLGLIRLLGYSFIHKGLLVQAFIHPSSYNRH-GGGCYCRLEFLC
SiDCL2d EELL-----TSSVKMYSRGKQKIKSKIMADVVEALIGAYLSSGGEVAALSFMKWLGVDINFDVAP--TSRH-----LPMNAEKLNNVRYLSLHYKFNDPSSLVEALTHGSCMLPDIIPRCYCRLEFLC
SiDCL2c EELM-----TSSDKMYSRIKQKIRSKRVADVVEALIGAYLSSGGEVAALSMKWLGMDIDFADAP--IQRH-----FPLNAEKLNNVRYLSLHYKFNDPSSLVEALTHGSCMLPDIIPRCYCRLEFLC
SiDCL2a EEFLL-----TSSDKMYSRGKQKFRSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDINFDVAP--LPRN-----FPMNAEKLNNVRYLSLHYKFNDPSSLVEALTHGSCMLPDIIPRCYCRLEFLC
SiDCL2b EVLL-----TSSDKMYSRGKQKIRSKRVADVVEALIGAYLSSGGEVAALSFMKWLGVDINFDVAP--MSRH-----FPMNAEKLNNVRYLSLHYKFNDPSSLVEALTHGSCMLPDIIPRCYCRLEFLC
AtDCL2 NDTL-----PESRNIYVASRIRNKRKISVADVVEALIGAYLSSGGEVAALSMKWLGVDINFDVAP--IQRD-----SPIQAEKLNNVRYLSLHYKFNDPSSLVEALTHGSCMLPDIIPRCYCRLEFLC
MiDCL2a EELL-----SDKRKIYVSGKRTWKGTITADAVEALIGAFIISTAGESAGILFLSRIGIDVDVFNIP--YQRH-----FOIRAEKLNNRAHLSLNNYKFNHSSSLVEALTHGSCMLPDIIPRCYCRLEFLC
MiDCL2b EELL-----SDTRKIYVSGKRTWKGTITADAVEALIGAFIISTAGESAGILFLNRIGIDVDVFNIP--YQRH-----FOIRAEKLNNRAHLSLNNYKFNHSSSLVEALTHGSCMLPDIIPRCYCRLEFLC
SiDCL1 GDEFDEETEEGELDNDSSGYRVLSSKTMADVVEALIGVYVVEGGKYAANHFMKWLGVEVDVDFNF--KETEYSIRCSIPENVLKSVEFDALQGALNIFSHNDKGLLEALTHASRPS-SGVSCYCRLEFLC
MiDCL1 HDDYDEEEMEDGELEGDSSYRVLSKTIADVVEALIGVYVVEGGKYAANHLSWIGIQVEVDPE--MIDCPIRPSYLPESILKSDVEALGALNIFKIDRSLLVEALTHASRPS-SGVSCYCRLEFLC
AtDCL1 SDVFDGEDMEGELGDLSSYRVLSKTIADVVEALIGVYVVEGGKYAANHLSWIGIQVEVDPE--EVDGTLKNNVNPESVLKSIDFVGLRALKYFKEKGLLEALTHASRPS-SGVSCYCRLEFLC
AtDCL3 PKFFTE-NMTIKIGKSCDMGHRWVSKSVSDCAEALIGAYVVGGLSASLHMKWLGIDVDVDFPNL--VVEAINRVSLRCYIPKEDLEIELRKLQHEFSAKFLLEALTHASRPS--SYSCYCRLEFLC
MiDCL3 GDFFTD-DTKVVVGKLCDKGHRWVSKTISDCVEALIGAYVVGGLVAAHLMKWLGIDANIEPSL--IIVEAITCASIRSYVPKTNELIKDINKVGYFHSVKFLLEALTHASVNE--FYCYCRLEFLC
SiDCL3 KKFLTE-DPKEVVGKHCDRGHRWVSKTISDCVEALIGAYVVGGLVAAHLMKWLGFKAELEPSL--VEDAINTASLYSYTPKAKDIEDLELKLAYKFSIKGLLEALTHATVQLEAGYSYCRLEFLC

RIBOc

Ribonuclease_3

1,830 1,840 1,850 1,860 1,870 1,880 1,890 1,900 1,910 1,920 1,930 1,940 1,950

AtDCL4 DAVLDYLMTSYFHTVFPKIKPGCLTDLRSLSVNNNEALANVAVSFSIKRFFCFESIYLHEVTEEDYTNFLASSPLASG--QS--EGPRCPKVLGDLVESLIGALFLDCGFNLNHWMTVMLSFIDPVKNLSN
MiDCL4 DAVLDYLMTSYFHTVFPKIKPGCLTDLRSLSVNNNEALANVAVDRSLNFI LFDSSGLSEAINNYVKFIETSPSSKK--FI--EGTKCPKALGDLVESLIGALFLDCGFNLSTWMTIMLSFFKPVLSNCGM
SiDCL4 DAVLDYLMTSYFHTVFPKIKPGCLTDLRSLSVNNNTAVVAVRQSFSEILCDSDLESITRYVNF IGRPDSTR--LG--EEPSCPKALGDLVESLIGALFLDCGFNLNRAWQILSFLKPVMSFTRIL
SiDCL2d DAVLDYVVTIHLHYFKYPGLTPGCLTDLRSASVNNNECVALSAVKAGLHKHILHSDLDLQVLQRHISTTVEDFDKLNLVSTFGWE--AETTYPKVLGDLVESLIGALFLDCGFNQDITFIQIRPLLEPLVTPQTL
SiDCL2c DAVLDYVVTIHLHYFKYPGLTPGCLTDLRSASVNNNECVAQCAIKASLHKHILHASPDQLRQICNTIEDFKN--PVSTFGWE--AETTYPKVLGDLVESLIGALFLDCGFNQDITFIQIRPLLEPLVTPQTL
SiDCL2a DAVLDYVVTIHLHYFKYPGLTPGCLTDLRSASVNNNECVAQSAVKAGLHKHILHASQDLRQICNTIEDFKN--PVSTFGWE--AETTYPKVLGDLVESLIGALFLDCGFNQDITFIQIRPLLEPLVTPQTL
SiDCL2b DAVLDYVVTIHLHYFKYPGLTPGCLTDLRSASVNNNECVAQSAVKAGLHKHILHASQDLRQICNTIEDFKN--PVSTFGWE--AETTYPKVLGDLVESLIGALFLDCGFNQDITFIQIRPLLEPLVTPQTL
AtDCL2 DAVLDYLITIKHYLDKYPCLSPGCLTDMRSASVNNNECVALSAVKANLHKHILHASHHLHKHISRTVSEFEQSSLSQSTFGWE--SDISFPKVLGDLVESLIGALFLDCGFNQDITFIQIRPLLEPLVTPQTL
MiDCL2a DAVLDYLITIKHYLNKYPGMCSCCLTDMRSASVNNNECVAQSSVKHGLHKHILHCSRRLHKOIHATVSEFEKSPSGSTFGWE--SESSFPMVLGDLVESLIGALFLDCGFNQDITFIQIRPLLEPLVTPQTL
MiDCL2b DAVLDYLITIKHYLNKYPGMCSPGCLTDLRSASVNNNECVAQSSVKHGLHKHILHCSNELSKQIFATVERFEKSPSGSTFGWE--SESSFPMVLGDLVESLIGALFLDCGFNQDITFIQIRPLLEPLVTPQTL
SiDCL1 DAVLDHLITRHLHFTYTDLPPIGRCLTDLRAAAVNNNEARVAVKHKHILHVRHGSALERQIRDFVKEVQDEL SKPGENS FGLGDCKAPKVLGDLVESLIGALFLDCGRNTAVMWKVFRLPHPMVTPETIL
MiDCL1 DAVLDHLITRHLHFTYTDLPPIGRCLTDLRAAAVNNNEARVAVKHKHILHVRHGSALERQIRDFVKEVQDEL SKPGENS FGLGDCKAPKVLGDLVESLIGALFLDCGRNTAVMWKVFRLPHPMVTPETIL
AtDCL1 DAVLDHLITRHLHFTYTDLPPIGRCLTDLRAAAVNNNEARVAVKHKHILHVRHGSALERQIRDFVKEVQDEL SKPGENS FGLGDCKAPKVLGDLVESLIGALFLDCGRNTAVMWKVFRLPHPMVTPETIL
AtDCL3 DSVLDLITRHLHFTYTDLPPIGRCLTDLRSASVNNNEARVAVKNNHILHVRQCATVLETOINDYIMSFQKPD-----TGRSIPSIQCPKALGDLVESLIGALFLDCSKLNLDEMVKIFKPLLEPLVTPQTL
MiDCL3 DAVLDLITIKHYLYQSRDIDPCECLTDLRSASVNNNEARVAVRNNLHKHILHQSSTLILSQITEYVKSFPPELSD-----TISSGPTTKAPKALGDLVESLIGALFLDCSKLNLDEMVKIFKPLLEPLVTPQTL
SiDCL3 DSVLDLITVITYLYQKFKDIDPCECLTDLRSASVNNNEARVAVRNNLHKHILHQSSTLILSQITEYVKSFPPELSD-----TISSGPTTKAPKALGDLVESLIGALFLDCSKLNLDEMVKIFKPLLEPLVTPQTL

Ribonuclease_3

AtDCL4
MiDCL4
SIDCL4
SIDCL2d
SIDCL2c
SIDCL2a
SIDCL2b
AtDCL2
MiDCL2a
MiDCL2b
SIDCL1
MiDCL1
AtDCL1
AtDCL3
MiDCL3
SIDCL3

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      2,090      2,100      2,110      2,120      2,130      2,140      2,150      2,160      2,170      2,180      2,190      2,200      2,210
-----NSER-----SSSYVIRR-----GLPQAPSK-T-----EDRL-----PQKAI I KAGGPSKKT-----AKSLIHEITAVANCWK PPH ECCEEE
-----NVDSDIFSDSDMSDNSSPAITQV---NRWSSLASKE-----VRRQPSSETV-----SDPN-----GDNE SPASGGPA NK S-----ARSHIHEITAVANCWK PPFYECCEEE
-----ETSESDCHLKVPVNEEL---ARSCNFKSKST-----RKLLSTEASVQCNSDQT I-----MSGNG-----SKEDAKATGGSKTES-----AKSR IHEITAVANCWK PPLFECCKET

DLELR TADSSFWDDR AKAQETLQALTDVKDRINLLTEFKTKVDDAVTIVNLTEEMDSIDAGLLEEAAGIIEELSKALDRFELTQLLSGPYDKEGAVISITA---GAGC---TDAQDWADMLLRMYVRW
DLELKTADSSFWDDR AKAQEILQALTDVKDRINLLTEFKTKVEDAVTIVNLTEEMDSIDAGLLEEA AVI IKELSKALDRFELTQLLSGPYDKEGSMNL FAMQHMAGAGAPLPLISLTQDWADMLLRMYVRW
-----AD-----DTKKKKKN---GNP SFTTRQTINDICLRKNWPMPL YRCVHEG
-----GDE-----NGKKKKKN---GNQTFTRQTINDICLRKNWPMPL FYRCVSEG
-----E--D-----QGEN-----ENGKKKN---GHQPFTRQTINDICLRKNWPMPL SYRCVKEG
-----S-----DRET-----L-----TSETTE-----IQSIVIPF IGPI N---MKKGGPRTIHEFCKKHLWPMPLTDTSEEK
-----Q-----TSDEYLPEQAAC-----KKLKGSE-----IQNPVCDSSKKAC-----SSTNATPIIAP I N---MKKGGPRTSIFQLCKTMLWPMPLTDTTEHK
-----M---ASRKKRKKVYLN N-----KTDE-----AQSVPSDCSTSSS-----YSNKDTQVIGPI N---MTRGGPRI SIFELCKKLQWPMPLSHESTERT
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DSRM_DCL_plant

AtDCL4
MiDCL4
SIDCL4
SIDCL2d
SIDCL2c
SIDCL2a
SIDCL2b
AtDCL2
MiDCL2a
MiDCL2b
SIDCL1
MiDCL1
AtDCL1
AtDCL3
MiDCL3
SIDCL3

```

      2,220      2,230      2,240      2,250      2,260      2,270      2,280      2,290      2,300      2,310      2,320      2,330      2,340
GP-----GHLKKS-----FVYKVIIEVEDAPNMTLCYGHARVTKKGA-----HHAQAALWCKKHSGLFC
GP-----SHLKKS-----FTYKVIIEIEGAPDIVLCFGAPQTKKAAA-----HYAAEGAYWYCKEGYWT
GP-----SHLKKE-----FTFRVLYEIEETSR-VIISYGHAAQAKKKDAA-----HHAAGALLWFKKEGYLL-----DN

GE-----K--QR-----YKTRV-----VEKSPGHEAGIKSATVEVEGRYAYGYLSGEKGTHRIVROSPFNAKGL-----RQTSFSGVEVMPLLRREESLDVEI
GE-----K--QR-----YKTRV-----VEKSPGHEAGIKSATVEVEGRYAYGYLSGEKGTHWIVROSPFNAKEGTWLSNINHMLPRTGLNHTPSSFAFSSPMTSFSGVEVMPLIPEESLDVEI
GP-----AHAKR-----FTYCVRVNIISDKGF-TDICI GHPMP SVKKAK-----DSAAALLLEL LNRYS
GP-----AHAKR-----FTFAYRVNNTTDRGW-TDICI GHPMP SVKKAK-----DSAAVL LLEL LNKWYS
GP-----AHAKR-----FTFCVRVNTSDRGW-TDICI GHPMP SVKKAK-----DSAAVL LLEL LNKTF S
SRTPFEFIDGGEKRTSFSSFTSTITIRIPNRE--AVMYAGHARPDKKS SF-----DSAVVELLYELERKIV I I QK
SRTPMIFDEISCKREGFNSI SKITTHIPGSG--NICTGPRADKKS SF-----DSAAALLMINSFEREGK I I SDS
SKSLIECGEGSDKRKVYNTFASRTISLTIPDYG--LIELTGDERADKKS SL-----DSAA LHMLYELERQGI I AIGNQ
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DSRM_DCL_plant