



US012385057B2

(12) **United States Patent**
Kwok et al.(10) **Patent No.:** US 12,385,057 B2
(45) **Date of Patent:** Aug. 12, 2025(54) **MODULATING LIGHT RESPONSE PATHWAYS IN PLANTS, INCREASING LIGHT-RELATED TOLERANCES IN PLANTS, AND INCREASING BIOMASS IN PLANTS**(71) Applicant: **Ceres, Inc.**, Thousand Oaks, CA (US)(72) Inventors: **Shing Kwok**, Alexandria, VA (US); **Kenneth Bounds**, Tarzana, CA (US); **Ryan Miller**, Sacramento, CA (US); **Sam Harris**, Newbury Park, CA (US); **James Burns**, Valley Village, CA (US); **Roger L. Pennell**, Malibu, CA (US); **Vijay Sharma**, Wildwood, MO (US); **Michael F. Portereiko**, Thousand Oaks, CA (US); **Han-Suk Kim**, Pinole, CA (US); **Gerard Magpantay**, Woodland Hills, CA (US)(73) Assignee: **Ceres, Inc.**, Thousand Oaks, CA (US)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 36 days.

(21) Appl. No.: **18/470,831**(22) Filed: **Sep. 20, 2023**(65) **Prior Publication Data**

US 2024/0102039 A1 Mar. 28, 2024

Related U.S. Application Data

(60) Division of application No. 17/481,090, filed on Sep. 21, 2021, now Pat. No. 11,926,836, which is a division of application No. 16/045,503, filed on Jul. 25, 2018, now Pat. No. 11,174,491, which is a division of application No. 13/630,902, filed on Sep. 28, 2012, now abandoned, which is a continuation-in-part of application No. 12/863,102, filed as application No. PCT/US2009/031292 on Jan. 16, 2009, now abandoned, said application No. 13/630,902 is a continuation-in-part of application No. 12/373,134, filed as application No. PCT/US2007/073154 on Jul. 10, 2007, now abandoned, said application No. 13/630,902 is a continuation-in-part of application No. 12/513,086, filed as application No. PCT/US2007/083495 on Nov. 2, 2007, now abandoned, said application No. 13/630,902 is a continuation-in-part of application No. 12/515,687, filed as application No. PCT/US2007/085237 on Nov. 20, 2007, now abandoned, said application No. 13/630,902 is a continuation-in-part of application No. 12/307,561, filed as application No. PCT/US2007/072877 on Jul. 5, 2007, now Pat. No. 8,344,210, said application No. 13/630,902 is a continuation-in-part of application No. 13/119,572, filed as application No. PCT/US2009/057116 on Sep. 16, 2009, now abandoned.

(60) Provisional application No. 61/021,943, filed on Jan. 18, 2008, provisional application No. 60/819,763,

filed on Jul. 10, 2006, provisional application No. 60/856,613, filed on Nov. 3, 2006, provisional application No. 60/860,145, filed on Nov. 20, 2006, provisional application No. 60/818,569, filed on Jul. 5, 2006, provisional application No. 61/097,789, filed on Sep. 17, 2008.

(51) **Int. Cl.****C12N 15/82** (2006.01)
C07K 14/41 (2006.01)
C07K 14/415 (2006.01)(52) **U.S. Cl.**CPC **C12N 15/8271** (2013.01); **C07K 14/415** (2013.01); **C12N 15/82** (2013.01); **C12N 15/8261** (2013.01); **Y02A 40/146** (2018.01)(58) **Field of Classification Search**CPC C12N 15/8271
See application file for complete search history.

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ABSTRACT

Methods and materials for modulating low light and/or shade tolerance, and red light specific responses in plants are disclosed. For example, nucleic acids encoding low light and/or SD+EODFR-tolerance polypeptides are disclosed as well as methods for using such nucleic acids to transform plant cells. Also disclosed are plants having increased low light and/or SD+EODFR tolerance. In addition, methods and materials involved in increasing UV-B tolerance in plants and methods and materials involved in modulating biomass levels in plants are provided.

11 Claims, 79 Drawing Sheets**Specification includes a Sequence Listing.**

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Figure 1

SEQ-ID-NO-3	MSSEQNGNSN	PSTSPVECT	KTPFRRRLQI	RQRVFAPKL	MEA_RRSRVS	50
SEQ-ID-NO-49	MISPF	STTPNVTN	TDSRDTIRRK	KRNKTKHH	QQDOI QINP-	43
SEQ-ID-NO-32	MASPI	ISIN-SPT	DLYRKKRQS	ASSAASPRR	NNAASA[AGD	42
SEQ-ID-NO-53	MI SI GGSS	SSSSAAAGV	RMGGAKRRGK	P-----	-CCAAPGAA	38
SEQ-ID-NO-55	MAPS	SI I AS-AAAID	FDRKRKRA-	-----	-GEACTEAD	32
SEQ-ID-NO-57	MAST	SSSTPAAEVE	FRCKRKRA-	-----	-AGAAPTQPS	32
SEQ-ID-NO-60	MASPI	SBSA-AAVE	ERGNSEERKRA	R-----	-GATGESEGS	32
SEQ-ID-NO-7	MASF	TPMLE-PAFD	TSLDFKPKP	R TLQT PSSC	PPNORI QRI K	43
SEQ-ID-NO-25	MVES	LF---PSI E	NTCESSRRKK	PRI SETAEAE	I EARRVNEES	40
SEQ-ID-NO-22	MASN	QSNCDVSSQ	EPNQORKKRR	KLTHETTESH	LQNDGTGETK	44
SEQ-ID-NO-36	MASF	DPMVDSNSD	TLRESNHKKR	R-----	I CDHAAADON	36
SEQ-ID-NO-3	SEEAPVRHLS	RWRWATTAAQK	VYSLKLYDAL	QRSR-----	-----	81
SEQ-ID-NO-49		KWKSQEFOO	YSTKLQAI	TRVNSSSTPR	-----	72
SEQ-ID-NO-32	GESHA	RWRSEKQQR	NSAKLVQAL	QOVRESSAA	ET--PSPTAK	84
SEQ-ID-NO-53	GT POT	RWRSGTQER	YGRRLLDAL	RATRSGAASS	AQ----PP--	76
SEQ-ID-NO-55	AERAP	KWTRRREHE	YSTRLLDAL	RLVRAGACVA	PS----PS--	70
SEQ-ID-NO-57	EMWTRRREHE	YSSRLLEAT	RLVRACPSA	AAAKAAPT--	69	
SEQ-ID-NO-60	EAQPS	KWTRRRAHE	YSSKLLDAI	RLVRSGGPSS	SA--EAPP--	72
SEQ-ID-NO-7	-----	RWRTQRDQH	YSSKLFQAL	RRSHRTS-	-----	69
SEQ-ID-NO-25	-----	RWKTNRVQO	YACKLVEAL	RRVRORSSI	SNNET DKLVS	81
SEQ-ID-NO-22	NOPTV	RWRTDTARR	YSSKLLEAL	RRSCRTTSRH	GE-----	80
SEQ-ID-NO-36	SAAAS	PWRSCLEEQR	YSPRLVEAL	RRTASSAAKP	R-----	71
SEQ-ID-NO-3	RSATVRDTA	DKMLATARG	AFRWSRAILV	S-RFGTSLRR	RRNTKPSAII	132
SEQ-ID-NO-49	RGKAVREAA	DRALAVTARG	RTRWSR[LM	T-RLK[KFRK	KKPNPVTALP	120
SEQ-ID-NO-32	KRGKAVREAA	DRALAVSARG	RT[NSRAI LA	N-R[KLFRK	QKRPPAAIP	133
SEQ-ID-NO-53	OPRAVKAAA	DSALALTARG	QSRWSRAI LL	A-[GAASCR	RRVLVKGCK	122
SEQ-ID-NO-55	PARQVREAA	DRALAVAARG	RSRWSRAI LA	S-[RRAHRVHR	VRLHAPAPAP	118
SEQ-ID-NO-57	RSRAVREAA	DRALAVAARG	RT[HWSRAI LA	S-HRRPLQAAH	RARLRAPASP	118
SEQ-ID-NO-60	RSRAVRESA	DRAI AVSARG	RTRWSRAI LA	S-HRRRIQAA[R	RARLFEATISP	121
SEQ-ID-NO-7	ASREVHETA	DRMLAVLAKG	TTRWSRAI LT	A-R---KVTK	HKKAKLPTNN	114
SEQ-ID-NO-25	CAARFVRDTA	DRMLAASARG	TTRWSRAI LA	S-RVRAKIKK	HRKAKKSTGN	130
SEQ-ID-NO-22	KREVRETA	DRMLAVVARG	KTRWSRAI LA	K-RARLLRVK	KVKKORVIA---	126
SEQ-ID-NO-36	AGOVRETA	DRMLAATARG	RTRWSRAI LS	RWRKLRI OHK	KAKKKEASS	120

Figure 1 (continued)

SEQ-ID-NO-3	-----	--AAAI RQSG CSGRN--RKR	SAVGN-----	RVRVL GGL	161
SEQ-ID-NO-49	-----	--STRSKKSR VNVFRLLKGKV VPSMQR-----	KVRFI GGL	152	
SEQ-ID-NO-32	AVI TTGSSSS	SNSGRWKKRR VTVVKLNKKS I PTVNR-----	KVRLV GRL	177	
SEQ-ID-NO-53	-----	--I RRHRRPP ARAAAAASAG F PPLLKERKV KDRLRVL GRL	160		
SEQ-ID-NO-55	APA -----	--LTTPRASPQ AGSSCSTSQAQ AQTLAR-----	KANIT GRL	153	
SEQ-ID-NO-57	-----	--PPRHGA SAAKG---TAA LPEVAR-----	KAMVL GRL	146	
SEQ-ID-NO-60	-----	--PSRHPS SSSCR---GPX APALAR-----	KAVVL GRL	149	
SEQ-ID-NO-7	-----	--FLRKPD I YRER---RK TPAVER-----	KLKVL GRL	141	
SEQ-ID-NO-25	-----	--CKSRKGQ TETNR---IK LPAVER-----	KLKI LGRL	158	
SEQ-ID-NO-22	-----	--DRKSP GSEKR---RK LPEMEK-----	KVKVL SRL	153	
SEQ-ID-NO-36	-----	--NCLKRTTRI GNGER---RNR LPAVOK-----	KARVL SRL	150	

SEQ-ID-NO-3	VPGCRRTALP	ELLDETADYI	A ALEMQVRAM	TAISKILSEL Q-----PST	205
SEQ-ID-NO-49	VPGCKKEPLP	VI LEEAIDYI	P ALEMQVRAM	SALFNLLSAS T-----SGA	196
SEQ-ID-NO-32	VPGCKKESVP	VI EEAATDYI	QAI FMQVRAM	KSLAEILLS-----GSN	218
SEQ-ID-NO-53	VPGCRKLDAP	DLEELTADYV	A ALEMQVRAM	RALADALAAA QLSSPPPPPAA	210
SEQ-ID-NO-55	VPGCRKLPPP	ALLSEASDYL	AAI FMQVRAM	A LAQALASAV A-----	194
SEQ-ID-NO-57	VPGCRKLSFP	ILLEAEIJIDYI	AAALOMQVRAM	T ALAEALSAV SSSSGAGSS	196
SEQ-ID-NO-60	VPGCRKLPPP	ALLAEASDYL	A ALEMQVRAM	T ALAEVLSTV SGSGSASSSG	199
SEQ-ID-NO-7	VPGCRKLSFS	NLI EEFISDYI	AAALEMQVRAM	TAIEFLLCGG TGGGPQPPAD	191
SEQ-ID-NO-25	VPGCRKVSVP	NLLDEATDYI	AAALEMQVRAM	E ALAEELLTA A A-----PRT	202
SEQ-ID-NO-22	VPGCRKVSFV	NLLLEEASDYL	AAALEMQVI KV M	TNLSEI LTVA GG-----GGG	198
SEQ-ID-NO-36	VPGCRKVSFP	NLLLEEATDYI	SALEMQVRAM	T ALAELLAVALA A-----PAS	194

SEQ-ID-NO-3	NLG SAL -----	211
SEQ-ID-NO-49	GVSSG -----	201
SEQ-ID-NO-32	SAPPPI -----	224
SEQ-ID-NO-53	ACDDEAEMER	220
SEQ-ID-NO-55	--PPP -----	197
SEQ-ID-NO-57	PSSSPA -----	202
SEQ-ID-NO-60	CSSSSPA -----	205
SEQ-ID-NO-7	RLPSINV -----	197
SEQ-ID-NO-25	TLTGT -----	207
SEQ-ID-NO-22	GGGSS -----	204
SEQ-ID-NO-36	LAGTLS ---	201

Figure 2

SEQ-ID-NO-93	MGKYMKKSKV	TN	-----ND	TEPTEP-----	--TSLGVRT R	28
SEQ-ID-NO-70	MGKYI RKSKI	DGAGAGAGGG	GGGGGGGESS	[A]LMDVVS[PS	SS[SLGV[TR	50
SEQ-ID-NO-80	----MRKA[KI	TN	-----D	LT[VVDL	--SCGVRT R	22
SEQ-ID-NO-99	MGKYI RKTRK	TE	-----D	M-----	--SPLCV[TR	22
SEQ-ID-NO-72	MGKYI RKAKI	AG	-----E	VAVMEL-----	SQASLGVRT R	29
SEQ-ID-NO-105	MGKYMRKPKV	SG	-----E	VAVMEV-----	AAAPLGVRT R	29
SEQ-ID-NO-119	MGKYMRKGKV	SG	-----E	VAVMEV-----	GGALLGVRT R	29
SEQ-ID-NO-115	MGKYMRKGKV	SG	-----E	VAVMEV-----P	GGALLGVRT R	30
SEQ-ID-NO-103	MGKYMRKGKV	SG	-----E	VAVMEV-----P	GGALLCVRT R	30
SEQ-ID-NO-109	MGKYMRKGKV	SG	-----E	VAVMEV-----P	GGALLGVRT R	30
SEQ-ID-NO-96	MAQVKARAF	AL	-----	-----A	MAASASSRKR	23
SEQ-D-NO-101	-----MEV	SD	-----D	V[DVP-----	TTTTK	17
SEQ-D-NO-102	-----MRKCKG	IE	-----E	V[MEV]-----SD	VDE[VPTTK	27
SEQ-D-NO-93	A[KTALK	RN	SSASDSALAC	DSS-----	-----	52
SEQ-D-NO-70	A[KSLALQQ	QQRCLLOKPS	SPSSSLPPTSA	SPNPPSKQKM	KKKQQQMND	99
SEQ-ID-NO-80	-AKTLALKKQ	QA-----LRLH	ASSASPPPPS	SPA-----	-----	50
SEQ-ID-NO-99	-AK[A]L[N	-----G	-----C	DGG-----	-----	34
SEQ-ID-NO-72	-AKTLALQ	-----RQ	KSS[SSPPTV	VSAPATGDC	-----	58
SEQ-ID-NO-105	-ARA[ALAMQ	-----ROP	QGAAVAKDQG	-----	-----	49
SEQ-ID-NO-119	-SRTLALQ	-----R-T	TSSOKPPEKG	EGDPGAGAGA	GA-----	60
SEQ-ID-NO-115	-SRTLALQ	-----R	--AQRPPDKG	EAGEAAC	-----	53
SEQ-ID-NO-103	-SRTLALQ	-----R	--AQRPLDKG	DAEDAAA	-----	53
SEQ-ID-NO-109	-SRTLALQ	-----R	--AQRPI.DKG	DAFDAAA	-----	53
SEQ-ID-NO-96	-RK[SIN	-----N	-----	-----	-----	30
SEQ-ID-NO-101	-RK[RKISD	-----	-----	-----	-----	24
SEQ-ID-NO-102	-RK[RKISD	-----	-----	-----	-----	34

Figure 2 (continued)

SEQ-ID-NO-93	-CYLQLRSRR	LEKPM-----	-----	-----	ALTEF	KOPPR	76
SEQ-ID-NO-70	GSYLQLRSRR	LOKPPPI VVI	RST KRRKQQR	-----RNET	CGRNP	NPNSN	143
SEQ-ID-NO-80	-CYLQLRSRR	LEKPPPVP	LHHGSPRRQQ	ORLGQNNNK	LGQD	SPSP	99
SEQ-ID-NO-99	-SYLQLRSRR	MKPFTVLEC	RRQKNGV	-----PKNP	NLVN	FNPNO	74
SEQ-ID-NO-72	-SFLQLRSRR	LEKPP---LV	VHHHVSKRHK	QQQGSKKDS	CVQNP	PNPSY	104
SEQ-ID-NO-105	EYLELRSRK	LEKLP-----	-----	-----	-PPP	PAAR	70
SEQ-ID-NO-119	-EYLELRSRK	LEKPP-----	-----	-----	-PHT	PPAKEK	83
SEQ-ID-NO-115	-EYLELRSRK	LEKPP-----	-----	-----	KEQAA	APAPK	77
SEQ-ID-NO-103	-EYLELRSRK	LEKPH-----	-----	-----	KDP	LPPPSAPATK	80
SEQ-ID-NO-109	-EYLELRSRK	LEKPH-----	-----	-----	KEHPP	PPAPA	77
SEQ-ID-NO-96	-NFVQIKSL	SATIVP-----	-----	-----	ATGE	RI SGESPASC	58
SEQ-ID-NO-101	-GDVKL	S-----	-----	-----	-----	PALLR	36
SEQ-ID-NO-102	-GDVKLMS	-----	-----	-----	-----	PPILLR	46
SEQ-ID-NO-93	I KESASKGRV	NSGS GSVRVD	CDDW-----	-----	-----	F GKS DA	106
SEQ-ID-NO-70	LDS RGDGSR	S DSVSESVVF	DKDK-----DLI	S-----	-----	EI NKDP	177
SEQ-ID-NO-80	LKPSSRVDKD	S GS QEREREGG	ESKEVEENN	N S-----	-----	NSKOLG	136
SEQ-ID-NO-99	I PN VCNSEE	GKVKEMENQ	K KE-----K	S-----	-----	CLGPED	106
SEQ-ID-NO-72	SRVRPCCCSN	SEKKKGEDI	V QEDNCNDNI	I NYSNLNNNHN	ESNDFFCGV	EA	154
SEQ-ID-NO-105	-----RR	AAAAERVEAE	A EAD-----	-----	-----	EV	88
SEQ-ID-NO-119	ETARRASAAA	AAA VRMPAAP	QAAE-----E	F-----	-----	EAEVEV	115
SEQ-ID-NO-115	----NGAATK	AAAAAASPAL	A EDE-----	-----	-----	VEV	100
SEQ-ID-NO-103	RGA GRKVATA	AAAAAAPHGL	A EDE-----	-----	-----	VEV	107
SEQ-ID-NO-109	TAT KRGAGRK	AMAAAQHVL	M EDE-----	-----	-----	VEV	104
SEQ-ID-NO-96	CSS GSVDDE	N P TKFSDE	V EST-----	-----	-----	RVTSTC	89
SEQ-ID-NO-101	CRSHTGVGDT	PAGNLVSPSG	SVNL-----	-----	-----	KENDDS	67
SEQ-ID-NO-102	CRSHSGVGDT	PAGS VSPSS	SVNL-----	-----	-----	NDAS	74

Figure 2 (continued)

SEQ-ID-NO-93	F G E N S P D F -	- - - - - E S R Q S	T R E S T P C N F T	E D L E T T M T P G	S S T K I S M R - - -	147
SEQ-ID-NO-70	F F G Q N F F D I F	F F H T Q S F N R T	T R E S T P C S L I	R R P E I M T T P G	S S T K L N I C V S	227
SEQ-ID-NO-80	S F G D N V L D I -	- E - - - S R D R S	T R E S T P C N L I T	R G I F E D T R T P G	S T T K P A S - - -	178
SEQ-ID-NO-99	S F G E N L L E F -	- E - - - G R K R T I	T R E S T P C S L I T	R D S D N I Q T P G	S S T R R T N - - -	148
SEQ-ID-NO-72	S F G E N I L D M -	- E - - - A R E R G	T R E S T P C S L I I	R D S E S I R T P G	S A T R P T N - - -	196
SEQ-ID-NO-105	S F G E N V L E S -	- E - - - A M G R G	T R E T T P C S L I I	R D S G T I S T P G	S T T R P S H - - -	130
SEQ-ID-NO-119	S F G D N V I D L D -	G D - - - A M E R S	T R E T T P C S L I I	R S S E M I S T P G	S T T K T N T - - -	159
SEQ-ID-NO-115	S F G E N V L D F -	- D - - - S M E R N	T R E T T P C S L I I	R N S E M I S T P G	S T T K S K I - S S	144
SEQ-ID-NO-103	S F C F N V I L D F -	- D - - - A M E R S	T R E T T P C S L I I	R N P E M I S T P G	S T T K S K I - S N	151
SEQ-ID-NO-109	S F G D N V L D L -	- D - - - T M E R S	T R E T T P C S L I I	R N P E M I S T P G	S T T K S K T S S N	149
SEQ-ID-NO-96	D O G E - - - - -	Q Q Q Q I	R R E E I S L T S E L	R - - - - - I T N S	S S P E V D S A E E	123
SEQ-ID-NO-101	N L D H D L A S C -	- - - - - C S R N G	S T E - - - - -	E N N V V A S A E S	K E A K L S S - - -	101
SEQ-ID-NO-102	N L D H D L A S Y -	- - - - - C L R N C	S S E - - - - -	E N S V V A S A E S	K E A K L S S - - -	108
SEQ-ID-NO-93	--T A F R D C - I	R D R D S S V P S T	S E L E E X F A Y A	E Q Q Q R L F M D	K Y N F D I V N D M	194
SEQ-ID-NO-70	E S N O R E D S - L	S R S H R R R P T T I	F E M D E F F S G A	E E E Q Q K Q F I E	K Y N F D P V N E O	276
SEQ-ID-NO-80	P T E S S R R I - Q	N S M Q R R I P T T I	F E M D E F F G P A	E E E Q L R Q F I E	K Y N F D P V S D K	227
SEQ-ID-NO-99	A N E A N G R V - P	N S I O P T I P T D	L E M E E F F T R A	E K E Q Q R K F I E	K Y N F D P V N E K	197
SEQ-ID-NO-72	S A D T N D R V - Q	N S T Q R H T P T S	H E M D E F F S L T	E E D O Q R O F I E	K Y N F D P V K D K	245
SEQ-ID-NO-105	- S N S H R R V - Q	A P A R H I T P C S	A E M N E F F S A A	E Q P Q Q Q A F I D	K Y N F D P V N D C	178
SEQ-ID-NO-119	S I S S R R R M - E	T S V C R Y V P S S	L E M E E F F A A A	E Q Q Q I Q A F R C	R Y N F C P V N D C	208
SEQ-ID-NO-115	S M I S R R R M - E	S S V C R F I P N S	L E M E E F F A A A	E Q H E Q H T F R E	K Y N F C P V N D S	193
SEQ-ID-NO-103	S M I S R R R M - E	T S I C R F I P S S	H E M E E F F S A A	E K Q E Q Q S F R E	K Y N F C P V N D C	200
SEQ-ID-NO-109	S T I S R R R I E E	T P S C R F I P S S	L E M E E F F S A A	E Q Q E Q H S F R E	K Y N F C P V N D C	199
SEQ-ID-NO-96	O I T O T K S L - - -	- - - P P O K M P T E	L E L D E F F A A A	E K D I T K R F S D	K Y N Y D I V K G V	169
SEQ-ID-NO-101	--- E R E R T ---	--- - - - P E K M P S F	K E I F D F F A V R	Q K A I F K R F R E	K Y N F D F E K E E	143
SEQ-ID-NO-102	--- E R Q R I ---	--- - - - P E K M P S E	K E I E F F A A R	Q K A I L K R F R K	K Y N F D F E K E E	150

Figure 2 (continued)

SEQ-ID-NO-93	PLTGRYEWVK	MSP	207
SEQ-ID-NO-70	PLPGRFFWTIK	VDD	289
SEQ-ID-NO-80	PLFGRYEWEEK	LDP	240
SEQ-ID-NO-99	PLFCRYEWVK	VNH	210
SEQ-ID-NO-72	PLPGRYQWEIK	MDP	258
SEQ-ID-NO-105	PLPCRYEWVK	LDL	190
SEQ-ID-NO-119	PLPGRYEWTRR	LDC	221
SEQ-ID-NO-115	PLPGRYEWTR	LGC	206
SEQ-ID-NO-103	PLPGRYEWA	LDC	213
SEQ-ID-NO-109	PLPGRYEWA	LDC	212
SEQ-ID-NC-96	SLEGRYEWVK	--	180
SEQ-ID-NO-101	PSEGRYEWVR	GS	156
SEQ-ID-NO-102	PLEGRYEWVR	GS	163

Figure 3

SEQ-ID-NO-129	S1ESSSKSNP	FQASSS1RNI	S---TDLRLG	LSFGTISS---	44	
SEQ-ID-NO-247	MS PPLELDYI GL	SAAAGGRPD D	DLKGTEELRLG	LPI-GCESPDR	41	
SEQ-ID-NO-302	---MSTDTGR	SSTESEVSDL	DYEETEELKLG	LPI-GCSRTAG	36	
SEQ-ID-NO-270	MDGGVG	YA-----DMD	AIKAIELRLG	LPI-GSHPPEK	30	
SEQ-ID-NO-236	MERTAT	YC-----KD	NLKATEELRLG	LPI-GI DEPEK	30	
SEQ-ID-NO-137	MV	FE-----KD	NLDATELRLG	LPI-AISKESL	26	
SEQ-ID-NO-300	ME	FE-----RD	NLDATELRLG	LPI-GTATRQS	26	
SEQ-ID-NO-303	ME	FE-----RD	NLFATELRLG	LPI-GTATQQL	26	
SEQ-ID-NO-133	MECSVG	YD-----ND	NLRATELRLG	LPI-GTEPVSI	30	
SEQ-ID-NO-209	ME NSL GK	YG-----KL	NLEATELRLG	LPI-GSDEPEK	31	
SEQ-ID-NO-201	MEK	-----DGL	ELEI TELRLG	LPI-GRDVTEK	25	
SEQ-ID-NO-231	MAR	-----FCL	GLEI TELRLG	LSCGEPK---	23	
SEQ-ID-NO-234	MEK	-----EDL	GLEI TELRLG	LPI-GAGGENN	25	
SEQ-ID-NO-129	RPAATTLE	LLPAKGA[KRG	FSDDEVVPPAP	I SAAGKGKEA	GTOYFNGGY	53
SEQ-ID-NO-247	S	-----ETEKKRIG	FAETVDSLGL	AESRSGDLGD	SGDEKDK[KVA	91
SEQ-ID-NO-302	PLPTTTT	---APTKRS	LDEDRAA-----	RSTICDFGSQA	RSTICDFGSQA	74
SEQ-ID-NO-270	QSSASTSA	---KYISKKRT	SSEMD-----	-----RREI SEGGR	61	
SEQ-ID-NO-236	-----RIISNKRA	LPDMNDDS-----	-----NSISGKENE	-----NSISGKENE	60	
SEQ-D-NO-137	EKOTPNNSL	---AKSNKRS	LPDMNEDPAG	SSRENNSTVS	-----OVAAKKCD	50
SEQ-D-NO-300	EKOTPSSNV	---TKSNKRS	LPDMNEDSAC	RSESSSV---	-SNEEKSHDQ	71
SEQ-D-NO-303	-----VRSNKRS	LQQVADDDCG	VN-----	-----SSNDKKSDE	68	
SEQ-D-NO-133	RSA	-----VRSNKRS	SPEASEEECI	SKGNMNSSD-	-----GCRSDDÖNL	58
SEQ-D-NO-209	M	-----MKKRG	FTEM MTSSG	SHSEQCESSV	-----GSDITSDQ	69
SEQ-D-NO-201	-----KNEKKRM	FSEIDG-----	-----VSSGVVDVEKV	-----GMEENGSG	61	
SEQ-D-NO-231	TDKDK	-----NKNKKRV	FSDE-----	-----GENSSSEE[D	45	
SEQ-ID-NO-234						51

Figure 3 (continued)

SEQ-ID-NO-129	GY[MAAPAVE]	DAE[MAAVER	E[EENECNSVG	S-----	-----FYYV	87
SEQ-ID-NO-247	APFQPAAKAO	VVGWPPVRSY	RKNIMATTIN	QLKSSKEDSD	TKQQQFFLYV	141
SEQ-ID-NO-302	GKP[AVKAQ	VVGWPPVRSF	RKNIAKSCT-	-	-	104
SEQ-ID-NO-270	AT[TRATKAO	VI CWPPPI RSY	RKNSEQAMKA	T-AEAAG	-	100
SEQ-ID-NO-236	QDSAPAKAO	VVGWPPVRSY	RKNMLQIKKS	ESDNSSG	-	100
SEQ-ID-NO-137	QETAPPTKAO	VVGWPPPI RSY	RKNSLQTKKT	E-AETSG	-	89
SEQ-ID-NO-300	FTAPPPI KAO	VVGWPPPI RSY	RKNOLQAKKO	E-AEAAG	-	110
SEQ-ID-NO-303	QETAPPT[R	VVGWPPPI RSY	RKNOLQAKKL	E-AEAAG	-	107
SEQ-ID-NO-133	TAP-PPPKAO	VVGWPPPI RSY	RKNNIQTKKN	E-SEGGE	-	96
SEQ-ID-NO-209	DNVVPAPAKAO	VVGWPPVRSY	RKNSLQKKE	EQAEGAG	-	109
SEQ-ID-NO-201	NE[PAVK[TQ	VVGWPPVCSY	RRKNSCKIEVS	T-TKVGL	-	99
SEQ-ID-NO-231	DRKSVDDKNO	VVGWPPVCSY	RKKNNMNEGSK	-	-	78
SEQ-D-NO-234	GK---KETKNO	VVGWPPVCSY	GKKNFVNNEPK	-	-	82
SEQ-D-NO-129	KVNMEGMPI G	RKIIDLMSLNG	YRDLITRLDF	MF-NA-----	SI LWAEEEDM	131
SEQ-D-NO-247	KVSMGDGAPYL	RKVDLKITYKN	YKDMVVALGK	MF-GF-----	RT[GKDASEN	186
SEQ-D-NO-302	KVAVDGAPYL	RKWDLCMYGG	YQOFLITAI ED	MF-SCTVRN	CPN[ERRLVDP	153
SEQ-D-NO-270	KVSMGDGT[YL	RKI DLEVYKG	YRELREALED	MF-[KC-----	-	137
SEQ-D-NO-236	KVSMDDGTYL	RKI DLKVYNS	YPELLKALON	MF-[KC-----	TI [CVYTEREG	144
SEQ-D-NO-137	KVSMGDGAPYL	RKI DLKVYKG	YPEL[KALED	MF-[KF-----	KV[GKYSEREG	133
SEQ-D-NO-300	KVSMGDGAPYL	RKI DLKVYKG	YPELLKALEE	MF-[KS-----	KVGEYSEREG	154
SEQ-D-NO-303	KVSMGDGAPYL	RKI DLKVYKG	YPELL[EMEE	MF-[KF-----	KVGEPSEREG	151
SEQ-D-NO-133	KVSMGDGAPYL	RKI DLKI YSG	YPELLOAI CN	MF-[KF-----	TI GEYSEREG	140
SEQ-D-NO-209	KVSMGDGAPYL	RKI DLKVYKG	YPELL[KALEN	MF-[KC-----	TFGQYSEREG	153
SEQ-D-NO-201	KVSMGDGAPYL	RKMDLGSSQG	MDDLAFA[LDK	MF-[GF-----	II-[G]VALKD	142
SEQ-D-NO-231	KVSMGDGAPYL	RKI DLCLHKG	YLELALALEK	LF-[DC-----	C-GI EEAALKD	121
SEQ-D-NO-234	KVSMGDGAPFL	RKI DLAMHKG	YSDLAFALDK	FE-[GC-----	Y-GI CEALKD	125

Figure 3 (continued)

SEQ-ID-NO-129	CNEKSHVILTY	ADEKEGDWMMV	GDVPWEMFLS	TMRRLKISRA	NYHY-----	175
SEQ-ID-NO-247	RKDGFYVIMTY	EDKDCDWMLV	GDVPWEMFTE	ACRRI RVMKS	SDM-VGLGVT	235
SEQ-ID-NO-302	VNGTEYVPTY	EDKDCDWMLV	GDVPWKMFTA	SCKRLRLMKR	SEA-NLAPRT	203
SEQ-ID-NO-270	CKGSEYAITTY	EDKDCDWMLV	GDVPWEMFIIS	SCKKLRI I RG	AEAI RGLGSS	187
SEQ-ID-NO-236	YNGSDYAPT	EDKDCDWMLV	GDVPWDMILN	SCRRLRI MKG	SEA-KGLHAY	193
SEQ-ID-NO-137	YNGSEFVPTY	EDKDCDWMLA	GDVPWEMFI N	ACKRLRI VRG	SEA-RGLGCV	182
SEQ-ID-NO-300	YNGSEHVPTY	EDKDCDWMLV	GDVPWDMFI N	SCKRLRI MKE	SEA-RGLGCA	203
SEQ-ID-NO-303	YNGSEYVPTY	EDKDCDWMLV	GDVPWEMFI N	SCKRLRI MKE	SEA-RGLGCA	200
SEQ-ID-NO-133	YKGSDYAPT	EDKDCDWMLV	GDVPWEMFI T	SCKRLRI MKG	SEA-RGLGCG	189
SEQ-ID-NO-209	YNGSEYAPT	EDKDCDWMLV	GDVPWNMFVS	SCKRLRI MKG	SEA-KGLGCF	202
SEQ-ID-NO-201	GDNCEYVIIY	EDKDCDWMLA	GDVPWGMFI E	SCRVRRI MKR	SEX-TGFGQX	191
SEQ-ID-NO-231	AENQEHVPI Y	EDKDCDWMLV	GDVPWEMFIE	SCKRLRI MKR	SDA-KGFDLQ	170
SEQ-ID-NO-234	AENAEHVPI Y	EDKDCDWMLV	GDVPWEMFRE	SCKRLRI MKR	SDA-KGFDLQ	174

SEQ-ID-NO-129	-----	-----	175
SEQ-ID-NO-247	RAGVSKKNKN	-----	245
SEQ-ID-NO-302	POGSTRAR	-----	211
SEQ-ID-NO-270	Q	-----	188
SEQ-ID-NO-236	RL	-----	195
SEQ-ID-NO-137	V	-----	183
SEQ-ID-NO-300	V	-----	204
SEQ-ID-NO-303	V	-----	201
SEQ-ID-NO-133	V	-----	190
SEQ-ID-NO-209	PXCLDE	-----	202
SEQ-ID-NO-201	PKGSLKRFI	-----	179
SEQ-ID-NO-231	PKGSLKGFI	E GVRK	188
SEQ-ID-NO-234			

Figure 4

SEQ-ID-NO-319	M E A G S E -- C E	N N R I S N - - - - -	- - - - - P N K N I S S	S N E G N A K P K R	31	
SEQ-ID-NO-331	M D D G D G A A P A	E G S A A S T P P P	A P P A A A A A A A	A A V S A G S T G A	SG S G E K T V K R	50
SEQ-ID-NO-317	M					1
SEQ-ID-NO-321	M E E S S E V H F G	E N R V S P	- - - - -	- - - - -	E K N L K R	22
SEQ-ID-NO-327	M E E V T E L I Q S E	E N K L S M	- - - - -	- - - - -	E K N K K R	22
SEQ-ID-NO-330	M E E S S E L Q P E	E N K V S A	- - - - -	- - - - -	E K F P K R	22
SEQ-ID-NO-319	Q M K T P F Q I E A	L E K A Y A L E T Y	P S E A T R A E L S	E K L G L S D R Q L	Q M W F C H R R L K	81
SEQ-ID-NO-331	M M K S P M Q L E V	L E K I Y A V E Q Y	P S E T L R A E L S	A K I G L S D R Q L	Q M W F C H R R L K	100
SEQ-ID-NO-317	M	A	P T E E M K G K L A	E E V G L T E K Q V	S G W F C H R R L K	42
SEQ-ID-NO-321	V K T P A Q V M A	L E N F Y N E H K Y	P T E E M K S E L A	D Q I G L T E K Q I	S S W F C H R R L K	72
SEQ-ID-NO-327	R L K T P A Q L K A	L E D F Y N D N K Y	P T E E M K S E L A	D E L E L T E K Q I	S G W F C H R R L K	72
SEQ-ID-NO-330	K L K T P A Q L K G	L E K F Y T E H K Y	P T E E L K L A I A	E E L E L T E K Q V	S G W F C H R R L K	72
SEQ-ID-NO-319	F - - - - - K K D N	P T I K O R K G A A	L P P E S P V D E L	R A V P C P D Y G S	G S G S G S S P Y M	126
SEQ-ID-NO-331	D R K P P T K R Q R	R E E E A A V P L	M A P P P V L P P P	A L F D S S G F L L	I G A S S P Y D E P	150
SEQ-ID-NO-317	D K R H V	K E D G N A L G S O	D R S S V W L O D R	G S G L R O D S C G	S T K D D Y W N P	87
SEQ-ID-NO-321	D - - - - - K R - L	R D E V C T N G R Q	D R S S C I I Q D R	G S G L R O D S C G	S T K D D Y R N L	116
SEQ-ID-NO-327	D - - - - - K K M L	N D E V C A N G R Q	D R S S C V I Q D R	G S G L V Q D S C G	S T K H V H Y R Y L	117
SEQ-ID-NO-330	D - - - - - K R - L	K E E A N A N G R Q	D R S S C V I Q D R	G S G L G O D S C G	S S K H C D Y K Y L	117
SEQ-ID-NO-319	D I R K L G G S - - - - -	- - - - -	- - - - - S S R G M M E D A P	T M - - - - -	146	
SEQ-ID-NO-331	P L P P M H S R - - - - -	- - - - -	- - - - - R G A G R S S A V P	R L S A P D T G - -	176	
SEQ-ID-NO-317	K P R E V E S Q R L	Y - - - - -	- - - - - M G	N A D G I - E D S T S	S D R I S S S L R K N	119
SEQ-ID-NO-321	D P R E V E S Q R L	Y G R D F H P A D L	T Y D R T S R Y T G	N W T G I - I D N S	S G S S S S L Q D K	165
SEQ-ID-NO-327	D P K E V E S H G L	Y N H G F S A A D I	T Y G H K N H R Y A	E N D S A T O N T S	S E S S S S L Q D R	167
SEQ-ID-NO-330	D P K E V E S N G L	Y N R D L S V A D M	T Y G R R N H F S E	N V S C M D D D T S	S E S S S M L Q E R	167
SEQ-ID-NO-319	- - - - - R R Y Y E S Q	Q S I V - - - - -	- - - - -	- - - - - E	158	
SEQ-ID-NO-331	- - - - - R R Y Y E P L	P V M L P P P V A	S M O L - - - - -	M P S - - - - - E	201	
SEQ-ID-NO-317	L V I S S K D G I R D	V E S S R Y V A H K	D V I Q - - - H P O F	M R S Y G Y N K P S	C Y L K V K G E I E	167
SEQ-ID-NO-321	F M C Q R E D P Y D	A E T S K Y L A Q N	G A A M P L I P K G	T D S E F G Y - K P S	C Y L K V K G E I E	214
SEQ-ID-NO-327	E L C Q C Q D P Y D	M E P S E H V T P N	G S L L P P N T K C	A N N M C H - K P S	C Y L K V K G E I E	216
SEQ-ID-NO-330	M Y P Q Q Q D P Y E	M E P S R Y - - - S	K A L P P L N P K G	A J N M G Y - K P S	C Y L K V K G E I E	213

Figure 4 (continued)

SEQ-ID-NO-319	L R A T A Q V E A Q	E G E P L R D D G P	M L C I E F D P L P	P D A F C A	-----	194
SEQ-ID-NO-331	L R V I H S V E S Q	E G E P L R D D G P	M L C I E F D P L P	P G S F C A P I	-----	239
SEQ-ID-NO-317	N F A I T A V K R Q	G R O Y Q F D G P	P L G V E F D P L P	P G A F E P O T N P	I V H E P I Y V G N	217
SEQ-ID-NO-321	N A A I T A V K M Q	G R G H Y K C D G P	P L G V E F D P L P	P G A F A S P S R D	P V S C P I Y V G D	264
SEQ-ID-NO-327	H A A I T A V K K O	G C K H Y R E D G P	P L S V E F D P L P	P E A F E C Q L A D	L A N E A Y Y A A N	266
SEQ-ID-NO-330	H A A I T A V K K O	G R N Y Q E D G P	P L G V E F D P L P	P G A F E C Q T E E	A V H E P Y H I A D	263
SEQ-ID-NO-319	-----	-----	-----	-----	-----	194
SEQ-ID-NO-331	-----	-----	-----	-----	-----	239
SEQ-ID-NO-317	O R R P H L P H L	G T R K S F N P G P	-----	-----	-----	237
SEQ-ID-NO-321	L A Q M S P D V S	C V R K Q S S L G A	F E A Q V L L V H A	G N L Y I L Q L S I	T S N D V C H P M F	314
SEQ-ID-NO-327	P A L P N S P E V S	A N K K Q S S L S S	-----	-----	-----	286
SEQ-ID-NO-330	P A L L N S P E I S	T V K S R P C L S S	-----	-----	-----	283
SEQ-ID-NO-319	-----	-----	-----	-----	-----	194
SEQ-ID-NO-331	-----	-----	-----	-----	-----	239
SEQ-ID-NO-317	I T T V T F T L L L	L P I Y H Q S C T G	T T S N Y A H N M F	P S S F R Y V P K K	G S V R P E N V M E	237
SEQ-ID-NO-321	-----	-----	-----	-----	-----	364
SEQ-ID-NO-327	-----	-----	-----	-----	-----	286
SEQ-ID-NO-330	-----	-----	-----	-----	-----	283
SEQ-ID-NO-319	-----	-----	-----	-----	-----	194
SEQ-ID-NO-331	-----	-----	-----	-----	-----	239
SEQ-ID-NO-317	Q G I F L Y D S S D	S I P P S S I S C T	S N E S L Y I L A V	S Y E I A R K S K L	H S P D P D S E D D	257
SEQ-ID-NO-321	-----	-----	-----	R Y D - V Y S T K M	S S H D S Y I E G A	413
SEQ-ID-NO-327	-----	-----	-----	R Y D - S Y F T K I	S S Q D S I	300
SEQ-ID-NO-330	-----	-----	-----	R Y D - S Y Y T K H	G S Q D T H M E G V	302
SEQ-ID-NO-319	-----	-----	-----	-----	-----	194
SEQ-ID-NO-331	-----	-----	-----	-----	-----	239
SEQ-D-NO-317	E H D D D D N I M V	G M E P G I R D K K	S F G E P R L K S P	S T S F Y N S V P R	H K S F K E T F K C	307
SEQ-ID-NO-321	N C N P E -----	----- P S D S H D R	K S H H H L E Q K P	T Y N G S N S N A C	G N S A M D M P D D	455
SEQ-ID-NO-327	D F G S L H D V H V	----- Q D K Q D K K	A L H G T K H R Q T	F Q S N A G R F P G	R N S S L D L Y E D	305
SEQ-ID-NO-330	-----	-----	-----	-----	-----	349

Figure 4 (continued)

SEQ-ID-NO-319

SEQ-ID-NO-331

SEQ-ID-NO-317

SEQ-ID-NO-321

SEQ-ID-NO-327

SEQ-ID-NO-330

SPREI	PVTNS	KRKGW-I	SSKIS	WAEGOSRNHLV	ANVONLSGS-	NICTNDS---	194
LACE	T SAYVN	KRHYRMSSKH	GFEERRSDSL	STHLCPSGR-	RVNSEKTEAW	239	
SI	GEASAYNN	TKNCRKGTKH	GFDCTRYDSC	SNPSDHYEEN	NLVVNOTDSL	352	
SI	CEA-AYN	TKNHRKDAKR	GVEGIRSDS	SNHSDRYEE-	NLPVKHSDFL	504	

SEQ-ID-NO-319

SEQ-ID-NO-331

SEQ-ID-NO-317

SEQ-ID-NO-321

SEQ-ID-NO-327

SEQ-ID-NO-330

-HDYDNNSN	GGR	-	-	-	KTIGYL	T KSSKL LPPSR	194
LHDGNDNPK	I VQ	-	-	-	RNNNTS	KHPFLMRGS	239
LHGYENSNLK	NVQ	-	-	-	RGEYAK	SKPSNSVHK	380
QNYENTNOK	NVRSVHADI	-	-	-	LQYDYNVNP	KKAPRSEH K SKPISNSI HNS	532

SEQ-ID-NO-319

SEQ-ID-NO-331

SEQ-ID-NO-317

SEQ-ID-NO-321

SEQ-ID-NO-327

SEQ-ID-NO-330

SRSFESMD-R	G PSSGMA-G	I	MHCERNQMK	MOREK---L	HSTDEPPVAK	194
GKSLDTTEE-R	ARCTII MEKED	I	KLHCEM[KRMK	CSDPVRVKR	HPTDEITIVAK	239
QVYLDTGERR	GLNKRMAKEE	I	KFDGDRKIKK	QYRDOPDEV-R	VLTNEMTVAK	423
RGSVDTEE-R	G SSRMTKDC	I	UKGDRKSKK	QYRDAGGA-G	MLSNETMVAK	581

SEQ-ID-NO-319

SEQ-ID-NO-331

SEQ-ID-NO-317

SEQ-ID-NO-321

SEQ-ID-NO-327

SEQ-ID-NO-330

-	-	IPE	PHNRTG	-	-	-	203
-	-	VME	PK	-	-	-	244
RVKHGYIQQV	YAPKSSSSYSF	I	ERKS	-	-	-	449
RFRVDFPQQ-	EHVAKASESE	I	RRRINTLTKR	LNPENMATGI	AFTEVVGALD	630	
WAKVDPLEQ-	YDVKQSSVAE	I	LEPRKS	-	-	-	458
RKANTFQP-	YNMKQMPVAE	I	EPRKT	-	-	-	520

SEQ-ID-NO-319

SEQ-ID-NO-331

SEQ-ID-NO-317

SEQ-ID-NO-321

SEQ-ID-NO-327

SEQ-ID-NO-330

---QI NRSCV	E LPSSL SGDD	I	TDDESSSSMD	-	-	-	244
VPI DI GRSAM	E RPSFS-ED	I	TPETSSSAE	-	-	-	476
-----QRSAA	F MPSSFS-ED	I	ETAETSSSAD	-	-	-	659
-----QRSAA	E MPSSFS-ED	I	ETADTSSSLD	-	-	-	482
-----QRSAA	E MPSSFS-ED	I	ETADTSSSLD	-	-	-	544

Figure 5

SEQ-ID-NO-401	MGLSNFIPSAS	EGVLPVLVIN	TMLSVAVLKN	MERSMLQVVI-	GGSA[A]ANGS	49	
SEQ-ID-NO-370	MGISSMPAPK	ESLLIYLLYH	AVVSI AALAG	LLRAALVFLG	LPAPPSSL--	48	
SEQ-ID-NO-409	MGISSMPAPK	ESLLIYLLYH	AVVSI AALAG	LLRAALVFLG	LPAPPSSL--	48	
SEQ-ID-NO-349	MGISSMPAPK	DSVVAYLLYN	TAVSI AILAD	MVRALVFLG	LPVPPS---A	47	
SEQ-ID-NO-357	MGISSMP[PK]	DSLMGFLVLYN	TAVSVAI LAG	LVRALVFLG	LAAPS---P	46	
SEQ-ID-NO-337	MGLSSLPGPS	EGLMCLVILVN	TALSI SI VKG	VRSFLG[VG]	SISPSSSSSP	50	
SEQ-ID-NO-339	MGLSSLPGPS	EGLMCLVILVN	TALSI SI VKG	LRSVLCLIG	RISPPSSAAA	50	
SEQ-ID-NO-395	MGLSSLPAPS	EGVLCVLLVN	TALSI SI EKG	VRTLHHVG	HLSSSSTS	50	
SEQ-ID-NO-417	MGLSSLPAPS	EGVLCVLLVN	TALSI SI VKG	IRSLLHVG	HLPP---P	46	
SEQ-ID-NO-437	MGLSSLPAPS	EGVLCVLLVN	TALSI SI VKG	VRSLHHVG	RLSPSASLP	50	
SEQ-ID-NO-355	MGF[PV--GYP	EVSMVNLFLY	TLSLSFLRS	TTSFSLFH	SDL-----	42	
SEQ-ID-NO-393	MGF[PV--GYS	ELMPRIVLH	MALLGYVRR	FIFRAFDAYG	GDLDDADVP	48	
SEQ-ID-NO-401	N-----I[EHD	SSSSSMERRY	SI -----	TQYKS[CHSH	DICR-----T	82	
SEQ-ID-NO-370	-----AGEDA	DGDQLTAAT	PA -----	GPSSLA	ERFRSRFRPA	RFGR---RRG	87
SEQ-ID-NO-409	-----AGEDA	DGDQLTAAT	PA -----	GPSSLA	ERFRSRFRPA	RFGR-RRCAA	89
SEQ-ID-NO-349	WED--GDDOL	AATAAAAAAA	AAAACGPSSA	DRFRSRFRPA	RFCR-RRGCC	94	
SEQ-ID-NO-357	WEGLADEHH	HHRQVVSSTS	PL -----	GPSSLA	DRFRSRVRPS	RFGR---RRGG	91
SEQ-ID-NO-337	SSVTSSSENS	STSESFDRV	CQ-----	PESYL	EEFRNRTPTL	RFES-[C]RCK	96
SEQ-ID-NO-339	AA---ASSEN	OTSDFDFRM	CQ-----	PESYL	EEFRNRTPTV	KFES-LCKCK	93
SEQ-ID-NO-395	PSS---PDSL	TAPESFEFH	SP-----	SESYI	EEFRSRTPTL	RFDS-VCCCK	94
SEQ-ID-NO-417	S---SDYTE	NLESEFDHL	NT-----	SESYI	EEFRSRTPTI	HFGAVMCSCCK	89
SEQ-ID-NO-437	S---SDNAE	DTRSELEFRL	SP-----	PENYI	EEFRSRMPSI	RFNT-VCSCE	92
SEQ-ID-NO-355	-----UDTDF	STTLPDISHI	HR-----	PTLSAI	ITLROFLPII	TFND-LAEGD	83
SEQ-ID-NO-393	W---PENSG	HRNLDHQQL	WOPQSFSVSA	MLLREALPMV	RYEE-LGAAG	93	
SEQ-ID-NO-401	SMAMVECCVC	[C]RFEANQEV	SELP-CKHMF	HRGCLOKWFD	NKHT[C]PLCR	131	
SEQ-ID-NO-370	AAAVPDCRVC	LVRFEADAVV	NRLP-CGHLF	HRACLETWLD	MDHAT[C]PLCR	136	
SEQ-ID-NO-409	ASPTDCRVC	LVRFEADAVV	NRLP-CGHLF	HRACLETWLD	YDHA[C]PLCR	138	
SEQ-ID-NO-349	AC-AADCRCV	LARFEPESMV	NRLP-CGHLF	HRACLEKWL	YDHA[C]PLCR	142	
SEQ-ID-NO-357	ACACACDCRVC	LARFEPESMV	NRLP-CGHLF	HRACLETWLD	YDHA[C]PLCR	140	
SEQ-ID-NO-337	KOADNECSVC	LSKFODDSEI	NKLK-CGHLF	HKTCLEKWI	YWNJ[T]CPLCR	145	
SEQ-ID-NO-339	KOADNECSVC	LSKFODDSEI	NKLK-CGHLF	HKTCLEKWI	YWNJ[T]CPLCR	142	
SEQ-ID-NO-395	-OPEHDCSVC	LTOFEPESEI	NRLS-CGHLF	HKMCLEKWL	YWNJ[T]CPLCR	142	
SEQ-ID-NO-417	-RPOHDCQVC	LTOFEPKSEI	NRLS-CGHLF	HKMCLEKWL	YWNJ[T]CPLCR	137	
SEQ-ID-NO-437	-OPEHDCSVC	LTOFEPESEI	NSLS-CGHLF	HKMCLEKWL	YWNJ[T]CPLCR	140	
SEQ-ID-NO-355	SSPPVGCAVC	LNFAGEEEFI	RCMANCRHM	HRTCVDRWL	HQOK[C]PLCR	133	
SEQ-ID-NO-393	QHVGDSCVVC	LYEEAAAEV	RRLSNQRHV	HRGCLOKRWL	HQOK[C]PLCR	143	

Replacement Sheet

Figure 5 (continued)

SEQ-ID-NO-401		134
SEQ-ID-NO-370		161
SEQ-ID-NO-409		164
SEQ-ID-NO-349		167
SEQ-ID-NO-357		163
SEQ-ID-NO-337		162
SEQ-ID-NO-339		160
SEQ-ID-NO-395		155
SEQ-ID-NO-417		150
SEQ-ID-NO-437		153
SEQ-ID-NO-355		180
SEQ-ID-NO-393		191
SRL	LPAA - AAADESWSPP APTLT -- AW	
SRL	LPAA1 TAADESWSPP APTLT -- AW	
FRL	-LP--- ATTESPSPS PATATPHFAR I	
LRL	-LP--- PAAADDYAAV AAGLAAREI-	
TPL	VVVRP--- EDFQQLSSN -----W-----	
TPL	VVVA---- ADDDQLVSS N-----W-----	
TPL	MP--- EDDTPC-----FQ-----	
TPL	-LP--- EEEASC-----FL-----	
TPL	-LP--- EEDASC-----FW-----	
THF	VPYHK MEDYNGRLWN DAASEDDIDD DVSLFSHRHD YYYIANASL-	
TPL	MPGEM PVAVD DQMWA AAGVPDSYYD DFFSFPPASA SPPSPTLLL P	
SEQ-ID-NO-401		134
SEQ-ID-NO-370		161
SEQ-ID-NO-409		164
SEQ-ID-NO-349		167
SEQ-ID-NO-337		163
SEQ-ID-NO-339		162
SEQ-ID-NO-395		160
SEQ-ID-NO-417		155
SEQ-ID-NO-437		150
SEQ-ID-NO-355		153
SEQ-ID-NO-393	HQLFSAS	198

Figure 6

SEQ-ID-NO-1842	MSSSCI PT GL	RLLD DMVKAA	ASPVG AHSSP	L RPAHYSSPS	S T L S I E A S I N A	50	
SEQ-ID-NO-456	-----	----- MCSNK	ASPVV GEE	-----	-KOSTRISSSKR	22	
SEQ-ID-NO-511	-----	----- ML MNC	DFNCDL FE	--QEAKRRS	-YPWARPCDG	29	
SEQ-ID-NO-498	-----	----- MF MNC	NENSNLLE	--NEAGRI S	-FPWARPCDG	29	
SEQ-ID-NO-478	-----	----- MI KOE	SNNI CNRE	--N-----	--NRGARACDT	23	
SEQ-ID-NO-481	-----	----- ML KQE	S	-----	--NWAQACDT	14	
SEQ-ID-NO-485	-----	----- MI KOE	S	-----	--NWAWQT CDT	14	
SEQ-ID-NO-496	-----	----- ML KKE	NSN	-----	--NWARVCDS	16	
SEQ-ID-NO-510	-----	----- ML KKE	KISGGFDRS	--S-----	--NNWARVCOS	23	
SEQ-ID-NO-536	-----	----- ML KEE	RTSGGETG	--E-----	--NNWARLCOT	23	
SEQ-ID-NO-474	-----	----- ML KQE	SSGGGGGD	-----	--NRARVCOT	21	
SEQ-ID-NO-475	-----	----- ML KQE	SSGSGGGD	-----	--NRARLCOT	21	
SEQ-ID-NO-457	-----	-----	-----	-----	--MPKPCDA	7	
SEQ-ID-NO-532	-----	----- MKVEE	QT	-----	--GAGQGGAGF	WGLAGRCPDT	32
SEQ-ID-NO-466	-----	----- MVI DT	TNVKGLTG	--R-----	--WGMAAKTCOT	21	
SEQ-ID-NO-508	-----	----- MGI ER	GCL KSL RG	--G-----	--WSVPPKLCDS	24	
SEQ-ID-NO-488	-----	-----	-----	-----	--MALKL CDS	8	
SEQ-ID-NO-494	-----	-----	-----	-----	--MATKL CDS	8	
SEQ-ID-NO-1842	SSSSAT SVSL	KRARA PRKRP	NOAYNEAAAL	--LASI HPSM	F PVNKSPKTA	98	
SEQ-ID-NO-456	I KKRKN	REATTI MEDK	SSSNIDASRK	--RTKTKKK	-----P	56	
SEQ-ID-NO-511	CHAAPS	SAVYC	HADAAYLCAS	CDTQVHSANR	--LASSHERV	RVCVSCESAA	77
SEQ-ID-NO-498	CHAAP	STVYC	CADAAYLCAS	CDTQVHSANR	--VASRHERV	RVCETICESAP	77
SEQ-ID-NO-478	CGSTI	CTVYC	HADASYL CNS	CDAQVHSANR	--VASRHKRV	RVCESCRAP	71
SEQ-ID-NO-481	CRSAACT	VYC	RADSAYL CTS	CDAOI HAANR	--LASRHERV	RVCESCRAP	62
SEQ-ID-NO-485	CRSAACT	VYC	RADSAYL CTN	CDAQVHAANR	--LASRHERV	RVCQSCERAP	62
SEQ-ID-NO-496	CHSAT	CTVYC	RADSAYL CAG	COARI HTASL	--MASRHERV	WVCEACERAP	64
SEQ-ID-NO-510	CHSAT	CTVYC	RADSAYI CAG	CDSRI HAASL	--MASRHERV	WVCEACERAP	71
SEQ-ID-NO-536	CRSAACT	VYC	RADSAYL CT	CDARVHAANH	--VASRHERV	WVCESCERAP	71
SEQ-ID-NO-474	CRAA	PCT VYC	RADSAYL CAG	CDARVHAANR	--VASRHERV	WVCEACERAP	69
SEQ-ID-NO-475	CRAAAC	CTVYC	RADSAYL CAG	CDARVHAANR	--VASRHERV	WVCESCERAP	69
SEQ-ID-NO-457	CHVSSA	AVFC	RADAAYLCVG	COOKVHANK	--LASRHERV	WMCEVCEMAP	55
SEQ-ID-NO-532	CAVDIAAR	LYC	RLDGAYLCAG	CDARAHQASS	--RHARV	WLCEVCEMAP	77
SEQ-ID-NO-466	CKSAAA	AI FC	RSDSAFMCLIS	CDSRI HSAND	KLVSCRHRV	WMCEVCEQAP	74
SEQ-ID-NO-508	CKLT	PIAFLFC	RSDSAFLCI N	CDSI HSANK	--LSSRHERV	WMCEVCEQAP	72
SEQ-ID-NO-488	CKSAT	GTLFC	RSDSAFLCVN	CDSKI HAANK	--LASRHRV	WLCEVCEQAP	56
SEQ-ID-NO-494	CKSTK	ATLFC	RSDSAFLCIT	CDSNL DAANK	--LASRHRV	TLCEVCEQAP	56

Figure 6 (continued)

SEQ-ID-NO-1842	PPRPPPQLSVL	AAALDASPDL	L ^P PPLPVLAADS	AFLLR ^D DDT ^P	-SPKPRSPSG	147
SEQ-ID-NO-456	KF ^L SLKLE[--LNTSHEI	I ^N E ^P NSK	--KSKKKN	NNKKQSKKKE	94
SEQ-ID-NO-511	AVLECHADSA	ALC ^T CDAQV	HSANPI AQ	--RHQRVP	VLPUPALA--	119
SEQ-ID-NO-498	AM ^L ACHADAA	ALC ^T ACDAQV	HSANPI AQ	--RHQRVP	VLPPLPAVA--	119
SEQ-ID-NO-478	AAFMC ^E ADDV	SLCTACDLEV	HSANPLAR--	--RHQRVP	VVP ^I GNSCS	115
SEQ-ID-NO-481	AAFFCKADAA	SLCTACDSQI	HSANPLAR--	--RHQRVP	ILPI SGCVAT	106
SEQ-ID-NO-485	AAFFCKADAA	SLCTACDSQI	HSANPLAR--	--RHQRVP	ILPI SGSMV-	105
SEQ-ID-NO-496	AAFLCKADAA	SLCASCDA ^D I	HSANPLAR--	--RHQRVP	IMPI PGTI YG	108
SEQ-ID-NO-510	AAFLCKADAA	SLCASCDA ^V I	HSANPLAR--	--RHQRVP	IMPI PGTL YG	115
SEQ-ID-NO-536	AAFLCKADAA	SLCAACDAEI	HSANPLAR--	--RHQRVP	ILPI SGSMMSG	115
SEQ-ID-NO-474	AALLCKADAA	SLCTACDADI	HSANPLAR--	--RHQRVP	ILPI SGCLHG	113
SEQ-ID-NO-475	AALLCKADAA	SLCTACDADI	HSANPLAR--	--RHQRVP	ILPI SGCLHG	113
SEQ-ID-NO-457	ANVTCKADAA	SLCMACD ^T DI	HSANPLAQ--	--RHERVP	VTPPLEES--	96
SEQ-ID-NO-532	AAVTCRADAA	ALCATICDADI	HSANPLAS--	--RHLLP	TIPFFGALAD	120
SEQ-ID-NO-466	AAVTCKADAA	ALCVACDSDI	HSANPLAR--	--RHERVP	VPDPFFDSA--	116
SEQ-ID-NO-508	ASVTCKADAA	ALCVTCDSDI	HSANPLAR--	--RHERVP	VEPFDFDSAES	116
SEQ-ID-NO-488	ATVTCKADAA	ALCVTCDRDI	HSANPLSH--	--ADERVP	VTPFYDSVINS	100
SEQ-ID-NO-494	AHVTCKADAA	ALCVSCDHDI	HSANPPAS--	--RHERIP	INTFHHN--	98
SEQ-ID-NO-1842	AKNCPSPAPV	----SSAFRD	FRTOPPS ^S ASL	DAVCADELGE	I DFDODDG ^F NA	193
SEQ-ID-NO-456	PD-----	TTPFKE	KKRATT	--TTLCCGEEK--	--EEEOYDTV	125
SEQ-ID-NO-511	-----	I PAASV	FAAEAA	--TTMYG-----	--DKEEGEEV	145
SEQ-ID-NO-498	-----	I PAASG	FAAEAE	--VTAHG-----	--DKEEGEEM	145
SEQ-ID-NO-478	SLA-----	TAHIT	VTEPEKR	--VV[--VOEDAKEI	142
SEQ-ID-NO-481	-----	NHHSSE	TTEPENI	--VVVGQ-----	--EEDEEA	132
SEQ-ID-NO-485	-----	LNHHSSE	TTETEDI	--VVVCQ-----	--EEDEEA	131
SEQ-ID-NO-496	PPAVHTITGG	SMMI GGT ^T GE	GTEDDGF	--ISLNODADDT	TIDEEDEDEA	155
SEQ-ID-NO-510	PPAVHTVS ^G G	SMMI GGT ^T GE	GTEDDGF	--LSLTODADDT	TIDEEDENEA	162
SEQ-ID-NO-536	PMA-----	NHHPSE	TAMTDTE	--NDMVVGREA	EDEDDEDEA	151
SEQ-ID-NO-474	SP-----	VCPAAAG	EETEDRFT	--TQECEETI	--SFEEDDEA	144
SEQ-ID-NO-475	SQ-----	VCPAAAG	EETEDRFT	--TQECEETI	--SFEEDDEA	147
SEQ-ID-NO-457	-----	ASPLRG	PDFCVLV	--SENCHDLLK	GCEDASVVEA	129
SEQ-ID-NO-532	-----	POPVPS	PSSAAAT	--QEDA EPIGSNEEA	148	
SEQ-ID-NO-466	-----	DSIVKS	SBFSFLV	--PTDPNTG	SNCQOEDVEI	146
SEQ-ID-NO-508	VVK-----	SSSAAA	AAAASFN	--FVMPFTDDG--	--YCQDDAEA	148
SEQ-ID-NO-488	ATD-----	SVPAVK	SAVNFLN	--DRYFSODVDGE	LEARREEAEA	136
SEQ-ID-NO-494	-----	KQQFFS	ESDPOAD	--	--VSTEEAEA	119

Figure 6 (continued)

SEQ-ID-NC-1812	DSI DVGDAAGCGLDGMGS LTVDVSGTARSDDSILSS SGI HPYLRLRLL	243
SEQ-ID-NC-456	AAYLFNSATD STISSIHDLL PSS---AATD YDCGGERNNL ---SPYDR---	167
SEQ-ID-NO-511	DISWLLLERDS DDDNN-----	180
SEQ-ID-NO-498	DISWLLRRNSD-----	179
SEQ-ID-NO-478	ASWLFPKNSD YH-----	173
SEQ-ID-NO-481	ASWLPPSVK NC-----	165
SEQ-ID-NO-485	ASWLPPSSLK NSCDNN-----	167
SEQ-ID-NO-496	ASWLNPBV K-----	189
SEQ-ID-NO-510	ASWLNPBV KNKNKNNINN N-----	206
SEQ-ID-NO-536	ASWLNPCK NS-----	185
SEQ-ID-NO-474	ASWLNPVK -----	176
SEQ-D-NO-475	ASWLNPVK -----	179
SEQ-D-NO-457	VSWLPPPKI -----	161
SEQ-D-NO-532	ASWLPEP -----	176
SEQ-D-NO-466	GSWLPPNPKL TM-----	178
SEQ-ID-NO-508	AAWLPNPNF GSKLN-----	183
SEQ-ID-NO-488	ASWLPPNPKA M-----	167
SEQ-ID-NO-494	ASWLQTPAN P-----	150
SEQ-ID-NO-1842	MVVCLAGRFE LGLGSQH GAR PSLNRALKR KR DDDGAWWWMWP AVPVKDLTI A	293
SEQ-ID-NO-456	----- QD HGSSSSSLL R TAMRKCASEE E-----	190
SEQ-ID-NO-511	S----- CN PCPGE FMRLO E-----	204
SEQ-ID-NO-498	T----- CD PRPEEQYRMO E-----	203
SEQ-ID-NO-478	----- AD YNSSMDYKFT S-----	196
SEQ-ID-NO-481	----- VD YSSSI DKRFX G-----	186
SEQ-ID-NO-485	----- ----- LVDYINKYQQ-----	177
SEQ-ID-NO-496	----- AE YGG DSQFN D-----	210
SEQ-ID-NO-510	----- AE YGG DSQFN D-----	227
SEQ-ID-NO-536	----- VE YNSSM INQFS D-----	206
SEQ-ID-NO-474	----- VT Y----- NSCTE NQCS D-----	195
SEQ-ID-NO-475	----- VE Y----- NSCIE NQCS D-----	198
SEQ-ID-NO-457	----- RP ESPKKQKV F-----	189
SEQ-ID-NO-532	----- ----- LDF VRS M-----	183
SEQ-ID-NO-466	----- ----- FEY QDSF QQQ D-----	189
SEQ-ID-NO-508	----- ----- FDYSNNF QNN N-----	194
SEQ-ID-NO-488	----- ----- DPKLEDAQEQ Q-----	184
SEQ-ID-NO-494	----- ----- NFVCV DAKTDSPEOH S-----	166

Figure 6 (continued)

SEQ-ID-NO-1842	P P A P P A P P N A A M P O A A A A	A A P ----- - E K K K S K K K K V V K A M A K G N F	335
SEQ-ID-NO-456	E T T E E R M W S Y S E V V E E V M S R	S G T ----- - Q P E R C C C G D G N D	224
SEQ-ID-NO-511	----- E V C E F A M P I S Q V G M	A S E ----- - Q P E S S M G M I G A E Q	233
SEQ-ID-NO-498	----- E G C E C M V P P P Q V V M	A S E ----- - Q O E S D Y G T I G A G O A	233
SEQ-ID-NO-478	C I V P E K N Y S G D R V V P L Q L E E	T R G ----- - N L R N K Q O N T Y G S S	233
SEQ-ID-NO-481	Y N V P O R S Y V A D G V V P L Q V G V	A N G ----- - H M M H E K H N F D F G F T	223
SEQ-ID-NO-485	Y N V P O R S Y V A D G V V P L Q V G V	I K S ----- - H M M H E E H N F D F G F T	214
SEQ-ID-NO-496	Y S V P O K S Y V E D S V V P V Q N G Q	R K S ----- L I L Y G T P Q Q Q Q S F H L N F D F G M E	255
SEQ-ID-NO-510	Y S V P O K S Y V E D S V V P V Q N G Q	R K S L I L Y H O P Q Q Q Q Q Q Q S F H L N F D F G M E	277
SEQ-ID-NO-536	C G V P Q K S F G G D G V V P L Q V E E	S R G ----- - Q L H H E Q S F O L A I T	243
SEQ-ID-NO-474	Y C V P P K S Y G G D R A M P I Q Y G E	G K D ----- - H Q Q R Q Y F N F D F G L E	233
SEQ-ID-NO-475	Y C V P P K S Y G G D R V V P I Q Y G E	G K D ----- - H Q Q R Q Y H N F D F G L E	236
SEQ-ID-NO-457	D D A T V T G I Q P D S V V P V H M P E	C S E ----- - D T D S L A H S M D P S F T	226
SEQ-ID-NO-532	D G I K A I G V P V A P S	----- E D D L A G G T L	205
SEQ-ID-NO-466	----- G A M D S V V P V Q T K P A T I	----- S M I N N E N C F D V D	217
SEQ-ID-NO-508	----- C S N A M N D S V V P V Q T K P A T I	----- P M M N H N E C C F D I D	227
SEQ-ID-NO-488	S C T T D G V V P E Q S K N M Q P	----- Q L V N D T S F D F S	214
SEQ-ID-NO-494	----- P G T A D G V V P V Q S H S K T V	----- T E H Y S D I N N D	193
SEQ-ID-NO-1842	E L L P N A K C K E E E A D A S V D D A	A A N G D G D S D S A P T N A P K A G I G L K L D A D E V L	385
SEQ-ID-NO-456	G R P S L A L K L D Y E Q . . . I M E A W	S D K G F L Y M D G E P E - Q T V P D L	261
SEQ-ID-NO-511	D A S M T A G T S T Y T A -- S I S N G	----- P F S S M E V G I P D N : R P D V	270
SEQ-ID-NO-498	----- A S V T A M T S T Y T A -- S I S N D	----- S F S S M E V G I V P D - N S R P D I	269
SEQ-ID-NO-478	G S ----- Q Y N N N G S I N H N	----- A Y N P I S M E T D F V P E - Q T A P D T	265
SEQ-ID-NO-481	----- N V S S E A S P I H M - V S I V P F - S V T S D A	-----	246
SEQ-ID-NO-485	----- N V S S E A S P I H M - V S I V P E - S T L S E T	-----	237
SEQ-ID-NO-496	Y D N S N T G Y - G Y P A -- S L S H S	V S I S S M D V S V V P F - S A Q S E T	291
SEQ-ID-NO-510	Y D N S N T G Y - G Y P A -- S L S H S	V S I S S M D V S V V P E - S A S S E T	313
SEQ-ID-NO-536	Y G S P G A L Y G S Y N G -- S M N H S I	V S M S S M D I M V V P E - S T A S D M	280
SEQ-ID-NO-474	Y E P S K A A C - S Y N G -- S I S D S	V S M S S M D V G V V P E - S T M S E I	269
SEQ-ID-NO-475	Y E P S K A A Y - S Y N G -- L I S Q S	V S M S S M D V G V V P E - S T M S E I	272
SEQ-ID-NO-457	K F P L S A K S G Y S Y G I S T L T Q S	S C S S S L D A A V V P D - S S L S D I	265
SEQ-ID-NO-532	----- F Y P E H ----- S M N H S I	M S T S E V V A V V P D A L I S A G G A	233
SEQ-ID-NO-466	F C R S K F P T F S Y O T K - S O S H S	V S S S S S L E V G V V P D G N S V S D I	256
SEQ-ID-NO-508	F C R S K L S S F N Y P S H - S I S H S	V S S S S S L D V G V V P D G N T V S E I	266
SEQ-ID-NO-488	A A S K P F V Y - G Y H A Q C L R Q S	V S S S S M D V S I V P D D N A M T D D	253
SEQ-ID-NO-494	F S T S K P F T Y N Y ----- N H S	V S S S S L E V G V V P D G N V M S E M	227

Figure 6 (continued)

SEQ-ID-NO-1842	KAWSDKGSMF	AEGSGP[E]--L	PTSAAEVRAK	--[A]D[D]LF	PENCAGGGV	430
SEQ-ID-NO-456	---HASADGF	NDGGEAGNLW	AVPEMETTER	--[L]WRGH	-----	293
SEQ-ID-NO-511	---S-NTN[Q]	RTSEAME[---L	AGHSLOMPVH	--FSSMD	-----	299
SEQ-ID-NO-498	---S-NSNL	LTSSEAME[---L	SCHSLOMPVH	--FSSMD	-----	298
SEQ-ID-NC-178	---T-VSHPK	THKGKTA-QL	PEPLI QI	--LSPMD	-----	292
SEQ-ID-NO-481	---T-VSHPR	SPKACTE[---E1.	PEAPVOM	--LSPME	-----	273
SEQ-ID-NO-185	---T-VSHPR	SPKVATE[---EL	HDA[P]OM	--LSPVE	-----	264
SEQ-ID-NO-496	---S-NSHPR	PPKGTD-LF	SGPPI QI PPQ	--LTPMD	-----	321
SEQ-ID-NO-510	---S-NSHPR	PPKGTD-LF	SGPPI OI PPQ	--LTPMD	-----	343
SEQ-ID-NO-536	---AVVSOLR	APKOTTD-LL	T[G]PPI OMMPQ	--LSPMD	-----	311
SEQ-ID-NO-474	---S-I-SOHR	PPKGTM[E]-LF	SSTAI QMPSQ	--LSPMD	-----	299
SEQ-ID-NO-475	---S-I-SOHR	TPKRLL[E]-LF	SSTAI QMPSQ	--LSPMD	-----	302
SEQ-ID-NO-457	---S-TPYLD	SOSSQDM--S	ARLPHOTCCP	--[D]IVD	-----	294
SEQ-ID-NO-532	-----P	APAPSVA[V]VA	SKCKE	-----	-----	249
SEQ-ID-NO-466	---S-YT[GLGR]	IMGDPSAPI W	AAIANNOAPP	OACVGGMD	-----	290
SEQ-ID-NO-508	---S-YNFGS	ESMVSGGVNS	SNQCVQGATQ	--LCGMD	-----	297
SEQ-ID-NO-488	---S-NPYNK	SMT SAME[---S	SHPAVQ	--LSSAD	-----	278
SEQ-ID-NO-494	---SYCGYGR	TEAVQ	--ITAAD	-----	-----	244

SEQ-ID-NO-1842	REASVLRYKE	KRRILFLFSKK	RYQVRKVNAA	DCRPRMKGRF	VRSPSI	476
SEQ-ID-NO-456	REASLLRYKE	KRONRLFSKR	RYQVRKLNA	EKRPRVKGRF	VKRIDS	339
SEQ-ID-NO-511	RDARVLRYKE	KKKARLFQKT	RYATRXAYA	EARPRI KGRF	AKRSDE	347
SEQ-ID-NO-498	REARVLRYKE	KKOTRKFQKT	RYATRKAYA	EARPRI KGRF	AKRSDE	346
SEQ-ID-NO-478	REARVLRYKE	KKKTRKFQKT	RYASRKAYA	ERRPRI NGRF	AKNSE	340
SEQ-ID-NO-481	RKARVLRYRE	KKKTRKFQKT	RYASRKAYA	EKRPRI KGRF	AKRNEVD	320
SEQ-ID-NO-485	RKARVMRYRE	KKKKRKFEKR	RYASRKAYA	EKRPRI KGRF	AKRNEVD	312
SEQ-ID-NO-496	REARVLRYRE	KKKNRKFEKT	RYASRKAYA	ETRPRI KGRF	AKRTDVE	369
SEQ-ID-NO-510	REARVLRYRE	KKKNRKFEKT	RYASRKAYA	ETRPRI KGRF	AKRTDVK	391
SEQ-ID-NO-536	REARVLRYRE	KKKTRKFQKT	RYASRKAYA	ETRPRI KGRF	AKRTDI	359
SEQ-ID-NO-474	REARVLRYRE	KKKTRKFQKT	RYASRKAYA	ETRPRI KGRF	AKRKDVE	347
SEQ-ID-NO-475	REARVLRYRE	KKKTRKFQKT	RYASRKAYA	ETRPRI KGRF	AKRKDVE	350
SEQ-ID-NO-457	REARVLRYKE	KRKQRKFFKT	RYASRKAYA	ESRPRI KGRF	AKRTDIS	342
SEQ-ID-NO-532	REARLMRYRE	KRNINRFQKT	RYASRKAYA	ETRPRI KGRF	AKRTAEDDAL	299
SEQ-ID-NO-466	REARVLRYRE	KRKNRKFFKT	RYASRKAYA	ESRPRI KGRF	AKRNETD	338
SEQ-ID-NO-508	REARVMRYRE	KRKNRKFFKT	RYASRKAYA	ETRPRI KGRF	AKRTEID	345
SEQ-ID-NO-488	REARVLRYRE	KRKNRKFFKT	RYASRKAYA	ETRPRI KGRF	AKRTEIE	326
SEQ-ID-NO-494	REARVMRYRE	KRKNRKFFKT	RYASRKAYA	ETRPRI KGRF	AKRTDLN	292

Figure 6 (continued)

SEQ-ID-NO-1842	--L R Q A L E E E	T -----	-----	-----	485
SEQ-ID-NO-456	-----	-----	-----	-----	339
SEQ-ID-NO-511	E-L D Q M L T I P	A [P -----	D-S G F I A T M L	W F -----	369
SEQ-ID-NO-498	E-E D H M L S P P	A [P -----	D-T S S Y N T V P	W F -----	369
SEQ-ID-NO-478	E-D Q E Y N T M	L M Y -----	C D-T G Y G I V P	S F Y G Q K	366
SEQ-ID-NO-481	-----	-----	D-T G Y G I V P	S F -----	342
SEQ-ID-NO-485	E-A D K A F S S M	V M F -----	D-T G Y G I V P	S F -----	335
SEQ-ID-NO-496	E-V D Q M F S T Q	L M T -----	D-S N Y G I V P	S F -----	391
SEQ-ID-NO-510	E-V D Q M F S T Q	L M T -----	D-S S Y G I V P	S F -----	413
SEQ-ID-NO-536	E-V D Q A F S T T	L M Q -----	E-S G Y G I V P	S F -----	381
SEQ-ID-NO-474	E-D D Q M F S S T	L M A -----	E-T G Y G I V P	S F -----	369
SEQ-ID-NO-475	E-D D R T F S S T	L M A -----	E-G -G C G I V P	S F -----	372
SEQ-ID-NO-457	E-Q -- F G S V	D S S -----	F G V V P	S F -----	358
SEQ-ID-NO-532	E-Q D G P F S P A	S S A -----	H L A S D-G D Y G V V P	S F -----	325
SEQ-ID-NO-466	E-V D H M Y N S A	S S A A T A A A F M	Y D-N Q Y G I V P	S F -----	368
SEQ-ID-NO-508	D-V D R L Y N P A	D P L S V P S S M L	M D-C P Y G V V P	T F -----	375
SEQ-ID-NO-488	E-A E P M -----	-----	-----	-----	340
SEQ-ID-NO-494	N-V N-L I G E D	E S Y -----	D G Y G V V P	S C -----	312

Figure 7

SEQ-ID-NO-634
SEQ-ID-NO-637

MHVKL	SLWLK	HVVVTI	LI YK	MEESKKY	KSM	VKOTMNKKKK	20	
Q				YRPPSRPLHH	NSVFI	SKKAM	EERSRNREQR	50

SEQ-ID-NO-634
SEQ-ID-NO-637

NNNKKGEGSG	SRSGLLOMKV	RRLQI	LI PGG	QICNHPDLL	SKTVVDYI	VHL	70	
KQTKKKTGRG	SGSOSI	QI KM	RKLRLVLI	PGG	RRLNQPDLLL	TKTADYI	MHL	100

SEQ-ID-NO-634
SEQ-ID-NO-637

KLKLRFLKAI	SEMYSL	86
ELRI RFLKAI	SDIYSLS	117

Figure 8

SEQ-ID-NO-826	MDPF	YTSFSDSLIS	I PDPHRS---P	VSDSSECSPK	-----	31
SEQ-ID-NO-813	MISF	SI-SEM LCS	--EYES---P	VT_GCEYC PK	-----	28
SEQ-ID-NO-809	MNSF	SA-FAEM GS	--FYFS---P	VT_VGGDYC PT	-----	28
SEQ-ID-NO-811	MSSF	SA-F SEM GS	--DYES---M	LSSVGDYSPT	-----	28
SEQ-ID-NO-808	MNSF	SA-SEM GS	--DYE-----	-PQGGDYC PT	-----	25
SEQ-ID-NO-804	MNSF	SA-FSEM GS	--DYES---P	VSSGGDYSPK	-----	28
SEQ-ID-NO-644	MNST	SA-FSEM GS	--DYES---S	VSSCGDYI PT	-----	28
SEQ-ID-NO-796	MNSF	SA-FSEM GS	--DYES---S	VSSGGDYI PT	-----	28
SEQ-ID-NO-797	MNSF	SA-FSEM GS	--DYES---S	VSSCGGYI PT	-----	28
SFQ-ID-NO-645	MNSF	SA-FSEM GS	--DYES---S	VSSCGDYI PT	-----	28
SEQ-ID-NO-767	MDSL	SLDYICSVSSP	--MSDS---G	SGNGASRPNN	---FSDEDVM	36
SEQ-ID-NO-1843	MATL	I O-FNT PYT S	L SADNIPTE	SSSTS DSYSTG	-TSFSDEEV M	42
SEQ-ID-NO-834	MNTT	SPPYSDPHPL	VCNWDSLNL P	DSDCGSEEL M	-----	34
SEQ-ID-NO-837	MSLLSVLDEQ	ECSYSSVLSD	---SS-I ---T	SSVTKGVOPG	-AI FSDEEV I	43
SEQ-ID-NO-838	MDGC	SNYYNDPPCE	-----S	SSASDTSRPM	FLTLSDKEV L	35
SEQ-ID-NO-830	MNI F	ETYYNSDSLIS	-----T	FSSSSSSSS	SSLFSEEF I	35
SEQ-ID-NO-840	MNI F	ETYYNSDSLIL	--TCS-----S	SSSSSSSEE	-----EVI	32
SEQ-ID-NO-832	MNI F	RSYYS DPLTE	--SSS-----S	FSDSSI YSPN	RAI FSDEEV I	38
SEQ-ID-NO-835	MNI F	RSYYS DPLTE	--SSS-----S	FSDSSI YSPN	RAI FSDEEV I	38
SEQ-ID-NO-831	MD F	R SYYS DPLAE	--CS-----S	SDSSSSSCN	RANLSDEEV I	37
SEQ-ID-NO-839	MD F	R SYYS DPLAE	--Y S-----S	SDSSSSSCN	RANHSDEEV M	37

Figure 8 (continued)

SEQ-ID-NO-826	LASSCPKKLA	GRKKFRET RH	PI YRGVQRQRN	SGKWVCEVRE	PNKKSRI WL G	81
SEQ-ID-NO-813	LAASCPKKPA	GRKKFRET RH	PVYRGVRQRN	SGKWVCEVRE	PNKKSRI WL G	78
SEQ-ID-NO-809	LATSCPKKPA	GRKKFRET RH	PI YRGVRRRN	SGKWVCEVRE	PNKKSRI WL G	78
SEQ-ID-NO-811	LATSCPKKPA	GRKKFRET RH	PVYRGVRORN	SGKWVCELRE	PNKKT RI WL G	78
SEQ-ID-NO-808	LATSCPKKPA	GRKKFRET RH	PI YRGVORN	SGKWVCEVRE	PNKKT RI WL G	75
SEQ-ID-NO-804	LATSCPKKPA	GRKKFRET RH	PI YRGVQRN	SGKWVCELRE	PNKKT RI WL G	78
SEQ-ID-NO-644	LASSCPKKPA	GRKKFRET RH	PI YRGVRRS	SGKWVCEVRE	PNKKT RI WL G	78
SEQ-ID-NO-796	LASSCPKKPA	GRKKFRET RH	PI YRGVRRRN	SGKWVCEVRE	PNKKT RI WL G	78
SEQ-ID-NO-797	LASSCPKKPA	GRKKFRET RH	PI YRGVRRRN	SGKWVCEVRE	PNKKT RI WL G	78
SEQ-ID-NO-645	LASSCPKKPA	GRKKFRET RH	PI YRGVRRRN	SGKWVCEVRE	PNKKT RI WL G	78
SEQ-ID-NO-767	LASCYPKKPA	GRKKFRET RH	PVFRGVRRRN	SGKWVCEVRE	PNKKSRI WL G	86
SEQ-ID-NO-1843	LASKNPKKRA	GRKKFRET RH	PI YRGVRRRD	SGKWVCEVRE	PNKKT RV WL G	92
SEQ-ID-NO-834	LASTHPKKRA	GRKKFRET RH	PVYRGVRRRN	SGKWVCEVRE	PNKKSRI WL G	84
SEQ-ID-NO-837	LASRNPKKRA	GRKKFRET RH	PVYRGVRRRN	SGKWVCEVRE	PNKKSRI WL G	93
SEQ-ID-NO-838	LASTCPKKRA	GRKKFRET RH	PVFRGVRRRN	SGKWVCEVRE	PNKKT RI WL G	85
SEQ-ID-NO-830	LASNPNPKRA	GRKKFRET RH	PI YRG RKRN	SGKWVCEVRF	PNKKT RI WL G	85
SEQ-ID-NO-840	LASNPNPKPA	GRKKFRET RH	PI YRG RKRN	SGKWVCEVRE	PNKKT RI WL G	82
SEQ-ID-NO-832	LASNPNPKPA	GRKKFRET RH	PVYRCVRKRN	SGKWVCEVRE	PNKKSRI WL G	88
SEQ-ID-NO-835	LASNPNPKPA	GRKKFRET RH	PVYRGVRKRN	SGKWVCEVRE	PNKKSRI WL G	88
SEQ-ID-NO-831	LASNPNPKRA	GRKKFRET RH	PVYRGVRKRN	SGKWVCEVRE	PNKKSRI WL G	87
SEQ-ID-NO-839	LASNPNPKRA	GRKKFRET RH	PVYRGVRKRN	SGKWVCELRE	PNKKSRI WL G	87

Figure 8 (continued)

SEQ-ID-NO-826	TFPTVEMAAR	AHDVAALALR	GRSACLNFAD	SAWRLP PES	TCPKEI ORAA	131
SEQ-ID-NO-813	TFPTAEI AAR	AHDVAAI A1 R	GKSACLNFAD	SAWRLP PET	TCPKEI QKAA	128
SEQ-ID-NO-809	TFPTAEMAAR	AHDVAAI AL R	GRSACLNFAD	SAWRLP PES	TCAKDI' QKAA	128
SEQ-ID-NO-811	TFQTAEMAAR	AHDVAAI ALR	GRSACLNFAD	SIVWRLP PES	TCAKDI' QKAA	128
SEQ-ID-NO-808	TFQTAEMAAR	AHDVAALALR	GRSACLNFAD	SAWRLP PES	TCAKDI' QKAA	125
SEQ-ID-NO-804	TFQTAEMAAR	AHDVAAI ALR	GRSACLNFAD	SAWRLP PES	TCAKEI QKAA	128
SEQ-ID-NO-644	TFQTAEMAAR	AHDVAALALR	GRSACLNFAD	SAWRLP PES	TCAKDI QKAA	128
SEQ-ID-NO-796	TFQTAEMAAR	AHDVAALALR	GRSACLNFAD	SAWRLP PES	TCAKDI QKAA	128
SEQ-ID-NO-797	TFQTAEMAAR	AHDVAALALR	GRSACLNFAD	SAWRLP PES	TCAKDI QKAA	128
SEQ-ID-NO-645	TFQTAEMAAR	AHDVAALALR	GRSACLNFAD	SAWRLP PES	TCAKDI QKAA	128
SEQ-ID-NO-767	TFPTTEMAAR	AHDVAALALR	GRLACLNFD	SAWRLPP PAS	TDPKDI QKAA	136
SEQ-ID-NO-1843	TYPTADMAAR	AHDVAALAMR	GRSACLNFAD	SIVWRLP PES	SNVKDI QKAA	142
SEQ-ID-NO-834	TFPTAEMAAR	AHDVAALALR	GRSACLNFAD	SAWRLHVP PAS	RDAKDI QKAA	134
SEQ-ID-NO-837	TFPTADMAAR	AHDVAALALR	GRSACLNFAD	SAWRLPTP PAS	SDAKDI QKAA	143
SEQ-ID-NO-838	TFPTAEMAAR	AHDVAAI ALR	GRSACLNFAD	SABRI VP PAS	SNAKDI QTAA	135
SEQ-ID-NO-830	TFPTAEMAAR	AHDVAALALR	GRSACLNFSD	SAWRLP PAS	SNSKDI QKAA	135
SEQ-ID-NO-840	TFPTAFAAMAAR	AHDVAALALR	GRSACLNFSD	SAWRLP PAS	SNSKDI QKAA	132
SEQ-ID-NO-832	TFPTAEMAAR	AHDVAAI AL R	GRSACLNFAD	SAWRLPP VP PAS	SDTJKDI QKAA	138
SEQ-ID-NO-835	TFPTAEMAAR	AHDVAAI AL R	GRSACLNFAD	SAWRLPP VP PAS	SDTJKDI QKAA	138
SEQ-ID-NO-831	TFPSAEMAAR	AHDVAAI ALK	GRSACLNFAD	SAWKLPI PAS	TDAKDI QKAA	137
SEQ-ID-NO-839	TFPSAEMAAR	AHDVAAI ALR	GRSACLNFAD	SAWKLPI PAS	TDAKDI QKAA	137

Figure 8 (continued)

SEQ-ID-NO-826	AEEAAIAFQNK	TATTTETT	TMVE	AVKPAEETVG	QTCCETMEFN	GVFYMAEEAV	181
SEQ-ID-NO-813	AEAAIAFOAE	I-NNNTTDI-H	GLD-MEETIV	EAIYTPEOQN	DVFYMDDEESM		174
SEQ-ID-NO-809	AEAAIAFOAE	M-SDTMISDH	GLD-MEETTV	EVIVTEEEQS	EVFYMDDEEAM		176
SEQ-ID-NO-811	AEAAIAFONE	LMSDTATTIDH	GLD-MEETLV	EAIYTAEOQ-	DTFYI DEETM		176
SEQ-ID-NO-808	AEAAIAFQDE	T-CDTTTEINH	GLD-MQETMV	EAIYTPEOSE	GAFYMDDEETM		173
SEQ-ID-NO-804	AEAAIAFQDE	M-CHMTTDIH	GLD-MEETLV	EAIYTPEOSO	DVFYMDDEEAM		176
SEQ-ID-NO-644	AEAAIAFQDE	M-CDATTDI-H	GFD-MEETLV	EAIYTAEOSE	NAFYMHDEAM		175
SEQ-ID-NO-796	AEAAIAFQDE	M-CDATTDI-H	GSD-MEETLV	EAIYTAEOSE	NAFYMHDEAM		175
SFQ-ID-NO-797	AEAAIAFQDE	M-CDATTDI-H	GFD-MEETLV	EAIYTAEOSE	NAFYMHDEAM		175
SEQ-ID-NO-645	AEAAIAFQDE	M-CDATTDI-H	GFD-MEETLV	EAIYTAEOSE	NAFYMHDEAM		175
SEQ-ID-NO-767	AEAAEVFRPV	DSAGDSSK--	--TAEN--	TAVEGTKESE	ENFFLDEEEAV		178
SEQ-ID-NO-1843	VKAEEAFRPT	E-TDVAV--	--[EES]--	--NELTG	NVFYMDDEESI		177
SEQ-ID-NO-834	AEAAEAFRPM	E-NDGVMQ--	--DER--	--REESEVRTPD	NVFYMDDEDV		174
SEQ-ID-NO-837	AEAAEAFRPE	GSLGVELTRT	[GDE]-VEKM-	--AGTAAG	DVFYMDDDAD		186
SEQ-ID-NO-838	AEAAEAFRPT	EESDEVCG--	--SPVAAP	SESTSASEQQ	GVFYMDDEEAV		179
SEQ-ID-NO-830	AEAAEITRPL	KESSEEVSG--	--ESDNST	SPTESENQEE	SSDFVDEEAI		179
SEQ-ID-NO-840	AOAEEFRSE	EVGESPE--	--	--TSENQEE	SSDFVDEEAI		167
SEQ-ID-NO-832	AEAAEAFRPL	KLEGI SKE--	--	--SSSSTPE	SMFFMDEEAL		173
SEQ-ID-NO-835	AEAAEAURPL	KLEGI SKE--	--	--SSSSTPE	SMFFMDEEAL		173
SEQ-ID-NO-831	AEAAEAFRSS	E-AE[NMPEYS	[GED]-TKEV--	--NSTPE	NMFYMDDEEAL		178
SEQ-ID-NO-839	AEAAEAFRSS	E-AE[NMPEYS	[GED]-TKEV--	--NSTPE	NMFYMDDEEAL		178

Figure 8 (continued)

SEQ-ID-NO-826	L[GMPREFENM	GEEMLLPPPE	-[CWNH]---N	-D[AC-DADV	SI.WSF--	220
SEQ-ID-NO-813	LEMPALLASM	AEGMLLPPPS	-VHF[G]---N	-YDFDC-DADV	SLWSY--	214
SEQ-ID-NO-809	FGMPRLANM	AEGMLLPPPS	-VQWGI---N	-YD[D]DC-DADV	SLWSY--	216
SEQ-ID-NO-811	FGMPSLANM	AEGMLLP[PS]	-I QMI N---N	-YDVEG-DADM	PLWSY--	216
SEQ-ID-NO-808	FGMPTELLDNM	AEGMLLP[PS]	-VQWNH---N	-YD[E]G-DGEV	PLWSY--	213
SEQ-ID-NO-804	LGMSLLDNM	AEGMLLP[PS]	-VQWNY---N	-DVVKG-DDDM	SLWSY--	216
SEQ-ID-NO-644	FEMPSLLANM	AEGMLLP[PS]	-VQMNH---N	-HEVDGDDDV	SLWSY--	216
SEQ-ID-NO-796	FEMPSLLANM	AEGMLLP[PS]	-VQWNH---N	-HEVDGDDDV	SLWSY--	216
SEQ-ID-NO-797	FEMPSLLANM	AEGMLLP[PS]	-VQWNH---N	-HEVDGDDDV	SLWSY--	216
SEQ-ID-NO-645	FEMPSLLANM	AEGMLLP[PS]	-VQWNH---N	-HEVDGDDDV	SLWSY--	216
SEQ-ID-NO-767	FGREKFLANM	AAGMMMSPPH	-SGMEK---DE	-DEL[FVDDCM	QLWSYSI	222
SEQ-ID-NO-1843	FEMQGFLADM	AEGMMLPPPR	T[EYDN---C	-QDDLEFFVDA	SLWSF--	219
SEQ-ID-NO-834	FGMPGELVNIM	AEGMLMPPPP	S[VADGY---G	-CDDMAADADM	SLWSYSI	218
SEQ-ID-NO-837	FGMPGLANI	AEGMLLPPPN	CCGYSGGDDSL	-DNMENNNTDM	SI.WSFISV	233
SEQ-ID-NO-838	FGMPGLLAQM	AEGMLLPPPH	--YSD---D	-DDVDM-CADV	PLWSFSI	219
SEQ-ID-NO-830	FFMPGLLANM	AEGMLLPPPO	-CAEMG---D	-H[VET DAYM	TLWNSYSI	222
SEQ-ID-NO-840	FFMPGLLANM	AEGMLLPPPO	-CAEMG---D	-HC[VET DAYM	TLWNSYSI	210
SEQ-ID-NO-832	FCMPGLLTNM	AEGMLLPPPO	-CAF1 G---D	-H-VETADADT	PLWSYSI	215
SEQ-ID-NO-835	FCMPGLLTNM	AEGMLLPPPO	-CAEI G---D	-H-VETADADT	PLWSYSI	215
SEQ-ID-NO-831	FCMPGLLANM	AEGMLLPPPO	-CSQI G---D	-HME[D]---DFDM	PLWSYSI	219
SEQ-ID-NO-839	FFMPGLLVNIM	AEGMLLPPPO	-CSQI G---D	-HMEA---DVDM	PLWSYSI	219

Figure 9

SEQ-ID-NO-850	MEK[S]-----	PRYRD-----	KA-----	11
SEQ-ID-NO-881	-MEPCT KQ---	-FLPM P-PQDPNSPS	SSTSSSSSSS TSPSHPYHRA	40
SEQ-ID-NO-895	-MSVFT KQ---	--LLPM PHQDPNSPS	SSISSSSSSS TSPSHPHRA	41
SEQ-ID-NO-885	-MEVPAV-----	-KQLL PMARCPNSPS	SSTTSSSPSP SAA	34
SEQ-ID-NO-898	-----	-MAHDPNSPS	SSTSSSSPSS AAAAASSSPS	29
SEQ-ID-NO-876	-----	-----	-----	19
SEQ-ID-NO-877	MDSI [S]-----	PKFDEENNNNN	NNNT -----	-----
SEQ-ID-NO-877	MDSI SSMRYQ FFKQSSLTSL	PSPKTQSNGH NHSHNQI PSP	RPI SLPSPKT	50
SEQ-ID-NO-853	-METSPRQTT NPN---FLAS	PKSLSPNSSET	SSTSSG-----	35
SEQ-ID-NO-857	METSPRHLD NQNQSQLFPS	PTSYSSSSNS NSNSSTTAT	TNNVALNNNI	49
SEQ-ID-NO-850	-----	-----	-----	-----
SEQ-ID-NO-881	KNL LPSPSSCF-----	-----TP-----	TRMVKDDM YETTFIRIDP	43
SEQ-ID-NO-895	-----QPP HPHNLPPS-----	-----PRP-----	VPRTIETTP FPTTFVQADT	73
SEQ-ID-NO-885	-----O-----	-----PRP-----	-----FPTTFVQADT	71
SEQ-ID-NO-888	-----APS PPPRQQS-----	-----QAP-----	-----FPTTFVQADT	67
SEQ-ID-NO-898	-----SHR PPPPPPPSSS-----	-----QAP-----	-----FPTTFVQADT	72
SEQ-ID-NO-876	-----	-----QAP-----	-----FPTTFVQADT	41
SEQ-ID-NO-877	QTQSNGHNHN HNHNQI PS-----	-----PKP-----	MTRSEPANS YPTTFVQADT	90
SEQ-ID-NO-853	-----NPP PFPFPFQQ-----	-----PKP-----	-----YPTTFVQADT	68
SEQ-ID-NO-857	-----NHP PPLPS-----	-----PKP-----	-----YPTTFVQADT	79
SEQ-ID-NO-850	SSFKQVVQQL-----	TG PK-----	N PTHQPDPRFP PFESTPP KA-----	79
SEQ-ID-NO-881	TSFKQIVQML-----	TGSEQS-----	S KSAAAATTNG SACNQAASGS	110
SEQ-ID-NO-895	TSFKQVVQML-----	TCAEQPTKND-----	A TTTAAAAPAGN GGGGOAA--G	110
SEQ-ID-NO-885	ASFKQVVQRL-----	TGSD-----	T P2PAOKPAKT HGHHHHHH--G	100
SEQ-ID-NO-898	ASFKQVVQML-----	TGSD-----	T TPPSQRPAK SNHHQHHHS	107
SEQ-ID-NO-876	TSFKQVVQML-----	TGSETAK-----	-----A AASSSSSSSK PANPPPMK	86
SEQ-ID-NO-877	TSFKQVVQML-----	TGSET-----	-----K QASTSTKAN HNHNIP---	124
SEQ-ID-NO-853	SSFKQVVQML-----	I GSSETAK-----	-----LASSTK PTFSPLSDSN LKTHI PPI KS	112
SEQ-ID-NO-857	SSFKQVVQML-----	TGSPKPKPTC-----	-----PNTSOVDPLP KTNNI PPI KS	129
SEQ-ID-NO-850	VTNKDSSSF-----	-RLSERRNS-----	MKHYNIN-----	111
SEQ-ID-NO-881	GPCRKKPSF-----	-KLYERRSS-----	LKNLKM-----	150
SEQ-ID-NO-895	GPCRKKPSF-----	-KLYERRSS-----	MKNLKM-----	148
SEQ-ID-NO-885	GGVCPKKPAF-----	-KLYERRIG-----	A PL-----	137
SEQ-ID-NO-898	APCRPKKQAF-----	-KLYERRSGV-----	A PLAMAAAAAA	152
SEQ-ID-NO-876	IPNKKQQPF-----	SKLYERRINS-----	A GAASSSPRK-----	131
SEQ-ID-NO-877	-----KKQQGF-----	I NERNSLHN-----	-----S NHNTNSPRK-----	163
SEQ-ID-NO-853	I PKNKQNSCF-----	-KLYERRNS-----	PLLPPIFI-----	154
SEQ-ID-NO-857	MPKKNQSSCF-----	-KLYERRNS-----	PLNPFAFGS-----	171

Figure 9 (continued)

SEQ-ID-NO-850	-----PEI L	TPTI LNFPAL	D-----SPDT PLM	S DPFY RRPCSF	S Q S P -- SDSK	152
SEQ-ID-NO-881	AA -----PFI I	SPSVLDFPSL	KLSSPVTPLT	GDPFFPPSPAS	SSGD-----	190
SEQ-ID-NO-895	AA -----PEI L	SPSVLDFPSL	R LSSPVTPLT	GDPFNRSPPAS	TSE S-----	188
SEQ-ID-NO-885	AA ... PEVL	SPSVLDFPSL	A L CSPVTPLT	A DPFNRSASA	SPGE-----	177
SEQ-ID-NO-898	AAQHQQOEAL	SPSVLDFPSL	A L SPVTPLV	A DPFNRSPPAS	A S S S -----	195
SEQ-ID-NO-876	-----ADI L	SPSI LDFFPAL	V L SPVTPLI	PDPFDRSNA	I DSE -----	168
SEQ-ID-NO-877	-----OEI L	SPSI LDFFPSL	V L SPVTPLI	PDPFNRSGSS	SSSSAARNCS	206
SEQ-ID-NO-853	-----PEI L	SPSI LDFFPSL	A L SPVTPLI	PDPFDRCSCG	N Y T N C I N N N V	197
SEQ-ID-NO-857	-----PEI L	SPSI LDFFPAL	V L SPVTPLI	PDPFDRCSCA	K Y T N -----	208
SEQ-ID-NO-850	PSFDDDOERS	KEKGFYLRP	SPSIT-----T P RD	T E P R L L S L F P	M T P I H S P A P S	200
SEQ-ID-NO-881	----AAERAA	ADKGFFLHP	SPRGAE-----P	--P R L L P L F P	V S S P R M A A A S	231
SEQ-ID-NO-895	---EAEAAA	AERGFLLHP	SPRGAE-----P	--P R L L P L F P	V T S P R M A A P A	230
SEQ-ID-NO-885	--QDEAFAAA	NORGFFLHP	SPRGAE-----P	--P R L L P L F P	V T S P K M A Q -----	219
SEQ-ID-NO-898	-ASPEEEAAA	AOKGFFLHP	SPRSA-----E	--P R L L P L F P	V T S P R V A S S S	239
SEQ-ID-NO-876	-----AFVKA	KEKGFFLHP	SPRD-----K	A Q P L L P L F P	T T S P R A S S G P	208
SEQ-ID-NO-877	SLDSIAEDKA	REKGFFLHP	SPRAA-----TSR D	S E P R L L P L F P	T S S P R A S G P S	256
SEQ-ID-NO-853	NLDKEAEKA	KEKGFYLHP	S P A S -----T P RD	S E P R L L P L F P	V T S P R V S G S S	245
SEQ-ID-NO-857	-----KEKA	KEKGFYLHP	S P G S -----S P R E	T E P R L L P L F P	T S P R I S G S V	250
SEQ-ID-NO-850	-----HD-----H					
SEQ-ID-NO-881	ATAAAPAE-----					204
SEQ-ID-NO-895	AA-----PSE-----					238
SEQ-ID-NO-885						235
SEQ-ID-NO-898						219
SEQ-ID-NO-876	SSSAAAAVAV	ASPSFE				255
SEQ-ID-NO-877	SSSAAPS-----					215
SEQ-ID-NO-853	SSSKYSAS-----					264
SEQ-ID-NO-857	T S-----					247
	N ... PSS-----					254

Figure 10

SEQ-ID-NO-948	-----MEG E-----D	DGQKLQQQQ	SPCSDNFSLA	AA-----SS	0
SEQ-ID-NO-950	-----MDA A-----D	-GQKLQQQQH	QPPCSDNFNS	LLAAAADSSS	0
SEQ-ID-NO-932	-----MER V-----D	DGQKLQQQ-	QPPCSD-NFS	LAGAA-----SS	33
SEQ-ID-NO-931	-----WNP KOTQE---E	DDSWEVRAFA	EDT-CNI NG-	-----TT	30
SEQ-ID-NO-1844	-----WNP NKI EEELE-DD	DESWEVKAFFE	QDTKCN SC-	-----TT	30
SEQ-ID-NO-911	MNGCAWMWNP	DESWEVKAFFE	QDTKCN SC-	-----TT	40
SEQ-ID-NO-907	-----WNH SKNEFE-DD	DESWEVKAFFE	QDTKCN YC-	-----TT	34
SEQ-ID-NO-922	-----WNP SKVERLE-DD	DESWEVKAFF	QDTKCN SC-	-----TT	31
SEQ-ID-NO-923	-----MHE M-----T	DPALSIYNFL	SREGAKRY-----PP	-----PP	26
SEQ-ID-NO-929	-----M-----M	EQEISLELTL	LHP SAS-----PP	-----PP	19
SEQ-ID-NO-936	-----MKS RLSSRLPWQQ	EELDLELSL	LPGDSOTE-----	-----	31
SEQ-ID-NO-947	-----	-----	-----	-----	0
SEQ-ID-NO-948	-----MSQET S-----KDEM	GGRSP	SGDGDKAEEE	26	
SEQ-ID-NO-950	-----MSOKTS-----KDEM	GGRSP	SGDGDKAEEE	26	
SEQ-ID-NO-932	-----LPPQVRS -----SSSY	T CGYCKKEFR	SAQGLGCHMN	I HRLDRA--R	70
SEQ-ID-NO-931	-----PPQVRS PPSSSSSSSY	T CGYCKKEFR	SAQGLGCHMN	V HRLDRA--R	79
SEQ-ID-NO-1844	-----MPAPPPQVRS SP-----SSSY	T CGYCKKEFR	SAQGLGCHMN	V HRLDRA--R	75
SEQ-ID-NO-911	-----MPPR-----S-----Y	T CTFCRREFR	SAQALGGHMN	V HRRDRDA--R	64
SEQ-ID-NO-907	-----MPPR-----S-----Y	T CNFCRREFR	SAQALGGHMN	V HRRDRASSR	76
SEQ-ID-NO-922	-----MPPR-----S-----Y	T CNFCRREFR	SAQALGGHMN	V HRRDRDA-SK	69
SEQ-ID-NO-923	-----MPPR-----S-----Y	T CNFCRREFR	SAQALGGHMN	V HRRDRDA-SK	69
SEQ-ID-NO-929	-----PPP-----STRTF	A CHFCRREFR	SSOALGGHQN	A HKLERA--A	63
SEQ-ID-NO-936	-----PPC-----Y-----F	VCMYCDRKFF	SSOALGGHQN	A HKYERS--L	53
SEQ-ID-NO-947	-----PPC-----F-----E	R CIVCDRKFY	TSOALGGHQN	A HKYERT--L	64
SEQ-ID-NO-948	-----REARSG-----	-----	-----	-----	33
SEQ-ID-NO-950	-----REARSG-----	-----	-----	-----	33
SEQ-ID-NO-932	-----HQQT-----SHRI AHPHN	PNPSCTMLDL	E-----S LSSL	LAHGA[A]-SSD	112
SEQ-ID-NO-931	-----HQQMVSS-----SHRT APPPSN	PNPSCAVLDL	G-----S LSSL	LAIRC[G]---CGC	124
SEQ-ID-NO-1844	-----HQQMV-----SHRI DAPPIN	PNPSCTMLDL	G-----S LSSL	LARGAAGGSN	119
SEQ-ID-NO-911	-----HOTDPC-----S-----S	-----	-----SSTF	I PTQEFPPN	97
SEQ-ID-NO-907	-----AHQSTM-----AAAARS GHGC	MLNS	CAPPLPTT[]	I QSTA-SNI	117
SEQ-ID-NO-922	-----AHQPAV-----RSGGGS	GGCRTTFLSS	CYF---PSTTL	I QSTA-SNS	109
SEQ-ID-NO-923	-----AHQPA-----AAAARS GGGS	RGGKTFLNS	CYI---PTATL	I QSTA-A-SNN	113
SEQ-ID-NO-929	-----ARRSTKP-----LHNFHHHHHH	NNNNNGSFHPS	SE-----IIDL	RPKPKPOKE[S]	107
SEQ-ID-NO-936	-----AKRRE-----AAALRAHGA	ATATGAPE[D]	AAA---AMGSR	DV[P]PARPOGTG	98
SEQ-ID-NO-947	-----AKRRE-----AAAFNAGGAG	R-----	-----A	SMVACA-ETV	93

Figure 10 (continued)

SEQ-ID-NO-948	GGIPVPAVKL AGN-----	-----RFSSEASS	33
SEQ-ID-NO-950	GGLPVPLEKQ LGD-----	-----RFSSEASS	33
SEQ-ID-NO-932	GGPAVPLEK MCN-----	-----RFSSEASS	132
SEQ-ID-NO-931	AGCLLYQLP NPNGVFTPAT	MNACATDSPS TLLSI TPYPH NNLI EKSLNF	144
SEQ-ID-NO-1844	EGSHFYQLO NPSGI FG---	----NSGDMV NLYGTTSFPP SNLFPSMLNS	139
SEQ-ID-NO-911	EGSHFYQLO NPSGI FG---	----NSGDMV NLYGTTSFPP SNLFPSMLNS	147
SEQ-ID-NO-907	EGSHFYQLO NPSGI FG---	----NSGDMV NLYGTTSFPP SNLFPSMLNS	160
SEQ-ID-NO-922	EGFSHFNQLQ NPNSMFG---	----NSSDMV NFYGTTPFPS SNLEFSLLNS	152
SEQ-ID-NO-923	EGSHFYQLO NPNSMFG---	----HSSDTV NFYGSSSFPS SNLDFSVLNS	156
SEQ-ID-NO-929	ARFFHNYPPLL EVE-----	-----PFHQHLH-----	126
SEQ-ID-NO-936	TGVVVVEDES ATR-----	-----MMDKOKA-----	118
SEQ-ID-NO-947	GARPRLEDAL APE-----	-----	106
SEQ-ID-NO-948	-----DODDDDEAQ TRGPYNCT-----	-----	50
SEQ-ID-NO-950	-----DODDDDEAQ TRGPYNCT-----	-----	50
SEQ-ID-NO-932	SAA-----TKDV EGKNEELRI G ACOSH-CDCAE ERLDLQLRLG	-----	168
SEQ-ID-NO-931	AAATN-----DYY\$ EVKNL ELRMC ACSSHGGDGTE ERLDLQLRLG	-----	183
SEQ-ID-NO-1844	AAT-----NDYS EGKTL ELRMC ACSSHGGDGTE ERLDLQLRLG	-----	176
SEQ-ID-NO-911	LVAPPENNTS HCYSIKAFPS ASIDNSNNIN SDNNFKELAH EELDLELRLG	-----	197
SEQ-ID-NO-907	PVEVPP-----RLI EYST GDEESI GSMK EAIGTSVD-----	EELDLELRLG	200
SEQ-ID-NO-922	SVEVPP-----RLI QYPT GDDEKAGSMK ETIRTSVN-----	EELDLELRLG	192
SEQ-ID-NO-923	PVLVPP-----RFI EYST GDEESI GSMK ETKRTSVG-----	EELDLELRLG	196
SEQ-ID-NO-929	-----A GTSIISHEYD TPPAEPSDH ANLDLITLRL-----	-----	156
SEQ-ID-NO-936	PAA-----DDDA PATAS\$SNMK RSSCYGYG-V EELDLSLR-----	-----	153
SEQ-ID-NO-947	-----RS SRLLLRDKG SSEHGGVERA DELDUSIRL-----	-----	137
SEQ-ID-NO-948	-----	FCRRGFPTAQ	60
SEQ-ID-NO-950	-----	FCRRGFPTAQ	60
SEQ-ID-NO-932	MS-----	-----	170
SEQ-ID-NO-931	Y-----	-----	184
SEQ-ID-NO-1844	Y-----	-----	177
SEQ-ID-NO-911	HRS-----	-----	200
SEQ-ID-NO-907	HHPPMEANHL EDSKSSSEET DKSEQSI DDM RTGRRSYECV FCKRGFSTAQ	-----	250
SEQ-ID-NO-922	HKP-----	-----	195
SEQ-ID-NO-923	HNP-----	-----	199
SEQ-ID-NO-929	-----	-----	156
SEQ-ID-NO-936	-----	-----	153
SEQ-ID-NO-947	-----	-----	137

Figure 10 (continued)

SEQ-ID-NO-948	ALGCHMNVR	KDRVGRATPS	SSSSTTAAAAA	RRSVSYDTLV	GLFLPPASGG	110
SEQ-ID-NO-950	ALGCHMNVR	KDRVGRATPS	SSSSTTAAAAA	RRSVSYDTLV	RLFRPPASGG	110
SEQ-ID-NO-932	-----	-----	-----	-----	-----	170
SEQ-ID-NO-931	-----	-----	-----	-----	-----	184
SEQ-ID-NO-1844	-----	-----	-----	-----	-----	177
SEQ-ID-NO-911	ALCCHMNI	HR	KDRVKSRPSS	VPI VSLSGNK	ADDKNYPSFR	200
SEQ-ID-NO-907	-----	-----	-----	-----	-----	300
SEQ-ID-NO-922	-----	-----	-----	-----	-----	195
SEQ-ID-NO-923	-----	-----	-----	-----	-----	199
SEQ-ID-NO-929	-----	-----	-----	-----	-----	156
SEQ-ID-NO-936	-----	-----	-----	-----	-----	153
SEQ-ID-NO-947	-----	-----	-----	-----	-----	137
SEQ-ID-NO-948	SEDAAASTAA	GGGCSLRSRT	AEPAPQELRL	FGRGAGRREE	GGGRDRRDRY	160
SEQ-ID-NO-950	SEDAAASTAA	GGGASLRSRT	AEPAPQELRL	FGRGAGRREE	GGGRDRRDRY	160
SEQ-ID-NO-932	-----	-----	-----	-----	-----	170
SEQ-ID-NO-931	-----	-----	-----	-----	-----	184
SEQ-ID-NO-1844	-----	-----	-----	-----	-----	177
SEQ-ID-NO-911	QPHYSI APEV	-----HV	SYQAFLPVSG	WGFRLLPPHTA	QLFVDNSKHR	200
SEQ-ID-NO-907	-----	-----	-----	-----	-----	342
SEQ-ID-NO-922	-----	-----	-----	-----	-----	195
SEQ-ID-NO-923	-----	-----	-----	-----	-----	199
SEQ-ID-NO-929	-----	-----	-----	-----	-----	156
SEQ-ID-NO-936	-----	-----	-----	-----	-----	153
SEQ-ID-NO-947	-----	-----	-----	-----	-----	137
SEQ-ID-NO-948	GCCSKDGDGN	GGHDHGEEEE	LDLELRLGGGS	GSAGS	195	
SEQ-ID-NO-950	GCCSKDGDGN	GGHDHGEEEE	LDLELRLGGGS	GSAGS	195	
SEQ-ID-NO-932	-----	-----	-----	-----	170	
SEQ-ID-NO-931	-----	-----	-----	-----	184	
SEQ-ID-NO-1844	-----	-----	-----	-----	177	
SEQ-ID-NO-911	NPFGEDDHEN	KKADCYNDKE	DELDLFIRLG	HDP--	207	
SEQ-ID-NO-907	-----	-----	-----TT	PPPSS	375	
SEQ-ID-NO-922	-----	-----	-----P--	-----	196	
SEQ-ID-NO-923	-----	-----	-----P--	-----	200	
SEQ-ID-NO-929	-----	-----	-----P--	-----	156	
SEQ-ID-NO-936	-----	-----	-----P--	-----	153	
SEQ-ID-NO-947	-----	-----	-----P--	-----	137	

Figure 11

SEQ-ID-NO-1005	MESLS-----	SKKRV	RNSD-----	ESVVD	SFAKRI	26
SEQ-ID-NO-953	MEKKLLDI TR	TDSA-EKKRV	RDESF D	EAVLD	SPEMKRL R-D	39
SEQ-ID-NO-971	MAEETLRTD	SAEPTDKKRV	RDES-D-----	GAVLD	SPEMKRL R-D	39
SEQ-ID-NO-963	MEIELLN-----	HKKRV	RUGS-D-----	ESOLD	FPEMKKI R-D	30
SEQ-ID-NO-955	MDELN-----	SKKRA	RDDS-N-----	ESGLD	SPDMKRL R-D	29
SEQ-ID-NO-977	MD-----	CKKRV	RDDS-D-----	ESVLE	SPEAKRL R-D	26
SEQ-ID-NO-979	MD-----	CKKRV	RDDS-D-----	ESI LE	SPEAKRL R-D	26
SEQ-ID-NO-999	MEDSR-----	DRKRR	RDEAEE-----	-OE	SPEAKRL RDD	28
SEQ-ID-NO-985	MESSSSLLL	SSYAGNNKRA	RDAADLE-----	VCSAAE	AEAAKMRPPE	42
SEQ-ID-NO-995	MESSSSLLL	SSYTGGNKRA	READLD-----	VASSAE	AEAAKRI RPE	42
SEQ-ID-NO-1015	MDSSNNNN---	NNKRA	RDAE-D-----	-E	ADEAKRL RAE	29
SEQ-ID-NO-1009	MESS-----	SHKRA	REAA-D-----	LAAAGDGLP	E---KRL RPE	31
SEQ-ID-NO-991	METS-----	SHKRA	REAV-D-----L	AAAAGEAVWP	EADAKRL RPQ	35
SEQ-ID-NO-993	METS-----	SHKRA	REAV-DLAAA	AAAAGEAVWP	ESDAKRL RPQ	38
SEQ-ID-NO-1005	LLDLI LDDSD	VC-TPSHDL	SFMKTFODEI	SPSPAPEF	-TG--- SST	68
SEQ-ID-NO-953	DLFDVLDSD	PE-PVSQDL	SVMKSFEDEL	STVTTTA	--QG--- SSIA	82
SEQ-ID-NO-971	DLFDVFDSD	PE-PVSQDL	SVMKSFEDEL	SS-----	-----AQPR	74
SEQ-ID-NO-963	DLFGLLDDSD	PD-SI QDLD	SVMKSFEQEI	SASSSSPV	--PVVDLTSES	76
SEQ-ID-NO-955	DLP-----	SL-PINQDLA	SVMKSFEEL	SAWPSITES	MPVVDLTSOS	76
SEQ-ID-NO-977	DLLEF FDDAD	DAI-PSSQDL	SVMKSLOEEI	SCV-----	-----ASDS	62
SEQ-ID-NO-9/9	DLLEFFDDAD	DAI-ASTQDL	SVMKSLQEEI	SCV-----	-----TSDY	62
SEQ-ID-NO-999	LFLDT LDDDA	FA-GDQDLA	SVMKSLEEEI	ALSSPPPP	--PPT-- RALV	71
SEQ-ID-NO-985	DLLDLLADDT	DA-AAAQDLA	SVMRSLEEEI	C-----	-----ADEL	76
SEQ-ID-NO-995	DLLDLLDDDA	DA-AAAQDLA	SVMRSLEEEI	C-----	-----AGDL	76
SEQ-ID-NO-1015	DLLDMLDDDT	DAGCAAQDLA	SVMRSFEEL	VAGDVA	-----CDVA	69
SEQ-ID-NO-1009	DLLDLLDDDA	DA-AAAQDLA	SVMRSLEEEI	GSFDEAGA	--PDA-- AAAF	75
SEQ-ID-NO-991	DLLDMLDDDI	EA-AAAQDLA	SVMRSLEEEI	ASFDEA	-----AEAA	74
SEQ-ID-NO-993	DLLDMLDEDI	DA-AAAQDLA	SVMRSLEEEI	ASFDEA	-----AEAA	77

Figure 11 (continued)

SEQ-ID-NO-1005	SGERPELGFL	FEASDDELGL	PPTE-----	IN	EKV[A]-----	99
SEQ-ID-NO-953	GEFQPDLCYL	LEASDDELGL	PPPPSI SPVP	VAKKEVTTET	VT[DLMRASS-	131
SEQ-ID-NO-971	GEFQPDLCYL	LEASDDELGL	PPPP--PPVS	VVEEVE[TET	VADLMVRASS-	121
SEQ-ID-NO-963	GEISOPDLGFL	LEASDDELGL	PPPS-----I N	LSSGEVKGGV	ETELARVDSA	122
SEQ-ID-NO-955	CDSQPDLCYL	LEASDDELGL	PPPI -----A	SITDAEGRSE	ATDLMRADS-	120
SEQ-ID-NO-977	GEISQOI GYL	LEASDDELGL	PPAC-----	NSSAPEEKNV	ETELVRVAS-	105
SEQ-ID-NO-979	CFISOAQI GYL	LEASDDDLGL	PPAC-----	NSSAPQEKEKIV	EAEELVRVAS-	105
SEQ-ID-NO-999	KTDQFDLGFL	LEASDDELGL	PPPV-----LS	SSDDGGEAPA	ADDPAAEQVA	117
SEQ-ID-NO-985	MPPPOPELGFL	LEASDDELGL	PPAA-----	GASSSSSDAG	GWEPE-----	115
SEQ-ID-NO-995	AAPQPELGFL	LEASDDELGL	PPAA-----G	AASSSSSDAG	GWEPE-----	116
SEQ-ID-NO-1015	PTTQPELGFL	LEASDDELGL	PPAT-----	ASSSFEEAAG	AGEPE-----	107
SEQ-ID-NO-1009	PAHQPELGFL	LEASDDELGL	PPAC-----	ASSSEEAVAA	ACAPD-----	114
SEQ-ID-NO-991	PSQQPELGFL	LEASDDELGL	PPAC-----SA	AAASEEAGL	AGPPE-----	115
SEQ-ID-NO-993	PSQQPELGFL	LEASDDELGL	PPAC-----S	AAASEEAGL	AGP[CPAAP-	121
SEQ-ID-NO-1005	[ESM]-[SE]-	[WGLDDEFI K...]	--YDSFESGF	VY --DGDNNI	NNGEYVALDG	142
SEQ-ID-NO-953	DSSGI-[DE]-	[WGFEDFVSN-]	--YCGLDFGS	GV --GDGG-	--DYVAVEEG	169
SEQ-ID-NO-971	DSSGI-[DE]-	[WGFEDHMPD-]	--YCSLDFGS	CV --CDCC-	--DYVTVIEG	159
SEQ-ID-NO-963	DSSGVGGE-[D]-	[WGFEDQILPT-]	--YDSFCLCV	GD --SNYSS-	--DYVGFOOD	162
SEQ-ID-NO-955	DSSGI-[HD]-	[WGFEEONPN-]	--YDSFEEGF	VDNFNDGT--	--VAYDG	158
SEQ-ID-NO-977	DSSGI-[GE]-	[MEFFEOIPR-]	--YDSFDLGM	GFGYECDTT-	--EYAAFCGG	146
SEQ-ID-NO-979	DSSGI-[GE]-	[MEFFEOIPR-]	--YDSFDLGM	GFGYECDAT-	--EYAAFCCE	146
SEQ-ID-NO-999	VEGVVFQ-	[WGLDDDI TGY]	--YDGFDLGI	GPDDRVDTTA	AAEDGV-YDG	164
SEQ-ID-NO-985	EAACLGEGO-	[WGFDEI DGA]	YAFCCGVAYSP	EAAAAAAA	AFWGDDGFDA	165
SEQ-ID-NO-995	EPAVGVGEQ-	[WGFDEI DGA]	YAFCCGVASSP	EAAAAAAA	AEWCDGGFDA	166
SEQ-ID-NO-1015	DAQGFCQ-	[WGFDEI DGG]	G-YTG[FALTS	PEAVAAAAAA	AEWDDDFDA	155
SEQ-ID-NO-1009	VIAACLDCQ-	[WGFDEI DGG]	--FCGYSPREA	AA---AAAAA	AAWDDDGFDA	158
SEQ-ID-NO-991	PAARI YGO-	[WGFDEI DGG]	--FCGYSPREA	AA---AAAAA	AAWDDDVFC	159
SEQ-ID-NO-993	AAAAL YGO-	[WAFDDEI DGG]	--FCGYSPREA	AA---AAAAA	AAWDDDVFGA	165

Figure 11 (continued)

SEQ-ID-NO-1005	-LFDYTDMGF	GSSDLT	--W	RPETLPAQ	166
SEQ-ID-NO-953	-LEFSDDCF	DSCDLFS	--W	RSESLPAE	194
SEQ-ID-NO-971	-LFDGS <u>G</u> CF	DSGDLFS	--W	RPESLPAE	184
SEQ-ID-NO-963	SLEYSNVCF	DSSDFSDLSM	RGGMPAE		190
SEQ-ID-NO-955	-LFEYSDVYY	DSSDI SGQLW	RPETL SAK		185
SEQ-ID-NO-977	-LFD <u>H</u> SDLYY	DS	-----W	RHETLPTQ	166
SEQ-ID-NO-979	-LFDHSODVYY	DS	-----W	RQ-----	160
SEQ-ID-NO-999	GLFDYADMVC	APPDFLD	-----		181
SEQ-ID-NO-985	GLFG <u>G</u> DFSF	GPSDLDV	--L	ROETMPAV	191
SEQ-ID-NO-995	GLFGFGDESF	GPSDLAM	--L	ROETMPAV	192
SEQ-ID-NO-1015	GLFGFGQDEV	A	-----L	RHETMPAV	175
SEQ-ID-NO-1009	GLFAFGDDAC	GASDLAA	--L	RHETMPAV	184
SEQ-ID-NO-991	GLFAFGDDAC	APSDLAA	--L	RHESMPAV	185
SEQ-ID-NO-993	GLFAFGDDAC	GPSDLAA	--L	RHETMPAV	191

Figure 12

SEQ-ID-NO-1024	MSRVLTCPPPL	VFARNHIVCVQ	NLVESTIKLKR	DLDSKKAAHR	I EKKEKKEKRR	50
SEQ-ID-NO-1039	MSRYFTISPPP	VYARNWANGQ	NLVESTIKLKR	DIVTSKKVHP	KEKKERKKDK	50
SEQ-ID-NO-1042	MSRCFPYPPP	VYLGNPVM	AVAEAEESTAK	CQKERERAHAK	--KKDKRSRDK	45
SEQ-ID-NO-1043	MSRCFPYPPP	GYVRNPWAV	AAACAOATTIK	LQKERERKAFK	--KEKRSRDR	48
SEQ-ID-NO-1040	MSRCFPFPPP	GYM	KLRFDL	DTPKKDRKKK	NRKE-DKNER	49
SEQ-ID-NO-1029	MSRCFPYPPP	GYQIE	-----	STKTRKEKEK	SITTESHKDIK	KEKKERRKRR
SEQ-ID-NO-1024	KEKKEI KREK	SHKHIS KAT-	-DNH EKL FL	PSKKVSE-DES	DSLEKSGLTD	97
SEQ-ID-NO-1039	KQKNEKIT E-	-----	-----VYL	PKOVS-DES	EQLEKSGLTD	82
SEQ-ID-NO-1042	KAPQLGEG ISK	HSKHN-HKKRK	LEDVSTI GDOE	PKKMVK-ESA	ELLEKSGLSE	94
SEQ-ID-NO-1043	KALPHGEI SK	HSKRT-HKKRK	HEDI NNADQK	SRKVSEMEPG	EQLEKSGLSE	98
SEQ-ID-NO-1040	KELKQKDSII	SHASF GGAMK	LKDINCKLL M	GED----YEN	EQLERSGCLTE	95
SEQ-ID-NO-1029	KENKDO CYT	VGKS HOKGK-	-----TFI	FRI-----EKK	EEAEKSDLTE	82
SEQ-ID-NO-1024	ELEEP---OKH	EGYL SDGSQN	SKKRI RDDSP	FAVESLI KAA	PVAOKP RIR	145
SEQ-ID-NO-1039	EHEKE-----	YLSDGQS	SKKR RREAS	PSVESNI KAT	PVTGNDP RIR	123
SEQ-ID-NO-1042	EHGAPCFVOM	FRDGPFSSSQD	BSKR RKA V	FSPSOA-----	-KNCGNI I RIK	138
SEQ-ID-NO-1043	EHGAPCFQT	VHGSPFESSQD	SSKR RKVVL	FSPSOA-----	-KNCGNI LRI K	142
SEQ-ID-NO-1040	ELEQPVSSPQ	EPIYSSDSTQS	SKRK RCT LL	FNQDHE-----	DAIKTR	136
SEQ-ID-NO-1029	EHNEPVCLDN	FCYLSDDGTR	SNKK RKL EQ	ATNDDK-----	--PRNVFRIR	125
SEQ-ID-NO-1024	M-----	VEKKPKKE EVP	T D P F AVVD	STTMVAKSLS-----	-----	174
SEQ-ID-NO-1039	F-----	VEKKPKDAEF	VVFQ EDLVC	STS-----	-----	146
SEQ-ID-NO-1042	LKS NQDPQSV	LLEKPRMFIQ	PIMQ-QMSEN	SSLSSKNSI-----	--NRKVNR	184
SEQ-ID-NO-1043	RRDQDSSAS	SEKENVQQT	P V H-QMGSV	SSLPSKKNSM-----	OPHNT EMMVR	190
SEQ-ID-NO-1040	L-----	SLTKHSEPEK	SKOGFOFGSC	STS VGI GDSL	TOETTRI DRP	177
SEQ-ID-NO-1029	L-----	PLTRKKEPDW	PLN--SEGIC	STS-GEADS	SGONEGVHLS	163
SEQ-ID-NO-1024	-----	-----	-----	-----	-----	174
SEQ-ID-NO-1039	-----	-----	-----	-----	-----	146
SEQ-ID-NO-1042	S-TAGQQWVN	GDSQAVQKSL	VTETLSRAMQ	RTVPQPAVKV	TRRADPQLSV	233
SEQ-ID-NO-1043	TASTQQQSI K	GDFQAV	-----LK	QGMPTPA-KV	MPRVDVPPSM	227
SEQ-ID-NO-1040	L-----	-----	-----	-----	-----	178
SEQ-ID-NO-1029	-----	-----	-----	-----	-----	163

Figure 12 (continued)

SEQ-ID-NO-1024							HQ	DVI TSSSI SSS	186
SEQ-ID-NO-1039							GT	EI SSSMSCHD	158
SEQ-ID-NO-1042	KAPVGRSDL	PPKFSGSVGP	SPARVTGRFC	PAPVKTQQR				EHPTSMVSQR	282
SEQ-ID-NO-1043	RASKERVGLR	PAEMLANVGP	SPSKAKQIVN	PAAAKVTQRV				DPPPAAKASOR	277
SEQ-ID-NO-1040							TKV	ETPNQJOLHRN	191
SEQ-ID-NO-1029							HQ	ETVNSKAJCTV	175
SEQ-ID-NO-1024	KTS						ELEKNL	PSISI RA DE	205
SEQ-ID-NO-1039	ENL						PLAISL	ESVETAI LSE	176
SEQ-ID-NO-1042	VDP	--OAKVS	QEEMGSAVCL	POAP	PPMLOPKPKDL			PVPKOREPILN	325
SEQ-ID-NO-1043	DPPLPSKVH	I DATRSFTKL	SQTEI KPEVQ	FPI	PKVPMVAM			PTINRQQIDT	327
SEQ-ID-NO-1040	SAS						-KMKPLQNL	VPMALLEANK	213
SEQ-ID-NO-1029	VGE						-LASPERM	PCLSMSCKKS	195
SEQ-ID-NO-1024	TKRK						RHRSKED	OYNALFDGWT	228
SEQ-ID-NO-1039	SKKKK						KHKT SKES	RYSSLFDEPV	199
SEQ-ID-NO-1042	SILPKEEPCFS	GRTVEADQGK	EAKLSRSDRK	KIHKT	TEKKINK		KFRDLFVTWN		375
SEQ-ID-NO-1043	SOPKEEPCSS	CRNAEAASVS	VEKQSksDRK	KSRKAEKKEK			KFKDLFVTWD		377
SEQ-ID-NO-1040	TVDDDE						SRCVIES	LYKSLC H	231
SEQ-ID-NO-1029	TYCHESGI SR	FKL PN					KKMRKADS	PYKVLI EDWV	228
SEQ-ID-NO-1024	PPSMCIADAS	SNONGDYWLF	GNKTOEVLKP	KA	--AVKV		DDDTMMRPGD		274
SEQ-ID-NO-1039	PPCLSI EEDD	CNS--DDWL	SGRRQENSST	KS	--T MDED		MVMNLDKSGE		244
SEQ-ID-NO-1042	PILLMENEGSD	CG--QDWLF	SSTRSSDGSM	AOPTV	PDGIG		PJHPMVQOQP		423
SEQ-ID-NO-1043	PPSME MDDMD	GD--QDWLF	GSTRKPDAGI	GN	--CREIVD		PLTSOSAEQF		423
SEQ-ID-NO-1040	IOPAYELFD	ALD--QDWLF	SSVKFEAKHV	SK	--K		OKTDAFRCSK		272
SEQ-ID-NC-1029	SPPOFELND	SDD--QEWLS	EASKRERHGN	K	--LN		ACRDVLICHES		270
SEQ-ID-NO-1024	SWPRAQFLS	EVIC YSL PYT	VPF						
SEQ-ID-NO-1039	SCFPSSQFLS	EVCT FSL PYT	VF						
SEQ-ID-NO-1042	YLOPRAFLP	DLHI YQI PYM	VPF						
SEQ-ID-NO-1043	SLOPRAHLP	DLFVYQI PYM	VPT						
SEQ-ID-NO-1040	SLWPRAQFM	EVRI EAL PYT	PF						
SEQ-ID-NO-1029	SIFPRGHYLP	EADMYALPYT	PF						

Figure 13

SEQ-ID-NO-1099	MAFLQDQFOR	H-YQQQQQQPQ	P-----	-----	--QTKSFRNL	28
SEQ-ID-NO-1139	MAPIPHHQL	H-I 000P000	S-----	-----	--KSYRDI Y	27
SEQ-ID-NO-1100	MALPHHHQL	H-I 000PHQQ	Q-----	-----	QOSKSYRDLY	30
SEQ-ID-NO-1101	MALPHHHQL	H-I 000PHQQ	Q-----	-----	--SKSYRDLY	29
SEQ-ID-NO-1105	MAVQAQHLSH	A-FPHDLHAY	N-----	-----	-----SV	22
SEQ-ID-NO-1134	MAVQAQYLSH	ASFPHDLGL	R-----	-----	-----	21
SEQ-ID-NO-1111	MAVEAHSLL	A-GGHKQLTS	A---GWPWT T	GDEARC----	ATARP HQQA	42
SEQ-ID-NO-1131	MAVEAHHLH	A-GGQRPOLL	AP-EGWAW-A	GDAACCEAPA	ATAAGQGQRR	48
SEQ-ID-NO-1047	MAVOAHHMNI	--FSOFTSPN	R-----	-----	-----DC	21
SEQ-ID-NO-1083	MPVQARHMNI	--FSPOLLSN	R-----	-----	-----	19
SEQ-ID-NO-1085	MAVEASYMNL	--LPSOLL--N	R-----	-----	ELI KSNQQLQ	29
SEQ-ID-NO-1053	-----MH-----	--EGSQLPL	Y-----	-----	-----	11
SEQ-ID-NO-1057	MAVEAPHTNL	N-FPSHL--N	R-----	-----	DFAKVNQANM	30
SEQ-ID-NO-1099	QT[E]GOMSQQ	MAFYNP[T]--D	L QDQS[QHPPY	[PPF]--GFA	PG[MI PA--D]	71
SEQ-ID-NO-1139	NNMDGQISTP	VAYFNGS--N	L PEOSQIPPY	PPFQVVG LA	PG-----L	68
SEQ-ID-NO-1100	NNMDGQITNP	VVYFNGS--N	L PEOSQSHPPY	PPFQVVG LA	PG-----T	71
SEQ-ID-NO-1101	NNMDGQITTP	VVYFNGS--N	L PEOSQSHPPY	PPFQVVG LA	PG-----T	70
SEQ-ID-NO-1105	GALEDEMTCG	SLFF-----	-PENLKRGP E	LEGAGNTVFG	DI PRVDP--T	63
SEQ-ID-NO-1134	-ALEGATAAG	SLFLDDH--C	CCAPAFPA A	AAGI GHTVLS	DLPRELT-C	67
SEQ-ID-NO-1111	FQLOQASCVG	VGVCLPA--A	APVSSAAA AP	PAPMIAQYA	ACCRLFVG-D	89
SEQ-ID-NO-1131	LAGKODQQQH	YRFQOPC--A	A-TPAAAAGP	RLVAPTGRY A	PGPOLCAA-D	94
SEQ-ID-NO-1047	VKFQEENMMHG	EFFECTGG--	---EVPLIT	GESFAVEPLA	AKANF----N	60
SEQ-ID-NO-1083	VNFKQDMNHG	EFTGEF--L	AVIDPLSNA A	KPSF-----	-----N	52
SEQ-ID-NO-1085	HQLNSDYMYN	TTTCMDSSA	LPOPAT: M PFS	DLSEYQSNF-	CDP-----N	72
SEQ-ID-NO-1053	-----	-----	-----	-----QPL	CHPNIS A--N	23
SEQ-ID-NO-1057	SLYNTQMDSG	LVFNEP-----	-----MPFT	DLSEYQSSLG	CDPMVSAKAS N	70

Figure 13 (continued)

SEQ-ID-NO-1099	GSDGCV-DLH	WNFGLE-----	--PERKRLKE	QDFLENNSQ-	SSVDFLQPR	113
SEQ-ID-NO-1139	VDDIGCL-DLO	MNYGLE-----	--PKRKRPKE	QDFLENNSQ-	SSI DFLQPR	111
SEQ-ID-NO-1100	ADDGCL-DLO	MNYGLE-----	--PKKKRPKE	QDFMENNNSQ-	SSV DLLQRR	114
SEQ-ID-NO-1101	ADDGCL-DLO	MNYGLE-----	--PKKKRPKE	QDFMENNNSQ-	SSV DLFQRR	113
SEQ-ID-NO-1105	WHDNITRSHG F-----	--AQRKRARV	VPEAPSYLE-	-----	-----	91
SEQ-ID-NO-1134	NDNNGA-CYG	F-----	--VPRKRARL	-DADESAGAL	MAAAAQQQR	104
SEQ-ID-NO-1111	AESGV-TFG	GGGAM-QQE-	--APRKRKRA	-----	-----	114
SEQ-ID-NO-1131	AESGV-TFG	GGGGG-AQQQ	AMAPRKRKRA	-----	-----	122
SEQ-ID-NO-1047	KAESGL-SYN	FTVPP-----	--LSTIKRQRD	FQFSDSNAPV	-----	92
SEQ-ID-NO-1083	KSESGL-TYN	FNSFNVVP--	--PPRKRPVR	SOYLDSDARF	ASAV-----	91
SEQ-ID-NO-1085	KADSGL-TYH	TP-----	--LORKRSRD	FTELTISL	-----	99
SEQ-ID-NO-1053	KADSGL-TTYN	MSI PVS-----	--APRKRSRD	SFTNGFDI	-----	55
SEQ-ID-NO-1057	KDPSGL-TYN	VPAVM-----	--APRKRSRD	SI NDNFDAF	-----	101
SEQ-ID-NO-1099	SVSTGLGLSL	DNTRLASTGD	SALLSLTG--	-----DDI	DRELQ-QQL	153
SEQ-ID-NO-1139	SVSTGLGLSL	DNCRLASSGD	SAFLGLVG-----	DDI	ERELQ-RODA	151
SEQ-ID-NO-1100	SVSTGLGLSL	DNRGLASSCD	SAFLGLVG-----	DDI	ERELQ-RODA	154
SEQ-ID-NO-1101	SVSTGLGLSL	DNCRLASSCD	SAFLGLVG-----	DDI	ERELQ-RODA	153
SEQ-ID-NO-1105	-NQRQGCLVP	VGDVLTHAVG	SCTASTSGRM	:NAACPPQDL	ESOLY-HQGM	139
SEQ-ID-NO-1134	MVLPPHCLVF	PGDVQSRAVG	CGAASTSGRA	GNAAGLSQGL	ESOLY-HQGV	153
SEQ-ID-NO-1111	-----	EQGQTP	PPVLTGTGA-----	ADV	AAQFO-QQLV	140
SEQ-ID-NO-1131	-----	CEGQ-P	APALRIAS-----	ADV	AARFO-QQLV	147
SEQ-ID-NO-1047	-----	KRRSMVAFD	SSSPSPSLIN-----	VEL	VSOI ONQQQS	121
SEQ-ID-NO-1083	-----	KLGSGPFG	SPS-SLI N-----	AEL	VIFI ONQQQL	119
SEQ-ID-NO-1085	-----	PAHQKNKI	SSDPSEFLN-----	OEI	LYOFO-NQOS	127
SEQ-ID-NO-1053	-----	YSLPQNNN	ISGASSDVA-----	DDV	FSOI O-QQH	82
SEQ-ID-NO-1057	-----	HASQKTKV	CPFSSSFID-----	QDI	IFQI O-QQOS	129

Figure 13 (continued)

SEQ-ID-NO-1099	ENDRFLKLQG	EQLROTILEK	VDATQLOSVS	IEDKVLQKL	REKEI	EVENI	203
SEQ-ID-NO-1139	EI DRYI KVQG	DRLRQAIILEK	VQANQI QTIVT	YVEEKVLOKL	RCKET	EVEDI	201
SEQ-ID-NO-1100	EI DRYI KVQG	DRLRQAVILEK	VQANQI QAI T	YVEEKVLOKL	REROT	EVDDI	204
SEQ-ID-NO-1101	EI DRYI KVQG	DRLRQAVILEK	VQANQI QAI T	YVEEKVLOKL	RERDT	EVDDI	203
SEQ-ID-NO-1105	EI DAVLRLLET	DRMRAGLEEA	RQOHVRAVVS	AFAAARRRL	RAAEAAELA		189
SEQ-ID-NO-1134	EI DALMRLLES	DRMRAGLEEA	RRRHARQVVA	TVERAAAGRL	RAAEAELERA		203
SEQ-ID-NO-1111	DVDRMLQHT	AKMWAGLREQ	RRRHAGQVVA	TNEAAAAAPRL	RAKEEELI QRM		190
SEQ-ID-NO-1131	DVDRMLQHT	SKMWADLREQ	RRRHAGQVVA	AVEAAAAKRI	RAKDEEI EHI		197
SEQ-ID-NO-1047	EI DRFVAQQT	EKLRI EI EAR	QQT QT RMLAS	AVONMIAKKL	KEKDEEI VRI		171
SEQ-ID-NO-1083	EI DRFVAQQT	EKLRI EI EAR	QQT QT OMLAS	AVONALAMKL	KEKDEEI LRM		169
SEQ-ID-NO-1085	EI DRMLAHHT	EKVRMELEEO	KMROSRMFVS	AI GEAMAKKL	KEKDOEI ORM		177
SEQ-ID-NC-1053	DI DRFI SDHT	EKLRLVEER	RKRQSRMFIT	AI QERVMKKL	KEKDEEI QRI		132
SEQ-ID-NC-1057	EI DRFI AEHN	QKVVRMELEDR	RKRQSRMIVS	AI QGGMVRKL	TEKDECI QRM		179
SEQ-ID-NO-1099	NKRNMELECDQ	MEIQISMEAGA	WODRARYNEN	MIAALKFNLO	QAYLQCRDSK		253
SEQ-ID-NC-1139	NKKNMELELR	TEQIALEANA	WODRAKYNEN	LINTLKVNLQ	HMYAQOSRDSK		251
SEQ-ID-NO-1100	NKKNMELELR	MEQIALEANA	WODRAKYNEN	LINTLKVNLQ	HMYAQOSRDSK		254
SEQ-ID-NC-1101	NKKNMELELR	MEQDLEANA	WODRAKYNEN	LINTLKVNLQ	HMYAQOSRDSK		253
SEQ-ID-NO-1105	RCRNAKLSER	FQICAEQGA	WFIVAKSHEA	VAAQLOATLD	QI LOSPCAAL		239
SEQ-ID-NC-1134	RCRNMELEER	ERQIMTAEGQA	MLSIVAKSHEA	VAAQLRATILD	QI LOSPCAAL		253
SEQ-ID-NO-1111	PRVNWALEER	VKSMMYMEAHM	WRDLAQSNDA	AVTALRCELO	OAI DAQTRR		240
SEQ-ID-NO-1131	GRLNWALEER	VRSLYMEAQV	WRDLAQSNEA	AANALRGELO	OAI DAQQAR		246
SEQ-ID-NO-1047	RNLNWLQER	VKSLSLYVENOI	WRDI AQTNEA	NANTLRTNLD	QVLAQLETFP		221
SEQ-ID-NO-1083	RNLNCVQER	VKSLSFVNEOI	WRDI AQTNEA	OANNLRTNLD	QVLAQIETLP		219
SEQ-ID-NO-1085	GKLNWALQER	VKSLSOMENOI	WRELAQTNES	TANLRSNL	QVLAHVGEER		227
SEQ-ID-NO-1053	GKLNWVLQFR	VKSLSLYVENOL	WRDLAQNEA	TANSLRNLE	QVLAHAGDSI		181
SEQ-ID-NO-1057	GKLNWVLQEK	VKSLSLYVETQI	WRDLAQNEA	TANSLSRNLE	QVIAHVSEDR		229

Figure 13 (continued)

SEQ-ID-NO-1099	-DSEVDDTAS	CCNGRSLD-	-FHLLSNE	NSNMKDLMK-	290
SEQ-ID-NO-1139	-DSEVDDTAS	CCNGRATD-	--LHLLCRD	SNEMKELMT-	288
SEQ-ID-NO-1100	-DSEVDDTAS	CCNGRATD-	--LHLLCRD	SKEMKELMT-	291
SEQ-ID-NO-1101	-DSEVDDTAS	CCNGRATD-	--LILLCRD	SKEMKELMT-	290
SEQ-ID-NO-1105	-DSEVDDTAS	CCFETPAG-	-----D	DAASKASA-	273
AATCAGD-	DGDAEDARS	CCFETPAG-	-----D	DAASKTPAA-	297
SEQ-ID-NO-1134	AVAGAAGAGG	AEDDAEDAQS	CCYETPCG-	GDNAGAD	276
SEQ-ID-NO-1111	-----RADDACS	CCCGENDVFI	TEAGAAENE	EACTSSSG-	287
SEQ-ID-NO-1131	--CG--GGVAL	AEDDAEDAQS	CCCGENDVA-	--AGSTGAG	DEGEDEAGT-
SEQ-ID-NO-1047	TAS-----	-AVVEDDAES	-SCGSC---	---CGDGG	EAVTAVGGG-
SEQ-ID-NO-1083	-----T	MENDVIES	-SCGSCVEG-	-----G	EATAVSGG-
SEQ-ID-NO-1085	-----	-AVMADDAOS	-SCGSNDAA-	---EAGNDTA	ASAAATGRG-
SEQ-ID-NO-1053	--CG--GG	-AALADDAAES	-SCGSNDQGW	REVVTTPQAQG	SCGAODNNKA
SEQ-ID-NO-1057	YI NG--GG	-AVMADDAES	-SCGSNDHG-	---RCPLAGG	EFGAMKDKLV
-----	-----CKAC	RVNEMTVLLL	PCKHLCCLKD	C-E SK-LSF C	322
-----	-----CKVC	RVNEVSMLLL	PCKHLCCKE	C-E SK-LSLC	320
-----	-----CRVC	RTNEVCMLLL	PCKHLCCKE	C-E SK-LSLC	323
-----	-----CRVC	RTNEVCMLLL	PCKHLCCKE	C-E SK-LSLC	322
-----	-----AACRAC	GEESCVLLL	PCRHLCLCSA	C-DAA-VDT C	307
-----	-----ALCKAC	GACEASMLLL	PCRHLCLCIRG	C-EAA-VDAC	331
SFQ-ID-NO-1111	-HVI RACAVC	GDNADVLLL	PCRHLCACAP	C-AAA-ARAC	313
SEQ-ID-NO-1131	-----PCT	RRMCTVG	GEAAEVLM	PCRHLCACAP	C-AGA-ARAC
SEQ-ID-NO-1047	-----	-----CKRC	GEREASVLVL	PCRHLCLCTV	CGGSAL LRT C
SEQ-ID-NO-1083	-----	-----CKRC	GEREASVLVL	PCRHLCLCTV	C-GSAI LRT C
SEQ-ID-NO-1085	-----RLCKNC	GERESSVLL	PCRHLCLCTM	C-GST-VRNC	279
SEQ-ID-NO-1053	VVVCNN-----	NRKCRKIC	GERESSVLL	PCRHLCLCTM	C-GST MV GTC
SEQ-ID-NO-1057	VVKDNNSSKN	I NHNRMCKKC	GERESSVLL	PCRHLCLCTL	C-GSNL GTC

Figure 13 (continued)

SEQ-ID-NO-1099	PLCQSSKF	G	MEVYIM--	337
SEQ-ID-NO-1139	PLCQSTKY	G	MEIYM--	335
SEQ-ID-NO-1100	PLCQSTKY	G	MEVYIM--	338
SEQ-ID-NO-1101	PLCQSTKY	G	MEVYIM--	337
SEQ-ID-NO-1105	PLCATTKNAS	L	HVLLSI-	323
SEQ-ID-NO-1134	PVCAATKNAS	L	HVLLSI-	347
SEQ-ID-NO-1111	PACGCAKNGS	V	CVNFS--	329
SEQ-ID-NO-1131	PACGCAKNGS	V	CVNFS--	341
SEQ-ID-NO-1047	PVCDMVNNAS	V	HVNMS-	304
SEQ-ID-NO-1083	PVCDSVNNAS	V	HVNMS-	296
SEQ-ID-NO-1085	PI CDSMDAS	V	HVNLSI-	310
SEQ-ID-NO-1053	PVCLSLTINAS	V	HVNML--	281
SEQ-ID-NO-1057	PVCDSVMDAS	V	HVNMA-	334

Figure 14

SEQ-ID-NO-1258	-----MDVTGCG GCG-----	---GQRPNFP LQLLGKKE---	25
SEQ-ID-NO-1263	-----MELEADH QNC-----	---RSRLNFP LQLEKKDID	0
SEQ-ID-NO-1211	M DGGDDLHHHH FHQHHQHHHQ	HQQQQRQNFP FQLLEKKEDN	28
SEQ-ID-NO-1215	M EGGDDHHHH FHHN-----	---OSRPNFP FQLLEK<TTN	41
SEQ-ID-NO-1264	-----MSN NDGV-----	-----	32
SEQ-ID-NO-1209	-----MTTRPDG GCG-----	-----	7
SEQ-ID-NO-1223	-----MTTRPAA ECG-----	-----	10
SEQ-ID-NO-1246	-----MDLSDIRNN NNDTAAVAT GCGAR-----	-----	10
SEQ-ID-NO-1151	-----MESQRNTANQ QSNSSGNKDH HGOKQESVAA SLQLVPLESR PSQLQQQHGS	-----	23
SEQ-ID-NO-1155	-----	-----	0
SEQ-ID-NO-1172	-----	-----	50

SEQ-ID-NO-1258	-----EQ T CESTOTAGA GGGGVVGANG SA-----	-----AAAP	53
SEQ-ID-NO-1263	-----MTTSSSDAPC VDHNQKSKNQ DK-----	-----KQQA	26
SEQ-ID-NO-1211	DVT -----EQ PCSTTSVFTA TTTA TTTTTT	SDNNDLHLAE QS-----KKPP	69
SEQ-ID-NO-1215	QEAASCSTSS PYPSLA SPT PSFNSNRS NOLVPASTPT TSDPANKKPP	-----	91
SEQ-ID-NO-1264	-----NP PSALAI SAD I ASN PSTTITIS TITLTAAASE TS-----KKPP	-----	70
SEQ-ID-NO-1209	-----MI SNSLI EHQR QQQQNLKOSI SD-----	-----GALV	35
SEQ-ID-NO-1223	-----GV GGDGAEGKQL PVAAAASNG AN-----	-----CALA	38
SEQ-ID-NO-1246	-----AAAHAAAAAD NKQLVPT SNG TV-----	-----	31
SEQ-ID-NO-1151	-----QL VDASLSI VPR STPPEDSTLIA TTSSST -----	-----ATAT	54
SEQ-ID-NO-1155	-----MGSI SNOI G VPSSSPSTS SL-----	-----AKPP	25
SEQ-ID-NO-1172	-----TTTTPSQGP SMGSISCQI G THPSSTSNS AV-----	-----TKS	85

SEQ-ID-NO-1258	PKRTSTKDRH TKVDGRGRRI	RMPALCAARV FQLTRELCHK FDCTTEWLL	103
SEQ-ID-NO-1263	KKPDTT KDRH TKVDGRGRRI	RMPALCAARV FQLTRELGHK SDGETIEWLL	76
SEQ-ID-NO-1211	PKRSSTKDRH TKVDGRGRRI	RMPALCAARV FQLTRELGHK SDGETIEWLL	119
SEQ-ID-NO-1215	PKRTSTKDRH TKVEGRGRRI	RMPALCAARV FQLTRELGHK SDGETIEWLL	141
SEQ-ID-NO-1264	PKRTSTKDRH TKVDGRGRRI	RMPALCAARV FQLTRELGHK SDGETIEWLL	120
SEQ-ID-NO-1209	VKKPFAKDRH SKVDGRGRRI	RMPALCAARV FQLTRELGHK SDGOTTIEWLL	85
SEQ-ID-NO-1223	VRKATSKDRH SKVDGRGRRI	RMPALCAARV FQLTRELGHK SDGOTTIEWLL	88
SEQ-ID-NO-1246	TRKAPSKDRH SKVDGRGRRI	RMPALCAARV FQLTRELGHK SDGOTTIEWLL	80
SEQ-ID-NO-1151	TTKRTSTKDRH TKVDGRGRRI	RMPALCAARV FOITRFI.GHK SDGETIEWLL	104
SEQ-ID-NO-1155	AAKRPTKDRH TKVDGRGRRI	RMPAYCAARV FQLTQELGIK SDGETIEWLL	75
SEQ-ID-NO-1172	TTKRPDKDRH TKVDGRGRRI	RMPAMCAARV FQLTRELGHK SDGETIEWLL	135

Figure 14 (continued)

SEQ-ID-NO-1258	QQAEPAVI AA	T GT GTI PANF	T SLN	SLRS	SGSSLS	PSH	LRLA	CLACP-	151
SEQ-ID-NO-1263	QQAEPAVI AA	T GT GTI PANY	SSLN	SLRS	S -RHHSIA	SH	YLAHN	N NI	123
SEQ-ID-NO-1211	QQAEPAVI AA	T GT GTI PANF	T SLN	SLRS	SGST MSAP	SH	YFR	CNYFN	168
SEQ-ID-NO-1215	QQAEPAVI AA	T GT GTI PANF	T SLN	SLRS	SGSSMSVPSQ	-LRSSYF	NPN	189	
SEQ-ID-NO-1264	QQAEPSVI AA	T GT GTI PANF	T SLN	SLRS	SGSSMSVPSQ	-LRSSYF	NPN	168	
SEQ-ID-NO-1209	RQAEPsi I AA	T GT GTI PANF	STAS	VSVRC	SS T STS	LN	CTLSSSL	DHK	134
SEQ-ID-NO-1223	RQAEPsi I AA	T GSGT PASF	STSSP	SSLP	PGA PHPQMPH	AIIAQPLAVSP			138
SEQ-ID-NO-1246	RQAEPsi I AA	T GT GTI PASF	STSSP	SSLP	SSO TLP AAA	----PFI	---		123
SEQ-ID-NO-1151	QCAEPAI VAA	T GT GTI PANF	STLS	VSLRS	SGST LSAPP	S	-KSV	PLYGAL	152
SEQ-ID-NO-1155	QQAEPAI I AA	T GT GTI PANF	STLN	VSLRS	SGST LSAPP	S	-KSAPLSEFH	S	123
SEQ-ID-NO-1172	QCAEPAI I AF	T GT GTI PANF	STLN	VSLRS	SGAI SAPAS	S	-KSAPLSFHG	S	183
SEQ-ID-NO-1258	-----RF	CGCARAADAW	DRVVG	GFGG	A	-----	-----	ADAPS	179
SEQ-ID-NO-1263	GHVYHDRNYF	NG -----	-----	VGLFSSE	N -----	-----	-----	NSFFF	148
SEQ-ID-NO-1211	TFSTSAAAAA	AAGLRSRAEW	DRSM MVMED	SRRSM LENTS	SI SAI	I.NFNP	-----		218
SEQ-ID-NO-1215	FSLQQRRTLF	PG -----	-----	GLSPSD	N -----	NSN	NNTSMLN	NFQ	222
SEQ-ID-NO-1264	NYTMMSQPRR	GFSFPG -----	-----	GLSSSE	S -----	SSSG	T I NFQQAAA		206
SEQ-ID-NO-1209	PFI -----	-----	-----	LG -----	-----	-----	-----		139
SEQ-ID-NO-1223	HHHHLPHAAP	FI -----	-----	LG -----	-----	-----	-----		152
SEQ-ID-NO-1246	-----	-----	-----	LG -----	-----	-----	-----		125
SEQ-ID-NO-1151	GLTIHQYDEQ	GGGGVFAAHT	SPILLGFHHQL	Q -----	H	QNQNQNQDPV			195
SEQ-ID-NO-1155	ALGFYNSN	GDEARRI GNS	TAMLGFHHQL	Y -----	P	QLLNPETHI R			163
SEQ-ID-NO-1172	GLAFYDANNA	SETRRAMASN	PPMLGFHHQL	Y -----	-----	-----	-----		215
SEQ-ID-NO-1258	SATSSSSPL	LLSFHSG SVG	LDMSPPSAST	SPA -----	-----	AA DL SRKR			220
SEQ-ID-NO-1263	SGNLNMQLA	KEEL DDDDDN	DN DN -----	-----	-----	NNNTGR K			179
SEQ-ID-NO-1211	MGNVNVI QOA	KOELREESCG	GGCLEVASD	S -----	-----	DSSLGRKR			257
SEQ-ID-NO-1215	SNNLTNMLOA	KOEVRDGNTN	SNANANAPSS	STTLDLSETS	GEESMGGRKR				272
SEQ-ID-NO-1264	NLNPSLMHOA	KOEMRENSNN	NNNSLE ---S	E -----	-----	EE NGRKR			242
SEQ-ID-NO-1209	-----	KRLREDSCG	GK -----	-----	-----	-----			150
SEQ-ID-NO-1223	-----	KRVRDDDCG	GN GN NGQAA	A -----	-----	-----			172
SEQ-ID-NO-1246	-----	KRA DDAAGA	DA -----	-----	-----	-----			136
SEQ-ID-NO-1151	ETIPEGENFS	RKRY RSVDSL	KENDRKQ -----	-----	-----	NE NKS LKE			231
SEQ-ID-NO-1155	SGCNPDNDYA	T KF RDDL FK	ETSQHNTETG	AI -----	-----	DANS PKP E			203
SEQ-ID-NO-1172	QNLV DDNYM	RK FRED FK	ETTQQQSIEI	I -----	-----	EAS NSAKS			254

Figure 14 (continued)

SEQ-ID-NO-1258	-----QQQQQ	YQQQ-MACYT	QSCIPAG ---	--T[VWMV[PSS	255
SEQ-ID-NO-1263	RSEDKD LQHNNYHMSN	MLQSITYGSI	PASHQI GHI P ATTLYMMINN	226	
SEQ-ID-NO-1211	PEDEL -----SOMGS	YLIQSSTGSL	PASHASN--- TAAFWMVAGH	295	
SEQ-ID-NO-1215	RSSCGSEOD LSSLLOHOMGS	YLMOSSAAGSI	PASHIQI --- PAN[VWMVANS	319	
SEQ-ID-NO-1264	R-AEDEL Q QHQ-HHQI GN	YLVOSSSTGPM	AASHASI --- PANFMTLANS	285	
SEQ-ID-NO-1209	-----DEMGS	FATPACFMAV	PARPDFG --- --QVWSFASH	180	
SEQ-ID-NO-1223	-----VTAAM	APAP-CFVAL	PARCDFG --- --QLWSFAIPP	201	
SEQ-ID-NO-1246	-----EPTVA	APAP-CFVAL	PCRADLG --- --QLWSFAAA	165	
SEQ-ID-NO-1151	S-----ETSGP	TAAP-MWAVA	PBSRSGA --- GNTFWMLPVG	263	
SEQ-ID-NO-1155	R[GMPEDQEPG LF	TTNV MPAAPMWAVA	PATTNGC --- -NAFWMLPVG	246	
SEQ-ID-NO-1172	RAGVQDQETA GSIRPTTNM	LPTC-MWAVA	PAATTNG --- GNTFWMLPVG	299	
SEQ-ID-NO-1258	---NAQAAGG GAPPGGGG	---ESWT	FPGSG-SGGG GGAATVYRGV	294	
SEQ-ID-NO-1263	---NNNTSHH DPNN	---CSMWA	SPSNS --- ---NI ENS	252	
SEQ-ID-NO-1211	---CNOAMSG GGSVCCNNG	SSDN-NP WA	IPSVG --- ---NSGVYRGA	334	
SEQ-ID-NO-1215	---NNQI MSG G	---DPI WT	FPSVN --- NSAAALYRGA	347	
SEQ-ID-NO-1264	---SNNNNNNN NNNNNNQGMG	S ---DPI WT	FPSVN NNSA AAAAXLYRGT	328	
SEQ-ID-NO-1209	---QEMFLQQ QQQQQQQPA	AALFVHQQQ	QQIAM ---	212	
SEQ-ID-NO-1223	---P	---EMMA	APAMA ---	212	
SEQ-ID-NO-1246	---PEMM	---VAAA	TPAMA ---	179	
SEQ-ID-NO-1151	TTAGNOMEIS SNNNTAAGHR	A ---PPMWP	FVNSAGGAG GGGAAATHFM	309	
SEQ-ID-NO-1155	---GGATAAS ATVPE	---AQMW	FPAHY ---	268	
SEQ-ID-NO-1172	---CGATPLS SVQE	---PQMWT	FPAAA --- AGVPSMQRVN	330	
SEQ-ID-NO-1258	-PSGLHFM NFPA[TPM	---A[L	P[GCGQLGLAG AGGG-GEGHP	330	
SEQ-ID-NO-1263	NI RGCLLNFM NF[HOPIJ]	---G[RGCCCGG	TAA---AEGQW	285	
SEQ-ID-NO-1211	MSAPGDI HFM NF-[ASPMLM	PGGOLGSGIV	GGGGGGGGNG GAQLSESNL	383	
SEQ-ID-NO-1215	VS-TSGLHFM NF-[PQPMALL	PGQQLG NS	CCCCGGGNTN MNMNMNECHL	394	
SEQ-ID-NO-1264	V--SSGLHFM NF-[PAPV	---A[L	PSQO CGNV ---LSEGQL	360	
SEQ-ID-NO-1209	-----	---CEASAARVG	NYLP ---GHL	228	
SEQ-ID-NO-1223	-----	---GEASAARVG	NYLPMAQANL	231	
SEQ-ID-NO-1246	-----	---GEASAARVG	NYLPMAQCNL	198	
SEQ-ID-NO-1151	AGTGFS-PMQYRGSP	---QLG-SF	AOPOPTONLG LSMP ---DSNL	350	
SEQ-ID-NO-1155	--SCGCR ---CNPV	---QLG-SMI	LQQQAGCQO LGLGVTETNM	303	
SEQ-ID-NO-1172	FCGGGCRV ---SSPV	---QLG-SMI	VQQQVGANQQ LGGLI SESNM	368	

Figure 14 (continued)

SEQ-ID-NO-1258	GIL	AALNAY	RAQAAQPDAC	AAAQNQAGGS	SQHRQHQHHG	GGCGGCDERH	379
SEQ-ID-NO-1263	GML	TAAAMNSY	RQ-----	--S[G]-----	---HASCSS	[N]OHNCGDDHQ	316
SEQ-ID-NO-1211	GML	AALNAY	RQI PAN-----	--CVS-----	---EPPGSA	CQHH[C]DDGR	417
SEQ-ID-NO-1215	SML	A[G]LSPY	RPVSDHHQGH	HQPSQS-----	---QSHHHR	[S]CSHEHDDRH	435
SEQ-ID-NO-1264	G---NFMNPy	RNI GG-----	--GGG-----	---ASESQA	S[S]H[C]DDRH	391	
SEQ-ID-NO-1209	NLL	ASLS	-	--CQA-----	---PC	SGRREDDQR-	249
SEQ-ID-NO-1223	NLL	ASFIS	-	--GGP-----	---GGAGQA	[T]RAEEETAH	257
SFQ-ID-NO-1246	NLL	AYFIS	-	--GGP-----	...APTAT	AGRAEEESAR	223
SEQ-ID-NO-1151	GMI	AALNSA	YSRGGNAN--	---ANAEQAN	NAVEHQEKQQ	QSDHDDDSRE	394
SEQ-ID-NO-1155	GLLGSGGMNV	M	SN-----	---NNRVCLK	MNL EOQHHHE	[N]OT Q[S]DSGD	342
SEQ-ID-NO-1172	GMI	GGVNPM	SSSRVGLG--	---MNL-----	---EHHNQD	[N]OP Q[S]DSGD	405
SEQ-ID-NO-1258							
SEQ-ID-NO-1263	ESMSASDS			387			
SEQ-ID-NO-1211	HHS			319			
SEQ-ID-NO-1215	DSTSQHS-			424			
SEQ-ID-NO-1264	DN-----			437			
SEQ-ID-NO-1209	DSTS[H]S-			398			
SEQ-ID-NO-1223	-----			249			
SEQ-ID-NO-1246	-----			257			
SEQ-ID-NO-1151	ENISNSEE-			223			
SEQ-ID-NO-1155	ENPATDSQ			401			
SEQ-ID-NO-1172	ENPNDSQ-			350			
				412			

Figure 15

SEQ-ID-NO-1301	-----MH PKARI HADP-----	A APEP DRI DGL	PDSLVLLI LN	32		
SEQ-ID-NO-1317	-----MH PKARI HADP-----	VLEV DQFDCL	PDSLVLLI LN	31		
SEQ-ID-NO-1303	MS ED--PACS RRSR CDLGGD	ER-WLS --G	FA CDDH FDRL	44		
SEQ-ID-NO-1326	MA ED--PACS RRM CDACDE	HCCWLSSSAG	GCCD DHFDRL	48		
SEQ-ID-NO-1279	MS SM---YSD PI HGT HPEP I	-----	DHF DRL	33		
SEQ-ID-NO-1285	MS SL---RA DP PI SKT HPEA E	AEAT TSCFC S	SSKI DHFDRL	48		
SEQ-ID-NO-1294	MA I LRSS SDP LLSRI HPEP I	-----	QE I DHFDNL	38		
SEQ-ID-NO-1277	MA VJ PRSDP P SRI HPEPP	-----Q	TLE I DHFDHL	40		
SEQ-ID-NO-1301	KLEDVHS LGR	CAAVSRRFND	VPLVHDVYV	KIDRVVAVDG	DPDDA NLSS	
SEQ-ID-NO-1317	KVEDVRS LGR	CSAVSKRF CG	LVS LVHDVYV	KIDRVVAVDG	DAE DT NLSS	
SEQ-ID-NO-1303	RI CDVK ALGR	CSLVS LRFHE	LVPLVDSV FV	RVD CVI P -DE	PPSSSSSPST	
SEQ-ID-NO-1326	RI CDVK ALGR	CSLVS RRF HD	LVPLVDSV LM	RVD CVI P -DD	PASSSSSSSS	
SEQ-ID-NO-1279	M GDVK M LGR	CCVVSRRFHS	LVPQVENVVM	RVD CVI S -DD	DCS PSSSVKIS	
SEQ-ID-NO-1285	KI CDVK ALGR	CCVVSRRFHS	LVPQVDNVVM	RVD CVI S -DD	DT SSSSSSI K	
SEQ-ID-NO-1294	NJ GDVK ALGR	CSVVKRFHS	LI PQVENVVF	RVD CVI S -DD	DSSSL LSDKP	
SEQ-ID-NO-1277	KI CDVK ALGR	CCVVSRRFHS	LVPQVDNV VM	RVD CVI S -DD	DSSSL SSI K	
SEQ-ID-NO-1301	-----P KPRH FSH	F KLM LFT T A	KP F QGM -----	RG	109	
SEQ-ID-NO-1317	-----P KPRN I FSH	F KLM LFT T I	KP F HSM -----	RN	108	
SEQ-ID-NO-1303	----PFSPTA SMV RAR GFSQ	ARI VLGGI V	KP I QAL QOI	SPAN SA SC	137	
SEQ-ID-NO-1326	PSAAPSSPTA SAR ART VFSQ	ARI VLGGI V	KP I QAL QOI	SPAN SA SV	145	
SEQ-ID-NO-1279	-----RADGP FST	FRLV FGGI S	KPL QAL QOF	GPERPISLYKT	120	
SEQ-ID-NO-1285	S HSSSSSGFSS	FRLV FGGI S	KP I QAL QOF	GT KVNS RN	136	
SEQ-ID-NO-1294	R SASA ASPFSA	FRLV F ---	KP I QAI QOF	KRSCSS SL	122	
SEQ-ID-NO-1277	R SGSS AGFS A	FRLV VGGI V	KPL QAL QOF	GT KRSS SS	128	
SEQ-ID-NO-1301	PG GAC -----	G RPLFP RL AOH	SPV DVL RGFS	HVRN L RVEL P	145	
SEQ-ID-NO-1317	PNCN -----	G RPLFA QL S OH	SPA QVL RNFT	H RNL RVEL P	143	
SEQ-ID-NO-1303	FPA SSDSSSPS SSSSS ---S	P PPPADV SHH	SPSEVL RSFK	EL RH L RI ELP	183	
SEQ-ID-NO-1326	LAASMTSSPS SSSSSSSSS-S	PPLFGD VSHH	SPSEVL RSFK	EL RR L RI ELP	194	
SEQ-ID-NO-1279	LNT SSSSS SLS	M CIGGGED I G	E RDQGGV I HH	SPT QVL RNFT	EL RFL RI ELP	169
SEQ-ID-NO-1285	GNC -----PS	SVA ADDD I M	E LDQAGV THH	SPT QVL KNFT	E1 RFL RI ELP	180
SEQ-ID-NO-1294	PSGS -----PS	E I SCCDD I C	E I EQCCV THH	SPT QVL KNFD	E1 KFLK I ELP	169
SEQ-ID-NO-1277	CGGS SSSSS	E I SCCDD D G	E I EQGGV THH	SPT QVL KNFD	E1 RYL RI ELP	178

Figure 15 (continued)

SEQ-ID-NO-1301	SGDVGT EEGV	LLKWRAYGS	TLDOSCVI LGG	TLVDR-----	-----	180
SEQ-ID-NO-1317	SGDVGT EEGV	LLKWRAYGS	TLDOSCVI LGG	TRVDR-----	-----	178
SEQ-ID-NO-1303	AGELDMDGVS	MLKWKADFGS	TLGSCVI LGA	SSASASPSPS	SAGSDS T STA	233
SEQ-ID-NO-1326	AGELSMEEGV	LLKWKADFGS	TLGSCVI LGA	SSACK-----	---DCGACAA	236
SEQ-ID-NO-1279	GGELGI DDGV	LLKWRADFGS	TLDOSCVI LGA	ASVFNHVFQ	VPDHCN D GFC	219
SEQ-ID-NO-1285	SGELGI DDGV	LLKWRADFGS	TLDNCVI LGA	ASVI TNN--K	I SSAMQOE NA	228
SEQ-ID-NO-1294	SGELCI DDGV	LLKWRADFGS	TLENBCVI LGA	SSVIP-----	-PTNSD K TEA	213
SEQ-ID-NO-1277	SGELGI DDGV	LLKWRADFGS	TLDNCVI LGA	SSVPPNPMR	VSQACDTTV	228
-----	-----	-----	-----	-----	-----	-----
SEQ-ID-NO-1301	-----KPAAGH	EPSAAEDGGS	MPESFYTNGC	LKLRVVWTI S	SLI AAST RHY	226
SEQ-ID-NO-1317	-----RPMGCE	HEPSLEDNGS	MPESFYTNGC	LKLRVVWTI S	SLI AAST RHY	224
SEQ-ID-NO-1303	P S --VDCGRT	EPODEVDSGS	PESFYTNNG	EKLRRVWTI S	SLI AAAARHY	281
SEQ-ID-NO-1326	PA--VDCGES	D-----EFGS	PESFYTNNG	LKLRVVWTI S	SLI AASARHY	279
SEQ-ID-NO-1279	INNCISNVNG	D-----DNGS	PESFYTNNG	LKLRVVWTI S	SLI AASARHY	264
SEQ-ID-NO-1285	AA--AAAADD	D-----DNGS	PESFYTNNG	LKLRVVWTI S	SLI AASARHY	271
SEQ-ID-NO-1294	SS--APVAAV	F-----DNGS	PESFYTNNG	LKLRVVWTI S	SLI AASARHY	256
SEQ-ID-NO-1277	VE --APCGSGS	D-----DNGS	PESFYTNNG	LKLRVVWTI S	SLI AASARHY	271
-----	-----	-----	-----	-----	-----	-----
SEQ-ID-NO-1301	LLRSI T KEHP	TLSLVLADA	DCQCTLCMGA	EQLAEFRESR	LSASACSNRT	276
SEQ-ID-NO-1317	LLRSI T KDHP	TLSLVLTD A	DCQCTLCMGA	EQLKEFRENQ	LSASACSNRT	274
SEQ-ID-NO-1303	LLQPI T ADHK	TLEFLDLTDA	DGQGVLTMDK	COLQELRVRP	VS T SRGSHRT	331
SEQ-ID-NO-1326	LLQPI T ADHT	TLESLDLTDA	DGQGVLTMDK	WQLQELRVKP	VSASCGSHRT	329
SEQ-ID-NO-1279	LLQPI T AEHK	TLDLSLVLTDA	DGQGVLCMNC	EQLQELRVKP	LSASSASKRT	314
SEQ-ID-NO-1285	LLQPI T AEHK	TLDLSVLADA	DGQGVLCMNR	EQEELRLVKP	LSASSASKRT	321
SEQ-ID-NO-1294	LLQPI T AEHK	TLDLSVLTDV	DGQGVLCMNR	DQEELRLVKP	LSASSASKRT	306
SEQ-ID-NO-1277	LLQPI T AEHK	TLDLSVLTD S	DGQGVLCMNR	DQEELRLVKP	LAASSASKRT	321
-----	-----	-----	-----	-----	-----	-----
SEQ-ID-NO-1301	QVPA C SMKLK	YAPYLELPGG	Q C QGATLVV	KP S CDAGC	CHVORKETEA	326
SEQ-ID-NO-1317	QVPA C NMKLK	YAPYLELPGG	A C QGATLVA	KPSTEGSNC	GHTSRKETDA	324
SEQ-ID-NO-1303	MP E LSMMLW	YAPCIELPGG	VLINGATLVA	KPSEEGTGD	TWNNGAAGAA	381
SEQ-ID-NO-1326	MPALSMRLW	YAPHIELPGG	VLINGATLVA	KPTEEA TRD	TVGSGTAGSA	379
SEQ-ID-NO-1279	LVPALNMRLW	YAPHIELPD C	VVI QGATLVA	RPSEQSASK	KEVSDAS---	361
SEQ-ID-NO-1285	LVPALNMRLW	YAPHIELPDG	VVLKGATLVA	RPSEQA TK	KDVSDFS---	368
SEQ-ID-NO-1294	LVPALNMRLW	YAPSLELPDC	VVLKGATLVA	RPSE SK	KEVODVS---	350
SEQ-ID-NO-1277	LVPALNMRLW	YAPT E LPDG	VVLKGATLVA	RPSE SK	KEVSD S ---	365

Figure 15 (continued)

SEQ-ID-NO-1301	---FVSCAFD	GPFRFAAKAL	MKRRTYLLLEM	NGF	356
SEQ-ID-NO-1317	---FISGAFD	GPFKMAVKAL	TKRRIYLLLEM	NGF	354
SEQ-ID-NO-1303	---		LKQRTYSLEM	NSF	411
SEQ-ID-NO-1326	---		LKQRTYSLEM	NSF	412
SEQ-ID-NO-1279	CCC MVSAFE	E PYRTAVGMI	VKRRTYCLEM	NSF	391
SEQ-ID-NO-1285	---		VKRRTYCLEM	NSF	398
SEQ-ID-NO-1294	---		VKRRTYCLEM	NSF	380
SEQ-ID-NO-1277	---		VKRRTYCLEM	NSF	395

Figure 16

SEQ-ID-NO-1427
 SEQ-ID-NO-1430
 SEQ-ID-NO-1419
 SEQ-ID-NO-1422
 SEQ-ID-NO-1347
 SEQ-ID-NO-1431
 SEQ-ID-NO-1429

-----	-----	MEFKATE	RLGL-P-----	GT-----	15
-----	-----	MEFKATE	RLGL-P-----	GT-----	16
MSPPLLDYI	GLSPAAAAAA	A-HDDLKGT E	LRCLC-P----	OSG-----	38
MSPPLELDYI	GLSPAAAAAA	AENDELKCTE	LRCLC-P----	CSG-----	39
-----	-----	MEL-----	GLS SPHKS SKLGFN--F		21
-----	-----	MEL-----Q	SGLA PI HS SI EGFD--PY		21
-----	-----	MEL-----Q	GLGL-PSEK TMKGDLNSY		23

SEQ-ID-NO-1427
 SEQ-ID-NO-1430
 SEQ-ID-NO-1419
 SEQ-ID-NO-1422
 SEQ-ID-NO-1347
 SEQ-ID-NO-1431
 SEQ-ID-NO-1429

E EEKKI HG S -----	SVVKNNNKR	QL-----	POTSE	43
FFF EKKI HG S -----	SVVKNNNKR	QL-----	POTSE	43
-SPDRVVVAATATTLD-----	T PAKGAKR	GFSDEA-----	PTPSP	73
-SPDRRVVAA TATTLD-----	T PAKGAKR	GFSDEA-----	PPPSP	74
D NKHC EG A -----	ASCLGTEKL	RFEATFGLGN VEECYMPKO		61
NSDLNNH RG SF-----	NIKYVKNNKR	SFDESF-----	--GDFSKPLP	56
V SEP KELL GS COLHLGSYSW	F NDNDKKR	SE DASEESS RNEDVPRFLP		73

SEQ-ID-NO-1427
 SEQ-ID-NO-1430
 SEQ-ID-NO-1419
 SEQ-ID-NO-1422
 SEQ-ID-NO-1347
 SEQ-ID-NO-1431
 SEQ-ID-NO-1429

ESVS SKVTN DE-----	H VESS	AAPP AKAKIV	CWPPI R-----	78
ESVS SKVTN DE-----	H VESS	AAPP AKAKIV	CWPPI R-----	78
GARSGKGKKV A EEED-----	DKVVAAT	PQVAKAQVV	CWPPI R-----	111
VATAGKGKKV A EEYD-----	EKKVAAAT	PQPAKAKQVV	GWPPV C-----	113
RLFALNCOPN EEDEDPLE-----	SESSI VY	DDEEENSEVV	GWPPV K CMI	106
-L VWS COPN EEDCRSEKK-----	NRSI HIS	NNECENH V	GWPP K-----	96
-L VWN NOPN EEDDPPKDLD	NHONYSFSSN	KSDGESDGIV	GWPP K-----	118

SEQ-ID-NO-1427
 SEQ-ID-NO-1430
 SEQ-ID-NO-1419
 SEQ-ID-NO-1422
 SEQ-ID-NO-1347
 SEQ-ID-NO-1431
 SEQ-ID-NO-1429

---SYRKNS HE-----	AD V-----			90
---SYRKNS HE-----	AD V-----			90
---SYRKNTM ST-----	T Q	LKGSKEDAEAK-----	OD	135
---NYRKNTM TT-----	T Q	LEGSKEDGDA K-----	QG	137
KYGSYHHRH RNHHHCPYHH	RGRRI TAMNN	NISNPTTATV GSSSSSS SS		156
---SWRKKEF HD-----	OQ	PEH RKANE N-----	QNR	122
---FKRKKL S RQ-----	NS	RVLEVNRADV NGCEDCOARS		149

Figure 16 (continued)

SEQ-ID-NO-1427	-GGI FVKVSM	DGAPYLRKID	LRYVGGYSEL	LKALETMFK-	L[] GEYSERE	138
SEQ-ID-NO-1430	-GGI FVKVSM	DGAPYLRKID	LRYVGGYSEL	LKALETMFK-	L[] GEYSERE	138
SEQ-ID-NO-1419	OGFLYVKVSM	DGAPYLRKID	LKTYKNYKDL	STALEKMFSG	FST[GKD]LSE	185
SEQ-ID-NO-1422	OGFLYVKVSM	DGAPYLRKID	LKTYKNYKDL	STALEKMFSG	FST[GKDCSXE]	187
SEQ-ID-NO-1347	RSSMYVKVKM	DGVATARKVD	LKFINSYESL	TNSLT MFT-	-----EYEDC	200
SEQ-ID-NO-1431	SKPLYYVKVN	MCGMGRQIN	LRLYNISYOTL	KDSLISMFV-	-----KQONF	166
SEQ-ID-NO-1429	SNSMYIKVKM	EMGIARKID	MSNYRCFSTL	KHTLDMFIG-	-----ICQ--	191
SEQ-ID-NO-1427	GYKQSEYAPT	YEDKDCDWML	VCDVPWDMFV	TSCKRLRI MK	GTEAKGLGCG	188
SEQ-ID-NO-1430	GYKQSEYAPT	YEDKDCDWML	VCDVPWD[V]	TSCKRLRI MK	GTEAKGLGCG	186
SEQ-ID-NO-1419	YRKDGSEYVLT	YEDKDCDWML	VCDVPWEMFA	DSCRRLRI MK	GSDAIGLAAPR	235
SEQ-ID-NO-1422	YRKDGSEYVLT	YEDKDCDWML	VCDVPWEMFA	DSCRRLRI MK	GSDAIGLAAPR	237
SEQ-ID-NO-1347	UREDFNYTFIT	FOKEGDWLL	RGDVITWKI FA	ESVHRI S I R	DRPCAYTRCL	250
SEQ-ID-NO-1431	EETGANYTLL	FQNKGGEWKL	TSHIWQSFI	GTMRRLAI LR	NCECET[]---	213
SEQ-ID-NO-1429	-ENSSNYRLT	YODREGDWLL	AEDVPPRNEL	GSMQLKLMLR	SSN-----	233
SEQ-ID-NO-1427	V-----		189			
SEQ-ID-NO-1430	V-----		187			
SEQ-ID-NO-1419	AADSKKNRN		244			
SEQ-ID-NO-1422	AADSKKNRN		246			
SEQ-ID-NO-1347	F-----		251			
SEQ-ID-NO-1431	-----		213			
SEQ-ID-NO-1429	-----		233			

Figure 17

SEQ-ID-NO-1480	-----MAAAPS[A]	GGV[EGSSSS	AAAAAA[AAAAA	TICPHIVD[E	36	
SEQ-ID-NO-1475	-----MA APS----GGGG	GGAGEGSSSSA	AAMM-----	-TIGAHGV[DQ	32	
SEQ-ID-NO-1477	-----MA APSAGAGGGS	GGAGEGSSSSS	AAAAAA[AA	-TIGAHGV[DQ	39	
SEQ-ID-NO-1471	MDEAGRASAP AVVTVTASA[A	APS[P]PPPP	A[ATAAAADP	PSPD[P]DALYE	50	
SEQ-ID-NO-1457	-----MD FNA3VPMS[--	FNA3VPMS[--	-----	-SLSP[LMNQ	18	
SEQ-ID-NO-1467	-----MD FNA3VPMS[--	FNA3VPMS[--	-----	-SLSP[LMNQ	18	
SEQ-ID-NO-1460	-----MGFS[F	FACI PMSR[T	ATAAVPVTEG	SSLSPLMNQ	33	
SEQ-ID-NO-1462	-----MD FDAGI PMSRS[G	CVCLPAVTEG	TSMSP[SLSE	31*		
SEQ-ID-NO-1480	--EAMW[QMN	[CEAMEAC	PYPER[CEPD	CSYYMRTGLC	RFGMTCKFNH	81
SEQ-ID-NO-1475	VTCAMW[QMN	[CDAMELG	PYPER[VGDPD	CSYYMRTGMC	RFGMTCKFNH	79
SEQ-ID-NO-1477	VACAMW[QMN	[CEAVELG	PYPER[CEPD	CSYYMRTGMC	RFGMTCKFNH	86
SEQ-ID-NO-1471	--LGMWQOMA	MSGATMQSG	PYPMRPGEPD	CTYYLRTGLC	RFGMSCRFNH	98
SEQ-ID-NO-1457	--DAMW[QMN	LSSDETMETG	SYPERPGEPD	CSYYI RTGLC	RFGSTCRFNH	65
SEQ-ID-NO-1467	--DAMW[QMN	LSSDETMETG	SYPERPCEPD	CSYYI RTGLC	RFGSTCRFNH	65
SEQ-ID-NO-1460	--DAMW[QMN	LRSSSETMESS	PYPERPGEPD	CSYYI RTGLC	RFGATCHFNH	80
SEQ-ID-NO-1462	--DAMW[QMN	LRSSSETMEAC	PYPFRPGEPD	CSYYI RTGLC	RFGATCRFNH	78
SFQ-ID-NO-1480	PADRKMVA[AA	ARMKGEYPOR	GOPECQYYL	KTGTCKFGAT	CXFTIIIPREKA	131
SEQ-ID-NO-1475	PADRKLAVAA	ARWKGEYPQR	GQPECQYYL	KTCTCKFGAT	CXFHHPREKA	129
SEQ-ID-NO-1477	PADRKLAVAA	ARMKGEYPQR	NGOPECQYYL	KTGTCKFGAT	CXFHHPREKA	136
SEQ-ID-NO-1471	PODRNTAI AS	ARMKGEYPER	VGOPECQYYL	KTGTCKFGPT	CXFHHPREKA	148
SEQ-ID-NO-1457	PRDRELVI AF	ARMRGEYPER	GQPECCEYYL	KTGTCKFGVT	CXFHHPRNKA	115
SEQ-ID-NO-1467	PRDRELVI AF	ARMRGEYPER	GOPECCEYYL	KTGTCKFGVT	CXFHHPRNKA	115
SEQ-ID-NO-1460	PPNRKLAI AA	ARWKGEFPGR	VGOPECQYYL	KTGTCKFCAT	CXFHHPRDKA	130
SEQ-ID-NO-1462	PPNRKLAI AA	ARMKGEFPER	GQPECQYYL	KTGTCKFGAT	CXFHHPRDKA	128
SEQ-ID-NO-1480	A[ATRVQLNA	GYPLRPNEK	ECAYYLRTGQ	CKFGSTCKFH	H--POPSNIM	179
SEQ-ID-NO-1475	AMATRVQLNE	LGYP[LRNEK	ECAYYLRTGQ	CKFGSTCKFH	H--PQPSI MM	177
SEQ-ID-NO-1477	AMATRVQLNE	LGYP[RPSEK	ECAYYLRTGQ	CKFGSTCKFH	H--POPSI MM	184
SEQ-ID-NO-1471	GIAGMVQLNF	LGYP[LRPNER	ECAYYLKTGQ	CKYGN[CKFN	H--PE[ENAV	196
SEQ-ID-NO-1457	GIAGRVLSLNM	LGYP[LRSLNEV	DCAYFLRTGH	CKFG[CKFN	HPOPOPTNMM	165
SEQ-ID-NO-1467	GIAGRVLSLNM	LGYP[LRSLNEV	DCAYFI RTGH	CKFG[CKFN	HPOPOPTNMM	165
SEQ-ID-NO-1460	GIAGRVLSLNI	LGYP[LRPNEI	ECAYYLRTGQ	CKFGSTCKFH	H--POPTNMM	178
SEQ-ID-NO-1462	GISGRVSLNI	LGYP[LPNEI	ECAYYLRTGQ	CKFGSTCKFH	H--POPTNMM	176

Figure 17 (continued)

SEQ-ID-NO-1480	VAVRGS-VYS	PGGSMSTSPSQT	H T Y P C A M - T N	MPLSRSASFI	ASPRWP[G]HSS	227
SEQ-ID-NO-1475	VAVRGS-VYS	PGGSMATSPGH	HAYQGAV-T S	MPLSRSASFI	ASPRWP[G]HSS	225
SEQ-ID-NO-1477	VAVRGS-GYS	PGGSMATSPGQ	HAYQGAV-T S	MPLSRSASFI	ASPRWP[G]HSS	232
SEQ-ID-NO-1471	AS[RGSPI]YP	PV[HNSC]TGP	HSYTCIM-AS	WTYPR-GSF	PSPRWQSPSN	244
SEQ-ID-NO-1457	VP-----	TSCQ	QSYP-----	WS--R-ASF	ASPRWQDPSS	192
SEQ-ID-NO-1467	VP-----	TSCQ	QSYP-----	WS--R-ASF	ASPRWQDPSS	192
SEQ-ID-NO-1460	VSLRGSP[YQ	TVFSPATPGQ	QSHPCQ-H TN	WS--R-ASF	PSPRWQGPSS	224
SEQ-ID-NO-1462	VFLRGSP[YP	TVSSP[T]PGQ	QSYPGGLAT	WS--R-ASF	TS[PRWQ]PSS	223
SEQ-ID-NO-1480	YAQVI VPPCL	VQVPGWNPYA	AQI GSSSSDD	QD RTAGCAQ	YYT GSRHSET	276
SEQ-ID-NO-1475	YAQVI VPPGL	VQVPGWNPYA	AQI GSSSSDD	QD RTPGAAQ	YYT GSRQSCF	274
SEQ-ID-NO-1477	YAQVLVPPGL	VQVPGWNPYT	AQI GSSSSED	QD OTPGAAQ	YYT GSRQSGT	281
SEQ-ID-NO-1471	YTPMI VPQGL	VQVPNWN[SP]	COM[PVSSPE	SRLQSPGAQQ	YYGTSRQGEA	294
SEQ-ID-NO-1457	YASII MPRGV	VPMQGWNPYS	GOLGSVSPSG	-----TGNDQ	NNRNLIQNET	237
SEQ-ID-NO-1467	YASLI MPQGV	VPMQGWNPYS	GOLGSVSPSG	-----TGNDQ	NNRNLIQNET	237
SEQ-ID-NO-1460	YASII LPQGM	VSVPGWNAAYS	GQ_ASVSSSE	NLQQTINVNHQ	I HGT SRQNES	274
SEQ-ID-NO-1462	YTPLI LPQGV	VSMPGWNAAYS	GQ_GSVSSPE	SQ_ODTGNSO	I MGT SRHSES	272
SEQ-ID-NO-1480	PNNMC---DQGM	FSSYQAG-SV	PI GLY[VOR]	ESI FPERPDQ	PECQFYMKTC	322
SEQ-ID-NO-1475	PGICG---DRCM	FSSYQAG-SV	PV GLYAVQT	ENVFPERPDQ	PECQFYMKTC	320
SEQ-ID-NO-1477	PCIIG---DQGM	FSSYQAG-SV	PV GLYAVQR	ENVFPERPDQ	PLCOFYMKTC	327
SEQ-ID-NO-1471	-SAG---NQGM	DSPYRSS-SF	PA POYALQR	ENVFPERPDQ	PLC[JYI KTG	339
SEQ-ID-NO-1457	I ESGSOSQGS	FSSYNPQSSV	PLQGYALPR	ENVFPERPGQ	PECQFYMKTC	287
SEQ-ID-NO-1467	I ESGSQSQGS	FSSYNPQCSV	PI GGYALPR	ENVFPERPGQ	PECQFYMKTC	287
SEQ-ID-NO-1460	ATAG---SQAS	FSELRSQ-SV	PV CVYALQR	ENVFPERPGQ	PECQFYMKTC	320
SEQ-ID-NO-1462	VNAG---SQGT	FSPYRSG-SA	PL QFYALQR	ESVFPFRPGQ	PECQFYMKTC	318
SEQ-ID-NO-1480	DCKFCAVCKF	HHPKERI I PT	PNCALSSLG	PLRPGEPI CT	FYSRYGI CKF	372
SEQ-ID-NO-1475	DCKFGSVCKF	HHIPRERI I PT	PNCALSPLG	PLRPGEPI CS	FYNRYGMCKF	370
SEQ-ID-NO-1477	DCKFC[V]CKF	HHPRERI I PA	PNCALSSLG	PLRPGEPI CS	FYSRYGMCKF	377
SEQ-ID-NO-1471	DCKFGAVCKF	HHPRMRSQPP	PDCILSPMGL	PLRPGEELCK	FYSRYGI CKF	389
SEQ-ID-NO-1457	DCKFGTVCKF	HHPRDRQAPP	PDCLLSSI GL	PLRPGEPLCV	FYT RYGI CKF	337
SEQ-ID-NO-1467	DCKFGTVCKF	HHPRDRQAPP	PDCLLSSI GL	PLRPGEPLCV	FYT RYGI CKF	337
SEQ-ID-NO-1460	DCKFGAVCKF	HHPRERVLPA	PDCVLSPI GL	PLRPGEPLCI	FYSRYGI CKF	370
SEQ-ID-NO-1462	DCKFGAVCRF	HHPRERLI PA	PDCVLSPI GL	PLRPGEPLCI	FYSRYGI CKF	368

Figure 17 (continued)

SEQ-ID-NO-1480	GPNCKFDH--	--PMGTVMYG	LATSPFTGDVIS	ARRML-----	-APMPAHSEW	412
SEQ-ID-NO-1475	GPNCKFHH--	--PMGNPMYGM	HSSPTSEAQ	TSRRM-----	LAHMPSHPEV	411
SEQ-ID-NO-1477	GPNCKFDH--	--PI GTVMYG	HSSPTSEVP	TSRRM-----	LAYVPSHPEV	418
SEQ-ID-NO-1471	GVNCKFDHPM	AAPMGVYAYG	YSASASPINAP	M-----	-----	420
SEQ-ID-NO-1457	GPSCKFDH--	--PMRVFTYD	NTASETDEV	-----	-----	362
SEQ-ID-NO-1467	GPSCKFDH--	--PMRVFTYD	NTASETDIFV	-----	-----	362
SEQ-ID-NO-1460	GPSCKFNH--	--PMGI FTYS	YSFSSPSDAP	VIICFGSSSG	TAGLNLSSEG	416
SEQ-ID-NO-1462	GPSCKFDH--	--PMGVFTYN	LTASSSADAP	VRRNLGSSSG	SPGLTLSSEG	414
SEQ-ID-NO-1480	SPDNMSGRSR	RI THSDSQOI	PSGERGIERE	AS-----	444	
SEQ-ID-NO-1475	SPDSOSGRSR	RI VHSDSQOI	PSWERITERE	AS-----	443	
SEQ-ID-NO-1477	LPDNGSGRSR	RI THSDSQOI	PSGERSIERE	AS-----	450	
SEQ-ID-NO-1471	-----GR	RLESPSGSA	YAS-----	-----	435	
SEQ-ID-NO-1457	-VETSTGKSR	RLSVSETRQA	AFTSSGKDIT	I DNT QQ	397	
SEQ-ID-NO-1467	-VETSTGKSR	RLSVSETRQA	AFTSSGKDIT	I DNT QQ	397	
SEQ-ID-NO-1460	LVEAVPTKPR	RLSLSENRQI	SPSDDI DAE	G-----	446	
SEQ-ID-NO-1462	LVEAGPTKPR	RLSLSEPRQM	PPEDDONIDT	G-----	445	

Figure 18

SEQ-ID-NO-1512	MSMSSMSG	GGGDAACRT	VVFRRDLRV	EDNPALAAA	RAGGEVVPAY	50
SEQ-ID-NO-1499	-----MSG	-----GGCS	VWFRRDLRV	EDNPALAAAV	RA-GAVVAVE	36
SEQ-ID-NO-1506	---MSNSCSC	C-----GGCS	VWFRRDLRV	EDNPALAAAV	RA-GPVI AVF	41
SEQ-ID-NO-1497	MSDSVSCCGS	-----GGCS	VWFRRDLRV	EDNPALAAAV	RA-GPVI ALF	43
SEQ-ID-NO-1502	MSDSVSCCGS	-----GGCS	VWFRRDLRV	EDNPALAAAV	RA-GPVNALF	43
SEQ-ID-NO-1512	VWAPEEDGPY	YPGRVSRWWL	SOSLKHLDAS	LRLGACKLY	TRRSAADAVMA	100
SEQ-ID-NO-1499	VWAPEEEGHY	YPGRVSRWWL	KQSLAHLDSS	LRSLGCT-LV	TKRSTD SVST	85
SEQ-ID-NO-1506	VWAPEEEGHY	DGRVSRWWL	KNSLAQLDSS	LRSLGTC-LI	TKRSTD SVAS	90
SEQ-ID-NO-1497	VWAPEEEGHY	HGRVSRWWL	KNSLAQLDSS	LRSLGTC-LI	TKRSTD SVAS	92
SEQ-ID-NO-1502	VWAPEEEGHY	HGRVSRWWL	KNSLAQLDSS	LRSLGTC-LI	TKRSTD SVAS	92
SEQ-ID-NO-1512	LLOLVRDIFTGA	TRLFFNHYD	PI SLVRDHRL	KEMMAEGLI	VQSFNADLLY	150
SEQ-ID-NO-1499	LLLEVIKSTGA	TQLFFNHYD	PLSLVRDHRA	KEVLTAQGI A	VRSFNADLLY	135
SEQ-ID-NO-1506	LLEVVKSTGA	SQIFFNHYD	PLSLVRDHRA	KDTLTAEGLA	VKSFNADLLY	140
SEQ-ID-NO-1497	LLDVVKSTGA	SQIFFNHYD	PLSLVRDHRA	KDVLTAQGI A	VRSFNADLLY	142
SEQ-ID-NO-1502	LLDVVKSTGA	SQIFFNHYD	PLSLVRDHRA	KDVLTAQGI A	VRSFNADLLY	142
SEQ-ID-NO-1512	EPWEVMDDEG	QSFTMFAPFW	NRCLSMPPYDP	AAPLLPPKR	NSGDLSMCPS	200
SEQ-ID-NO-1499	EPWDVNDAQG	RPFITFATFW	DRCLSMPPDP	EAPLLPPKRI	SGDHSRCPS	185
SEQ-ID-NO-1506	EPWEVTDELG	RPFMSFAFW	ERCLSMPPYDP	ESPLLPPKKI	SGDVSCKVA	190
SEQ-ID-NO-1497	EPWEVTDELG	RPFMSFAFW	ERCLSMPPYDP	ESPLLPPKKI	SGDVSCKVA	192
SEQ-ID-NO-1502	EPWEVTDELG	RPFMSFAFW	ERCLSMPPYDP	ESPLLPPKKI	SGDVSCKVA	192
SEQ-ID-NO-1512	DDLI FEDDSE	RGSNALLARA	WSPGWQNADK	ALTAFNGPL	HYSMNRKKA	250
SEQ-ID-NO-1499	CMVFCDELE	KGSNALLARA	WSPGWSNAADR	ALTTFI NGPL	EYSKNRRKA	235
SEQ-ID-NO-1506	DTLI FEDESE	KGSNALLARA	WSPGWSNADK	ALTTFI NGPL	EYSKNRRKA	240
SEQ-ID-NO-1497	DPLVFEEDSE	KGSNALLARA	WSPGWSNGDK	ALTTFI NGPL	EYSKNRRKA	242
SEQ-ID-NO-1502	DPLVFEEDSE	KGSNALLARA	WSPGWSNGDK	ALTTFI NGPL	EYSKNRRKA	242
SEQ-ID-NO-1512	DSASTSLLSP	YLHFGCELSVR	KVFLVLRMKQ	MWSNEGNA	AEEESCTLFRL	300
SEQ-ID-NO-1499	DSATTSFLSP	HLHFGCEVSVR	KVFLVRLI KQ	VLWANEGNKA	GEESVNLFLK	285
SEQ-ID-NO-1506	DSATTSFLSP	HLHFGCEVSVR	KVFLLRLI KQ	VAWANEGNQA	GEESVNLFLK	290
SEQ-ID-NO-1497	DSATTSFLSP	HLHFGCEVSVR	KVFLVRLI KQ	VAWANEGNEA	GEESVNLFLK	292
SEQ-ID-NO-1502	DSATTSFLSP	HLHFGCEVSVR	KVFLVRLI KQ	VAWANEGNEA	GEESVNLFLK	292

Figure 18 (continued)

SEQ-ID-NO-1512	SI GLREYSRY	LSFNHPOSHE	KPLL AHLRFF	PWV NECYFK	I WROQRT GYP	350
SEQ-ID-NO-1499	SI GLREYSRY	LSFNHPYSHE	RPLLGHKLFFF	PWVVDGCGYFK	AWRQRGRT GYP	335
SEQ-ID-NO-1506	SI GLREYSRY	SFNHPYSHE	RPLLGHKLFFF	PWAVDENYFK	AWRQRGRT GYP	340
SEQ-ID-NO-1497	SI GLREYSRY	SFNHPYSHE	RPLLGHKLFFF	PWAVDENYFK	AWRQRGRT GYP	342
SEQ-ID-NO-1502	SI GLREYSRY	SFNHPYSHE	RPLLGHKLFFF	PWAVDENYFK	AWRQRGRT GYP	342
SEQ-ID-NO-1512	LVDAGMRELW	ATCWLHDRI R	VVVSSFFVVKV	QLPWRWGGMK	YFWDTL LDAD	400
SEQ-ID-NO-1499	LVDAGMRELW	ATGWLHDRI R	VVVASFFVVKV	QLPWRWGGMK	YFWDTL LDAD	385
SEQ-ID-NO-1506	LVDAGMRELW	ATGWLHDRI R	VVVSSFFVVKV	QLPWRWGGMK	YFWD1LL DAD	390
SEQ-ID-NO-1497	LVDAGMRELW	ATGWLHDRI R	VVVSSFFVVKV	QLPWRWGGMK	YFWDTL LDAD	392
SEQ-ID-NO-1502	LVDAGMRELW	ATGWLHDRI R	VVVSSFFVVKV	QLPWRWGGMK	YFWDTL LDAD	392
SEQ-ID-NO-1512	LESDALGWQY	SGSLPDGREG	LDRI DNPQFE	GYKFDPHGEY	VRRWLPELAR	450
SEQ-ID-NO-1499	LESDALGWQY	TGTLPDGREG	FDRI DNPQFE	GYKFDPNGEY	VRRWLPELAR	435
SEQ-ID-NO-1506	LFSDALGWQY	TGTLPDSRE	FDRI DNPQFE	GYKFDPNGEY	VRRWLPELSR	440
SEQ-ID-NO-1497	LESDALGWQY	TGTLPDSRE	FDRI DNPQFE	GYKFDPNCFY	VRRWLPELSR	442
SEQ-ID-NO-1502	LESDALGWQY	TGTLPDSRE	FDRI DNPQFE	GYKFDPNGEY	VRRWLPELSR	442
SEQ-ID-NO-1512	LPTEWI HHPW	DAPASVLOQA	CVELGSNYP	PI VGLDAANA	RLDEALSEMW	500
SEQ-ID-NO-1499	LPTEWI HHPW	NAPESVLQAA	GI ELCGSNYP	PI VGI DAAKV	RLDEALSEMW	485
SEQ-ID-NO-1506	LPTEWI HHPW	NAPESVLQAA	GI ELCGSNYP	PI VGI DEAKA	RLHEALSQMW	490
SEQ-ID-NO-1497	LPTDWI HHPW	NAPESVLQAA	GI ELCGSNYP	PI VGLDEAKA	RLHEALSQMW	492
SEQ-ID-NO-1502	LPTDWI HHPW	NAPESVLQAA	CI ELCGSNYP	PI VGLDEAKA	RLHEALSQMW	492
SEQ-ID-NO-1512	QLEASRAAM	DNGMEEGLGD	SSE--VPPI E	FPRELQMEVD	REPARYTANV	548
SEQ-ID-NO-1499	QLEASRAAI	ENGTEEGLGD	SSE--SAPI A	FPQDI NMEEN	HEPVNR--NP	531
SEQ-ID-NO-1506	QLEASRAAI	ENGSEEGLGD	STEFVEAPI E	FPRDI TMEET	-EPTRL--NP	537
SEQ-ID-NO-1497	QLEASRAAI	ENGSEEGLGD	SAEVEEAPI E	FPRDI TMEET	-EPIHL--NP	539
SEQ-ID-NO-1502	QLEASRAAI	ENGSEEGLGD	SAEVEEAPI E	FPRDI TMEET	-EPTRL--NP	539
SEQ-ID-NO-1512	LT TARRHEDO	MVPTMTSSLN	RA - ETELSA	DEMNDSR	AEVPT R-VNF	594
SEQ-ID-NO-1499	PATNRRYEDO	MVPSMTSSF	RI - EDEETSS	DVRNSTGDGR	AEVPRD-VNV	579
SEQ-ID-NO-1506	--VHRYEDO	MVPSITSSL	RPEEDQESSL	SLRNSSCDSR	AEVPRNMVNT	584
SEQ-ID-NO-1497	--NRRYEDO	MVPSITSSL	RPEEDESSL	NLRNSVGDSR	AEVPRNMVNT	586
SEQ-ID-NO-1502	--NRRYEDO	MVPSITSSL	RPEEDESSL	NLRNSVGDSR	AEVPRNMVNT	586

Figure 18 (continued)

SEQ-ID-NO-1512	EPAI ERE ENF	RTT AGN VART	NGI HEH NNFQ	OPO HMRM RNL	APS VSEASSG	644
SEQ-ID-NO-1499	NQDP FRRDT LN	QGF VQS VHD	NSL PFFN ---	VVRGLANME	DSTA ESSSSG	625
SEQ-ID-NO-1506	NQAR QFEE ARA	DPV SNOV --- T	AMI PEFN ---	I RI VAENTE	ESTAE SSSSG	628
SEQ-ID-NO-1497	NOA QR --- RA	EPAS NOV --- T	AMI PEFN ---	I RI VAESTE	DSTA ESSSSG	628
SEQ-ID-NO-1502	NOA QR --- RA	EPAS NOV --- T	AMI PEFN ---	I RI VAFSTE	DSTA ESSSSG	628
WT GRECCVVP	VWSPPA ASDH	SET FASDEAD	[--- SSRSY	DRHP POSH RI	690	
RRER DGGI VP	VWSPPASS Y	SFQFV DENG	G --- AJ SSY	LPRHP QSHQI	671	
RRER DGGI VP	EWSG ----- Y	SEQFA SEENG	GGGTTSSY	LQN H --- HEI	670	
RRER SGGI VP	EWS PG --- Y	SEQFP SEENG	GGGTTSSY	LQN H --- HEI	671	
RRER SGGI VP	EWS PG --- Y	SEQFP SEENG	GGGTTSSY	LQN H --- HEI	671	
SEQ-ID-NO-1512	MNW S0LSQSL	700				
SEQ-ID-NO-1499	LNW RRL SQT G	681				
SEQ-ID-NO-1506	VNW RRL SQT G	680				
SEQ-ID-NO-1497	INWR RL SQT G	681				
SEQ-ID-NO-1502	LNW RRL SQT G	681				

Figure 19

SEQ-ID-NO-1612	----C ₅ S ₁ C ₅ L ₁	P ₁ -P ₂ F ₁ A ₂ K ₃ T ₄ Y ₅ E ₆	M ₁ V ₂ D ₃ D ₄ L ₅ I ₆ S ₇ I ₈	N ₁ S ₂ I ₃	V ₁ S ₂ W ₃ S ₄ V ₅ S ₆ S ₇ K ₈ F ₉	V ₁ W ₂ N ₃ P ₄ P ₅ E ₆ F ₇ A ₈ R ₉	50
SEQ-ID-NO-1597	APTPM ₁ L ₂ N ₃ A ₄ N ₅ A ₆	P ₁ P ₂ F ₁ L ₃ S ₄ K ₅ T ₆ Y ₇	M ₁ V ₂ D ₃ D ₄ P ₅ S ₆ I ₇	D ₁ A ₂ I ₃	V ₁ S ₂ W ₃ S ₄ A ₅ T ₆ N ₇ S ₈	V ₁ V ₂ W ₃ D ₄ P ₅ E ₆ F ₇ A ₈ R ₉	69
SLO-ID-NO-1609	VTAAC ₁ AQ ₂ R ₃ S ₄ V ₅	P ₁ T ₂ P ₃ F ₄ L ₅ S ₆ K ₇ T ₈ Y ₉	L ₁ V ₂ D ₃ D ₄ P ₅ A ₆ N ₇ T ₈	D ₁ D ₂ I ₃	S ₁ W ₂ N ₃ D ₄ G ₅ S ₆ A ₇ F ₈	V ₁ W ₂ R ₃ P ₄ A ₅ E ₆ F ₇ A ₈ R ₉	73
SEQ-ID-NO-1614	VVG ₁ C ₂ G ₃ R ₄ T ₅ V ₆	P ₁ T ₂ P ₃ F ₄ L ₅ T ₆ K ₇ Y ₈ Q ₉	L ₁ V ₂ D ₃ D ₄ P ₅ A ₆ N ₇ T ₈	D ₁ D ₂ V ₃	S ₁ W ₂ N ₃ D ₄ G ₅ S ₆ A ₇ F ₈	V ₁ W ₂ R ₃ P ₄ A ₅ E ₆ F ₇ A ₈ R ₉	67
SEQ-ID-NO-1589	-GTAES ₁ S ₂ Q ₃ R ₄ S ₅ I ₆	P ₁ T ₂ P ₃ F ₄ L ₅ T ₆ K ₇ Y ₈ Q ₉	L ₁ V ₂ D ₃ D ₄ P ₅ A ₆ N ₇ T ₈	D ₁ D ₂ V ₃	S ₁ W ₂ N ₃ D ₄ G ₅ S ₆ A ₇ F ₈	V ₁ W ₂ N ₃ P ₄ T ₅ V ₆ F ₇ A ₈ R ₉	63
SEQ-ID-NO-1587	GGCGD ₁ S ₂ Q ₃ R ₄ S ₅ I ₆	P ₁ T ₂ P ₃ F ₄ L ₅ T ₆ K ₇ Y ₈ Q ₉	L ₁ V ₂ D ₃ D ₄ P ₅ A ₆ N ₇ T ₈	D ₁ D ₂ V ₃	S ₁ W ₂ N ₃ D ₄ G ₅ S ₆ A ₇ F ₈	V ₁ W ₂ R ₃ P ₄ A ₅ E ₆ F ₇ A ₈ R ₉	96
SEQ-ID-NO-1596	--T ₁ E ₂ Q ₃ R ₄ S ₅ I ₆	P ₁ T ₂ P ₃ F ₄ L ₅ T ₆ K ₇ Y ₈ Q ₉	L ₁ V ₂ D ₃ D ₄ P ₅ A ₆ N ₇ T ₈	D ₁ D ₂ V ₃	S ₁ W ₂ N ₃ D ₄ G ₅ S ₆ A ₇ F ₈	V ₁ W ₂ R ₃ P ₄ A ₅ E ₆ F ₇ A ₈ R ₉	61
SEQ-ID-NO-1591	SGSGD ₁ S ₂ Q ₃ R ₄ S ₅ I ₆	P ₁ T ₂ P ₃ F ₄ L ₅ T ₆ K ₇ Y ₈ Q ₉	L ₁ V ₂ D ₃ D ₄ P ₅ A ₆ N ₇ T ₈	D ₁ D ₂ V ₃	S ₁ W ₂ N ₃ D ₄ G ₅ S ₆ A ₇ F ₈	V ₁ W ₂ R ₃ P ₄ A ₅ E ₆ F ₇ A ₈ R ₉	76
SEQ-ID-NO-1603	VFTM ₁ ESQ ₂ R ₃ S ₄ V ₅	P ₁ A ₂ P ₃ F ₄ L ₅ T ₆ K ₇ Y ₈ Q ₉	L ₁ V ₂ D ₃ D ₄ P ₅ A ₆ N ₇ T ₈	D ₁ D ₂ V ₃	S ₁ W ₂ N ₃ D ₄ G ₅ S ₆ A ₇ F ₈	V ₁ W ₂ R ₃ P ₄ A ₅ E ₆ F ₇ A ₈ R ₉	51
SEQ-ID-NO-1605	---MSQRT ₁ A ₂	P ₁ A ₂ P ₃ F ₄ L ₅ T ₆ K ₇ Y ₈ Q ₉	L ₁ V ₂ D ₃ D ₄ P ₅ A ₆ N ₇ T ₈	D ₁ D ₂ V ₃	S ₁ W ₂ N ₃ D ₄ G ₅ S ₆ A ₇ F ₈	S ₁ W ₂ N ₃ E ₄ T ₅ F ₆	46
SEQ-ID-NO-1606	---MSQRT ₁ V ₂	P ₁ A ₂ P ₃ F ₄ L ₅ T ₆ K ₇ Y ₈ Q ₉	L ₁ V ₂ D ₃ D ₄ P ₅ A ₆ N ₇ T ₈	D ₁ D ₂ V ₃	S ₁ W ₂ N ₃ D ₄ G ₅ S ₆ A ₇ F ₈	V ₁ W ₂ K ₃ T ₄ A ₅ F ₆ K ₇ A ₈ K ₉	46

SEQ-ID-NO-1612	DLLPRFFKHN	NFSSFTI RQL N	TYGFKKI DPE	QWEFANDDFW	RCPH MKN	100
SEQ-ID-NO-1597	DLLPKFFKHN	NFSSFVRLQN	TYGFRKVDPD	RWFANEGLF	RCKQOLLKS	119
SEQ-ID-NO-1609	DLLPKYFKHN	NFSSFVRLQN	TYGFRKI VPD	RWFENDCFR	RGEKRLLCDI	123
SEQ-ID-NO-1614	DLLPKYFKHN	NFSSFVRLQN	TYGFRKI VPD	RWFENDCFR	RGERALLCEI	117
SEQ-ID-NO-1589	DLLPKYFKHN	NFSSFVRLQN	TYGFRKVVPD	RWEFSNDYFR	RGEKRLLCEI	113
SEQ-ID-NO-1587	DLLPKYFKHN	NFSSFVRLQN	TYGFRKVVPD	RWEFSNDYFR	RGEKRLLCEI	113
SEQ-ID-NO-1596	DLLPKYFKHN	NFSSFVRLQN	TYGFRKVVPD	RWEFSNDYFR	RGEKRLLCEI	113
SEQ-ID-NC-1591	DLLPKYFKHN	NFSSFVRLQN	TYGFRKVVPD	RWEFSNDYFR	RGEKRLLCEI	113
SEQ-ID-NO-1603	DLLPNFFKHN	NFSSFVRLQN	TYGFKKVVAD	RWFENDCFR	RGERALLRDI	111
SEQ-ID-NO-1605	DLLPKYFKHN	NFSSFVRLQN	TYGFRKI VPD	KWFEFANENFK	RCKQELLTAI	96
SEQ-ID-NO-1606	DLPVTFKHN	NFSSFVRLQN	TYGFRKI VPD	KWFEFANENFK	RQKQELLTAI	96

Figure 19 (continued)

SEQ-ID-NO-1612	HRRKPVHSHS	LQLNQAQGPL	GDEERQGFTD	GI EKLKRDKE	RLLVELQ-KF	149	
SEQ-ID-NO-1597	SRRKPAHGHT	QQQAQQPHGQ	SSSVGACVEV	GKFGLEEEVE	RLKRDKNVIM	169	
SEQ-ID-NO-1609	HRRKV	-----SPTAGA	VIVAAARAAA	P-----	-----MA	148	
SEQ-ID-NO-1614	HRRKV	-----TPPAPA	AITAAVA-AA	P-----	-----MA	141	
SEQ-ID-NO-1589	QRRKL	-----SSPTAAA	VIVAPVTVA	P-----	-----MA	139	
SEQ-ID-NO-1587	QRRKL SQPAM	AAAAAAAHAA	VIAASAVTVA	V-----	-----V	180	
SEQ-ID-NO-1596	QRRKL	-----LPVPPAAA	PAANTANTV	V-----	-----VA	139	
SEQ-ID-NO-1591	QRRKL	-----SITMAASA	VISASVTVAA	P-----	-----TV	152	
SEQ-ID-NO-1603	HRRKT	-----	-----	-----	-----PQ	108	
SEQ-ID-NO-1605	RRRK	-----VTS	PAGGK	SVAGCAS	-----	117	
SEQ-ID-NO-1606	RRRK	-----VTP	PAGGK	SVVPGTS	-----	117	
SEQ-ID-NO-1612	QHEWQTYEIQI	HCSNDRLEK	-----EOK	QHKMVSSI	SH VLOKPVLAVN	193	
SEQ-ID-NO-1597	QELVRLRQOQ	QTIDSQLQT	MQRQLQGMEQR	QQQMMSFLAK	AVQSPOFFAQ	219	
SEQ-ID-NO-1609	LPV	-----GS	PVYSGEEQ	-----LSS	SSPEPSLQQ	175	
SEQ-ID-NO-1614	LPVTTRDGS	PVLSGEEQ	-----V	-----S	SSSSFEPPLV	172	
SEQ-ID-NO-1589	KPI	-----IS	PSNSGDEQSP	-----V	-----SASSP	162	
SEQ-ID-NO-1587	AHI	-----VS	PSNSGEEQ	-----V	-----SNSSPAAAAA	206	
SEQ-ID-NO-1596	APAVH	-----VS	PITS	-----SGDEQ	-----V	163	
SEQ-ID-NO-1591	ARA	-----VS	PANSGDDQ	-----C	-----STSSP	173	
SEQ-ID-NO-1603	HYQQQYEQS	PQIFOPDE	-----S	-----C	WI DSP	134	
SEQ-ID-NO-1605	-----AS	PONSCDDI	-----C	-----SS	STSSP	135	
SEQ-ID-NO-1606	-----AS	PDSGEDL	-----C	-----SS	STSSP	135	
SEQ-ID-NO-1612	IIPITFMDR	KRRLPRSGHY	YDESSI	EADAI	ETISOMPREN	AENTIVTLN	243
SEQ-ID-NO-1597	FVQQONDNSNR	RIEVNKRR	---LKQDGIA	EITIEATPPD	GQIVKYQPMM	266	
SEQ-ID-NO-1609	HPPAPSGSG	-----SGG	---VVGDVG	EENERLREN	ARLARELGOM	214	
SEQ-ID-NO-1614	LPQAPSGSG	-----SGG	---VASGDVG	DENERLREN	AQLARELSQM	211	
SEQ-ID-NO-1589	---SRLNQAG	-----	---TVMAELM	KENEKLRKEN	VOLNQOLSEM	196	
SEQ-ID-NO-1587	AI GCVVGGC	---SLORTTSC	---TAPELV	EENERLRKDN	ERLRKEMTKL	250	
SEQ-ID-NO-1596	---I AGNNNNN	---TVHRTTSC	---TAPELL	EENERLRKEN	IQLSNELSQL	206	
SEQ-ID-NO-1591	---CGACTACC	ANSF	---TTPPEIL	EENERLRKEN	SALSIELTQL	218	
SEQ-ID-NO-1603	---LPSPKSNT	-----	---DLTALS	EDNQRLRKDN	FMLSELSTM	169	
SEQ-ID-NO-1605	---DSKNPG	---SDVTPGKL	---SOFTDLS	DENEKLKKDN	QMLSSSELVQA	176	
SEQ-ID-NO-1606	---DSKNPG	---SDVTPGK	---SOFADLS	DENEKLKKDN	QMLSSELAQA	175	

Figure 19 (continued)

SEQ-ID-NO-1612	V E R L D O L E S S	V A F W E I A H D I	I G D N F Q A Q : Q S	N M D F D E S T S C	A D S P S I	S C A Q	293
SEQ-ID-NO-1597	N E T A K A M I _ R X	I M K W D T P R V E I	S F I N K N P D N Y L	I G D G T S P S S A	M D S S S S T	W S N	316
SEQ-ID-NO-1609	K K L C N N I _ L L	M S K Y A A T Q Q P	D A A K E F A A A G	-----	- N C T G	E S S D A A A P P	257
SEQ-ID-NO-1614	R K L C N N I _ L L	M S K Y A F S T Q Q L	D A A N A S S A A C	N N N N N N N C S G	E S A E A T	F L P	261
SEQ-ID-NO-1589	K S I _ C N N I _ F S L	M S N Y A S S O S E	-----	-----	-----	-----	N I S P
SEQ-ID-NO-1587	K G L Y A N I _ Y T L	M A N F T P C Q E D	-----	-----	-----	-----	C A H I L P
SEQ-ID-NO-1596	K G L C N N I _ L S L	M T N Y A S G F S R	Q Q L E S S T S A	-----	-----	-----	-----
SEQ-ID-NO-1591	R G L C N N I _ M V L	M N N Y A S P O L E	G N S C G N S N N	-----	-----	-----	N L A E
SEQ-ID-NO-1603	K N L Y N D I _ I Y F	I Q N H V S P A S P	F E O R S N N S A	-----	-----	-----	T I L K L V E
SEQ-ID-NO-1605	K K Q C N C L V A F	L S D Q Y V K V A P D	M I N R I M S Q G	-----	-----	-----	T P
SEQ-ID-NO-1606	K K Q C D E L V A F	L N Q Y V K V A P D	M I N R I S Q G	-----	-----	-----	T
SEQ-ID-NO-1612	D D V D M R P K --	- S S G I D M N S E	P T A A A A V P D P L	A S K D Q P A G I T	-----	V A A T C V	336
SEQ-ID-NO-1597	S G V T L Q E V	- P F S S V Q S T Q	I P M S T G T Q G H	I P S A E K -----	-----	P E I L S M	355
SEQ-ID-NO-1609	C P S I L E L L	- P S C R A D P A P	A A A C T D H E D D	E K A C -----	-----	A R L F G V	294
SEQ-ID-NO-1614	L P A V L D L M	- P S C P G A A S A	A A P V S D N E E G	M M S -----	-----	A K L F G V	297
SEQ-ID-NO-1589	V H K P L D F L	- P A K R L S C G E	S V E E T S -----	-----	-----	-----	P R I F G V
SEQ-ID-NO-1587	E G K P L D L L	- P F E R Q E M S E	A I M A S E I E T G	I G L K L G E D L T	-----	P R L F G V	318
SEQ-ID-NO-1596	G K A P L E L L	- P A K H V S S A D	D A L H V C G A A G	A A A C A T G N A A	E A E V P K I	F G V	290
SEQ-ID-NO-1591	V K A A L E L L	- P E ----- V A D	E V A V E S G R P R G	G A A A T E S E V S	-----	P R L F G V	288
SEQ-ID-NO-1603	L D S S S P Q L	- P N D K D C N S S	S -----	-----	-----	-----	V K L F G V
SEQ-ID-NO-1605	S C S S L E E L V K	E V G G V K D L E E	Q G S Y N D N D K	E D D D E K G D T	-----	L K L F G V	252
SEQ-ID-NO-1606	S C S S Y G E L	- V K E V I G G V N	D L E A Q G S D D D	E K G D T -----	-----	L K L F G V	243
SEQ-ID-NO-1612	N D V F W E Q F T	E D P G -----	-----	-----	-----	-----	350
SEQ-ID-NO-1597	P Q A A S A N V M	K D G T H A A S T I	P T S Q A D V I M P	D I P S V P E I V P	K S I L D I	P E D N	405
SEQ-ID-NO-1609	S I G - R K R M R	D E S D H H A -----	-----	-----	-----	-----	309
SEQ-ID-NO-1614	S I G - R K R M R	H D G G D -----	-----	-----	-----	-----	311
SEQ-ID-NO-1589	P I C C A A K R A R	E E S E G V A T E A	A T A A D E T -----	-----	Q L Q L Q	Q -----	283
SEQ-ID-NO-1587	S I G - V K R A R	R E E E L G A A E E	E D D D R R -----	-----	E A A A Q	E -----	348
SEQ-ID-NO-1596	S I G - L K R C R	T I C E ----- A E P	E G E D Q N Q M Q T	R A Q T Q S Q S S Q	E -----	-----	326
SEQ-ID-NO-1591	S I G - C F K R V R	I D E E ----- E E E	E G N -----	-----	R Q Q T E	G -----	312
SEQ-ID-NO-1603	P I D G - K K R V H	-----	-----	-----	-----	-----	238
SEQ-ID-NO-1605	L L K - E K K K K	R G -----	-----	-----	-----	-----	262
SEQ-ID-NO-1606	L L K - E N K K K K	R G -----	-----	-----	-----	-----	253

Figure 19 (continued)

SEQ-ID-NO-1612	--ASETQEVQ SER-----	--KDCDGRKN EGKPNDHSKF WWN[RNANNL	389
SEQ-ID-NO-1597	YMAPETDDGF MDPSSSLGSLP	DLDCLSPGA DJ DLLSNS: MDDLLOTPI P	455
SEQ-ID-NO-1609	--GVCAAEVK AEP-----	VDARPDDQO RQRNATEPQS WPI YRPRPVY	348
SEQ-ID-NO-1614	--DDIAATVK AEP-----	MDGRPHGK DE QSA -ETQA WPI YRPRPVY	349
SEQ-ID-NO-1589	--PGCSEI K LEP-----	LDCCONRGR DDDRGQI QDAP WL RQFHANQ	322
SEQ-ID-NO-1587	--CEQISSDVK AEP-----	ME ENNSCINHNGS WLE DKG -----	377
SEQ-ID-NO-1596	--PDHGSDVK SEP-----	LD DS DYCQDHDPH WLE -----	355
SEQ-ID-NO-1591	--KEHESDVK AEP-----	LD GS SGNSDHQDOR -----	337
SEQ-ID-NO-1603	--PSN-----	LD -----	243
SEQ-ID-NO-1605	--PDENIETC GCR-----	GK MMKFDYNGP WMKMSPAGE	295
SEQ-ID-NO-1606	--PDENADIS GSR-----	GK MMKFTDYNLP WMKMSAPGE	286
SEQ-ID-NO-1612	SEPMGHVGQA EKT-----	-----	402
SEQ-ID-NO-1597	EDFEANI DEI SRGNFVQPTE NGWDNNTOPL DOLTEQMGLL SSDAKRI	-----	502
SEQ-ID-NO-1609	HPLRACNGSG SAGSDHDGSN DSR-----	-----	371
SEQ-ID-NO-1614	OPI RACNGYE YDRAGSDQDG SNST-----	-----	373
SEQ-ID-NO-1589	RVCN-----	-----	326
SEQ-ID-NO-1587	-----	-----	377
SEQ-ID-NO-1596	-----	-----	355
SEQ-ID-NO-1591	-----	-----	337
SEQ-ID-NO-1603	-----	-----	243
SEQ-ID-NO-1605	SSKVCN-----	-----	301
SEQ-ID-NO-1606	SNKVCN-----	-----	292

Figure 20

Figure 20 (continued)

SEQ-ID-NO-1646	-----	-----	-----	-----	-----	16
SEQ-ID-NO-1648	-----	-----	-----	-----	-----	11
SEQ-ID-NO-1650	-----	-----	-----	-----	-----	13
SEQ-ID-NO-1642	-----	-----	-----	-----	-----	16
SEQ-ID-NO-1644	-----	-----	-----	-----	-----	29
SEQ-ID-NO-1651	QMLSSNDRI S	VQLEGNAKVE	LGKSESDPTT	MRKERNGSGA	CESDHPARLI	245
SEQ-ID-NO-1653	QMLSSNDRI S	VQLEGNAKVE	LGKSESDPTT	MRKERNGSGA	CESDHPARLI	246
SEQ-ID-NO-1637	-----	-----	DPNSLL	LYCKTESGAN	DFNIDF	82
SEQ-ID-NO-1635	-----	-----	TPPP--	SPDPDLF	CSSSTP-----	71
 SEQ-ID-NO-1646	-----	-----	-----	-----	-----	16
SEQ-ID-NO-1648	-----	-----	-----	-----	-----	11
SEQ-ID-NO-1650	-----	-----	-----	-----	-----	13
SEQ-ID-NO-1642	-----	-----	-----	-----	-----	16
SEQ-ID-NO-1644	-----	-----	-----	-----	-----	29
SEQ-ID-NO-1651	EPRLLTIVTN	CDFGGADSM	SKELGSAI HP	SVSKDRNVEN	ESGGASVCTF	295
SEQ-ID-NO-1653	EPRLLTIVTN	CDFGGADSM	SKELGSAI HP	SVSKDRNVEN	ESGGASVCTF	296
SEQ-ID-NO-1637	-----	-----	-----	-----	-----	82
SEQ-ID-NO-1635	-----	-----	-----	-----	-----	71
 SEQ-ID-NO-1646	-----	-----	-----	-----	-----	16
SEQ-ID-NO-1648	-----	-----	-----	-----	-----	11
SEQ-ID-NO-1650	-----	-----	-----	-----	-----	13
SEQ-ID-NO-1642	-----	-----	-----	-----	-----	16
SEQ-ID-NO-1644	-----	-----	-----	-----	-----	29
SEQ-ID-NO-1651	ALHNRNCHSS	CVESELELLN	AKYDLGPRDC	KESQEGPGLC	SLI SEERTVA	345
SEQ-ID-NO-1653	ALHNRNCHSS	CVESELEMLN	AKYDLGPRDC	KESQEGPGLC	SLI SEERTVA	346
SEQ-ID-NO-1637	-----	NCSLD FLESSID---	-----	-----	CTVS-----S	99
SEQ-ID-NO-1635	-----	HCLD CI PSSVD	-----	-----	SLGDFNGPI S	94
 SEQ-ID-NO-1646	-----	-----	-----	-----	-----	16
SEQ-ID-NO-1648	-----	-----	-----	-----	-----	11
SEQ-ID-NO-1650	-----	-----	-----	-----	-----	13
SEQ-ID-NO-1642	-----	F N DGVNE-----	-----	-----	EE-----	25
SEQ-ID-NO-1644	-----	-----	-----	-----	-----	29
SEQ-ID-NO-1651	AFGDATAFTFE	ERGNTSSGLE	ACKGSHCLDP	VEPKLMDSCA	TH----ALEG	391
SEQ-ID-NO-1653	AEGDATAFTFE	ERGNTSSGLE	ACKGSHCLDP	VEPKLMDSCA	TH----ALEG	392
SEQ-ID-NO-1637	KVGNEKF --D	SGSGKKEKLE	VS-CGYLCNS	PEARLMKSRV	DY----SGVNV	143
SEQ-ID-NO-1635	SLGEEDK--E	D---KDDCI K	VNREGYLCNS	MEARLLKSRI	CLGFDSGI HE	139

Figure 20 (continued)

SEQ-ID-NO-1646	-----I SD DLDD-----	-----NC FPA -----	28
SEQ-ID-NO-1648	-----A DLDD-----	-----NG FPA -----	21
SEQ-ID-NO-1650	-----A DLDD-----	-----NG FPD -----	23
SEQ-ID-NO-1642	EDEEGFVFND DVEE-----	-----NE EEE -----	44
SEQ-ID-NO-1644	-DDDAASFDAL RLDD-----	-----EG FPS -----	47
SEQ-ID-NO-1651	DGCDPFEI GT QLNE I NLCM E-DYTEGPLS NKVACLEGNG MDCGSFNSSC	-----	410
SEQ-ID-NO-1653	DGCDPFFI GT QLNE I NLCM E-DYTEGPLS NKVACLEGNG MDCGSFNSSC	-----	441
SEQ-ID-NO-1637	GNEEDTEENS ELLDALIKLCT EEEESEAREK I KVNC--NG DEC -----C	-----	184
SEQ-ID-NO-1635	DDEGFVESNS ELDVLI NLC S ESEGCRSG---EFSL ---GK DDS	-----	175
SEQ-ID-NO-1646	----- SPPT APAT -----	-----	36
SEQ-ID-NO-1648	-----LPSSPA A-----	-----	28
SEQ-ID-NO-1650	-----LPSSPA A-----	-----	30
SEQ-ID-NO-1642	-----	-----	44
SEQ-ID-NO-1644	-----QQ LPI E SPSP -----	-----	57
SEQ-ID-NO-1651	EVQCPLCGSN I SDSLSEELRL VHTNSCLDGD KPAKEPN S-----	-----	478
SEQ-ID-NO-1653	EVQCPLCGSN I SDSLSEELRL VHTNSCLDGD KPAKEPN S-----	-----	479
SEQ-ID-NO-1637	FVLCPLCGTD I SDSLSEEFR L VHTNECLDKE ENSVTYV SVF RI LVVLGGDD	-----	234
SEQ-ID-NO-1635	-I QCPLCSMD I SSSLSEEQRQ VHSNTCLDKS YNQPSEQDSL RKCENLSS-----	-----	222
SEQ-ID-NO-1646	-----S SFAD DFYRSGI DWS	-----	51
SEQ-ID-NO-1648	-----FAE DFYRSGI DWS	-----	45
SEQ-ID-NO-1650	-----A TTS S GFAE DFYRSGI DWS	-----	50
SEQ-ID-NO-1642	-----GFA S DFYRSGI DWS	-----	58
SEQ-ID-NO-1644	-----FAA DFYRSGI DWS	-----	77
SEQ-ID-NO-1651	-----DNQ NEP-CGESNV E-KRRVMEWL RN GLSKYEE I F I KEEDWE	-----	519
SEQ-ID-NO-1653	-----DNQ NEP-CGESNV E-KRRVMEWL RN GLSKYEE I F I KEEDWE	-----	520
SEQ-ID-NO-1637	GRPEVVPRGV ECPVCGPKK V-VSPVVKWL RN GLERYEE DFVREE DWE	-----	283
SEQ-ID-NO-1635	----LI KESI DDPVQLPQLV TDLSPVLKWL RSLGLAKYED VFI REE DWD	-----	268
SEQ-ID-NO-1646	SLQ-----AP PSHRRRPADC TT EKF -- CCP LVQKNLFQAW	-----	84
SEQ-ID-NO-1648	SLR-----APP PLGPPRRAPG V XERG -- GGS AVQSSLFQAW	-----	79
SEQ-ID-NO-1650	SLR-----APP PRRPPEGAAAG VKEKGKEGGS LVQSSLFQAW	-----	86
SEQ-ID-NO-1642	OL-----VED EETMSSSVKK MKQSN-----L FQI W	-----	83
SEQ-ID-NO-1644	SL-----LTP EROSLSSCKK LKQAN-----L FQI W	-----	102
SEQ-ID-NO-1651	T L QMLTEEDL LGMGI T S L GP RKKTAHALCE LRKKN----D DANDLAADML	-----	565
SEQ-ID-NO-1653	T L QMLTEEDL LGMGI I S L GP RKKIAHALCE LRKKN----N DANDLAADML	-----	566
SEQ-ID-NO-1637	T L QMLTEEDL FGIGVTA L GP RKKIVHALSE LRKGS-NHAI EAHCDAHAFG	-----	332
SEQ-ID-NO-1635	T L QSLTEEDL LSI GI T S L GP RKKIVNALSG VRDPF-ASSA EVOAQSHCTS	-----	317

Figure 20 (continued)

SEQ-ID-NO-1646	GLEKP---AS CMI E███VC---	-----GPPVQ	KN F QAWG O	KPPREEAQG	123
SEQ-ID-NO-1648	GI EKPRR DG RGA DSS---	-----LVIQ	RSL FOAWG E	RPORE-----	113
SEQ-ID-NO-1650	GI ERPRREFG AGACDSS---	-----LVIQ	RSL FOAWG E	RPKRF-----	121
SEQ-ID-NO-1642	GL QEINS PDTT KMK---	-----Q	TDL QSWGL O	KP-----	110
SEQ-ID-NO-1644	GF KRNV EIS PNQ GYCDVV	GEGSVSSEKK	SVKRGNWGST	L RD-----	145
SEQ-ID-NO-1651	NLENTKKAKI PMNG-----	-----N	KLI TEYFRCP	SSDO-----	594
SEQ-ID-NO-1653	NLENTKKAKI PMNG-----	-----N	KLI TEYFRCP	SSDO-----	595
SEQ-ID-NO-1637	EMSSRSRSHGA EMOVEASKI I	GDDTSKPTAN	KLI T DYFPGS	VPI K-----	376
SEQ-ID-NO-1635	SHVTER██DK STTRKAS---	--EPKKPTAN	KLI TEFEPGQ	AT-----	354
SEQ-ID-NO-1646	VPVCAGA GSSS SPSPS VAGS	·GRKRRWCGS	DEN--GASRK	PVA CPFYKQI	169
SEQ-ID-NO-1648	---GLGAGDS SPSS SLSGSL	LA RKRRRGST	EEERVAAK K	PLACPFYKKI	159
SEQ-ID-NO-1650	---CCGAGDA SPSPSRSGCSW	SGRKRRRGGP	EEFVAAAAMN	PR CPFYKKI	168
SEQ-ID-NO-1642	---SPFT SPA SNSAKTTSA	LGKRRRDSSF	SND-----S	PR CPFYKKL	151
SEQ-ID-NO-1644	---TCKVVEN SKST GKRKS F	HCEK R-----	-----V	TRSCPFYKKM	178
SEQ-ID-NO-1651	---ROKKACK VNT PSNL NSQ	KNSNAKATGC	RRTVKQ K	VKDTP WCCI	638
SEQ-ID-NO-1653	---ROKKACK VNT PSNL NSQ	KNSNAKATGG	RRTVKQ K	VKDTP WCCI	639
SEQ-ID-NO-1637	---KKT SMI S KEORGAEKISQ	PG VRKQGVK	NYTKKG K	FKDI PLWCSI	420
SEQ-ID-NO-1635	---ECTK RT APK VAEKIS P	SDSSS RAVR	RNGNNNG K	SKV PHWC	398
SEQ-ID-NO-1646	PGTPFTVDAF RYCAVE WCSA	YFL SHF H DH	YGLLT K WCH	GPI YCTALTA	219
SEQ-ID-NO-1648	PGTPFTVDAF RYGOVE GCSA	YFL SHF H DH	YGLLT K WCH	GPI YCSAI TA	209
SEQ-ID-NO-1650	PGTPFTVDAF RYGEVEGCSA	YFL SHF H DH	YGLLT K WCH	GPI YCSALTA	218
SEQ-ID-NO-1642	PGTPFTVDAF RYGCVOGCSA	YFL THF HADH	Y GLT KAWSH	GPI YCSSLTS	201
SEQ-ID-NO-1644	PGT FTVDAF RYGOVEECSA	YFL SHF HADH	YGLLSK MSH	GPI YCS LTG	228
SEQ-ID-NO-1651	PGTPFRVDAF RYFL RGDCICH	WF LTHFHV DH	Y GLT KSFCH	GKI YCSSVTA	687
SEQ-ID-NO-1653	PGTPFRVDAF RYFL LRGDCICH	WF LTHFHV DH	Y GLT KSFCH	GKI YCSSVTA	688
SEQ-ID-NO-1637	PGTPFRVDAF KY-L RGDCSII	WF LTHFHM DH	Y GLT RFSCH	GKI YCSL TA	469
SEQ-ID-NO-1635	PGTPFRVDAF KY-LTR DCICH	WF LTHFHL DH	Y GLT KSF SH	GKI YCSL VTA	447
SEQ-ID-NO-1646	RLVKM L S D SAY C PLELD	TEY DGKV	TF FANHCPG	AALI HFRPSD	269
SEQ-ID-NO-1648	RLVKMCL SVN SEM C PLELD	TEY EGVT V	T LEANHCPG	AALI HFRLSD	259
SEQ-ID-NO-1650	RLVKMCL SVN SD C PLELD	TEY EGVT V	T LEANHCPG	AALI HFRLSD	268
SEQ-ID-NO-1642	RLLRLS LSVN PSS HPELD	VEY E NGI KV	T LEANHCPG	AALI HFRLLD	251
SEQ-ID-NO-1644	RLVOMCL YVN PSY C PLEFD	TEY DGI KV	T LEANHCPG	AALI HFELPN	278
SEQ-ID-NO-1651	NLVHYK G P WDR LHV PLN	EKT T AGVN	TC DANHCPG	AV I FEPSN	737
SEQ-ID-NO-1653	NLVHYK G P WDR LHV PLN	EKT T AGVN	TC DANHCPG	AV I FEPSN	738
SEQ-ID-NO-1637	KLVN K G P WDSL HV PLN	OKI C AGVD	TC DANHCPG	S I I FEPP N	519
SEQ-ID-NO-1635	KLVNM K G P WERLOV LDLG	OKV N SGI DV	TC DANHCPG	S MI LFEPAN	497

Figure 20 (continued)

SEQ-ID-NO-1646	GKTYLHTGDF	RASKSMQLHP	LLQTSCISLL	YLDTTYCNPK	YKFPPQEDVI	319
SEQ-ID-NO-1648	GKFCYLHTGDF	RASKTMQSHP	LLORGRVNLLV	YLDTTYCNPK	YKFPPQEDVI	309
SEQ-ID-NO-1650	GKTYLHTGDF	RASRSMOELHP	LLORGRINLL	YLDTTYCNPK	YKFPPQCDVI	318
SEQ-ID-NO-1642	GFCYLHTGDF	RASKOMQTHP	LLFNORVHV	YLDTTYCNPK	YKFPSKEDV	301
SEQ-ID-NO-1644	GOCYLHTGDF	RACKLMQDYH	LFVNKRNV	YLDTTYCNPK	YKFPSKDDVL	328
SEQ-ID-NO-1651	GKAVLHTGDF	RFSESEMANNR	VQSSPIHTL	YLDTTYCNPK	YDPTQEIVI	787
SEQ-ID-NO-1653	GKAVLHTGDF	RFSESEMANNR	VQSSPIHTL	YLDTTYCNPK	YDPTQEIVI	788
SEQ-ID-NO-1637	GKAVLHTGDF	RFSEKMMTMDP	VIQMSSHTL	YLDTTYCNP	-----AOEAVI	563
SEQ-ID-NO-1635	GKAVLHTGDF	BYSEEMSNNW-	CSHSSL	YLDTTYCNPQ	YDPTQEAVI	545
SEQ-ID-NO-1646	DFVVIRTAQRY	LKKOPKTLIV	VGAYSIKGEN	VYLAI SOALE	VPI YIDASRR	369
SEQ-ID-NO-1648	DFVVIRIIQRY	LKKOPKTLIV	VGAYSIKGEN	VYLAI SOALC	AII YTIDASRR	359
SEQ-ID-NO-1650	DFVVIRSTRRY	LKKOPKTLIV	VGAYSIKGEN	VYLAI SOALE	VPI YIDASRR	368
SEQ-ID-NO-1642	SYVVRITKDF	LRKOPKTLIV	VGYSYIKGEC	VYLAI AKALC	VKI FANASRR	351
SEQ-ID-NO-1644	NYVVKTTNNH	LKKYPRTLVV	VGAYSIKGEN	VYLAI SKAIG	VKI HVNASRR	378
SEQ-ID-NO-1651	QFVI EAI QAE	AFN-PKTLFL	GSYTI GKER	LYMEVARLQ	KKI YYCAAKL	836
SEQ-ID-NO-1653	QFVI EAI QAE	AFN-PKTLFL	GSYTI GKER	LYMEVARLQ	KKI YYCAAKL	837
SEQ-ID-NO-1637	QFVI EAI QAE	AFN-PKTLFL	GSYTI GKER	LLEVARVILH	KKVYVNMMAKF	612
SEQ-ID-NO-1635	QFVVAI QAE	AFN-PKTLFL	GSYTI GKER	LLEVARVILR	EKI YI NPAKL	594
SEQ-ID-NO-1646	RLHSFGWP-	DLSKRSSCN	QSSPLHVLPL	ASLQHENLKK	YLET-LDORF	417
SEQ-ID-NO-1648	RLYSFGWP-	DLSKRCSCN	QSSPLHVLPI	CSINHENLKK	YMFT-I NGRF	407
SEQ-ID-NO-1650	RLHSFGWK-	DLSKRCSCN	QSSALHVLPL	GSVNHENWKK	YLGT-LNQDF	416
SEQ-ID-NO-1642	RLQSGFWD-	DLSKNLSTDG	KATCLHVLPM	SSLKVERDIE	HLKI -YREQY	399
SEQ-ID-NO-1644	RLLEYDCP-	DYSQRLOTNC	NNLHHVLVPM	SBLRIETLKE	YLKTLYKEQF	426
SEQ-ID-NO-1651	OILKHLGLPQ	EIMHWFTANE	AESHI HVVPM	WTIASFKRMK	YLSTOYADRF	886
SEQ-ID-NO-1653	OILKHLGLPQ	EIMHWFTANE	AESHI HVVPM	WLASFKRMK	YLSTOYADRF	887
SEQ-ID-NO-1637	RLLECLGFPE	EDMRMTLINE	QESHI HVVPM	WTLASFKRLK	HLSSQYAGRF	662
SEQ-ID-NO-1635	KLLECLGFSK	DDIQWFTVKE	EESHI HVVPL	WLASFKRLK	HVANRYTNR	644
SEQ-ID-NO-1646	LAVLAFRPTG	WTFSEAAAGKE	DLIKPSSRG	RVTI YGVVPS	FHSSFSELRD	467
SEQ-ID-NO-1648	LAVLAFRPTG	WTFSEATGKH	DLIKPSSNA	NVTI YGVVPS	EHSSFTELRD	457
SEQ-ID-NO-1650	LAVLAFRPTG	WTFSEATGKQ	DLIKPNSNG	SVTI YGVVPS	EHSSFTEL---	463
SEQ-ID-NO-1642	GAVLAFRPTG	WTYSEKIGEH	DLIKPTSRG	KTI YGVVPS	EHSSFTELRE	449
SEQ-ID-NO-1644	TISVLAFRPTG	WTFSEKIGND	LALIKPMNSNG	NITI YGVVPS	EHSSFTELRD	476
SEQ-ID-NO-1651	DLVAFCPTG	WSFCK--GKK	RIPCRKWQQG	AI RYEVPS	EHSSFTELRE	934
SEQ-ID-NO-1653	DLVAFCPTG	WSFCK--GKK	RTPCRKWQQG	AI RYEVPS	EHSSFTELRE	935
SEQ-ID-NO-1637	TLIVAFSPTG	WTFCGK--GKK	KSPGRRRCQQC	TII RYEVPS	EHOSFTELRE	710
SEQ-ID-NO-1635	SLIVAFSPTG	WTSCGK--TKK	KSPGRRRLQQG	TI RYEVPS	EHSSFTELKE	692

Figure 20 (continued)

SEQ-ID-NO-1646
SEQ-ID-NO-1648
SEQ-ID-NO-1650
SEQ-ID-NO-1642
SEQ-ID-NO-1644
SEQ-ID-NO-1651
SEQ-ID-NO-1653
SEQ-ID-NO-1637
SEQ-ID-NO-1635

FLKFLRPQKV	PTVNVGNA	NRDKM A YIFR	EWLKG	503
FVMLLKPKQK	PTVNGNAT	SRDKM A HFR	EWLKS	493
-----	-----	-----	-----	463
FVQFLRPDKI	PTVNNCNAG	TREK M SCFR	EWLRP-	484
FVQFLRPDKI	PTVNVCNA	NREK M SYFR	DWLKG-	511
FVRFISPEHI	PSVNNNDGPD	SANAMLAQLL	ND-----	966
FVRFISPEHI	PSVNNNDGPD	SANAMLAQLL	ND-----	967
FVKFVSPENI	PSVNNNDGPD	SANDMVSLL	S-----	741
FVQKVSPEVI	PSVNNNDGPD	SAAAMVSLLV	T-----	723

Figure 21

SFQ-ID-NO-1561	MATYYSS-P	GSE RDSQ	---	T MYS	AES GN	V SYPV	PS-A	GNFLY	38	
SEQ-ID-NO-1563	MATYYSS-P	CSE RDSQ	---	NMYS	RD	GNASYPM	PS-A	GNLLY	39	
SEQ-ID-NO-1565	MATYYHGGA	GT DI QI	---	Sgt	DGLO	LML MN	PS-YEG	---	33	
SEQ-ID-NO-1566	---	MYDQTS	DN	QADHQ	QQHNNL	GNSN	NNI	QT LML MN	PN	
SEQ-ID-NO-1540	---	---	---	---	ACSD	GGLO	LT	LMN	PTT YVO	47
SEQ-ID-NO-1567	MATYFHG-N	PPEI S	---	---	GGSA	DGL	OTL	LMN	PSGYI N	34
SEQ-ID-NO-1543	MATYFHG-N	NSEI Q	---	---	GGSA	DGL	OTL	LMN	PA-YVO	33
SEQ-ID-NO-1547	MSTYFHG-	NPEI Q	---	---	AST	DGL	OTL	VLM MN	PA-YVO	31
	MATYFHG	NPEI QAA	---	---	AASA	EGL	OTL	VLM MN	PT-YVO	34
SEQ-ID-NO-1561	TNNASSGPyT	EFSG	VQPO	-ON	MEL	---	GHP	SAMS HDS	S--SNEAT NM	82
SEQ-ID-NO-1563	TNNSI SGPyT	EFSG	LIQSQ	-ON	CNCME	MPDP	GHP	SMSQDS	S--ARESDML	85
SEQ-ID-NO-1565	GDAAAAAAAP	GAANMM	LN	SAV	TSM	PV	SFG	HOPCPSS	S--SAOHFV	80
SEQ-ID-NO-1556	TDTIOHLQQQ	QNOHQ	LLFLN	SAPAG	GNAL	SHAN	--QHA	P--LQOQHFV	92	
SEQ-ID-NO-1540	TODNDNSNNN	NNNSNNNN	---	TNT	NTNNNN	SSFVF	DSHA	POPNAISQOFV	83	
SEQ-ID-NO-1567	SDTPQPPP	HA	GN	LVFLN	SAAT	LAGNG	NT SI	QQQHNLS	S--HAPPQFV	77
SEQ-ID-NO-1543	SDTPPPP	PAN	---	LLFLN	PNSL	---	---	---	P--POT QOLM	60
SEQ-ID-NO-1547	SETPPPQSN	N	---	LVFLN	AAA	SANSL	SPPPH	LSGH	P--SNT QOFV	78
SEQ-ID-NO-1561	GSS	TE QR	SF	GP	KDMR	NEM	MH	MDGAHS	SGSDL	118
SEQ-ID-NO-1563	GSHQ	-GQR	SF	GP	VKDM	NEM	MH	MDGS	STADL	120
SEQ-ID-NO-1565	GI	PL	---	---	QAPP	AS	Q	---	---	90
SEQ-ID-NO-1556	GVPL	---	PAV	SL	HDD	NI	HCL	ORMW	NNQDQSQQVI	135
SEQ-ID-NO-1540	GI	PL	SCHEA	AS	ST	AA	DNI	S	VPSST VVSAT	111
SEQ-ID-NO-1567	GVPL	---	S	AE	QSM	VAH	HD	S	---	103
SEQ-ID-NO-1543	GI	PL	PAT	SAA	NQG	P	SHD	S	---	89
SEQ-ID-NO-1547	GI	PL	---	DPN	SHEA	S	PL	HGL	PRV	99
SEQ-ID-NO-1561	---	---	---	---	---	---	---	---	---	154
SEQ-ID-NO-1563	---	---	---	---	---	---	---	---	---	156
SEQ-ID-NO-1565	---	---	---	---	---	---	---	---	---	156
SEQ-ID-NO-1556	---	---	---	---	---	---	---	---	---	127
SEQ-ID-NO-1540	SCCGTT	DLA	SOLAF	CRP	I	V	VSPT	---	---	177
SEQ-ID-NO-1567	---	---	---	---	---	---	VDPT	HOQA	ACET PR	144
SEQ-ID-NO-1543	---	---	---	---	---	---	ADPN	---	SAAREAT R	132
SEQ-ID-NO-1547	---	---	---	---	---	---	DPS	---	CSARET PR	118
	---	---	---	---	---	---	DST	---	STARET PR	128

Figure 21 (continued).

SEQ-ID-NO-1561	THI LAPSYPH	WSAKQDLLTP	NSYQC-----	----DDNRMK	NMOSEASHA	195
SEQ-ID-NO-1563	TQI LAPSLPY	WSMVKPDMISP	HSMHD-----	SLRVDDI RIMK	SMOSEASRAI	201
SEQ-ID-NO-1565	AVLS--LSSR	EAAFPVTMAA	VVAAG-----	DEGKYLQAVA	QGMASHGOMV	170
SEQ-ID-NO-1566	PQQQQQI SFM	NNJSS-----	PSPR-----	TINNVITI	RGTM DGCSS--NMI	214
SEQ-ID-NO-1540	SQ00000QHH	QOHOPI IIVGF	GSGHGEEDI RV	GSCTGSGV	NGIAN-----	190
SEQ-ID-NO-1567	AG-----GSG	EDARV-----	--SAG-----	GSASSAS	NGVSGI QSVL	163
SEQ-ID-NO-1543	SLQQ-----PGYG	SQAOA-----	--VSD-----	GSASSGSGVH	NRNSGVQSVF	154
SEQ-ID-NO-1547	SQOO-----CGFC	SQAOAVSGED	I RVSC-----	GLVSFGSGV	NGVPGMQGV	171
SEQ-ID-NO-1561	RNSKYLKAAQ	ELLDEIVSVW	KCV-----	KOKT	DKGPAEACK-----ADGK	235
SEQ-ID-NO-1563	WNSRYLKAAQ	ELLDEVVNJV	KNI-----	KOKA	QKEQVEAGK-----TDAK	241
SEQ-ID-NO-1565	MSSKYLKAAQ	ELLDEVVSVS	KGWDDVKA	AAA	AKSPASV/K-----KK	211
SEQ-ID-NO-1556	LSSKYLKAAQ	ELLDEVVNIV	GKSN-----	KDD	QIKKDNMSNKE LI-----PLVS	258
SEQ-ID-NO-1540	VSSKYLKAAQ	ELLDEVVNAD	SDDMMNAKSOL	FSSKGKGSCGN	D-----KPVG	235
SEQ-ID-NO-1567	NSKYLKATQ	ELLDEVVNVN	GG-----	KVES	VKRSFEKN-----KVVG	202
SEQ-ID-NO-1543	LSSKYLKAAQ	ELLDEVVNVN	TTGI-----	TKSEL	LAKKGGGGNN HSNSSSKAVG	203
SEQ-ID-NO-1547	LSSKYLKATE	ELLDEVVNVN	SNGI -----	KSEI	SKRSNGI SSN NSN-----KVIG	216
SEQ-ID-NO-1561	ETDGGIKSEG	V---SSNPQES	CANAAAELST	AEKQELQNK	AKLMMLDEV	283
SEQ-ID-NO-1563	ETEGGLKSEG	V---SSNPQES	AANAAPELST	AERQELQNK	AKLMMLDEV	289
SEQ-ID-NO-1565	EDSEGVSGGG	EDDGGAKSG	GAPPPPEMST	AERQELQMKK	QKLI NMLDEV	261
SEQ-ID-NO-1556	DVNTNSGGG	G---CESSSRQ	KNEVA-----	ELTT	AQRQELQMKK AKLLAMLEEV	306
SEQ-ID-NO-1540	ESSAAGGEG	S---GGAAFAA	GKR-PVELQ	AEROEI OMKK	AKLSNMHLEV	282
SEQ-ID-NO-1567	ESSATAVSGDC	G---SVGGDG	GKR-STELST	JERQEYQMKK	AKLI NMLDEV	249
SEQ-ID-NO-1543	ESS---VAGDG	S---GGEAG	EKH-AAELTT	AEKOEI OMKK	AKLI NMLDEV	248
SEQ-ID-NO-1547	ESS---TGEQ	S---G-EGEAS	GKR-GPELST	AEROEI FMKK	AKLMSMLDEV	259
SEQ-ID-NO-1561	DRKYKHYHQ	MQLVMSSFINM	VACAGAAKPM	TAVALOTI SR	HFRCLKDAI N	333
SEQ-ID-NO-1563	DRKYKHYHQ	MQLVNSSFDV	VACGGAALKPM	TAVALOTI SR	HFRCLKDAI N	339
SEQ-ID-NO-1565	EQRYRQYHQ	MOVVVASFEA	VAGGGSAARTY	TALALRTI SR	QFRCLRDIA A	311
SEQ-ID-NO-1556	EQRYRQYHQ	MOI VSSFEQ	VAGVGSIAKSY	TQALHA SK	QFRCLKDAI S	356
SEQ-ID-NO-1540	EQRYRQYHQ	MOMVI SSFEQ	AAGI GSAKSY	TSLALKTI SR	QFRCLKEAI A	332
SEQ-ID-NO-1567	EQRYRQYHQ	MOMVI SSFEQ	VAGI GSARTY	TALALOTI SK	QFRCLKDAI T	299
SEQ-ID-NO-1543	EQRYRQYHQ	MOI VISSFEQ	AAGI GSAKTY	TALALKTI SK	QFRCLKDAI S	298
SEQ-ID-NO-1547	EQRYRQYHQ	MQL VISSFEQ	AAGI GSAKTY	TALALKTI SK	QFRCLKDAI T	309

Figure 21 (continued)

SEQ-ID-NO-1561	DQI SVI RKKL	GEDDNT SGKE	GKL -- TRL RY	DQO ROQRA	FQO YGML QO-	380
SEQ-ID-NO-1563	DQI NVI RKKL	GEEENSSSGKE	GKL -- TRL RY	DQO L RQORA	FQO YGML PQ-	386
SEQ-ID-NO-1565	GOVRAASRAL	GEAVIDADGGC	GRT VGSRL RY	DQO L RQORA	EQQLGMMQS	360
SEQ-ID-NO-1556	EOVKATPSKSL	G EDEGLGGI	KI EGSR LKF	VDHHL RQORA	E QQL GMMOP	402
SEQ-ID-NO-1540	GOI KAANKSL	G EEDSVSGV	GRT EGSR LKF	VDHHL RQORA	E QQL GMQ H	381
SEQ-ID-NO-1567	GOI RAANKSL	G EDDSFGGI	KI EGSR LKY	VDHHL RQORA	I QQL GMQ H	345
SEQ-ID-NO-1543	DQI RAANKSL	G EEDDVCGA	AKI EGSR LKF	VDHHL RQORA	I QQL GMQ H	347
SEQ-ID-NO-1547	GOI KAANKSL	G EEDOLGG	KI EGSR LKF	VDHHL RQORA	I QQL GMQ H	355
SEQ-ID-NO-1561	--NAWRPQRG	LPENSVSI LR	AWL FEHFL HP	YPKDSEKJ ML	SRQTGLTRSQ	428
SEQ-ID-NO-1563	--NAWRPQRG	LPENSVTI LR	AWL FEHFL HP	YPKDSEKJ ML	ARQTGLTRSQ	434
SEQ-ID-NO-1565	--SAWRPORG	LPERSVSI LR	AWL FEHFL HP	YPKDSDKI ML	AKQTGLTRSQ	408
SEQ-ID-NO-1556	--NAWRPQRG	LPERAVSVLR	AWL FEHFL HP	YPKDSDKI ML	AKQTGLTRSQ	450
SEQ-ID-NO-1540	SNNAWRPORG	LPERAVSVLR	AWL FEHFL HP	YPKDSDKHML	AKQTGLTRSQ	431
SEQ-ID-NO-1567	--NAWRPQRG	LPERSVSVLR	AWL FEHFL HP	YPKDSDKHML	AKQTGLTRSQ	393
SEQ-ID-NO-1543	--NAWRPQRG	LPERSVSVLR	AWL FEHFL HP	YPKDSDKHML	AKQTGLTRSQ	395
SEQ-ID-NO-1547	--NAWRPORG	LPERSVSVLR	AWL FEHFL HP	YPKDSDKHML	AKQTGLTRSQ	403
SEQ-ID-NO-1561	[SNWFI NARV]	RLWKPMI EDM	YKEEICAEEL	DS ---- NSSS	DNGQRN KDKA	474
SEQ-ID-NO-1563	SNWFI NARV	RLWKPMI EDM	YKEEICDI EQI	DS ---- NSSS	DNAPRSKCKM	480
SEQ-ID-NO-1565	VSNWFI NARV	RLWKPMVEEM	YLEETKDQDG	GG --- CAGAG	DEGSKPGGSK	455
SEQ-ID-NO-1556	VSNWFI NARV	RLWKPMVEEM	YLEEVKNOEO	NS --- SNT SG	DNKNKETNLS	497
SEQ-ID-NO-1540	VSNWFI NARV	RLWKPMVEEM	YMEEMKEQAK	NMCSMEZTPL	DQSNEDSASK	481
SEQ-ID-NO-1567	VSNWFI NARV	RLWKPMVEEM	YTEEMKEQEM	NG SEDNKSS	KH DEDTSMK	442
SEQ-ID-NO-1543	VSNWFI NARV	RLWKPMVEEM	YLEEI KEQEQ	NGT SDOKFSK	TENHEDSASK	445
SEQ-ID-NO-1547	VSKWFI NARV	RLWKPMVEEM	YMEEI KEQEO	NG SEDKTSK	SEHNEDAASR	452
SEQ-ID-NO-1561	PPEEENEDL	-----	-----	---CP P SQA	CQT SOLGE SK	500
SEQ-ID-NO-1563	ASSEDKEDL	-----	-----	---KSSTIPRM	CESSOLSESR	506
SEQ-ID-NO-1565	GGGAGVNGGV	VDSA AKM ---	-DSKAH -- M	ESGGGVHPSL	LELAGDHOAQ	499
SEQ-ID-NO-1556	APNEEKQPO	TSSL LOD ---	-CTT QAE -- I	SISI STSP	A G A S I HH JAHN	541
SEQ-ID-NO-1540	STSNOEK	---	---	---	SPM ADT NH HMNP N	501
SEQ-ID-NO-1567	STTPQQVPTS	ETESKSF ---	-NSKODI PI V	SYSI QST SPI	GVNVRNNNSG	488
SEQ-ID-NO-1543	STA PS CONPG	ENDK VSL ---	----- M	SISI ASTSPL	AG NA HQDSR	482
SEQ-ID-NO-1547	SVLQEKGSVN	GNL TRSF KSL	DNSPDAPS A	SIT SST SPV	GG NL RINOSG	501

Figure 21 (continued)

SEQ-ID-NO-1561	A	VGCVNGFS	CVL	-----A	GGFHTEANPDI	D-----SFM	SMLK-----	533			
SEQ-ID-NO-1563	AS	-GTIMNVG	GAA	-----	VGFONEANPDI	D-----SFM	NLMK-----	537			
SEQ-ID-NO-1565	AGFYDDDDDFD	GGA	--AAALD	Q	QLKKARTEE	O--OAAAFHV	SDVATLHAHA	545			
SEQ-ID-NO-1556	FSFLGSFINME	NT	TTVDHI	E	NNAKKPRNIID	MHKFSPSII	LSVEM-----	586			
SEQ-ID-NO-1540	HN	--GDL	E	GVT	GSPKRLRTSID	E-----	-TMMO-----	528			
SEQ-ID-NO-1567	FSF	--TELD	GI	T	--GMO	AASPKRTRNHE	-LQSPNIV	KSNET-----	522		
SEQ-ID-NO-1543	FSI	GSSELE	GI	T	--Q	GSPKKPRRSNE	-LQSPTSV	PSMNM-----	519		
SEQ-ID-NO-1547	FSF	MGSSELD	GI	T	--Q	GSPKKPRSHD	-I OSPTSV	PSINM-----	538		
SEQ-ID-NO-1561	-----AQRPG	E	TECT G	LHDA	VAHH-----	SD	DGARFM-----	-----A	562		
SEQ-ID-NO-1563	-----DORSNE	G	DGGGL	LVHNA	VAHH-----	QD	ENARFM-----	-----A	566		
SEQ-ID-NO-1565	AAAAAARHDE	V	VSHRELL	MKF	MESGSA-GAG	AGAAARDHHH	EHHGCMGYS	-----	594		
SEQ-ID-NO-1556	-----EAKARE	S	TINKSFT	NPL	EEEROGI RSD	CCYPFMGN	-----	MA-----A	605		
SEQ-ID-NO-1540	-----PI NADF	S	SNEKLTMKI	-----	CDRO-----SR	DGYCFMGNQT	NFI AGFC	-----Q	565		
SEQ-ID-NO-1567	-----NN	N	NNNEQISMKF	-----	CDRO-----SR	DGYCFMGNT	DFMCCLG	-----Q	559		
SEQ-ID-NO-1543	-----DMNOSE	A	ASND	VSMKF	-----SK	DGYSF MGT NT	DFMCCLG	-----Q	554		
SEQ-ID-NO-1547	-----DJKPGE	A	ANNEQVSMKF	-----	CDERO-----SR	DGYSF1 GGQT	NFI GFG	-----Q	579		
SEQ-ID-NO-1561	YHL	AE	GRY	-----	-----CNS	NVSLTLGLPH	AENS LAVPPN	595			
SEQ-ID-NO-1563	YHL	AE	GRY	-----	-----CN-G	NVSLTLGLPH	SGSSLSV-HN	597			
SEQ-ID-NO-1565	FAPAPY	GQFA	T	--EQ	--FAF	AGHGGGGCGG	GVSLTLCLPH	G-----AE	633		
SEQ-ID-NO-1556	YAMGDFGRFD	G	PHDOQ	--MTA	NFH	--CN-N	GVSLTLCLPP	SEN-LAM-PV	647		
SEQ-ID-NO-1540	YQMDMEMSRFD	V	VVSQELMAQ	RYS	--CNN	GVSLTLCLPH	COS-LS	-----ST	609		
SEQ-ID-NO-1567	YPMEEI	GRFD	A	--EQ	--FTP	RFS	GVSLTLCLPH	CDI-L	-----SC	598	
SEQ-ID-NO-1543	YPI GEI	GRFD	A	--EQ	--FAP	RFP	--GN--	GVSLTLCLPH	CEN-LSL	SG	593
SEQ-ID-NO-1547	YPMGEI	GRFD	G	--EQ	--FTP	RFS	--GN--	GVSLTLCLPH	CEN-LSL	SG	618
SEQ-ID-NO-1561	TOPGF	-----	PGV	RDODMMNATA	-----	PP	LNVAS	-----SSEM	625		
SEQ-ID-NO-1563	AQDSF	-----	AGV	GDODLYNATA	-----	P	LGVS	-----TSSD	626		
SEQ-ID-NO-1565	QTASFLMTSS	-----	-----	NGSDGAGHVA	-----	-----	-----	CGGGY	658		
SEQ-ID-NO-1556	SONYLSNE	-----	LGSRPEI	QSH	-----	-----	-----	YNRMGY	672		
SEQ-ID-NO-1540	HHQGF	MOTHH	G	PI GRRVK	GETEEYCPAT	I NGGSSTTA	HSSAAAAAA	-----	659		
SEQ-ID-NO-1567	THOSFMPNON	H	OLGRRLDI	SEONEFG	-----	-----	-----	DSSAAF	630		
SEQ-ID-NO-1543	THQNFLPNQT	M	OMGRRLDI	DEPNEFGAI	N	-----	PPTPHSSAAY	-----	632		
SEQ-ID-NO-1547	THQFLPNQN	I	OLGRRVEI	GEPENEYGAI	N	-----	TSTPHSSAY	-----	657		

Figure 21 (continued)

SEQ-ID-NO-1561
SEQ-ID-NO-1563
SEQ-ID-NO-1565
SEQ-ID-NO-1556
SEQ-ID-NO-1540
SEQ-ID-NO-1567
SEQ-ID-NO-1543
SEQ-ID-NO-1547

DSASQ	DQQQ	QRORF	EPSP	MHDFVA	----	-	651	
ES	---	MNQMD	QRQRF	EQSPL	LHDFVA	----	-	649
D	---	MNMQS	-TKSF	-AAQL	MRDFVA	----	-	678
EN	---	D F QS	CNKRF	PTQL	LPDFV I GNLG T	----	-	699
NG	---	MNI QN	-OKRYI	-VAQL	LPDFVA	----	-	680
ES	---	MNMQN	-PKRF	-AAQL	LPDFVA	----	-	651
ES	---	NL QN	-RKRF	-VAQL	LPDFVA	----	-	653
ES	---	DI QN	-RKRF	-IAQL	LPDFVA	----	-	678

Figure 22

SEQ-ID-NO-544	MSNSCSGGGG	CSTVWFRRLD	RVEDNPALAA	AVRAGPMLAV	FVWAPEEEGH	50
SEQ-ID-NO-539	-----MAA	CTIVWFRRLD	RLEDNPALAA	AAHACTVVFV	FVWSPLAEQG	43
SEQ-ID-NO-549	-----MAGSE	RTVVWFRRLD	RI DDPNALAS	AARDGAVLPV	FI WCPADEGQ	45
SEQ-ID-NO-543	-----MSTNK	KTI VWFRRDL	RI EDNPALAA	AAFEGSVFPV	FI WCPEEEQG	45
SEQ-ID-NO-538	-----MKMDK	KTI VWFRRDL	RI EDNPALAA	AAHEGSVFPV	FI WCPEEEQG	45
SEQ-ID-NO-542	-----MTTNIK	KTI VWFRRDL	RI EDNPALAA	AAHOGSVFPV	FI WCPEEEQG	45
SEQ-ID-NO-547	-----MESNY	KTI VWFRRDL	RI EDNPALAA	AARNGSVLPV	FI WCPKEEGQ	45
SEQ-ID-NO-548	-----MESNS	KTI VWFRRDL	RI EDNPALAA	AARNGSVFPV	FI WSPKEEGQ	45
SEQ-ID-NO-541	-----MDRS	KTI VWFRRDL	RI EDNPALAA	AARDGCMFPV	FI WCPKEEGQ	44
SEQ-ID-NO-545	-----MN	RTI VWFRRDL	RI EDNPALAA	AARDGSVFPV	FI CCPKEEGQ	42
SEQ-ID-NO-546	-----MGSN	RTI VWFRRDL	RI EDNPALAA	AARDGSVFPV	FI WCPKEECQ	44
SEQ-ID-NO-544	YOPGRVSRWW	LKNSLAQLDS	SLRSLGLCIL	TKRSTDVSAS	LLEMVKSTGQ	100
SEQ-ID-NO-539	FHPGRVSRWW	LKQSLIHLEL	SLKJLGSPLI	ERKSPDPLS	LLEIAEATGA	93
SEQ-ID-NO-549	FYPGRGSRWW	LKQSLPHLSQ	SLESLGCPLV	LI RAEESTLEA	LLRCITDSVGA	95
SEQ-ID-NO-543	FYPGRASRWW	MKQSLAHLTQ	SLKALGSEPT	LI KTHNTVSA	LLDCRATGQ	95
SEQ-ID-NO-538	FYPGRASRWW	MKQSLAHLSQ	SLKALGSDLT	LI KTHNTVSA	LLDCIRVTGA	95
SEQ-ID-NO-542	FYPGRASRWW	MKQSLAHLSP	SLKALGSEL	LI KTHNTVSA	LLDCIRVTGA	95
SEQ-ID-NO-547	FYPGRVSRWW	LKQSLIHLKQ	SLKSLGAELV	LMKAQSTLSA	LLTECVDAVGA	95
SEQ-ID-NO-548	FYPGRVSRWW	LKQSLIHLHQ	SLKSLGAELV	LI KAQSTLSA	LLDCIEAVGA	95
SEQ-ID-NO-541	FYPGRVSRWW	LKQSLAHLQ	SLKSLGAELV	LI KTHNTVAA	LLDCIEGA	94
SEQ-ID-NO-545	FYPGRVSRWW	LKQSLYHLDO	SLKSLGAELV	MI KTGSTLKA	LLECVNIAVQA	92
SEQ-ID-NO-546	FYPGRVSRWW	LKQSLAHLDO	SLKSLGAELV	LI KTGSTLNA	LLECVNIAIQA	94
SEQ-ID-NO-544	SQIFFNHLYD	PLSLVRDHRA	KDAITAEGCA	VKSFNADLLY	EPWEVIDEKG	150
SEQ-ID-NO-539	TQVEYNHLYD	PVSLVRDHRY	KQGLSORGI	VFTNGDLLY	EPWEVYDEEG	143
SEQ-ID-NO-549	TRLVYNHLYD	PVSLVRDDKI	KKELSALGI	QSFGNDLLY	EPWEIYDDSG	145
SEQ-ID-NO-543	TKVVFNHLYD	PVSLVRDHTV	KEKLVERGI	VQSYNGDLLY	EPWEIYCEKG	145
SEQ-ID-NO-538	TKVVFNHLYD	PVSLVRDHTV	KEKLVERGI	VQSYNGDLLY	EPWEIYCEKG	145
SEQ-ID-NO-542	TKVVFNHLYD	PVSLVRDHTV	KEKLVELGI	VQSFNGDLLY	EPWEIYCEKG	145
SEQ-ID-NO-547	TKVYYNHLYD	PVSLVRDHNI	KOKLGDLGI	VQSYNGDLLN	EPWEVYDDDG	145
SEQ-ID-NO-548	TKVYYNHLYD	PVSLVRDHNI	KOKLGELGI	VQSYNGDLLN	EPWEVYDDDG	145
SEQ-ID-NO-541	TRVVFNHLYD	PVSLVRDHNI	KEKLVELGI	VQSYNGDLLY	EPWEIYDERG	144
SEQ-ID-NO-545	TKVVFNHLYD	PVSLVRDHNI	KEKLVELGI	VQSYNGDLLH	EPWDIYDESG	142
SEQ-ID-NO-546	TKVVFNHLYD	PVSLVRDHNI	KEKLVELGI	VKSNGDLLY	EPWELYDEKG	144

Figure 22 (continued)

SEQ-ID-NO-544	RPFNSMFAFW	ERCLSMPYDP	ESPLLPPKKI	LSGLLLHHTL	SEI VSYPL	I	200
SEQ-ID-NO-539	GAFTVYEAFW	KKCMMSMPFEP	EAPELLPPIR	-----	-----	I	174
SEQ-ID-NO-549	LAFTTFNMYW	EKCMELPIDA	-SPSLAPWK	-----	-----	V	175
SEQ-ID-NO-543	KPFTINFSYW	KKCLCDMPVES	-VMI PPPWR	-----	-----	I	175
SEQ-ID-NO-538	KPFTSFNSYW	KKCLCDMSIES	-VMLPPPWR	-----	-----	M	175
SEQ-ID-NO-542	KPFTSFSSYW	KKCLCDMSIES	-VMLPPPWR	-----	-----	I	175
SEQ-ID-NO-547	KMFTTFDAYW	EKSLSIQNEP	-VSQI PPPWR	-----	-----	I	175
SEQ-ID-NO-548	KNFTTFDAYW	EKSRLRQKEP	-VSHLPPPWR	-----	-----	I	175
SEQ-ID-NO-541	HAFTTFFEAYW	DRCLHMQMEP	-VSHLPPPWR	-----	-----	V	174
SEQ-ID-NO-545	HAFTTFDPFW	SRCLQMQMKIT	-YSTI PPQ	-----	-----	I	172
SEQ-ID-NO-546	HAFTTFDPFW	ERCLHKQMEP	-VSII PPWQ	-----	-----	I	174
SEQ-ID-NO-544	TLFVLAGDVS	KCVADETTLE	-DESEKGSNA	LLARAWSPGW	SNADKALTTEF	249	
SEQ-ID-NO-539	G---PTGKIV	GCNAEELGLE	-DEFEKSSNA	LLARAWCPGW	CFANKSLDSF	220	
SEQ-ID-NO-549	PVP-CLESVR	SCSVDLGLE	SSKDEESSNA	LLRAWSPGW	RRAEKMLTEEF	224	
SEQ-ID-NO-543	PLT-FACTVW	ACSI EELGLE	-NEAEKPSNA	LLTRAWSPGW	SNADKILTEF	223	
SEQ-ID-NO-538	PTAAAEAIW	ACSI EELGLE	-NEAEKPSNA	LLTRAWSPGW	SNADKLLNEF	224	
SEQ-ID-NO-542	PTAAVEAVW	ACSI EELGLE	-NDAEKPSNA	LLTRAWSPGW	SNADKLLNEF	224	
SEQ-ID-NO-547	O---AAGSVK	MCSVEELGLE	-NESEKSSNA	LLGKOWAPGW	SNADKALTEF	221	
SEQ-ID-NO-548	P---AAGSVK	MCSVEELGLE	-NESEKSSNA	LLGKOWAPGW	SNADKALTEF	221	
SEQ-ID-NO-541	P---AGTGVW	KCSVEELGLE	-DEAEKSSNS	LLGRGMSPGW	SNADKALTEF	220	
SEQ-ID-NO-545	P---AGRVE	KHSI EQLGLE	-DEIETSSNA	LLSRAWSPGW	SKSDKALTEF	218	
SEQ-ID-NO-546	P---AKGKVE	RCSI EDLGLE	-NELEKPSNA	LLGRGMSPGW	SNANKALTEF	220	
SEQ-ID-NO-544	NGPTEYSK	NRRRADSAT	--TSLLSPHL	HFGEVSVRKV	FHLLRI KQVA	296	
SEQ-ID-NO-539	LRSPLI DYAR	DRKADGASG	--T SLLSPHL	HFGELSVRKI	FHEVRI KROI T	270	
SEQ-ID-NO-549	VSHGOLLEYSK	HGMKVEGAT	--TSLLSPYL	HFGEVSVRKV	YQLVRMQQIK	271	
SEQ-ID-NO-543	EKOLIDYAK	NSKKVVGNS	--TSLLSPYL	HGEI SVRRV	FOCARMKQI T	270	
SEQ-ID-NO-538	EKOLIDYAK	NSKKVVGNS	--TSLLSPYL	HGEI SVRH	FOCARMKQI I	271	
SEQ-ID-NO-542	DKOLIYYAK	NSNKVVGNA	--TSLLSPYL	HYGEI SVRRV	FOCARMKQI I	271	
SEQ-ID-NO-547	VESNLAYSK	DRLRVGGNS	--TSLLSPYL	HGEVSVRKV	FNSVRLKQI L	268	
SEQ-ID-NO-548	VENOLLLAYSK	DRLRVGGNS	--TSLLSPYL	HGEVSVRKV	FNSVRLKQI L	268	
SEQ-ID-NO-541	AEOHLLDYME	SRLKVG-TS	--TSLLSPYL	HFGELSVRKV	FQCIVQLKQL	266	
SEQ-ID-NO-545	VENHLLDYSK	NRLNLCVDS	--TSLLSPYL	HFGELSVRKV	FQIVRLKQI L	265	
SEQ-ID-NO-546	MDKQLLNYSK	NRDKVGGDS	--TSLLSPYL	HFGELSVRKV	FOMARVKQI S	267	

Figure 22 (continued)

SEQ-ID-NO-544	WA[EGNQAGE	ESVNLFLKST	GLREYSRYI S	FNHPSHERP	LLGHLKFFPW	346
SEQ-ID-NO-539	WAREGNAGGE	ASVNMFRLAL	GFREYSRYLS	FHFPTFHRS	LLANLKSFPW	320
SEQ-ID-NO-549	WENEGCTSEAE	ESIHFIMRSI	GLREYSRYLC	FNFPTTHEKS	LLGNLKHFPW	321
SEQ-ID-NO-543	WARDRKNQGV	ESAVFLRLC	GLRDYSRYIC	FNFPTTHEQS	LLSHLRFFFNW	320
SEQ-ID-NO-538	WARDKNSEGE	ESADLFLRLC	GLREYSRYJC	FNFPTTHEQS	LLSHLRFFFNW	321
SEQ-ID-NO-542	WARDKNSEGE	ESTDFLFLKGJ	GLREYSRYIC	FNFPTTHEQS	LLSHLRFFFNW	321
SEQ-ID-NO-547	WTKEGNSMVCK	DSATIYLRAI	GLREYSRYIC	FNFPTFHRS	LLNNLRFFFNW	318
SEQ-ID-NO-548	WTKEGNSMVGD	ESASLYLRAI	GLREYSRYIC	FNFPTFHRS	LLNNLKFFPW	318
SEQ-ID-NO-541	WAKEENIMGK	ESVTFLRLRSI	GLREYSRYLC	FNFPTFHRS	LLRNLKYPFW	316
SEQ-ID-NO-545	WKNEGNGVGE	ESATFLRLAI	GFREYSRYLC	FSFPTVERP	LLGNLKFFPW	315
SEQ-ID-NO-546	WGNEGNSMVCK	ESVFLRLAI	GLREYSRYLC	FNFPTFHRS	LLGHLSEFPW	317
SEQ-ID-NO-544	A[DENYFKAW	RQGRGYPLV	DAGMRELWAT	GWLHDRI RVV	VSSFVKMLQ	396
SEQ-ID-NO-539	RADEGYFKAW	RQGRGYPLV	DAGMRELWAT	GWAHNRIRVV	VASFVKFLQ	370
SEQ-ID-NO-549	KVDEERFKSW	RQGRGYPLV	DAGMRELWAT	GWHNRIRVI	ISSFAVKFLL	371
SEQ-ID-NO-543	DADVEERFKAW	RQGRGYPLV	DAGMRELWAT	GWMMHNRIRVI	VSSFAVKFLL	370
SEQ-ID-NO-538	DADVDFKFKAW	RQGRGYPLV	DAGMRELWAT	GWMMHNRIRVI	VSSFAVKFLL	371
SEQ-ID-NO-542	DADVDFKFKAW	RQGRGYPLV	DAGMRELWAT	GWMMHNRIRVI	VSSFAVKFLL	371
SEQ-ID-NO-547	NADQAHFKAW	RQGRGYPLV	DAGMRELWAT	GWVHNKIRVI	VSSFVKFLL	368
SEQ-ID-NO-548	NADQARFKAW	RQGRGYPLV	DAGMRELWAT	GWI HNKIRVI	VASFVKFLL	368
SEQ-ID-NO-541	NDNQVFRKAW	RQGRGYPLV	DAGMRELWAT	GWI HNKIRVI	VSSFAVKML	366
SEQ-ID-NO-545	NTDPSKFKAW	RQGRGYPLV	DAGMRELWAT	GWI HNKMRVI	VSSFAVKML	365
SEQ-ID-NO-546	NADPSNFKFW	RQGRGYPLV	DAGMRELWAT	GWMMHNRIRVI	VSSFAVKML	367
SEQ-ID-NO-544	LPWRWGMKYF	WDTLLDADLE	SDALGWQYIT	GTLPDSSREFD	RIDNPQEFGY	446
SEQ-ID-NO-539	LPWRWGMKYF	WDLVLLDADLE	CDVLGWQYIS	GSLPDGHED	RIDNPQEFGY	420
SEQ-ID-NO-549	PWLGWMKYF	WDVLLDADLE	SDILGWQYIS	GSLPDGHEL	RLDNPEVDGQ	421
SEQ-ID-NO-543	LPWKWGMKYF	WDTLLDADLE	CDILGWQYIS	GSLPDGHED	RLDNPALQGA	420
SEQ-ID-NO-538	LPWKWGMKYF	WDTLLDADLE	CDILGWQYIS	GSI PDGHELD	RLDNPALQGA	421
SEQ-ID-NO-542	LPWKWGMKYF	WDTLLDADLE	CDILLCWQYIS	GSLPDGHED	RLDNPALQGA	421
SEQ-ID-NO-547	LPWQWGMKYF	WDTLLDADLE	SDILGWQYIS	GSLPDGHELE	RLDNPEVQGF	418
SEQ-ID-NO-548	LPWQWGMKYF	WDTLLDADLE	SDILGWQYIS	GSLPDGHELE	RLDNPEVQGF	418
SEQ-ID-NO-541	LPWRWGMKYF	WDTLLDADLE	SDILGWQYIS	GSLPDGHED	RLDNPETQGS	416
SEQ-ID-NO-545	PWKGWMKYF	WDTLLDADLE	SDILGWQYIS	GSLPDGHED	RLDDPETQGT	415
SEQ-ID-NO-546	LPWKWGMKYF	WDTLLDADLE	CDILGWQYIS	GCLPDGHELE	RLDPEI LGA	417

Figure 22 (continued)

SEQ-ID-NO-544	KFDPINEYVR	RWLPELSRLP	I EWI HHPWNAI	PESVLDAAIGI	ELGSNYPRPI	496
SEQ-ID-NO-539	RFDPCDGYVR	RWIPELARLP	N NEWHHWPDA	PPSALRAAGV	ELGTNYPRPI	470
SEQ-ID-NO-549	KYDPDGIVVR	TWIPELARMP	T EWI HHPWDA	PSOILEVAGV	ELGFNYPKPI	471
SEQ-ID-NO-543	KYDPEGEYI R	QWLPELARLP	T EWI HHPWDA	PLTVLKASGV	ELGTNYAKPI	470
SEQ-ID-NO-538	KYDPEGEYI R	QWLPELARLP	T EWI HHPWDA	PLTVLKASGV	ELGTNYAKPI	471
SEQ-ID-NO-542	KFDPEGEYI R	QWLPELARLP	I EWI HHPWDA	PLTVLKASGV	ELGFNYVKPI	471
SEQ-ID-NO-547	NYDPEGEYVR	HWLPELARMP	A EWI HHPWDA	PLTVLKAAVG	ELGMNYPNPI	468
SEQ-ID-NO-548	NYDPEGEYVR	HWLPELARMP	A EWI HHPWDA	PLTVLKAAVG	ELCMNYPNPI	468
SEQ-ID-NO-541	KFDPEGEYVR	RWLPELARMP	A EWI HHPWDA	S AVLKAAGV	ELGNYPKPI	465
SEQ-ID-NO-545	KYDPEGEYI R	QWLPELARI P	T EWI HHPWNA	PLTVLKASGI	ELGQNYPKPI	465
SEQ-ID-NO-546	KFDPEGEYVR	QWLPELARMP	I EWI HHPWNA	PLSVLRASGV	ELGQNYPNPI	467
SEQ-ID-NO-544	VGLDEAKARL	HEALSQMWQL	E AASRAAI EN	GSEEGLGDSI	EFVE-----	540
SEQ-ID-NO-539	VEI GAERERL	QASLAEMWER	DAAMKAALAN	GEEESLGFI V	EVAGTGGPEH	520
SEQ-ID-NO-549	VDLHIAREOL	DDSI S TM WQI	DIAEKLAFTID	G--EVVEDNL	SNI -----	512
SEQ-ID-NO-543	VDI DTARELL	TKAI SRTREA	Q MI GAA----	--PDEI VADSF	-----	505
SEQ-ID-NO-538	VDI DTARELL	AKAI SRTREA	Q MI GAA----	--PDEI VADSF	-----	507
SEQ-ID-NO-542	VDI DTARELL	TIKAI SRTREA	Q MI GAA----	--PDEI VADSF	-----	507
SEQ-ID-NO-547	DVDVARDRL	MQAI T TM REK	EAANNTSHAN	GT VIEVVFDNS	ENVG-----	512
SEQ-ID-NO-548	DVDVARDRL	MQAI F TM REK	EAANANAADDAN	GT NEVVFDNS	ENVG-----	512
SEQ-ID-NO-541	DI DLARERL	MEAI FKMWE M	EAARASNTN	GT NEVVVDNT	DDT-----	509
SEQ-ID-NO-545	E1 DLAREQL	TQAI FKMWE D	EAASKASTSE	NKHEVVDDOS	-----	504
SEQ-ID-NO-546	DI DLAREKL	TQAI FKMWE	QAASKASCSE	ARDEVVVDN	-----	506
SEQ-ID-NO-544	APLEFPROIT	MEETEPTRL-	N PVRRYEDOM	VPSITTSLIR	PEEDQESSLS	589
SEQ-ID-NO-539	ERMDVPR-VM	VHMORDADM	SCNSERRDQL	VPELVPN---	-----	555
SEQ-ID-NO-549	KTFDI PK-VV	L---RETSP-	CA---LPI DQR	VPHA-----	-----	539
SEQ-ID-NO-543	EALEAAN-T	V---KEHGY-	CPL---SSNDQQ	VPSDV-----	-----	532
SEQ-ID-NO-538	EALCANT---	I---KEPGL-	CPSVSSNDQQ	VPSAV-----	-----	535
SEQ-ID-NO-542	GALEGNT---	V---KET GL-	CPSVSSNDQQ	VPSAV-----	-----	535
SEQ-ID-NO-547	DSASIPKDDM	V---KGKEP-	CPSSESSYDQR	VPSMQ-----	-----	543
SEQ-ID-NO-548	DSVNPK--V	V---KGKVP-	CPSSESSYDQR	VPSMO-----	-----	540
SEQ-ID-NO-541	ENLATPK-VV	L---KDKVT-	CPTNSSNDQR	VPTNQN-----	-----	540
SEQ-ID-NO-545	ENLSPK-VF	L---KDKAPR	GATSSSSNDQK	VPIEONP-----	-----	537
SEQ-ID-NO-546	ENODIPK-VI	I---KDKGP	CVI SANDQK	VPALPDP-----	-----	538

Figure 22 (continued)

SEQ-ID-NO-544	L	RNSGGDSRA	EVPRNMV-NT	NDQRCFARA	DPVSNQVTA-	627
SEQ-ID-NO-539	-	DPH RAHES	I MNPSAA-MV	EDGEFAAGRAA	VPMVFASVRR	603
SEQ-ID-NO-549	-	SSKDHN-	- LKSKV -LR	ASNSSEI ---	CVDM-	563
SEQ-ID-NO-543	-	RYSGS---	- KRMKPAAE-	EEREEMKKLR	GFNEVI ---	561
SEQ-ID-NO-538	-	RYNGS---	- KRMKP-EE	EEFRDMKKSR	GFD- ---	560
SEQ-ID-NO-542	-	RYNGS---	- KRMKH-VE	EEFRDMKKSR	GFDE- ---	561
SEQ-ID-NO-547	--	NVGTYR-	- KRPKP-EE	ETKKLNDNKL	SYKNERI K--	574
SEQ-ID-NO-548	--	KGSTINK	- KRPNP-VE	EKKFKDNLWL	SCKI KTEGK-	572
SEQ-ID-NO-541	--	SKN PAYR	- KRISKY-ME	FERPOPDKLH	NDGNVVG---	572
SEQ-ID-NO-545	KI	DPPPNR	- KKQKC-MD	KDREODSLS	NLSKRTDTG-	571
SEQ-ID-NO-546	KI	KNELPVR	- KRKKG-ME	EXPKEOES	NEKDSK---	569
SEQ-ID-NO-544	-----	-----	-----	-----	-----	662
SEQ-ID-NO-539	-----	-----	-----	-----	-----	651
SEQ-ID-NO-549	-----	-----	-----	-----	-----	594
SEQ-ID-NO-543	-----	-----	-----	-----	-----	588
SEQ-ID-NO-538	-----	-----	-----	-----	-----	580
SEQ-ID-NO-542	-----	-----	-----	-----	-----	587
SEQ-ID-NO-547	-----	-----	-----	-----	-----	605
SEQ-ID-NO-548	-----	-----	-----	-----	-----	603
SEQ-ID-NO-541	-----	-----	-----	-----	-----	602
SEQ-ID-NO-545	-----	-----	-----	-----	-----	600
SEQ-ID-NO-546	-----	-----	-----	-----	-----	600
SEQ-ID-NO-544	-----	-----	-----	-----	-----	694
SEQ-ID-NO-539	-----	-----	-----	-----	-----	697
SEQ-ID-NO-549	-----	-----	-----	-----	-----	634
SEQ-ID-NO-543	-----	-----	-----	-----	-----	611
SEQ-ID-NO-538	HSC	SSA EVHSII	QDHG	GSI -----V	GPSRYLLQEA	GRNYVDEVED
SEQ-ID-NO-542	HSC	SLV SECKNL	EG--	-----	I QDS	SDOI
SEQ-ID-NO-547	HSC	SLV SECKNL	EG--	-----	I QDP	SDOI
SEQ-ID-NO-548	RTI	TMS HORKSFDD	-	-----	-EASS	HVKLQKEEE
SEQ-ID-NO-541	QAI	SMS YDI KSFDG	-	-----	-EASS	HVKLQNEEE
SEQ-ID-NO-545	QYC	SS SECKPLQE	-	-----	-SESS	DLRQPLQAJ
SEQ-ID-NO-546	DOC	-----	-----	-----	-----	NLKWSWQEO

Figure 22 (continued)

SEQ-ID-NO-544	VNWRRLS <u>Q</u> <u>T</u> <u>G</u>	-----	704
SEQ-ID-NO-539	SNKQAE <u>E</u> <u>E</u> <u>D</u> F	YVPKLVKWTQ PRKRRVKQDG	727
SEQ-ID-NO-549	SSTA <u>D</u> <u>S</u> <u>G</u> <u>S</u> I	SRQRKAA-----	651
SEQ-ID-NO-543	---T <u>S</u> <u>L</u> <u>G</u> KNG	-----	618
SEQ-ID-NO-538	---T <u>S</u> <u>L</u> <u>G</u> KNG	CK-----	612
SEQ-ID-NO-542	---T <u>K</u> <u>L</u> <u>G</u> KNG	-----	617
SEQ-ID-NO-547	DT-----	-----	635
SEQ-ID-NO-548	DMEI <u>N</u> <u>S</u> <u>C</u> <u>K</u> NE	-----	641
SEQ-ID-NO-541	EMEQ <u>S</u> <u>S</u> <u>S</u> <u>K</u> D <u>G</u>	KQLHFI V-----	646
SEQ-ID-NO-545	DMEQ <u>S</u> <u>S</u> <u>S</u> <u>G</u> <u>K</u> D <u>G</u>	PT-----	600
SEQ-ID-NO-546	DMEQ <u>S</u> <u>S</u> <u>S</u> <u>G</u> <u>K</u> D <u>G</u>	PT-----	629

Figure 23

SEQ-ID-NO-606	--MDYSSSMHQ	-NVNGVSSCS	[QDYQNQKKP	LSATRPAPE	QSLRCPRCDS	47
SEQ-ID-NO-609	--MNFISSGQP	-DQMSSQSVE	-----	KKPKP-HPE	OALKCPRCDS	35
SEQ-ID-NO-607	MGMDSSSGQQ	-QQMSNOSLE	SMLTC SKGEQ	DKKPKPPQPE	ALKCPRCDS	48
SEQ-ID-NO-608	--MDSSSEFQQ	HQQMSNOSLE	SMLTC SKGEQ	DKKAKP-QPE	ALKCPRCDS	46
SEQ-ID-NO-606	TNTKFCYYNN	YSLSQPRYFC	KSCRYYWTKG	GLRNPIGG	AYRKHKRS-S	96
SEQ-ID-NO-609	TNTKFCYYNN	YSLSQPRYFC	KSCRYYWTKG	GTLRNPVGCG	GCRKRRRE--S	82
SEQ-ID-NO-607	NNTKFCYYNN	YSLSQPRYFC	KSCRYYWTKG	GTLRNPVGCG	GCRKNKRSSS	98
SEQ-ID-NO-608	BNTKFCYYNN	YSLSQPRYFC	KSCRYYWTKG	GTLRNPVGCG	GCRKNKRSSS	96
SEQ-ID-NO-606	SATKSLRTTP	EPMIMTADGKS	FPTASFGYNN	NN SNEOME	----LGLA-	139
SEQ-ID-NO-609	SSIKRAQGQT	LTPNLNPLT	EPHLSYDSND	FTLAVAREOK	QSSCOLCYN-	131
SEQ-ID-NO-607	ASSKRSQDQP	FQENPNPLTC	FPSLSYDSND	LT LALARLQK	---CHLGFDH	145
SEQ-ID-NO-608	SVSRRIQDQA	FVNINPNPVTC	FPSLSYDSND	LT LALARLQK	---COLGFDH	143
SEQ-ID-NO-606	---YALLNQ	P-----	--LCVSSSHLG	FG-SSQSPMA	MDGM-----YG	170
SEQ-ID-NO-609	DHDLSLGNP	T-----TG	SECDLGNNSG	MNPSANPSF	LDAIRTGFE	174
SEQ-ID-NO-607	FHDFSI LGNO	T-----N	TSCGLNNHG	MNHSSNNQGF	FEAL-----MG	183
SEQ-ID-NO-608	EHDFSI LGNH	ANSNI NI NTN	TSCAVLNHHG	MNHSSNNHGF	FEAL-----MG	189
SEQ-ID-NO-606	ITSHOMENTG	PAFCNGGGG	-----	-----	-----	189
SEQ-ID-NO-609	TONH-LONLY	CWYGNGLGE	VDNNGNSGVVG	VSGEMMLPYD	QVI NSNATTQ	223
SEQ-ID-NO-607	SONN-VONLY	Y-----MGE	VDNCAANGNG	NGEMMLPYD	HE-MSTATTQ	224
SEQ-ID-NO-608	SONN-VONLY	YGYGNRDME	VDNGNV---	SGEMMLPYD	HE-MSI ATTQ	232
SEQ-ID-NO-606	-----	MEQMATSDPN	RVLMGFPWQM	NMGCCSGHGH	GHVDODID-SG	228
SEQ-ID-NO-609	SVSV-MKQE	MCSNREOSER	RVLGFPWQM	N-----AD	FNI CEDLDSG	263
SEQ-ID-NO-607	AVTVTTMKQE	MCNVREQEN	RVLLGFPWQF	N-----NGD	TNMAEMDHLG	268
SEQ-ID-NO-608	AVTVTTMKQE	MCNVREQNES	RVLLGFPWQF	N-----NGD	SNMDEIDHSG	276
SEQ-ID-NO-606	REF--WSSIV	NYINTG-----	ALL	245		
SEQ-ID-NO-609	RT-AWNSET	NSW-GELQD	PLM	285		
SEQ-ID-NO-607	RAG-WNGLT	SSWCHGLLNS	PLM	289		
SEQ-ID-NO-608	RAG-WNGLT	SPW-HGLLNS	PLM	296		

Figure 24

SEQ-ID-NO-579	MVRTL-----	PERSY---SC	SSAKREMASYSC	GCCCCAALNLS	31	
SEQ-ID-NO-570	MERSASAVGVN DGRFGCGNOFY	SPSFSSSSSS	SSMRHVNYS	CSCGYELNLS	50	
SEQ-ID-NO-578	MDRSASAVGK K DGGFGCGNHL	SPSFSL---SS	SSMRHVNYS	CSCGYELNLS	47	
SEQ-ID-NO-576	MD[DA]FKRG -----GH---	FNNTYI---SC	SSQRD[DM]YSC	GTCCGYELNLS	38	
SEQ-ID-NO-574	MEKSK-[VGKG] -AYLN	NCN----PHNSFSSSS	ASQRHVSYS	C[G]CGYELNLS	44	
SEQ-ID-NO-572	MEKSV-FVKD VQQLNCN---	LHSF---SS	V[SQRD]M[YSC]	GSCGYELNLS	43	
SEQ-ID-NO-579	SSILRNTANI G	SKYGKDI RKG	VI SFFAI DES	RFTOLDEVSC	MPYFH-SRRSW	81
SEQ-ID-NO-570	STNRITSTI G	SKYGKSMKSG	I I SFFNI DEG	RFSQVDEFQC	MPHF-SRYSW	99
SEQ-ID-NO-578	STNRITSSI G	SKYGKSMKIG	I I SFFNI DEG	RFSQVDEFQC	MPHF-SRYSW	96
SEQ-ID-NO-576	SSNRNTASI G	SKYGKSI KRG	I I SFFSI DES	RFTQVDEIQC	VPHFD-KHWSW	87
SEQ-ID-NO-574	SSNRNTSSI G	SKYGKSI KRG	I I SFFF[] DES	RFTQVDEFQC	I PFF-SRNSW	93
SEQ-ID-NO-572	SSSRNTATI G	SKYGKLI KRG	MI SFFNI DET	RFTQVDEFQC	RPFY-SKHWSW	92
SEQ-ID-NO-579	GLFRKRTRLL	CRKCGCRI GN	AYEDEIDSILY	DGSDDLHMSS	ECYSMSSGKK	131
SEQ-ID-NO-570	GLFRRTKLL	CRKCNNYI CN	ASQEKA-PEY	ALVTQNSDPT	SP-RIGSMVK	147
SEQ-ID-NO-578	GLFRRKTKLL	CRQCNYYI GN	ASYDKAPPEY	ALVTQNSDPR	KG-VTDIMTK	145
SEQ-ID-NO-576	GLFRRRTKLL	CRKCGNHI GN	AYNGYT-SSE	PLVSDGAESS	PSSKVMMSHTK	136
SEQ-ID-NO-574	GLFRRRTALL	CRKCGNNI GL	AYDDKA-SAY	PLVADGSDSS	SMSEVSKHRK	142
SEQ-ID-NO-572	GLFRRTKLL	CRKCGNHI GD	AYDDKS-SGY	PFMLDGSDSS	SGTEPSNHRK	141
SEQ-ID-NO-579	YDKI NALQP	ST-DDSGMPF	TL		152	
SEQ-ID-NO-570	YDRI RSLQP	SS-----AY	AL		163	
SEQ-ID-NO-578	YDRI RALQP	SS-----GVA	SL		162	
SEQ-ID-NO-576	YDRI CALQP	SSSEESDIPV	FA		158	
SEQ-ID-NO-574	YDVKI RALQP	SSVDFSTPI	HT		164	
SEQ-ID-NO-572	YDVRI RALQP	STAEGLGOSPL	FA			

**MODULATING LIGHT RESPONSE
PATHWAYS IN PLANTS, INCREASING
LIGHT-RELATED TOLERANCES IN
PLANTS, AND INCREASING BIOMASS IN
PLANTS**

**CROSS-REFERENCE TO RELATED
APPLICATIONS**

This application is a divisional of U.S. patent application Ser. No. 17/481,090, filed Sep. 21, 2021, which is a divisional of U.S. patent application Ser. No. 16/045,503 filed Jul. 25, 2018 which application is a divisional of U.S. patent application Ser. No. 13/630,902 filed Sep. 28, 2012, which application is a continuation-in-part application of and claims priority to U.S. patent application Ser. No. 12/863,102, filed Apr. 11, 2011, which is a National Stage application under 35 U.S.C. § 371 of International Application No. PCT/US2009/031292, filed Jan. 16, 2009, which claims the benefit of priority under 35 U.S.C. § 119(e) to U.S. Provisional Patent Application Ser. No. 61/021,943, filed Jan. 18, 2008. U.S. patent application Ser. No. 13/630,902, filed Sep. 28, 2012, is also a continuation-in-part application of and claims priority to U.S. patent application Ser. No. 12/373,134, filed Apr. 6, 2010, which is a National Stage application under 35 U.S.C. § 371 of International Application No. PCT/US2007/073154, filed Jul. 10, 2007, which claims the benefit of priority under 35 U.S.C. § 119(e) to U.S. Provisional Patent Application Ser. No. 60/819,763, filed Jul. 10, 2006. U.S. patent application Ser. No. 13/630,902 filed Sep. 28, 2012, is also a continuation-in-part application of and claims priority to U.S. patent application Ser. No. 12/513,086, filed Apr. 23, 2010, which is a National Stage application under 35 U.S.C. § 371 of International Application No. PCT/US2007/083495, filed Nov. 2, 2007, which claims the benefit of priority under 35 U.S.C. § 119(e) to U.S. Provisional Patent Application Ser. No. 60/856,613, filed Nov. 3, 2006. U.S. patent application Ser. No. 13/630,902 filed Sep. 28, 2012, is also a continuation-in-part application of and claims priority to U.S. patent application Ser. No. 12/515,687, filed Apr. 6, 2010, which is a National Stage application under 35 U.S.C. § 371 of International Application No. PCT/US2007/085237, filed Nov. 20, 2007, which claims the benefit of priority under 35 U.S.C. § 119(e) to U.S. Provisional Patent Application Ser. No. 60/860,145, filed Nov. 20, 2006. U.S. patent application Ser. No. 13/630,902 filed Sep. 28, 2012, is also a continuation-in-part application of and claims priority to U.S. patent application Ser. No. 12/307,561, filed Nov. 23, 2009, which is a National Stage application under 35 U.S.C. § 371 of International Application No. PCT/US2007/072877, filed Jul. 5, 2007, which claims priority under 35 U.S.C. § 119(e) to U.S. Provisional Patent Application Ser. No. 60/818,569, filed Jul. 5, 2006. U.S. patent application Ser. No. 13/630,902 filed Sep. 28, 2012, is also a continuation-in-part application of and claims priority to U.S. patent application Ser. No. 13/119,572, filed Aug. 10, 2011, which is a National Stage application under 35 U.S.C. § 371 of International Application No. PCT/US2009/057116, filed Sep. 16, 2009, which claims the benefit of priority under 35 U.S.C. § 119(e) to U.S. Provisional Patent Application Ser. No. 61/097,789, filed Sep. 17, 2008. The disclosures of these prior applications are considered part of (and are incorporated by reference in their entirety in) the disclosure of this application.

INCORPORATION OF SEQUENCE LISTING

The Sequence listing contained in the file named CRES026USD4_ST26.xml, which is 6,805 kilobytes (size

as measured in Microsoft Windows®), was created on Sep. 14, 2023, was filed herewith by electronic submission on Sep. 20, 2023, and is incorporated by reference herein.

TECHNICAL FIELD

This document relates to methods and materials involved in plant shade and/or low light tolerance, and red light specific responses. For example, this document provides plants having increased shade and/or low light tolerance as well as materials and methods for making plants having increased shade and/or low light tolerance. This document also relates to methods and materials involved in increasing UV-B tolerance in plants and methods and materials involved in modulating biomass levels in plants.

BACKGROUND

Light is the source of energy that fuels plant growth through photosynthesis. Light is also a developmental signal that modulates morphogenesis, such as de-etiolation and the transition to reproductive development. Since plants cannot choose their surroundings, they are forced to adapt their growth to ambient light conditions and have evolved complex mechanisms for monitoring the quantity and quality of the surrounding light. For example, many kinds of plants respond to growth under dense canopies or at high densities by growing faster and taller (Cerdan and Chory (2003) *Nature*, 423:881). Densely planted crops tend to place energy into stem and petiole elongation to lift the leaves into the sunlight rather than putting energy into storage or reproductive structures. The response to low light conditions and/or shade conditions negatively affects crop yields by reducing the amount of harvestable products such as seeds, fruits and tubers. In addition, tall spindly plants tend to be less wind resistant and lodge more easily, further reducing crop yield.

There is a continuing need for plants that can thrive under less than optimal environmental conditions. One strategy to improve a plant's ability to withstand suboptimal environmental conditions relies upon traditional plant breeding methods. Another approach involves genetic manipulation of plant characteristics through the introduction of exogenous nucleic acids conferring a desirable trait.

SUMMARY

The spectral energy distribution of daylight is dramatically altered by vegetation. Light reflected from neighboring vegetation is depleted in red (R) wavelengths, but remains rich in far-red (FR) wavelengths. It is desirable to have plants that exhibit increased shade tolerance. Plants having increased shade tolerance described herein exhibit an increased tolerance to shade conditions, in particular, Short Day plus End-of-Day Far-Red (SD+EODFR) conditions. Wild-type plants typically exhibit shade avoidance responses to SD+EODFR conditions, whereas the SD+EODFR-tolerant plants described herein display a reduction in the level of shade avoidance responses relative to the level of shade avoidance responses displayed by non-SD+EODFR-tolerant plants.

The quantity of light can dictate the eventual biomass and yield of plants. Wild-type plants typically exhibit low light responses, whereas the low light-tolerant plants described herein display a reduction in the level of low light responses relative to the level of low light responses displayed by non-low light-tolerant plants.

Increasing the SD+EODFR and/or low light tolerance of plants can increase the crop yields of such plants, which can benefit both food consumers and producers. This document provides methods and materials related to plants having increased shade and/or low light tolerance. For example, this document provides transgenic plants having increased SD+EODFR and/or low light tolerance, nucleic acids used to generate transgenic plants having increased SD+EODFR and/or low light tolerance, and methods for making plants having increased SD+EODFR and/or low light tolerance. Such plants may be useful to produce biomass which may be converted to a liquid fuel or other chemicals and/or to produce crops with increased yield and/or quality.

Methods of producing a plant are provided herein. In one aspect, a method comprises growing a plant cell comprising an exogenous nucleic acid. The exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide. The Hidden Markov Model (HMM) bit score of the amino acid sequence of the polypeptide is greater than about 20, using an HMM generated from the amino acid sequences depicted in one of FIGS. 1-24. A plant produced from the cell has a difference in low light or SD+EODFR tolerance as compared to a control plant that does not comprise the exogenous nucleic acid.

In another aspect, the exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide having 80 percent or greater sequence identity to an amino acid sequence set forth in SEQ ID NOs:3, 5, 7, 9, 10, 12, 14, 16, 18, 20, 22, 24, 25, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 49, 51, 53, 55, 57, 59, 60, 61, 62, 63, 65, 67, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 89, 90, 91, 93, 95, 96, 97, 98, 99, 100, 101, 102, 103, 105, 107, 109, 111, 113, 115, 116, 117, 118, 119, 120, 121, 122, 124, 126, 129, 130, 131, 132, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 188, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 262, 264, 266, 268, 270, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 306, 308, 310, 312, 314, 317, 319, 321, 323, 325, 327, 329, 330, 331, 332, 334, 337, 339, 341, 343, 344, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 357, 359, 361, 362, 364, 365, 366, 367, 368, 370, 372, 374, 376, 378, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 456, 457, 458, 459, 460, 462, 464, 466, 468, 470, 472, 474, 475, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 491, 493, 494, 495, 496, 497, 498, 499, 501, 503, 505, 507, 508, 509, 510, 511, 512, 514, 515, 516, 518, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 538, 539, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 552, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 567, 570, 572, 574, 576, 578, 579, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 601, 603, 606, 607, 608, 609, 611, 613, 615, 616, 617, 618, 620, 621, 622, 624, 625, 626, 628, 629, 631, 634, 636, 637, 638, 639, 641, 644, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 675, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 695, 697, 699, 701, 702, 704, 706, 708, 709, 711, 712, 713, 714, 716, 718, 720, 721, 723, 725, 726, 728, 730, 732, 734, 736, 738, 740, 741, 742, 743, 744, 745, 747, 749, 750, 751, 753, 755, 757, 759, 761, 762, 763, 764, 765, 767,

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In one aspect, the polypeptide further comprises a CDI domain having 70 percent or greater sequence identity to the CDI domain of SEQ ID NO:70. In another aspect, the polypeptide further comprises an AUX/IAA domain having 70 percent or greater sequence identity to the AUX/IAA domain of SEQ ID NO:129 or SEQ ID NO:1347. In another aspect, the polypeptide further comprises a homeobox domain having 70 percent or greater sequence identity to the homeobox domain of SEQ ID NO:317. In another aspect, the polypeptide further comprises a zf_C3HC4 domain having 70 percent or greater sequence identity to the zf_C3HC4 domain of SEQ ID NO:337. In another aspect, the polypeptide further comprises a B-box zinc finger domain having 70 percent or greater sequence identity to the B-box zinc finger domain of SEQ ID NO:456 and a CCT motif having 70 percent or greater sequence identity to the CCT motif of SEQ ID NO:456. In another aspect, the polypeptide further comprises a FAD_binding_7 domain

having 70 percent or greater sequence identity to the FAD_binding_7 domain of SEQ ID NO:538 or SEQ ID NO:1497 and a DNA photolyase domain having 70 percent or greater sequence identity to the DNA photolyase domain of SEQ ID NO:538 or SEQ ID NO:1497. In another aspect, the polypeptide further comprises a zf_Dof domain having 70 percent or greater sequence identity to the zf_Dof domain of SEQ ID NO:606. In another aspect, the polypeptide further comprises an AP2 domain having 70 percent or greater sequence identity to the AP2 domain of SEQ ID NO:645. In another aspect, the polypeptide further comprises a VQ motif having 70 percent or greater sequence identity to the VQ motif of SEQ ID NO:850. In another aspect, the polypeptide further comprises a zf_C2H2 domain having 70 percent or greater sequence identity to the zf_C2H2 domain of SEQ ID NO:907. In another aspect, the polypeptide further comprises a TCP domain having 70 percent or greater sequence identity to the TCP domain of SEQ ID NO:1151. In another aspect, the polypeptide further comprises an F-box domain having 70 percent or greater sequence identity to the F-box domain of SEQ ID NO:1277. In another aspect, the polypeptide further comprises a zf_CCCCH domain having 70 percent or greater sequence identity to the zf_CCCCH domain of SEQ ID NO:1457. In another aspect, the polypeptide further comprises a POX domain having 70 percent or greater sequence identity to the POX domain of SEQ ID NO:1540 and a homeobox domain having 70 percent or greater sequence identity to the homeobox domain of SEQ ID NO:1540. In another aspect, the polypeptide further comprises an HSF-type DNA-binding domain having 70 percent or greater sequence identity to the HSF-type DNA-binding domain of SEQ ID NO:1587. In another aspect, the polypeptide further comprises a SAM_1 domain having 70 percent or greater sequence identity to the SAM_1 domain of SEQ ID NO:1635 and a DRMBL domain having 70 percent or greater sequence identity to the DRMBL domain of SEQ ID NO:1635.

In another aspect, a method of producing a plant comprises growing a plant cell comprising an exogenous nucleic acid, where the exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence, or a fragment thereof, set forth in SEQ ID NOS:1, 2, 4, 6, 8, 11, 13, 15, 17, 19, 21, 23, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 50, 52, 54, 56, 58, 64, 66, 68, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 92, 94, 104, 106, 108, 110, 112, 114, 123, 125, 127, 128, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 263, 265, 267, 269, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 305, 307, 309, 311, 313, 315, 316, 318, 320, 322, 324, 326, 328, 333, 335, 336, 338, 340, 342, 345, 356, 358, 360, 363, 369, 371, 373, 375, 377, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 455, 461, 463, 465, 467, 469, 471, 473, 476, 490, 492, 500, 502, 504, 506, 513, 517, 519, 537, 540, 551, 553, 566, 568, 569, 571, 573, 575, 577, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 602, 604, 605, 610, 612, 614, 619, 623, 627, 630, 632, 633, 635, 640, 642, 643, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 677, 679, 681, 683, 685, 687, 689, 691, 693, 696, 698, 700, 703, 705, 707, 710, 715, 717, 719, 722, 724, 727, 729, 731, 733, 735, 737, 739, 746, 748, 752, 754, 756, 758, 760, 766, 768,

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Methods of modulating low light tolerance in a plant are provided herein. In one aspect, a method comprises introducing into a plant cell an exogenous nucleic acid, that comprises a regulatory region operably linked to a nucleo-

tide sequence encoding a polypeptide. The HMM bit score of the amino acid sequence of the polypeptide is greater than about 20, using an HMM generated from the amino acid sequences depicted in one of FIGS. 1-24. A plant produced from the plant cell has a difference in low light tolerance as compared to a control plant that does not comprise the exogenous nucleic acid.

In another aspect, a method comprises introducing into a plant cell an exogenous nucleic acid that comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide having 80 percent or greater sequence identity to an amino acid sequence set forth in SEQ ID NOs:3, 5, 7, 9, 10, 12, 14, 16, 18, 20, 22, 24, 25, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 49, 51, 53, 55, 57, 59, 60, 61, 62, 63, 65, 67, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 89, 90, 91, 93, 95, 96, 97, 98, 99, 100, 101, 102, 103, 105, 107, 109, 111, 113, 115, 116, 117, 118, 119, 120, 121, 122, 124, 126, 129, 130, 131, 132, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 188, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 262, 264, 266, 268, 270, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 306, 308, 310, 312, 314, 317, 319, 321, 323, 325, 327, 329, 330, 331, 332, 334, 337, 339, 341, 343, 344, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 357, 359, 361, 362, 364, 365, 366, 367, 368, 370, 372, 374, 376, 378, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 456, 457, 458, 459, 460, 462, 464, 466, 468, 470, 472, 474, 475, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 491, 493, 494, 495, 496, 497, 498, 499, 501, 503, 505, 507, 508, 509, 510, 511, 512, 514, 515, 516, 518, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 538, 539, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 552, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 567, 570, 572, 574, 576, 578, 579, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 601, 603, 606, 607, 608, 609, 611, 613, 615, 616, 617, 618, 620, 621, 622, 624, 625, 626, 628, 629, 631, 634, 636, 637, 638, 639, 641, 644, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 675, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 695, 697, 699, 701, 702, 704, 706, 708, 709, 711, 712, 713, 714, 716, 718, 720, 721, 723, 725, 726, 728, 730, 732, 734, 736, 738, 740, 741, 742, 743, 744, 745, 747, 749, 750, 751, 753, 755, 757, 759, 761, 762, 763, 764, 765, 767, 769, 771, 773, 774, 776, 778, 779, 780, 782, 783, 784, 786, 788, 790, 792, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 826, 827, 829, 830, 831, 832, 833, 834, 835, 837, 838, 839, 840, 841, 843, 845, 847, 850, 851, 853, 855, 857, 859, 861, 862, 863, 864, 865, 866, 868, 870, 872, 874, 876, 877, 879, 881, 883, 885, 887, 889, 891, 893, 895, 897, 898, 900, 902, 904, 907, 909, 911, 913, 915, 917, 919, 920, 922, 923, 924, 926, 928, 929, 930, 931, 932, 934, 936, 937, 938, 939, 940, 941, 943, 945, 947, 948, 949, 950, 953, 955, 957, 959, 961, 963, 965, 966, 967, 969, 971, 973, 975, 977, 979, 981, 983, 985, 987, 989, 991, 993, 995, 997, 999, 1001, 1003, 1005, 1007, 1009, 1011, 1013, 1014, 1015, 1016, 1018, 1024, 1025, 1027, 1029, 1030, 1032, 1033, 1035, 1037, 1039, 1040, 1042, 1043, 1044, 1047, 1049, 1051, 1053, 1055, 1057, 1059, 1061, 1063, 1065, 1067, 1068, 1069, 1071, 1072, 1073,

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In another aspect, a method comprises introducing into a plant cell an exogenous nucleic acid, that comprises a regulatory region operably linked to a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence set forth in SEQ ID NOs: 1, 2, 4, 6, 8, 11, 13, 15, 17, 19, 21, 23, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 50, 52, 54, 56, 58, 64, 66, 68, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 92, 94, 104, 106, 108, 110, 112, 114, 123, 125, 127, 128, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 263, 265, 267, 269, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 305, 307, 309, 311, 313, 315, 316, 318, 320, 322, 324, 326, 328, 333, 335, 336, 338, 340, 342, 345, 356, 358, 360, 363, 369, 371, 373, 375, 377, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 455, 461, 463, 465, 467, 469, 471, 473, 476, 490, 492, 500, 502, 504, 506, 513, 517, 519, 537, 540, 551, 553, 566, 568, 569, 571, 573, 575, 577, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 602, 604, 605, 610, 612, 614, 619, 623, 627, 630, 632, 633, 635, 640, 642, 643, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 677, 679, 681, 683, 685, 687, 689, 691, 693, 696, 698, 700, 703, 705, 707, 710, 715, 717, 719, 722, 724, 727, 729, 731, 733, 735, 737, 739, 746, 748, 752, 754, 756, 758, 760, 766, 768, 770, 772, 775, 777, 781, 785, 787, 789, 791, 793, 825, 828, 836, 842, 844, 846, 848, 849, 852, 854, 856, 858, 860, 867, 869, 871, 873, 875, 878, 880, 882, 884, 886, 888, 890, 892, 894, 896, 899, 901, 903, 905, 906, 908, 910, 912, 914, 916, 918, 921, 925, 927, 933, 935, 942, 944, 946, 951, 952, 954, 956, 958, 960, 962, 964, 968, 970, 972, 974, 976, 978, 980, 982, 984, 986, 988, 990,

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Methods of modulating SD+EODFR tolerance in a plant are provided herein. In one aspect, a method comprises introducing into a plant cell an exogenous nucleic acid, that comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide. The HMM bit score of the amino acid sequence of the polypeptide is greater than about 20, using an HMM generated from the amino acid sequences depicted in one of FIG. 16 or 24-27. A plant produced from the plant cell has a difference in SD+EODFR tolerance as compared to a control plant that does not comprise the exogenous nucleic acid.

In another aspect, a method comprises introducing into a plant cell an exogenous nucleic acid that comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide having 80 percent or greater sequence identity to an amino acid sequence set forth in SEQ ID NOs:538, 539, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 552, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 567, 570, 572, 574, 576, 578, 579, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 601, 603, 606, 607, 608, 609, 611, 613, 615, 616, 617, 618, 620, 621, 622, 624, 625, 626, 628, 629, 631, 1347, 1349, 1351, 1352, 1353, 1355, 1357, 1358, 1360, 1362, 1364, 1366, 1367, 1368, 1370, 1372, 1374, 1375, 1377, 1379, 1381, 1383, 1385, 1387, 1389, 1391, 1393, 1395, 1397, 1399, 1401, 1402, 1404, 1406, 1408, 1410, 1411, 1412, 1413, 1414, 1415, 1417, 1419, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1429, 1430, 1431, 1433, 1434, 1435, 1436, 1438, 1439, 1440, 1442, 1444, 1446, 1448, 1450, 1452, 1540, 1541, 1543, 1545, 1547, 1549, 1551, 1553, 1554, 1555, 1556, 1557, 1558, 1559, 1561, 1563, 1564, 1565, 1566, 1567, 1568, 1570, 1572, 1574, 1576, 1578, 1580, 1582, 1584, 1679, 1681, 1682, 1748, 1750, 1751, 1752, 1850, 1852, 1854, 1856, 1858, 1859, 1860, 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1869, 1870, 1871, 1873, 1875, 1877, 1879, 1881, 1883, 1885, 1887, 1889, 1891, 1893, 1895, 1897, 1899, 1901, 1903, 1905, 1907, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, or 2278. A plant produced from the plant cell has a difference in SD+EODFR tolerance as compared to a control plant that does not comprise the exogenous nucleic acid.

In another aspect, a method comprises introducing into a plant cell an exogenous nucleic acid, that comprises a regulatory region operably linked to a nucleotide sequence having 80 percent or greater sequence identity to a nucleotide sequence set forth in SEQ ID NOs:537, 540, 551, 553, 566, 568, 569, 571, 573, 575, 577, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 602, 604, 605, 610, 612, 614, 619, 623, 627, 630, 1345, 1346, 1348, 1350, 1354, 1356, 1359, 1361, 1363, 1365, 1369, 1371, 1373, 1376, 1378, 1380, 1382, 1384, 1386, 1388, 1390, 1392, 1394, 1396, 1398, 1400, 1403, 1405, 1407, 1409, 1416, 1418, 1420, 1428, 1432, 1437, 1441, 1443, 1445, 1447, 1449, 1451, 1537, 1538, 1539, 1542, 1544, 1546, 1548, 1550, 1552, 1560, 1562, 1569, 1571, 1573, 1575, 1577, 1579, 1581, 1583, 1678, 1680, 1747, 1749, 1849, 1851, 1853, 1855, 1857, 1868, 1872, 1874, 1876, 1878, 1880, 1882, 1884, 1886, 1888, 1890, 1892, 1894, 1896, 1898, 1900, 1902, 1904, 1906, and 2267, or a fragment thereof. A plant produced from the plant cell has a difference in SD+EODFR tolerance as compared to a control plant that does not comprise the exogenous nucleic acid.

Plant cells comprising an exogenous nucleic acid are provided herein. In one aspect, the exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide. The HMM bit score of the amino acid sequence of the polypeptide is greater than about 20, using an HMM based on the amino acid sequences depicted in one of FIGS. 1-24. A plant produced from the cells has a difference in low light or SD+EODFR tolerance as compared to a control plant that does not comprise the exogenous nucleic acid. In another aspect, the exogenous nucleic acid comprises a regulatory region operably linked to a nucleotide sequence encoding a polypeptide having 80 percent or greater sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:3, 5, 7, 9, 10, 12, 14, 16, 18, 20, 22, 24, 25, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 49, 51, 53, 55, 57, 59, 60,

61, 62, 63, 65, 67, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 89, 90, 91, 93, 95, 96, 97, 98, 99, 100, 101, 102, 103, 105, 107, 109, 111, 113, 115, 116, 117, 118, 119, 120, 121, 122, 124, 126, 129, 130, 131, 132, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 188, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 262, 264, 266, 268, 270, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 306, 308, 310, 312, 314, 317, 319, 321, 323, 325, 327, 329, 330, 331, 332, 334, 337, 339, 341, 343, 344, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 357, 359, 361, 362, 364, 365, 366, 367, 368, 370, 372, 374, 376, 378, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 456, 457, 458, 459, 460, 462, 464, 466, 468, 470, 472, 474, 475, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 491, 493, 494, 495, 496, 497, 498, 499, 501, 503, 505, 507, 508, 509, 510, 511, 512, 514, 515, 516, 518, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 538, 539, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 552, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 567, 570, 572, 574, 576, 578, 579, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 601, 603, 606, 607, 608, 609, 611, 613, 615, 616, 617, 618, 620, 621, 622, 624, 625, 626, 628, 629, 631, 634, 636, 637, 638, 639, 641, 644, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 675, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 695, 697, 699, 701, 702, 704, 706, 708, 709, 711, 712, 713, 714, 716, 718, 720, 721, 723, 725, 726, 728, 730, 732, 734, 736, 738, 740, 741, 742, 743, 744, 745, 747, 749, 750, 751, 753, 755, 757, 759, 761, 762, 763, 764, 765, 767, 769, 771, 773, 774, 776, 778, 779, 780, 782, 783, 784, 786, 788, 790, 792, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 826, 827, 829, 830, 831, 832, 833, 834, 835, 837, 838, 839, 840, 841, 843, 845, 847, 850, 851, 853, 855, 857, 859, 861, 862, 863, 864, 865, 866, 868, 870, 872, 874, 876, 877, 879, 881, 883, 885, 887, 889, 891, 893, 895, 897, 898, 900, 902, 904, 907, 909, 911, 913, 915, 917, 919, 920, 922, 923, 924, 926, 928, 929, 930, 931, 932, 934, 936, 937, 938, 939, 940, 941, 943, 945, 947, 948, 949, 950, 953, 955, 957, 959, 961, 963, 965, 966, 967, 969, 971, 973, 975, 977, 979, 981, 983, 985, 987, 989, 991, 993, 995, 997, 999, 1001, 1003, 1005, 1007, 1009, 1011, 1013, 1014, 1015, 1016, 1018, 1024, 1025, 1027, 1029, 1030, 1032, 1033, 1035, 1037, 1039, 1040, 1042, 1043, 1044, 1047, 1049, 1051, 1053, 1055, 1057, 1059, 1061, 1063, 1065, 1067, 1068, 1069, 1071, 1072, 1073, 1074, 1075, 1077, 1078, 1080, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1098, 1099, 1100, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1115, 1117, 1119, 1121, 1123, 1125, 1127, 1129, 1131, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1141, 1143, 1145, 1147, 1149, 1151, 1153, 1155, 1157, 1159, 1160, 1161, 1162, 1164, 1166, 1168, 1170, 1172, 1174, 1176, 1178, 1180, 1182, 1184, 1186, 1188, 1190, 1192, 1194, 1196, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1206, 1208, 1209, 1211, 1213, 1214, 1215, 1216, 1217, 1219, 1221, 1223, 1225, 1227, 1229, 1230, 1232, 1234, 1236, 1238, 1240, 1242, 1244, 1246, 1248, 1250, 1252, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1266, 1268, 1270, 1272, 1274, 1277, 1279, 1281, 1283, 1285, 1287, 1289, 1291, 1293, 1294, 1295,

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15

2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2266, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2280, 2282, 2284, 2286, 2288, 2290, 2292, 2294, 2296, 2298, 2300, 2302, 2304, 2306, 2308, 2310, 2312, 2314, 2316, 2318, 2320, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2350, 2352, 2354, 2356, 2358, 2360, 2362, 2364, 2366, 2368, 2370, 2372, 2374, 2375, 2376, 2377, 2378, 2379, 2380, and 2381.

Also provided herein is a method of identifying whether a polymorphism is associated with variation in low light or SD+EODFR tolerance. The method includes the steps of: determining whether one or more genetic polymorphisms in a population of plants is associated with the locus for a polypeptide selected from the group consisting of the polypeptides depicted in FIGS. 1-24 and functional homologs thereof; and measuring the correlation between variation in the low light or SD+EODFR tolerance in plants of the population and the presence of the genetic polymorphisms in plants of the population, thereby identifying whether or not one or more genetic polymorphisms are associated with variation in low light or SD+EODFR tolerance. The population of plants can be a population of switchgrass, sorghum, sugar cane, or miscanthus plants.

A method of making a plant line is also provided herein. The method includes the steps of: determining whether one or more genetic polymorphisms in a population of plants is associated with the locus for a polypeptide selected from the group consisting of the polypeptides depicted in FIGS. 1-24 and functional homologs thereof; identifying one or more plants in the population in which the presence of at least one allele at the one or more genetic polymorphisms is associated with variation in low light or SD+EODFR tolerance; crossing each of the identified plants with itself or a different plant to produce seed; crossing at least one progeny plant grown from the seed with itself or a different plant; and repeating the crossing steps for an additional 0-5 generations to make the plant line, wherein the allele is present in the plant line. The population of plants can be a population of switchgrass plants.

In another aspect, this document provides a method of producing a plant. The method comprises growing a plant cell comprising an exogenous nucleic acid, wherein the exogenous nucleic acid is effective for down-regulating an endogenous nucleic acid in the plant cell. The endogenous nucleic acid can encode a polypeptide. The HMM bit score of the amino acid sequence of the polypeptide can be greater than about 210. The HMM can be based on the amino acid sequences depicted in one of FIGS. 6, 11, and 21. The plant produced from the cell can have an increase in hypocotyl length as compared to a control plant that does not comprise the exogenous nucleic acid.

In another aspect, a transgenic plant cell is provided. The plant cell comprises an exogenous nucleic acid. The exogenous nucleic acid is effective for down-regulating an endogenous nucleic acid in the plant cell. The endogenous nucleic acid can encode a polypeptide. The HMM bit score of the amino acid sequence of the polypeptide is greater than about 210. The HMM is based on the amino acid sequences depicted in one of FIGS. 6, 11, and 21.

16

A transgenic plant is also provided. The transgenic plant comprises a plant cell comprising an exogenous nucleic acid. The exogenous nucleic acid is effective for down-regulating an endogenous nucleic acid in the plant cell. The endogenous nucleic acid can encode a polypeptide. The HMM bit score of the amino acid sequence of the polypeptide is greater than about 210. The HMM is based on the amino acid sequences depicted in one of FIGS. 6, 11, and 21. The plant has an increase in hypocotyl length as compared to a control plant that does not comprise the plant cell.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. Although methods and materials similar or equivalent to those described herein can be used to practice the invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

DESCRIPTION OF THE DRAWINGS

FIG. 1 is an alignment of At4g37295 (Ceres Seedline ME05268; SEQ ID NO:3) with homologous and/or orthologous amino acid sequences including Ceres CLONE ID no. 1844057 (SEQ ID NO:7), Ceres ANNOT ID no. 1469148 (SEQ ID NO:22), Public GI ID no. 18390998 (SEQ ID NO:25), Ceres CLONE ID no. 1065656 (SEQ ID NO:32), Ceres CLONE ID no. 1652677 (SEQ ID NO:36), Public GI ID no. 92874556 (SEQ ID NO:49), Ceres CLONE ID no. 1329161 (SEQ ID NO:53), Ceres CLONE ID no. 1030378 (SEQ ID NO:55), Ceres CLONE ID no. 1413787 (SEQ ID NO:57), and Public GI ID no. 125543598 (SEQ ID NO:60). In all the alignment figures shown herein, a dash in an aligned sequence represents a gap, i.e., a lack of an amino acid at that position. Identical amino acids or conserved amino acid substitutions among aligned sequences are identified by boxes. FIG. 1 and the other alignment figures provided herein were generated using the program MUSCLE version 3.52.

FIG. 2 is an alignment of At2g32710 (Ceres Seedline ME06120; SEQ ID NO:70) with homologous and/or orthologous amino acid sequences including Ceres CLONE ID no. 1975934 (SEQ ID NO:72), Ceres ANNOT ID no. 1529913 (SEQ ID NO:80), Ceres CLONE ID no. 977794 (SEQ ID NO:93), Public GI ID no. 42362378 (SEQ ID NO:96), Public GI ID no. 23899378 (SEQ ID NO:99), Public GI ID no. 15963346 (SEQ ID NO:101), Public GI ID no. 15963344+B816 (SEQ ID NO:102), Public GI ID no. 92429657 (SEQ ID NO:103), Ceres CLONE ID no. 746644 (SEQ ID NO:105), Ceres CLONE ID no. 623089 (SEQ ID NO:109), Ceres CLONE ID no. 1913678 (SEQ ID NO:115), and Public GI ID no. 115450609 (SEQ ID NO:119).

FIG. 3 is an alignment of At2g46990 (Ceres Seedline ME09503; SEQ ID NO:129) with homologous and/or orthologous amino acid sequences including Public GI ID no. 34550779 (SEQ ID NO:133), Ceres CLONE ID no. 1932235 (SEQ ID NO:137), Ceres CLONE ID no. 981738 (SEQ ID NO:201), Ceres CLONE ID no. 565974 (SEQ ID NO:202).

NO:209), Public GI ID no. 1352058 (SEQ ID NO:231), Public GI ID no. 11131101 (SEQ ID NO:234), Public GI ID no. 4887018 (SEQ ID NO:236), Public GI ID no. 4887018 (SEQ ID NO:236), Ceres CLONE ID no. 644455 (SEQ ID NO:247), Ceres CLONE ID no. 1731500 (SEQ ID NO:270), Public GI ID no. 20269063 (SEQ ID NO:300), Public GI ID no. 50404477 (SEQ ID NO:302), and Public GI ID no. 62125392 (SEQ ID NO:303).

FIG. 4 is an alignment of At4g03250 (Ceres Seedline ME10007; SEQ ID NO:317) with homologous and/or orthologous amino acid sequences including Ceres CLONE ID no. 1842125 (SEQ ID NO:319), Ceres ANNOT ID no. 1461360 (SEQ ID NO:321), Ceres CLONE ID no. 480906 (SEQ ID NO:327), Public GI ID no. 92889352 (SEQ ID NO:330), and Public GI ID no. 56201850 (SEQ ID NO:331).

FIG. 5 is an alignment of At2g04240 (Ceres Seedline ME10852; SEQ ID NO:337), Ceres CLONE ID no. 952050 (SEQ ID NO:339) with homologous and/or orthologous amino acid sequences including Public GI ID no. 115477050 (SEQ ID NO:349), Public GI ID no. 87162911 (SEQ ID NO:355), Ceres CLONE ID no. 1790901 (SEQ ID NO:357), Ceres CLONE ID no. 1460088 (SEQ ID NO:370), Ceres CLONE ID no. 1734065 (SEQ ID NO:393), Ceres CLONE ID no. 473509 (SEQ ID NO:395), Ceres CLONE ID no. 849918 (SEQ ID NO:401), Ceres CLONE ID no. 633470 (SEQ ID NO:409), Ceres CLONE ID no. 1808334 (SEQ ID NO:417), and Ceres ANNOT ID no. 1525600 (SEQ ID NO:437).

FIG. 6 is an alignment of At5g14370 (Ceres Seedline ME11939; SEQ ID NO:456) with homologous and/or orthologous amino acid sequences including Public GI ID no. 58430585 (SEQ ID NO:457), Ceres CLONE ID no. 1842825 (SEQ ID NO:466), Ceres ANNOT ID no. 1449721 (SEQ ID NO:474), Public GI ID no. 41323978 (SEQ ID NO:475), Public GI ID no. 2895186 (SEQ ID NO:478), Public GI ID no. 22854950 (SEQ ID NO:481), Public GI ID no. 116010474 (SEQ ID NO:485), Public GI ID no. 4091804 (SEQ ID NO:488), Public GI ID no. 60459257 (SEQ ID NO:494), Public GI ID no. 45544881 (SEQ ID NO:496), Public GI ID no. 36789802 (SEQ ID NO:498), Public GI ID no. 92875402 (SEQ ID NO:508), Public GI ID no. 118406898 (SEQ ID NO:510), Public GI ID no. 107770485 (SEQ ID NO:511), Public GI ID no. 21655154 (SEQ ID NO:532), Public GI ID no. 90657642 (SEQ ID NO:536), and Ceres CLONE ID no. 1569555 (SEQ ID NO:1842).

FIG. 7 is an alignment of At1g70270 (Ceres Seedline ME13456; SEQ ID NO:634) with homologous and/or orthologous amino acid sequences including Public GI ID no. 98961985 (SEQ ID NO:637).

FIG. 8 is an alignment of At4g25480 (Ceres Seedline ME15935; SEQ ID NO:644) with homologous and/or orthologous amino acid sequences including SEQ ID NO:645, Ceres CLONE ID no. 1849479 (SEQ ID NO:767), Public GI ID no. 89275008 (SEQ ID NO:796), Public GI ID no. 120400525 (SEQ ID NO:797), Public GI ID no. 98980426 (SEQ ID NO:804), Public GI ID no. 71983373 (SEQ ID NO:808), Public GI ID no. 41351817 (SEQ ID NO:809), Public GI ID no. 76446191 (SEQ ID NO:811), Public GI ID no. 5616086 (SEQ ID NO:813), Ceres CLONE ID no. 1052602 (SEQ ID NO:826), Public GI ID no. 72068957 (SEQ ID NO:830), Public GI ID no. 71534113 (SEQ ID NO:831), Public GI ID no. 37147896 (SEQ ID NO:832), Public GI ID no. 92918850 (SEQ ID NO:834), Public GI ID no. 40647095 (SEQ ID NO:835), Ceres ANNOT ID no. 1527711 (SEQ ID NO:837), Public GI ID

no. 71041116 (SEQ ID NO:838), Public GI ID no. 12003384 (SEQ ID NO:839), Public GI ID no. 18535580 (SEQ ID NO:840), and Public GI ID no. 115353971 (SEQ ID NO:1843).

FIG. 9 is an alignment of At2g33780 (Ceres SEEDLINE ID no. ME16594, SEQ ID NO:850) with homologous and/or orthologous amino acid sequences including Ceres CLONE ID no. 1833093 (SEQ ID NO:853), Ceres ANNOT ID no. 1502190 (SEQ ID NO:857), Ceres CLONE ID no. 565641 (SEQ ID NO:876), Public GI ID no. 87240507 (SEQ ID NO:877), Ceres CLONE ID no. 1325382 (SEQ ID NO:881), Ceres CLONE ID no. 1558265 (SEQ ID NO:885), Ceres CLONE ID no. 1823669 (SEQ ID NO:895), and Public GI ID no. 115464921 (SEQ ID NO:898).

FIG. 10 is an alignment of At4g17810 (Ceres SEEDLINE ID no. ME16597, SEQ ID NO:907) with homologous and/or orthologous amino acid sequences including Ceres CLONE ID no. 1940797 (SEQ ID NO:909), Ceres ANNOT ID no. 1538900 (SEQ ID NO:911), Ceres CLONE ID no. 1126868 (SEQ ID NO:922), Public GI ID no. 89257684 (SEQ ID NO:923), Public GI ID no. 124360460 (SEQ ID NO:929), Public GI ID no. 62865694 (SEQ ID NO:931), Public GI ID no. 62865692 (SEQ ID NO:932), Ceres CLONE ID no. 260368 (SEQ ID NO:936), Ceres CLONE ID no. 1873510 (SEQ ID NO:947), Public GI ID no. 125541662 (SEQ ID NO:948), Public GI ID no. 48716268 (SEQ ID NO:950), and Public GI ID no. 62865696 (SEQ ID NO:1844).

FIG. 11 is an alignment of At1g13360 (Ceres SEEDLINE ID no. ME16630, SEQ ID NO:953) with homologous and/or orthologous amino acid sequences including Ceres CLONE ID no. 1798705 (SEQ ID NO:955), Ceres ANNOT ID no. 1458907 (SEQ ID NO:963), Ceres CLONE ID no. 1090409 (SEQ ID NO:971), Ceres CLONE ID no. 479817 (SEQ ID NO:977), Ceres CLONE ID no. 1041793 (SEQ ID NO:979), Ceres CLONE ID no. 684633 (SEQ ID NO:985), Ceres CLONE ID no. 371815 (SEQ ID NO:991), Ceres CLONE ID no. 1686460 (SEQ ID NO:993), Ceres CLONE ID no. 1448595 (SEQ ID NO:995), Ceres CLONE ID no. 1734477 (SEQ ID NO:999), Ceres CLONE ID no. 1605693 (SEQ ID NO:1005), Ceres CLONE ID no. 1757400 (SEQ ID NO:1009), and Public GI ID no. 115434334 (SEQ ID NO:1015).

FIG. 12 is an alignment of At1g75860 (Ceres SEEDLINE ID no. ME17128, SEQ ID NO:1024) with homologous and/or orthologous amino acid sequences including Ceres ANNOT ID no. 1452905 (SEQ ID NO:1029), Ceres CLONE ID no. 956176 (SEQ ID NO:1039), Public GI ID no. 92870366 (SEQ ID NO:1040), Ceres CLONE ID no. 294166 (SEQ ID NO:1042), and Public GI ID no. 125543067 (SEQ ID NO:1043).

FIG. 13 is an alignment of At4g19700 (Ceres SEEDLINE ID no. ME17578, SEQ ID NO:1047) with homologous and/or orthologous amino acid sequences including Ceres CLONE ID no. 1837694 (SEQ ID NO:1053), Ceres ANNOT ID no. 1483367 (SEQ ID NO:1057), Ceres CLONE ID no. 1077781 (SEQ ID NO:1083), Ceres CLONE ID no. 471026 (SEQ ID NO:1085), Public GI ID no. 92888885 (SEQ ID NO:1099), Public GI ID no. 45544873 (SEQ ID NO:1100), Public GI ID no. 45758663 (SEQ ID NO:1101), Ceres CLONE ID no. 772927 (SEQ ID NO:1105), Ceres CLONE ID no. 895080 (SEQ ID NO:1111), Ceres CLONE ID no. 1806128 (SEQ ID NO:1113), Public GI ID no. 115458192 (SEQ ID NO:1134), and Public GI ID no. 82470795 (SEQ ID NO:1139).

FIG. 14 is an alignment of At1g58100 (Ceres SEEDLINE ID no. ME18158, SEQ ID NO:1151) with homologous and/or orthologous amino acid sequences including Ceres

CLONE ID no. 1851526 (SEQ ID NO:1155), Ceres ANNOT ID no. 1486769 (SEQ ID NO:1172), Public GI ID no. 83032232 (SEQ ID NO:1209), Ceres CLONE ID no. 1620420 (SEQ ID NO:1211), Public GI ID no. 92892428 (SEQ ID NO:1215), Ceres CLONE ID no. 884742 (SEQ ID NO:1223), Ceres CLONE ID no. 1821559 (SEQ ID NO:1246), Public GI ID no. 51535021 (SEQ ID NO:1258), Public GI ID no. 113205304 (SEQ ID NO:1263), and Public GI ID no. 37719051 (SEQ ID NO:1264).

FIG. 15 is an alignment of At5g46170 (Ceres SEEDLINE ID no. ME18314, SEQ ID NO:1277) with homologous and/or orthologous amino acid sequences including Ceres CLONE ID no. 1926352 (SEQ ID NO:1279), Ceres ANNOT ID no. 1448905 (SEQ ID NO:1285), Public GI ID no. 15236865 (SEQ ID NO:1294), Ceres CLONE ID no. 934771 (SEQ ID NO:1301), Ceres CLONE ID no. 338386 (SEQ ID NO:1303), Ceres CLONE ID no. 1780691 (SEQ ID NO:1317), and Public GI ID no. 115464819 (SEQ ID NO:1326).

FIG. 16 is an alignment of At4g32280 (Ceres SEEDLINE ID no. ME18408, SEQ ID NO:1347) with homologous and/or orthologous amino acid sequences including Ceres CLONE ID no. 285028 (SEQ ID NO:1419), Ceres CLONE ID no. 100969565 (SEQ ID NO:1422), Public GI ID no. 1352057 (SEQ ID NO:1427), Ceres ANNOT ID no. 1453784 (SEQ ID NO:1429), Public GI ID no. 452777 (SEQ ID NO:1430), and Public GI ID no. 92873297 (SEQ ID NO:1431).

FIG. 17 is an alignment of At3g02830 (Ceres SEEDLINE ID no. ME19304, SEQ ID NO:1457) with homologous and/or orthologous amino acid sequences including Ceres CLONE ID no. 1924904 (SEQ ID NO:1460), Ceres ANNOT ID no. 1543346 (SEQ ID NO:1462), Public GI ID no. 18396338 (SEQ ID NO:1467), Ceres CLONE ID no. 833872 (SEQ ID NO:1471), Ceres CLONE ID no. 1579587 (SEQ ID NO:1475), Ceres CLONE ID no. 1786411 (SEQ ID NO:1477), and Public GI ID no. 108864370 (SEQ ID NO:1480).

FIG. 18 is an alignment of At4g08920 (Ceres SEEDLINE ID no. ME19738, SEQ ID NO:1497) with homologous and/or orthologous amino acid sequences including Ceres ANNOT ID no. 1443463 (SEQ ID NO:1499), Public GI ID no. 13605525 (SEQ ID NO:1502), Public GI ID no. 94965681 (SEQ ID NO:1506), and Public GI ID no. 28201254 (SEQ ID NO:1512).

FIG. 19 is an alignment of At4g11660 (Ceres SEEDLINE ID no. ME20871, SEQ ID NO:1587) with homologous and/or orthologous amino acid sequences including Ceres CLONE ID no. 1839577 (SEQ ID NO:1589), Ceres ANNOT ID no. 1491567 (SEQ ID NO:1591), Ceres CLONE ID no. 574505 (SEQ ID NO:1596), Public GI ID no. 56117815 (SEQ ID NO:1597), Public GI ID no. 92874021 (SEQ ID NO:1603), Public GI ID no. 123684 (SEQ ID NO:1605), Public GI ID no. 5821136 (SEQ ID NO:1606), Ceres CLONE ID no. 283366 (SEQ ID NO:1609), Public GI ID no. 16118447 (SEQ ID NO:1612), and Public GI ID no. 125562434 (SEQ ID NO:1614).

FIG. 20 is an alignment of At2g45700 (Ceres SEEDLINE ID no. ME21508, SEQ ID NO:1635) with homologous and/or orthologous amino acid sequences including Ceres ANNOT ID no. 1508307 (SEQ ID NO:1637), Public GI ID no. 1495267 (SEQ ID NO:1642), Public GI ID no. 87241310 (SEQ ID NO:1644), Ceres CLONE ID no. 938390 (SEQ ID NO:1646), Ceres CLONE ID no. 272338 (SEQ ID NO:1648), Ceres CLONE ID no. 1993510 (SEQ

ID NO:1650), Public GI ID no. 125563862 (SEQ ID NO:1651), and Public GI ID no. 125605833 (SEQ ID NO:1653).

FIG. 21 is an alignment of At2g35940 (Ceres SEEDLINE ID no. ME19971, SEQ ID NO:1540) with homologous and/or orthologous amino acid sequences including Ceres CLONE ID no. 1943265 (SEQ ID NO:1543), Ceres ANNOT ID no. 1454522 (SEQ ID NO:1547), Public GI ID no. 31323447 (SEQ ID NO:1556), Ceres CLONE ID no. 1583941 (SEQ ID NO:1561), Ceres CLONE ID no. 1792942 (SEQ ID NO:1563), Public GI ID no. 77548772 (SEQ ID NO:1565), and Public GI ID no. 84453182 (SEQ ID NO:1567).

FIG. 22 is an alignment of At1g04400 (Ceres SEEDLINE ID no. ME12006, SEQ ID NO:538) with homologous and/or orthologous amino acid sequences including Public GI ID no. 5731739 (SEQ ID NO:539), Ceres ANNOT ID no. 1538045 (SEQ ID NO:541), Public GI ID no. 29467479 (SEQ ID NO:542), Public GI ID no. 133921974 (SEQ ID NO:543), Public GI ID no. 113197027 (SEQ ID NO:544), Public GI ID no. 92879277 (SEQ ID NO:545), Public GI ID no. 45935260 (SEQ ID NO:546), Public GI ID no. 8101444 (SEQ ID NO:547), Public GI ID no. 78217443 (SEQ ID NO:548), and Public GI ID no. 28372347 (SEQ ID NO:549).

FIG. 23 is an alignment of At3g45610 (Ceres SEEDLINE ID no. ME12899, SEQ ID NO:606) with homologous and/or orthologous amino acid sequences including Public GI ID no. 92873064 (SEQ ID NO:607), Public GI ID no. 37051125 (SEQ ID NO:608), and Public GI ID no. 112363376 (SEQ ID NO:609).

FIG. 24 is an alignment of At4g08330 (Ceres SEEDLINE ID no. ME12596, SEQ ID NO:570) with homologous and/or orthologous amino acid sequences including Ceres CLONE ID no. 1919714 (SEQ ID NO:572), Ceres ANNOT ID no. 1443290 (SEQ ID NO:574), Ceres CLONE ID no. 1042157 (SEQ ID NO:576), Ceres CLONE ID no. 1384304 (SEQ ID NO:578), and Public GI ID no. 115464375 (SEQ ID NO:579).

DETAILED DESCRIPTION

This document provides methods and materials related to modulating tolerance of plants to Short Day plus End-of-Day Far-Red (SD+EODFR) conditions or low light irradiation. In some embodiments, the plants may have increased SD+EODFR tolerance and increased low light tolerance. The methods can include transforming a plant cell with a nucleic acid encoding an SD+EODFR and/or low light-tolerance polypeptide, wherein expression of the polypeptide results in increased SD+EODFR and/or low light tolerance. Plant cells produced using such methods can be grown to produce plants having an increased SD+EODFR and/or low light tolerance. Such plants can also be used to produce crops, plant products, biomass, and/or nitrogen fixing plants in shady or low light areas, such as under the canopy of another crop. For example, the methods and materials provided herein can be used to produce a legume (a member of Fabaceae, e.g., peas, beans, lupins, lentils, chick peas, vethes, soybeans, clovers, alfalfas, and peanuts) having an increased SD+EODFR and/or low light tolerance and which can be grown under the canopy of a taller crop (e.g., corn, switchgrass, sorghum, sugar cane, or miscanthus). In other embodiments, the taller plant is a nitrogen fixing plant (e.g., a member of Fabaceae, such as tamarind, mimosa, acacia, and carob) and the SD+EODFR and/or low

21

light tolerant plant is a shorter plant, such as corn, switchgrass, sorghum, sugar cane, or miscanthus.

I. DEFINITIONS

“Amino acid” refers to one of the twenty biologically occurring amino acids and to synthetic amino acids, including D/L optical isomers.

“Cell type-preferential promoter” or “tissue-preferential promoter” refers to a promoter that drives expression preferentially in a target cell type or tissue, respectively, but may also lead to some transcription in other cell types or tissues as well.

“Control plant” refers to a plant that does not contain the exogenous nucleic acid present in a transgenic plant of interest, but otherwise has the same or similar genetic background as such a transgenic plant. A suitable control plant can be a non-transgenic wild type plant, a non-transgenic segregant from a transformation experiment, or a transgenic plant that contains an exogenous nucleic acid other than the exogenous nucleic acid of interest.

“Domains” are groups of substantially contiguous amino acids in a polypeptide that can be used to characterize protein families and/or parts of proteins. Such domains have a “fingerprint” or “signature” that can comprise conserved primary sequence, secondary structure, and/or three-dimensional conformation. Generally, domains are correlated with specific in vitro and/or in vivo activities. A domain can have a length of from 10 amino acids to 400 amino acids, e.g., 10 to 50 amino acids, or 25 to 100 amino acids, or 35 to 65 amino acids, or 35 to 55 amino acids, or 45 to 60 amino acids, or 200 to 300 amino acids, or 300 to 400 amino acids.

“Down-regulation” refers to regulation that decreases the level of an expression product (mRNA, polypeptide, or both) relative to basal or native states.

“Exogenous” with respect to a nucleic acid indicates that the nucleic acid is part of a recombinant nucleic acid construct, or is not in its natural environment. For example, an exogenous nucleic acid can be a sequence from one species introduced into another species, i.e., a heterologous nucleic acid. Typically, such an exogenous nucleic acid is introduced into the other species via a recombinant nucleic acid construct. An exogenous nucleic acid can also be a sequence that is native to an organism and that has been reintroduced into cells of that organism. An exogenous nucleic acid that includes a native sequence can often be distinguished from the naturally occurring sequence by the presence of non-natural sequences linked to the exogenous nucleic acid, e.g., non-native regulatory sequences flanking a native sequence in a recombinant nucleic acid construct. In addition, stably transformed exogenous nucleic acids typically are integrated at positions other than the position where the native sequence is found. It will be appreciated that an exogenous nucleic acid may have been introduced into a progenitor and not into the cell under consideration. For example, a transgenic plant containing an exogenous nucleic acid can be the progeny of a cross between a stably transformed plant and a non-transgenic plant. Such progeny are considered to contain the exogenous nucleic acid.

“Expression” refers to the process of converting genetic information of a polynucleotide into RNA through transcription, which is catalyzed by an enzyme, RNA polymerase, and into protein, through translation of mRNA on ribosomes.

“Heterologous polypeptide” as used herein refers to a polypeptide that is not a naturally occurring polypeptide in a plant cell, e.g., a transgenic *Panicum virgatum* plant

22

transformed with and expressing the coding sequence for a nitrogen transporter polypeptide from a *Zea mays* plant.

“Isolated nucleic acid” as used herein includes a naturally-occurring nucleic acid, provided one or both of the sequences immediately flanking that nucleic acid in its naturally-occurring genome is removed or absent. Thus, an isolated nucleic acid includes, without limitation, a nucleic acid that exists as a purified molecule or a nucleic acid molecule that is incorporated into a vector or a virus. A nucleic acid existing among hundreds to millions of other nucleic acids within, for example, cDNA libraries, genomic libraries, or gel slices containing a genomic DNA restriction digest, is not to be considered an isolated nucleic acid.

“Modulation” of the level of tolerance to a stimulus (e.g., low light conditions or SD+EODFR conditions) refers to the change in the level of tolerance of the indicated stimulus that is observed as a result of expression of, or transcription from, an exogenous nucleic acid in a plant cell. The change in level is measured relative to the corresponding level in control plants.

“Nucleic acid” and “polynucleotide” are used interchangeably herein, and refer to both RNA and DNA, including cDNA, genomic DNA, synthetic DNA, and DNA or RNA containing nucleic acid analogs. Polynucleotides can have any three-dimensional structure. A nucleic acid can be double-stranded or single-stranded (i.e., a sense strand or an antisense strand). Non-limiting examples of polynucleotides include genes, gene fragments, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, siRNA, micro-RNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, nucleic acid probes and nucleic acid primers. A polynucleotide may contain unconventional or modified nucleotides.

“Operably linked” refers to the positioning of a regulatory region and a sequence to be transcribed in a nucleic acid so that the regulatory region is effective for regulating transcription or translation of the sequence. For example, to operably link a coding sequence and a regulatory region, the translation initiation site of the translational reading frame of the coding sequence is typically positioned between one and about fifty nucleotides downstream of the regulatory region. A regulatory region can, however, be positioned as much as about 5,000 nucleotides upstream of the translation initiation site, or about 2,000 nucleotides upstream of the transcription start site.

“Polypeptide” as used herein refers to a compound of two or more subunit amino acids, amino acid analogs, or other peptidomimetics, regardless of post-translational modification, e.g., phosphorylation or glycosylation. The subunits may be linked by peptide bonds or other bonds such as, for example, ester or ether bonds. Full-length polypeptides, truncated polypeptides, point mutants, insertion mutants, splice variants, chimeric proteins, and fragments thereof are encompassed by this definition.

“Progeny” includes descendants of a particular plant or plant line. Progeny of an instant plant include seeds formed on F₁, F₂, F₃, F₄, F₅, F₆ and subsequent generation plants, or seeds formed on BC₁, BC₂, BC₃, and subsequent generation plants, or seeds formed on F₁BC₁, F₁BC₂, F₁BC₃, and subsequent generation plants. The designation F₁ refers to the progeny of a cross between two parents that are genetically distinct. The designations F₂, F₃, F₄, F₅ and F₆ refer to subsequent generations of self- or sib-pollinated progeny of an F₁ plant.

“Regulatory region” refers to a nucleic acid having nucleotide sequences that influence transcription or translation initiation and rate, and stability and/or mobility of a

transcription or translation product. Regulatory regions include, without limitation, promoter sequences, enhancer sequences, response elements, protein recognition sites, inducible elements, protein binding sequences, 5' and 3' untranslated regions (UTRs), transcriptional start sites, termination sequences, polyadenylation sequences, introns, and combinations thereof. A regulatory region typically comprises at least a core (basal) promoter. A regulatory region also may include at least one control element, such as an enhancer sequence, an upstream element or an upstream activation region (UAR). For example, a suitable enhancer is a cis-regulatory element (-212 to -154) from the upstream region of the octopine synthase (ocs) gene. Fromm et al., *The Plant Cell*, 1:977-984 (1989).

"Up-regulation" refers to regulation that increases the level of an expression product (mRNA, polypeptide, or both) relative to basal or native states.

"Vector" refers to a replicon, such as a plasmid, phage, or cosmid, into which another DNA segment may be inserted so as to bring about the replication of the inserted segment. Generally, a vector is capable of replication when associated with the proper control elements. The term "vector" includes cloning and expression vectors, as well as viral vectors and integrating vectors. An "expression vector" is a vector that includes a regulatory region.

II. POLYPEPTIDES

Polypeptides described herein include SD+EODFR and/or low light tolerance polypeptides. SD+EODFR and/or low light tolerance polypeptides can be effective to increase SD+EODFR and/or low light tolerance when expressed in a plant or plant cell. Such polypeptides typically contain at least one domain indicative of SD+EODFR and/or low light tolerance polypeptides, as described in more detail herein. SD+EODFR and/or low light tolerance polypeptides typically have an HMM bit score that is greater than 20 for an HMM model based on one of the alignments set forth in FIGS. 1-24, as described in more detail herein. In some embodiments, SD+EODFR and/or low light tolerance polypeptides have greater than 40% identity to SEQ ID NO:3, SEQ ID NO:70, SEQ ID NO:129, SEQ ID NO:317, SEQ ID NO:337, SEQ ID NO:456, SEQ ID NO:538, SEQ ID NO:570, SEQ ID NO:606, SEQ ID NO:634, SEQ ID NO:644, SEQ ID NO:850, SEQ ID NO:907, SEQ ID NO:953, SEQ ID NO:1024, SEQ ID NO:1047, SEQ ID NO:1151, SEQ ID NO:1277, SEQ ID NO:1347, SEQ ID NO:1457, SEQ ID NO:1497, SEQ ID NO:1540, SEQ ID NO:1587, SEQ ID NO:1630, or SEQ ID NO:1635 as described in more detail herein.

Polypeptides described herein include red light specific response pathway polypeptides. Red light specific response pathway polypeptides can be effective to decrease hypocotyl length when over-expressed in a plant or plant cell. Such polypeptides typically contain at least one domain indicative of red light specific response pathway polypeptides, as described in more detail herein. Red light specific response pathway polypeptides typically have an HMM bit score that is greater than for an HMM model based on one of the alignments set forth in FIGS. 6, 11, and 24, as described in more detail herein. In some embodiments, red light specific response pathway polypeptides have greater than 40% identity to SEQ ID NO:456, SEQ ID NO:953, or SEQ ID NO:1540 as described in more detail herein.

A. Domains Indicative of SD+EODFR and/or Low Light Tolerance Polypeptides

A low light tolerance polypeptide can contain a cyclin dependent kinase inhibitor (CDI) domain. Cell cycle progression is negatively controlled by cyclin-dependent kinases inhibitors (CDIs). CDIs are involved in cell cycle arrest at the G1 phase. The motif is also present in SEQ ID NO:70, which sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At2g32710 (SEQ ID NO:69), that is predicted to encode a cyclin-dependent kinase inhibitor 4 (KIP4) polypeptide.

A low light tolerance polypeptide can contain an AUX/IAA domain, which is predicted to be characteristic of an Aux/IAA transcriptional repressor. AUX/IAA proteins act as repressors of auxin-induced gene expression, possibly through modulating the activity of DNA-binding auxin response factors (ARFs). SEQ ID NO:129 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At2g46990 (SEQ ID NO:127), that is predicted to encode an auxin-induced IAA21 polypeptide. An SD+EODFR tolerance and low light tolerance polypeptide can also contain an AUX/IAA domain. SEQ ID NO:1347 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At1g32280 (SEQ ID NO:1345), that is predicted to encode an auxin-responsive IAA29 polypeptide containing an AUX/IAA domain.

A low light tolerance polypeptide can contain a homeobox domain. Homeobox domains bind DNA through a helix-turn-helix (HTH) structure. The HTH motif is characterised by two alpha-helices, which make intimate contacts with the DNA and are joined by a short turn. The second helix binds to DNA via a number of hydrogen bonds and hydrophobic interactions, which occur between specific side chains and the exposed bases and thymine methyl groups within the major groove of the DNA. The first helix helps to stabilise the structure. SEQ ID NO:317 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At4g03250 (SEQ ID NO:315), that is predicted to encode a polypeptide containing a homeobox domain.

A low light tolerance polypeptide can contain a C3HC4 type zinc-finger (zf_C3HC4) domain. The C3HC4 type zinc-finger (RING finger) is a cysteine-rich domain of 40 to 60 residues that coordinates two zinc ions, and has the consensus sequence: C-X2-C-X(9-39)-C-X(1-3)-H-X(2-3)-C-X2-C-X(4-48)-C-X2-C where X is any amino acid. Many proteins containing a RING finger play a role in the ubiquitination pathway. SEQ ID NO:337 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At2g04240 (SEQ ID NO:335), that is predicted to encode a polypeptide containing zf_C3HC4 domain.

A low light tolerance polypeptide can contain a B-box zinc finger (zf-B_box) domain and a CCT motif A B-box zinc finger domain is about 40 amino acids in length. One or two copies of this domain are generally associated with a ring finger and a coiled coil motif B-box zinc finger domains are found in transcription factors, ribonucleoproteins and protooncoproteins, but no function is clearly assigned. The CCT (CONSTANS, CO-like, and TOC1) motif is a highly conserved basic domain of about 43 amino acids, and is found near the C-terminus of plant proteins often involved in light signal transduction. The CCT motif is found in association with other domains, such as B-box zinc finger domains, GATA-type zinc finger domains, ZIM motifs, or response regulatory domains. The CCT motif contains a putative nuclear localization signal within the second half of the CCT motif, has been shown to be involved in nuclear localization, and likely has a role in protein-protein interaction. SEQ ID NO:456 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At5g14370

(SEQ ID NO:454), that is predicted to encode a polypeptide containing a B-box zinc finger domain and a CCT motif.

An SD+EODFR tolerance polypeptide can contain a DNA photolyase domain and a FAD_binding_7 domain (FAD binding domain of DNA photolyase). DNA photolyases are enzymes that repair mismatched pyrimidine dimers in DNA that are induced by exposure to ultra-violet light. Proteins containing a FAD_binding_7 domain include *Arabidopsis* cryptochromes 1 (CRY1) and 2 (CRY2), which are blue light photoreceptors that mediate blue light-induced gene expression. SEQ ID NO:538 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At1g04400 (SEQ ID NO:537), that is predicted to encode a cryptochrome 2 apoprotein polypeptide containing a FAD_binding_7 domain and a DNA photolyase domain. A low light-tolerance polypeptide can also FAD_binding_7 domain and a DNA photolyase domain. SEQ ID NO:1497 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At4g08920 (SEQ ID NO:1496), that is predicted to encode a cryptochrome 1 (CRY1), flavin-type blue-light photoreceptor apoprotein polypeptide containing a FAD_binding_7 domain and a DNA photolyase domain.

An SD+EODFR tolerance polypeptide can contain a zf_Dof domain, which is predicted to be characteristic of a Dof domain zinc finger polypeptide. SEQ ID NO:606 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At3g45610 (SEQ ID NO:605), that is predicted to encode a polypeptide containing a zf_Dof domain.

A low light tolerance polypeptide can contain an AP2 domain, which is predicted to be characteristic of an ERF/AP2 transcription factor. AP2 domains are typically about 60 amino acid residues in length. SEQ ID NO:645 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At4g25480 (SEQ ID NO:642), that is predicted to encode a DREB subfamily A-1 polypeptide of the ERF/AP2 transcription factor family containing an AP2 domain.

A low light tolerance polypeptide can contain a VQ motif. VQ motifs are short conserved motifs of FXhVQChTG, where X is any amino acid and h is a hydrophobic amino acid, that is found in a variety of plant proteins. SEQ ID NO:850 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At2g33780 (SEQ ID NO:848), that is predicted to encode a polypeptide containing a VQ motif.

A low light tolerance polypeptide can contain a zf_C2H2 domain, which is predicted to be characteristic of a C2H2-type zinc finger. C2H2 zinc fingers are composed of two short beta strands followed by an alpha helix. The amino terminal part of the helix binds the major groove of DNA. The two conserved cysteines and histidines of a C2H2 zinc finger domain coordinate a zinc ion. SEQ ID NO:907 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At4g17810 (SEQ ID NO:905), that is predicted to encode a polypeptide containing a zf_C2H2 domain.

A low light tolerance polypeptide can contain a TCP domain, which is predicted to be characteristic of a TCP family transcription factor. The TCP family of transcription factors is named after its first characterized members, TB1, CYC and PCF1 and PCF2. TCP domains are predicted to form non-canonical basic-Helix-Loop-Helix (bHLP) structures. The TCP domains found in two rice DNA-binding proteins, PCF1 and PCF2, have been shown to be involved in DNA-binding and dimerization. SEQ ID NO:1151 sets forth the amino acid sequence of an *Arabidopsis* clone,

identified herein as At1g58100 (SEQ ID NO:1150), that is predicted to encode a polypeptide containing a TCP domain.

A low light tolerance polypeptide can contain an F-box domain. F-box domains have a role in mediating protein-protein interactions in a variety of contexts, such as polyubiquitination, transcription elongation, centromere binding and translational repression. Two motifs that are commonly found associated with F-box domains are leucine rich repeats and WD repeats. SEQ ID NO:1277 sets forth the 10 amino acid sequence of an *Arabidopsis* clone, identified herein as At5g46170 (SEQ ID NO:1276), that is predicted to encode a polypeptide containing an F-box domain.

A low light tolerance polypeptide can contain a zf_CCCCH domain, which is predicted to be characteristic of a C-x8-15 C-x5-C-x3-H type zinc finger polypeptide. The zf-CCCH domain is often found associated with proteins that interact with the 3' untranslated region of various mRNAs. SEQ ID NO:1457 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At3g02830 (SEQ ID NO:1456), that is predicted to encode a polypeptide containing a zf_CCCCH domain.

An SD+EODFR tolerance and low light tolerance polypeptide can contain a POX domain and a homeobox domain. POX domains are often found in plant proteins with a 25 homeobox domain, indicating that such proteins are likely transcription factors. SEQ ID NO:1540 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At2g35940 (SEQ ID NO:1537), that is predicted to encode a BEL1-like homeodomain 1 polypeptide containing a POX 30 domain and a homeobox domain.

A low light tolerance polypeptide can contain an HSF-type DNA-binding domain, which is predicted to be characteristic of heat shock factor transcription activator. Heat shock factor transcription activators are often found associated with heat shock protein promoters during heat shock. SEQ ID NO:1587 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At4g11660 (SEQ ID NO:1586), that is predicted to encode a polypeptide containing an HSF-type DNA-binding domain.

A low light tolerance polypeptide can contain a sterile alpha motif (SAM_1) domain and a DNA repair metallo-beta-lactamase (DRMBL) domain, which is predicted to be characteristic of a DNA repair metallo-beta-lactamase. SEQ ID NO:1635 sets forth the amino acid sequence of an 45 *Arabidopsis* clone, identified herein as Ceres At2g45700 (SEQ ID NO:1634), that is predicted to encode a polypeptide containing a SAM domain and a DRMBL domain.

B. Domains Indicative of Red Light Specific Response Pathway Polypeptides

A red light specific response pathway polypeptide can contain a B-box zinc finger (zf-B_box) domain and a CCT motif A B-box zinc finger domain is about 40 amino acids in length. One or two copies of this domain are generally associated with a ring finger and a coiled coil motif B-box 55 zinc finger domains are found in transcription factors, ribonucleoproteins and protooncoproteins, but no function is clearly assigned. The CCT (CONSTANS, CO-like, and TOC1) motif is a highly conserved basic domain of about 43 amino acids, and is found near the C-terminus of plant proteins often involved in light signal transduction. The CCT motif is found in association with other domains, such as B-box zinc finger domains, GATA-type zinc finger domains, ZIM motifs, or response regulatory domains. The CCT motif contains a putative nuclear localization signal 60 within the second half of the CCT motif, has been shown to be involved in nuclear localization, and likely has a role in protein-protein interaction. SEQ ID NO:456 sets forth the 65

amino acid sequence of an *Arabidopsis* clone, identified herein as At5g14370 (SEQ ID NO:454), that is predicted to encode a polypeptide containing a B-box zinc finger domain and a CCT motif.

A red light specific response pathway polypeptide can contain a POX domain and a homeobox domain. POX domains are often found in plant proteins with a homeobox domain, indicating that such proteins are likely transcription factors. SEQ ID NO:1540 sets forth the amino acid sequence of an *Arabidopsis* clone, identified herein as At2g35940 (SEQ ID NO:1537), that is predicted to encode a BELL-like homeodomain 1 polypeptide containing a POX domain and a homeobox domain.

C. Functional Homologs Identified by Reciprocal BLAST

In some embodiments, one or more functional homologs of a reference SD+EODFR and/or low light tolerance polypeptide defined by one or more of the pfam descriptions indicated above are suitable for use as SD+EODFR and/or low light tolerance polypeptides. A functional homolog is a polypeptide that has sequence similarity to a reference polypeptide, and that carries out one or more of the biochemical or physiological function(s) of the reference polypeptide. A functional homolog and the reference polypeptide may be natural occurring polypeptides, and the sequence similarity may be due to convergent or divergent evolutionary events. As such, functional homologs are sometimes designated in the literature as homologs, or orthologs, or paralogs. Variants of a naturally occurring functional homolog, such as polypeptides encoded by mutants of a wild type coding sequence, may themselves be functional homologs. Functional homologs can also be created via site-directed mutagenesis of the coding sequence for an SD+EODFR and/or low light tolerance polypeptide, or by combining domains from the coding sequences for different naturally-occurring SD+EODFR and/or low light tolerance polypeptides ("domain swapping"). The term "functional homolog" is sometimes applied to the nucleic acid that encodes a functionally homologous polypeptide.

Functional homologs can be identified by analysis of nucleotide and polypeptide sequence alignments. For example, performing a query on a database of nucleotide or polypeptide sequences can identify homologs of SD+EODFR and/or low light tolerance polypeptides. Sequence analysis can involve BLAST, Reciprocal BLAST, or PSI-BLAST analysis of nonredundant databases using an SD+EODFR and/or low light tolerance polypeptide amino acid sequence as the reference sequence. Amino acid sequence is, in some instances, deduced from the nucleotide sequence. Those polypeptides in the database that have greater than 40% sequence identity are candidates for further evaluation for suitability as an SD+EODFR and/or low light tolerance polypeptide. Amino acid sequence similarity allows for conservative amino acid substitutions, such as substitution of one hydrophobic residue for another or substitution of one polar residue for another. If desired, manual inspection of such candidates can be carried out in order to narrow the number of candidates to be further evaluated. Manual inspection can be performed by selecting those candidates that appear to have domains present in SD+EODFR and/or low light tolerance polypeptides, e.g., conserved functional domains.

Conserved regions can be identified by locating a region within the primary amino acid sequence of an SD+EODFR and/or low light tolerance polypeptide that is a repeated sequence, forms some secondary structure (e.g., helices and beta sheets), establishes positively or negatively charged domains, or represents a protein motif or domain. See, e.g.,

the Pfam web site describing consensus sequences for a variety of protein motifs and domains on the World Wide Web at sanger.ac.uk/Software/Pfam/and pfam.janelia.org/. A description of the information included at the Pfam database is described in Sonnhammer et al., *Nucl. Acids Res.*, 26:320-322 (1998); Sonnhammer et al., *Proteins*, 28:405-420 (1997); and Bateman et al., *Nucl. Acids Res.*, 27:260-262 (1999). Conserved regions also can be determined by aligning sequences of the same or related polypeptides from closely related species. Closely related species preferably are from the same family. In some embodiments, alignment of sequences from two different species is adequate.

Typically, polypeptides that exhibit at least about 40% amino acid sequence identity are useful to identify conserved regions. Conserved regions of related polypeptides exhibit at least 45% amino acid sequence identity (e.g., at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% amino acid sequence identity). In some embodiments, a conserved region exhibits at least 92%, 94%, 96%, 98%, or 99% amino acid sequence identity.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:3 are provided in FIG. 1. Such functional homologs include Ceres CLONE ID no. 1844057 (SEQ ID NO:7), Ceres ANNOT ID no. 1469148 (SEQ ID NO:22), Public GI ID no. 18390998 (SEQ ID NO:25), Ceres CLONE ID no. 1065656 (SEQ ID NO:32), Ceres CLONE ID no. 1652677 (SEQ ID NO:36), Public GI ID no. 92874556 (SEQ ID NO:49), Ceres CLONE ID no. 1329161 (SEQ ID NO:53), Ceres CLONE ID no. 1030378 (SEQ ID NO:55), Ceres CLONE ID no. 1413787 (SEQ ID NO:57), and Public GI ID no. 125543598 (SEQ ID NO:60). Other functional homologs of SEQ ID NO:3 include Ceres CLONE ID no. 1793691 (SEQ ID NO:5), Ceres CLONE ID no. 1933784 (SEQ ID NO:9), Ceres CLONE ID no. 100030408 (SEQ ID NO:10), Ceres CLONE ID no. 1837059 (SEQ ID NO:12), Ceres CLONE ID no. 1793801 (SEQ ID NO:14), Ceres CLONE ID no. 1855480 (SEQ ID NO:16), Ceres CLONE ID no. 1915644 (SEQ ID NO:18), Ceres CLONE ID no. 1898104 (SEQ ID NO:20), Ceres ANNOT ID no. 1464241 (SEQ ID NO:24), Public GI ID no. 18697627 (SEQ ID NO:26), Ceres CLONE ID no. 9391 (SEQ ID NO:28), Ceres CLONE ID no. 111154 (SEQ ID NO:30), Ceres CLONE ID no. 973975 (SEQ ID NO:34), Ceres CLONE ID no. 676695 (SEQ ID NO:38), Ceres CLONE ID no. 680331 (SEQ ID NO:40), Ceres CLONE ID no. 654515 (SEQ ID NO:42), Ceres CLONE ID no. 626154 (SEQ ID NO:44), Ceres CLONE ID no. 710603 (SEQ ID NO:46), Ceres CLONE ID no. 648076 (SEQ ID NO:48), Ceres CLONE ID no. 749439 (SEQ ID NO:51), Ceres CLONE ID no. 295936 (SEQ ID NO:59), Public GI ID no. 125525139 (SEQ ID NO:61), Public GI ID no. 115452643 (SEQ ID NO:62), Public GI ID no. 24059889 (SEQ ID NO:63), Ceres ANNOT ID no. 6012747 (SEQ ID NO:65), Ceres ANNOT ID no. 6027628 (SEQ ID NO:67), and sequences identified as functional homologs of the sequences of FIG. 1, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:3 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:3.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:70 are provided in FIG. 2. Such functional homologs include Ceres CLONE ID no. 1975934 (SEQ ID NO:72), Ceres ANNOT ID no. 1529913 (SEQ ID NO:80), Ceres CLONE ID no. 977794 (SEQ ID NO:93), Public GI ID no. 42362378 (SEQ ID NO:96),

Public GI ID no. 23899378 (SEQ ID NO:99), Public GI ID no. 15963346 (SEQ ID NO:101), Public GI ID no. 15963344+B816 (SEQ ID NO:102), Public GI ID no. 92429657 (SEQ ID NO:103), Ceres CLONE ID no. 746644 (SEQ ID NO:105), Ceres CLONE ID no. 623089 (SEQ ID NO:109), Ceres CLONE ID no. 1913678 (SEQ ID NO:115), and Public GI ID no. 115450609 (SEQ ID NO:119). Other functional homologs of SEQ ID NO:70 include Ceres CLONE ID no. 1835084 (SEQ ID NO:74), Ceres CLONE ID no. 1846153 (SEQ ID NO:76), Ceres CLONE ID no. 1930884 (SEQ ID NO:78), Ceres ANNOT ID no. 1493858 (SEQ ID NO:82), Ceres ANNOT ID no. 1498646 (SEQ ID NO:84), Ceres ANNOT ID no. 1440974 (SEQ ID NO:86), Ceres CLONE ID no. 1189183 (SEQ ID NO:88), Public GI ID no. 26450253 (SEQ ID NO:89), Public GI ID no. 15239719 (SEQ ID NO:90), Public GI ID no. 15230194 (SEQ ID NO:91), Ceres CLONE ID no. 630905 (SEQ ID NO:95), Public GI ID no. 42362389 (SEQ ID NO:97), Public GI ID no. 70906129 (SEQ ID NO:98), Public GI ID no. 23899381 (SEQ ID NO:100), Ceres CLONE ID no. 298166 (SEQ ID NO:107), Ceres CLONE ID no. 1448390 (SEQ ID NO:111), Ceres CLONE ID no. 1734216 (SEQ ID NO:113), Public GI ID no. 125542322 (SEQ ID NO:116), Public GI ID no. 125532331 (SEQ ID NO:117), Public GI ID no. 125541233 (SEQ ID NO:118), Public GI ID no. 125584844 (SEQ ID NO:120), Public GI ID no. 115482472 (SEQ ID NO:121), Public GI ID no. 125575112 (SEQ ID NO:122), Ceres ANNOT ID no. 6003994 (SEQ ID NO:124), Ceres ANNOT ID no. 6068427 (SEQ ID NO:126), and sequences identified as functional homologs of the sequences of FIG. 2, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:70 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:70.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:129 are provided in FIG. 3. Such functional homologs include Public GI ID no. 34550779 (SEQ ID NO:133), Ceres CLONE ID no. 1932235 (SEQ ID NO:137), Ceres CLONE ID no. 981738 (SEQ ID NO:201), Ceres CLONE ID no. 565974 (SEQ ID NO:209), Public GI ID no. 1352058 (SEQ ID NO:231), Public GI ID no. 11131101 (SEQ ID NO:234), Public GI ID no. 4887018 (SEQ ID NO:236), Public GI ID no. 4887018 (SEQ ID NO:247), Ceres CLONE ID no. 644455 (SEQ ID NO:270), Public GI ID no. 20269063 (SEQ ID NO:300), Public GI ID no. 50404477 (SEQ ID NO:302), and Public GI ID no. 62125392 (SEQ ID NO:303). Other functional homologs of SEQ ID NO:129 include Public GI ID no. 32396293 (SEQ ID NO:130), Public GI ID no. 32396299 (SEQ ID NO:131), Public GI ID no. 32396295 (SEQ ID NO:132), Ceres CLONE ID no. 1855369 (SEQ ID NO:135), Ceres CLONE ID no. 1948456 (SEQ ID NO:139), Ceres CLONE ID no. 1920182 (SEQ ID NO:141), Ceres CLONE ID no. 1835797 (SEQ ID NO:143), Ceres CLONE ID no. 1794204 (SEQ ID NO:145), Ceres CLONE ID no. 1853542 (SEQ ID NO:147), Ceres CLONE ID no. 1838776 (SEQ ID NO:149), Ceres CLONE ID no. 1854675 (SEQ ID NO:151), Ceres CLONE ID no. 1833078 (SEQ ID NO:153), Ceres CLONE ID no. 1850667 (SEQ ID NO:155), Ceres CLONE ID no. 1918745 (SEQ ID NO:157), Ceres CLONE ID no. 1929487 (SEQ ID NO:159), Ceres ANNOT ID no. 1497918 (SEQ ID NO:161), Ceres ANNOT ID no. 1459563 (SEQ ID NO:163), Ceres ANNOT ID no. 1452610 (SEQ ID NO:165), Ceres ANNOT ID no. 1496539 (SEQ ID NO:167), Ceres ANNOT ID no.

1498819 (SEQ ID NO:169), Ceres ANNOT ID no. 1446583 (SEQ ID NO:171), Ceres ANNOT ID no. 1535123 (SEQ ID NO:173), Ceres ANNOT ID no. 1463397 (SEQ ID NO:175), Ceres ANNOT ID no. 1499563 (SEQ ID NO:177), Ceres ANNOT ID no. 1495753 (SEQ ID NO:179), Ceres ANNOT ID no. 1488767 (SEQ ID NO:181), Ceres ANNOT ID no. 1522920 (SEQ ID NO:185), Ceres ANNOT ID no. 1469532 (SEQ ID NO:187), Public GI ID no. 15219692 (SEQ ID NO:188), Public GI ID no. 18420964 (SEQ ID NO:189), Ceres CLONE ID no. 1342080 (SEQ ID NO:191), Ceres CLONE ID no. 123105 (SEQ ID NO:193), Ceres CLONE ID no. 32727 (SEQ ID NO:195), Ceres CLONE ID no. 41161 (SEQ ID NO:197), Ceres CLONE ID no. 37274 (SEQ ID NO:199), Ceres CLONE ID no. 538020 (SEQ ID NO:203), Ceres CLONE ID no. 476244 (SEQ ID NO:205), Ceres CLONE ID no. 1623662 (SEQ ID NO:207), Ceres CLONE ID no. 626817 (SEQ ID NO:211), Ceres CLONE ID no. 537469 (SEQ ID NO:213), Ceres CLONE ID no. 582463 (SEQ ID NO:215), Ceres CLONE ID no. 1069818 (SEQ ID NO:217), Ceres CLONE ID no. 511737 (SEQ ID NO:219), Ceres CLONE ID no. 565422 (SEQ ID NO:221), Ceres CLONE ID no. 514595 (SEQ ID NO:223), Ceres CLONE ID no. 566396 (SEQ ID NO:225), Ceres CLONE ID no. 612705 (SEQ ID NO:227), Ceres CLONE ID no. 564134 (SEQ ID NO:229), Public GI ID no. 92872146 (SEQ ID NO:230), Public GI ID no. 11131103 (SEQ ID NO:232), Public GI ID no. 416641 (SEQ ID NO:233), Public GI ID no. 11131105 (SEQ ID NO:235), Public GI ID no. 4887016 (SEQ ID NO:237), Public GI ID no. 4887022 (SEQ ID NO:238), Public GI ID no. 81074526 (SEQ ID NO:239), Ceres CLONE ID no. 742023 (SEQ ID NO:241), Ceres CLONE ID no. 576268 (SEQ ID NO:243), Ceres CLONE ID no. 615386 (SEQ ID NO:245), Ceres CLONE ID no. 756966 (SEQ ID NO:249), Ceres CLONE ID no. 1052710 (SEQ ID NO:251), Ceres CLONE ID no. 697018 (SEQ ID NO:253), Ceres CLONE ID no. 618577 (SEQ ID NO:255), Ceres CLONE ID no. 935194 (SEQ ID NO:257), Ceres CLONE ID no. 1557429 (SEQ ID NO:259), Ceres CLONE ID no. 305337 (SEQ ID NO:261), Ceres CLONE ID no. 100872943 (SEQ ID NO:262), Ceres CLONE ID no. 305454 (SEQ ID NO:264), Ceres CLONE ID no. 1534670 (SEQ ID NO:266), Ceres CLONE ID no. 207963 (SEQ ID NO:268), Public GI ID no. 20257219 (SEQ ID NO:271), Ceres CLONE ID no. 1876818 (SEQ ID NO:273), Ceres CLONE ID no. 1817533 (SEQ ID NO:275), Ceres CLONE ID no. 1958631 (SEQ ID NO:277), Ceres CLONE ID no. 1963215 (SEQ ID NO:279), Ceres CLONE ID no. 1770022 (SEQ ID NO:281), Ceres CLONE ID no. 1796223 (SEQ ID NO:283), Ceres CLONE ID no. 2016695 (SEQ ID NO:285), Ceres CLONE ID no. 1757085 (SEQ ID NO:287), Ceres CLONE ID no. 1769256 (SEQ ID NO:289), Ceres CLONE ID no. 1994871 (SEQ ID NO:291), Public GI ID no. 17154533 (SEQ ID NO:292), Public GI ID no. 125557426 (SEQ ID NO:293), Public GI ID no. 125524736 (SEQ ID NO:294), Public GI ID no. 125527656 (SEQ ID NO:295), Public GI ID no. 125599342 (SEQ ID NO:296), Public GI ID no. 125569626 (SEQ ID NO:297), Public GI ID no. 115465401 (SEQ ID NO:298), Public GI ID no. 40539038 (SEQ ID NO:299), Public GI ID no. 20269059 (SEQ ID NO:301), Public GI ID no. 110826446 (SEQ ID NO:304), Ceres ANNOT ID no. 6029073 (SEQ ID NO:306), Ceres ANNOT ID no. 6011329 (SEQ ID NO:308), Ceres ANNOT ID no. 6034498 (SEQ ID NO:310), Ceres ANNOT ID no. 6095057 (SEQ ID NO:312), Ceres ANNOT ID no. 6095058 (SEQ ID NO:314), and sequences identified as functional homologs of the sequences of FIG. 3, as set forth in the sequence listing. In some cases, a functional homolog of

SEQ ID NO:129 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:129.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:317 are provided in FIG. 4. Such functional homologs include Ceres CLONE ID no. 1842125 (SEQ ID NO:319), Ceres ANNOT ID no. 1461360 (SEQ ID NO:321), Ceres CLONE ID no. 480906 (SEQ ID NO:327), Public GI ID no. 92889352 (SEQ ID NO:330), and Public GI ID no. 56201850 (SEQ ID NO:330). Other functional homologs of SEQ ID NO:317 include Ceres ANNOT ID no. 1440334 (SEQ ID NO:323), Ceres ANNOT ID no. 1493205 (SEQ ID NO:325), Ceres CLONE ID no. 482270 (SEQ ID NO:329), Public GI ID no. 125571531 (SEQ ID NO:332), Ceres ANNOT ID no. 6042411 (SEQ ID NO:334), and sequences identified as functional homologs of the sequences of FIG. 4, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:317 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:317.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:337 are provided in FIG. 5. Such functional homologs include Ceres CLONE ID no. 952050 (SEQ ID NO:339), Public GI ID no. 115477050 (SEQ ID NO:349), Public GI ID no. 87162911 (SEQ ID NO:355), Ceres CLONE ID no. 1790901 (SEQ ID NO:357), Ceres CLONE ID no. 1460088 (SEQ ID NO:370), Ceres CLONE ID no. 1734065 (SEQ ID NO:393), Ceres CLONE ID no. 473509 (SEQ ID NO:395), Ceres CLONE ID no. 849918 (SEQ ID NO:401), Ceres CLONE ID no. 633470 (SEQ ID NO:409), Ceres CLONE ID no. 1808334 (SEQ ID NO:417), and Ceres ANNOT ID no. 1525600 (SEQ ID NO:437). Other functional homologs of SEQ ID NO:337 include Ceres CLONE ID no. 1265097 (SEQ ID NO:341), Ceres CLONE ID no. 942980 (SEQ ID NO:343), Public GI ID no. 37901055 (SEQ ID NO:344), Ceres CLONE ID no. 1609912 (SEQ ID NO:346), Public GI ID no. 76446335 (SEQ ID NO:347), Public GI ID no. 125560204 (SEQ ID NO:348), Public GI ID no. 125303087 (SEQ ID NO:350), Public GI ID no. 115460088 (SEQ ID NO:351), Public GI ID no. 125591385 (SEQ ID NO:352), Public GI ID no. 115447931 (SEQ ID NO:353), Public GI ID no. 92893514 (SEQ ID NO:354), Ceres CLONE ID no. 2019320 (SEQ ID NO:359), Ceres CLONE ID no. 1890013 (SEQ ID NO:361), Public GI ID no. 20340241 (SEQ ID NO:362), Ceres CLONE ID no. 25801 (SEQ ID NO:364), Public GI ID no. 9743343 (SEQ ID NO:365), Public GI ID no. 15238072 (SEQ ID NO:366), Public GI ID no. 15222553 (SEQ ID NO:367), Public GI ID no. 21554155 (SEQ ID NO:368), Ceres CLONE ID no. 374439 (SEQ ID NO:372), Ceres CLONE ID no. 1465572 (SEQ ID NO:374), Ceres CLONE ID no. 1565524 (SEQ ID NO:376), Ceres CLONE ID no. 322302 (SEQ ID NO:378), Ceres CLONE ID no. 101136485 (SEQ ID NO:379), Ceres CLONE ID no. 1376133 (SEQ ID NO:381), Ceres CLONE ID no. 1374381 (SEQ ID NO:383), Ceres CLONE ID no. 1566473 (SEQ ID NO:385), Ceres CLONE ID no. 318088 (SEQ ID NO:387), Ceres CLONE ID no. 1452604 (SEQ ID NO:389), Ceres CLONE ID no. 337906 (SEQ ID NO:391), Ceres CLONE ID no. 1662513 (SEQ ID NO:397), Ceres CLONE ID no. 1662527 (SEQ ID NO:399), Ceres CLONE ID no. 571184 (SEQ ID NO:403), Ceres CLONE ID no. 665689 (SEQ ID

NO:405), Ceres CLONE ID no. 1365853 (SEQ ID NO:407), Ceres CLONE ID no. 1052457 (SEQ ID NO:411), Ceres CLONE ID no. 579918 (SEQ ID NO:413), Ceres CLONE ID no. 863299 (SEQ ID NO:415), Ceres CLONE ID no. 1855611 (SEQ ID NO:419), Ceres CLONE ID no. 1845975 (SEQ ID NO:421), Ceres CLONE ID no. 1808298 (SEQ ID NO:423), Ceres CLONE ID no. 1841236 (SEQ ID NO:425), Ceres CLONE ID no. 1808269 (SEQ ID NO:427), Ceres CLONE ID no. 1850628 (SEQ ID NO:429), Ceres CLONE ID no. 1846911 (SEQ ID NO:431), Ceres CLONE ID no. 1916014 (SEQ ID NO:433), Ceres CLONE ID no. 1842594 (SEQ ID NO:435), Ceres ANNOT ID no. 1472192 (SEQ ID NO:439), Ceres ANNOT ID no. 1447489 (SEQ ID NO:441), Ceres ANNOT ID no. 1513000 (SEQ ID NO:443), Ceres ANNOT ID no. 1438658 (SEQ ID NO:445), Ceres ANNOT ID no. 1497255 (SEQ ID NO:447), Ceres ANNOT ID no. 6092104 (SEQ ID NO:449), Ceres ANNOT ID no. 6041700 (SEQ ID NO:451), Ceres ANNOT ID no. 6007297 (SEQ ID NO:453), and sequences identified as functional homologs of the sequences of FIG. 5, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:337 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:337.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:456 are provided in FIG. 6. Such functional homologs include Public GI ID no. 58430585 (SEQ ID NO:457), Ceres CLONE ID no. 1842825 (SEQ ID NO:466), Ceres ANNOT ID no. 1449721 (SEQ ID NO:474), Public GI ID no. 41323978 (SEQ ID NO:475), Public GI ID no. 2895186 (SEQ ID NO:478), Public GI ID no. 22854950 (SEQ ID NO:481), Public GI ID no. 116010474 (SEQ ID NO:485), Public GI ID no. 4091804 (SEQ ID NO:488), Public GI ID no. 60459257 (SEQ ID NO:494), Public GI ID no. 45544881 (SEQ ID NO:496), Public GI ID no. 36789802 (SEQ ID NO:498), Public GI ID no. 92875402 (SEQ ID NO:508), Public GI ID no. 118406898 (SEQ ID NO:510), Public GI ID no. 107770485 (SEQ ID NO:511), Public GI ID no. 21655154 (SEQ ID NO:532), Public GI ID no. 90657642 (SEQ ID NO:536), and Ceres CLONE ID no. 1569555 (SEQ ID NO:1842). Other homologs of SEQ ID NO:456 include Public GI ID no. 66841018 (SEQ ID NO:458), Public GI ID no. 66841020 (SEQ ID NO:459), Public GI ID no. 108859343 (SEQ ID NO:460), Ceres CLONE ID no. 1937613 (SEQ ID NO:462), Ceres CLONE ID no. 1834027 (SEQ ID NO:464), Ceres ANNOT ID no. 1477832 (SEQ ID NO:468), Ceres ANNOT ID no. 1482536 (SEQ ID NO:470), Ceres ANNOT ID no. 1478227 (SEQ ID NO:472), Ceres CLONE ID no. 19906 (SEQ ID NO:478), Public GI ID no. 2895184 (SEQ ID NO:479), Public GI ID no. 2895188 (SEQ ID NO:480), Public GI ID no. 11037313 (SEQ ID NO:482), Public GI ID no. 22854908 (SEQ ID NO:483), Public GI ID no. 40787165 (SEQ ID NO:484), Public GI ID no. 116010475 (SEQ ID NO:486), Public GI ID no. 3341723 (SEQ ID NO:487), Public GI ID no. 4091806 (SEQ ID NO:489), Ceres CLONE ID no. 523203 (SEQ ID NO:491), Ceres CLONE ID no. 463157 (SEQ ID NO:493), Public GI ID no. 61611678 (SEQ ID NO:495), Public GI ID no. 45544887 (SEQ ID NO:497), Public GI ID no. 36789793 (SEQ ID NO:481), Ceres CLONE ID no. 907473 (SEQ ID NO:501), Ceres CLONE ID no. 1674443 (SEQ ID NO:503), Ceres CLONE ID no. 1559496 (SEQ ID NO:505), Ceres CLONE ID no. 530984 (SEQ ID NO:507), Public GI ID no. 61611682 (SEQ ID NO:509), Public GI ID no.

36789785 (SEQ ID NO:512), Ceres CLONE ID no. 702632 (SEQ ID NO:514), Public GI ID no. 61657299 (SEQ ID NO:515), Public GI ID no. 10946337 (SEQ ID NO:516), Ceres CLONE ID no. 1996408 (SEQ ID NO:518), Ceres CLONE ID no. 1725313 (SEQ ID NO:520), Public GI ID no. 78058606 (SEQ ID NO:521), Public GI ID no. 125538317 (SEQ ID NO:522), Public GI ID no. 125556324 (SEQ ID NO:523), Public GI ID no. 125548890 (SEQ ID NO:524), Public GI ID no. 93211100 (SEQ ID NO:525), Public GI ID no. 115444217 (SEQ ID NO:526), Public GI ID no. 115467558 (SEQ ID NO:527), Public GI ID no. 11094209 (SEQ ID NO:528), Public GI ID no. 125596830 (SEQ ID NO:529), Public GI ID no. 115469296 (SEQ ID NO:530), Public GI ID no. 115447239 (SEQ ID NO:531), Public GI ID no. 21667485 (SEQ ID NO:533), Public GI ID no. 21667475 (SEQ ID NO:534), Public GI ID no. 21655158 (SEQ ID NO:535), and sequences identified as functional homologs of the sequences of FIG. 6, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:456 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:456.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:634 are provided in FIG. 7. Such functional homologs include Public GI ID no. 98961985 (SEQ ID NO:637). Other functional homologs of SEQ ID NO:634 include Ceres CLONE ID no. 1916112 (SEQ ID NO:636), Public GI ID no. 9369405 (SEQ ID NO:638), Public GI ID no. 9369406 (SEQ ID NO:639), Ceres CLONE ID no. 1238706 (SEQ ID NO:641), and sequences identified as functional homologs of the sequences of FIG. 7, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:634 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:634.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:644 are provided in FIG. 8. Such functional homologs include SEQ ID NO:645, Ceres CLONE ID no. 1849479 (SEQ ID NO:767), Public GI ID no. 89275008 (SEQ ID NO:796), Public GI ID no. 120400525 (SEQ ID NO:797), Public GI ID no. 98980426 (SEQ ID NO:804), Public GI ID no. 71983373 (SEQ ID NO:808), Public GI ID no. 41351817 (SEQ ID NO:809), Public GI ID no. 76446191 (SEQ ID NO:811), Public GI ID no. 5616086 (SEQ ID NO:813), Ceres CLONE ID no. 1052602 (SEQ ID NO:826), Public GI ID no. 72068957 (SEQ ID NO:830), Public GI ID no. 71534113 (SEQ ID NO:831), Public GI ID no. 37147896 (SEQ ID NO:832), Public GI ID no. 92918850 (SEQ ID NO:834), Public GI ID no. 40647095 (SEQ ID NO:835), Ceres ANNOT ID no. 1527711 (SEQ ID NO:837), Public GI ID no. 71041116 (SEQ ID NO:838), Public GI ID no. 12003384 (SEQ ID NO:839), Public GI ID no. 18535580 (SEQ ID NO:840), and Public GI ID no. 115353971 (SEQ ID NO:1843). Other functional homologs of SEQ ID NO:644 include Ceres CLONE ID no. 991178 (SEQ ID NO:647), Ceres CLONE ID no. 1626038 (SEQ ID NO:649), Ceres CLONE ID no. 341615 (SEQ ID NO:651), Ceres CLONE ID no. 1832518 (SEQ ID NO:653), Ceres CLONE ID no. 1832588 (SEQ ID NO:655), Ceres CLONE ID no. 1936806 (SEQ ID NO:657), Ceres CLONE ID no. 973892 (SEQ ID NO:659), Ceres CLONE ID no. 565251 (SEQ ID NO:661), Ceres CLONE ID no. 681088 (SEQ ID NO:663), Ceres CLONE ID no.

707775 (SEQ ID NO:665), Ceres CLONE ID no. 453357 (SEQ ID NO:667), Ceres CLONE ID no. 1916958 (SEQ ID NO:669), Ceres CLONE ID no. 1940632 (SEQ ID NO:671), Ceres CLONE ID no. 476784 (SEQ ID NO:673), Ceres CLONE ID no. 1869284 (SEQ ID NO:675), Public GI ID no. 125540662 (SEQ ID NO:676), Ceres CLONE ID no. 1648272 (SEQ ID NO:678), Ceres CLONE ID no. 1987804 (SEQ ID NO:680), Ceres CLONE ID no. 1675695 (SEQ ID NO:682), Ceres CLONE ID no. 1169111 (SEQ ID NO:684), Ceres CLONE ID no. 572121 (SEQ ID NO:686), Ceres CLONE ID no. 1674836 (SEQ ID NO:688), Ceres ANNOT ID no. 1486207 (SEQ ID NO:690), Ceres CLONE ID no. 2023610 (SEQ ID NO:692), Ceres ANNOT ID no. 1496976 (SEQ ID NO:694), Public GI ID no. 116310031 (SEQ ID NO:695), Ceres CLONE ID no. 1626363 (SEQ ID NO:697), Ceres ANNOT ID no. 1483747 (SEQ ID NO:699), Ceres ANNOT ID no. 1471330 (SEQ ID NO:701), Ceres CLONE ID no. 101144964 (SEQ ID NO:702), Ceres ANNOT ID no. 1439439 (SEQ ID NO:704), Ceres CLONE ID no. 1446565 (SEQ ID NO:706), Ceres CLONE ID no. 1951962 (SEQ ID NO:708), Ceres CLONE ID no. 100960656 (SEQ ID NO:709), Ceres CLONE ID no. 285154 (SEQ ID NO:711), Public GI ID no. 61968916 (SEQ ID NO:712), Public GI ID no. 118026854 (SEQ ID NO:713), Public GI ID no. 63098612 (SEQ ID NO:714), Ceres ANNOT ID no. 1522310 (SEQ ID NO:716), Ceres CLONE ID no. 1854375 (SEQ ID NO:718), Ceres CLONE ID no. 709819 (SEQ ID NO:720), Public GI ID no. 115447695 (SEQ ID NO:721), Ceres CLONE ID no. 1726356 (SEQ ID NO:723), Ceres CLONE ID no. 1762419 (SEQ ID NO:725), Public GI ID no. 63098606 (SEQ ID NO:726), Ceres CLONE ID no. 1766572 (SEQ ID NO:728), Ceres CLONE ID no. 281871 (SEQ ID NO:730), Ceres CLONE ID no. 1560970 (SEQ ID NO:732), Ceres CLONE ID no. 1760747 (SEQ ID NO:734), Ceres ANNOT ID no. 1438772 (SEQ ID NO:736), Ceres ANNOT ID no. 1447378 (SEQ ID NO:738), Ceres ANNOT ID no. 1453360 (SEQ ID NO:740), Public GI ID no. 33637698 (SEQ ID NO:741), Public GI ID no. 118026860 (SEQ ID NO:742), Public GI ID no. 60116232 (SEQ ID NO:743), Public GI ID no. 115477639 (SEQ ID NO:744), Public GI ID no. 126567023 (SEQ ID NO:745), Ceres CLONE ID no. 988971 (SEQ ID NO:747), Ceres CLONE ID no. 1464521 (SEQ ID NO:749), Public GI ID no. 63098610 (SEQ ID NO:750), Public GI ID no. 126566972 (SEQ ID NO:751), Ceres CLONE ID no. 1556129 (SEQ ID NO:753), Ceres CLONE ID no. 1761385 (SEQ ID NO:755), Ceres ANNOT ID no. 1488325 (SEQ ID NO:757), Ceres ANNOT ID no. 1460483 (SEQ ID NO:759), Ceres CLONE ID no. 1837825 (SEQ ID NO:761), Public GI ID no. 27228310 (SEQ ID NO:762), Public GI ID no. 117653881 (SEQ ID NO:763), Public GI ID no. 115480233 (SEQ ID NO:764), Public GI ID no. 37694048 (SEQ ID NO:765), Ceres CLONE ID no. 1934653 (SEQ ID NO:769), Ceres CLONE ID no. 1608106 (SEQ ID NO:771), Ceres CLONE ID no. 1604576 (SEQ ID NO:773), Public GI ID no. 55824656 (SEQ ID NO:774), Ceres CLONE ID no. 1620272 (SEQ ID NO:776), Ceres CLONE ID no. 1853170 (SEQ ID NO:778), Public GI ID no. 79013962 (SEQ ID NO:779), Public GI ID no. 98975385 (SEQ ID NO:780), Ceres ANNOT ID no. 1438775 (SEQ ID NO:782), Public GI ID no. 23495460 (SEQ ID NO:783), Public GI ID no. 98975377 (SEQ ID NO:784), Ceres ANNOT ID no. 1438776 (SEQ ID NO:786), Ceres CLONE ID no. 1853601 (SEQ ID NO:788), Ceres CLONE ID no. 1609048 (SEQ ID NO:790), Ceres CLONE ID no. 322305 (SEQ ID NO:792), Ceres CLONE ID no. 1823713 (SEQ ID NO:794), Public GI ID no. 3660548 (SEQ ID NO:795), Public GI ID no.

56154991 (SEQ ID NO:798), Public GI ID no. 2980802 (SEQ ID NO:799), Public GI ID no. 7269398 (SEQ ID NO:800), Public GI ID no. 18416557 (SEQ ID NO:801), Public GI ID no. 56154992 (SEQ ID NO:802), Public GI ID no. 4091984 (SEQ ID NO:803), Public GI ID no. 1899058 (SEQ ID NO:805), Public GI ID no. 56154990 (SEQ ID NO:806), Public GI ID no. 18416562 (SEQ ID NO:807), Public GI ID no. 38683266 (SEQ ID NO:810), Public GI ID no. 39983638 (SEQ ID NO:812), Public GI ID no. 38426954 (SEQ ID NO:814), Public GI ID no. 38426948 (SEQ ID NO:815), Public GI ID no. 38146944 (SEQ ID NO:816), Public GI ID no. 38426952 (SEQ ID NO:817), Public GI ID no. 20303011 (SEQ ID NO:818), Public GI ID no. 66269982 (SEQ ID NO:819), Public GI ID no. 89212816 (SEQ ID NO:820), Public GI ID no. 20303015 (SEQ ID NO:821), Public GI ID no. 38426950 (SEQ ID NO:822), Public GI ID no. 15242244 (SEQ ID NO:823), Public GI ID no. 116831599 (SEQ ID NO:824), Public GI ID no. 66269671 (SEQ ID NO:827), Ceres ANNOT ID no. 1468919 (SEQ ID NO:829), Public GI ID no. 57903606 (SEQ ID NO:833), Public GI ID no. 45826358 (SEQ ID NO:841), Ceres ANNOT ID no. 6085912 (SEQ ID NO:843), Ceres ANNOT ID no. 6026171 (SEQ ID NO:845), Ceres ANNOT ID no. 6031706 (SEQ ID NO:847), and sequences listing identified as functional homologs of the sequences of FIG. 8, as set forth in the sequence. In some cases, a functional homolog of SEQ ID NO:644 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:644.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:850 are provided in FIG. 9. Such functional homologs include Ceres CLONE ID no. 1833093 (SEQ ID NO:853), Ceres ANNOT ID no. 1502190 (SEQ ID NO:857), Ceres CLONE ID no. 565641 (SEQ ID NO:876), Public GI ID no. 87240507 (SEQ ID NO:877), Ceres CLONE ID no. 1325382 (SEQ ID NO:881), Ceres CLONE ID no. 1558265 (SEQ ID NO:885), Ceres CLONE ID no. 1823669 (SEQ ID NO:895), and Public GI ID no. 115464921 (SEQ ID NO:898). Other functional homologs of SEQ ID NO:850 include Ceres CLONE ID no. 100040598 (SEQ ID NO:851), Ceres CLONE ID no. 1847967 (SEQ ID NO:855), Ceres ANNOT ID no. 1449186 (SEQ ID NO:859), Ceres ANNOT ID no. 1466723 (SEQ ID NO:861), Public GI ID no. 21805688 (SEQ ID NO:862), Public GI ID no. 9795609 (SEQ ID NO:863), Public GI ID no. 13877535 (SEQ ID NO:864), Public GI ID no. 15232547 (SEQ ID NO:865), Public GI ID no. 15238851 (SEQ ID NO:866), Ceres CLONE ID no. 123863 (SEQ ID NO:868), Ceres CLONE ID no. 652496 (SEQ ID NO:870), Ceres CLONE ID no. 1656707 (SEQ ID NO:872), Ceres CLONE ID no. 1660346 (SEQ ID NO:874), Ceres CLONE ID no. 678878 (SEQ ID NO:879), Ceres CLONE ID no. 340102 (SEQ ID NO:883), Ceres CLONE ID no. 330491 (SEQ ID NO:887), Ceres CLONE ID no. 992304 (SEQ ID NO:889), Ceres CLONE ID no. 1509925 (SEQ ID NO:891), Ceres CLONE ID no. 1543852 (SEQ ID NO:893), Ceres CLONE ID no. 1785736 (SEQ ID NO:897), Ceres ANNOT ID no. 6079909 (SEQ ID NO:900), Ceres ANNOT ID no. 6040353 (SEQ ID NO:902), Ceres ANNOT ID no. 6100173 (SEQ ID NO:904), and sequences listing identified as functional homologs of the sequences of FIG. 9, as set forth in the sequence. In some cases, a functional homolog of SEQ ID NO:850 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%,

70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:850.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:907 are provided in FIG. 10. Such functional homologs include Ceres CLONE ID no. 1940797 (SEQ ID NO:909), Ceres ANNOT ID no. 1538900 (SEQ ID NO:911), Ceres CLONE ID no. 1126868 (SEQ ID NO:922), Public GI ID no. 89257684 (SEQ ID NO:923), Public GI ID no. 124360460 (SEQ ID NO:929), Public GI ID no. 62865694 (SEQ ID NO:931), Public GI ID no. 62865692 (SEQ ID NO:932), Ceres CLONE ID no. 260368 (SEQ ID NO:936), Ceres CLONE ID no. 1873510 (SEQ ID NO:947), Public GI ID no. 125541662 (SEQ ID NO:948), Public GI ID no. 48716268 (SEQ ID NO:950), and Public GI ID no. 62865696 (SEQ ID NO:1844). Other functional homologs of SEQ ID NO:907 include Ceres ANNOT ID no. 1529131 (SEQ ID NO:913), Ceres ANNOT ID no. 1454060 (SEQ ID NO:915), Ceres ANNOT ID no. 1442787 (SEQ ID NO:917), Ceres ANNOT ID no. 1452648 (SEQ ID NO:919), Public GI ID no. 2245140 (SEQ ID NO:920), Public GI ID no. 89274212 (SEQ ID NO:924), Ceres CLONE ID no. 1104523 (SEQ ID NO:926), Ceres CLONE ID no. 654265 (SEQ ID NO:928), Public GI ID no. 42627704 (SEQ ID NO:930), Ceres CLONE ID no. 887222 (SEQ ID NO:934), Public GI ID no. 62865690 (SEQ ID NO:937), Public GI ID no. 64175600 (SEQ ID NO:938), Public GI ID no. 64175634 (SEQ ID NO:939), Public GI ID no. 64175606 (SEQ ID NO:940), Public GI ID no. 64175648 (SEQ ID NO:941), Ceres CLONE ID no. 312184 (SEQ ID NO:943), Ceres CLONE ID no. 380740 (SEQ ID NO:945), Public GI ID no. 125531536 (SEQ ID NO:949), and sequences identified as functional homologs of the sequences of FIG. 10, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:907 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:907.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:953 are provided in FIG. 11. Such functional homologs include Ceres CLONE ID no. 1798705 (SEQ ID NO:955), Ceres ANNOT ID no. 1458907 (SEQ ID NO:963), Ceres CLONE ID no. 1090409 (SEQ ID NO:971), Ceres CLONE ID no. 479817 (SEQ ID NO:977), Ceres CLONE ID no. 1041793 (SEQ ID NO:979), Ceres CLONE ID no. 684633 (SEQ ID NO:985), Ceres CLONE ID no. 371815 (SEQ ID NO:991), Ceres CLONE ID no. 1686460 (SEQ ID NO:993), Ceres CLONE ID no. 1448595 (SEQ ID NO:995), Ceres CLONE ID no. 1734477 (SEQ ID NO:999), Ceres CLONE ID no. 1605693 (SEQ ID NO:1005), Ceres CLONE ID no. 1757400 (SEQ ID NO:1009), and Public GI ID no. 115434334 (SEQ ID NO:1015). Other functional homologs of SEQ ID NO:953 include Ceres CLONE ID no. 1793754 (SEQ ID NO:957), Ceres CLONE ID no. 1938045 (SEQ ID NO:959), Ceres CLONE ID no. 1850004 (SEQ ID NO:961), Ceres ANNOT ID no. 1489548 (SEQ ID NO:965), Public GI ID no. 22329538 (SEQ ID NO:966), Public GI ID no. 18404714 (SEQ ID NO:967), Ceres CLONE ID no. 1110032 (SEQ ID NO:969), Ceres CLONE ID no. 1095353 (SEQ ID NO:973), Ceres CLONE ID no. 872121 (SEQ ID NO:975), Ceres CLONE ID no. 562208 (SEQ ID NO:981), Ceres CLONE ID no. 1042364 (SEQ ID NO:983), Ceres CLONE ID no. 1031873 (SEQ ID NO:987), Ceres CLONE ID no. 1377698 (SEQ ID NO:989), Ceres CLONE ID no. 1742945 (SEQ ID NO:997), Ceres CLONE ID no. 1742053 (SEQ ID NO:998).

NO:1001), Ceres CLONE ID no. 1728365 (SEQ ID NO:1003), Ceres CLONE ID no. 1609807 (SEQ ID NO:1007), Ceres CLONE ID no. 1778566 (SEQ ID NO:1011), Ceres CLONE ID no. 2020580 (SEQ ID NO:1013), Public GI ID no. 125524285 (SEQ ID NO:1014), Public GI ID no. 125568898 (SEQ ID NO:1016), Ceres ANNOT ID no. 6055303 (SEQ ID NO:1018), and sequences identified as functional homologs of the sequences of FIG. 11, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:953 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:953.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1024 are provided in FIG. 12. Such functional homologs include Ceres ANNOT ID no. 1452905 (SEQ ID NO:1029), Ceres CLONE ID no. 956176 (SEQ ID NO:1039), Public GI ID no. 92870366 (SEQ ID NO:1040), Ceres CLONE ID no. 294166 (SEQ ID NO:1042), and Public GI ID no. 125543067 (SEQ ID NO:1043). Other functional homologs of SEQ ID NO:1024 include SEQ ID NO:1025, Ceres ANNOT ID no. 1442522 (SEQ ID NO:1027), Public GI ID no. 8778818 (SEQ ID NO:1030), Ceres CLONE ID no. 108095 (SEQ ID NO:1032), Public GI ID no. 18394821 (SEQ ID NO:1033), Ceres CLONE ID no. 6332 (SEQ ID NO:1035), Ceres CLONE ID no. 1069047 (SEQ ID NO:1037), Public GI ID no. 115480956 (SEQ ID NO:1044), and sequences identified as functional homologs of the sequences of FIG. 12, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:1024 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1024.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1047 are provided in FIG. 13. Such functional homologs include Ceres CLONE ID no. 1837694 (SEQ ID NO:1053), Ceres ANNOT ID no. 1483367 (SEQ ID NO:1057), Ceres CLONE ID no. 1077781 (SEQ ID NO:1083), Ceres CLONE ID no. 471026 (SEQ ID NO:1085), Public GI ID no. 92888885 (SEQ ID NO:1099), Public GI ID no. 45544873 (SEQ ID NO:1100), Public GI ID no. 45758663 (SEQ ID NO:1101), Ceres CLONE ID no. 772927 (SEQ ID NO:1105), Ceres CLONE ID no. 895080 (SEQ ID NO:1111), Ceres CLONE ID no. 1806128 (SEQ ID NO:1131), Public GI ID no. 115458192 (SEQ ID NO:1134), and Public GI ID no. 82470795 (SEQ ID NO:1139). Other functional homologs of SEQ ID NO:1047 include Ceres CLONE ID no. 1837746 (SEQ ID NO:1049), Ceres CLONE ID no. 1834764 (SEQ ID NO:1051), Ceres CLONE ID no. 1853547 (SEQ ID NO:1055), Ceres ANNOT ID no. 1474088 (SEQ ID NO:1059), Ceres ANNOT ID no. 1536919 (SEQ ID NO:1061), Ceres ANNOT ID no. 1467033 (SEQ ID NO:1063), Ceres ANNOT ID no. 1485401 (SEQ ID NO:1065), Ceres ANNOT ID no. 1486505 (SEQ ID NO:1067), Public GI ID no. 17065054 (SEQ ID NO:1068), Public GI ID no. 30694690 (SEQ ID NO:1069), Ceres CLONE ID no. 12997 (SEQ ID NO:1071), Public GI ID no. 30694694 (SEQ ID NO:1072), Public GI ID no. 42572167 (SEQ ID NO:1073), Public GI ID no. 110739742 (SEQ ID NO:1074), Public GI ID no. 18412263 (SEQ ID NO:1075), Ceres CLONE ID no. 36412 (SEQ ID NO:1077), Public GI ID no. 18399792 (SEQ ID NO:1078), Ceres CLONE ID no. 924 (SEQ ID NO:1080), Public GI ID no. 15238000 (SEQ

ID NO:1081), Ceres CLONE ID no. 1626330 (SEQ ID NO:1087), Ceres CLONE ID no. 1650419 (SEQ ID NO:1089), Ceres CLONE ID no. 1641329 (SEQ ID NO:1091), Ceres CLONE ID no. 1620406 (SEQ ID NO:1093), Ceres CLONE ID no. 546832 (SEQ ID NO:1095), Ceres CLONE ID no. 1243138 (SEQ ID NO:1097), Public GI ID no. 92887260 (SEQ ID NO:1098), Ceres CLONE ID no. 885628 (SEQ ID NO:1103), Ceres CLONE ID no. 1376391 (SEQ ID NO:1107), Ceres CLONE ID no. 465893 (SEQ ID NO:1109), Ceres CLONE ID no. 218243 (SEQ ID NO:1113), Ceres CLONE ID no. 1558456 (SEQ ID NO:1115), Ceres CLONE ID no. 343008 (SEQ ID NO:1117), Ceres CLONE ID no. 218463 (SEQ ID NO:1119), Ceres CLONE ID no. 1565409 (SEQ ID NO:1121), Ceres CLONE ID no. 1060968 (SEQ ID NO:1123), Ceres CLONE ID no. 236111 (SEQ ID NO:1125), Ceres CLONE ID no. 285598 (SEQ ID NO:1127), Ceres CLONE ID no. 225881 (SEQ ID NO:1129), Ceres CLONE ID no. 1811383 (SEQ ID NO:1133), Public GI ID no. 49388268 (SEQ ID NO:1135), Public GI ID no. 125590268 (SEQ ID NO:1136), Public GI ID no. 115444009 (SEQ ID NO:1137), Public GI ID no. 115447993 (SEQ ID NO:1138), Ceres ANNOT ID no. 6033842 (SEQ ID NO:1141), Ceres ANNOT ID no. 6029952 (SEQ ID NO:1143), Ceres ANNOT ID no. 6035837 (SEQ ID NO:1145), Ceres ANNOT ID no. 6035830 (SEQ ID NO:1147), Ceres ANNOT ID no. 6029981 (SEQ ID NO:1149), and sequences identified as functional homologs of the sequences of FIG. 13, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:1047 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1047.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1151 are provided in FIG. 14. Such functional homologs include Ceres CLONE ID no. 1851526 (SEQ ID NO:1155), Ceres ANNOT ID no. 1486769 (SEQ ID NO:1172), Public GI ID no. 83032232 (SEQ ID NO:1209), Ceres CLONE ID no. 1620420 (SEQ ID NO:1211), Public GI ID no. 92892428 (SEQ ID NO:1215), Ceres CLONE ID no. 884742 (SEQ ID NO:1223), Ceres CLONE ID no. 1821559 (SEQ ID NO:1246), Public GI ID no. 51535021 (SEQ ID NO:1258), Public GI ID no. 113205304 (SEQ ID NO:1263), and Public GI ID no. 37719051 (SEQ ID NO:1264). Other functional homologs of SEQ ID NO:1151 include Ceres CLONE ID no. 1918070 (SEQ ID NO:1153), Ceres CLONE ID no. 1948426 (SEQ ID NO:1157), Ceres CLONE ID no. 1937875 (SEQ ID NO:1159), Ceres CLONE ID no. 100056542 (SEQ ID NO:1160), Public GI ID no. 5731257 (SEQ ID NO:1161), Ceres CLONE ID no. 100058043 (SEQ ID NO:1162), Ceres CLONE ID no. 1838288 (SEQ ID NO:1164), Ceres CLONE ID no. 1793597 (SEQ ID NO:1166), Ceres ANNOT ID no. 1543031 (SEQ ID NO:1168), Ceres ANNOT ID no. 1489643 (SEQ ID NO:1170), Ceres ANNOT ID no. 1479721 (SEQ ID NO:1174), Ceres ANNOT ID no. 1449170 (SEQ ID NO:1176), Ceres ANNOT ID no. 1493696 (SEQ ID NO:1178), Ceres ANNOT ID no. 1543534 (SEQ ID NO:1180), Ceres ANNOT ID no. 1440815 (SEQ ID NO:1182), Ceres ANNOT ID no. 1490137 (SEQ ID NO:1184), Ceres ANNOT ID no. 1451054 (SEQ ID NO:1186), Ceres ANNOT ID no. 1456669 (SEQ ID NO:1188), Ceres ANNOT ID no. 1509865 (SEQ ID NO:1190), Ceres ANNOT ID no. 1447910 (SEQ ID

NO:1192), Ceres ANNOT ID no. 1471068 (SEQ ID NO:1194), Ceres ANNOT ID no. 1504118 (SEQ ID NO:1196), Ceres CLONE ID no. 1343621 (SEQ ID NO:1198), Public GI ID no. 15218305 (SEQ ID NO:1199), Public GI ID no. 15219640 (SEQ ID NO:1200), Public GI ID no. 18409345 (SEQ ID NO:1201), Public GI ID no. 6522545 (SEQ ID NO:1202), Public GI ID no. 15237274 (SEQ ID NO:1203), Public GI ID no. 26452377 (SEQ ID NO:1204), Ceres CLONE ID no. 33629 (SEQ ID NO:1206), Ceres CLONE ID no. 1064407 (SEQ ID NO:1208), Ceres CLONE ID no. 1656310 (SEQ ID NO:1213), Public GI ID no. 92885257 (SEQ ID NO:1214), Public GI ID no. 92868571 (SEQ ID NO:1216), Public GI ID no. 53689778 (SEQ ID NO:1217), Ceres CLONE ID no. 835598 (SEQ ID NO:1219), Ceres CLONE ID no. 575649 (SEQ ID NO:1221), Ceres CLONE ID no. 376567 (SEQ ID NO:1225), Ceres CLONE ID no. 1284191 (SEQ ID NO:1227), Ceres CLONE ID no. 367175 (SEQ ID NO:1229), Ceres CLONE ID no. 100748296 (SEQ ID NO:1230), Ceres CLONE ID no. 1597176 (SEQ ID NO:1232), Ceres CLONE ID no. 375636 (SEQ ID NO:1234), Ceres CLONE ID no. 288123 (SEQ ID NO:1236), Ceres CLONE ID no. 303582 (SEQ ID NO:1238), Ceres CLONE ID no. 1604759 (SEQ ID NO:1240), Ceres CLONE ID no. 1955192 (SEQ ID NO:1242), Ceres CLONE ID no. 2008687 (SEQ ID NO:1244), Ceres CLONE ID no. 1995843 (SEQ ID NO:1248), Ceres CLONE ID no. 2008591 (SEQ ID NO:1250), Ceres CLONE ID no. 2046826 (SEQ ID NO:1252), Ceres CLONE ID no. 1985573 (SEQ ID NO:1254), Public GI ID no. 125541129 (SEQ ID NO:1255), Public GI ID no. 125528922 (SEQ ID NO:1256), Public GI ID no. 115487590 (SEQ ID NO:1257), Public GI ID no. 115448671 (SEQ ID NO:1259), Public GI ID no. 125596564 (SEQ ID NO:1260), Public GI ID no. 125573161 (SEQ ID NO:1261), Public GI ID no. 48716463 (SEQ ID NO:1262), Ceres ANNOT ID no. 6054246 (SEQ ID NO:1266), Ceres ANNOT ID no. 6086570 (SEQ ID NO:1268), Ceres ANNOT ID no. 6024957 (SEQ ID NO:1270), Ceres ANNOT ID no. 6016867 (SEQ ID NO:1272), Ceres ANNOT ID no. 6091369 (SEQ ID NO:1274), and sequences identified as functional homologs of the sequences of FIG. 14, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:1151 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1151.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1277 are provided in FIG. 15. Such functional homologs include Ceres CLONE ID no. 1926352 (SEQ ID NO:1279), Ceres ANNOT ID no. 1448905 (SEQ ID NO:1285), Public GI ID no. 15236865 (SEQ ID NO:1294), Ceres CLONE ID no. 934771 (SEQ ID NO:1301), Ceres CLONE ID no. 338386 (SEQ ID NO:1303), Ceres CLONE ID no. 1780691 (SEQ ID NO:1317), and Public GI ID no. 115464819 (SEQ ID NO:1326). Other functional homologs of SEQ ID NO:1277 include Ceres CLONE ID no. 1848576 (SEQ ID NO:1281), Ceres CLONE ID no. 1981528 (SEQ ID NO:1283), Ceres ANNOT ID no. 1465978 (SEQ ID NO:1287), Ceres ANNOT ID no. 1504997 (SEQ ID NO:1289), Ceres ANNOT ID no. 1451909 (SEQ ID NO:1291), Ceres ANNOT ID no. 1461635 (SEQ ID NO:1293), Public GI ID no. 18397400 (SEQ ID NO:1295), Ceres CLONE ID no. 16226 (SEQ ID NO:1297), Public GI ID no. 18411823 (SEQ

ID NO:1298), Public GI ID no. 15219845 (SEQ ID NO:1299), Ceres CLONE ID no. 1276710 (SEQ ID NO:1305), Ceres CLONE ID no. 1479310 (SEQ ID NO:1307), Ceres CLONE ID no. 376230 (SEQ ID NO:1309), Ceres CLONE ID no. 1290713 (SEQ ID NO:1311), Ceres CLONE ID no. 321681 (SEQ ID NO:1313), Ceres CLONE ID no. 1869072 (SEQ ID NO:1315), Ceres CLONE ID no. 1818502 (SEQ ID NO:1319), Ceres CLONE ID no. 1750477 (SEQ ID NO:1321), Public GI ID no. 125552947 (SEQ ID NO:1322), Public GI ID no. 125527862 (SEQ ID NO:1323), Public GI ID no. 125543660 (SEQ ID NO:1324), Public GI ID no. 125528123 (SEQ ID NO:1325), Public GI ID no. 115440195 (SEQ ID NO:1327), Public GI ID no. 115452717 (SEQ ID NO:1328), Public GI ID no. 115440629 (SEQ ID NO:1329), Public GI ID no. 115464599 (SEQ ID NO:1330), Public GI ID no. 20161462 (SEQ ID NO:1331), Public GI ID no. 125586076 (SEQ ID NO:1332), Ceres CLONE ID no. 1823216 (SEQ ID NO:1334), Ceres ANNOT ID no. 6040230 (SEQ ID NO:1336), Ceres ANNOT ID no. 6015489 (SEQ ID NO:1338), Ceres ANNOT ID no. 6042890 (SEQ ID NO:1340), Ceres ANNOT ID no. 6040033 (SEQ ID NO:1342), Ceres ANNOT ID no. 6018414 (SEQ ID NO:1344), and sequences identified as functional homologs of the sequences of FIG. 15, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:1277 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1277.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1347 are provided in FIG. 16. Such functional homologs include Ceres CLONE ID no. 285028 (SEQ ID NO:1419), Ceres CLONE ID no. 100969565 (SEQ ID NO:1422), Public GI ID no. 1352057 (SEQ ID NO:1427), Ceres ANNOT ID no. 1453784 (SEQ ID NO:1429), Public GI ID no. 452777 (SEQ ID NO:1430), and Public GI ID no. 92873297 (SEQ ID NO:1431). Other functional homologs of SEQ ID NO:1347 include Ceres ANNOT ID no. 1452612 (SEQ ID NO:1349), Ceres CLONE ID no. 520455 (SEQ ID NO:1351), Public GI ID no. 75271810 (SEQ ID NO:1352), Public GI ID no. 115489446 (SEQ ID NO:1353), Ceres CLONE ID no. 499878 (SEQ ID NO:1355), Ceres ANNOT ID no. 1491840 (SEQ ID NO:1357), Public GI ID no. 125587204 (SEQ ID NO:1358), Ceres CLONE ID no. 320997 (SEQ ID NO:1360), Ceres ANNOT ID no. 1455585 (SEQ ID NO:1362), Ceres ANNOT ID no. 1499460 (SEQ ID NO:1364), Ceres CLONE ID no. 334484 (SEQ ID NO:1366), Ceres CLONE ID no. 100819481 (SEQ ID NO:1367), Public GI ID no. 115462401 (SEQ ID NO:1368), Ceres CLONE ID no. 1448136 (SEQ ID NO:1370), Ceres CLONE ID no. 277751 (SEQ ID NO:1372), Ceres ANNOT ID no. 1491839 (SEQ ID NO:1374), Ceres CLONE ID no. 100913241 (SEQ ID NO:1375), Ceres CLONE ID no. 1053224 (SEQ ID NO:1377), Ceres CLONE ID no. 425766 (SEQ ID NO:1379), Ceres CLONE ID no. 485480 (SEQ ID NO:1381), Ceres CLONE ID no. 474845 (SEQ ID NO:1383), Ceres CLONE ID no. 354561 (SEQ ID NO:1385), Ceres CLONE ID no. 540858 (SEQ ID NO:1387), Ceres CLONE ID no. 2032994 (SEQ ID NO:1389), Ceres CLONE ID no. 2015315 (SEQ ID NO:1391), Ceres CLONE ID no. 2016149 (SEQ ID NO:1393), Ceres CLONE ID no. 1922843 (SEQ ID NO:1395), Ceres CLONE ID no. 2000263 (SEQ ID

NO:1397), Ceres CLONE ID no. 1943510 (SEQ ID NO:1399), Ceres CLONE ID no. 1835498 (SEQ ID NO:1401), Ceres CLONE ID no. 101116694 (SEQ ID NO:1402), Ceres CLONE ID no. 1930596 (SEQ ID NO:1404), Ceres CLONE ID no. 846036 (SEQ ID NO:1406), Ceres CLONE ID no. 941614 (SEQ ID NO:1408), Ceres CLONE ID no. 238788 (SEQ ID NO:1410), Public GI ID no. 125554220 (SEQ ID NO:1411), Public GI ID no. 125559895 (SEQ ID NO:1412), Public GI ID no. 75252070 (SEQ ID NO:1413), Public GI ID no. 115466632 (SEQ ID NO:1414), Public GI ID no. 125541525 (SEQ ID NO:1415), Ceres CLONE ID no. 1805110 (SEQ ID NO:1417), Ceres CLONE ID no. 1725309 (SEQ ID NO:1421), Ceres CLONE ID no. 100861679 (SEQ ID NO:1423), Public GI ID no. 75226278 (SEQ ID NO:1424), Public GI ID no. 125525030 (SEQ ID NO:1425), Public GI ID no. 115435474 (SEQ ID NO:1426), Ceres CLONE ID no. 1728516 (SEQ ID NO:1433), Public GI ID no. 115467910 (SEQ ID NO:1434), Public GI ID no. 15239950 (SEQ ID NO:1435), Public GI ID no. 4887012 (SEQ ID NO:1436), Ceres ANNOT ID no. 1478544 (SEQ ID NO:1438), Public GI ID no. 90811713 (SEQ ID NO:1439), Public GI ID no. 25989504 (SEQ ID NO:1440), Ceres CLONE ID no. 1113354 (SEQ ID NO:1442), Ceres CLONE ID no. 1113630 (SEQ ID NO:1444), Ceres ANNOT ID no. 6072030 (SEQ ID NO:1446), Ceres ANNOT ID no. 6025654 (SEQ ID NO:1448), Ceres ANNOT ID no. 6091150 (SEQ ID NO:1450), Ceres ANNOT ID no. 6100390 (SEQ ID NO:1452), and sequences identified as functional homologs of the sequences of FIG. 16, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:1347 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1347.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1457 are provided in FIG. 17. Such functional homologs include Ceres CLONE ID no. 1924904 (SEQ ID NO:1460), Ceres ANNOT ID no. 1543346 (SEQ ID NO:1462), Public GI ID no. 18396338 (SEQ ID NO:1467), Ceres CLONE ID no. 833872 (SEQ ID NO:1471), Ceres CLONE ID no. 1579587 (SEQ ID NO:1475), Ceres CLONE ID no. 1786411 (SEQ ID NO:1477), and Public GI ID no. 108864370 (SEQ ID NO:1480). Other functional homologs of SEQ ID NO:1457 include SEQ ID NO:1458, Ceres ANNOT ID no. 1532932 (SEQ ID NO:1464), Ceres ANNOT ID no. 1489955 (SEQ ID NO:1466), Public GI ID no. 4928917 (SEQ ID NO:1468), Public GI ID no. 6728979 (SEQ ID NO:1469), Ceres CLONE ID no. 285780 (SEQ ID NO:1473), Public GI ID no. 125528863 (SEQ ID NO:1478), Public GI ID no. 125536365 (SEQ ID NO:1479), Public GI ID no. 108864369 (SEQ ID NO:1481), Public GI ID no. 115488274 (SEQ ID NO:1482), Public GI ID no. 125577099 (SEQ ID NO:1483), Public GI ID no. 125573110 (SEQ ID NO:1484), Public GI ID no. 124359159 (SEQ ID NO:1485), Public GI ID no. 62901479 (SEQ ID NO:1486), Ceres ANNOT ID no. 6016783 (SEQ ID NO:1488), Ceres ANNOT ID no. 6020759 (SEQ ID NO:1490), Ceres ANNOT ID no. 6028676 (SEQ ID NO:1492), Ceres ANNOT ID no. 6028677 (SEQ ID NO:1494), and sequences identified as functional homologs of the sequences of FIG. 17, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:1457 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%,

70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1457.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1497 are provided in FIG. 18. Such functional homologs include Ceres ANNOT ID no. 1443463 (SEQ ID NO:1499), Public GI ID no. 13605525 (SEQ ID NO:1502), Public GI ID no. 94965681 (SEQ ID NO:1506), and Public GI ID no. 28201254 (SEQ ID NO:1512). Other functional homologs of SEQ ID NO:1497 include Ceres ANNOT ID no. 1504954 (SEQ ID NO:1501), Public GI ID no. 2499553 (SEQ ID NO:1503), Public GI ID no. 738308 (SEQ ID NO:1504), Public GI ID no. 4325368 (SEQ ID NO:1505), Ceres CLONE ID no. 919923 (SEQ ID NO:1508), Ceres CLONE ID no. 1659764 (SEQ ID NO:1510), Public GI ID no. 125539984 (SEQ ID NO:1511), Public GI ID no. 21740729 (SEQ ID NO:1513), Public GI ID no. 115458700 (SEQ ID NO:1514), Public GI ID no. 125590574 (SEQ ID NO:1515), Public GI ID no. 16444957 (SEQ ID NO:1516), Ceres CLONE ID no. 1784494 (SEQ ID NO:1518), Public GI ID no. 77963980 (SEQ ID NO:1519), Public GI ID no. 124361190 (SEQ ID NO:1520), Public GI ID no. 37725007 (SEQ ID NO:1521), Public GI ID no. 45935258 (SEQ ID NO:1522), Public GI ID no. 15559008 (SEQ ID NO:1523), Public GI ID no. 38037416 (SEQ ID NO:1524), Public GI ID no. 77963974 (SEQ ID NO:1525), Ceres ANNOT ID no. 6112581 (SEQ ID NO:1527), Public GI ID no. 56553448 (SEQ ID NO:1528), Public GI ID no. 23506659 (SEQ ID NO:1529), Ceres ANNOT ID no. 6118060 (SEQ ID NO:1531), Public GI ID no. 46446306 (SEQ ID NO:1532), Public GI ID no. 114321405 (SEQ ID NO:1533), Public GI ID no. 83858274 (SEQ ID NO:1534), Public GI ID no. 154250969 (SEQ ID NO:1535), Public GI ID no. 83594235 (SEQ ID NO:1536), and sequences identified as functional homologs of the sequences of FIG. 18, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:1497 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1497.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1587 are provided in FIG. 19. Such functional homologs include Ceres CLONE ID no. 1839577 (SEQ ID NO:1589), Ceres ANNOT ID no. 1491567 (SEQ ID NO:1591), Ceres CLONE ID no. 574505 (SEQ ID NO:1596), Public GI ID no. 56117815 (SEQ ID NO:1597), Public GI ID no. 92874021 (SEQ ID NO:1603), Public GI ID no. 123684 (SEQ ID NO:1605), Public GI ID no. 5821136 (SEQ ID NO:1606), Ceres CLONE ID no. 283366 (SEQ ID NO:1609), Public GI ID no. 16118447 (SEQ ID NO:1612), and Public GI ID no. 125562434 (SEQ ID NO:1614). Other functional homologs of SEQ ID NO:1587 include Ceres ANNOT ID no. 1438739 (SEQ ID NO:1593), Public GI ID no. 89274218 (SEQ ID NO:1594), Public GI ID no. 115521211 (SEQ ID NO:1598), Public GI ID no. 115521213 (SEQ ID NO:1599), Public GI ID no. 115521217 (SEQ ID NO:1600), Public GI ID no. 115521209 (SEQ ID NO:1601), Public GI ID no. 115521215 (SEQ ID NO:1602), Public GI ID no. 11386827 (SEQ ID NO:1604), Public GI ID no. 25052685 (SEQ ID NO:1607), Ceres CLONE ID no. 1440437 (SEQ ID NO:1611), Public GI ID no. 125564440 (SEQ ID NO:1613), Public GI ID no. 116309817 (SEQ ID NO:1615), Public GI ID no. 125549382 (SEQ ID NO:1616), Public GI ID no. 52077317 (SEQ ID NO:1617), Public GI ID no. 115477655 (SEQ ID NO:1618), Public GI ID no. 42408097 (SEQ ID NO:1619).

NO:1619), Public GI ID no. 115459982 (SEQ ID NO:1620), Public GI ID no. 33591096 (SEQ ID NO:1621), Ceres CLONE ID no. 484753 (SEQ ID NO:1623), Ceres ANNOT ID no. 6035291 (SEQ ID NO:1625), and sequences identified as functional homologs of the sequences of FIG. 19, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:1587 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1587.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1635 are provided in FIG. 20. Such functional homologs include Ceres ANNOT ID no. 1508307 (SEQ ID NO:1637), Public GI ID no. 1495267 (SEQ ID NO:1642), Public GI ID no. 87241310 (SEQ ID NO:1644), Ceres CLONE ID no. 938390 (SEQ ID NO:1646), Ceres CLONE ID no. 272338 (SEQ ID NO:1648), Ceres CLONE ID no. 1993510 (SEQ ID NO:1650), Public GI ID no. 125563862 (SEQ ID NO:1651), and Public GI ID no. 125605833 (SEQ ID NO:1653). Other functional homologs of SEQ ID NO:1635 include Public GI ID no. 6899919 (SEQ ID NO:1632), Ceres ANNOT ID no. 1455110 (SEQ ID NO:1639), Ceres ANNOT ID no. 1525218 (SEQ ID NO:1641), Public GI ID no. 15231597 (SEQ ID NO:1643), Public GI ID no. 125548147 (SEQ ID NO:1652), Public GI ID no. 51091343 (SEQ ID NO:1654), Public GI ID no. 115479355 (SEQ ID NO:1655), Ceres ANNOT ID no. 6042086 (SEQ ID NO:1657), Ceres ANNOT ID no. 6029903 (SEQ ID NO:1659), and sequences identified as functional homologs of the sequences of FIG. 20, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:1635 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1635.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:1540 are provided in FIG. 21. Such functional homologs include Ceres CLONE ID no. 1943265 (SEQ ID NO:1543), Ceres ANNOT ID no. 1454522 (SEQ ID NO:1547), Public GI ID no. 31323447 (SEQ ID NO:1556), Ceres CLONE ID no. 1583941 (SEQ ID NO:1561), Ceres CLONE ID no. 1792942 (SEQ ID NO:1563), Public GI ID no. 77548772 (SEQ ID NO:1565), and Public GI ID no. 84453182 (SEQ ID NO:1567). Other functional homologs of SEQ ID NO:1540 include Public GI ID no. 31746344 (SEQ ID NO:1541), Ceres CLONE ID no. 1926640 (SEQ ID NO:1545), Ceres ANNOT ID no. 1475125 (SEQ ID NO:1549), Ceres ANNOT ID no. 1439653 (SEQ ID NO:1551), Ceres ANNOT ID no. 1461995 (SEQ ID NO:1553), Public GI ID no. 13877517 (SEQ ID NO:1554), Public GI ID no. 7239157 (SEQ ID NO:1555), Public GI ID no. 22652125 (SEQ ID NO:1557), Public GI ID no. 22652115 (SEQ ID NO:1558), Public GI ID no. 22652117 (SEQ ID NO:1559), Public GI ID no. 125535858 (SEQ ID NO:1564), Public GI ID no. 125578581 (SEQ ID NO:1566), Public GI ID no. 13752407 (SEQ ID NO:1568), Ceres ANNOT ID no. 6098817 (SEQ ID NO:1570), Ceres ANNOT ID no. 6039430 (SEQ ID NO:1572), Ceres ANNOT ID no. 6068141 (SEQ ID NO:1574), Ceres ANNOT ID no. 6033916 (SEQ ID NO:1576), Ceres ANNOT ID no. 6034399 (SEQ ID NO:1578), Ceres ANNOT ID no. 6068617 (SEQ ID NO:1580), Ceres ANNOT ID no. 6026318 (SEQ ID NO:1582), Ceres ANNOT ID no. 6107650 (SEQ ID NO:1584), and sequences identified as functional homologs

of the sequences of FIG. 21, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:1540 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1540.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:538 are provided in FIG. 22. Such functional homologs include Public GI ID no. 5731739 (SEQ ID NO:539), Ceres ANNOT ID no. 1538045 (SEQ ID NO:541), Public GI ID no. 29467479 (SEQ ID NO:542), Public GI ID no. 133921974 (SEQ ID NO:543), Public GI ID no. 113197027 (SEQ ID NO:544), Public GI ID no. 92879277 (SEQ ID NO:545), Public GI ID no. 45935260 (SEQ ID NO:546), Public GI ID no. 8101444 (SEQ ID NO:547), Public GI ID no. 78217443 (SEQ ID NO:548), and Public GI ID no. 28372347 (SEQ ID NO:549). Other functional homologs of SEQ ID NO:538 include Public GI ID no. 16416405 (SEQ ID NO:550), Ceres ANNOT ID no. 1484634 (SEQ ID NO:552), Ceres ANNOT ID no. 1451869 (SEQ ID NO:554), Public GI ID no. 25407462 (SEQ ID NO:555), Public GI ID no. 29467481 (SEQ ID NO:556), Public GI ID no. 29467477 (SEQ ID NO:557), Public GI ID no. 45935264 (SEQ ID NO:558), Public GI ID no. 5524201 (SEQ ID NO:559), Public GI ID no. 78217441 (SEQ ID NO:560), Public GI ID no. 3551221 (SEQ ID NO:561), Public GI ID no. 3551219 (SEQ ID NO:562), Public GI ID no. 23954324 (SEQ ID NO:563), Public GI ID no. 125582937 (SEQ ID NO:564), Public GI ID no. 83764373 (SEQ ID NO:565), Ceres ANNOT ID no. 6045327 (SEQ ID NO:567), and sequences identified as functional homologs of the sequences of FIG. 22, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:538 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:538.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:606 are provided in FIG. 23. Such functional homologs include Public GI ID no. 92873064 (SEQ ID NO:607), Public GI ID no. 37051125 (SEQ ID NO:608), and Public GI ID no. 112363376 (SEQ ID NO:609). Other functional homologs of SEQ ID NO:606 include Ceres CLONE ID no. 1938524 (SEQ ID NO:611), Ceres ANNOT ID no. 1473601 (SEQ ID NO:613), Ceres ANNOT ID no. 1468397 (SEQ ID NO:615), Public GI ID no. 21554185 (SEQ ID NO:616), Public GI ID no. 18424330 (SEQ ID NO:617), Public GI ID no. 8885571 (SEQ ID NO:618), Ceres CLONE ID no. 20852 (SEQ ID NO:620), Public GI ID no. 21553763 (SEQ ID NO:621), Public GI ID no. 18401763 (SEQ ID NO:622), Ceres CLONE ID no. 16423 (SEQ ID NO:624), Public GI ID no. 112363380 (SEQ ID NO:625), Public GI ID no. 6092016 (SEQ ID NO:626), Ceres CLONE ID no. 770468 (SEQ ID NO:628), Public GI ID no. 113205234 (SEQ ID NO:629), Ceres ANNOT ID no. 6094775 (SEQ ID NO:631), and sequences identified as functional homologs of the sequences of FIG. 23, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:606 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:606.

Amino acid sequences of functional homologs of the polypeptide set forth in SEQ ID NO:570 are provided in

FIG. 24. Such functional homologs include Ceres CLONE ID no. 1919714 (SEQ ID NO:572), Ceres ANNOT ID no. 1443290 (SEQ ID NO:574), Ceres CLONE ID no. 1042157 (SEQ ID NO:576), Ceres CLONE ID no. 1384304 (SEQ ID NO:578), and Public GI ID no. 115464375 (SEQ ID NO:579). Other functional homologs of SEQ ID NO:570 include Ceres CLONE ID no. 100028078 (SEQ ID NO:580), Ceres ANNOT ID no. 1452096 (SEQ ID NO:582), Ceres ANNOT ID no. 1503869 (SEQ ID NO:584), Ceres ANNOT ID no. 1525651 (SEQ ID NO:586), Ceres CLONE ID no. 1645639 (SEQ ID NO:588), Ceres CLONE ID no. 603237 (SEQ ID NO:590), Ceres CLONE ID no. 340925 (SEQ ID NO:592), Ceres CLONE ID no. 293238 (SEQ ID NO:594), Ceres CLONE ID no. 483742 (SEQ ID NO:596), Ceres CLONE ID no. 1460255 (SEQ ID NO:598), Ceres CLONE ID no. 1400107 (SEQ ID NO:600), Public GI ID no. 115440865 (SEQ ID NO:601), Ceres ANNOT ID no. 6016008 (SEQ ID NO:603), and sequences identified as functional homologs of the sequences of FIG. 24, as set forth in the sequence listing. In some cases, a functional homolog of SEQ ID NO:570 has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:570.

The identification of conserved regions in an SD+EODFR and/or low light tolerance polypeptide facilitates production of variants of SD+EODFR and/or low light tolerance polypeptides. Variants of SD+EODFR and/or low light tolerance polypeptides typically have 10 or fewer conservative amino acid substitutions within the primary amino acid sequence, e.g., 7 or fewer conservative amino acid substitutions, 5 or fewer conservative amino acid substitutions, or between 1 and 5 conservative substitutions. A useful variant polypeptide can be constructed based on one of the alignments set forth in FIGS. 1-24. Such a polypeptide includes the conserved regions, arranged in the order depicted in the Figure from amino-terminal end to carboxy-terminal end. Such a polypeptide may also include zero, one, or more than one amino acid in positions marked by dashes. When no amino acids are present at positions marked by dashes, the length of such a polypeptide is the sum of the amino acid residues in all conserved regions. When amino acids are present at all positions marked by dashes, such a polypeptide has a length that is the sum of the amino acid residues in all conserved regions and all dashes.

D. Functional Homologs Identified by HMMER

In some embodiments, useful SD+EODFR and/or low light tolerance polypeptides include those that fit a Hidden Markov Model based on the polypeptides set forth in any one of FIGS. 1-24. A Hidden Markov Model (HMM) is a statistical model of a consensus sequence for a group of functional homologs. See, Durbin et al., *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids*, Cambridge University Press, Cambridge, UK (1998). An HMM is generated by the program HMMER 2.3.2 with default program parameters, using the sequences of the group of functional homologs as input. The multiple sequence alignment is generated by ProbCons (Do et al., *Genome Res.*, 15(2):330-40 (2005)) version 1.11 using a set of default parameters: -c, -consistency REPS of 2; -ir, -iterative-refinement REPS of 100; -pre, -pre-training REPS of 0. ProbCons is a public domain software program provided by Stanford University.

The default parameters for building an HMM (hmmbuild) are as follows: the default “architecture prior” (archpri) used by MAP architecture construction is 0.85, and the default

cutoff threshold (idlevel) used to determine the effective sequence number is 0.62. HMMER 2.3.2 was released Oct. 3, 2003 under a GNU general public license, and is available from various sources on the World Wide Web such as hmmer.janelia.org; hmmer.wustl.edu; and fr.com/hmmer232/. Hmmbuild outputs the model as a text file.

The HMM for a group of functional homologs can be used to determine the likelihood that a candidate SD+EODFR and/or low light tolerance polypeptide sequence is a better fit to that particular HMM than to a null HMM generated using a group of sequences that are not structurally or functionally related. The likelihood that a candidate polypeptide sequence is a better fit to an HMM than to a null HMM is indicated by the HMM bit score, a number generated when the candidate sequence is fitted to the HMM profile using the HMMER hmmsearch program. The following default parameters are used when running hmmsearch: the default E-value cutoff (E) is 10.0, the default bit score cutoff (T) is negative infinity, the default number of sequences in a database (Z) is the real number of sequences in the database, the default E-value cutoff for the per-domain ranked hit list (domE) is infinity, and the default bit score cutoff for the per-domain ranked hit list (domT) is negative infinity. A high HMM bit score indicates a greater likelihood that the candidate sequence carries out one or more of the biochemical or physiological function(s) of the polypeptides used to generate the HMM. A high HMM bit score is at least 20, and often is higher. Slight variations in the HMM bit score of a particular sequence can occur due to factors such as the order in which sequences are processed for alignment by multiple sequence alignment algorithms such as the ProbCons program. Nevertheless, such HMM bit score variation is minor.

The SD+EODFR and/or low light tolerance polypeptides discussed below fit the indicated HMM with an HMM bit score greater than 20 (e.g., greater than 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, or 500). In some embodiments, the HMM bit score of an SD+EODFR and/or low light tolerance polypeptide discussed below is about 50%, 60%, 70%, 80%, 90%, or 95% of the HMM bit score of a functional homolog provided in the Sequence Listing. In some embodiments, an SD+EODFR and/or low light tolerance polypeptide discussed below fits the indicated HMM with an HMM bit score greater than 20, and has a domain indicative of an SD+EODFR and/or low light tolerance polypeptide. In some embodiments, an SD+EODFR and/or low light tolerance polypeptide discussed below fits the indicated HMM with an HMM bit score greater than 20, and has 70% or greater sequence identity (e.g., 75%, 80%, 85%, 90%, 95%, or 100% sequence identity) to an amino acid sequence shown in any one of FIGS. 1-24.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 170 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 1. Such polypeptides include At4g37295 (SEQ ID NO:3), Ceres CLONE ID no. 1844057 (SEQ ID NO:7), Ceres ANNOT ID no. 1469148 (SEQ ID NO:22), Public GI ID no. 18390998 (SEQ ID NO:25), Ceres CLONE ID no. 1065656 (SEQ ID NO:32), Ceres CLONE ID no. 1652677 (SEQ ID NO:36), Public GI ID no. 92874556 (SEQ ID NO:49), Ceres CLONE ID no. 1329161 (SEQ ID NO:53), Ceres CLONE ID no. 1030378 (SEQ ID NO:55), Ceres CLONE ID no. 1413787 (SEQ ID NO:57), Public GI ID no. 125543598 (SEQ ID NO:60), Ceres CLONE ID no. 1793691 (SEQ ID NO:5), Ceres CLONE ID no. 1933784 (SEQ ID NO:9), Ceres CLONE ID no. 100030408 (SEQ ID NO:10), Ceres CLONE ID no. 1837059 (SEQ ID NO:12), Ceres CLONE

ID no. 1793801 (SEQ ID NO:14), Ceres CLONE ID no. 1855480 (SEQ ID NO:16), Ceres CLONE ID no. 1915644 (SEQ ID NO:18), Ceres CLONE ID no. 1898104 (SEQ ID NO:20), Ceres ANNOT ID no. 1464241 (SEQ ID NO:24), Public GI ID no. 18697627 (SEQ ID NO:26), Ceres CLONE ID no. 9391 (SEQ ID NO:28), Ceres CLONE ID no. 111154 (SEQ ID NO:30), Ceres CLONE ID no. 973975 (SEQ ID NO:34), Ceres CLONE ID no. 676695 (SEQ ID NO:38), Ceres CLONE ID no. 680331 (SEQ ID NO:40), Ceres CLONE ID no. 654515 (SEQ ID NO:42), Ceres CLONE ID no. 626154 (SEQ ID NO:44), Ceres CLONE ID no. 710603 (SEQ ID NO:46), Ceres CLONE ID no. 648076 (SEQ ID NO:48), Ceres CLONE ID no. 749439 (SEQ ID NO:51), Ceres CLONE ID no. 295936 (SEQ ID NO:59), Public GI ID no. 125525139 (SEQ ID NO:61), Public GI ID no. 115452643 (SEQ ID NO:62), Public GI ID no. 24059889 (SEQ ID NO:63), Ceres ANNOT ID no. 6012747 (SEQ ID NO:65), Ceres ANNOT ID no. 6027628 (SEQ ID NO:67), and sequences identified as functional homologs of the sequences of FIG. 1, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 80 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 2. Such polypeptides include At2g32710 (SEQ ID NO:70), Ceres CLONE ID no. 1975934 (SEQ ID NO:72), Ceres ANNOT ID no. 1529913 (SEQ ID NO:80), Ceres CLONE ID no. 977794 (SEQ ID NO:93), Public GI ID no. 42362378 (SEQ ID NO:96), Public GI ID no. 23899378 (SEQ ID NO:99), Public GI ID no. 15963346 (SEQ ID NO:101), Public GI ID no. 15963344+B816 (SEQ ID NO:102), Public GI ID no. 92429657 (SEQ ID NO:103), Ceres CLONE ID no. 746644 (SEQ ID NO:105), Ceres CLONE ID no. 623089 (SEQ ID NO:109), Ceres CLONE ID no. 1913678 (SEQ ID NO:115), Public GI ID no. 115450609 (SEQ ID NO:119), Ceres CLONE ID no. 1835084 (SEQ ID NO:74), Ceres CLONE ID no. 1846153 (SEQ ID NO:76), Ceres CLONE ID no. 1930884 (SEQ ID NO:78), Ceres ANNOT ID no. 1493858 (SEQ ID NO:82), Ceres ANNOT ID no. 1498646 (SEQ ID NO:84), Ceres ANNOT ID no. 1440974 (SEQ ID NO:86), Ceres CLONE ID no. 1189183 (SEQ ID NO:88), Public GI ID no. 26450253 (SEQ ID NO:89), Public GI ID no. 15239719 (SEQ ID NO:90), Public GI ID no. 15230194 (SEQ ID NO:91), Ceres CLONE ID no. 630905 (SEQ ID NO:95), Public GI ID no. 42362389 (SEQ ID NO:97), Public GI ID no. 70906129 (SEQ ID NO:98), Public GI ID no. 23899381 (SEQ ID NO:100), Ceres CLONE ID no. 298166 (SEQ ID NO:107), Ceres CLONE ID no. 1448390 (SEQ ID NO:111), Ceres CLONE ID no. 1734216 (SEQ ID NO:113), Public GI ID no. 125542322 (SEQ ID NO:116), Public GI ID no. 125532331 (SEQ ID NO:117), Public GI ID no. 125541233 (SEQ ID NO:118), Public GI ID no. 125584844 (SEQ ID NO:120), Public GI ID no. 115482472 (SEQ ID NO:121), Public GI ID no. 125575112 (SEQ ID NO:122), Ceres ANNOT ID no. 6003994 (SEQ ID NO:124), Ceres ANNOT ID no. 6068427 (SEQ ID NO:126), and sequences identified as functional homologs of the sequences of FIG. 2, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 80 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 3. Such polypeptides include Public GI ID no. 34550779 (SEQ ID NO:133), Ceres CLONE ID no. 1932235 (SEQ ID NO:137), Ceres CLONE ID no. 981738 (SEQ ID NO:201), Ceres CLONE ID no. 565974 (SEQ ID NO:209), Public GI ID no. 1352058 (SEQ ID NO:231), Public GI ID no. 11131101 (SEQ ID NO:234), Public GI ID no. 4887018

(SEQ ID NO:236), Public GI ID no. 4887018 (SEQ ID NO:236), Ceres CLONE ID no. 644455 (SEQ ID NO:247), Ceres CLONE ID no. 1731500 (SEQ ID NO:270), Public GI ID no. 20269063 (SEQ ID NO:300), Public GI ID no. 50404477 (SEQ ID NO:302), Public GI ID no. 62125392 (SEQ ID NO:303), Public GI ID no. 32396293 (SEQ ID NO:130), Public GI ID no. 32396299 (SEQ ID NO:131), Public GI ID no. 32396295 (SEQ ID NO:132), Ceres CLONE ID no. 1855369 (SEQ ID NO:135), Ceres CLONE ID no. 1948456 (SEQ ID NO:139), Ceres CLONE ID no. 1920182 (SEQ ID NO:141), Ceres CLONE ID no. 1835797 (SEQ ID NO:143), Ceres CLONE ID no. 1794204 (SEQ ID NO:145), Ceres CLONE ID no. 1853542 (SEQ ID NO:147), Ceres CLONE ID no. 1838776 (SEQ ID NO:149), Ceres CLONE ID no. 1854675 (SEQ ID NO:151), Ceres CLONE ID no. 1833078 (SEQ ID NO:153), Ceres CLONE ID no. 1850667 (SEQ ID NO:155), Ceres CLONE ID no. 1918745 (SEQ ID NO:157), Ceres CLONE ID no. 1929487 (SEQ ID NO:159), Ceres ANNOT ID no. 1497918 (SEQ ID NO:161), Ceres ANNOT ID no. 1459563 (SEQ ID NO:163), Ceres ANNOT ID no. 1452610 (SEQ ID NO:165), Ceres ANNOT ID no. 1496539 (SEQ ID NO:167), Ceres ANNOT ID no. 1498819 (SEQ ID NO:169), Ceres ANNOT ID no. 1446583 (SEQ ID NO:171), Ceres ANNOT ID no. 1535123 (SEQ ID NO:173), Ceres ANNOT ID no. 1463397 (SEQ ID NO:175), Ceres ANNOT ID no. 1499563 (SEQ ID NO:177), Ceres ANNOT ID no. 1488767 (SEQ ID NO:181), Ceres ANNOT ID no. 1522920 (SEQ ID NO:185), Ceres ANNOT ID no. 1469532 (SEQ ID NO:187), Public GI ID no. 15219692 (SEQ ID NO:188), Public GI ID no. 18420964 (SEQ ID NO:189), Ceres CLONE ID no. 1342080 (SEQ ID NO:191), Ceres CLONE ID no. 123105 (SEQ ID NO:193), Ceres CLONE ID no. 32727 (SEQ ID NO:195), Ceres CLONE ID no. 41161 (SEQ ID NO:197), Ceres CLONE ID no. 37274 (SEQ ID NO:199), Ceres CLONE ID no. 538020 (SEQ ID NO:203), Ceres CLONE ID no. 476244 (SEQ ID NO:205), Ceres CLONE ID no. 1623662 (SEQ ID NO:207), Ceres CLONE ID no. 626817 (SEQ ID NO:211), Ceres CLONE ID no. 537469 (SEQ ID NO:213), Ceres CLONE ID no. 582463 (SEQ ID NO:215), Ceres CLONE ID no. 1069818 (SEQ ID NO:217), Ceres CLONE ID no. 511737 (SEQ ID NO:219), Ceres CLONE ID no. 565422 (SEQ ID NO:221), Ceres CLONE ID no. 514595 (SEQ ID NO:223), Ceres CLONE ID no. 566396 (SEQ ID NO:225), Ceres CLONE ID no. 612705 (SEQ ID NO:227), Ceres CLONE ID no. 564134 (SEQ ID NO:229), Public GI ID no. 92872146 (SEQ ID NO:230), Public GI ID no. 11131103 (SEQ ID NO:232), Public GI ID no. 416641 (SEQ ID NO:233), Public GI ID no. 11131105 (SEQ ID NO:235), Public GI ID no. 4887016 (SEQ ID NO:237), Public GI ID no. 4887022 (SEQ ID NO:238), Public GI ID no. 81074526 (SEQ ID NO:239), Ceres CLONE ID no. 742023 (SEQ ID NO:241), Ceres CLONE ID no. 576268 (SEQ ID NO:243), Ceres CLONE ID no. 615386 (SEQ ID NO:245), Ceres CLONE ID no. 756966 (SEQ ID NO:249), Ceres CLONE ID no. 1052710 (SEQ ID NO:251), Ceres CLONE ID no. 697018 (SEQ ID NO:253), Ceres CLONE ID no. 618577 (SEQ ID NO:255), Ceres CLONE ID no. 935194 (SEQ ID NO:257), Ceres CLONE ID no. 1557429 (SEQ ID NO:259), Ceres CLONE ID no. 305337 (SEQ ID NO:261), Ceres CLONE ID no. 100872943 (SEQ ID NO:262), Ceres CLONE ID no. 305454 (SEQ ID NO:264), Ceres CLONE ID no. 1534670 (SEQ ID NO:266), Ceres CLONE ID no. 207963 (SEQ ID NO:268), Public GI ID no. 20257219 (SEQ ID NO:271), Ceres CLONE ID no. 1876818 (SEQ ID NO:273), Ceres CLONE ID no. 1817533 (SEQ ID NO:275), Ceres CLONE

ID no. 1958631 (SEQ ID NO:277), Ceres CLONE ID no. 1963215 (SEQ ID NO:279), Ceres CLONE ID no. 1770022 (SEQ ID NO:281), Ceres CLONE ID no. 1796223 (SEQ ID NO:283), Ceres CLONE ID no. 2016695 (SEQ ID NO:285), Ceres CLONE ID no. 1757085 (SEQ ID NO:287), Ceres CLONE ID no. 1769256 (SEQ ID NO:289), Ceres CLONE ID no. 1994871 (SEQ ID NO:291), Public GI ID no. 17154533 (SEQ ID NO:292), Public GI ID no. 125557426 (SEQ ID NO:293), Public GI ID no. 125524736 (SEQ ID NO:294), Public GI ID no. 125527656 (SEQ ID NO:295), Public GI ID no. 125599342 (SEQ ID NO:296), Public GI ID no. 125569626 (SEQ ID NO:297), Public GI ID no. 115465401 (SEQ ID NO:298), Public GI ID no. 40539038 (SEQ ID NO:299), Public GI ID no. 20269059 (SEQ ID NO:301), Public GI ID no. 110826446 (SEQ ID NO:304), Ceres ANNOT ID no. 6029073 (SEQ ID NO:306), Ceres ANNOT ID no. 6011329 (SEQ ID NO:308), Ceres ANNOT ID no. 6034498 (SEQ ID NO:310), Ceres ANNOT ID no. 6095057 (SEQ ID NO:312), Ceres ANNOT ID no. 6095058 (SEQ ID NO:314), and sequences identified as functional homologs of the sequences of FIG. 3, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 200 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 4. Such polypeptides include At4g03250 (Ceres Seedline ME10007; SEQ ID NO:317), Ceres CLONE ID no. 1842125 (SEQ ID NO:319), Ceres ANNOT ID no. 1461360 (SEQ ID NO:321), Ceres CLONE ID no. 480906 (SEQ ID NO:327), Public GI ID no. 92889352 (SEQ ID NO:330), Public GI ID no. 56201850 (SEQ ID NO:330), Ceres ANNOT ID no. 1440334 (SEQ ID NO:323), Ceres ANNOT ID no. 1493205 (SEQ ID NO:325), Ceres CLONE ID no. 482270 (SEQ ID NO:329), Public GI ID no. 125571531 (SEQ ID NO:332), Ceres ANNOT ID no. 6042411 (SEQ ID NO:334), and sequences identified as functional homologs of the sequences of FIG. 4, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 80 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 5. Such polypeptides include At2g04240 (SEQ ID NO:337), Ceres CLONE ID no. 952050 (SEQ ID NO:339), Public GI ID no. 115477050 (SEQ ID NO:349), Public GI ID no. 87162911 (SEQ ID NO:355), Ceres CLONE ID no. 1790901 (SEQ ID NO:357), Ceres CLONE ID no. 1460088 (SEQ ID NO:370), Ceres CLONE ID no. 1734065 (SEQ ID NO:393), Ceres CLONE ID no. 473509 (SEQ ID NO:395), Ceres CLONE ID no. 849918 (SEQ ID NO:401), Ceres CLONE ID no. 633470 (SEQ ID NO:409), Ceres CLONE ID no. 1808334 (SEQ ID NO:417), Ceres ANNOT ID no. 1525600 (SEQ ID NO:437), Ceres CLONE ID no. 1265097 (SEQ ID NO:341), Ceres CLONE ID no. 942980 (SEQ ID NO:343), Public GI ID no. 37901055 (SEQ ID NO:344), Ceres CLONE ID no. 1609912 (SEQ ID NO:346), Public GI ID no. 76446335 (SEQ ID NO:347), Public GI ID no. 125560204 (SEQ ID NO:348), Public GI ID no. 125303087 (SEQ ID NO:350), Public GI ID no. 115460088 (SEQ ID NO:351), Public GI ID no. 125591385 (SEQ ID NO:352), Public GI ID no. 115447931 (SEQ ID NO:353), Public GI ID no. 92893514 (SEQ ID NO:354), Ceres CLONE ID no. 2019320 (SEQ ID NO:359), Ceres CLONE ID no. 1890013 (SEQ ID NO:361), Public GI ID no. 20340241 (SEQ ID NO:362), Ceres CLONE ID no. 25801 (SEQ ID NO:364), Public GI ID no. 9743343 (SEQ ID NO:365), Public GI ID no. 15238072 (SEQ ID NO:366), Public GI ID no. 15222553 (SEQ ID NO:367), Public GI ID no. 21554155

(SEQ ID NO:368), Ceres CLONE ID no. 374439 (SEQ ID NO:372), Ceres CLONE ID no. 1465572 (SEQ ID NO:374), Ceres CLONE ID no. 1565524 (SEQ ID NO:376), Ceres CLONE ID no. 322302 (SEQ ID NO:378), Ceres CLONE ID no. 101136485 (SEQ ID NO:379), Ceres CLONE ID no. 1376133 (SEQ ID NO:381), Ceres CLONE ID no. 1374381 (SEQ ID NO:383), Ceres CLONE ID no. 1566473 (SEQ ID NO:385), Ceres CLONE ID no. 318088 (SEQ ID NO:387), Ceres CLONE ID no. 1452604 (SEQ ID NO:389), Ceres CLONE ID no. 337906 (SEQ ID NO:391), Ceres CLONE ID no. 1662513 (SEQ ID NO:397), Ceres CLONE ID no. 1662527 (SEQ ID NO:399), Ceres CLONE ID no. 571184 (SEQ ID NO:403), Ceres CLONE ID no. 665689 (SEQ ID NO:405), Ceres CLONE ID no. 1365853 (SEQ ID NO:407), Ceres CLONE ID no. 1052457 (SEQ ID NO:411), Ceres CLONE ID no. 579918 (SEQ ID NO:413), Ceres CLONE ID no. 863299 (SEQ ID NO:415), Ceres CLONE ID no. 1855611 (SEQ ID NO:419), Ceres CLONE ID no. 1845975 (SEQ ID NO:421), Ceres CLONE ID no. 1808298 (SEQ ID NO:423), Ceres CLONE ID no. 1841236 (SEQ ID NO:425), Ceres CLONE ID no. 1808269 (SEQ ID NO:427), Ceres CLONE ID no. 1850628 (SEQ ID NO:429), Ceres CLONE ID no. 1846911 (SEQ ID NO:431), Ceres CLONE ID no. 1916014 (SEQ ID NO:433), Ceres CLONE ID no. 1842594 (SEQ ID NO:435), Ceres ANNOT ID no. 1472192 (SEQ ID NO:439), Ceres ANNOT ID no. 1447489 (SEQ ID NO:441), Ceres ANNOT ID no. 1513000 (SEQ ID NO:443), Ceres ANNOT ID no. 1438658 (SEQ ID NO:445), Ceres ANNOT ID no. 1497255 (SEQ ID NO:447), Ceres ANNOT ID no. 6092104 (SEQ ID NO:449), Ceres ANNOT ID no. 6041700 (SEQ ID NO:451), Ceres ANNOT ID no. 6007297 (SEQ ID NO:453), and sequences identified as functional homologs of the sequences of FIG. 5, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 60 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 6. Such polypeptides include At5g14370 (SEQ ID NO:456), Public GI ID no. 58430585 (SEQ ID NO:457), Ceres CLONE ID no. 1842825 (SEQ ID NO:466), Ceres ANNOT ID no. 1449721 (SEQ ID NO:474), Public GI ID no. 41323978 (SEQ ID NO:475), Public GI ID no. 2895186 (SEQ ID NO:478), Public GI ID no. 22854950 (SEQ ID NO:481), Public GI ID no. 116010474 (SEQ ID NO:485), Public GI ID no. 4091804 (SEQ ID NO:488), Public GI ID no. 60459257 (SEQ ID NO:494), Public GI ID no. 45544881 (SEQ ID NO:496), Public GI ID no. 36789802 (SEQ ID NO:498), Public GI ID no. 92875402 (SEQ ID NO:508), Public GI ID no. 118406898 (SEQ ID NO:510), Public GI ID no. 107770485 (SEQ ID NO:511), Public GI ID no. 90657642 (SEQ ID NO:536), Ceres CLONE ID no. 1569555 (SEQ ID NO:1842) Public GI ID no. 66841018 (SEQ ID NO:458), Public GI ID no. 66841020 (SEQ ID NO:459), Public GI ID no. 108859343 (SEQ ID NO:460), Ceres CLONE ID no. 1937613 (SEQ ID NO:462), Ceres CLONE ID no. 1834027 (SEQ ID NO:464), Ceres ANNOT ID no. 1477832 (SEQ ID NO:468), Ceres ANNOT ID no. 1482536 (SEQ ID NO:470), Ceres ANNOT ID no. 1478227 (SEQ ID NO:472), Ceres CLONE ID no. 19906 (SEQ ID NO:478), Public GI ID no. 2895184 (SEQ ID NO:479), Public GI ID no. 2895188 (SEQ ID NO:480), Public GI ID no. 11037313 (SEQ ID NO:482), Public GI ID no. 22854908 (SEQ ID NO:483), Public GI ID no. 40787165 (SEQ ID NO:484), Public GI ID no. 116010475 (SEQ ID NO:486), Public GI ID no. 3341723 (SEQ ID NO:487), Public GI ID no. 4091806 (SEQ ID NO:489), Ceres CLONE ID no. 523203 (SEQ ID NO:491), Ceres CLONE ID no.

463157 (SEQ ID NO:493), Public GI ID no. 61611678 (SEQ ID NO:495), Public GI ID no. 45544887 (SEQ ID NO:497), Public GI ID no. 36789793 (SEQ ID NO:481), Ceres CLONE ID no. 907473 (SEQ ID NO:501), Ceres CLONE ID no. 1674443 (SEQ ID NO:503), Ceres CLONE ID no. 1559496 (SEQ ID NO:505), Ceres CLONE ID no. 530984 (SEQ ID NO:507), Public GI ID no. 61611682 (SEQ ID NO:509), Public GI ID no. 36789785 (SEQ ID NO:512), Ceres CLONE ID no. 702632 (SEQ ID NO:514), Public GI ID no. 61657299 (SEQ ID NO:515), Public GI ID no. 10946337 (SEQ ID NO:516), Ceres CLONE ID no. 1996408 (SEQ ID NO:518), Ceres CLONE ID no. 1725313 (SEQ ID NO:520), Public GI ID no. 78058606 (SEQ ID NO:521), Public GI ID no. 125538317 (SEQ ID NO:522), Public GI ID no. 125556324 (SEQ ID NO:523), Public GI ID no. 125548890 (SEQ ID NO:524), Public GI ID no. 93211100 (SEQ ID NO:525), Public GI ID no. 115444217 (SEQ ID NO:526), Public GI ID no. 115467558 (SEQ ID NO:527), Public GI ID no. 11094209 (SEQ ID NO:528), Public GI ID no. 125596830 (SEQ ID NO:529), Public GI ID no. 115469296 (SEQ ID NO:530), Public GI ID no. 115447239 (SEQ ID NO:531), Public GI ID no. 21655154 (SEQ ID NO:532), Public GI ID no. 21667485 (SEQ ID NO:533), Public GI ID no. 21667475 (SEQ ID NO:534), Public GI ID no. 21655158 (SEQ ID NO:535), and sequences identified as functional homologs of the sequences of FIG. 6, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 20 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 7. Such polypeptides include At1g70270 (SEQ ID NO:634), Public GI ID no. 98961985 (SEQ ID NO:637), Ceres CLONE ID no. 1916112 (SEQ ID NO:636), Public GI ID no. 9369405 (SEQ ID NO:638), Public GI ID no. 9369406 (SEQ ID NO:639), Ceres CLONE ID no. 1238706 (SEQ ID NO:641), and sequences identified as functional homologs of the sequences of FIG. 7, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 80 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 8. Such polypeptides include At4g25480 (SEQ ID NO:644), SEQ ID NO:645, Ceres CLONE ID no. 1849479 (SEQ ID NO:767), Public GI ID no. 89275008 (SEQ ID NO:796), Public GI ID no. 120400525 (SEQ ID NO:797), Public GI ID no. 98980426 (SEQ ID NO:804), Public GI ID no. 71983373 (SEQ ID NO:808), Public GI ID no. 41351817 (SEQ ID NO:809), Public GI ID no. 76446191 (SEQ ID NO:811), Public GI ID no. 5616086 (SEQ ID NO:813), Ceres CLONE ID no. 1052602 (SEQ ID NO:826), Public GI ID no. 72068957 (SEQ ID NO:830), Public GI ID no. 71534113 (SEQ ID NO:831), Public GI ID no. 37147896 (SEQ ID NO:832), Public GI ID no. 92918850 (SEQ ID NO:834), Public GI ID no. 40647095 (SEQ ID NO:835), Ceres ANNOT ID no. 1527711 (SEQ ID NO:837), Public GI ID no. 71041116 (SEQ ID NO:838), Public GI ID no. 12003384 (SEQ ID NO:839), Public GI ID no. 18535580 (SEQ ID NO:840), Ceres CLONE ID no. 991178 (SEQ ID NO:647), Ceres CLONE ID no. 1626038 (SEQ ID NO:649), Ceres CLONE ID no. 341615 (SEQ ID NO:651), Ceres CLONE ID no. 1832518 (SEQ ID NO:653), Ceres CLONE ID no. 1832588 (SEQ ID NO:655), Ceres CLONE ID no. 1936806 (SEQ ID NO:657), Ceres CLONE ID no. 973892 (SEQ ID NO:659), Ceres CLONE ID no. 565251 (SEQ ID NO:661), Ceres CLONE ID no. 681088 (SEQ ID NO:663), Ceres CLONE ID no. 707775 (SEQ ID NO:665), Ceres CLONE ID no. 453357 (SEQ ID NO:667), Ceres CLONE

ID no. 1916958 (SEQ ID NO:669), Ceres CLONE ID no. 1940632 (SEQ ID NO:671), Ceres CLONE ID no. 476784 (SEQ ID NO:673), Ceres CLONE ID no. 1869284 (SEQ ID NO:675), Public GI ID no. 125540662 (SEQ ID NO:676), Ceres CLONE ID no. 1648272 (SEQ ID NO:678), Ceres CLONE ID no. 1987804 (SEQ ID NO:680), Ceres CLONE ID no. 1675695 (SEQ ID NO:682), Ceres CLONE ID no. 1169111 (SEQ ID NO:684), Ceres CLONE ID no. 572121 (SEQ ID NO:686), Ceres CLONE ID no. 1674836 (SEQ ID NO:688), Ceres ANNOT ID no. 1486207 (SEQ ID NO:690), Ceres CLONE ID no. 2023610 (SEQ ID NO:692), Ceres ANNOT ID no. 1496976 (SEQ ID NO:694), Public GI ID no. 116310031 (SEQ ID NO:695), Ceres CLONE ID no. 1626363 (SEQ ID NO:697), Ceres ANNOT ID no. 1483747 (SEQ ID NO:699), Ceres ANNOT ID no. 1471330 (SEQ ID NO:701), Ceres CLONE ID no. 101144964 (SEQ ID NO:702), Ceres ANNOT ID no. 1439439 (SEQ ID NO:704), Ceres CLONE ID no. 1446565 (SEQ ID NO:706), Ceres CLONE ID no. 1951962 (SEQ ID NO:708), Ceres CLONE ID no. 100960656 (SEQ ID NO:709), Ceres CLONE ID no. 285154 (SEQ ID NO:711), Public GI ID no. 61968916 (SEQ ID NO:712), Public GI ID no. 118026854 (SEQ ID NO:713), Public GI ID no. 63098612 (SEQ ID NO:714), Ceres ANNOT ID no. 1522310 (SEQ ID NO:716), Ceres CLONE ID no. 1854375 (SEQ ID NO:718), Ceres CLONE ID no. 709819 (SEQ ID NO:720), Public GI ID no. 115447695 (SEQ ID NO:721), Ceres CLONE ID no. 1726356 (SEQ ID NO:723), Ceres CLONE ID no. 1762419 (SEQ ID NO:725), Public GI ID no. 63098606 (SEQ ID NO:726), Ceres CLONE ID no. 1766572 (SEQ ID NO:728), Ceres CLONE ID no. 281871 (SEQ ID NO:730), Ceres CLONE ID no. 1560970 (SEQ ID NO:732), Ceres CLONE ID no. 1760747 (SEQ ID NO:734), Ceres ANNOT ID no. 1438772 (SEQ ID NO:736), Ceres ANNOT ID no. 1447378 (SEQ ID NO:738), Ceres ANNOT ID no. 1453360 (SEQ ID NO:740), Public GI ID no. 33637698 (SEQ ID NO:741), Public GI ID no. 118026860 (SEQ ID NO:742), Public GI ID no. 60116232 (SEQ ID NO:743), Public GI ID no. 115477639 (SEQ ID NO:744), Public GI ID no. 126567023 (SEQ ID NO:745), Ceres CLONE ID no. 988971 (SEQ ID NO:747), Ceres CLONE ID no. 1464521 (SEQ ID NO:749), Public GI ID no. 63098610 (SEQ ID NO:750), Public GI ID no. 126566972 (SEQ ID NO:751), Ceres CLONE ID no. 1556129 (SEQ ID NO:753), Ceres CLONE ID no. 1761385 (SEQ ID NO:755), Ceres ANNOT ID no. 1488325 (SEQ ID NO:757), Ceres ANNOT ID no. 1460483 (SEQ ID NO:759), Ceres CLONE ID no. 1837825 (SEQ ID NO:761), Public GI ID no. 27228310 (SEQ ID NO:762), Public GI ID no. 117653881 (SEQ ID NO:763), Public GI ID no. 115480233 (SEQ ID NO:764), Public GI ID no. 37694048 (SEQ ID NO:765), Ceres CLONE ID no. 1934653 (SEQ ID NO:769), Ceres CLONE ID no. 1608106 (SEQ ID NO:771), Ceres CLONE ID no. 1604576 (SEQ ID NO:773), Public GI ID no. 55824656 (SEQ ID NO:774), Ceres CLONE ID no. 1620272 (SEQ ID NO:776), Ceres CLONE ID no. 1853170 (SEQ ID NO:778), Public GI ID no. 79013962 (SEQ ID NO:779), Public GI ID no. 98975385 (SEQ ID NO:780), Ceres ANNOT ID no. 1438775 (SEQ ID NO:782), Public GI ID no. 23495460 (SEQ ID NO:783), Public GI ID no. 98975377 (SEQ ID NO:784), Ceres ANNOT ID no. 1438776 (SEQ ID NO:786), Ceres CLONE ID no. 1853601 (SEQ ID NO:788), Ceres CLONE ID no. 1609048 (SEQ ID NO:790), Ceres CLONE ID no. 322305 (SEQ ID NO:792), Ceres CLONE ID no. 1823713 (SEQ ID NO:794), Public GI ID no. 3660548 (SEQ ID NO:795), Public GI ID no. 56154991 (SEQ ID NO:798), Public GI ID no. 2980802 (SEQ ID NO:799), Public GI ID no. 7269398 (SEQ ID NO:800)

NO:800), Public GI ID no. 18416557 (SEQ ID NO:801), Public GI ID no. 56154992 (SEQ ID NO:802), Public GI ID no. 4091984 (SEQ ID NO:803), Public GI ID no. 1899058 (SEQ ID NO:805), Public GI ID no. 56154990 (SEQ ID NO:806), Public GI ID no. 18416562 (SEQ ID NO:807), Public GI ID no. 38683266 (SEQ ID NO:810), Public GI ID no. 39983638 (SEQ ID NO:812), Public GI ID no. 38426954 (SEQ ID NO:814), Public GI ID no. 38426948 (SEQ ID NO:815), Public GI ID no. 38146944 (SEQ ID NO:816), Public GI ID no. 38426952 (SEQ ID NO:817), Public GI ID no. 20303011 (SEQ ID NO:818), Public GI ID no. 66269982 (SEQ ID NO:819), Public GI ID no. 89212816 (SEQ ID NO:820), Public GI ID no. 20303015 (SEQ ID NO:821), Public GI ID no. 38426950 (SEQ ID NO:822), Public GI ID no. 15242244 (SEQ ID NO:823), Public GI ID no. 116831599 (SEQ ID NO:824), Public GI ID no. 66269671 (SEQ ID NO:827), Ceres ANNOT ID no. 1468919 (SEQ ID NO:829), Public GI ID no. 57903606 (SEQ ID NO:833), Public GI ID no. 45826358 (SEQ ID NO:841), Ceres ANNOT ID no. 6085912 (SEQ ID NO:843), Ceres ANNOT ID no. 6026171 (SEQ ID NO:845), Ceres ANNOT ID no. 6031706 (SEQ ID NO:847), Public GI ID no. 115353971 (SEQ ID NO:1843), and sequences identified as functional homologs of the sequences of FIG. 8, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 170 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 9. Such polypeptides include A2g33780 (SEQ ID NO:850), Ceres CLONE ID no. 1833093 (SEQ ID NO:853), Ceres ANNOT ID no. 1502190 (SEQ ID NO:857), Ceres CLONE ID no. 565641 (SEQ ID NO:876), Public GI ID no. 87240507 (SEQ ID NO:877), Ceres CLONE ID no. 1325382 (SEQ ID NO:881), Ceres CLONE ID no. 1558265 (SEQ ID NO:885), Ceres CLONE ID no. 1823669 (SEQ ID NO:895), Public GI ID no. 115464921 (SEQ ID NO:898), Ceres CLONE ID no. 1000040598 (SEQ ID NO:851), Ceres CLONE ID no. 1847967 (SEQ ID NO:855), Ceres ANNOT ID no. 1449186 (SEQ ID NO:859), Ceres ANNOT ID no. 1466723 (SEQ ID NO:861), Public GI ID no. 21805688 (SEQ ID NO:862), Public GI ID no. 9795609 (SEQ ID NO:863), Public GI ID no. 13877535 (SEQ ID NO:864), Public GI ID no. 15232547 (SEQ ID NO:865), Public GI ID no. 15238851 (SEQ ID NO:866), Ceres CLONE ID no. 123863 (SEQ ID NO:868), Ceres CLONE ID no. 652496 (SEQ ID NO:870), Ceres CLONE ID no. 1656707 (SEQ ID NO:872), Ceres CLONE ID no. 1660346 (SEQ ID NO:874), Ceres CLONE ID no. 678878 (SEQ ID NO:879), Ceres CLONE ID no. 340102 (SEQ ID NO:883), Ceres CLONE ID no. 330491 (SEQ ID NO:887), Ceres CLONE ID no. 992304 (SEQ ID NO:889), Ceres CLONE ID no. 1509925 (SEQ ID NO:891), Ceres CLONE ID no. 1543852 (SEQ ID NO:893), Ceres CLONE ID no. 1785736 (SEQ ID NO:897), Ceres ANNOT ID no. 6079909 (SEQ ID NO:900), Ceres ANNOT ID no. 6040353 (SEQ ID NO:902), Ceres ANNOT ID no. 6100173 (SEQ ID NO:904), and sequences identified as functional homologs of the sequences of FIG. 9, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 80 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 10. Such polypeptides include At4g17810 (SEQ ID NO:907), Ceres CLONE ID no. 1940797 (SEQ ID NO:909), Ceres ANNOT ID no. 1538900 (SEQ ID NO:911), Ceres CLONE ID no. 1126868 (SEQ ID NO:922), Public GI ID no. 89257684 (SEQ ID NO:923), Public GI ID no. 124360460 (SEQ ID NO:929), Public GI ID no. 62865694

(SEQ ID NO:931), Public GI ID no. 62865692 (SEQ ID NO:932), Ceres CLONE ID no. 260368 (SEQ ID NO:936), Ceres CLONE ID no. 1873510 (SEQ ID NO:947), Public GI ID no. 125541662 (SEQ ID NO:948), Public GI ID no. 48716268 (SEQ ID NO:950), Ceres ANNOT ID no. 1529131 (SEQ ID NO:913), Ceres ANNOT ID no. 1454060 (SEQ ID NO:915), Ceres ANNOT ID no. 1442787 (SEQ ID NO:917), Ceres ANNOT ID no. 1452648 (SEQ ID NO:919), Public GI ID no. 2245140 (SEQ ID NO:920), Public GI ID no. 89274212 (SEQ ID NO:924), Ceres CLONE ID no. 1104523 (SEQ ID NO:926), Ceres CLONE ID no. 654265 (SEQ ID NO:928), Public GI ID no. 42627704 (SEQ ID NO:930), Ceres CLONE ID no. 887222 (SEQ ID NO:934), Public GI ID no. 62865690 (SEQ ID NO:937), Public GI ID no. 64175600 (SEQ ID NO:938), Public GI ID no. 64175634 (SEQ ID NO:939), Public GI ID no. 64175606 (SEQ ID NO:940), Public GI ID no. 64175648 (SEQ ID NO:941), Ceres CLONE ID no. 312184 (SEQ ID NO:943), Ceres CLONE ID no. 380740 (SEQ ID NO:945), Public GI ID no. 125531536 (SEQ ID NO:949), Public GI ID no. 62865696 (SEQ ID NO:1844), and sequences identified as functional homologs of the sequences of FIG. 10, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 60 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 11. Such polypeptides include At1g13360 (SEQ ID NO:951), Ceres CLONE ID no. 1798705 (SEQ ID NO:955), Ceres ANNOT ID no. 1458907 (SEQ ID NO:963), Ceres CLONE ID no. 1090409 (SEQ ID NO:971), Ceres CLONE ID no. 479817 (SEQ ID NO:977), Ceres CLONE ID no. 1041793 (SEQ ID NO:979), Ceres CLONE ID no. 684633 (SEQ ID NO:985), Ceres CLONE ID no. 371815 (SEQ ID NO:991), Ceres CLONE ID no. 1686460 (SEQ ID NO:993), Ceres CLONE ID no. 1448595 (SEQ ID NO:995), Ceres CLONE ID no. 1734477 (SEQ ID NO:999), Ceres CLONE ID no. 1605693 (SEQ ID NO:1005), Ceres CLONE ID no. 1757400 (SEQ ID NO:1009), Public GI ID no. 115434334 (SEQ ID NO:1015), Ceres CLONE ID no. 1793754 (SEQ ID NO:957), Ceres CLONE ID no. 1938045 (SEQ ID NO:959), Ceres CLONE ID no. 1850004 (SEQ ID NO:961), Ceres ANNOT ID no. 1489548 (SEQ ID NO:965), Public GI ID no. 22329538 (SEQ ID NO:966), Public GI ID no. 18404714 (SEQ ID NO:967), Ceres CLONE ID no. 1110032 (SEQ ID NO:969), Ceres CLONE ID no. 1095353 (SEQ ID NO:973), Ceres CLONE ID no. 872121 (SEQ ID NO:975), Ceres CLONE ID no. 562208 (SEQ ID NO:981), Ceres CLONE ID no. 1042364 (SEQ ID NO:983), Ceres CLONE ID no. 1031873 (SEQ ID NO:987), Ceres CLONE ID no. 1377698 (SEQ ID NO:989), Ceres CLONE ID no. 1742945 (SEQ ID NO:997), Ceres CLONE ID no. 1742053 (SEQ ID NO:1001), Ceres CLONE ID no. 1728365 (SEQ ID NO:1003), Ceres CLONE ID no. 1609807 (SEQ ID NO:1007), Ceres CLONE ID no. 1778566 (SEQ ID NO:1011), Ceres CLONE ID no. 2020580 (SEQ ID NO:1013), Public GI ID no. 125524285 (SEQ ID NO:1014), Public GI ID no. 125568898 (SEQ ID NO:1016), Ceres ANNOT ID no. 6055303 (SEQ ID NO:1018), and sequences identified as functional homologs of the sequences of FIG. 11, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 140 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 12. Such polypeptides include At1g75860 (SEQ ID NO:1024), Ceres ANNOT ID no. 1452905 (SEQ ID NO:1029), Ceres CLONE ID no. 956176 (SEQ ID NO:1039), Public GI ID no. 92870366 (SEQ ID NO:1040),

Ceres CLONE ID no. 294166 (SEQ ID NO:1042), Public GI ID no. 125543067 (SEQ ID NO:1043), SEQ ID NO:1025, Ceres ANNOT ID no. 1442522 (SEQ ID NO:1027), Public GI ID no. 8778818 (SEQ ID NO:1030), Ceres CLONE ID no. 108095 (SEQ ID NO:1032), Public GI ID no. 18394821 (SEQ ID NO:1033), Ceres CLONE ID no. 6332 (SEQ ID NO:1035), Ceres CLONE ID no. 1069047 (SEQ ID NO:1037), Public GI ID no. 115480956 (SEQ ID NO:1044), and sequences identified as functional homologs of the sequences of FIG. 12, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 80 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 13. Such polypeptides include At4g19700 (SEQ ID NO:1047), Ceres CLONE ID no. 1837694 (SEQ ID NO:1053), Ceres ANNOT ID no. 1483367 (SEQ ID NO:1057), Ceres CLONE ID no. 1077781 (SEQ ID NO:1083), Ceres CLONE ID no. 471026 (SEQ ID NO:1085), Public GI ID no. 92888885 (SEQ ID NO:1099), Public GI ID no. 45544873 (SEQ ID NO:1100), Public GI ID no. 45758663 (SEQ ID NO:1101), Ceres CLONE ID no. 772927 (SEQ ID NO:1105), Ceres CLONE ID no. 895080 (SEQ ID NO:1111), Ceres CLONE ID no. 1806128 (SEQ ID NO:1131), Public GI ID no. 115458192 (SEQ ID NO:1134), Public GI ID no. 82470795 (SEQ ID NO:1139), Ceres CLONE ID no. 1837746 (SEQ ID NO:1049), Ceres CLONE ID no. 1834764 (SEQ ID NO:1051), Ceres CLONE ID no. 1853547 (SEQ ID NO:1055), Ceres ANNOT ID no. 1474088 (SEQ ID NO:1059), Ceres ANNOT ID no. 1536919 (SEQ ID NO:1061), Ceres ANNOT ID no. 1467033 (SEQ ID NO:1063), Ceres ANNOT ID no. 1485401 (SEQ ID NO:1065), Ceres ANNOT ID no. 1486505 (SEQ ID NO:1067), Public GI ID no. 17065054 (SEQ ID NO:1068), Public GI ID no. 30694690 (SEQ ID NO:1069), Ceres CLONE ID no. 12997 (SEQ ID NO:1071), Public GI ID no. 30694694 (SEQ ID NO:1072), Public GI ID no. 42572167 (SEQ ID NO:1073), Public GI ID no. 110739742 (SEQ ID NO:1074), Public GI ID no. 18412263 (SEQ ID NO:1075), Ceres CLONE ID no. 36412 (SEQ ID NO:1077), Public GI ID no. 18399792 (SEQ ID NO:1078), Ceres CLONE ID no. 924 (SEQ ID NO:1080), Public GI ID no. 15238000 (SEQ ID NO:1081), Ceres CLONE ID no. 1626330 (SEQ ID NO:1087), Ceres CLONE ID no. 1650419 (SEQ ID NO:1089), Ceres CLONE ID no. 1641329 (SEQ ID NO:1091), Ceres CLONE ID no. 1620406 (SEQ ID NO:1093), Ceres CLONE ID no. 546832 (SEQ ID NO:1095), Ceres CLONE ID no. 1243138 (SEQ ID NO:1097), Public GI ID no. 92887260 (SEQ ID NO:1098), Ceres CLONE ID no. 885628 (SEQ ID NO:1103), Ceres CLONE ID no. 1376391 (SEQ ID NO:1107), Ceres CLONE ID no. 465893 (SEQ ID NO:1109), Ceres CLONE ID no. 218243 (SEQ ID NO:1113), Ceres CLONE ID no. 1558456 (SEQ ID NO:1115), Ceres CLONE ID no. 343008 (SEQ ID NO:1117), Ceres CLONE ID no. 218463 (SEQ ID NO:1119), Ceres CLONE ID no. 1565409 (SEQ ID NO:1121), Ceres CLONE ID no. 1060968 (SEQ ID NO:1123), Ceres CLONE ID no. 236111 (SEQ ID NO:1125), Ceres CLONE ID no. 285598 (SEQ ID NO:1127), Ceres CLONE ID no. 225881 (SEQ ID NO:1129), Ceres CLONE ID no. 1811383 (SEQ ID NO:1133), Public GI ID no. 49388268 (SEQ ID NO:1135), Public GI ID no. 125590268 (SEQ ID NO:1136), Public GI ID no. 115444009 (SEQ ID NO:1137), Public GI ID no. 115447993 (SEQ ID NO:1138), Ceres ANNOT ID no. 6033842 (SEQ ID NO:1141), Ceres ANNOT ID no. 6029952 (SEQ ID NO:1143), Ceres ANNOT ID no.

6035837 (SEQ ID NO:1145), Ceres ANNOT ID no. 6035830 (SEQ ID NO:1147), Ceres ANNOT ID no. 6029981 (SEQ ID NO:1149), and sequences identified as functional homologs of the sequences of FIG. 13, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 80 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 14. Such polypeptides include At1g58100 (SEQ ID NO:1151), Ceres CLONE ID no. 1851526 (SEQ ID NO:1155), Ceres ANNOT ID no. 1486769 (SEQ ID NO:1172), Public GI ID no. 83032232 (SEQ ID NO:1209), Ceres CLONE ID no. 1620420 (SEQ ID NO:1211), Public GI ID no. 92892428 (SEQ ID NO:1215), Ceres CLONE ID no. 884742 (SEQ ID NO:1223), Ceres CLONE ID no. 1821559 (SEQ ID NO:1246), Public GI ID no. 51535021 (SEQ ID NO:1258), Public GI ID no. 113205304 (SEQ ID NO:1263), Public GI ID no. 37719051 (SEQ ID NO:1264), Ceres CLONE ID no. 1918070 (SEQ ID NO:1153), Ceres CLONE ID no. 1948426 (SEQ ID NO:1157), Ceres CLONE ID no. 1937875 (SEQ ID NO:1159), Ceres CLONE ID no. 100056542 (SEQ ID NO:1160), Public GI ID no. 5731257 (SEQ ID NO:1161), Ceres CLONE ID no. 100058043 (SEQ ID NO:1162), Ceres CLONE ID no. 1838288 (SEQ ID NO:1164), Ceres CLONE ID no. 1793597 (SEQ ID NO:1166), Ceres ANNOT ID no. 1543031 (SEQ ID NO:1168), Ceres ANNOT ID no. 1489643 (SEQ ID NO:1170), Ceres ANNOT ID no. 1479721 (SEQ ID NO:1174), Ceres ANNOT ID no. 1449170 (SEQ ID NO:1176), Ceres ANNOT ID no. 1493696 (SEQ ID NO:1178), Ceres ANNOT ID no. 1543534 (SEQ ID NO:1180), Ceres ANNOT ID no. 1440815 (SEQ ID NO:1182), Ceres ANNOT ID no. 1490137 (SEQ ID NO:1184), Ceres ANNOT ID no. 1451054 (SEQ ID NO:1186), Ceres ANNOT ID no. 1456669 (SEQ ID NO:1188), Ceres ANNOT ID no. 1509865 (SEQ ID NO:1190), Ceres ANNOT ID no. 1447910 (SEQ ID NO:1192), Ceres ANNOT ID no. 1471068 (SEQ ID NO:1194), Ceres ANNOT ID no. 1504118 (SEQ ID NO:1196), Ceres CLONE ID no. 1343621 (SEQ ID NO:1198), Public GI ID no. 15218305 (SEQ ID NO:1199), Public GI ID no. 15219640 (SEQ ID NO:1200), Public GI ID no. 18409345 (SEQ ID NO:1201), Public GI ID no. 6522545 (SEQ ID NO:1202), Public GI ID no. 15237274 (SEQ ID NO:1203), Public GI ID no. 26452377 (SEQ ID NO:1204), Ceres CLONE ID no. 33629 (SEQ ID NO:1206), Ceres CLONE ID no. 1064407 (SEQ ID NO:1208), Ceres CLONE ID no. 1656310 (SEQ ID NO:1213), Public GI ID no. 92885257 (SEQ ID NO:1214), Public GI ID no. 92868571 (SEQ ID NO:1216), Public GI ID no. 53689778 (SEQ ID NO:1217), Ceres CLONE ID no. 835598 (SEQ ID NO:1219), Ceres CLONE ID no. 575649 (SEQ ID NO:1221), Ceres CLONE ID no. 376567 (SEQ ID NO:1225), Ceres CLONE ID no. 1284191 (SEQ ID NO:1227), Ceres CLONE ID no. 367175 (SEQ ID NO:1229), Ceres CLONE ID no. 100748296 (SEQ ID NO:1230), Ceres CLONE ID no. 1597176 (SEQ ID NO:1232), Ceres CLONE ID no. 375636 (SEQ ID NO:1234), Ceres CLONE ID no. 288123 (SEQ ID NO:1236), Ceres CLONE ID no. 303582 (SEQ ID NO:1238), Ceres CLONE ID no. 1604759 (SEQ ID NO:1240), Ceres CLONE ID no. 1955192 (SEQ ID NO:1242), Ceres CLONE ID no. 2008687 (SEQ ID NO:1244), Ceres CLONE ID no. 1995843 (SEQ ID NO:1248), Ceres CLONE ID no. 2008591 (SEQ ID NO:1250), Ceres CLONE ID no. 2046826 (SEQ ID NO:1252), Ceres CLONE ID no. 1985573 (SEQ ID NO:1255).

NO:1254), Public GI ID no. 125541129 (SEQ ID NO:1255), Public GI ID no. 125528922 (SEQ ID NO:1256), Public GI ID no. 115487590 (SEQ ID NO:1257), Public GI ID no. 115448671 (SEQ ID NO:1259), Public GI ID no. 125596564 (SEQ ID NO:1260), Public GI ID no. 125573161 (SEQ ID NO:1261), Public GI ID no. 48716463 (SEQ ID NO:1262), Ceres ANNOT ID no. 6054246 (SEQ ID NO:1266), Ceres ANNOT ID no. 6086570 (SEQ ID NO:1268), Ceres ANNOT ID no. 6024957 (SEQ ID NO:1270), Ceres ANNOT ID no. 6016867 (SEQ ID NO:1272), Ceres ANNOT ID no. 6091369 (SEQ ID NO:1274), and sequences identified as functional homologs of the sequences of FIG. 14, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 180 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 15. Such polypeptides include At5g46170 (SEQ ID NO:1277), Ceres CLONE ID no. 1926352 (SEQ ID NO:1279), Ceres ANNOT ID no. 1448905 (SEQ ID NO:1285), Public GI ID no. 15236865 (SEQ ID NO:1294), Ceres CLONE ID no. 934771 (SEQ ID NO:1301), Ceres CLONE ID no. 338386 (SEQ ID NO:1303), Ceres CLONE ID no. 1780691 (SEQ ID NO:1317), Public GI ID no. 115464819 (SEQ ID NO:1326), Ceres CLONE ID no. 1848576 (SEQ ID NO:1281), Ceres CLONE ID no. 1981528 (SEQ ID NO:1283), Ceres ANNOT ID no. 1465978 (SEQ ID NO:1287), Ceres ANNOT ID no. 1504997 (SEQ ID NO:1289), Ceres ANNOT ID no. 1451909 (SEQ ID NO:1291), Ceres ANNOT ID no. 1461635 (SEQ ID NO:1293), Public GI ID no. 18397400 (SEQ ID NO:1295), Ceres CLONE ID no. 16226 (SEQ ID NO:1297), Public GI ID no. 18411823 (SEQ ID NO:1298), Public GI ID no. 15219845 (SEQ ID NO:1299), Ceres CLONE ID no. 1276710 (SEQ ID NO:1305), Ceres CLONE ID no. 1479310 (SEQ ID NO:1307), Ceres CLONE ID no. 376230 (SEQ ID NO:1309), Ceres CLONE ID no. 1290713 (SEQ ID NO:1311), Ceres CLONE ID no. 321681 (SEQ ID NO:1313), Ceres CLONE ID no. 1869072 (SEQ ID NO:1315), Ceres CLONE ID no. 1818502 (SEQ ID NO:1319), Ceres CLONE ID no. 1750477 (SEQ ID NO:1321), Public GI ID no. 125552947 (SEQ ID NO:1322), Public GI ID no. 125527862 (SEQ ID NO:1323), Public GI ID no. 125543660 (SEQ ID NO:1324), Public GI ID no. 125528123 (SEQ ID NO:1325), Public GI ID no. 115440195 (SEQ ID NO:1327), Public GI ID no. 115452717 (SEQ ID NO:1328), Public GI ID no. 115440629 (SEQ ID NO:1329), Public GI ID no. 115464599 (SEQ ID NO:1330), Public GI ID no. 20161462 (SEQ ID NO:1331), Public GI ID no. 125586076 (SEQ ID NO:1332), Ceres CLONE ID no. 1823216 (SEQ ID NO:1334), Ceres ANNOT ID no. 6040230 (SEQ ID NO:1336), Ceres ANNOT ID no. 6015489 (SEQ ID NO:1338), Ceres ANNOT ID no. 6042890 (SEQ ID NO:1340), Ceres ANNOT ID no. 6040033 (SEQ ID NO:1342), Ceres ANNOT ID no. 6018414 (SEQ ID NO:1344), and sequences identified as functional homologs of the sequences of FIG. 15, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 60 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 16. Such polypeptides include At4g32280 (SEQ ID NO:1347), Ceres CLONE ID no. 285028 (SEQ ID NO:1419), Ceres CLONE ID no. 100969565 (SEQ ID NO:1422), Public GI ID no. 1352057 (SEQ ID NO:1427), Ceres ANNOT ID no. 1453784 (SEQ ID NO:1429), Public

GI ID no. 452777 (SEQ ID NO:1430), Public GI ID no. 92873297 (SEQ ID NO:1431), Ceres ANNOT ID no. 1452612 (SEQ ID NO:1349), Ceres CLONE ID no. 520455 (SEQ ID NO:1351), Public GI ID no. 75271810 (SEQ ID NO:1352), Public GI ID no. 115489446 (SEQ ID NO:1353), Ceres CLONE ID no. 499878 (SEQ ID NO:1355), Ceres ANNOT ID no. 1491840 (SEQ ID NO:1357), Public GI ID no. 125587204 (SEQ ID NO:1358), Ceres CLONE ID no. 320997 (SEQ ID NO:1360), Ceres ANNOT ID no. 1455585 (SEQ ID NO:1362), Ceres ANNOT ID no. 1499460 (SEQ ID NO:1364), Ceres CLONE ID no. 334484 (SEQ ID NO:1366), Ceres CLONE ID no. 100819481 (SEQ ID NO:1367), Public GI ID no. 115462401 (SEQ ID NO:1368), Ceres CLONE ID no. 1448136 (SEQ ID NO:1370), Ceres CLONE ID no. 277751 (SEQ ID NO:1372), Ceres ANNOT ID no. 1491839 (SEQ ID NO:1374), Ceres CLONE ID no. 100913241 (SEQ ID NO:1375), Ceres CLONE ID no. 1053224 (SEQ ID NO:1377), Ceres CLONE ID no. 425766 (SEQ ID NO:1379), Ceres CLONE ID no. 485480 (SEQ ID NO:1381), Ceres CLONE ID no. 474845 (SEQ ID NO:1383), Ceres CLONE ID no. 354561 (SEQ ID NO:1385), Ceres CLONE ID no. 540858 (SEQ ID NO:1387), Ceres CLONE ID no. 2032994 (SEQ ID NO:1389), Ceres CLONE ID no. 2015315 (SEQ ID NO:1391), Ceres CLONE ID no. 2016149 (SEQ ID NO:1393), Ceres CLONE ID no. 1922843 (SEQ ID NO:1395), Ceres CLONE ID no. 2000263 (SEQ ID NO:1397), Ceres CLONE ID no. 1943510 (SEQ ID NO:1399), Ceres CLONE ID no. 1835498 (SEQ ID NO:1401), Ceres CLONE ID no. 101116694 (SEQ ID NO:1402), Ceres CLONE ID no. 1930596 (SEQ ID NO:1404), Ceres CLONE ID no. 846036 (SEQ ID NO:1406), Ceres CLONE ID no. 941614 (SEQ ID NO:1408), Ceres CLONE ID no. 238788 (SEQ ID NO:1410), Public GI ID no. 125554220 (SEQ ID NO:1411), Public GI ID no. 125559895 (SEQ ID NO:1412), Public GI ID no. 75252070 (SEQ ID NO:1413), Public GI ID no. 115466632 (SEQ ID NO:1414), Public GI ID no. 125541525 (SEQ ID NO:1415), Ceres CLONE ID no. 1805110 (SEQ ID NO:1417), Ceres CLONE ID no. 1725309 (SEQ ID NO:1421), Ceres CLONE ID no. 100861679 (SEQ ID NO:1423), Public GI ID no. 75226278 (SEQ ID NO:1424), Public GI ID no. 125525030 (SEQ ID NO:1425), Public GI ID no. 115435474 (SEQ ID NO:1426), Ceres CLONE ID no. 1728516 (SEQ ID NO:1433), Public GI ID no. 115467910 (SEQ ID NO:1434), Public GI ID no. 15239950 (SEQ ID NO:1435), Public GI ID no. 4887012 (SEQ ID NO:1436), Ceres ANNOT ID no. 1478544 (SEQ ID NO:1438), Public GI ID no. 90811713 (SEQ ID NO:1439), Public GI ID no. 25989504 (SEQ ID NO:1440), Ceres CLONE ID no. 1113354 (SEQ ID NO:1442), Ceres CLONE ID no. 1113630 (SEQ ID NO:1444), Ceres ANNOT ID no. 6072030 (SEQ ID NO:1446), Ceres ANNOT ID no. 6025654 (SEQ ID NO:1448), Ceres ANNOT ID no. 6091150 (SEQ ID NO:1450), Ceres ANNOT ID no. 6100390 (SEQ ID NO:1452), and sequences identified as functional homologs of the sequences of FIG. 16, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 270 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 17. Such polypeptides include At3g02830 (SEQ ID NO:1457), Ceres CLONE ID no. 1924904 (SEQ ID NO:1460), Ceres ANNOT ID no. 1543346 (SEQ ID NO:1462), Public GI ID no. 18396338 (SEQ ID NO:1467), Ceres CLONE ID no. 833872 (SEQ ID NO:1471), Ceres CLONE ID no. 1579587 (SEQ ID NO:1475), Ceres CLONE

ID no. 1786411 (SEQ ID NO:1477), Public GI ID no. 108864370 (SEQ ID NO:1480), SEQ ID NO:1458, Ceres ANNOT ID no. 1532932 (SEQ ID NO:1464), Ceres ANNOT ID no. 1489955 (SEQ ID NO:1466), Public GI ID no. 4928917 (SEQ ID NO:1468), Public GI ID no. 6728979 (SEQ ID NO:1469), Ceres CLONE ID no. 285780 (SEQ ID NO:1473), Public GI ID no. 125528863 (SEQ ID NO:1478), Public GI ID no. 125536365 (SEQ ID NO:1479), Public GI ID no. 108864369 (SEQ ID NO:1481), Public GI ID no. 115488274 (SEQ ID NO:1482), Public GI ID no. 125577099 (SEQ ID NO:1483), Public GI ID no. 125573110 (SEQ ID NO:1484), Public GI ID no. 124359159 (SEQ ID NO:1485), Public GI ID no. 62901479 (SEQ ID NO:1486), Ceres ANNOT ID no. 6016783 (SEQ ID NO:1488), Ceres ANNOT ID no. 6020759 (SEQ ID NO:1490), Ceres ANNOT ID no. 6028676 (SEQ ID NO:1492), Ceres ANNOT ID no. 6028677 (SEQ ID NO:1494), and sequences identified as functional homologs of the sequences of FIG. 17, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 70 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 18. Such polypeptides include At4g08920 (SEQ ID NO:1497), Ceres ANNOT ID no. 1443463 (SEQ ID NO:1499), Public GI ID no. 13605525 (SEQ ID NO:1502), Public GI ID no. 94965681 (SEQ ID NO:1506), Public GI ID no. 28201254 (SEQ ID NO:1512), Ceres ANNOT ID no. 1504954 (SEQ ID NO:1501), Public GI ID no. 2499553 (SEQ ID NO:1503), Public GI ID no. 738308 (SEQ ID NO:1504), Public GI ID no. 4325368 (SEQ ID NO:1505), Ceres CLONE ID no. 919923 (SEQ ID NO:1508), Ceres CLONE ID no. 1659764 (SEQ ID NO:1510), Public GI ID no. 125539984 (SEQ ID NO:1511), Public GI ID no. 21740729 (SEQ ID NO:1513), Public GI ID no. 115458700 (SEQ ID NO:1514), Public GI ID no. 125590574 (SEQ ID NO:1515), Public GI ID no. 16444957 (SEQ ID NO:1516), Ceres CLONE ID no. 1784494 (SEQ ID NO:1518), Public GI ID no. 77963980 (SEQ ID NO:1519), Public GI ID no. 110.124361190 (SEQ ID NO:1520), Public GI ID no. 37725007 (SEQ ID NO:1521), Public GI ID no. 45935258 (SEQ ID NO:1522), Public GI ID no. 1559008 (SEQ ID NO:1523), Public GI ID no. 38037416 (SEQ ID NO:1524), Public GI ID no. 77963974 (SEQ ID NO:1525), Ceres ANNOT ID no. 6112581 (SEQ ID NO:1527), Public GI ID no. 56553448 (SEQ ID NO:1528), Public GI ID no. 23506659 (SEQ ID NO:1529), Ceres ANNOT ID no. 6118060 (SEQ ID NO:1531), Public GI ID no. 46446306 (SEQ ID NO:1532), Public GI ID no. 114321405 (SEQ ID NO:1533), Public GI ID no. 83858274 (SEQ ID NO:1534), Public GI ID no. 154250969 (SEQ ID NO:1535), Public GI ID no. 83594235 (SEQ ID NO:1536), and sequences identified as functional homologs of the sequences of FIG. 18, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 130 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 19. Such polypeptides include At4g11660 (SEQ ID NO:1587), Ceres CLONE ID no. 1839577 (SEQ ID NO:1589), Ceres ANNOT ID no. 1491567 (SEQ ID NO:1591), Ceres CLONE ID no. 574505 (SEQ ID NO:1596), Public GI ID no. 56117815 (SEQ ID NO:1597), Public GI ID no. 92874021 (SEQ ID NO:1603), Public GI ID no. 123684 (SEQ ID NO:1605), Public GI ID no. 5821136 (SEQ ID NO:1606), Ceres CLONE ID no. 283366 (SEQ ID NO:1609), Public GI ID no. 16118447 (SEQ ID NO:1612), Public GI ID no. 125562434 (SEQ ID NO:1614),

Ceres ANNOT ID no. 1438739 (SEQ ID NO:1593), Public GI ID no. 89274218 (SEQ ID NO:1594), Public GI ID no. 115521211 (SEQ ID NO:1598), Public GI ID no. 115521213 (SEQ ID NO:1599), Public GI ID no. 115521217 (SEQ ID NO:1600), Public GI ID no. 115521209 (SEQ ID NO:1601), Public GI ID no. 115521215 (SEQ ID NO:1602), Public GI ID no. 11386827 (SEQ ID NO:1604), Public GI ID no. 25052685 (SEQ ID NO:1607), Ceres CLONE ID no. 1440437 (SEQ ID NO:1611), Public GI ID no. 125564440 (SEQ ID NO:1613), Public GI ID no. 116309817 (SEQ ID NO:1615), Public GI ID no. 125549382 (SEQ ID NO:1616), Public GI ID no. 52077317 (SEQ ID NO:1617), Public GI ID no. 115477655 (SEQ ID NO:1618), Public GI ID no. 42408097 (SEQ ID NO:1619), Public GI ID no. 115459982 (SEQ ID NO:1620), Public GI ID no. 33591096 (SEQ ID NO:1621), Ceres CLONE ID no. 484753 (SEQ ID NO:1623), Ceres ANNOT ID no. 6035291 (SEQ ID NO:1625), and sequences identified as functional homologs of the sequences of FIG. 19, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 570 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 20. Such polypeptides include At2g45700 (SEQ ID NO:1635), Ceres ANNOT ID no. 1508307 (SEQ ID NO:1637), Public GI ID no. 1495267 (SEQ ID NO:1642), Public GI ID no. 87241310 (SEQ ID NO:1644), Ceres CLONE ID no. 938390 (SEQ ID NO:1646), Ceres CLONE ID no. 272338 (SEQ ID NO:1648), Ceres CLONE ID no. 1993510 (SEQ ID NO:1650), Public GI ID no. 125563862 (SEQ ID NO:1651), Public GI ID no. 125605833 (SEQ ID NO:1653), Public GI ID no. 6899919 (SEQ ID NO:1632), Ceres ANNOT ID no. 1455110 (SEQ ID NO:1639), Ceres ANNOT ID no. 1525218 (SEQ ID NO:1641), Public GI ID no. 15231597 (SEQ ID NO:1643), Public GI ID no. 125548147 (SEQ ID NO:1652), Public GI ID no. 51091343 (SEQ ID NO:1654), Public GI ID no. 115479355 (SEQ ID NO:1655), Ceres ANNOT ID no. 6042086 (SEQ ID NO:1657), Ceres ANNOT ID no. 6029903 (SEQ ID NO:1659), and sequences identified as functional homologs of the sequences of FIG. 20, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 150 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 21. Such polypeptides include At2g35940 (SEQ ID NO:1540), Ceres CLONE ID no. 1943265 (SEQ ID NO:1543), Ceres ANNOT ID no. 1454522 (SEQ ID NO:1547), Public GI ID no. 31323447 (SEQ ID NO:1556), Ceres CLONE ID no. 1583941 (SEQ ID NO:1561), Ceres CLONE ID no. 1792942 (SEQ ID NO:1563), Public GI ID no. 77548772 (SEQ ID NO:1565), Public GI ID no. 84453182 (SEQ ID NO:1567), Public GI ID no. 31746344 (SEQ ID NO:1541), Ceres CLONE ID no. 1926640 (SEQ ID NO:1545), Ceres ANNOT ID no. 1475125 (SEQ ID NO:1549), Ceres ANNOT ID no. 1439653 (SEQ ID NO:1551), Ceres ANNOT ID no. 1461995 (SEQ ID NO:1553), Public GI ID no. 13877517 (SEQ ID NO:1554), Public GI ID no. 7239157 (SEQ ID NO:1555), Public GI ID no. 22652125 (SEQ ID NO:1557), Public GI ID no. 22652115 (SEQ ID NO:1558), Public GI ID no. 22652117 (SEQ ID NO:1559), Public GI ID no. 125535858 (SEQ ID NO:1564), Public GI ID no. 125578581 (SEQ ID NO:1566), Public GI ID no. 13752407 (SEQ ID NO:1568), Ceres ANNOT ID no. 6098817 (SEQ ID NO:1570), Ceres ANNOT ID no. 6039430 (SEQ ID NO:1572), Ceres ANNOT ID no. 6068141 (SEQ ID NO:1574), Ceres

61

ANNOT ID no. 6033916 (SEQ ID NO:1576), Ceres ANNOT ID no. 6034399 (SEQ ID NO:1578), Ceres ANNOT ID no. 6068617 (SEQ ID NO:1580), Ceres ANNOT ID no. 6026318 (SEQ ID NO:1582), Ceres ANNOT ID no. 6107650 (SEQ ID NO:1584), and sequences identified as functional homologs of the sequences of FIG. 21, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 1340 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 22. Such polypeptides include At1g04400 (SEQ ID NO:538), Public GI ID no. 5731739 (SEQ ID NO:539), Ceres ANNOT ID no. 1538045 (SEQ ID NO:541), Public GI ID no. 29467479 (SEQ ID NO:542), Public GI ID no. 133921974 (SEQ ID NO:543), Public GI ID no. 113197027 (SEQ ID NO:544), Public GI ID no. 92879277 (SEQ ID NO:545), Public GI ID no. 45935260 (SEQ ID NO:546), Public GI ID no. 8101444 (SEQ ID NO:547), Public GI ID no. 78217443 (SEQ ID NO:548), Public GI ID no. 28372347 (SEQ ID NO:549), Public GI ID no. 16416405 (SEQ ID NO:550), Ceres ANNOT ID no. 1484634 (SEQ ID NO:552), Ceres ANNOT ID no. 1451869 (SEQ ID NO:554), Public GI ID no. 25407462 (SEQ ID NO:555), Public GI ID no. 29467481 (SEQ ID NO:556), Public GI ID no. 29467477 (SEQ ID NO:557), Public GI ID no. 45935264 (SEQ ID NO:558), Public GI ID no. 5524201 (SEQ ID NO:559), Public GI ID no. 78217441 (SEQ ID NO:560), Public GI ID no. 3551221 (SEQ ID NO:561), Public GI ID no. 3551219 (SEQ ID NO:562), Public GI ID no. 23954324 (SEQ ID NO:563), Public GI ID no. 125582937 (SEQ ID NO:564), Public GI ID no. 83764373 (SEQ ID NO:565), Ceres ANNOT ID no. 6045327 (SEQ ID NO:567), and sequences identified as functional homologs of the sequences of FIG. 22, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 80 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 23. Such polypeptides include At3g45610 (SEQ ID NO:606), Public GI ID no. 92873064 (SEQ ID NO:607), Public GI ID no. 37051125 (SEQ ID NO:608), Public GI ID no. 112363376 (SEQ ID NO:609), Ceres CLONE ID no. 1938524 (SEQ ID NO:611), Ceres ANNOT ID no. 1473601 (SEQ ID NO:613), Ceres ANNOT ID no. 1468397 (SEQ ID NO:615), Public GI ID no. 21554185 (SEQ ID NO:616), Public GI ID no. 18424330 (SEQ ID NO:617), Public GI ID no. 8885571 (SEQ ID NO:618), Ceres CLONE ID no. 20852 (SEQ ID NO:620), Public GI ID no. 21553763 (SEQ ID NO:621), Public GI ID no. 18401763 (SEQ ID NO:622), Ceres CLONE ID no. 16423 (SEQ ID NO:624), Public GI ID no. 112363380 (SEQ ID NO:625), Public GI ID no. 6092016 (SEQ ID NO:626), Ceres CLONE ID no. 770468 (SEQ ID NO:628), Public GI ID no. 113205234 (SEQ ID NO:629), Ceres ANNOT ID no. 6094775 (SEQ ID NO:631), and sequences identified as functional homologs of the sequences of FIG. 23, as set forth in the sequence listing.

Polypeptides are shown in the sequence listing that have HMM bit scores greater than 110 when fitted to an HMM generated from the amino acid sequences set forth in FIG. 24. Such polypeptides include At4g08330 (SEQ ID NO:570), Ceres CLONE ID no. 1919714 (SEQ ID NO:572), Ceres ANNOT ID no. 1443290 (SEQ ID NO:574), Ceres CLONE ID no. 1042157 (SEQ ID NO:576), Ceres CLONE ID no. 1384304 (SEQ ID NO:578), Public GI ID no. 115464375 (SEQ ID NO:579), Ceres CLONE ID no. 100028078 (SEQ ID NO:580), Ceres ANNOT ID no. 1452096 (SEQ ID NO:582), Ceres ANNOT ID no. 1503869 (SEQ ID NO:584), Ceres ANNOT ID no. 1525651 (SEQ ID

62

NO:586), Ceres CLONE ID no. 1645639 (SEQ ID NO:588), Ceres CLONE ID no. 603237 (SEQ ID NO:590), Ceres CLONE ID no. 340925 (SEQ ID NO:592), Ceres CLONE ID no. 293238 (SEQ ID NO:594), Ceres CLONE ID no. 483742 (SEQ ID NO:596), Ceres CLONE ID no. 1460255 (SEQ ID NO:598), Ceres CLONE ID no. 1400107 (SEQ ID NO:600), Public GI ID no. 115440865 (SEQ ID NO:601), Ceres ANNOT ID no. 6016008 (SEQ ID NO:603), and sequences identified as functional homologs of the sequences of FIG. 24, as set forth in the sequence listing.

E. Percent Identity

In some embodiments, an SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to one of the amino acid sequences set forth in SEQ ID NO:3, SEQ ID NO:70, SEQ ID NO:129, SEQ ID NO:317, SEQ ID NO:337, SEQ ID NO:456, SEQ ID NO:538, SEQ ID NO:570, SEQ ID NO:606, SEQ ID NO:634, SEQ ID NO:644, SEQ ID NO:850, SEQ ID NO:907, SEQ ID NO:953, SEQ ID NO:1024, SEQ ID NO:1047, SEQ ID NO:1151, SEQ ID NO:1277, SEQ ID NO:1347, SEQ ID NO:1457, SEQ ID NO:1497, SEQ ID NO:1540, SEQ ID NO:1587, SEQ ID NO:1630, and SEQ ID NO:1635. Polypeptides having such a percent sequence identity often have a domain indicative of an SD+EODFR and/or low light-tolerance polypeptide and/or have an HMM bit score that is greater than 20, as discussed above. Amino acid sequences of SD+EODFR and/or low light-tolerance polypeptides having at least 40% sequence identity to one of the amino acid sequences set forth in SEQ ID NO:3, SEQ ID NO:70, SEQ ID NO:129, SEQ ID NO:317, SEQ ID NO:337, SEQ ID NO:456, SEQ ID NO:538, SEQ ID NO:570, SEQ ID NO:606, SEQ ID NO:634, SEQ ID NO:644, SEQ ID NO:850, SEQ ID NO:907, SEQ ID NO:953, SEQ ID NO:1024, SEQ ID NO:1047, SEQ ID NO:1151, SEQ ID NO:1277, SEQ ID NO:1347, SEQ ID NO:1457, SEQ ID NO:1497, SEQ ID NO:1540, SEQ ID NO:1587, and SEQ ID NO:1635 are provided in FIGS. 1-24.

“Percent sequence identity” refers to the degree of sequence identity between any given reference sequence, e.g., SEQ ID NO:3, and a candidate SD+EODFR and/or low light-tolerance sequence. A candidate sequence typically has a length that is from 80 percent to 200 percent of the length of the reference sequence, e.g., 82, 85, 87, 89, 90, 93, 95, 97, 99, 100, 105, 110, 115, 120, 130, 140, 150, 160, 170, 180, 190, or 200 percent of the length of the reference sequence. A percent identity for any candidate nucleic acid or polypeptide relative to a reference nucleic acid or polypeptide can be determined as follows. A reference sequence (e.g., a nucleic acid sequence or an amino acid sequence) is aligned to one or more candidate sequences using the computer program ClustalW (version 1.83, default parameters), which allows alignments of nucleic acid or polypeptide sequences to be carried out across their entire length (global alignment). Chenna et al., Nucleic Acids Res., 31(13):3497-500 (2003).

ClustalW calculates the best match between a reference and one or more candidate sequences, and aligns them so that identities, similarities and differences can be determined. Gaps of one or more residues can be inserted into a reference sequence, a candidate sequence, or both, to maximize sequence alignments. For fast pairwise alignment of nucleic acid sequences, the following default parameters are used: word size: 2; window size: 4; scoring method: percentage; number of top diagonals: 4; and gap penalty: 5. For multiple sequence alignment of nucleic acid sequences, the

following parameters are used: gap opening penalty: 10.0; gap extension penalty: 5.0; and weight transitions: yes. For fast pairwise alignment of protein sequences, the following parameters are used: word size: 1; window size: 5; scoring method: percentage; number of top diagonals: 5; gap penalty: 3. For multiple alignment of protein sequences, the following parameters are used: weight matrix: blosum; gap opening penalty: 10.0; gap extension penalty: 0.05; hydrophilic gaps: on; hydrophilic residues: Gly, Pro, Ser, Asn, Asp, Gln, Glu, Arg, and Lys; residue-specific gap penalties: on. The ClustalW output is a sequence alignment that reflects the relationship between sequences. ClustalW can be run, for example, at the Baylor College of Medicine Search Launcher site (searchlauncher.bcm.tmc.edu/multi-align/multi-align.html) and at the European Bioinformatics Institute site on the World Wide Web (ebi.ac.uk/clustalw).

To determine percent identity of a candidate nucleic acid or amino acid sequence to a reference sequence, the sequences are aligned using ClustalW, the number of identical matches in the alignment is divided by the length of the reference sequence, and the result is multiplied by 100. It is noted that the percent identity value can be rounded to the nearest tenth. For example, 78.11, 78.12, 78.13, and 78.14 are rounded down to 78.1, while 78.15, 78.16, 78.17, 78.18, and 78.19 are rounded up to 78.2.

In some cases, an SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:3. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:3 are provided in FIG. 1. Such polypeptides include Ceres CLONE ID no. 1844057 (SEQ ID NO:7), Ceres ANNOT ID no. 1469148 (SEQ ID NO:22), Public GI ID no. 18390998 (SEQ ID NO:25), Ceres CLONE ID no. 1065656 (SEQ ID NO:32), Ceres CLONE ID no. 1652677 (SEQ ID NO:36), Public GI ID no. 92874556 (SEQ ID NO:49), Ceres CLONE ID no. 1329161 (SEQ ID NO:53), Ceres CLONE ID no. 1030378 (SEQ ID NO:55), Ceres CLONE ID no. 1413787 (SEQ ID NO:57), and Public GI ID no. 125543598 (SEQ ID NO:60).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:70. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:70 are provided in FIG. 2. Such polypeptides include Ceres CLONE ID no. 1975934 (SEQ ID NO:72), Ceres ANNOT ID no. 1529913 (SEQ ID NO:80), Ceres CLONE ID no. 977794 (SEQ ID NO:93), Public GI ID no. 42362378 (SEQ ID NO:96), Public GI ID no. 23899378 (SEQ ID NO:99), Public GI ID no. 15963346 (SEQ ID NO:101), Public GI ID no. 15963344+B816 (SEQ ID NO:102), Public GI ID no. 92429657 (SEQ ID NO:103), Ceres CLONE ID no. 746644 (SEQ ID NO:105), Ceres CLONE ID no. 623089 (SEQ ID NO:109), Ceres CLONE ID no. 1913678 (SEQ ID NO:115), and Public GI ID no. 115450609 (SEQ ID NO:119).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:129. Amino acid sequences of polypeptides

having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:129 are provided in FIG. 3. Such polypeptides include Public GI ID no. 34550779 (SEQ ID NO:133), Ceres CLONE ID no. 1932235 (SEQ ID NO:137), Ceres CLONE ID no. 981738 (SEQ ID NO:201), Ceres CLONE ID no. 565974 (SEQ ID NO:209), Public GI ID no. 1352058 (SEQ ID NO:231), Public GI ID no. 11131101 (SEQ ID NO:234), Public GI ID no. 4887018 (SEQ ID NO:236), Public GI ID no. 4887018 (SEQ ID NO:236), Ceres CLONE ID no. 644455 (SEQ ID NO:247), Ceres CLONE ID no. 1731500 (SEQ ID NO:270), Public GI ID no. 20269063 (SEQ ID NO:300), Public GI ID no. 50404477 (SEQ ID NO:302), and Public GI ID no. 62125392 (SEQ ID NO:303).

15 In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:317. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:317 are provided in FIG. 4. Such polypeptides include Ceres CLONE ID no. 1842125 (SEQ ID NO:319), Ceres ANNOT ID no. 1461360 (SEQ ID NO:321), Ceres CLONE ID no. 480906 (SEQ ID NO:327), Public GI ID no. 92889352 (SEQ ID NO:330), and Public GI ID no. 56201850 (SEQ ID NO:330).

20 In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:337. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:337 are provided in FIG. 5. Such polypeptides include At2g04240 Ceres CLONE ID no. 952050 (SEQ ID NO:339), Public GI ID no. 115477050 (SEQ ID NO:349), Public GI ID no. 87162911 (SEQ ID NO:355), Ceres CLONE ID no. 1790901 (SEQ ID NO:357), Ceres CLONE ID no. 1460088 (SEQ ID NO:370), Ceres CLONE ID no. 1734065 (SEQ ID NO:393), Ceres CLONE ID no. 473509 (SEQ ID NO:395), Ceres CLONE ID no. 849918 (SEQ ID NO:401), Ceres CLONE ID no. 633470 (SEQ ID NO:409), Ceres CLONE ID no. 1808334 (SEQ ID NO:417), and Ceres ANNOT ID no. 1525600 (SEQ ID NO:437).

25 In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:456. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:456 are provided in FIG. 6. Such polypeptides include Public GI ID no. 58430585 (SEQ ID NO:457), Ceres CLONE ID no. 1842825 (SEQ ID NO:466), Ceres ANNOT ID no. 1449721 (SEQ ID NO:474), Public GI ID no. 41323978 (SEQ ID NO:475), Public GI ID no. 2895186 (SEQ ID NO:478), Public GI ID no. 22854950 (SEQ ID NO:481), Public GI ID no. 116010474 (SEQ ID NO:485), Public GI ID no. 4091804 (SEQ ID NO:488), Public GI ID no. 60459257 (SEQ ID NO:494), Public GI ID no. 45544881 (SEQ ID NO:496), Public GI ID no. 36789802 (SEQ ID NO:498), Public GI ID no. 92875402 (SEQ ID NO:508), Public GI ID no. 118406898 (SEQ ID NO:510), Public GI ID no. 107770485 (SEQ ID NO:511), Public GI ID no. 21655154 (SEQ ID NO:532), Public GI ID

no. 90657642 (SEQ ID NO:536), and Ceres CLONE ID no. 1569555 (SEQ ID NO:1842).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:634. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:634 are provided in FIG. 7. Such polypeptides include Public GI ID no. 98961985 (SEQ ID NO:637).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:644. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:644 are provided in FIG. 8. Such polypeptides include SEQ ID NO:645, Ceres CLONE ID no. 1849479 (SEQ ID NO:767), Public GI ID no. 89275008 (SEQ ID NO:796), Public GI ID no. 120400525 (SEQ ID NO:797), Public GI ID no. 98980426 (SEQ ID NO:804), Public GI ID no. 71983373 (SEQ ID NO:808), Public GI ID no. 41351817 (SEQ ID NO:809), Public GI ID no. 76446191 (SEQ ID NO:811), Public GI ID no. 5616086 (SEQ ID NO:813), Ceres CLONE ID no. 1052602 (SEQ ID NO:826), Public GI ID no. 72068957 (SEQ ID NO:830), Public GI ID no. 71534113 (SEQ ID NO:831), Public GI ID no. 37147896 (SEQ ID NO:832), Public GI ID no. 92918850 (SEQ ID NO:834), Public GI ID no. 40647095 (SEQ ID NO:835), Ceres ANNOT ID no. 1527711 (SEQ ID NO:837), Public GI ID no. 71041116 (SEQ ID NO:838), Public GI ID no. 12003384 (SEQ ID NO:839), Public GI ID no. 18535580 (SEQ ID NO:840), and Public GI ID no. 115353971 (SEQ ID NO:1843).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:850. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:850 are provided in FIG. 9. Such polypeptides include Ceres CLONE ID no. 1833093 (SEQ ID NO:853), Ceres ANNOT ID no. 1502190 (SEQ ID NO:857), Ceres CLONE ID no. 565641 (SEQ ID NO:876), Public GI ID no. 87240507 (SEQ ID NO:877), Ceres CLONE ID no. 1325382 (SEQ ID NO:881), Ceres CLONE ID no. 1558265 (SEQ ID NO:885), Ceres CLONE ID no. 1823669 (SEQ ID NO:895), and Public GI ID no. 115464921 (SEQ ID NO:898).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:907. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:907 are provided in FIG. 10. Such polypeptides include Ceres CLONE ID no. 1940797 (SEQ ID NO:909), Ceres ANNOT ID no. 1538900 (SEQ ID NO:911), Ceres CLONE ID no. 1126868 (SEQ ID NO:922), Public GI ID no. 89257684 (SEQ ID NO:923), Public GI ID no. 124360460 (SEQ ID NO:929), Public GI ID no. 62865694 (SEQ ID NO:931), Public GI ID no. 62865692

(SEQ ID NO:932), Ceres CLONE ID no. 260368 (SEQ ID NO:936), Ceres CLONE ID no. 1873510 (SEQ ID NO:947), Public GI ID no. 125541662 (SEQ ID NO:948), Public GI ID no. 48716268 (SEQ ID NO:950), and Public GI ID no. 62865696 (SEQ ID NO:1844).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:953. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:953 are provided in FIG. 11. Such polypeptides include Ceres CLONE ID no. 1798705 (SEQ ID NO:955), Ceres ANNOT ID no. 1458907 (SEQ ID NO:963), Ceres CLONE ID no. 1090409 (SEQ ID NO:971), Ceres CLONE ID no. 479817 (SEQ ID NO:977), Ceres CLONE ID no. 1041793 (SEQ ID NO:979), Ceres CLONE ID no. 684633 (SEQ ID NO:985), Ceres CLONE ID no. 371815 (SEQ ID NO:991), Ceres CLONE ID no. 1686460 (SEQ ID NO:993), Ceres CLONE ID no. 1448595 (SEQ ID NO:995), Ceres CLONE ID no. 1734477 (SEQ ID NO:999), Ceres CLONE ID no. 1605693 (SEQ ID NO:1005), Ceres CLONE ID no. 1757400 (SEQ ID NO:1009), and Public GI ID no. 115434334 (SEQ ID NO:1015).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1024. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:1024 are provided in FIG. 12. Such polypeptides include Ceres ANNOT ID no. 1452905 (SEQ ID NO:1029), Ceres CLONE ID no. 956176 (SEQ ID NO:1039), Public GI ID no. 92870366 (SEQ ID NO:1040), Ceres CLONE ID no. 294166 (SEQ ID NO:1042), and Public GI ID no. 125543067 (SEQ ID NO:1043).

In some cases, an SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1047. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:1047 are provided in FIG. 13. Such polypeptides include Ceres CLONE ID no. 1837694 (SEQ ID NO:1053), Ceres ANNOT ID no. 1483367 (SEQ ID NO:1057), Ceres CLONE ID no. 1077781 (SEQ ID NO:1083), Ceres CLONE ID no. 471026 (SEQ ID NO:1085), Public GI ID no. 92888885 (SEQ ID NO:1099), Public GI ID no. 45544873 (SEQ ID NO:1100), Public GI ID no. 45758663 (SEQ ID NO:1101), Ceres CLONE ID no. 772927 (SEQ ID NO:1105), Ceres CLONE ID no. 895080 (SEQ ID NO:1111), Ceres CLONE ID no. 1806128 (SEQ ID NO:1131), Public GI ID no. 115458192 (SEQ ID NO:1134), and Public GI ID no. 82470795 (SEQ ID NO:1139).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1151. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:1151 are provided in FIG. 14. Such polypeptides include Ceres CLONE ID no. 1851526 (SEQ ID NO:1155), Ceres ANNOT ID no. 1486769 (SEQ

ID NO:1172), Public GI ID no. 83032232 (SEQ ID NO:1209), Ceres CLONE ID no. 1620420 (SEQ ID NO:1211), Public GI ID no. 92892428 (SEQ ID NO:1215), Ceres CLONE ID no. 884742 (SEQ ID NO:1223), Ceres CLONE ID no. 1821559 (SEQ ID NO:1246), Public GI ID no. 51535021 (SEQ ID NO:1258), Public GI ID no. 113205304 (SEQ ID NO:1263), and Public GI ID no. 37719051 (SEQ ID NO:1264).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1277 Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:1277 are provided in FIG. 15. Such polypeptides include Ceres CLONE ID no. 1926352 (SEQ ID NO:1279), Ceres ANNOT ID no. 1448905 (SEQ ID NO:1285), Public GI ID no. 15236865 (SEQ ID NO:1294), Ceres CLONE ID no. 934771 (SEQ ID NO:1301), Ceres CLONE ID no. 338386 (SEQ ID NO:1303), Ceres CLONE ID no. 1780691 (SEQ ID NO:1317), and Public GI ID no. 115464819 (SEQ ID NO:1326).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1347 Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:1347 are provided in FIG. 16. Such polypeptides include Ceres CLONE ID no. 285028 (SEQ ID NO:1419), Ceres CLONE ID no. 100969565 (SEQ ID NO:1422), Public GI ID no. 1352057 (SEQ ID NO:1427), Ceres ANNOT ID no. 1453784 (SEQ ID NO:1429), Public GI ID no. 452777 (SEQ ID NO:1430), and Public GI ID no. 92873297 (SEQ ID NO:1431).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1457 Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:1457 are provided in FIG. 17. Such polypeptides include Ceres CLONE ID no. 1924904 (SEQ ID NO:1460), Ceres ANNOT ID no. 1543346 (SEQ ID NO:1462), Public GI ID no. 18396338 (SEQ ID NO:1467), Ceres CLONE ID no. 833872 (SEQ ID NO:1471), Ceres CLONE ID no. 1579587 (SEQ ID NO:1475), Ceres CLONE ID no. 1786411 (SEQ ID NO:1477), and Public GI ID no. 108864370 (SEQ ID NO:1480).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1497 Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:1497 are provided in FIG. 18. Such polypeptides include Ceres ANNOT ID no. 1443463 (SEQ ID NO:1499), Public GI ID no. 13605525 (SEQ ID NO:1502), Public GI ID no. 94965681 (SEQ ID NO:1506), and Public GI ID no. 28201254 (SEQ ID NO:1512).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1587 Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:1587 are provided in FIG. 19. Such polypeptides include Ceres CLONE ID no. 1839577 (SEQ ID NO:1589), Ceres ANNOT ID no. 1491567 (SEQ ID NO:1591), Ceres CLONE ID no. 574505 (SEQ ID NO:1596), Public GI ID no. 56117815 (SEQ ID NO:1597), Public GI ID no. 92874021 (SEQ ID NO:1603), Public GI ID no. 123684 (SEQ ID NO:1605), Public GI ID no. 5821136 (SEQ ID NO:1606), Ceres CLONE ID no. 283366 (SEQ ID NO:1609), Public GI ID no. 16118447 (SEQ ID NO:1612), and Public GI ID no. 125562434 (SEQ ID NO:1614).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1635 Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:1635 are provided in FIG. 20. Such polypeptides include Ceres ANNOT ID no. 1508307 (SEQ ID NO:1637), Public GI ID no. 1495267 (SEQ ID NO:1642), Public GI ID no. 87241310 (SEQ ID NO:1644), Ceres CLONE ID no. 938390 (SEQ ID NO:1646), Ceres CLONE ID no. 272338 (SEQ ID NO:1648), Ceres CLONE ID no. 1993510 (SEQ ID NO:1650), Public GI ID no. 125563862 (SEQ ID NO:1651), and Public GI ID no. 125605833 (SEQ ID NO:1653).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1540 Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:1540 are provided in FIG. 21. Such polypeptides include Ceres CLONE ID no. 1943265 (SEQ ID NO:1543), Ceres ANNOT ID no. 1454522 (SEQ ID NO:1547), Public GI ID no. 31323447 (SEQ ID NO:1556), Ceres CLONE ID no. 1583941 (SEQ ID NO:1561), Ceres CLONE ID no. 1792942 (SEQ ID NO:1563), Public GI ID no. 77548772 (SEQ ID NO:1565), and Public GI ID no. 84453182 (SEQ ID NO:1567).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:538. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:538 are provided in FIG. 22. Such polypeptides include Public GI ID no. 5731739 (SEQ ID NO:539), Ceres ANNOT ID no. 1538045 (SEQ ID NO:541), Public GI ID no. 29467479 (SEQ ID NO:542), Public GI ID no. 133921974 (SEQ ID NO:543), Public GI ID no. 113197027 (SEQ ID NO:544), Public GI ID no. 92879277 (SEQ ID NO:545), Public GI ID no. 45935260 (SEQ ID NO:546), Public GI ID no. 8101444 (SEQ ID NO:547), Public GI ID no. 78217443 (SEQ ID NO:548), and Public GI ID no. 28372347 (SEQ ID NO:549).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:606. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:606 are provided in FIG. 23. Such polypeptides include Public GI ID no. 92873064 (SEQ ID NO:607), Public GI ID no. 37051125 (SEQ ID NO:608), and Public GI ID no. 112363376 (SEQ ID NO:609).

In some cases, a SD+EODFR and/or low light-tolerance polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:570. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:570 are provided in FIG. 24. Such polypeptides include Ceres CLONE ID no. 1919714 (SEQ ID NO:572), Ceres ANNOT ID no. 1443290 (SEQ ID NO:574), Ceres CLONE ID no. 1042157 (SEQ ID NO:576), Ceres CLONE ID no. 1384304 (SEQ ID NO:578), and Public GI ID no. 115464375 (SEQ ID NO:579).

In some cases, a red light specific response pathway polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:456. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:456 are provided in FIG. 6. Such polypeptides include Public GI ID no. 58430585 (SEQ ID NO:457), Ceres CLONE ID no. 1842825 (SEQ ID NO:466), Ceres ANNOT ID no. 1449721 (SEQ ID NO:474), Public GI ID no. 41323978 (SEQ ID NO:475), Public GI ID no. 2895186 (SEQ ID NO:478), Public GI ID no. 22854950 (SEQ ID NO:481), Public GI ID no. 116010474 (SEQ ID NO:485), Public GI ID no. 4091804 (SEQ ID NO:488), Public GI ID no. 60459257 (SEQ ID NO:494), Public GI ID no. 45544881 (SEQ ID NO:496), Public GI ID no. 36789802 (SEQ ID NO:498), Public GI ID no. 92875402 (SEQ ID NO:508), Public GI ID no. 118406898 (SEQ ID NO:510), Public GI ID no. 107770485 (SEQ ID NO:511), Public GI ID no. 21655154 (SEQ ID NO:532), Public GI ID no. 90657642 (SEQ ID NO:536), and Ceres CLONE ID no. 1569555 (SEQ ID NO:1842).

In some cases, red light specific response pathway polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:953. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:953 are provided in FIG. 11. Such polypeptides include Ceres CLONE ID no. 1798705 (SEQ ID NO:955), Ceres ANNOT ID no. 1458907 (SEQ ID NO:963), Ceres CLONE ID no. 1090409 (SEQ ID NO:971), Ceres CLONE ID no. 479817 (SEQ ID NO:977), Ceres CLONE ID no. 1041793 (SEQ ID NO:979), Ceres CLONE ID no. 684633 (SEQ ID NO:985), Ceres CLONE ID no. 371815 (SEQ ID NO:991), Ceres CLONE ID no. 1686460 (SEQ ID NO:993), Ceres CLONE ID no. 1448595 (SEQ ID NO:995), Ceres CLONE ID no. 1734477 (SEQ ID NO:999), Ceres CLONE ID no. 1605693 (SEQ ID NO:1005), Ceres CLONE ID no. 1757400 (SEQ ID NO:1009), and Public GI ID no. 115434334 (SEQ ID NO:1015).

In some cases, a red light specific response pathway polypeptide has an amino acid sequence with at least 40% sequence identity, e.g., 50%, 52%, 56%, 59%, 61%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the amino acid sequence set forth in SEQ ID NO:1540. Amino acid sequences of polypeptides having greater than 40% sequence identity to the polypeptide set forth in SEQ ID NO:1540 are provided in FIG. 21. Such polypeptides include Ceres CLONE ID no. 1943265 (SEQ ID NO:1543), Ceres ANNOT ID no. 1454522 (SEQ ID NO:1547), Public GI ID no. 31323447 (SEQ ID NO:1556), Ceres CLONE ID no. 1583941 (SEQ ID NO:1561), Ceres CLONE ID no. 1792942 (SEQ ID NO:1563), Public GI ID no. 77548772 (SEQ ID NO:1565), and Public GI ID no. 84453182 (SEQ ID NO:1567).

F. Other Sequences

It should be appreciated that an SD+EODFR and/or low light-tolerance polypeptide and red light specific response pathway polypeptide can include additional amino acids that are not involved in an SD+EODFR and/or low light tolerance, or a red light specific response pathway, and thus such a polypeptide can be longer than would otherwise be the case. For example, an SD+EODFR and/or low light-tolerance polypeptide can include a purification tag, a chloroplast transit peptide, a mitochondrial transit peptide, an amyloplast peptide, or a leader sequence added to the amino or carboxy terminus. In some embodiments, an SD+EODFR and/or low light-tolerance polypeptide includes an amino acid sequence that functions as a reporter, e.g., a green fluorescent protein or yellow fluorescent protein.

III. NUCLEIC ACIDS

Nucleic acids described herein include nucleic acids that are effective to modulate SD+EODFR and/or low light tolerance when transcribed in a plant or plant cell. Such nucleic acids include, without limitation, those that encode an SD+EODFR and/or low light-tolerance polypeptide and those that can be used to inhibit expression of an SD+EODFR and/or low light-tolerance polypeptide or a red light specific response pathway polypeptide via a nucleic acid based method.

A. Nucleic Acids Encoding SD+EODFR and/or Low Light-Tolerance Polypeptides

Nucleic acids encoding SD+EODFR and/or low light-tolerance polypeptides are described herein. Such nucleic acids include SEQ ID NOS:1, 2, 4, 6, 8, 11, 13, 15, 17, 19, 21, 23, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 50, 52, 54, 56, 58, 64, 66, 68, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 92, 94, 104, 106, 108, 110, 112, 114, 123, 125, 127, 128, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 263, 265, 267, 269, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 305, 307, 309, 311, 313, 315, 316, 318, 320, 322, 324, 326, 328, 333, 335, 336, 338, 340, 342, 345, 356, 358, 360, 363, 369, 371, 373, 375, 377, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 455, 461, 463, 465, 467, 469, 471, 473, 476, 490, 500, 502, 504, 506, 513, 517, 519, 537, 540, 551, 553, 566, 568, 569, 571, 573, 575, 577, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 602, 604, 605, 610, 612, 614, 619, 623, 627, 630, 632, 633, 635, 640, 642, 643, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666,

668, 670, 672, 674, 677, 679, 681, 683, 685, 687, 689, 691, 693, 696, 698, 700, 703, 705, 707, 710, 715, 717, 719, 722, 724, 727, 729, 731, 733, 735, 737, 739, 746, 748, 752, 754, 756, 758, 760, 766, 768, 770, 772, 775, 777, 781, 785, 787, 789, 791, 793, 825, 828, 836, 842, 844, 846, 848, 849, 852, 854, 856, 858, 860, 867, 869, 871, 873, 875, 878, 880, 882, 884, 886, 888, 890, 892, 894, 896, 899, 901, 903, 905, 906, 908, 910, 912, 914, 916, 918, 921, 925, 927, 933, 935, 942, 944, 946, 951, 952, 954, 956, 958, 960, 962, 964, 968, 970, 972, 974, 976, 978, 980, 982, 984, 986, 988, 990, 992, 994, 996, 998, 1000, 1002, 1004, 1006, 1008, 1010, 1012, 1017, 1019, 1020, 1021, 1022, 1023, 1026, 1028, 1031, 1034, 1036, 1038, 1041, 1045, 1046, 1048, 1050, 1052, 1054, 1056, 1058, 1060, 1062, 1064, 1066, 1070, 1076, 1079, 1082, 1084, 1086, 1088, 1090, 1092, 1094, 1096, 1102, 1104, 1106, 1108, 1110, 1112, 1114, 1116, 1118, 1120, 1122, 1124, 1126, 1128, 1130, 1132, 1140, 1142, 1144, 1146, 1148, 1150, 1152, 1154, 1156, 1158, 1163, 1165, 1167, 1169, 1171, 1173, 1175, 1177, 1179, 1181, 1183, 1185, 1187, 1189, 1191, 1193, 1195, 1197, 1205, 1207, 1210, 1212, 1218, 1220, 1222, 1224, 1226, 1228, 1231, 1233, 1235, 1237, 1239, 1241, 1243, 1245, 1247, 1249, 1251, 1253, 1265, 1267, 1269, 1271, 1273, 1275, 1276, 1278, 1280, 1282, 1284, 1286, 1288, 1290, 1292, 1296, 1300, 1302, 1304, 1306, 1308, 1310, 1312, 1314, 1316, 1318, 1320, 1333, 1335, 1337, 1339, 1341, 1343, 1345, 1346, 1348, 1350, 1354, 1356, 1359, 1361, 1363, 1365, 1369, 1371, 1373, 1376, 1378, 1380, 1382, 1384, 1386, 1388, 1390, 1392, 1394, 1396, 1398, 1400, 1403, 1405, 1407, 1409, 1416, 1418, 1420, 1428, 1432, 1437, 1441, 1443, 1445, 1447, 1449, 1451, 1453, 1454, 1455, 1456, 1459, 1461, 1463, 1465, 1470, 1472, 1474, 1476, 1487, 1489, 1491, 1493, 1495, 1496, 1498, 1500, 1507, 1509, 1517, 1526, 1530, 1537, 1538, 1539, 1542, 1544, 1546, 1548, 1550, 1552, 1560, 1562, 1569, 1571, 1573, 1575, 1577, 1579, 1581, 1583, 1585, 1586, 1588, 1590, 1592, 1595, 1608, 1610, 1622, 1624, 1626, 1627, 1628, 1629, 1633, 1634, 1636, 1638, 1640, 1645, 1647, 1649, 1656, 1658, 1660, 1662, 1664, 1666, 1668, 1670, 1672, 1674, 1676, 1678, 1680, 1683, 1685, 1687, 1689, 1691, 1693, 1695, 1697, 1706, 1708, 1710, 1712, 1714, 1716, 1718, 1724, 1726, 1728, 1731, 1733, 1735, 1737, 1747, 1749, 1753, 1755, 1757, 1759, 1761, 1763, 1765, 1779, 1781, 1783, 1785, 1787, 1789, 1791, 1793, 1795, 1797, 1799, 1801, 1803, 1841, 1849, 1851, 1853, 1855, 1857, 1868, 1872, 1874, 1876, 1878, 1880, 1882, 1884, 1886, 1888, 1890, 1892, 1894, 1896, 1898, 1900, 1902, 1904, 1906, 1908, 1910, 1912, 1914, 1916, 1918, 1920, 1922, 1924, 1926, 1928, 1930, 1932, 1934, 1936, 1938, 1940, 1942, 1944, 1946, 1948, 1950, 1952, 1954, 1956, 1958, 1960, 1962, 1964, 1966, 1968, 1970, 1972, 1974, 1976, 1978, 1980, 1982, 1984, 1986, 1988, 1990, 1992, 1994, 1996, 1998, 2000, 2002, 2004, 2006, 2008, 2010, 2012, 2014, 2016, 2018, 2020, 2022, 2024, 2026, 2028, 2068, 2071, 2073, 2075, 2077, 2079, 2082, 2086, 2088, 2090, 2092, 2094, 2096, 2098, 2100, 2102, 2104, 2106, 2108, 2110, 2112, 2122, 2124, 2126, 2128, 2130, 2132, 2134, 2145, 2147, 2149, 2151, 2153, 2155, 2157, 2159, 2161, 2163, 2165, 2167, 2169, 2171, 2173, 2175, 2177, 2179, 2181, 2265, 2267, 2279, 2281, 2283, 2285, 2287, 2289, 2291, 2293, 2295, 2297, 2299, 2301, 2303, 2305, 2307, 2309, 2311, 2313, 2315, 2317, 2319, 2321, 2349, 2351, 2353, 2355, 2357, 2359, 2361, 2363, 2365, 2367, 2369, 2371, and 2373 as described in more detail below. A nucleic acid also can be a fragment that is at least 40% (e.g., at least 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 99%) of the length of the full-length nucleic acid set forth in SEQ ID NOS:1, 2, 4, 6, 8, 11, 13, 15, 17, 19,

21, 23, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 50, 52, 54, 56, 58, 64, 66, 68, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 92, 94, 104, 106, 108, 110, 112, 114, 123, 125, 127, 128, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 263, 265, 267, 269, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 305, 307, 309, 311, 313, 315, 316, 318, 320, 322, 324, 326, 328, 333, 335, 336, 338, 340, 342, 345, 356, 358, 360, 363, 369, 371, 373, 375, 377, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 455, 461, 463, 465, 467, 469, 471, 473, 476, 490, 492, 500, 502, 504, 506, 513, 517, 519, 537, 540, 551, 553, 566, 568, 569, 571, 573, 575, 577, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 602, 604, 605, 610, 612, 614, 619, 623, 627, 630, 632, 633, 635, 640, 642, 643, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 677, 679, 681, 683, 685, 687, 689, 691, 693, 696, 698, 700, 703, 705, 707, 710, 715, 717, 719, 722, 724, 727, 729, 731, 733, 735, 737, 739, 746, 748, 752, 754, 756, 758, 760, 766, 768, 770, 772, 775, 777, 781, 785, 787, 789, 791, 793, 825, 828, 836, 842, 844, 846, 848, 849, 852, 854, 856, 858, 860, 867, 869, 871, 873, 875, 878, 880, 882, 884, 886, 888, 890, 892, 894, 896, 899, 901, 903, 905, 906, 908, 910, 912, 914, 916, 918, 921, 925, 927, 933, 935, 942, 944, 946, 951, 952, 954, 956, 958, 960, 962, 964, 968, 970, 972, 974, 976, 978, 980, 982, 984, 986, 988, 990, 992, 994, 996, 998, 1000, 1002, 1004, 1006, 1008, 1010, 1012, 1017, 1019, 1020, 1021, 1022, 1023, 1026, 1028, 1031, 1034, 1036, 1038, 1041, 1045, 1046, 1048, 1050, 1052, 1054, 1056, 1058, 1060, 1062, 1064, 1066, 1070, 1076, 1079, 1082, 1084, 1086, 1088, 1090, 1092, 1094, 1096, 1102, 1104, 1106, 1108, 1110, 1112, 1114, 1116, 1118, 1120, 1122, 1124, 1126, 1128, 1130, 1132, 1140, 1142, 1144, 1146, 1148, 1150, 1152, 1154, 1156, 1158, 1163, 1165, 1167, 1169, 1171, 1173, 1175, 1177, 1179, 1181, 1183, 1185, 1187, 1189, 1191, 1193, 1195, 1197, 1205, 1207, 1210, 1212, 1218, 1220, 1222, 1224, 1226, 1228, 1231, 1233, 1235, 1237, 1239, 1241, 1243, 1245, 1247, 1249, 1251, 1253, 1265, 1267, 1269, 1271, 1273, 1275, 1276, 1278, 1280, 1282, 1284, 1286, 1288, 1290, 1292, 1296, 1300, 1302, 1304, 1306, 1308, 1310, 1312, 1314, 1316, 1318, 1320, 1333, 1335, 1337, 1339, 1341, 1343, 1345, 1346, 1348, 1350, 1354, 1356, 1359, 1361, 1363, 1365, 1369, 1371, 1373, 1376, 1378, 1380, 1382, 1384, 1386, 1388, 1390, 1392, 1394, 1396, 1398, 1400, 1403, 1405, 1407, 1409, 1416, 1418, 1420, 1428, 1432, 1437, 1441, 1443, 1445, 1447, 1449, 1451, 1453, 1454, 1455, 1456, 1459, 1461, 1463, 1465, 1470, 1472, 1474, 1476, 1487, 1489, 1491, 1493, 1495, 1496, 1498, 1500, 1507, 1509, 1517, 1526, 1530, 1537, 1538, 1539, 1542, 1544, 1546, 1548, 1550, 1552, 1560, 1562, 1569, 1571, 1573, 1575, 1577, 1579, 1581, 1583, 1585, 1586, 1588, 1590, 1592, 1595, 1608, 1610, 1622, 1624, 1626, 1627, 1628, 1629, 1633, 1634, 1636, 1638, 1640, 1645, 1647, 1649, 1656, 1658, 1660, 1662, 1664, 1666, 1668, 1670, 1672, 1674, 1676, 1678, 1680, 1683, 1685, 1687, 1689, 1691, 1693, 1695, 1697, 1706, 1708, 1710, 1712, 1714, 1716, 1718, 1724, 1726, 1728, 1731, 1733, 1735, 1737, 1747, 1749, 1753, 1755, 1757, 1759, 1761, 1763, 1765, 1779, 1781, 1783, 1785, 1787, 1789, 1791, 1793, 1795, 1797, 1799, 1801, 1803, 1841, 1849, 1851, 1853, 1855, 1857, 1868, 1872, 1874, 1876, 1878, 1880, 1882, 1884, 1886, 1888, 1890, 1892, 1894, 1896, 1898, 1900, 1902, 1904, 1906, 1908, 1910, 1912, 1914, 1916, 1918, 1920, 1922, 1924, 1926, 1928, 1930, 1932, 1934, 1936, 1938, 1940, 1942, 1944, 1946, 1948, 1950, 1952, 1954, 1956, 1958, 1960, 1962, 1964, 1966, 1968, 1970, 1972, 1974, 1976, 1978, 1980, 1982, 1984, 1986, 1988, 1990, 1992, 1994, 1996, 1998, 2000, 2002, 2004, 2006, 2008, 2010, 2012, 2014, 2016, 2018, 2020, 2022, 2024, 2026, 2028, 2068, 2071, 2073, 2075, 2077, 2079, 2082, 2086, 2088, 2090, 2092, 2094, 2096, 2098, 2100, 2102, 2104, 2106, 2108, 2110, 2112, 2122, 2124, 2126, 2128, 2130, 2132, 2134, 2145, 2147, 2149, 2151, 2153, 2155, 2157, 2159, 2161, 2163, 2165, 2167, 2169, 2171, 2173, 2175, 2177, 2179, 2181, 2265, 2267, 2279, 2281, 2283, 2285, 2287, 2289, 2291, 2293, 2295, 2297, 2299, 2301, 2303, 2305, 2307, 2309, 2311, 2313, 2315, 2317, 2319, 2321, 2349, 2351, 2353, 2355, 2357, 2359, 2361, 2363, 2365, 2367, 2369, 2371, and 2373 as described in more detail below. A nucleic acid also can be a fragment that is at least 40% (e.g., at least 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 99%) of the length of the full-length nucleic acid set forth in SEQ ID NOS:1, 2, 4, 6, 8, 11, 13, 15, 17, 19,

example, an SD+EODFR and/or low light-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, e.g., 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1585 or SEQ ID NO:1586.

An SD+EODFR and/or low light-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1626, SEQ ID NO:1627, SEQ ID NO:1628, or SEQ ID NO:1629. Alternatively, an SD+EODFR and/or low light-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1626, SEQ ID NO:1627, SEQ ID NO:1628, or SEQ ID NO:1629. For example, an SD+EODFR and/or low light-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, e.g., 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1626, SEQ ID NO:1627, SEQ ID NO:1628, or SEQ ID NO:1629.

An SD+EODFR and/or low light-tolerance nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1633 or SEQ ID NO:1634. Alternatively, an SD+EODFR and/or low light-tolerance nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1633 or SEQ ID NO:1634. For example, an SD+EODFR and/or low light-tolerance nucleic acid can have a nucleotide sequence with at least 80% sequence identity, e.g., 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1633 or SEQ ID NO:1634.

B. Nucleic Acids Encoding Red Light Specific Response Pathway Polypeptides

Nucleic acids encoding red light specific response pathway polypeptides are described herein. Such nucleic acids include SEQ ID NOs: 454, 455, 461, 463, 465, 467, 469, 471, 473, 476, 490, 492, 500, 502, 504, 506, 513, 517, 519, 951, 952, 954, 956, 958, 960, 962, 964, 968, 970, 972, 974, 976, 978, 980, 982, 984, 986, 988, 990, 992, 994, 996, 998, 1000, 1002, 1004, 1006, 1008, 1010, 1012, 1017, 1537, 1538, 1539, 1542, 1544, 1546, 1548, 1550, 1552, 1560, 1562, 1569, 1571, 1573, 1575, 1577, 1579, 1581, 1583, 1660, 1662, 1664, 1666, 1668, 1670, 1672, 1674, 1676, 1779, 1781, 1783, 1785, 1787, 1789, 1791, 1793, 1795, 1797, 1799, 1801, 1803, 1841, and 2267 as described in more detail below. A nucleic acid also can be a fragment that is at least 40% (e.g., at least 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 99%) of the length of the full-length nucleic acid set forth in SEQ ID NOs: 454, 455, 461, 463, 465, 467, 469, 471, 473, 476, 490, 492, 500, 502, 504, 506, 513, 517, 519, 951, 952, 954, 956, 958, 960, 962, 964, 968, 970, 972, 974, 976, 978, 980, 982, 984, 986, 988, 990, 992, 994, 996, 998, 1000, 1002, 1004, 1006, 1008, 1010, 1012, 1017, 1537, 1538, 1539, 1542, 1544, 1546, 1548, 1550, 1552, 1560, 1562, 1569, 1571, 1573, 1575, 1577, 1579, 1581, 1583, 1660, 1662, 1664, 1666, 1668, 1670, 1672, 1674, 1676, 1779, 1781, 1783, 1785, 1787, 1789, 1791, 1793, 1795, 1797, 1799, 1801, 1803, 1841, and 2267.

A red light specific response pathway nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:454 or SEQ ID NO:455. Alternatively, a red light specific response pathway nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:454 or SEQ ID NO:455. For example, a red light specific response pathway nucleic acid can have a nucleotide sequence with at least 80% sequence identity, e.g., 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:454 or SEQ ID NO:455.

A red light specific response pathway nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:951 or SEQ ID NO:952. Alternatively, a red light specific response pathway nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:951 or SEQ ID NO:952. For example, a red light specific response pathway nucleic acid can have a nucleotide sequence with at least 80% sequence identity, e.g., 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:951 or SEQ ID NO:952.

A red light specific response pathway nucleic acid can comprise the nucleotide sequence set forth in SEQ ID NO:1537, SEQ ID NO:1538, or SEQ ID NO:1539. Alternatively, a red light specific response pathway nucleic acid can be a variant of the nucleic acid having the nucleotide sequence set forth in SEQ ID NO:1537, SEQ ID NO:1538, or SEQ ID NO:1539. For example, a red light specific response pathway nucleic acid can have a nucleotide sequence with at least 80% sequence identity, e.g., 81%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity, to the nucleotide sequence set forth in SEQ ID NO:1537, SEQ ID NO:1538, or SEQ ID NO:1539.

Isolated nucleic acid molecules can be produced by standard techniques. For example, polymerase chain reaction (PCR) techniques can be used to obtain an isolated nucleic acid containing a nucleotide sequence described herein. PCR can be used to amplify specific sequences from DNA as well as RNA, including sequences from total genomic DNA or total cellular RNA. Various PCR methods are described, for example, in *PCR Primer: A Laboratory Manual*, Dieffenbach and Dveksler, eds., Cold Spring Harbor Laboratory Press, 1995. Generally, sequence information from the ends of the region of interest or beyond is employed to design oligonucleotide primers that are identical or similar in sequence to opposite strands of the template to be amplified. Various PCR strategies also are available by which site-specific nucleotide sequence modifications can be introduced into a template nucleic acid. Isolated nucleic acids also can be chemically synthesized, either as a single nucleic acid molecule (e.g., using automated DNA synthesis in the 3' to 5' direction using phosphoramidite technology) or as a series of oligonucleotides. For example, one or more pairs of long oligonucleotides (e.g., >100 nucleotides) can be synthesized that contain the desired sequence, with each pair containing a short segment of complementarity (e.g., about 15 nucleotides) such that a duplex is formed when the oligonucleotide pair is annealed. DNA polymerase is used to extend the oligonucleotides, resulting in a single, double-stranded nucleic acid molecule per oligonucleotide pair, which then can be ligated into a vector. Isolated nucleic acids of the invention also can be obtained by mutagenesis of, e.g., a naturally occurring DNA.

C. Use of Nucleic Acids to Modulate Expression of Polypeptides Expression of an SD+EODFR and/or Low Light-Tolerance Polypeptide

A nucleic acid encoding one of the SD+EODFR and/or low light-tolerance polypeptides described herein can be used to express the polypeptide in a plant species of interest, typically by transforming a plant cell with a nucleic acid having the coding sequence for the polypeptide operably linked in sense orientation to one or more regulatory regions. It will be appreciated that because of the degeneracy of the genetic code, a number of nucleic acids can encode a particular SD+EODFR and/or low light-tolerance polypeptide; i.e., for many amino acids, there is more than one nucleotide triplet that serves as the codon for the amino acid.

Thus, codons in the coding sequence for a given SD+EODFR and/or low light-tolerance polypeptide can be modified such that optimal expression in a particular plant species is obtained, using appropriate codon bias tables for that species.

In some cases, expression of an SD+EODFR and/or low light-tolerance polypeptide inhibits one or more functions of an endogenous polypeptide. For example, a nucleic acid that encodes a dominant negative polypeptide can be used to inhibit protein function. A dominant negative polypeptide typically is mutated or truncated relative to an endogenous wild type polypeptide, and its presence in a cell inhibits one or more functions of the wild type polypeptide in that cell, i.e., the dominant negative polypeptide is genetically dominant and confers a loss of function. The mechanism by which a dominant negative polypeptide confers such a phenotype can vary but often involves a protein-protein interaction or a protein-DNA interaction. For example, a dominant negative polypeptide can be an enzyme that is truncated relative to a native wild type enzyme, such that the truncated polypeptide retains domains involved in binding a first protein but lacks domains involved in binding a second protein. The truncated polypeptide is thus unable to properly modulate the activity of the second protein. See, e.g., US 2007/0056058. As another example, a point mutation that results in a non-conservative amino acid substitution in a catalytic domain can result in a dominant negative polypeptide. See, e.g., US 2005/032221. As another example, a dominant negative polypeptide can be a transcription factor that is truncated relative to a native wild type transcription factor, such that the truncated polypeptide retains the DNA binding domain(s) but lacks the activation domain(s). Such a truncated polypeptide can inhibit the wild type transcription factor from binding DNA, thereby inhibiting transcription activation.

D. Use of Nucleic Acids to Inhibit Expression of a Red Light Specific Response Pathway Polypeptide

Polynucleotides and recombinant constructs described herein can be used to inhibit expression of a red light specific response pathway polypeptide in a plant species of interest. See, e.g., Matzke and Birchler, *Nature Reviews Genetics*, 6:24-35 (2005); Akashi et al., *Nature Reviews Mol. Cell Biology*, 6:413-422 (2005); Mittal, *Nature Reviews Genetics*, 5:355-365 (2004); and *Nature Reviews RNA interference collection*, October 2005 at nature.com/reviews/focus/mai. A number of nucleic acid based methods, including antisense RNA, ribozyme directed RNA cleavage, post-transcriptional gene silencing (PTGS), e.g., RNA interference (RNAi), and transcriptional gene silencing (TGS) are known to inhibit gene expression in plants. Suitable polynucleotides include full-length nucleic acids encoding red light specific response pathway polypeptides or fragments of such full-length nucleic acids. In some embodiments, a complement of the full-length nucleic acid or a fragment thereof can be used. Typically, a fragment is at least 10 nucleotides, e.g., at least 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 30, 35, 40, 50, 80, 100, 200, 500 nucleotides or more. Generally, higher homology can be used to compensate for the use of a shorter sequence.

Antisense technology is one well-known method. In this method, a nucleic acid of a gene to be repressed is cloned and operably linked to a regulatory region and a transcription termination sequence so that the antisense strand of RNA is transcribed. The recombinant construct is then transformed into plants, as described herein, and the anti-sense strand of RNA is produced. The nucleic acid need not be the entire sequence of the gene to be repressed, but

typically will be substantially complementary to at least a portion of the sense strand of the gene to be repressed.

In another method, a nucleic acid can be transcribed into a ribozyme, or catalytic RNA, that affects expression of an mRNA. See, U.S. Pat. No. 6,423,885. Ribozymes can be designed to specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. Heterologous nucleic acids can encode ribozymes designed to cleave particular mRNA transcripts, thus preventing expression of a polypeptide. Hammerhead ribozymes are useful for destroying particular mRNAs, although various ribozymes that cleave mRNA at site-specific recognition sequences can be used. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target RNA contains a 5'-UG-3' nucleotide sequence. The construction and production of hammerhead ribozymes is known in the art. See, for example, U.S. Pat. No. 5,254,678 and WO 02/46449 and references cited therein. Hammerhead ribozyme sequences can be embedded in a stable RNA such as a transfer RNA (tRNA) to increase cleavage efficiency in vivo. Perriman et al., *Proc. Natl. Acad. Sci. USA*, 92(13):6175-6179 (1995); de Feyter and Gaudron, *Methods in Molecular Biology*, Vol. 74, Chapter 43, "Expressing Ribozymes in Plants", Edited by Turner, P. C., Humana Press Inc., Totowa, NJ. RNA endoribonucleases which have been described, such as the one that occurs naturally in *Tetrahymena thermophila*, can be useful. See, for example, U.S. Pat. Nos. 4,987,071 and 6,423,885.

PTGS, e.g., RNAi, can also be used to inhibit the expression of a gene. For example, a construct can be prepared that includes a sequence that is transcribed into an RNA that can anneal to itself, e.g., a double stranded RNA having a stem-loop structure. In some embodiments, one strand of the stem portion of a double stranded RNA comprises a sequence that is similar or identical to the sense coding sequence or a fragment thereof of a red light specific response pathway polypeptide, and that is from about 10 nucleotides to about 2,500 nucleotides in length. The length of the sequence that is similar or identical to the sense coding sequence can be from 10 nucleotides to 500 nucleotides, from 15 nucleotides to 300 nucleotides, from 20 nucleotides to 100 nucleotides, or from 25 nucleotides to 100 nucleotides. The other strand of the stem portion of a double stranded RNA comprises a sequence that is similar or identical to the antisense strand or a fragment thereof of the coding sequence of the red light specific response pathway polypeptide, and can have a length that is shorter, the same as, or longer than the corresponding length of the sense sequence. In some cases, one strand of the stem portion of a double stranded RNA comprises a sequence that is similar or identical to the 3' or 5' untranslated region, or a fragment thereof, of an mRNA encoding a red light specific response pathway polypeptide, and the other strand of the stem portion of the double stranded RNA comprises a sequence that is similar or identical to the sequence that is complementary to the 3' or 5' untranslated region, respectively, or a fragment thereof, of the mRNA encoding the red light specific response pathway polypeptide. In other embodiments, one strand of the stem portion of a double stranded RNA comprises a sequence that is similar or identical to the sequence of an intron, or a fragment thereof, in the pre-mRNA encoding a red light specific response pathway polypeptide, and the other strand of the stem portion comprises a sequence that is similar or identical to the sequence

81

that is complementary to the sequence of the intron, or a fragment thereof, in the pre-mRNA.

The loop portion of a double stranded RNA can be from 3 nucleotides to 5,000 nucleotides, e.g., from 3 nucleotides to 25 nucleotides, from 15 nucleotides to 1,000 nucleotides, from 20 nucleotides to 500 nucleotides, or from 25 nucleotides to 200 nucleotides. The loop portion of the RNA can include an intron or a fragment thereof. A double stranded RNA can have zero, one, two, three, four, five, six, seven, eight, nine, ten, or more stem-loop structures.

A construct including a sequence that is operably linked to a regulatory region and a transcription termination sequence, and that is transcribed into an RNA that can form a double stranded RNA, is transformed into plants as described herein. Methods for using RNAi to inhibit the expression of a gene are known to those of skill in the art. See, e.g., U.S. Pat. Nos. 5,034,323; 6,326,527; 6,452,067; 6,573,099; 6,753,139; and 6,777,588. See also WO 97/01952; WO 98/53083; WO 99/32619; WO 98/36083; and U.S. Patent Publications 20030175965, 20030175783, 20040214330, and 20030180945.

Constructs containing regulatory regions operably linked to nucleic acid molecules in sense orientation can also be used to inhibit the expression of a gene. The transcription product can be similar or identical to the sense coding sequence, or a fragment thereof, of a red light specific response pathway polypeptide. The transcription product also can be unpolyadenylated, lack a 5' cap structure, or contain an unspliceable intron. Methods of inhibiting gene expression using a full-length cDNA as well as a partial cDNA sequence are known in the art. See, e.g., U.S. Pat. No. 5,231,020.

In some embodiments, a construct containing a nucleic acid having at least one strand that is a template for both sense and antisense sequences that are complementary to each other is used to inhibit the expression of a gene. The sense and antisense sequences can be part of a larger nucleic acid molecule or can be part of separate nucleic acid molecules having sequences that are not complementary. The sense or antisense sequence can be a sequence that is identical or complementary to the sequence of an mRNA, the 3' or 5' untranslated region of an mRNA, or an intron in a pre-mRNA encoding a red light specific response pathway polypeptide, or a fragment of such sequences. In some embodiments, the sense or antisense sequence is identical or complementary to a sequence of the regulatory region that drives transcription of the gene encoding a red light specific response pathway polypeptide. In each case, the sense sequence is the sequence that is complementary to the antisense sequence.

The sense and antisense sequences can be a length greater than about 10 nucleotides (e.g., 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or more nucleotides). For example, an antisense sequence can be 21 or 22 nucleotides in length. Typically, the sense and antisense sequences range in length from about 15 nucleotides to about 30 nucleotides, e.g., from about 18 nucleotides to about 28 nucleotides, or from about 21 nucleotides to about 25 nucleotides.

In some embodiments, an antisense sequence is a sequence complementary to an mRNA sequence, or a fragment thereof, encoding a red light specific response pathway polypeptide described herein. The sense sequence complementary to the antisense sequence can be a sequence present within the mRNA of the red light specific response pathway polypeptide. Typically, sense and antisense sequences are

82

designed to correspond to a 15-30 nucleotide sequence of a target mRNA such that the level of that target mRNA is reduced.

In some embodiments, a construct containing a nucleic acid having at least one strand that is a template for more than one sense sequence (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10 or more sense sequences) can be used to inhibit the expression of a gene. Likewise, a construct containing a nucleic acid having at least one strand that is a template for more than one antisense sequence (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10 or more antisense sequences) can be used to inhibit the expression of a gene. For example, a construct can contain a nucleic acid having at least one strand that is a template for two sense sequences and two antisense sequences. The multiple sense sequences can be identical or different, and the multiple antisense sequences can be identical or different. For example, a construct can have a nucleic acid having one strand that is a template for two identical sense sequences and two identical antisense sequences that are complementary to the two identical sense sequences. Alternatively, an isolated nucleic acid can have one strand that is a template for (1) two identical sense sequences 20 nucleotides in length, (2) one antisense sequence that is complementary to the two identical sense sequences 20 nucleotides in length, (3) a sense sequence 30 nucleotides in length, and (4) three identical antisense sequences that are complementary to the sense sequence 30 nucleotides in length. The constructs provided herein can be designed to have a suitable arrangement of sense and antisense sequences. For example, two identical sense sequences can be followed by two identical antisense sequences or can be positioned between two identical antisense sequences.

A nucleic acid having at least one strand that is a template for one or more sense and/or antisense sequences can be operably linked to a regulatory region to drive transcription of an RNA molecule containing the sense and/or antisense sequence(s). In addition, such a nucleic acid can be operably linked to a transcription terminator sequence, such as the terminator of the nopaline synthase (nos) gene. In some cases, two regulatory regions can direct transcription of two transcripts: one from the top strand, and one from the bottom strand. See, for example, Yan et al., *Plant Physiol.*, 141: 1508-1518 (2006). The two regulatory regions can be the same or different. The two transcripts can form double-stranded RNA molecules that induce degradation of the target RNA. In some cases, a nucleic acid can be positioned within a T-DNA or plant-derived transfer DNA (P-DNA) such that the left and right T-DNA border sequences, or the left and right border-like sequences of the P-DNA, flank or are on either side of the nucleic acid. See, US 2006/0265788. The nucleic acid sequence between the two regulatory regions can be from about 15 to about 300 nucleotides in length. In some embodiments, the nucleic acid sequence between the two regulatory regions is from about 15 to about 200 nucleotides in length, from about 15 to about 100 nucleotides in length, from about 15 to about 50 nucleotides in length, from about 18 to about 50 nucleotides in length, from about 18 to about 40 nucleotides in length, from about 18 to about 30 nucleotides in length, or from about 18 to about 25 nucleotides in length.

In some nucleic-acid based methods for inhibition of gene expression in plants, a suitable nucleic acid can be a nucleic acid analog. Nucleic acid analogs can be modified at the base moiety, sugar moiety, or phosphate backbone to improve, for example, stability, hybridization, or solubility of the nucleic acid. Modifications at the base moiety include deoxyuridine for deoxythymidine, and 5-methyl-2'-de-

oxycytidine and 5-bromo-2'-deoxycytidine for deoxycytidine. Modifications of the sugar moiety include modification of the 2' hydroxyl of the ribose sugar to form 2'-O-methyl or 2'-O-allyl sugars. The deoxyribose phosphate backbone can be modified to produce morpholino nucleic acids, in which each base moiety is linked to a six-membered morpholino ring, or peptide nucleic acids, in which the deoxypyrophosphate backbone is replaced by a pseudopeptide backbone and the four bases are retained. See, for example, Summerton and Weller, 1997, *Antisense Nucleic Acid Drug Dev.*, 7:187-195; Hyrup et al., *Bioorgan. Med. Chem.*, 4:5-23 (1996). In addition, the deoxypyrophosphate backbone can be replaced with, for example, a phosphorothioate or phosphorodithioate backbone, a phosphoroamidite, or an alkyl phosphotriester backbone.

E. Constructs/Vectors

Recombinant constructs provided herein can be used to transform plants or plant cells in order to modulate SD+EODFR, low light tolerance, and/or red light specific response pathways. A recombinant nucleic acid construct can comprise a nucleic acid encoding an SD+EODFR and/or low light-tolerance polypeptide as described herein, operably linked to a regulatory region suitable for expressing the SD+EODFR and/or low light-tolerance polypeptide in the plant or cell. Thus, a nucleic acid can comprise a coding sequence that encodes any of the SD+EODFR and/or low light-tolerance polypeptides as set forth in SEQ ID NOs:3, 5, 7, 9, 10, 12, 14, 16, 18, 20, 22, 24, 25, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 49, 51, 53, 55, 57, 59, 60, 61, 62, 63, 65, 67, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 89, 90, 91, 93, 95, 96, 97, 98, 99, 100, 101, 102, 103, 105, 107, 109, 111, 113, 115, 116, 117, 118, 119, 120, 121, 122, 124, 126, 129, 130, 131, 132, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 188, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 262, 264, 266, 268, 270, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 306, 308, 310, 312, 314, 317, 319, 321, 323, 325, 327, 329, 330, 331, 332, 334, 337, 339, 341, 343, 344, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 357, 359, 361, 362, 364, 365, 366, 367, 368, 370, 372, 374, 376, 378, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 456, 457, 458, 459, 460, 462, 464, 466, 468, 470, 472, 474, 475, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 491, 493, 494, 495, 496, 497, 498, 499, 501, 503, 505, 507, 508, 509, 510, 511, 512, 514, 515, 516, 518, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 538, 539, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 552, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 567, 570, 572, 574, 576, 578, 579, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 601, 603, 606, 607, 608, 609, 611, 613, 615, 616, 617, 618, 620, 621, 622, 624, 625, 626, 628, 629, 631, 634, 636, 637, 638, 639, 641, 644, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 675, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 695, 697, 699, 701, 702, 704, 706, 708, 709, 711, 712, 713, 714, 716, 718, 720, 721, 723, 725, 726, 728, 730, 732, 734, 736, 738, 740, 741, 742, 743, 744, 745, 747, 749, 750, 751, 753, 755, 757, 759, 761, 762, 763, 764, 765, 767, 769, 771, 773, 774, 776, 778, 779, 780, 782, 783, 784, 786, 788, 790, 792, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804,

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1822, 1823, 1824, 1825, 1826, 1827, 1828, 1829, 1830, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838, 1839, 1840, 1842, 1843, 1844, 1845, 1846, 1847, 1848, 1850, 1852, 1854, 1856, 1858, 1859, 1860, 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1869, 1870, 1871, 1873, 1875, 1877, 1879, 1881, 1883, 1885, 1887, 1889, 1891, 1893, 1895, 1897, 1899, 1901, 1903, 1905, 1907, 1909, 1911, 1913, 1915, 1917, 1919, 1921, 1923, 1925, 1927, 1929, 1931, 1933, 1935, 1937, 1939, 1941, 1943, 1945, 1947, 1949, 1951, 1953, 1955, 1957, 1959, 1961, 1963, 1965, 1967, 1969, 1971, 1973, 1975, 1977, 1979, 1981, 1983, 1985, 1987, 1989, 1991, 1993, 1995, 1997, 1999, 2001, 2003, 2005, 2007, 2009, 2011, 2013, 2015, 2017, 2019, 2021, 2023, 2025, 2027, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2069, 2070, 2072, 2074, 2076, 2078, 2080, 2081, 2083, 2084, 2085, 2087, 2089, 2091, 2093, 2095, 2097, 2099, 2101, 2103, 2105, 2107, 2109, 2111, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2123, 2125, 2127, 2129, 2131, 2133, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2146, 2148, 2150, 2152, 2154, 2156, 2158, 2160, 2162, 2164, 2166, 2168, 2170, 2172, 2174, 2176, 2178, 2180, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2266, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2280, 2282, 2284, 2286, 2288, 2289, 2290, 2292, 2294, 2296, 2298, 2300, 2302, 2304, 2306, 2308, 2310, 2312, 2314, 2316, 2318, 2320, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2350, 2352, 2354, 2356, 2358, 2360, 2362, 2364, 2366, 2368, 2370, 2372, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381. Examples of nucleic acids encoding SD+EODFR and/or low light-tolerance polypeptides are described herein. The SD+EODFR and/or low light-tolerance polypeptide encoded by a recombinant nucleic acid can be a native SD+EODFR and/or low light-tolerance polypeptide, or can be heterologous to the cell. In some cases, the recombinant construct contains a nucleic acid that inhibits expression of an SD+EODFR and/or low light-tolerance polypeptide, operably linked to a regulatory region. Examples of suitable regulatory regions are described in the section entitled "Regulatory Regions."

Vectors containing recombinant nucleic acid constructs such as those described herein also are provided. Suitable vector backbones include, for example, those routinely used in the art such as plasmids, viruses, artificial chromosomes, BACs, YACs, or PACs. Suitable expression vectors include, without limitation, plasmids and viral vectors derived from, for example, bacteriophage, baculoviruses, and retroviruses. Numerous vectors and expression systems are commercially available from such corporations as Novagen (Madison, WI), Clontech (Palo Alto, CA), Stratagene (La Jolla, CA), and Invitrogen/Life Technologies (Carlsbad, CA).

The vectors provided herein also can include, for example, origins of replication, scaffold attachment regions

(SARs), and/or markers. A marker gene can confer a selectable phenotype on a plant cell. For example, a marker can confer biocide resistance, such as resistance to an antibiotic (e.g., kanamycin, G418, bleomycin, or hygromycin), or an herbicide (e.g., glyphosate, chlorsulfuron or phosphinothricin). In addition, an expression vector can include a tag sequence designed to facilitate manipulation or detection (e.g., purification or localization) of the expressed polypeptide. Tag sequences, such as luciferase, β -glucuronidase (GUS), green fluorescent protein (GFP), glutathione S-transferase (GST), polyhistidine, c-myc, hemagglutinin, or FlagTM tag (Kodak, New Haven, CT) sequences typically are expressed as a fusion with the encoded polypeptide. Such tags can be inserted anywhere within the polypeptide, including at either the carboxyl or amino terminus.

F. Regulatory Regions

The choice of regulatory regions to be included in a recombinant construct depends upon several factors, including, but not limited to, efficiency, selectability, inducibility, desired expression level, and cell- or tissue-preferential expression. It is a routine matter for one of skill in the art to modulate the expression of a coding sequence by appropriately selecting and positioning regulatory regions relative to the coding sequence. Transcription of a nucleic acid can be modulated in a similar manner.

Some suitable regulatory regions initiate transcription only, or predominantly, in certain cell types. Methods for identifying and characterizing regulatory regions in plant genomic DNA are known, including, for example, those described in the following references: Jordano et al., *Plant Cell*, 1:855-866 (1989); Bustos et al., *Plant Cell*, 1:839-854 (1989); Green et al., *EMBO J.*, 7:4035-4044 (1988); Meier et al., *Plant Cell*, 3:309-316 (1991); and Zhang et al., *Plant Physiology*, 110:1069-1079 (1996).

Examples of various classes of regulatory regions are described below. Some of the regulatory regions indicated below as well as additional regulatory regions are described in more detail in U.S. Patent Application Ser. Nos. 60/505, 689; 60/518,075; 60/544,771; 60/558,869; 60/583,691; 60/619,181; 60/637,140; 60/757,544; 60/776,307; 10/957, 569; 11/058,689; 11/172,703; 11/208,308; 11/274,890; 60/583,609; 60/612,891; 11/097,589; 11/233,726; 11/408, 791; 11/414,142; 10/950,321; 11/360,017; PCT/US05/ 011105; PCT/US05/23639; PCT/US05/034308; PCT/US05/ 034343; and PCT/US06/038236; PCT/US06/040572; and PCT/US07/62762.

For example, the sequences of regulatory regions p326, YP0144, YP0190, p13879, YP0050, p32449, 21876, YP0158, YP0214, YP0380, PT0848, PT0633, YP0128, YP0275, PT0660, PT0683, PT0758, PT0613, PT0672, PT0688, PT0837, YP0092, PT0676, PT0708, YP0396, YP0007, YP0111, YP0103, YP0028, YP0121, YP0008, YP0039, YP0115, YP0119, YP0120, YP0374, YP0101, YP0102, YP0110, YP0117, YP0137, YP0285, YP0212, YP0097, YP0107, YP0088, YP0143, YP0156, PT0650, PT0695, PT0723, PT0838, PT0879, PT0740, PT0535, PT0668, PT0886, PT0585, YP0381, YP0337, PT0710, YP0356, YP0385, YP0384, YP0286, YP0377, PD1367, PT0863, PT0829, PT0665, PT0678, YP0086, YP0188, YP0263, PT0743 and YP0096 are set forth in the sequence listing of PCT/US06/040572; the sequence of regulatory region PT0625 is set forth in the sequence listing of PCT/ US05/034343; the sequences of regulatory regions PT0623, YP0388, YP0087, YP0093, YP0108, YP0022 and YP0080 are set forth in the sequence listing of U.S. patent application Ser. No. 11/172,703; the sequence of regulatory region PR0924 is set forth in the sequence listing of PCT/US07/

62762; and the sequences of regulatory regions p530c10, pOsFIE2-2, pOsMEA, pOsYp102, and pOsYp285 are set forth in the sequence listing of PCT/US06/038236.

It will be appreciated that a regulatory region may meet criteria for one classification based on its activity in one plant species, and yet meet criteria for a different classification based on its activity in another plant species.

i. Broadly Expressing Promoters

A promoter can be said to be "broadly expressing" when it promotes transcription in many, but not necessarily all, plant tissues. For example, a broadly expressing promoter can promote transcription of an operably linked sequence in one or more of the shoot, shoot tip (apex), and leaves, but weakly or not at all in tissues such as roots or stems. As another example, a broadly expressing promoter can promote transcription of an operably linked sequence in one or more of the stem, shoot, shoot tip (apex), and leaves, but can promote transcription weakly or not at all in tissues such as reproductive tissues of flowers and developing seeds. Non-limiting examples of broadly expressing promoters that can be included in the nucleic acid constructs provided herein include the p326, YP0144, YP0190, p13879, YP0050, p32449, 21876, YP0158, YP0214, YP0380, PT0848, and PT0633 promoters. Additional examples include the cauliflower mosaic virus (CaMV) 35S promoter, the mannopine synthase (MAS) promoter, the 1' or 2' promoters derived from T-DNA of *Agrobacterium tumefaciens*, the figwort mosaic virus 34S promoter, actin promoters such as the rice actin promoter, and ubiquitin promoters such as the maize ubiquitin-1 promoter. In some cases, the CaMV 35S promoter is excluded from the category of broadly expressing promoters.

ii. Root Promoters

Root-active promoters confer transcription in root tissue, e.g., root endodermis, root epidermis, or root vascular tissues. In some embodiments, root-active promoters are root-preferential promoters, i.e., confer transcription only or predominantly in root tissue. Root-preferential promoters include the YP0128, YP0275, PT0625, PT0660, PT0683, and PT0758 promoters. Other root-preferential promoters include the PT0613, PT0672, PT0688, and PT0837 promoters, which drive transcription primarily in root tissue and to a lesser extent in ovules and/or seeds. Other examples of root-preferential promoters include the root-specific subdomains of the CaMV 35S promoter (Lam et al., *Proc. Natl. Acad. Sci. USA*, 86:7890-7894 (1989)), root cell specific promoters reported by Conkling et al., *Plant Physiol.*, 93:1203-1211 (1990), and the tobacco RD2 promoter.

iii. Maturing Endosperm Promoters

In some embodiments, promoters that drive transcription in maturing endosperm can be useful. Transcription from a maturing endosperm promoter typically begins after fertilization and occurs primarily in endosperm tissue during seed development and is typically highest during the cellularization phase. Most suitable are promoters that are active predominantly in maturing endosperm, although promoters that are also active in other tissues can sometimes be used. Non-limiting examples of maturing endosperm promoters that can be included in the nucleic acid constructs provided herein include the napin promoter, the Arcelin-5 promoter, the phaseolin promoter (Bustos et al., *Plant Cell*, 1(9):839-853 (1989)), the soybean trypsin inhibitor promoter (Riggs et al., *Plant Cell*, 1(6):609-621 (1989)), the ACP promoter (Baerson et al., *Plant Mol. Biol.*, 22(2):255-267 (1993)), the stearoyl-ACP desaturase promoter (Slocombe et al., *Plant Physiol.*, 104(4):167-176 (1994)), the soybean α' subunit of β -conglycinin promoter (Chen et al., *Proc. Natl. Acad. Sci.*

USA, 83:8560-8564 (1986)), the oleosin promoter (Hong et al., *Plant Mol. Biol.*, 34(3):549-555 (1997)), and zein promoters, such as the 15 kD zein promoter, the 16 kD zein promoter, 19 kD zein promoter, 22 kD zein promoter and 27 kD zein promoter. Also suitable are the Osgt-1 promoter from the rice glutelin-1 gene (Zheng et al., *Mol. Cell Biol.*, 13:5829-5842 (1993)), the beta-amylase promoter, and the barley hordein promoter. Other maturing endosperm promoters include the YP0092, PT0676, and PT0708 promoters.

iv. Ovary Tissue Promoters

Promoters that are active in ovary tissues such as the ovule wall and mesocarp can also be useful, e.g., a polygalacturonidase promoter, the banana TRX promoter, the melon actin promoter, YP0396, and PT0623. Examples of promoters that are active primarily in ovules include YP0007, YP0111, YP0092, YP0103, YP0028, YP0121, YP0008, YP0039, YP0115, YP0119, YP0120, and YP0374.

v. Embryo Sac/Early Endosperm Promoters

To achieve expression in embryo sac/early endosperm, regulatory regions can be used that are active in polar nuclei and/or the central cell, or in precursors to polar nuclei, but not in egg cells or precursors to egg cells. Most suitable are promoters that drive expression only or predominantly in polar nuclei or precursors thereto and/or the central cell. A pattern of transcription that extends from polar nuclei into early endosperm development can also be found with embryo sac/early endosperm-preferential promoters, although transcription typically decreases significantly in later endosperm development during and after the cellularization phase. Expression in the zygote or developing embryo typically is not present with embryo sac/early endosperm promoters.

Promoters that may be suitable include those derived from the following genes: *Arabidopsis viviparous-1* (see, GenBank No. U93215); *Arabidopsis atmycl* (see, Urao (1996) *Plant Mol. Biol.*, 32:571-57; Conceicao (1994) *Plant*, 5:493-505); *Arabidopsis FIE* (GenBank No. AF129516); *Arabidopsis MEA*; *Arabidopsis FIS2* (GenBank No. AF096096); and FIE 1.1 (U.S. Pat. No. 6,906,244). Other promoters that may be suitable include those derived from the following genes: maize MAC1 (see, Sheridan (1996) *Genetics*, 142: 1009-1020); maize Cat3 (see, GenBank No. L05934; Abler (1993) *Plant Mol. Biol.*, 22:10131-1038). Other promoters include the following *Arabidopsis* promoters: YP0039, YP0101, YP0102, YP0110, YP0117, YP0119, YP0137, DME, YP0285, and YP0212. Other promoters that may be useful include the following rice promoters: p530c10, pOsFIE2-2, pOsMEA, pOsYp102, and pOsYp285.

vi. Embryo Promoters

Regulatory regions that preferentially drive transcription in zygotic cells following fertilization can provide embryo-preferential expression. Most suitable are promoters that preferentially drive transcription in early stage embryos prior to the heart stage, but expression in late stage and maturing embryos is also suitable. Embryo-preferential promoters include the barley lipid transfer protein (Ltp1) promoter (*Plant Cell Rep* (2001) 20:647-654), YP0097, YP0107, YP0088, YP0143, YP0156, PT0650, PT0695, PT0723, PT0838, PT0879, and PT0740.

vii. Photosynthetic Tissue Promoters

Promoters active in photosynthetic tissue confer transcription in green tissues such as leaves and stems. Most suitable are promoters that drive expression only or predominantly in such tissues. Examples of such promoters include the ribulose-1,5-bisphosphate carboxylase (RbcS) promoters such as the RbcS promoter from eastern larch

(*Larix laricina*), the pine cab6 promoter (Yamamoto et al., *Plant Cell Physiol.*, 35:773-778 (1994)), the Cab-1 promoter from wheat (Fejes et al., *Plant Mol. Biol.*, 15:921-932 (1990)), the CAB-1 promoter from spinach (Lubberstedt et al., *Plant Physiol.*, 104:997-1006 (1994)), the cab1R promoter from rice (Luan et al., *Plant Cell*, 4:971-981 (1992)), the pyruvate orthophosphate dikinase (PPDK) promoter from corn (Matsuoka et al., *Proc. Natl. Acad. Sci. USA*, 90:9586-9590 (1993)), the tobacco LhcB1*2 promoter (Cerdan et al., *Plant Mol. Biol.*, 33:245-255 (1997)), the *Arabidopsis thaliana* SUC2 sucrose-H⁺ symporter promoter (Truernit et al., *Planta*, 196:564-570 (1995)), and thylakoid membrane protein promoters from spinach (psaD, psaF, psaE, PC, FNR, atpC, atpD, cab, rbcS). Other photosynthetic tissue promoters include PT0535, PT0668, PT0886, YP0144, YP0380 and PT0585.

viii. Vascular Tissue Promoters

Examples of promoters that have high or preferential activity in vascular bundles include YP0087, YP0093, YP0108, YP0022, and YP0080. Other vascular tissue-preferential promoters include the glycine-rich cell wall protein GRP 1.8 promoter (Keller and Baumgartner, *Plant Cell*, 3(10):1051-1061 (1991)), the *Commelinina* yellow mottle virus (CoYMV) promoter (Medberry et al., *Plant Cell*, 4(2):185-192 (1992)), and the rice tungro bacilliform virus (RTBV) promoter (Dai et al., *Proc. Natl. Acad. Sci. USA*, 101(2):687-692 (2004)).

ix. Inducible Promoters

Inducible promoters confer transcription in response to external stimuli such as chemical agents or environmental stimuli. For example, inducible promoters can confer transcription in response to hormones such as gibberellic acid or ethylene, or in response to light or drought. Examples of drought-inducible promoters include YP0380, PT0848, YP0381, YP0337, PT0633, YP0374, PT0710, YP0356, YP0385, YP0396, YP0388, YP0384, PT0688, YP0286, YP0377, PD1367, and PD0901. Examples of nitrogen-inducible promoters include PT0863, PT0829, PT0665, and PT0886. Examples of shade-inducible promoters include PR0924 and PT0678. An example of a promoter induced by salt is rd29A (Kasuga et al. (1999) *Nature Biotech* 17: 287-291).

x. Basal Promoters

A basal promoter is the minimal sequence necessary for assembly of a transcription complex required for transcription initiation. Basal promoters frequently include a "TATA box" element that may be located between about 15 and about 35 nucleotides upstream from the site of transcription initiation. Basal promoters also may include a "CCAAT box" element (typically the sequence CCAAT) and/or a GGGCG sequence, which can be located between about 40 and about 200 nucleotides, typically about 60 to about 120 nucleotides, upstream from the transcription start site.

xi. Other Promoters

Other classes of promoters include, but are not limited to, shoot-preferential, callus-preferential, trichome cell-preferential, guard cell-preferential such as PT0678, tuber-preferential, parenchyma cell-preferential, and senescence-preferential promoters. Promoters designated YP0086, YP0188, YP0263, PT0758, PT0743, PT0829, YP0119, and YP0096, as described in the above-referenced patent applications, may also be useful.

xii. Other Regulatory Regions

A 5' untranslated region (UTR) can be included in nucleic acid constructs described herein. A 5' UTR is transcribed, but is not translated, and lies between the start site of the transcript and the translation initiation codon and may

include the +1 nucleotide. A 3' UTR can be positioned between the translation termination codon and the end of the transcript. UTRs can have particular functions such as increasing mRNA stability or attenuating translation. Examples of 3' UTRs include, but are not limited to, polyadenylation signals and transcription termination sequences, e.g., a nopaline synthase termination sequence.

It will be understood that more than one regulatory region may be present in a recombinant polynucleotide, e.g., 10 introns, enhancers, upstream activation regions, transcription terminators, and inducible elements. Thus, for example, more than one regulatory region can be operably linked to the sequence of a polynucleotide encoding an SD+EODFR and/or low light-tolerance polypeptide.

Regulatory regions, such as promoters for endogenous genes, can be obtained by chemical synthesis or by subcloning from a genomic DNA that includes such a regulatory region. A nucleic acid comprising such a regulatory region can also include flanking sequences that contain restriction 20 enzyme sites that facilitate subsequent manipulation.

IV. TRANSGENIC PLANTS AND PLANT CELLS

A. Transformation

The invention also features transgenic plant cells and plants comprising at least one recombinant nucleic acid construct described herein. A plant or plant cell can be transformed by having a construct integrated into its genome, i.e., can be stably transformed. Stably transformed cells typically retain the introduced nucleic acid with each cell division. A plant or plant cell can also be transiently transformed such that the construct is not integrated into its genome. Transiently transformed cells typically lose all or some portion of the introduced nucleic acid construct with each cell division such that the introduced nucleic acid cannot be detected in daughter cells after a sufficient number of cell divisions. Both transiently transformed and stably transformed transgenic plants and plant cells can be useful in the methods described herein.

Transgenic plant cells used in methods described herein can constitute part or all of a whole plant. Such plants can be grown in a manner suitable for the species under consideration, either in a growth chamber, a greenhouse, or in a field. Transgenic plants can be bred as desired for a particular purpose, e.g., to introduce a recombinant nucleic acid into other lines, to transfer a recombinant nucleic acid to other species, or for further selection of other desirable traits. Alternatively, transgenic plants can be propagated vegetatively for those species amenable to such techniques. As used herein, a transgenic plant also refers to progeny of an initial transgenic plant provided the progeny inherits the transgene. Seeds produced by a transgenic plant can be grown and then selfed (or outcrossed and selfed) to obtain seeds homozygous for the nucleic acid construct.

Transgenic plants can be grown in suspension culture, or tissue or organ culture. For the purposes of this invention, solid and/or liquid tissue culture techniques can be used. When using solid medium, transgenic plant cells can be placed directly onto the medium or can be placed onto a filter that is then placed in contact with the medium. When using liquid medium, transgenic plant cells can be placed onto a flotation device, e.g., a porous membrane that contacts the liquid medium. A solid medium can be, for example, Murashige and Skoog (MS) medium containing agar and a suitable concentration of an auxin, e.g., 2,4-dichlorophenoxyacetic acid (2,4-D), and a suitable concentration of a cytokinin, e.g., kinetin.

When transiently transformed plant cells are used, a reporter sequence encoding a reporter polypeptide having a reporter activity can be included in the transformation procedure and an assay for reporter activity or expression can be performed at a suitable time after transformation. A suitable time for conducting the assay typically is about 1-21 days after transformation, e.g., about 1-14 days, about 1-7 days, or about 1-3 days. The use of transient assays is particularly convenient for rapid analysis in different species, or to confirm expression of a heterologous SD+EODFR and/or low light-tolerance polypeptide whose expression has not previously been confirmed in particular recipient cells.

Techniques for introducing nucleic acids into monocotyledonous and dicotyledonous plants are known in the art, and include, without limitation, *Agrobacterium*-mediated transformation, viral vector-mediated transformation, electroporation and particle gun transformation, e.g., U.S. Pat. Nos. 5,538,880; 5,204,253; 6,329,571 and 6,013,863. If a cell or cultured tissue is used as the recipient tissue for transformation, plants can be regenerated from transformed cultures if desired, by techniques known to those skilled in the art.

B. Screening/Selection

A population of transgenic plants can be screened and/or selected for those members of the population that have a trait or phenotype conferred by expression of the transgene. For example, a population of progeny of a single transformation event can be screened for those plants having a desired level of expression of an SD+EODFR and/or low light-tolerance polypeptide or nucleic acid. Physical and biochemical methods can be used to identify expression levels. These include Southern analysis or PCR amplification for detection of a polynucleotide; Northern blots, S1 RNase protection, primer-extension, or RT-PCR amplification for detecting RNA transcripts; enzymatic assays for detecting enzyme or ribozyme activity of polypeptides and polynucleotides; and protein gel electrophoresis, Western blots, immunoprecipitation, and enzyme-linked immunoassays to detect polypeptides. Other techniques such as *in situ* hybridization, enzyme staining, and immunostaining also can be used to detect the presence or expression of polypeptides and/or polynucleotides. Methods for performing all of the referenced techniques are known. As an alternative, a population of plants comprising independent transformation events can be screened for those plants having a desired trait, such as a modulated level SD+EODFR and/or low light tolerance. Selection and/or screening can be carried out over one or more generations, and/or in more than one geographic location. In some cases, transgenic plants can be grown and selected under conditions which induce a desired phenotype or are otherwise necessary to produce a desired phenotype in a transgenic plant. In addition, selection and/or screening can be applied during a particular developmental stage in which the phenotype is expected to be exhibited by the plant. Selection and/or screening can be carried out to choose those transgenic plants having a statistically significant difference in SD+EODFR and/or low light tolerance level relative to a control plant that lacks the transgene. Selected or screened transgenic plants have an altered phenotype as compared to a corresponding control plant, as described in the "Transgenic Plant Phenotypes" section herein.

C. Plant Species

The polynucleotides and vectors described herein can be used to transform a number of monocotyledonous and dicotyledonous plants and plant cell systems, including species from one of the following families: Acanthaceae, Aliaceae, Alstroemeriaeae, Amaryllidaceae, Apocynaceae,

Arecaceae, Asteraceae, Berberidaceae, Bixaceae, Brassicaceae, Bromeliaceae, Cannabaceae, Caryophyllaceae, Cephalotaxaceae, Chenopodiaceae, Colchicaceae, Cucurbitaceae, Dioscoreaceae, Ephedraceae, Erythroxylaceae, Euphorbiaceae, Fabaceae, Lamiaceae, Linaceae, Lycopodiaceae, Malvaceae, Melanthiaceae, Musaceae, Myrtaceae, Nymphaeaceae, Papaveraceae, Pinaceae, Plantaginaceae, Poaceae, Rosaceae, Rubiaceae, Salicaceae, Sapindaceae, Solanaceae, Taxaceae, Theaceae, or Vitaceae.

- 10 Suitable species may include members of the genus *Abelmoschus*, *Abies*, *Acer*, *Agrostis*, *Allium*, *Alstroemeria*, *Ananas*, *Andrographis*, *Andropogon*, *Artemisia*, *Arundo*, *Atropa*, *Berberis*, *Beta*, *Bixa*, *Brassica*, *Calendula*, *Camellia*, *Camptotheca*, *Cannabis*, *Capsicum*, *Carthamus*, *Catharanthus*, *Cephalotaxus*, *Chrysanthemum*, *Cinchona*, *Citrus*, *Coffea*, *Colchicum*, *Coleus*, *Cucumis*, *Cucurbita*, *Cynodon*, *Datura*, *Dianthus*, *Digitalis*, *Dioscorea*, *Elaeis*, *Ephedra*, *Erianthus*, *Erythroxylum*, *Eucalyptus*, *Festuca*, *Fragaria*, *Galanthus*, *Glycine*, *Gossypium*, *Helianthus*, *Hevea*, *Hordeum*, *Hyoscyamus*, *Jatropha*, *Lactuca*, *Linum*, *Lolium*, *Lupinus*, *Lycopersicon*, *Lycopodium*, *Manihot*, *Medicago*, *Mentha*, *Misanthus*, *Musa*, *Nicotiana*, *Oryza*, *Panicum*, *Papaver*, *Parthenium*, *Pennisetum*, *Petunia*, *Phalaris*, *Phleum*, *Pinus*, *Poa*, *Poinsettia*, *Populus*, *Rauwolfia*, *Ricinus*, *Rosa*, *Saccharum*, *Salix*, *Sanguinaria*, *Scopolia*, *Secale*, *Solanum*, *Sorghum*, *Spartina*, *Spinacea*, *Tanacetum*, *Taxus*, *Theobroma*, *Triticosecale*, *Triticum*, *Uniola*, *Veratrum*, *Vitis*, and *Zea*.

Suitable species include *Panicum* spp. or hybrids thereof, *Sorghum* spp. or hybrids thereof, sudangrass, *Misanthus* spp. or hybrids thereof, *Saccharum* spp. or hybrids thereof, *Erianthus* spp., *Populus* spp., *Andropogon gerardii* (big bluestem), *Pennisetum purpureum* (elephant grass) or hybrids thereof (e.g., *Pennisetum purpureum**x**Pennisetum typhoidum*), *Phalaris arundinacea* (reed canarygrass), *Cynodon dactylon* (bermudagrass), *Festuca arundinacea* (tall fescue), *Spartina pectinata* (prairie cord-grass), *Medicago sativa* (alfalfa), *Arundo donax* (giant reed) or hybrids thereof, *Secale cereale* (rye), *Salix* spp. (willow), *Eucalyptus* spp. (eucalyptus), *Triticosecale* (triticum—wheat X rye) and bamboo.

In some embodiments, a suitable species can be a wild, weedy, or cultivated sorghum species such as, but not limited to, *Sorghum alnum*, *Sorghum amplum*, *Sorghum angustum*, *Sorghum arundinaceum*, *Sorghum bicolor* (such as bicolor, guinea, caudatum, kafir, and durra), *Sorghum brachypodium*, *Sorghum bulbosum*, *Sorghum burmahicum*, *Sorghum controversum*, *Sorghum drummondii*, *Sorghum ecarinatum*, *Sorghum exstans*, *Sorghum grande*, *Sorghum halepense*, *Sorghum interjectum*, *Sorghum intrans*, *Sorghum laxiflorum*, *Sorghum leiocladium*, *Sorghum macrosperrum*, *Sorghum matarankense*, *Sorghum miliaceum*, *Sorghum nigrum*, *Sorghum nitidum*, *Sorghum plumbosum*, *Sorghum propinquum*, *Sorghum purpleosericum*, *Sorghum stipoides*, *Sorghum sudanense*, *Sorghum timorense*, *Sorghum trichocladum*, *Sorghum versicolor*, *Sorghum virgatum*, *Sorghum vulgare*, or hybrids such as *Sorghum**x**alnum*, *Sorghum**x*sudangrass or *Sorghum**x**drummondii*.

Suitable species also include *Helianthus annuus* (sunflower), *Carthamus tinctorius* (safflower), *Jatropha curcas* (jatropha), *Ricinus communis* (castor), *Elaeis guineensis* (palm), *Linum usitatissimum* (flax), and *Brassica juncea*.

Suitable species also include *Beta vulgaris* (sugarbeet), and *Manihot esculenta* (cassava).

Suitable species also include *Lycopersicon esculentum* (tomato), *Lactuca sativa* (lettuce), *Musa paradisiaca* (banana), *Solanum tuberosum* (potato), *Brassica oleracea*

(broccoli, cauliflower, Brussels sprouts), *Camellia sinensis* (tea), *Fragaria ananassa* (strawberry), *Theobroma cacao* (cocoa), *Coffea arabica* (coffee), *Vitis vinifera* (grape), *Ananas comosus* (pineapple), *Capsicum annuum* (hot & sweet pepper), *Allium cepa* (onion), *Cucumis melo* (melon), *Cucumis sativus* (cucumber), *Cucurbita maxima* (squash), *Cucurbita moschata* (squash), *Spinacea oleracea* (spinach), *Citrullus lanatus* (watermelon), *Abelmoschus esculentus* (okra), and *Solanum melongena* (eggplant).

Suitable species also include *Papaver somniferum* (opium poppy), *Papaver orientale*, *Taxus baccata*, *Taxus brevifolia*, *Artemisia annua*, *Cannabis sativa*, *Camptotheca acuminata*, *Catharanthus roseus*, *Vinca rosea*, *Cinchona officinalis*, *Colchicum autumnale*, *Veratrum californica*, *Digitalis lanata*, *Digitalis purpurea*, *Dioscorea* spp., *Andrographis paniculata*, *Atropa belladonna*, *Datura stramonium*, *Berberis* spp., *Cephalotaxus* spp., *Ephedra sinica*, *Ephedra* spp., *Erythroxylum coca*, *Galanthus woronowii*, *Scopolia* spp., *Lycopodium serratum* (= *Huperzia serrata*), *Lycopodium* spp., *Rauwolfia serpentina*, *Rauwolfia* spp., *Sanguinaria canadensis*, *Hyoscyamus* spp., *Calendula officinalis*, *Chrysanthemum parthenium*, *Coleus forskohlii*, and *Tanacetum parthenium*.

Suitable species also include *Parthenium argentatum* (guayule), *Hevea* spp. (rubber), *Mentha spicata* (mint), *Mentha piperita* (mint), *Bixa orellana*, and *Alstroemeria* spp.

Suitable species also include *Rosa* spp. (rose), *Dianthus caryophyllus* (carnation), *Petunia* spp. (petunia) and *Poinsettia pulcherrima* (poinsettia). Suitable species also include *Nicotiana tabacum* (tobacco), *Lupinus albus* (lupin), *Uniola paniculata* (oats), bentgrass (*Agrostis* spp.), *Populus tremuloides* (aspen), *Pinus* spp. (pine), *Abies* spp. (fir), *Acer* spp. (maple), *Hordeum vulgare* (barley), *Poa pratensis* (bluegrass), *Lolium* spp. (ryegrass) and *Phleum pratense* (timothy).

Thus, the methods and compositions can be used over a broad range of plant species, including species from the dicot genera *Brassica*, *Carthamus*, *Glycine*, *Gossypium*, *Helianthus*, *Jatropha*, *Parthenium*, *Populus*, and *Ricinus*; and the monocot genera *Elaeis*, *Festuca*, *Hordeum*, *Lolium*, *Oryza*, *Panicum*, *Pennisetum*, *Phleum*, *Poa*, *Saccharum*, *Secale*, *Sorghum*, *Triticosecale*, *Triticum*, and *Zea*. In some embodiments, a plant is a member of the species *Panicum virgatum* (switchgrass), *Sorghum bicolor* (sorghum, sudangrass), *Miscanthus giganteus* (miscanthus), *Saccharum* sp. (energycane), *Populus balsamifera* (poplar), *Zea mays* (corn), *Glycine max* (soybean), *Brassica napus* (canola), *Triticum aestivum* (wheat), *Gossypium hirsutum* (cotton), *Oryza sativa* (rice), *Helianthus annuus* (sunflower), *Medicago sativa* (alfalfa), *Beta vulgaris* (sugarbeet), or *Pennisetum glaucum* (pearl millet).

In certain embodiments, the polynucleotides and vectors described herein can be used to transform a number of monocotyledonous and dicotyledonous plants and plant cell systems, wherein such plants are hybrids of different species or varieties of a specific species (e.g., *Saccharum* sp. \times *Miscanthus* sp., *Panicum virgatum* \times *Panicum amarum*, *Panicum virgatum* \times *Panicum amarulum*, and *Pennisetum purpureum* \times *Pennisetum typhoidum*).

D. Transgenic Plant Phenotypes

The light in shady environments is enriched in FR wavelengths relative to the light in non-shady environments. Red wavelengths typically range from a photon irradiance of about 630 nm to a photon irradiance of about 700 nm.

Far-red wavelengths typically range from a photon irradiance of about 700 nm to a photon irradiance of about 750 nm.

In some embodiments, a plant in which expression of an SD+EODFR and/or low light-tolerance polypeptide is modulated can have increased SD+EODFR and/or low light tolerance. The phenotype of a transgenic plant in which expression of an SD+EODFR and/or low light-tolerance polypeptide is modulated and a corresponding control plant that either lacks the transgene or does not express the transgene can be evaluated under particular environmental conditions that are useful for simulating shade, i.e., Short Day plus End-of-Day Far-Red (SD+EODFR) conditions. SD+EODFR conditions consist of a light period followed by a pulse of far-red-enriched light conditions followed by a 14 hour dark period. The light period is from about 9.0 to about 9.6 hours with a red:far-red ratio of about 5.5, with the following fluence rates: blue₄₅₀=12 $\mu\text{mol}/\text{m}^2/\text{s}$, red 633=22 $\mu\text{mol}/\text{m}^2/\text{s}$, far-red₇₄₀=4 $\mu\text{mol}/\text{m}^2/\text{s}$, PPFD₄₀₀₋₇₀₀=55 $\mu\text{mol}/\text{m}^2/\text{s}$. The pulse of far-red-enriched light conditions is from about 0.4 to about 1.0 hours with a red:far-red ratio of about 0.14 with the following fluence rates: blue₄₅₀=0.004 $\mu\text{mol}/\text{m}^2/\text{s}$, red 633=10 $\mu\text{mol}/\text{m}^2/\text{s}$, far-red₇₄₀=70 $\mu\text{mol}/\text{m}^2/\text{s}$, PPFD₄₀₀₋₇₀₀=8 $\mu\text{mol}/\text{m}^2/\text{s}$. Sources of lighting equipment appropriate for producing and maintaining SD+EODFR conditions are known to those in art.

The phenotype of a transgenic plant in which expression of an SD+EODFR and/or low light-tolerance polypeptide is modulated and a corresponding control plant can also be evaluated under conditions of low light irradiance. Low light conditions are conditions under which a plant is exposed to an irradiance of about 0.01 $\mu\text{mol}/\text{m}^2/\text{s}$ of light to about 20 $\mu\text{mol}/\text{m}^2/\text{s}$ of light at room temperature and about 70% relative humidity. For example, conditions under which a plant is exposed to 0.01, 1, 5, 10, 15, or 20 $\mu\text{mol}/\text{m}^2/\text{s}$ of light are low light conditions. Sources of lighting and other equipment appropriate for controlling light conditions are known to those in art.

Low light conditions typically have light of a combination of wavelengths, such as white light. White light can be supplied, e.g., by 32 watt fluorescent bulbs (Sylvania, F_{032/841}/ECO, Danvers, MA), providing a red:far-red ratio of 13:1. Red wavelengths typically range from a photon irradiance of about 630 to about 700 nm. Far-red wavelengths typically range from a photon irradiance of about 700 to about 750 nm.

In some embodiments, the phenotype of a transgenic plant is assayed under low light conditions in which there is continuous low light during the light period of a light/dark cycle. Continuous low light conditions can be, for example, 16 hours of irradiance with 0.01 to 20 $\mu\text{mol}/\text{m}^2/\text{s}$ of light alternating with 8 hours of darkness. The phenotype of a transgenic plant is assayed once the plant has been exposed to continuous low light conditions during the light period of the light/dark cycle for seven days.

In some embodiments, the phenotype of a transgenic plant is assayed under red light conditions in which there is continuous red light. Continuous red light conditions can be, for example, continuous irradiance with about -15 $\mu\text{mol}/\text{m}^2/\text{s}$ of light with a red light to far-red light ratio (R:FR) of about 80. Continuous red light can be supplied by a LED array that can be used to activate and deactivate the plant photoreceptor phytochrome (e.g., SNAP-LITE™ Quantum Devices, WI). The phenotype of a transgenic plant is assayed once the plant has been exposed to continuous red light conditions for about five days.

95

In some embodiments, the phenotype of a transgenic plant is assayed under far-red light conditions in which there is continuous far-red light. Continuous far-red light conditions can be, for example, continuous irradiance with about 5 $\mu\text{mol}/\text{m}^2/\text{s}$ of light with a R:FR of about 0.10. Continuous far-red light can be supplied by a LED array that can be used to activate and deactivate the plant photoreceptor phytochrome (e.g., SNAP-LITETM Quantum Devices, WI). The phenotype of a transgenic plant is assayed once the plant has been exposed to continuous far-red light conditions for about five days.

In some embodiments, the phenotype of a transgenic plant is assayed under natural daylight or other broad spectrum light conditions. Natural daylight conditions, can be, for example, full sun or other natural irradiation of green house or field grown transgenic plants. Broad spectrum conditions can be irradiation supplied by a fluorescent lamp with continuous fluence rates of about 12 $\mu\text{mol}/\text{m}^2/\text{s}$ of blue 450 light, 22 $\mu\text{mol}/\text{m}^2/\text{s}$ of red 633 light, 4 $\mu\text{mol}/\text{m}^2/\text{s}$ far-red 740 light, and photosynthetically active radiation (PAR₄₀₀₋₇₀₀) of about 55 $\mu\text{mol}/\text{m}^2/\text{s}$, with a R:FR of about 5. Other broad spectrum conditions can be, for example, continuous broad-spectrum light during the light period of a light/dark photocycle. In some cases, continuous broad spectrum light can be 16 hours of irradiance of about 15 to 55 $\mu\text{mol}/\text{m}^2/\text{s}$ PAR₄₀₀₋₇₀₀, alternating with 8 hours of darkness, with a dark period of 8 hours, for example. In some cases, continuous broad spectrum light can be 12 hours of irradiance of about to 55 $\mu\text{mol}/\text{m}^2/\text{s}$ PAR₄₀₀₋₇₀₀, alternating with 12 hours of darkness, for example. The phenotype of a transgenic plant is assayed during maturation and/or once the plant has reached maturity.

As compared to a control plant that does not express an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions, a transgenic plant expressing an SD+EODFR and/or low light-tolerance polypeptide can exhibit one or more of the following phenotypes under SD+EODFR conditions or low light conditions: decreases in extension growth, acceleration in leaf development, decreased apical dominance, increased chloroplast development, alterations in flowering and seed/fruit production, and an increase in storage organ deposition.

As compared to a control plant that does not overexpress a red specific light response pathway polypeptide grown under continuous red light or far-red light conditions, a transgenic plant overexpressing a red light specific response pathway polypeptide can exhibit decreases in hypocotyl length under continuous red light or natural daylight conditions, but has similar hypocotyl length under continuous far-red light or dark conditions.

Typically, a difference (e.g., an increase or a decrease) in a morphological feature in a transgenic plant or cell relative to a control plant or cell is considered statistically significant at $p \leq 0.05$ with an appropriate parametric or non-parametric statistic, e.g., Chi-square test, Student's t-test, Mann-Whitney test, or F-test. In some embodiments, a difference in the dimensions of any individual morphological feature is statistically significant at $p < 0.01$, $p < 0.005$, or $p < 0.001$. A statistically significant difference in, for example, a morphological feature in a transgenic plant compared to the corresponding morphological feature a control plant indicates that expression of the recombinant nucleic acid present in the transgenic plant confers the alteration in the morphological feature.

Examples of a decrease in extension growth include, without limitation, decreased petiole length, decreased hypocotyl length, decreased internode spacing, and

96

decreased leaf elongation in cereals, when comparing a transgenic plant expressing an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions to a control plant that does not express an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions. A decrease in extension growth can be a decrease of from about 0.25% to about 90%, e.g., from about 0.25% to about 15%, from about 5% to about 50%, from about 5% to about 10%, from about 25% to about 50%, from about 1% to about 30%, from about 50% to about 90%, from about 20% to about 40%, from about 1% to about 5%, from about 0.5% to about 2%, from about 15% to about 50%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 55%, about 60%, about 65%, about 70%, about 75%, or about 80%.

One suitable phenotype to measure is hypocotyl length. When wild-type seedlings are grown under SD+EODFR conditions or low light conditions, the hypocotyl length is typically significantly increased relative to the hypocotyl length found in wild-type seedlings grown under control light conditions. Thus, seedlings of a transgenic plant and seedlings of a corresponding control plant that either lacks the transgene or does not express the transgene can be grown under SD+EODFR conditions or low light conditions and at the appropriate time, hypocotyl lengths from seedlings of each group can be measured. Under SD+EODFR conditions or low light conditions, a seedling in which the expression of an SD+EODFR and/or low light-tolerance polypeptide is increased can have a statistically significantly shorter hypocotyl length than a seedling of a corresponding control plant that either lacks the transgene or does not express the transgene. The hypocotyl length can be shorter by at least 20 percent, e.g., 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, or 80 percent, as compared to the hypocotyl length in a corresponding control plant that does not express the transgene.

When wild-type seedlings are grown under continuous red-light conditions, the hypocotyl length is typically significantly decreased relative to the hypocotyl length found in wild-type seedlings grown under continuous far-red light conditions. Thus, seedlings of a transgenic plant and seedlings of a corresponding control plant that either lacks the transgene or does not express the transgene can be grown under continuous red-light conditions or far-red light conditions and at the appropriate time, hypocotyl lengths from seedlings of each group can be measured. Under red light conditions, a seedling in which the expression of a red light specific response pathway polypeptide is increased can have a statistically significantly shorter hypocotyl length than a seedling of a corresponding control plant that either lacks the transgene or does not express the transgene. The hypocotyl length can be shorter by at least 20 percent, e.g., 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, or 80 percent, as compared to the hypocotyl length in a corresponding control plant that does not express the transgene. Under far-red conditions, a seedling in which the expression of a red light specific response pathway polypeptide is increased can have a hypocotyl of similar length to a corresponding control plant that either lacks the transgene or does not express the transgene.

In contrast, a seedling in which the expression of a red light specific response pathway polypeptide is decreased can have a statistically significantly longer hypocotyl length than a seedling of a corresponding control plant that either lacks the transgene or does not express the transgene. The hypocotyl length can be longer by at least 20 percent, e.g., 20, 25,

30, 35, 40, 45, 50, 55, 60, 65, 70, 75, or 80 percent, as compared to the hypocotyl length in a corresponding control plant that does not express the transgene. Under far-red conditions, a seedling in which the expression of a red light specific response pathway polypeptide is decreased can have a hypocotyl of similar length to a corresponding control plant that either lacks the transgene or does not express the transgene.

Another suitable phenotype can be overall plant height of mature plants. When wild-type plants are grown under natural light or other broad spectrum light conditions, the plant height at maturity can be significantly decreased relative to the plant height found in wild-type plants grown under low light conditions. Thus, the transgenic plant and a corresponding control plant that either lacks the transgene or does not express the transgene can be grown under natural light conditions or low light conditions and at maturity, the height of the plants from each group can be measured. Under natural light or other broad spectrum light conditions, a mature plant in which the expression of a red light specific response pathway polypeptide is decreased can have a statistically significantly taller plant than a mature plant of a corresponding control plant that either lacks the transgene or does not express the transgene. The plant height can be taller by at least 20 percent, e.g., 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, or 75 percent, as compared to the height in a corresponding control plant that does not express the transgene.

Another suitable phenotype can be rate of plant growth. The rate of plant growth can be determined by measuring differences in fresh weight (T/acre), or differences in sub-apical cell expansion, over a period of time, for example. When wild-type plants are grown under natural light or other broad spectrum light conditions, the rate of plant growth can be significantly slower relative to the rate of plant growth found in wild-type plants grown under low light conditions. Thus, the transgenic plant and a corresponding control plant that either lacks the transgene or does not express the transgene can be grown under natural light conditions or low light conditions and during maturation, the rate of plant growth for plants from each group can be measured. Under natural light or other broad spectrum light conditions, a plant in which the expression of a red light specific response pathway polypeptide is decreased can have a statistically significantly increased rate of plant growth, than a plant of a corresponding control plant that either lacks the transgene or does not express the transgene. The rate of growth can be increased by at least 2 percent, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, or more than 60 percent, as compared to the growth rate in a corresponding control plant that does not express the transgene. Another suitable phenotype to measure can be dry matter yield of stem parts, or above ground parts, excluding inflorescence and seed parts of a plant. When wild-type plants are grown under natural light or other broad spectrum light conditions, the dry matter yield can be significantly decreased relative to the dry matter yield found in wild-type plants grown under low light conditions. Thus, the transgenic plant and a corresponding control plant that either lacks the transgene or does not express the transgene can be grown under natural light conditions or low light conditions and at harvest, the dry matter yield of the plants from each group can be measured. Under natural light or other broad spectrum light conditions, a mature plant in which the expression of a red light specific response pathway polypeptide is decreased can have a statistically significantly greater dry matter yield than a mature plant of a

corresponding control plant that either lacks the transgene or does not express the transgene. Dry matter yield (DMY) yield is calculated using the fresh matter weight (FMW) and a measurement of weight percent moisture (M) in the following equation. $DMY=((100-M)/100)*FMW$. For example, the dry matter yield can be increased by at least 2 percent, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, or more than 60 percent, as compared to the dry matter yield level in a corresponding control plant that does not express the transgene.

Another suitable phenotype to measure is petiole length. When wild-type seedlings are grown under SD+EODFR conditions or low light conditions, the petiole length is typically significantly increased relative to the petiole length found in wild-type seedlings grown under control light conditions. Thus, seedlings of a transgenic plant and seedlings of a corresponding control plant that either lacks the transgene or does not express the transgene can be grown under SD+EODFR conditions or low light conditions and at the appropriate time, petiole lengths from seedlings of each group can be measured. Under SD+EODFR conditions or low light conditions, a seedling in which the expression of an SD+EODFR and/or low light-tolerance polypeptide is increased can have a statistically significantly shorter petiole length than a seedling of a corresponding control plant that either lacks the transgene or does not express the transgene. The petiole length can be shorter by at least 20 percent, e.g., 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, or 75 percent, as compared to the petiole length in a corresponding control plant that does not express the transgene.

Examples of acceleration in leaf development include, without limitation, increased leaf thickness and increased leaf area growth when comparing a transgenic plant expressing an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions to a control plant that does not express an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions. Leaf thickness or leaf area growth can be increased by about 0.25% to about 200% (e.g., about 0.25% to about 2%, about 0.5% to about 5%, about 0.5% to about 15%, about 2% to about 10%, about 5% to about 35%, about 10% to about 25%, about 20% to about 80%, about 50% to about 200%, about 100% to about 200%, about 100% to about 150%, about 5%, about 10%, about 20%, about 35%, about 50%, about 70%, about 90%, about 120%, about 180%, or about 200%) in a transgenic plant expressing an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions as compared to a control plant that does not express an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions.

Examples of decreased apical dominance include, without limitation, increased branching and increased tillering when comparing a transgenic plant expressing an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions to a control plant that does not express an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions. Branching and tillering can be increased by about 0.25% to about 200% (e.g., about 0.25% to about 2%, about 0.5% to about 5%, about 0.5% to about 15%, about 2% to about 10%, about 5% to about 35%, about 10% to about 25%, about 20% to about 80%, about 50% to about 200%, about 100% to about 200%, about 100% to about 200%, about 100% to about 150%, about 5%, about 10%, about 20%, about 35%, about 50%, about 70%, about 90%, about 120%, about 180%, or about 200%) in a transgenic plant expressing an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions. Branching and tillering can be increased by about 0.25% to about 200% (e.g., about 0.25% to about 2%, about 0.5% to about 5%, about 0.5% to about 15%, about 2% to about 10%, about 5% to about 35%, about 10% to about 25%, about 20% to about 80%, about 50% to about 200%, about 100% to about 200%, about 100% to about 150%, about 5%, about 10%, about 20%, about 35%, about 50%, about 70%, about 90%, about 120%, about 180%, or about 200%) in a transgenic plant expressing an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions.

99

about 35%, about 50%, about 70%, about 90%, about 120%, about 180%, or about 200%) in a transgenic plant expressing an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions as compared to a control plant that does not express an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions.

Examples of increased apical dominance include, without limitation, decreased branching and decreased tillering when comparing a transgenic plant in which a red light specific response pathway polypeptide is down-regulated to a control plant that either lacks the transgene or does not express the transgene grown natural light or other broad spectrum light conditions. Branching and tillering can be decreased by about 0.25% to about 200% (e.g., about 0.25% to about 2%, about 0.5% to about 5%, about 0.5% to about 15%, about 2% to about 10%, about 5% to about 35%, about 10% to about 25%, about 20% to about 80%, about 50% to about 200%, about 100% to about 200%, about 100% to about 150%, about 5%, about 10%, about 20%, about 35%, about 50%, about 70%, about 90%, about 120%, about 180%, or about 200%) in a transgenic plant in which a red light specific response pathway polypeptide is down-regulated grown under natural light or other broad spectrum light conditions as compared to a control plant that either lacks the transgene or does not express the transgene grown natural light or other broad spectrum light conditions.

Examples of increased chloroplast development include, without limitation, increased chlorophyll synthesis and a change in the chlorophyll a:b ratio when comparing a transgenic plant expressing an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions to a control plant that does not express an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions. Chlorophyll synthesis and/or the chlorophyll a:b ratio can be about 0.25% to about 200% (e.g., about 0.25% to about 2%, 0.25% to about 0.5%, about 0.25% to about 1.5%, about 0.5% to about 1%, about 0.5% to about 5%, about 0.5% to about 15%, about 2% to about 10%, about 5% to about 35%, about 10% to about 25%, about 20% to about 80%, about 50% to about 200%, about 100% to about 200%, about 100% to about 100% to about 150%, about 5%, about 10%, about 20%, about 35%, about 50%, about 70%, about 90%, about 120%, about 180%, or about 200%) greater in a transgenic plant expressing an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions as compared to a control plant that does not express an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions.

Examples of alterations in flowering and seed/fruit production include, without limitation, a decreased rate of flowering, an increase in seed set, and an increase of fruit development when comparing a transgenic plant expressing an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions to a control plant that does not express an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions. The rate of flowering can be a decreased from about 0.25% to about 90% (e.g., from about 0.25% to about 15%, from about 5% to about 50%, from about 5% to about 10%, from about 25% to about 50%, from about 1% to about 30%, from about 50% to about 90%, from about 20% to about 40%, from about 1% to about 5%, from about 0.5% to about 2%, from about 15% to about 50%, about 20%, about 25%, about 30%, about

100

35%, about 40%, about 45%, about 50%, about 55%, about 60%, about 65%, about 70%, about 75%, or about 80%) in a transgenic plant expressing an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions as compared to a control plant that does not express an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions. Seed or fruit weight can be increased by about 0.25% to about 200% (e.g., about 0.25% to about 2%, about 0.5% to about 5%, about 0.5% to about 15%, about 2% to about 10%, about 5% to about 35%, about 10% to about 25%, about 20% to about 80%, about 50% to about 200%, about 100% to about 200%, about 100% to about 150%, about 5%, about 10%, about 20%, about 35%, about 50%, about 70%, about 90%, about 120%, about 180%, or about 200%) in a transgenic plant expressing an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions as compared to a control plant that does not express an SD+EODFR and/or low light-tolerance polypeptide grown under SD+EODFR conditions or low light conditions.

The phenotype of a transgenic plant is evaluated relative to a control plant. A plant is said "not to express" a polypeptide when the plant exhibits less than 10%, e.g., less than 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, 0.01%, or 0.001% of the amount of polypeptide or mRNA encoding the polypeptide exhibited by the plant of interest. Expression can be evaluated using methods including, for example, RT-PCR, Northern blots, 5' RNase protection, primer extensions, Western blots, protein gel electrophoresis, immunoprecipitation, enzyme-linked immunoassays, chip assays, and mass spectrometry. It should be noted that if a polypeptide is expressed under the control of a tissue-preferential or broadly expressing promoter, expression can be evaluated in the entire plant or in a selected tissue. Similarly, if a polypeptide is expressed at a particular time, e.g., at a particular time in development or upon induction, expression can be evaluated selectively at a desired time period.

V. PLANT BREEDING

Genetic polymorphisms are discrete allelic sequence differences in a population. Typically, an allele that is present at 1% or greater is considered to be a genetic polymorphism. The discovery that polypeptides disclosed herein can modulate SD+EODFR and/or low light tolerance is useful in plant breeding, because genetic polymorphisms exhibiting a degree of linkage with loci for such polypeptides are more likely to be correlated with variation in SD+EODFR and/or low light tolerance. For example, genetic polymorphisms linked to the loci for such polypeptides are more likely to be useful in marker-assisted breeding programs to create lines having SD+EODFR and/or low light tolerance.

Thus, one aspect of the invention includes methods of identifying whether one or more genetic polymorphisms are associated with variation in SD+EODFR and/or low light tolerance. Such methods involve determining whether genetic polymorphisms in a given population exhibit linkage with the locus for one of the polypeptides depicted in FIGS. 1-24 and/or a functional homolog thereof. The correlation is measured between variation in SD+EODFR and/or low light tolerance in plants of the population and the presence of the genetic polymorphism(s) in plants of the population, thereby identifying whether or not the genetic polymorphism(s) are associated with variation for the trait. If the presence of a particular allele is statistically significantly correlated with a

101

desired modulation in SD+EODFR and/or low light tolerance, the allele is associated with variation for the trait and is useful as a marker for the trait. If, on the other hand, the presence of a particular allele is not significantly correlated with the desired modulation, the allele is not associated with variation for the trait and is not useful as a marker.

Such methods are applicable to populations containing the naturally occurring endogenous polypeptide rather than an exogenous nucleic acid encoding the polypeptide, i.e., populations that are not transgenic for the exogenous nucleic acid. It will be appreciated, however, that populations suitable for use in the methods may contain a transgene for another, different trait, e.g., herbicide resistance.

Genetic polymorphisms that are useful in such methods include simple sequence repeats (SSRs, or microsatellites), rapid amplification of polymorphic DNA (RAPDs), single nucleotide polymorphisms (SNPs), amplified fragment length polymorphisms (AFLPs) and restriction fragment length polymorphisms (RFLPs). SSR polymorphisms can be identified, for example, by making sequence specific probes and amplifying template DNA from individuals in the population of interest by PCR. If the probes flank an SSR in the population, PCR products of different sizes will be produced. See, e.g., U.S. Pat. No. 5,766,847. Alternatively, SSR polymorphisms can be identified by using PCR product(s) as a probe against Southern blots from different individuals in the population. See, U. H. Refseth et al., (1997) Electrophoresis 18: 1519. The identification of RFLPs is discussed, for example, in Alonso-Blanco et al. (Methods in Molecular Biology, vol. 82, "Arabidopsis Protocols", pp. 137-146, J. M. Martinez-Zapater and J. Salinas, eds., c. 1998 by Humana Press, Totowa, NJ); Burr ("Mapping Genes with Recombinant Inbreds", pp. 249-254, in Freeling, M. and V. Walbot (Ed.), The Maize Handbook, c. 1994 by Springer-Verlag New York, Inc.: New York, NY, USA; Berlin Germany; Burr et al. Genetics (1998) 118: 519; and Gardiner, J. et al., (1993) Genetics 134: 917). The identification of AFLPs is discussed, for example, in EP 0 534 858 and U.S. Pat. No. 5,878,215.

In some embodiments, the methods are directed to breeding a plant line. Such methods use genetic polymorphisms identified as described above in a marker assisted breeding program to facilitate the development of lines that have a desired alteration in SD+EODFR and/or low light tolerance. Once a suitable genetic polymorphism is identified as being associated with variation for the trait, one or more individual plants are identified that possess the polymorphic allele correlated with the desired variation. Those plants are then used in a breeding program to combine the polymorphic allele with a plurality of other alleles at other loci that are correlated with the desired variation. Techniques suitable for use in a plant breeding program are known in the art and include, without limitation, backcrossing, mass selection, pedigree breeding, bulk selection, crossing to another population and recurrent selection. These techniques can be used alone or in combination with one or more other techniques in a breeding program. Thus, each identified plants is selfed or crossed a different plant to produce seed which is then germinated to form progeny plants. At least one such progeny plant is then selfed or crossed with a different plant to form a subsequent progeny generation. The breeding program can repeat the steps of selfing or outcrossing for an additional 0 to 5 generations as appropriate in order to achieve the desired uniformity and stability in the resulting plant line, which retains the polymorphic allele. In most breeding programs, analysis for the particular polymorphic

102

allele will be carried out in each generation, although analysis can be carried out in alternate generations if desired.

In some cases, selection for other useful traits is also carried out, e.g., selection for fungal resistance or bacterial resistance. Selection for such other traits can be carried out before, during or after identification of individual plants that possess the desired polymorphic allele.

VI. ARTICLES OF MANUFACTURE

Transgenic plants provided herein have various uses in the agricultural and energy production industries. For example, transgenic plants described herein can be used to make animal feed and food products. Such plants, however, are often particularly useful as a feedstock for energy production.

Transgenic plants described herein often produce higher yields of grain and/or biomass per hectare, relative to control plants that lack the exogenous nucleic acid. In some embodiments, such transgenic plants provide equivalent or even increased yields of grain and/or biomass per hectare relative to control plants when grown under conditions of low light conditions and/or SD+EODFR conditions. Thus, such transgenic plants can be used to provide yield stability under environmentally stressful conditions such as low light conditions and/or SD+EODFR conditions. By providing higher yields under environmentally stressful conditions such as low light conditions and/or SD+EODFR conditions, the transgenic plants described herein improve profitability for farmers and processors as well as decrease costs to consumers.

Seeds from transgenic plants described herein can be conditioned and bagged in packaging material by means known in the art to form an article of manufacture. Packaging material such as paper and cloth are well known in the art. A package of seed can have a label, e.g., a tag or label secured to the packaging material, a label printed on the packaging material, or a label inserted within the package, that describes the nature of the seeds therein.

VII. OTHER POLYPEPTIDES, NUCLEIC ACIDS, PLANT CELLS, PLANTS, AND METHODS

In some cases, this document provides methods and materials involved in plant UV-B tolerance. For example, this document provides seeds and plants having cells comprising an exogenous nucleic acid encoding a polypeptide having UV-B tolerance activity as described in U.S. Patent Application Publication No. 2010-0192261 (U.S. patent application Ser. No. 12/373,134), which is incorporated by reference herein in its entirety. In some cases, a plant can include a polypeptide or nucleic acid or can be made to include a polypeptide or nucleic acid such that the sequence of such a polypeptide or nucleic acid is as set forth in one of the identified sequences of U.S. Patent Application Publication No. 2010-0192261 (U.S. patent application Ser. No. 12/373,134) (e.g., SEQ ID NOS:1-119 of U.S. Patent Application Publication No. 2010-0192261 (U.S. patent application Ser. No. 12/373,134)), or is a homolog or ortholog thereof as described in U.S. Patent Application Publication No. 2010-0192261 (U.S. patent application Ser. No. 12/373,134), or has at least 80% sequence identity (e.g., at least 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity) to an identified sequence of U.S. Patent Application Publication No. 2010-0192261 (U.S. patent application Ser. No. 12/373,134), as set forth in U.S. Patent Application Publication No. 2010-0192261 (U.S. patent application Ser.

103

No. 12/373,134). SEQ ID NOs:1-119 of U.S. Patent Application Publication No. 2010-0192261 (U.S. patent application Ser. No. 12/373,134), together with the identified activities for each of SEQ ID NOs:1-119, the described homologs and orthologs of SEQ ID NOs:1-119 and their associated activities, the sequences having at least 80% sequence identity (e.g., at least 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity) to SEQ ID NOs:1-119 and their associated activities, the phenotypes of plants containing any one of SEQ ID NOs:1-119 or the described homologs of SEQ ID NOs:1-119 or the described orthologs of SEQ ID NOs:1-119 or the described sequences having at least 80% sequence identity to any one of SEQ ID NOs:1-119, and the working examples and data set forth in Examples 1-6 of U.S. Patent Application Publication No. 2010-0192261 (U.S. patent application Ser. No. 12/373,134) are incorporated by reference herein.

In some cases, this document provides methods and materials involved in tolerance of plants to low light conditions. For example, this document provides transgenic plants and seeds comprising nucleic acids encoding polypeptides that confer tolerance to conditions of low light irradiance as described in U.S. Patent Application Publication No. 2010-0205688 (U.S. Patent Application Ser. No. 12/513,086), which is incorporated by reference herein in its entirety. In some cases, a plant can include a polypeptide or nucleic acid or can be made to include a polypeptide or nucleic acid such that the sequence of such a polypeptide or nucleic acid is as set forth in one of the identified sequences of U.S. Patent Application Publication No. 2010-0205688 (U.S. Patent Application Ser. No. 12/513,086) (e.g., SEQ ID NOs:1-149 of U.S. Patent Application Publication No. 2010-0205688 (U.S. patent application Ser. No. 12/513,086)), or is a homolog or ortholog thereof as described in U.S. Patent Application Publication No. 2010-0205688 (U.S. patent application Ser. No. 12/513,086), or has at least 80% sequence identity (e.g., at least 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity) to an identified sequence of U.S. Patent Application Publication No. 2010-0205688 (U.S. patent application Ser. No. 12/513,086), as set forth in U.S. Patent Application Publication No. 2010-0205688 (U.S. patent application Ser. No. 12/513,086). SEQ ID NOs:1-149 of U.S. Patent Application Publication No. 2010-0205688 (U.S. patent application Ser. No. 12/513,086), together with the identified activities for each of SEQ ID NOs:1-149, the described homologs and orthologs of SEQ ID NOs:1-149 and their associated activities, the sequences having at least 80% sequence identity (e.g., at least 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity) to SEQ ID NOs:1-149 and their associated activities, the phenotypes of plants containing any one of SEQ ID NOs:1-149 or the described homologs of SEQ ID NOs:1-149 or the described orthologs of SEQ ID NOs:1-149 or the described sequences having at least 80% sequence identity to any one of SEQ ID NOs:1-149, and the working examples and data set forth in Examples 1-8 of U.S. Patent Application Publication No. 2010-0205688 (U.S. Patent Application Ser. No. 12/513,086) are incorporated by reference herein.

In some cases, this document provides methods and materials involved in shade tolerance in plants. For example, this document provides plants having increased shade tolerance as well as materials and methods for making plants having increased shade tolerance and plant products derived from plants having increased shade tolerance as described in U.S. Patent Application Publication No. 2010-0199378 (U.S. patent application Ser. No. 12/515,687), which is incorporated by reference herein in its entirety. In some

104

cases, a plant can include a polypeptide or nucleic acid or can be made to include a polypeptide or nucleic acid such that the sequence of such a polypeptide or nucleic acid is as set forth in one of the identified sequences of U.S. Patent Application Publication No. 2010-0199378 (U.S. patent application Ser. No. 12/515,687) (e.g., SEQ ID NOs:1-171 of U.S. Patent Application Publication No. 2010-0199378 (U.S. Patent Application Ser. No. 12/515,687)), or is a homolog or ortholog thereof as described in U.S. Patent Application Publication No. 2010-0199378 (U.S. Patent Application Ser. No. 12/515,687), or has at least 80% sequence identity (e.g., at least 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity) to an identified sequence of U.S. Patent Application Publication No. 2010-0199378 (U.S. patent application Ser. No. 12/515,687), as set forth in U.S. Patent Application Publication No. 2010-0199378 (U.S. patent application Ser. No. 12/515,687). SEQ ID NOs:1-171 of U.S. Patent Application Publication No. 2010-0199378 (U.S. Patent Application Ser. No. 12/515,687), together with the identified activities for each of SEQ ID NOs:1-171, the described homologs and orthologs of SEQ ID NOs:1-171 and their associated activities, the sequences having at least 80% sequence identity (e.g., at least 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity) to SEQ ID NOs:1-171 and their associated activities, the phenotypes of plants containing any one of SEQ ID NOs:1-171 or the described homologs of SEQ ID NOs:1-171 or the described orthologs of SEQ ID NOs:1-171 or the described sequences having at least 80% sequence identity to any one of SEQ ID NOs:1-171, and the working examples and data set forth in Examples 1-11 of U.S. Patent Application Publication No. 2010-0199378 (U.S. Patent Application Ser. No. 12/515,687) are incorporated by reference herein.

In some cases, this document provides methods and materials involved in tolerance of plants to low light conditions. For example, this document provides transgenic plants and seeds comprising nucleic acids encoding polypeptides that confer tolerance to conditions of low light irradiance as described in U.S. Patent Application Publication No. 2010-0119688 (U.S. patent application Ser. No. 12/307,561), which is incorporated by reference herein in its entirety. In some cases, a plant can include a polypeptide or nucleic acid or can be made to include a polypeptide or nucleic acid such that the sequence of such a polypeptide or nucleic acid is as set forth in one of the identified sequences of U.S. Patent Application Publication No. 2010-0119688 (U.S. patent application Ser. No. 12/307,561) (e.g., SEQ ID NOs:1-146 of U.S. Patent Application Publication No. 2010-0119688 (U.S. patent application Ser. No. 12/307,561)), or is a homolog or ortholog thereof as described in U.S. Patent Application Publication No. 2010-0119688 (U.S. patent application Ser. No. 12/307,561), or has at least 80% sequence identity (e.g., at least 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity) to an identified sequence of U.S. Patent Application Publication No. 2010-0119688 (U.S. patent application Ser. No. 12/307,561), as set forth in U.S. Patent Application Publication No. 2010-0119688 (U.S. patent application Ser. No. 12/307,561). SEQ ID NOs:1-146 of U.S. Patent Application Publication No. 2010-0119688 (U.S. patent application Ser. No. 12/307,561), together with the identified activities for each of SEQ ID NOs:1-146, the described homologs and orthologs of SEQ ID NOs:1-146 and their associated activities, the sequences having at least 80% sequence identity (e.g., at least 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity) to SEQ ID NOs:1-146 and their associated activities, the

105

phenotypes of plants containing any one of SEQ ID NOS: 1-146 or the described homologs of SEQ ID NOS:1-146 or the described orthologs of SEQ ID NOS:1-146 or the described sequences having at least 80% sequence identity to any one of SEQ ID NOS:1-146, and the working examples and data set forth in Examples 1-22 of U.S. Patent Application Publication No. 2010-0119688 (U.S. patent application Ser. No. 12/307,561) are incorporated by reference herein.

In some cases, this document provides methods and materials involved in modulating biomass levels in plants. For example, this document provides plants having increased biomass levels as well as materials and methods for making plants and plant products having increased biomass levels as described in International Patent Application Publication No. WO 2010/033564 and U.S. patent application Ser. No. 13/119,572, which are incorporated by reference herein in their entireties. In some cases, a plant can include a polypeptide or nucleic acid or can be made to include a polypeptide or nucleic acid such that the sequence of such a polypeptide or nucleic acid is as set forth in one of the identified sequences of International Patent Application Publication No. WO 2010/033564 and U.S. patent application Ser. No. 13/119,572 (e.g., SEQ ID NOS:1-638 of International Patent Application Publication No. WO 2010/033564 and U.S. patent application Ser. No. 13/119,572), or is a homolog or ortholog thereof as described in International Patent Application Publication No. WO 2010/033564 and U.S. patent application Ser. No. 13/119,572, or has at least 80% sequence identity (e.g., at least 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity) to an identified sequence of International Patent Application Publication No. WO 2010/033564 and U.S. patent application Ser. No. 13/119,572, as set forth in International Patent Application Publication No. WO 2010/033564 and U.S. patent application Ser. No. 13/119,572. SEQ ID NOS:1-638 of International Patent Application Publication No. WO 2010/033564 and U.S. patent application Ser. No. 13/119,572, together with the identified activities for each of SEQ ID NOS:1-638, the described homologs and orthologs of SEQ ID NOS:1-638 and their associated activities, the sequences having at least 80% sequence identity (e.g., at least 80%, 85%, 90%, 95%, 97%, 98%, or 99% sequence identity) to SEQ ID NOS:1-638 and their associated activities, the phenotypes of plants containing any one of SEQ ID NOS:1-638 or the described homologs of SEQ ID NOS:1-638 or the described orthologs of SEQ ID NOS:1-638 or the described sequences having at least 80% sequence identity to any one of SEQ ID NOS:1-638, and the working examples and data set forth in Examples 1-11 of International Patent Application Publication No. WO 2010/033564 and U.S. patent application Ser. No. 13/119,572 are incorporated by reference herein.

The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

VIII. EXAMPLES

Example 1—Transgenic *Arabidopsis* Plants

The following symbols are used in the Examples with respect to *Arabidopsis* transformation: T₁: first generation transformant; T₂: second generation, progeny of self-pollinated T₁ plants; T₃: third generation, progeny of self-pollinated T₂ plants; T₄: fourth generation, progeny of self-pollinated T₃ plants. Independent transformations are referred to as events.

106

Nucleic acids were isolated from *Arabidopsis thaliana* plants, and cloned into a Ti plasmid vector, CRS338 or CRS 811, under the control of a 35S promoter. Each construct contained a phosphinothricin acetyltransferase gene which confers Finale™ resistance to transformed plants. Wild-type *Arabidopsis thaliana* ecotype Wassilewskija (Ws) plants were transformed separately with each construct. The transformations were performed essentially as described in Bechtold et al., *C.R. Acad. Sci. Paris*, 316:1194-1199 (1993).

Transgenic *Arabidopsis* lines containing SEQ ID NO:1, SEQ ID NO:69, SEQ ID NO:127, SEQ ID NO:315, SEQ ID NO:335, SEQ ID NO:454, SEQ ID NO:537, SEQ ID NO:568, SEQ ID NO:604, SEQ ID NO:632, SEQ ID NO:642, SEQ ID NO:848, SEQ ID NO:905, SEQ ID NO:951, SEQ ID NO:1023, SEQ ID NO:1045, SEQ ID NO:1150, SEQ ID NO:1276, SEQ ID NO:1345, SEQ ID NO:1456, SEQ ID NO:1496, SEQ ID NO:1539, SEQ ID NO:1586, SEQ ID NO:1629, or SEQ ID NO:1634 were designated, ME05268, ME06120, ME09503, ME10007, ME10852, ME11939, ME12006, ME12596, ME12899, ME13456, ME15935, ME16594, ME16597, ME16630, ME17128, ME17578, ME18158, ME18314, ME18408, ME19304, ME19738, ME19971, ME20871, ME21199, or ME21508, respectively. The presence of each vector containing a nucleic acid described above in the respective transgenic *Arabidopsis* line transformed with the vector was confirmed by Finale™ resistance, PCR amplification from green leaf tissue extract, and/or sequencing of PCR products.

Example 2—Identification of Transgenic Plants Tolerant to Low Light Conditions

Wild-type and transgenic seeds were sterilized, plated on solid 0.5x MS medium containing 5 g/L sucrose, and stratified at 4° C. in the dark for three days. After stratification, plates containing the seeds were allowed to reach room temperature. The plates were then transferred to a Conviron walk-in growth chamber (Controlled Environments Inc., Pambina, ND) at 22° C. and 70% humidity with a 16:8 hour light:dark cycle. Lighting was supplied by 32 watt fluorescent bulbs (Sylvania, F032/841/ECO, Danvers, MA), providing a red:far-red ratio of 13:1. The plates were covered with three layers of shade cloth (New York wire, charcoal fiberglass screen, 857650; Home Depot, Atlanta, GA) such that the irradiance was about 10 μmol/m²/s. The plates were rotated daily and monitored for changes in hypocotyl elongation. After 48 hours, the plates were scored for late germinators, which were eliminated from consideration as candidate plants having reduced hypocotyl elongation under low light conditions. Each seedling was transplanted to an 8x8 cm well of a flat containing a total of 18 wells (three wells by six wells) and measuring 24 cm by 48 cm in size.

Seedlings maintained under conditions of irradiance with about 10 pimol/m² ls of light fbr seven days at 22° C. were analyzed for hypocotyl length. The hypocotyls of individual seedlings were determined to be “long” or “short” based on qualitative observation.

Example 3—Identification of Transgenic Plants Tolerant to Short Day Plus End-of-Day-Far-Red (SD+EODFR) Conditions

A Short Day plus End-of-Day-Far-Red (SD+EODFR) assay was carried out on seedlings in order to evaluate the effect of SD+EODFR conditions on hypocotyl length. For

the SD+EODFR assay, seeds were plated on 0.5% sucrose, 1×MS media (PhytoTech) agar plates, cold-treated for 3-4 days at 4° C., then germinated for 2 days under continuous white light at about 60 $\mu\text{mol}/\text{m}^2/\text{s}$ in walk-in Conviron growth chambers. Seedlings were then exposed to SD+EODFR conditions for 4 days. SD+EODFR conditions were 9.5 hours light, followed by a 30 minute pulse of far-red light at the end of each light cycle, alternating with 14 hours of darkness. Two Gro-Lux (Sylvania, 24660) and two Cool White (Phillips) lights at about 60 $\mu\text{mol}/\text{m}^2/\text{s}$ PPFD, with a red: far-red ratio of about 5.5, were used for the light cycle; the fluence rates under these conditions were: blue₄₅₀=12 $\mu\text{mol}/\text{m}^2/\text{s}$, red₆₃₃=22 $\mu\text{mol}/\text{m}^2/\text{s}$, far-red₇₄₀=4 $\mu\text{mol}/\text{m}^2/\text{s}$, PPFD₄₀₀₋₇₀₀=55 $\mu\text{mol}/\text{m}^2/\text{s}$. The far-red pulse was generated by 3 SNAP-LITE Far-red light boxes (Quantum devices, SL1515-670-735) at about 8 $\mu\text{mol}/\text{m}^2/\text{s}$ PPFD, with a red: far-red ratio of about 0.14; the fluence rates under these conditions were: blue₄₅₀=0.004 $\mu\text{mol}/\text{m}^2/\text{s}$, red₆₃₃=ss, far-red₇₄₀=70 $\mu\text{mol}/\text{m}^2/\text{s}$, PPFD₄₀₀₋₇₀₀=8 $\mu\text{mol}/\text{m}^2/\text{s}$. Control seedlings were cultured exactly as above except that they did not receive the far-red pulse; that is, following germination, they were exposed for two days to a cycle of 10 hours of light alternating with 14 hours of darkness under 2 Gro-Lux and 2 Cool white lights at about 60 $\mu\text{mol}/\text{m}^2/\text{s}$ PPFD, with a red: far-red ratio of about 5.5. Plates were rotated on the third day after plating and hypocotyl length was characterized on the fourth day after plating. The hypocotyls of individual seedlings were determined to be "long" or "short" based on qualitative observation.

Seedlings were then sprayed with sterile Finale® (concentration=0.63%), on two subsequent days, then allowed to grow for 24 hours before chlorophyll fluorescence imaging was done to determine the Finale® resistant:Finale® sensitive ratio. Finale® sensitivity was determined by placing plates of Finale® treated seedlings in a chlorophyll fluorescence imager (CF Imager, Technologica Limited, UK). Finale® resistant seedlings appeared red and Finale® sensitive seedlings appeared blue. Hypocotyl lengths from Finale® resistant seedlings and Finale® sensitive seedlings were then subjected to a Chi-squared analysis to determine statistical significance.

Example 4—Results for ME05268, ME06120, ME09503, ME10007, ME10852, ME11939, ME13456, ME15935, ME16594, ME16597, ME16630, ME17128, ME17578, ME18158, ME18314, ME19304, ME19738, ME20871, ME21199, and ME21508 Events

T₃ and T₄ seed from event -03 of ME05268, T₂ and T₃ seed from event -04 of ME05268, T₂ and T₃ seed from events -11 and -12 of ME06120, T₂ and T₃ seed from events -03 and -07 of ME09503, T₂ and T₃ seed from events -02 and -05 of ME10007, T₂ and T₃ seed from events -03 and -04 of ME10852, T₂ and T₃ seed from events -01, -02, and -03 of ME11939, T₂ and T₃ seed from events -02 and -05 of ME13456, T₂ and T₃ seed from events -03 and -04 of ME15935, T₃ and T₄ seed from events -02 and -05 of ME16594, T₂ and T₃ seed from events -01, -04, and -06 of ME16597, T₂ and T₃ seed from events -01, -02, and -04 of ME16630, T₂ and T₃ seed from events -02, -03, and -03 of ME17128, T₂ and T₃ seed from events -01 and -03 of ME17578, T₂ and T₃ seed from events -01, -03, and -04 of ME18158, T₂ and T₃ seed from events -01, -02, -03, and -04 of ME18314, T₂ and T₃ seed from events -07 and -08 of ME19304, T₂ and T₃ seed from events -02 and -05 of ME19738, T₂ and T₃ seed from events -03, -05, and -10 of

ME20871, T₂ and T₃ seed from events -01, -03 and -05 of ME21199, T₂ and T₃ seed from events -01 and -05 of ME21508 was grown under low light conditions and evaluated for hypocotyl length as described in Example 2.

A Chi-square test was performed to compare transgenic seedlings and corresponding non-transgenic segregants having a short or a long hypocotyl. A hypocotyl having a length similar to the hypocotyl length typically exhibited by wild-type *Arabidopsis* seedlings grown under normal light conditions (e.g., about 100 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light) was considered a short hypocotyl, whereas a hypocotyl having a length similar to that typically exhibited by wild-type *Arabidopsis* seedlings grown under low light conditions (e.g., about 10 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light) was considered a long hypocotyl. Wild-type *Arabidopsis* seeds grown for seven days at 22° C. under conditions of irradiance with about 100 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light and a 16:8 hour light:dark cycle typically form hypocotyls that are about 1-3 mm in length. Under conditions of irradiance with about 10 $\mu\text{mol}/\text{m}^2/\text{s}$ of white light, the hypocotyls typically are about 5-7 mm in length.

Seedlings from event -03 of ME05268; event -04 of ME05268; events -11 and -12 of ME06120; events -03 and -07 of ME09503; events -02 and -05 of ME10007; events -03 and -04 of ME10852; events -01, -02, and -03 of ME11939; events -02 and -05 of ME13456; events -03 and -04 of ME15935; events -02 and -05 of ME16594; events -01, -04, and -06 of ME16597; events -01, -02, and -04 of ME16630; events -02, -03, and -03 of ME17128; events -01 and -03 of ME17578; events -01, -03, and -04 of ME18158; events -01, -02, -03, and -04 of ME18314; events -07 and -08 of ME19304; events -02 and -05 of ME19738; events -03, -05, and -10 of ME20871; events -01, -03 and -05 of ME21199; and events -01 and -05 of ME21508 displayed a short hypocotyl under low light conditions in both the T₂ and T₃ generations, and the transgene was linked to the short hypocotyl phenotype with a confidence level of p<0.05 (Tables 1-23).

T₃ or T₄ data designated with -99 are data obtained from seed pooled from multiple individual plants of the indicated generation and event.

45

TABLE 1

Plants	Hypocotyl length in seedlings from ME05268			Chi-Square	p-value
	Short Hypo-cotyl	Long Hypo-cotyl			
T ₃ seedlings from event -03-99 of ME05268	32	6	54.35	1.68E-13	
T ₃ non-transgenic segregants of event -03-99 of ME05268	0	37			
T ₄ seedlings from event -03-99-99 of ME05268	69	3	53.00	1.68E-13	
T ₄ non-transgenic segregants of event -03-99-99 of ME05268	0	7			
T ₂ seedlings from event -04 of ME05268	55	9	17.98	2.23E-05	
T ₂ non-transgenic segregants of event -04 of ME05268	0	4			
T ₃ seedlings from event -04-99 of ME05268	52	8	40.81	1.68E-10	
T ₃ non-transgenic segregants of event -04-99 of ME05268	0	14			

US 12,385,057 B2

109

TABLE 2

Hypocotyl length in seedlings from ME06120					
Plants	Short Hypo-cotyl	Long Hypo-cotyl	Chi-Square	p-value	
T ₂ seedlings from event -11 of ME06120	26	4	16.89	3.96E-05	
T ₂ non-transgenic segregants of event -11 of ME05268	1	7			
T ₃ seedlings from event -11-99 of ME06120	52	3	37.89	7.48E-10	
T ₃ non-transgenic segregants of event -11-99 of ME06120	4	13			
T ₂ seedlings from event -12 of ME06120	27	2	14.43	1.45E-04	
T ₂ non-transgenic segregants of event -12 of ME06120	0	2			
T ₃ seedlings from event -12-99 of ME06120	46	0	39.93	2.63E-10	
T ₃ non-transgenic segregants of event -12-99 of ME06120	1	4			

TABLE 3

Hypocotyl length in seedlings from ME09503					
Plants	Short Hypo-cotyl	Long Hypo-cotyl	Chi-Square	p-value	
T ₂ seedlings from event -03 of ME09503	34	4	35.47	2.59E-09	
T ₂ non-transgenic segregants of event -03 of ME09503	1	16			
T ₃ seedlings from event -03-99 of ME09503	55	0	68.85	1.06E-16	
T ₃ non-transgenic segregants of event -03-99 of ME09503	1	18			
T ₂ seedlings from event -07 of ME09503	46	1	44.94	2.03E-11	
T ₂ non-transgenic segregants of event -07 of ME09503	2	12			
T ₃ seedlings from event -07-99 of ME09503	72	1	56.91	4.56E-14	
T ₃ non-transgenic segregants of event -07-99 of ME09503	1	6			

TABLE 4

Hypocotyl length in seedlings from ME10007					
Plants	Short Hypo-cotyl	Long Hypo-cotyl	Chi-Square	p-value	
T ₂ seedlings from event -02 of ME10007	57	3	42.15	8.45E-11	
T ₂ non-transgenic segregants of event -02 of ME10007	5	15			
T ₃ seedlings from event -02-99 of ME10007	50	8	40.30	2.18E-10	
T ₃ non-transgenic segregants of event -02-99 of ME10007	2	19			
T ₂ seedlings from event -05 of ME10007	58	0	37.14	1.10E-09	
T ₂ non-transgenic segregants of event -05 of ME10007	9	11			
T ₃ seedlings from event -05-99 of ME10007	49	6	39.36	3.53E-10	
T ₃ non-transgenic segregants of event -05-99 of ME10007	3	18			

110

TABLE 5

Hypocotyl length in seedlings from ME10852					
Plants	Short Hypo-cotyl	Long Hypo-cotyl	Chi-Square	p-value	
T ₂ seedlings from event -03 of ME10852	57	1	48.97	2.59E-12	
T ₂ non-transgenic segregants of event -03 of ME10852	5	15			
T ₃ seedlings from event -03-99 of ME10852	55	0	35.66	2.59E-09	
T ₃ non-transgenic segregants of event -03-99 of ME10852	11	13			
T ₂ seedlings from event -04 of ME10852	57	0	71.00	3.57E-17	
T ₂ non-transgenic segregants of event -04 of ME10852	0	14			
T ₃ seedlings from event -04-99 of ME10852	63	3	57.75	2.97E-14	
T ₃ non-transgenic segregants of event -04-99 of ME10852	0	11			

TABLE 6

Hypocotyl length in seedlings from ME11939					
Plants	Short Hypo-cotyl	Long Hypo-cotyl	Chi-Square	p-value	
T ₂ seedlings from event -01 of ME11939	32	6	29.39	5.93E-08	
T ₂ non-transgenic segregants of event -01 of ME11939	0	13			
T ₃ seedlings from event -01-99 of ME11939	47	0	52.88	3.55E-13	
T ₃ non-transgenic segregants of event -01-99 of ME11939	2	14			
T ₂ seedlings from event -02 of ME11939	42	5	23.34	1.35E-06	
T ₂ non-transgenic segregants of event -02 of ME11939	4	11			
T ₃ seedlings from event -02-99 of ME11939	46	2	44.94	2.03E-11	
T ₃ non-transgenic segregants of event -02-99 of ME11939	1	12			
T ₂ seedlings from event -05 of ME11939	45	8	27.72	1.40E-07	
T ₂ non-transgenic segregants of event -05 of ME11939	4	16			
T ₃ seedlings from event -05-99 of ME11939	33	0	27.59	1.50E-07	
T ₃ non-transgenic segregants of event -05-99 of ME11939	3	7			

TABLE 7

Hypocotyl length in seedlings from ME13456					
Plants	Short Hypo-cotyl	Long Hypo-cotyl	Chi-Square	p-value	
T ₂ seedlings from event -02 of ME13456	18	1	12.28	4.58E-04	
T ₂ non-transgenic segregants of event -02 of ME13456	3	6			
T ₃ seedlings from event -02-99 of ME13456	47	3	34.55	4.16E-09	
T ₃ non-transgenic segregants of event -02-99 of ME13456	1	8			
T ₂ seedlings from event -05 of ME13456	14	2	13.13	2.91E-04	
T ₂ non-transgenic segregants of event -05 of ME13456	0	5			

US 12,385,057 B2

111

TABLE 7-continued

Hypocotyl length in seedlings from ME13456				
Plants	Short Hypo-cotyl	Long Hypo-cotyl	Chi-Square	p-value
T ₃ seedlings from event -05-99 of ME13456	21	3	23.42	1.30E-06
T ₃ non-transgenic segregants of event -05-99 of ME13456	1	13		

TABLE 8

Hypocotyl length in seedlings from ME15935				
Plants	Short Hypo-cotyl	Long Hypo-cotyl	Chi-Square	p-value
T ₂ seedlings from event -03 of ME15935	44	2	33.90	5.81E-09
T ₂ non-transgenic segregants of event -03 of ME15935	2	12		
T ₃ seedlings from event -03-99 of ME15935	53	3	51.86	5.97E-13
T ₃ non-transgenic segregants of event -03-99 of ME15935	1	15		
T ₂ seedlings from event -04 of ME15935	23	0	33.00	9.22E-09
T ₂ non-transgenic segregants of event -04 of ME15935	0	10		
T ₃ seedlings from event -04-99 of ME15935	58	0	41.24	1.34E-10
T ₃ non-transgenic segregants of event -04-99 of ME15935	2	4		

TABLE 9

Hypocotyl length in seedlings from ME16594				
Plants	Short Hypo-cotyl	Long Hypo-cotyl	Chi-Square	p-value
T ₂ seedlings from event -02 of ME16594	16	0	37.14	1.10E-09
T ₂ non-transgenic segregants of event -02 of ME16594	12	52		
T ₃ seedlings from event -02-99 of ME16594	46	10	10.18	1.42E-03
T ₃ non-transgenic segregants of event -02-99 of ME16594	4	7		
T ₂ seedlings from event -05 of ME16594	35	2	52.10	5.28E-13
T ₂ non-transgenic segregants of event -05 of ME16594	4	33		
T ₃ seedlings from event -05-99 of ME16594	41	11	5.14	2.34E-02
T ₃ non-transgenic segregants of event -05-99 of ME16594	5	6		

TABLE 10

Hypocotyl length in seedlings from ME16597				
Plants	Short Hypo-cotyl	Long Hypo-cotyl	Chi-Square	p-value
T ₂ seedlings from event -01 of ME16597	18	6	16.99	3.77E-05
T ₂ non-transgenic segregants of event -01 of ME16597	0	11		

112

TABLE 10-continued

Hypocotyl length in seedlings from ME16597				
Plants	Short Hypo-cotyl	Long Hypo-cotyl	Chi-Square	p-value
T ₃ seedlings from event -01-99 of ME16597	69	3	55.76	8.20E-04
T ₃ non-transgenic segregants of event -01-99 of ME16597	0	8		
T ₂ seedlings from event -04 of ME16597	25	3	21.88	2.91E-06
T ₂ non-transgenic segregants of event -04 of ME16597	0	7		
T ₃ seedlings from event -04-99 of ME16597	54	5	32.49	1.20E-08
T ₃ non-transgenic segregants of event -04-99 of ME16597	3	11		
T ₂ seedlings from event -04 of ME16597	44	5	34.14	5.12E-09
T ₂ non-transgenic segregants of event -04 of ME16597	4	17		
T ₃ seedlings from event -04-99 of ME16597	49	4	43.99	3.30E-11
T ₃ non-transgenic segregants of event -04-99 of ME16597	3	18		

TABLE 11

Hypocotyl length in seedlings from ME16630				
Plants	Short Hypo-cotyl	Long Hypo-cotyl	Chi-Square	p-value
T ₂ seedlings from event -01 of ME16630	49	7	49.26	2.24E-12
T ₂ non-transgenic segregants of event -01 of ME16630	0	20		
T ₃ seedlings from event -01-99 of ME16630	59	1	55.63	8.75E-14
T ₃ non-transgenic segregants of event -01-99 of ME16630	0	6		
T ₂ seedlings from event -02 of ME16630	32	9	25.13	5.36E-07
T ₂ non-transgenic segregants of event -02 of ME16630	4	22		
T ₃ seedlings from event -02-99 of ME16630	43	6	33.59	6.79E-09
T ₃ non-transgenic segregants of event -02-99 of ME16630	2	15		
T ₂ seedlings from event -04 of ME16630	60	9	19.53	9.89E-06
T ₂ non-transgenic segregants of event -04 of ME16630	0	4		
T ₃ seedlings from event -04-99 of ME16630	65	9	12.14	4.94E-04
T ₃ non-transgenic segregants of event -04-99 of ME16630	0	2		

55

TABLE 12

Hypocotyl length in seedlings from ME17128				
Plants	Short Hypo-cotyl	Long Hypo-cotyl	Chi-Square	p-value
T ₂ seedlings from event -02 of ME17128	31	0	38.00	7.07E-10
T ₂ non-transgenic segregants of event -02 of ME17128	0	7		

65

US 12,385,057 B2

113

TABLE 12-continued

Hypocotyl length in seedlings from ME17128				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₃ seedlings from event -02-99 of ME17128	68	0	70.78	4.00E-17
T ₃ non-transgenic segregants of event -02-99 of ME17128	1	10		
T ₂ seedlings from event -03 of ME17128	21	11	11.05	8.86E-04
T ₂ non-transgenic segregants of event -03 of ME17128	0	8		
T ₃ seedlings from event -03-99 of ME17128	74	0	80.00	3.74E-19
T ₃ non-transgenic segregants of event -03-99 of ME17128	0	6		
T ₂ seedlings from event -04 of ME17128	28	4	18.06	2.14E-05
T ₂ non-transgenic segregants of event -04 of ME17128	1	7		
T ₃ seedlings from event -04-99 of ME17128	62	0	39.42	3.41E-10
T ₃ non-transgenic segregants of event -04-99 of ME17128	7	9		

TABLE 13

Hypocotyl length in seedlings from ME17578				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event-01 of ME17578	32	1	32.42	1.24E-08
T ₂ non-transgenic segregants of event-01 of ME17578	0	6		
T ₃ seedlings from event-01-99 of ME17578	63	0	69.06	9.56E-17
T ₃ non-transgenic segregants of event-01-99 of ME17578	1	12		
T ₂ seedlings from event-03 of ME17578	20	0	30.00	4.32E-08
T ₂ non-transgenic segregants of event-03 of ME17578	0	10		
T ₃ seedlings from event-03-99 of ME17578	29	4	19.26	1.14E-05
T ₃ non-transgenic segregants of event-03-99 of ME17578	14	24		

TABLE 14

Hypocotyl length in seedlings from ME18158				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event-01 of ME18158	23	2	22.31	2.33E-06
T ₂ non-transgenic segregants of event-01 of ME18158	2	11		
T ₃ seedlings from event-01-99 of ME18158	61	0	54.93	1.25E-13
T ₃ non-transgenic segregants of event-01-99 of ME18158	1	5		
T ₂ seedlings from event-02 of ME18158	25	5	7.62	5.78E-03
T ₂ non-transgenic segregants of event-02 of ME18158	0	2		
T ₃ seedlings from event-02-99 of ME18158	70	0	7.88	5.01E-03
T ₃ non-transgenic segregants of event-02-99 of ME18158	8	1		

114

TABLE 14-continued

Hypocotyl length in seedlings from ME18158				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event-04 of ME18158	22	3	27.17	1.86E-07
T ₂ non-transgenic segregants of event-04 of ME18158	0	13		
T ₃ seedlings from event-04-99 of ME18158	22	3	49.13	2.40E-12
T ₃ non-transgenic segregants of event-04-99 of ME18158	0	13		

TABLE 15

Hypocotyl length in seedlings from ME18314				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event-01 of ME18314	13	14	5.72	1.67E-02
T ₂ non-transgenic segregants of event-01 of ME18314	1	11		
T ₃ seedlings from event-01-99 of ME18314	62	0	47.75	4.85E-12
T ₃ non-transgenic segregants of event-01-99 of ME18314	2	5		
T ₂ seedlings from event-02 of ME18314	16	9	4.48	3.43E-02
T ₂ non-transgenic segregants of event-02 of ME18314	0	3		
T ₃ seedlings from event-02-99 of ME18314	56	0	46.67	8.41E-12
T ₃ non-transgenic segregants of event-02-99 of ME18314	4	10		
T ₂ seedlings from event-03 of ME18314	18	6	4.78	2.88E-02
T ₂ non-transgenic segregants of event-03 of ME18314	6	9		
T ₃ seedlings from event-03-99 of ME18314	37	0	42.00	9.13E-11
T ₃ non-transgenic segregants of event-03-99 of ME18314	0	5		
T ₂ seedlings from event-04 of ME18314	24	3	20.84	4.99E-06
T ₂ non-transgenic segregants of event-04 of ME18314	2	11		
T ₃ seedlings from event-04-99 of ME18314	67	0	79.00	6.21E-19
T ₃ non-transgenic segregants of event-04-99 of ME18314	0	12		

TABLE 16

Hypocotyl length in seedlings from ME19304				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event-07 of ME19304	28	1	29.22	6.48E-08
T ₂ non-transgenic segregants of event-07 of ME19304	1	9		
T ₃ seedlings from event-07-99 of ME19304	57	0	40.51	1.95E-10
T ₃ non-transgenic segregants of event-07-99 of ME19304	8	12		
T ₂ seedlings from event-08 of ME19304	18	11	7.67	5.62E-03
T ₂ non-transgenic segregants of event-08 of ME19304	0	6		
T ₃ seedlings from event-08-99 of ME19304	69	0	63.61	1.52E-15

115

TABLE 16-continued

Hypocotyl length in seedlings from ME19304					
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value	
T ₃ non-transgenic segregants of event-08-99 of ME19304	2	9			

TABLE 17

Hypocotyl length in seedlings from ME19738					
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value	
T ₂ seedlings from event-02 of ME19738	32	0	20.84	4.99E-06	
T ₂ non-transgenic segregants of event-02 of ME19738	0	7			
T ₃ seedlings from event-02-99 of ME19738	68	0	80.00	3.74E-19	
T ₃ non-transgenic segregants of event-02-99 of ME19738	0	12			
T ₂ seedlings from event-05 of ME19738	22	6	15.76	7.20E-05	
T ₂ non-transgenic segregants of event-05 of ME19738	1	10			
T ₃ seedlings from event-05-99 of ME19738	65	1	66.48	3.54E-16	
T ₃ non-transgenic segregants of event-05-99 of ME19738	0	9			

TABLE 18

Hypocotyl length in seedlings from ME20871					
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value	
T ₂ seedlings from event-03 of ME20871	27	8	10.03	1.54E-03	
T ₂ non-transgenic segregants of event-03 of ME20871	0	4			
T ₃ seedlings from event-03-99 of ME20871	51	10	12.35	4.41E-04	
T ₃ non-transgenic segregants of event-03-99 of ME20871	0	3			
T ₂ seedlings from event-05 of ME20871	32	0	40.00	2.54E-10	
T ₂ non-transgenic segregants of event-05 of ME20871	0	8			
T ₃ seedlings from event-05-99 of ME20871	61	0	68.52	1.26E-16	
T ₃ non-transgenic segregants of event-05-99 of ME20871	1	13			
T ₂ seedlings from event-10 of ME20871	26	0	27.24	1.80E-07	
T ₂ non-transgenic segregants of event-10 of ME20871	1	6			
T ₃ seedlings from event-10-99 of ME20871	52	1	48.91	2.68E-12	
T ₃ non-transgenic segregants of event-10-99 of ME20871	1	9			

TABLE 19

Hypocotyl length in seedlings from ME21199					
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value	
T ₂ seedlings from event-01 of ME21199	29	0	29.83	4.72E-08	

116

TABLE 19-continued

Hypocotyl length in seedlings from ME21199					
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value	
T ₂ non-transgenic segregants of event-01 of ME21199	1	6			
T ₃ seedlings from event-01-99 of ME21199	62	0	78.00	1.03E-18	
T ₃ non-transgenic segregants of event-01-99 of ME21199	0	16			
T ₂ seedlings from event-03 of ME21199	19	0	9.44	2.12E-03	
T ₂ non-transgenic segregants of event-03 of ME21199	7	5			
T ₃ seedlings from event-03-99 of ME21199	68	0	55.03	1.19E-13	
T ₃ non-transgenic segregants of event-03-99 of ME21199	3	8			
T ₂ seedlings from event-05 of ME21199	26	0	20.41	6.26E-06	
T ₂ non-transgenic segregants of event-05 of ME21199	4	7			
T ₃ seedlings from event-05-99 of ME21199	31	1	17.88	2.35E-05	
T ₃ non-transgenic segregants of event-05-99 of ME21199	5	7			

TABLE 20

Hypocotyl length in seedlings from ME21508					
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value	
T ₂ seedlings from event-01 of ME21508	20	5	15.76	7.19E-05	
T ₂ non-transgenic segregants of event-01 of ME21508	2	12			
T ₃ seedlings from event-01-99 of ME21508	74	0	80.00	3.74E-19	
T ₃ non-transgenic segregants of event-01-99 of ME21508	0	6			
T ₂ seedlings from event-05 of ME21508	23	8	15.71	7.85E-05	
T ₂ non-transgenic segregants of event-05 of ME21508	0	9			
T ₃ seedlings from event-05-99 of ME21508	65	0	78.00	1.03E-18	
T ₃ non-transgenic segregants of event-05-99 of ME21508	0	13			

There were no observable or statistically significant differences between T₂ ME05268, ME06120, ME09503, ME10007, ME10852, ME11939, ME13456, ME15935, ME16594, ME16597, ME16630, ME17128, ME17578, ME18158, ME18314, ME19304, ME19738, ME20871, ME21199, and ME21508 plants and control plants in germination, onset of flowering, rosette area, fertility, and general morphology/architecture.

Example 5—Results for ME12006, ME12596, and ME12899 Events

T₂ and T₃ seed from events -03, -02, and -03 of ME12006, T₂ and T₃ seed from events -08 and -09 of ME12596, and T₂ and T₃ seed from events -05 and -06 of ME12899 was grown under SD+EODFR conditions and evaluated for hypocotyl length as described in Example 3. Seedlings from events -03, -02, and -03 of ME12006; events -08 and -09 of ME12596; and events -05 and -06 of ME12899 displayed a short hypocotyl under SD+EODFR conditions in both the T₂ and T₃ generations, and the trans-

gene was linked to the short hypocotyl phenotype with a confidence level of $p<0.05$ (Tables 21-23).

TABLE 21

Plants	Hypocotyl length in seedlings from ME12006			
	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event-01 of ME12006	22	2	8.89	2.87E-03
T ₂ non-transgenic segregants of event-01 of ME12006	8	8		
T ₃ seedlings from event-01-03 of ME12006	27	3	7.50	6.17E-03
T ₃ non-transgenic segregants of event-01-03 of ME12006	5	5		
T ₂ seedlings from event-02 of ME12006	20	20	12.23	4.70E-04
T ₂ non-transgenic segregants of event-02 of ME12006	6	10		
T ₃ seedlings from event-02-01 of ME12006	23	4	12.61	3.84E-04
T ₃ non-transgenic segregants of event-02-01 of ME12006	2	7		
T ₂ seedlings from event-03 of ME12006	24	4	7.94	4.83E-03
T ₂ non-transgenic segregants of event-03 of ME12006	4	6		
T ₃ seedlings from event-03-04 of ME12006	19	2	8.82	2.99E-03
T ₃ non-transgenic segregants of event-03-04 of ME12006	2	4		

TABLE 22

Plants	Hypocotyl length in seedlings from ME12596			
	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event-08 of ME12596	22	4	18.75	1.487E-05
T ₂ non-transgenic segregants of event-08 of ME12596	2	12		
T ₃ seedlings from event-08-01 of ME12596	18	4	10.21	1.40E-04
T ₃ non-transgenic segregants of event-08-01 of ME12596	4	10		
T ₂ seedlings from event-09 of ME12596	21	5	8.12	4.39E-03
T ₂ non-transgenic segregants of event-09 of ME12596	5	9		
T ₃ seedlings from event-09-01 of ME12596	20	4	5.08	2.42E-02
T ₃ non-transgenic segregants of event-09-01 of ME12596	8	8		

TABLE 23

Plants	Hypocotyl length in seedlings from ME12899			
	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event-05 of ME12899	24	4	10.98	9.23E-04
T ₂ non-transgenic segregants of event-05 of ME12899	4	8		
T ₃ seedlings from event-05-99 of ME12899	27	3	7.5	6.17E-03
T ₃ non-transgenic segregants of event-05-99 of ME12899	5	5		
T ₂ seedlings from event-06 of ME12899	26	2	23.22	1.445E-06
T ₃ non-transgenic segregants of event-06 of ME12899				

TABLE 23-continued

Hypocotyl length in seedlings from ME12899						
Plants	Short Hypocotyl		Long Hypocotyl		Chi-Square	p-value
	Plants	Short Hypocotyl	Long Hypocotyl			
T ₂ non-transgenic segregants of event-06 of ME12899		2				
T ₃ seedlings from event-06-99 of ME12899		21	3		6.77	9.264E-03
T ₃ non-transgenic segregants of event-06-99 of ME12899		8	8			

There were no observable or statistically significant differences between T₂ ME12006, ME12596, and ME12899 plants and control plants in germination, onset of flowering, rosette area, fertility, and general morphology/architecture.

Example 6—Results for ME18408 and ME19971 Events

T₂ and T₃ seed from events -01, -02, and -03 of ME18408, and T₂ and T₃ seed from events -01, -02, -03, and -05 of ME19971 was grown under low light conditions and SD+EOFDR conditions as described in Examples 2 and 3, respectively, and evaluated for hypocotyl length.

Seedlings from events -01, -02, and -03 of ME18408, and events -01, -02, -03, and -05 of ME19971 displayed a short hypocotyl under SD+EOFDR conditions in both the T₂ and T₃ generations, and the transgene was linked to the short hypocotyl phenotype with a confidence level of $p<0.05$ (Tables 24 and 26). Seedlings from events -01, and -02 of ME18408, and events -01, -02, -03, and -05 of ME19971 displayed a short hypocotyl under SD+EOFDR conditions in both the T₂ and T₃ generations, and the transgene was linked to the short hypocotyl phenotype with a confidence level of $p<0.05$ (Tables 25 and 27).

TABLE 24

Hypocotyl length in seedlings from ME18408 grown under low light conditions					
Plants	Short Hypocotyl		Long Hypocotyl		
	Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	
T ₂ seedlings from event-01 of ME18408		63	2	44.58	2.44E-11
T ₂ non-transgenic segregants of event-01 of ME18408		0	4		
T ₃ seedlings from event-01-99 of ME18408		40	6	35.90	2.08E-09
T ₃ non-transgenic segregants of event-01-99 of ME18408		1	16		
T ₂ seedlings from event-02 of ME18408		38	7	28.67	8.58E-08
T ₂ non-transgenic segregants of event-02 of ME18408		3	17		
T ₃ seedlings from event-02-99 of ME18408		39	17	10.98	9.20E-04
T ₃ non-transgenic segregants of event-02-99 of ME18408		5	14		
T ₂ seedlings from event-03 of ME18408		30	1	25.76	3.86E-07
T ₂ non-transgenic segregants of event-03 of ME18408		7	15		
T ₃ seedlings from event-03-99 of ME18408		23	5	21.74	3.12E-06
T ₃ non-transgenic segregants of event-03-99 of ME18408		11	32		

119

TABLE 25

Hypocotyl length in seedlings from ME18408 grown under SD + EODFR conditions				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event-01 of ME18408	22	5	6.18	1.29E-02
T ₂ non-transgenic segregants of event-01 of ME18408	5	7		
T ₃ seedlings from event-01-99 of ME18408	19	8	10.71	1.06E-03
T ₃ non-transgenic segregants of event-01-99 of ME18408	1	9		
T ₂ seedlings from event-02 of ME18408	25	5	4.44	3.50E-02
T ₂ non-transgenic segregants of event-02 of ME18408	5	5		
T ₃ seedlings from event-02-99 of ME18408	22	3	6.8	9.13E-03
T ₃ non-transgenic segregants of event-02-99 of ME18408	7	7		

TABLE 26

Hypocotyl length in seedlings from ME19971 grown under low light conditions				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event-01 of ME19971	8	0	18.00	2.21E-05
T ₂ non-transgenic segregants of event-01 of ME19971	0	10		
T ₃ seedlings from event-01-99 of ME19971	37	0	61.00	5.71E-15
T ₃ non-transgenic segregants of event-01-99 of ME19971	0	24		
T ₂ seedlings from event-02 of ME19971	16	2	19.64	9.37E-06
T ₂ non-transgenic segregants of event-02 of ME19971	0	9		
T ₃ seedlings from event-02-99 of ME19971	36	0	29.19	6.56E-08
T ₃ non-transgenic segregants of event-02-99 of ME19971	1	3		
T ₂ seedlings from event-03 of ME19971	14	1	19.08	1.25E-05
T ₂ non-transgenic segregants of event-03 of ME19971	0	8		
T ₃ seedlings from event-03-99 of ME19971	34	0	46.00	1.18E-11
T ₃ non-transgenic segregants of event-03-99 of ME19971	0	12		
T ₂ seedlings from event-05 of ME19971	26	0	29.00	7.24E-08
T ₂ non-transgenic segregants of event-05 of ME19971	0	3		
T ₃ seedlings from event-05-99 of ME19971	42	0	47.94	4.39E-12
T ₃ non-transgenic segregants of event-05-99 of ME19971	3	16		

TABLE 27

Hypocotyl length in seedlings from ME19971 grown under SD + EODFR conditions				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ seedlings from event-01 of ME19971	30	2	30.00	4.32E-08

120

TABLE 27-continued

Hypocotyl length in seedlings from ME19971 grown under SD + EODFR conditions				
Plants	Short Hypocotyl	Long Hypocotyl	Chi-Square	p-value
T ₂ non-transgenic segregants of event-01 of ME19971	0	8		
T ₃ seedlings from event-01-04 of ME19971	22	0	32.00	1.542E-08
T ₃ non-transgenic segregants of event-01-04 of ME19971	0	10		
T ₂ seedlings from event-02 of ME19971	24	4	17.60	2.721E-05
T ₂ non-transgenic segregants of event-02 of ME19971	2	10		
T ₃ seedlings from event-02-04 of ME19971	22	6	16.16	5.811E-05
T ₃ non-transgenic segregants of event-02-04 of ME19971	0	8		
T ₂ seedlings from event-03 of ME19971	28	0	40.00	2.54E-10
T ₂ non-transgenic segregants of event-03 of ME19971	0	12		
T ₃ seedlings from event-03-06 of ME19971	24	0	17.49	2.895E-05
T ₃ non-transgenic segregants of event-03-06 of ME19971	4	6		
T ₂ seedlings from event-05 of ME19971	24	2	24.35	8.034E-07
T ₂ non-transgenic segregants of event-05 of ME19971	2	12		
T ₃ seedlings from event-05-02 of ME19971	25	4	6.13	1.33E-02
T ₃ non-transgenic segregants of event-05-02 of ME19971	3	4		

There were no observable or statistically significant differences between T₂ ME18408 and ME19971 plants and control plants in germination, onset of flowering, rosette area, fertility, and general morphology/architecture.

Example 7—Determination of Functional Homologs by Reciprocal BLAST

A candidate sequence was considered a functional homolog of a reference sequence if the candidate and reference sequences encoded proteins having a similar function and/or activity. A process known as Reciprocal BLAST (Rivera et al., *Proc. Natl. Acad. Sci. USA*, 95:6239-6244 (1998)) was used to identify potential functional homolog sequences from databases consisting of all available public and proprietary peptide sequences, including NR from NCBI and peptide translations from Ceres clones.

Before starting a Reciprocal BLAST process, a specific reference polypeptide was searched against all peptides from its source species using BLAST in order to identify polypeptides having BLAST sequence identity of 80% or greater to the reference polypeptide and an alignment length of 85% or greater along the shorter sequence in the alignment. The reference polypeptide and any of the aforementioned identified polypeptides were designated as a cluster.

The BLASTP version 2.0 program from Washington University at Saint Louis, Missouri, USA was used to determine BLAST sequence identity and E-value. The BLASTP version 2.0 program includes the following parameters: 1) an E-value cutoff of 1.0e-5; 2) a word size of 5; and 3) the -postsw option. The BLAST sequence identity was calculated based on the alignment of the first BLAST HSP (High-scoring Segment Pairs) of the identified potential functional homolog sequence with a specific reference polypeptide. The number of identically matched residues in the

121

BLAST HSP alignment was divided by the HSP length, and then multiplied by 100 to get the BLAST sequence identity. The HSP length typically included gaps in the alignment, but in some cases gaps were excluded.

The main Reciprocal BLAST process consists of two rounds of BLAST searches; forward search and reverse search. In the forward search step, a reference polypeptide sequence, "polypeptide A," from source species SA was BLASTed against all protein sequences from a species of interest. Top hits were determined using an E-value cutoff of 10^{-5} and a sequence identity cutoff of 35%. Among the top hits, the sequence having the lowest E-value was designated as the best hit, and considered a potential functional homolog or ortholog. Any other top hit that had a sequence identity of 80% or greater to the best hit or to the original reference polypeptide was considered a potential functional homolog or ortholog as well. This process was repeated for all species of interest.

In the reverse search round, the top hits identified in the forward search from all species were BLASTed against all protein sequences from the source species SA. A top hit from the forward search that returned a polypeptide from the aforementioned cluster as its best hit was also considered as a potential functional homolog.

Functional homologs were identified by manual inspection of potential functional homolog sequences. Representative functional homologs for SEQ ID NO:3, SEQ ID NO:70, SEQ ID NO:129, SEQ ID NO:317, SEQ ID NO:337, SEQ ID NO:456, SEQ ID NO:538, SEQ ID NO:570, SEQ ID NO:606, SEQ ID NO:634, SEQ ID NO:644, SEQ ID NO:850, SEQ ID NO:907, SEQ ID NO:953, SEQ ID NO:1024, SEQ ID NO:1047, SEQ ID NO:1151, SEQ ID NO:1277, SEQ ID NO:1347, SEQ ID NO:1457, SEQ ID NO:1497, SEQ ID NO:1540, SEQ ID NO:1587, SEQ ID NO:1630, and SEQ ID NO:1635 are shown in FIGS. 1-24, respectively.

Example 8—Determination of Functional Homologs by Hidden Markov Models

Hidden Markov Models (HMMs) were generated by the program HMMER 2.3.2. To generate each HMM, the default HMMER 2.3.2 program parameters, configured for glocal alignments, were used.

An HMM was generated using the sequences shown in FIG. 1 as input. These sequences were fitted to the model and a representative HMM bit score for each sequence is shown in the Sequence Listing. Additional sequences were fitted to the model, and representative HMM bit scores for any such additional sequences are shown in the Sequence Listing. The results indicate that these additional sequences are functional homologs of SEQ ID NO:3.

The procedure above was repeated and an HMM was generated for each group of sequences shown in FIGS. 2-24, using the sequences shown in each Figure as input for that HMM. A representative bit score for each sequence is shown in the Sequence Listing. Additional sequences were fitted to certain HMMs, and representative HMM bit scores for such additional sequences are shown in the Sequence Listing. The results indicate that these additional sequences are functional homologs of the sequences used to generate that HMM.

Example 9—Identification of Transgenic Plants Exhibiting a Red Light-Specific Short Hypocotyl Phenotype

Wild type and transgenic seeds were surface-sterilized, plated on solid 0.5× MS medium containing 5 g/L sucrose, 0.5 g/L MES, 7 g/L Agar (adjusted to pH 5.7), and stratified at 4° C. in the dark for three to four days. After stratification,

122

plates were acclimated to room temperature, wrapped in micropore tape, and exposed to continuous white light having a fluence rate of ~60 mmol/m²/s PAR, and a red:far-red ratio (R:FR) of ~5.3. After 24 hours, plates from wild type controls and transgenic lines were moved to one of three light conditions: (1) white light conditions at a lower fluence rate (~15 mmol/m²/s PAR, R:FR=~5.0), (2) red-light conditions (SNAP-LITE™ Red/Far-Red light box (Quantum Devices), at ~15 μmol/m²/s PAR, R:FR=~80), or (3) far-red conditions (SNAP-LITE™ Red/Far-red light box, at ~15 μmol/m²/s PAR, R:FR=~0.10). Seedlings were maintained under continuous light conditions for five days. The hypocotyls of individual seedlings were determined to be "tall" or "short" based on qualitative observation.

A hypocotyl having a length similar to the hypocotyl length typically exhibited by wild-type *Arabidopsis* seedlings grown under the same light conditions was considered a tall hypocotyl. A hypocotyl having reduced length relative to the hypocotyl length typically exhibited by wild-type *Arabidopsis* seedlings grown under the same light conditions was considered a short hypocotyl. Transgenic seedlings from ten Ceres SEEDLINE ID nos. failed to germinate, or germinated poorly, under continuous red light (ME10007, ME10852, ME11961, ME15935, ME17128, ME18158, ME18314, ME19304, ME20871, and ME21508).

Transgenic seedlings from eight Ceres SEEDLINE ID nos. (ME11939, ME16630, ME19971, ME05268, ME13456, ME13629, ME16597, and ME17578) exhibited short hypocotyls when grown under continuous red light. Transgenic seedlings from three of these (ME11939, ME16630, and ME19971) exhibited tall hypocotyls under continuous far-red light exposure, indicating that the short hypocotyl phenotype was red-light specific in these three seed lines. In contrast, the other five seedlings (ME05268, ME13456, ME13629, ME16597, and ME17578) exhibited a short-hypocotyl phenotype when grown under far-red light, indicating that the short-hypocotyl phenotype exhibited by ME05268, ME13456, ME13629, ME16597, and ME17578 was not red-light specific (See, e.g., Parks and Spaulding, Proc. Natl. Acad. Sci., 96: 14142-14146 (1999) describing different molecular mechanisms for suppression of hypocotyl elongation under continuous red and far-red light conditions).

A similar red light-dependent short hypocotyl phenotype has been observed in transgenic plants overexpressing the photochemically and biologically functional photoreceptor, Phytochrome B (Phy B) (Wagner et al., Plant Cell, 3: 1275-1288 (1991)). Phy B null mutants exhibit a long hypocotyl seedling phenotype and increased plant height (Kebrom and Brutnell, J Exp. Bot., 58: 3079-3089 (2007)). These observations suggest that transgene modulation of light response pathways can produce plants exhibiting either increased grain yield, or increased biomass. See Pennell et al., U.S. Pat. App. Ser. No. 61/097,789, "Transgenic Plants Having Increased Biomass," filed Sep. 17, 2008, incorporated by reference herein. Thus, transgenic plants comprising nucleic acid sequences that down-regulate expression of a At5g14370 polypeptide (SEQ ID NO: 456) (FIG. 6), a At1g13360 polypeptide (SEQ ID NO: 953) (FIG. 11), a At2g35940 polypeptide (SEQ ID NO: 1540) (FIG. 21), and sequences identified as functional homologs of these sequences (see FIGS. 6, 11, 21 and sequence listing) are predicted to exhibit a tall hypocotyl phenotype under conditions of normal or low light.

OTHER EMBODIMENTS

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

SEQUENCE LISTING

The patent contains a lengthy sequence listing. A copy of the sequence listing is available in electronic form from the USPTO web site (<https://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US12385057B2>). An electronic copy of the sequence listing will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed is:

1. A method of modulating a trait in a dicotyledonous plant, said method comprising
 - introducing into a dicotyledonous plant cell an exogenous nucleic acid, said exogenous nucleic acid comprising a nucleotide sequence encoding a polypeptide having 95 percent or greater sequence identity to the amino acid sequence of SEQ ID NO:1635, wherein the nucleotide sequence is operably linked to a heterologous regulatory region;
 - producing a dicotyledonous plant from said dicotyledonous plant cell; and
 - selecting a dicotyledonous plant for increased low light tolerance or SD+EODFR tolerance as compared to a control plant that does not comprise said nucleic acid.
2. A dicotyledonous plant cell comprising an exogenous nucleic acid, said exogenous nucleic acid comprising a nucleotide sequence encoding a polypeptide having 95 percent or greater sequence identity to the amino acid sequence of SEQ ID NO:1635;
 - wherein the nucleotide sequence is operably linked to a heterologous regulatory region;
 - wherein a dicotyledonous plant produced from said cell has increased low light tolerance or SD+EODFR tolerance as compared to a control plant that does not comprise said nucleic acid.
3. A dicotyledonous plant comprising an exogenous nucleic acid, said exogenous nucleic acid comprising:
 - a nucleotide sequence encoding a polypeptide having 95 percent or greater sequence identity to the amino acid sequence of SEQ ID NO: 1635;
 - wherein the nucleotide sequence is operably linked to a heterologous regulatory region;
 - wherein the dicotyledonous plant has increased low light tolerance or SD+EODFR tolerance as compared to a control plant that does not comprise said nucleic acid.
4. The method of claim 1, wherein said polypeptide has 97 percent or greater sequence identity to the amino acid sequence of SEQ ID NO:1635.
5. The method of claim 1, wherein said polypeptide sequence comprises the amino sequence of SEQ ID NO:1635.
6. The method of claim 1, wherein said nucleotide sequence comprises the polynucleotide sequence of SEQ ID NO:1633 or SEQ ID NO:1634.
7. The dicotyledonous plant of claim 3, wherein said polypeptide has 97 percent or greater sequence identity to the amino acid sequence of SEQ ID NO: 1635.
8. The dicotyledonous plant of claim 3, wherein said polypeptide sequence comprises the amino acid sequence of SEQ ID NO:1635.
9. The dicotyledonous plant of claim 3, wherein said nucleotide sequence comprises the polynucleotide sequence of SEQ ID NO:1633 or SEQ ID NO:1634.
10. The dicotyledonous plant of claim 3, wherein the plant is selected for having increased low light tolerance.
11. The dicotyledonous plant of claim 3, wherein the plant is selected for having increased SD+EODFR tolerance.

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