US 20110167516A1

(19) **United States**

(12) **Patent Application Publication**

Gordon-Kamm et al.

(10) **Pub. No.: US 2011/0167516 A1**

(43) **Pub. Date: Jul. 7, 2011**

(54) **METHODS AND COMPOSITIONS FOR THE INTRODUCTION AND REGULATED EXPRESSION OF GENES IN PLANTS**

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(21) Appl. No.: **12/982,180**

(22) Filed: **Dec. 30, 2010**

Related U.S. Application Data

(60) Provisional application No. 61/291,257, filed on Dec. 30, 2009.

Publication Classification

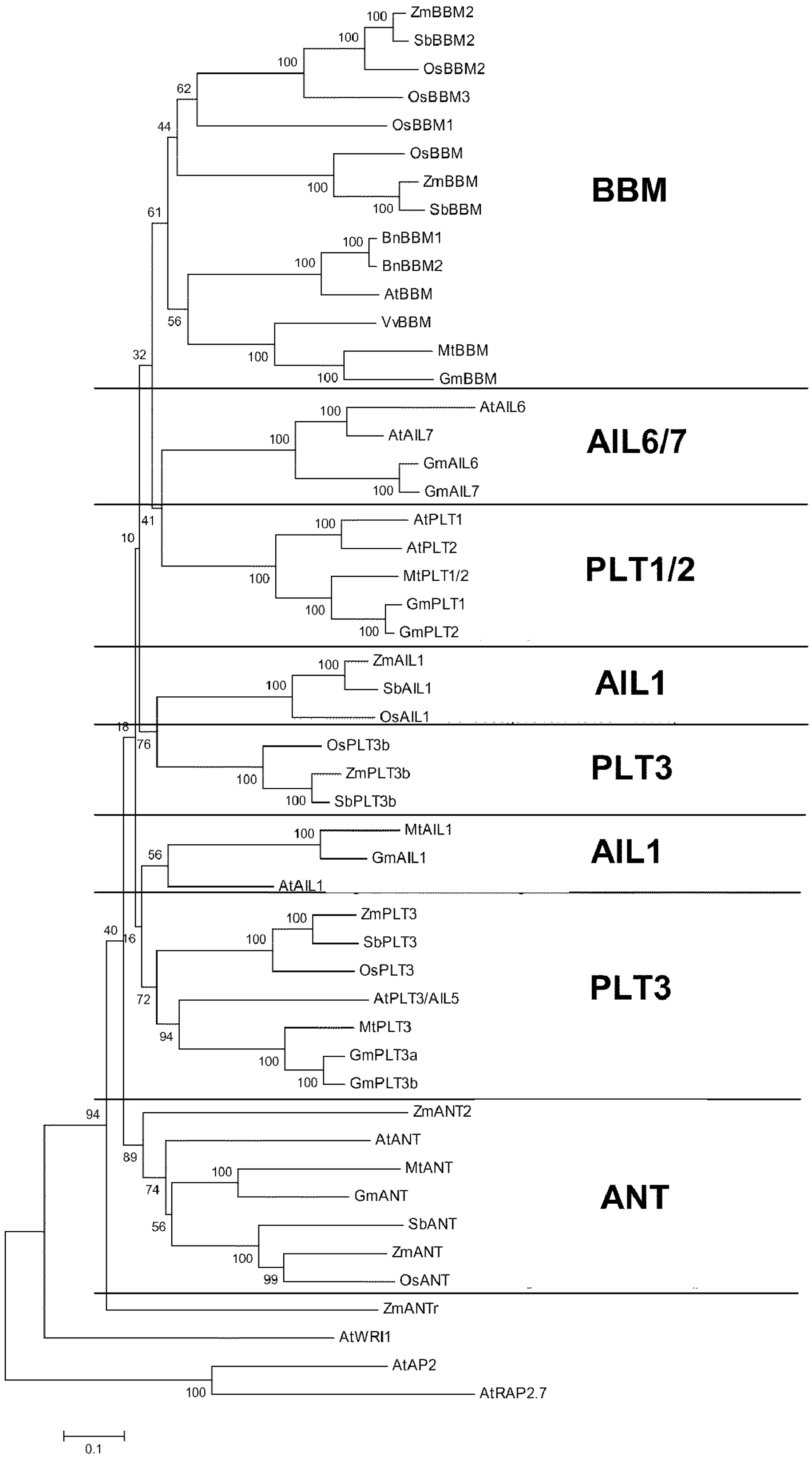
(51) **Int. Cl.**

A01H 5/00	(2006.01)
C07H 21/04	(2006.01)
C12N 15/63	(2006.01)
C12N 5/10	(2006.01)
A01H 5/10	(2006.01)
C12N 15/82	(2006.01)

(52) **U.S. Cl.** **800/278**; 536/24.1; 435/320.1; 435/419; 800/298; 435/468

(57) **ABSTRACT**

Compositions and methods are provided for the introduction and the regulated expression of genes in plants. Compositions include promoter constructs that provide a level of activity useful for the regulated expression of site-specific recombinases, while avoiding premature excision. Further provided are isolated polynucleotides encoding novel babyboom polypeptides, expression cassettes, and plants comprising the same. Methods for the introduction of genes into plants are provided, including methods for plastid transformation and methods for the transformation of tissues from mature seeds and leaves.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100 BnBBM2
AtBBM
56 VvBBM
32
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100 GmBBM
100 AtAIL6
AIL6/7
100 AtAIL7
GmAIL6
100 GmAIL7
41
100 AtPLT1
10
AtPLT2
PLT1/2
MtPLT1/2
100
GmPLT1
100
100 GmPLT2
100 ZmAIL1
AIL1
100 SbAIL1
OsAIL1
18
76
OsPLT3b
PLT3
100 ZmPLT3b
100 SbPLT3b
100 MtAIL1
AIL1
56 GmAIL1
AtAIL1
100 ZmPLT3
40
16
100 SbPLT3
OsPLT3
PLT3
72 AtPLT3/AIL5
94
MtPLT3
100 GmPLT3a
100 GmPLT3b
94 ZmANT2
AtANT
89
100 MtANT
74 GmANT
ANT
56 SbANT
100 ZmANT
99 OsANT
ZmANTr
AtWRI1
AtAP2
100 AtRAP2.7
0.1

FIG. 1

	SEQ ID NO:		
GmPLT3b	70	(221)	YEKELEEMKNMTRQEFVASLRRKSSGFSRGA
GmPLT3a	71	(217)	YEKELEEMKNMTRQEFVASLRRKSSGFSRGA
OsBBM	14	(353)	YEKELEEMKHMTRQEFVASLRRKSSGFSRGA
VvBBM	6	(278)	YEKEIEEMKHMTRQEYVASLRRKSSGFSRGA
GmBBM	2	(339)	YEKELEEMKHMTRQEYVASLRRKSSGFSRGA
ZmPLT3b	72	(210)	YEKELEEMKSMTRQEFIASLRRKSSGFSRGA
AtBBM	22	(280)	YEKEVEEMKHMTRQEYVASLRRKSSGFSRGA
OsPLT3	73	(214)	YEKELEEMKHMTRQEFVASLRRKSSGFSRGA
ZmBBM	10	(343)	YEKELEDMKHMTRQEFVASLRRKSSGFSRGA
BnBBM2	26	(280)	YEKEIEEMKHMTRQEYVASLRRKSSGFSRGA
BnBBM1	24	(280)	YEKEVEEMKHMTRQEYVASLRRKSSGFSRGA
OsBBM1	16	(238)	YEKELDEMKHMNRQEFVASLRRKSSGFSRGA
AtPLT3/AIL5	74	(273)	YESELEEMKHMTRQEFVASLRRKSSGFSRGA
AtPLT2	75	(260)	YEKEVEEMKNMTRQEFVASIRRKSSGFSRGA
SbPLT3b	76	(205)	YEKELEEMKSMTRQEFIASLRRKSSGFSRGA
OsAIL1	77	(323)	YEKELEEMKHMTRQEFIAHLRRNSSGFSRGA
SbBBM	4	(347)	YEKELEDMKHMTRQEFVASLRRKSSGFSRGA
MtBBM	8	(329)	YEKEVEEMKHMTRQEYVASLRRKSSGFSRGA
SbBBM2	28	(356)	YEKELEEMKHMTRQEYIAYLRRNSSGFSRGA
ZmBBM2	12	(349)	YEKELEEMKHMTRQEYIAYLRRNSSGFSRGA
GmPLT2	78	(234)	YEKELDEMKHMTRQEFVAAIRRKSSGFSRGA
OsBBM3	20	(349)	YEKELEEMKHMTRQEYIAHLRRNSSGFSRGA
MtPLT3	79	(229)	YEKEIDDMKNMTRQEFVASLRRKSSGFSRGA
ZmPLT3	80	(197)	YEKEVEEMKNMTRQEFVASLRRKSSGFSRGA
OsPLT3b	81	(200)	YETELEEMKSMTRQEFIASLRRKSSGFSRGA
GmPLT1	82	(239)	YEKELDEMKHMTRQEFVAAIRRKSSGFSRGA
AtPLT1	83	(251)	YEKEVEEMKHMTRQEFVAAIRRKSSGFSRGA
OsBBM2	18	(370)	YEKELDEMKHMTRQEYIAYLRRNSSGFSRGA
MtPLT1/2	84	(233)	YEKEIDEMKHMTRQEFVASIRRKSSGFSRGA
ZmAIL1	85	(341)	YEKELEEMKHMSRQEFIAHLRRNSSGFSRGA
GmAIL1	86	(272)	YEKELEEMKHMTRQEFVANLRRKSSGFSRGA
SbPLT3	87	(208)	YEKELEEMKTMTRQEFVASLRRKSSGFSRGA
GmAIL6	88	(291)	YSKEVEEMKHVTKQEFIASLRRKSSGFSRGA
AtAIL6	89	(323)	YSKEVEEMKHMTKQEFIASLRRKSSGFSRGA
MtAIL1	90	(318)	YDKELEEMKHMTRQEFVANLRRKSSGFSRGA
SbAIL1	91	(333)	YEKELEEMKHMSRQEFIAHLRRNSSGFSRGA
AtANT	92	(353)	YQKEIEDMKNMTRQEYVAHLRRKSSGFSRGA
SbANT	93	(353)	YQEELEEMKNMTRQEYVAHLRRKSSGFSRGA
GmAIL7	94	(290)	YSKEVEEMKHVTKQEFIASLRRKSSGFSRGA
ZmANT	67	(372)	YREELEEMKNMTRQEYVAHLRRKSSGFSRGA
OsANT	95	(372)	YQEELEEMKNMSRQEYVAHLRRKSSGFSRGA
AtAIL7	96	(243)	YSKELEEMNHMTKQEFIASLRRKSSGFSRGA
ZmANT2	97	(354)	YRDELEEMKGMTRQEFVAHLRRRSSGFSRGA
MtANT	98	(380)	YQNQLEEMKNMTRQEYVAHLRRKSSGFSRGA
GmANT	99	(334)	YQVQLEEMKNMSRQEYVAHLRRKSSGFSRGA
AtAIL1	100	(293)	YEKEIEELNNMNRQEFVAMLRRNSSGFSRGA
ZmANTr	101	(218)	YIREIQDMQNMNRRDVVASLRRKSSGFSRGA
AtWRI1	102	(135)	YTKELEEMQRVTKEEYLASLRRQSSGFSRGV
AtAP2	103	(191)	YDDDLKQMTNLTKEEFVHVLRRQSTGFPRGS
AtRAP2.7	104	(213)	YEEDMKQVQNLSKEEFVHILRRQSTGFSRGS
Consensus	48		YEKELEEMK1MTRQE23A4LRRKSSGFSRGA

1= H or N; 2= F or Y; 3= V or I; 4=S or H

FIG. 2A

	SEQ ID NO:		
SbBBM	4	(378)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
OsBBM	13	(384)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
ZmBBM	10	(374)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
GmPLT3b	70	(252)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
GmPLT3a	71	(248)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
MtPLT3	79	(260)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
AtPLT3/AIL5	74	(304)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
SbBBM2	28	(387)	SKYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEEAA
OsBBM2	18	(401)	SKYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEEAA
ZmBBM2	12	(380)	SKYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEEAA
GmPLT2	78	(265)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEEAA
GmPLT1	82	(270)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEEAA
ZmPLT3b	72	(241)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
AtAIL1	100	(324)	SVYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
SbPLT3b	76	(236)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
OsPLT3b	81	(231)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
OsBBM1	16	(269)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAA
MtPLT1/2	84	(264)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEEAA
SbAIL1	91	(364)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
OsAIL1	77	(354)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
ZmAIL1	85	(372)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
AtPLT2	75	(291)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEEAA
AtPLT1	83	(282)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEEAA
OsBBM3	20	(380)	SKYRGVTRHHQHGRWQARIGRVAGNKDIYLGTFSTEEEAA
VvBBM	6	(309)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
GmANT	99	(365)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
GmBBM	2	(370)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
MtBBM	8	(360)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
SbANT	93	(384)	SMYRGVTRHHQHGRWQARIGRVSGNKDLYLGTFSTQEEAA
GmAIL1	86	(303)	SVYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
MtAIL1	90	(349)	SVYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
SbPLT3	87	(239)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEEAA
ZmPLT3	80	(228)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEEAA
AtBBM	22	(311)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAA
OsANT	95	(403)	SIYRGVTRHHQHGRWQARIGRVSGNKDLYLGTFSTQEEAA
BnBBM2	26	(311)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAA
BnBBM1	24	(311)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAA
MtANT	98	(412)	SMYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAA
AtANT	92	(384)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAA
AtAIL6	89	(354)	SIYRGVTRHHQQGRWQARIGRVAGNKDLYLGTFATEEEAA
ZmANT	67	(403)	SIYRGVTRHHQHGRWQARIGRVSGNKDLYLGTFSTQEEAA
OsPLT3	73	(245)	SIYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTEEEAA
GmAIL7	94	(321)	SIYRGVTRHHQQGRWQARIGRVAGNKDLYLGTFATEEEAA
GmAIL6	88	(322)	SIYRGVTRHHQQGRWQARIGRVAGNKDLYLGTFATEEEAA
AtAIL7	96	(274)	SIYRGVTRHHQQGRWQARIGRVAGNKDLYLGTFATEEEAA
ZmANT2	97	(385)	SIYRGVTRHHQQGRWQSRIGRVAGNKDLYLGTFTTQEEAA
ZmANTr	101	(249)	SIYRGVTKHHQHGRWQARIGRVAGNKDLYLGTFATEQEAA
AtWRI1	102	(166)	SKYRGVARHHHNGRWEARIGRVFGNKYLYLGTYNTQEEAA
Consensus	49		S1YRGVTRHHQHGRWQARIGRVAGNKDLYLGTFST2EEAA

FIG. 2B

	SEQ ID NO:		
SbBBM	4	(418)	EAYDIAAIKFRGLNAVTNFDMSR
OsBBM	14	(424)	EAYDIAAIKFRGLNAVTNFDMSR
ZmBBM	10	(414)	EAYDIAAIKFRGLNAVTNFDMSR
GmPLT3b	70	(292)	EAYDIAAIKFRGLNAVTNFDMSR
GmPLT3a	71	(288)	EAYDIAAIKFRGLNAVTNFDMSR
MtPLT3	79	(300)	EAYDIAAIKFRGLNAVTNFDMSR
AtPLT3/AIL5	74	(344)	EAYDIAAIKFRGLNAVTNFDISR
SbBBM2	28	(427)	EAYDIAAIKFRGLNAVTNFDMSR
OsBBM2	18	(441)	EAYDIAAIKFRGLNAVTNFDMSR
ZmBBM2	12	(420)	EAYDIAAIKFRGLNAVTNFDMSR
GmPLT2	78	(305)	EAYDIAAIKFRGLNAVTNFDMSR
GmPLT1	82	(310)	EAYDIAAIKFRGLNAVTNFDMSR
ZmPLT3b	72	(281)	EAYDIAAIKFRGLNAVTNFDMSR
AtAIL1	100	(364)	EAYDIAAIKFRGLNAVTNFDINR
SbPLT3b	76	(276)	EAYDIAAIKFRGLNAVTNFDMSR
OsPLT3b	81	(271)	EAYDIAAIKFRGLNAVTNFDMSR
OsBBM1	16	(309)	EAYDIAAIKFRGLNAVTNFDMSR
MtPLT1/2	84	(304)	EAYDIAAIKFRGLNAVTNFDMTR
SbAIL1	91	(404)	EAYDIAAIKFRGLNAVTNFDISK
OsAIL1	77	(394)	EAYDIAAIKFRGLNAVTNFDISK
ZmAIL1	85	(412)	EAYDIAAIKFRGLNAVTNFDISK
AtPLT2	75	(331)	EAYDIAAIKFRGLNAVTNFEINR
AtPLT1	83	(322)	EAYDIAAIKFRGLNAVTNFEINR
OsBBM3	20	(420)	EAYDIAAIKFRGLNAVTNFDMSR
VvBBM	6	(349)	EAYDIAAIKFRGLNAVTNFDMSR
GmANT	99	(405)	EAYDIAAIKFRGANAVTNFDISR
GmBBM	2	(410)	EAYDVAAIKFRGLSAVTNFDMSR
MtBBM	8	(400)	EAYDVAAIKFRGLSAVTNFDMSR
SbANT	93	(424)	EAYDIAAIKFRGLNAVTNFDITR
GmAIL1	86	(343)	EAYDIAAIKFRGTSAVTNFDISR
MtAIL1	90	(389)	EAYDIAAIKFRGTSAVTNFDISR
SbPLT3	87	(279)	EAYDIAAIKFRGLNAVTNFEISR
ZmPLT3	80	(268)	EAYDIAAIKFRGLNAVTNFEISR
AtBBM	22	(351)	EAYDIAAIKFRGLSAVTNFDMNR
OsANT	95	(443)	EAYDVAAIKFRGLNAVTNFDITR
BnBBM2	26	(351)	EAYDIAAIKFRGLTAVTNFDMNR
BnBBM1	24	(351)	EAYDIAAIKFRGLTAVTNFDMNR
MtANT	98	(452)	EAYDIAAIKFRGANAVTNFDIIK
AtANT	92	(424)	EAYDVAAIKFRGTNAVTNFDITR
AtAIL6	89	(394)	EAYDIAAIKFRGINAVTNFEMNR
ZmANT	67	(443)	EAYDVAAIKFRGLSAVTNFDITR
OsPLT3	73	(285)	EAYDIAAIKFRGLNAVTNFEIGR
GmAIL7	94	(361)	EAYDIAAIKFRGANAVTNFEMNR
GmAIL6	88	(362)	EAYDIAAIKFRGANAVTNFEMNR
AtAIL7	96	(314)	EAYDIAAIKFRGINAVTNFEMNR
ZmANT2	97	(425)	EAYDIAAIKFRGLNAVTNFDIAR
ZmANTr	101	(289)	EAYDIAALKFRGENAVTNFEPSR
AtWRI1	102	(206)	AAYDMAAIEYRGANAVTNFDISN
Consensus	49		EAYD3AAIKFRGLNAVTNF456R

1= I or M; 2= Q or E; 3= I or V; 4= D or E; 5=M or I; 6=S or N

FIG. 2B (continued)

	SEQ ID NO:		
SbBBM	4	(276)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQTRK
ZmBBM	10	(272)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQTRK
VvBBM	6	(207)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQTRK
GmBBM	2	(268)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQTRK
OsBBM	14	(282)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQTRK
MtBBM	8	(261)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQTRK
SbBBM2	28	(285)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
OsBBM3	20	(278)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
OsBBM2	18	(302)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
ZmBBM2	12	(278)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
GmPLT3b	70	(150)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
GmPLT3a	71	(146)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
MtPLT3	79	(161)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
ZmANT	67	(301)	SQYRGVTRHRWTGRYEAHLWDNSCRKEGQTRK
GmAIL1	86	(204)	SQYRGVTRHRWTGRYEAHLWDNSCRKEGQTRK
MtAIL1	90	(250)	SQYRGVTRHRWTGRYEAHLWDNSCRKEGQTRK
SbANT	93	(285)	SQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRK
OsANT	95	(304)	SQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRK
GmANT	99	(267)	SQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRK
GmAIL6	88	(223)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQARK
MtANT	98	(312)	SQYRGVTRHRWTGRYEAHLWDNSCKKEGQSRK
BnBBM2	26	(209)	SIYRGVTRHRWTGRYEAHLWDNSCKREGQTRK
BnBBM1	24	(209)	SIYRGVTRHRWTGRYEAHLWDNSCKREGQTRK
AtBBM	22	(209)	SIYRGVTRHRWTGRYEAHLWDNSCKREGQTRK
SbPLT3	87	(140)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
ZmPLT3	80	(126)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
GmPLT2	78	(163)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
GmPLT1	82	(168)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
OsPLT3	73	(143)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
GmAIL7	94	(223)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQARK
AtAIL6	89	(253)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQARK
AtPLT2	75	(189)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
OsPLT3b	81	(129)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
AtPLT1	83	(180)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
AtPLT3/AIL5	74	(202)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
SbPLT3b	76	(134)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
ZmPLT3b	72	(139)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQSRK
ZmANT2	97	(283)	SRYRGVTRHRWTGRYEAHLWDNSCRKDGQTRK
AtAIL7	96	(172)	SIYRGVTRHRWTGRYEAHLWDNSCRREGQARK
MtPLT1/2	84	(165)	SIYRGVTKHRWTGRYEAHLWDNSCRREGQSRK
SbAIL1	91	(265)	SQFRGVTRHRWTGRYEAHLWDNTCRKEGQTRK
OsAIL1	77	(252)	SQFRGVTRHRWTGRYEAHLWDNTCRKEGQTRK
ZmAIL1	85	(270)	SQFRGVTRHRWTGRYEAHLWDNTCRKEGQTRK
OsBBM1	16	(167)	SIYRGVTKHRWTGRYEAHLWDNSCRREGQTRK
AtAIL1	100	(222)	SQYRGVTRHRWTGRYEAHLWDNSCKKEGQTRR
AtANT	92	(282)	SQYRGVTRHRWTGRYEAHLWDNSFKKEGHSRK
ZmANTr	101	(147)	SIYRGVTRHRWTGRYEAHLWDNTCRKEGQKRK
AtWRI1	102	(64)	SIYRGVTRHRWTGRFEAHLWDKSSWNSIQNKK
Consensus	50		S0YRGVTRHRWTGRYEAHLWDNSCR1EGQ2RK

FIG. 2C

	SEQ ID NO:		
SbBBM	4	(308)	GRQGGYDKEEKAARAYDLAALKYWGPTTTTNFPVNN
ZmBBM	10	(307)	VYLGGYDKEEKAARAYDLAALKYWGATTTTNFPVSN
VvBBM	6	(242)	VYLGGYDKEEKAARAYDLAALKYWGTTTTTNFPISN
GmBBM	2	(303)	VYLGGYDKEEKAARAYDLAALKYWGTTTTTNFPISH
OsBBM	14	(317)	VYLGGYDKEEKAARAYDLAALKYWGPTTTTNFPVNN
MtBBM	8	(293)	GRQGGYDKEEKAARAYDLAALKYWGTTTTTNFPISH
SbBBM2	28	(320)	VYLGGYDKEDKAARAYDLAALKYWGTTTTTNFPISN
OsBBM3	20	(313)	VYLGGYDKEDKAARAYDLAALKYWGTTTTTNFPMSN
OsBBM2	18	(334)	GRQGGYDKEDKAARAYDLAALKYWGTTTTTNFPISN
ZmBBM2	12	(313)	VYLGGYDKEDKAARAYDLAALKYWGTTTTTNFPISN
GmPLT3b	70	(185)	VYLGGYDKEDKAARAYDLAALKYWGPTTTTNFPISN
GmPLT3a	71	(181)	VYLGGYDKEDKAARAYDLAALKYWGPTTTTNFPISN
MtPLT3	79	(193)	GRQGGYDKEEKAARAYDLAALKYWGPTTTTNFPISN
ZmANT	67	(336)	VYLGGYDVEEKAARAYDLAALKYWGTSTHVNFPVED
GmAIL1	86	(236)	GRQGGYDKEEKAAKAYDLAALKYWGPTTHINFPLST
MtAIL1	90	(282)	GRQGGYDKEEKAAKAYDLAALKYWGPTTHINFPLST
SbANT	93	(317)	GRQGGYDMEEKAARAYDLAALKYWGPSTHINFPLED
OsANT	95	(336)	GRQGGYDMEEKAARAYDLAALKYWGPSTHINFPLED
GmANT	99	(298)	GRQGGYDMEEKAARAYDLAALKYWGPSTHINFSIEN
GmAIL6	88	(255)	GRQGGYDKEEKAARAYDLAALKYWGPTATTNFPVSN
MtANT	98	(344)	GRQGGYDMEEKAARAYDQAALKYWGPSTHINFPLEN
BnBBM2	26	(244)	VYLGGYDKEEKAARAYDLAALKYWGTTTTTNFPMSE
BnBBM1	24	(244)	VYLGGYDKEEKAARAYDLAALKYWGTTTTTNFPMSE
AtBBM	22	(244)	VYLGGYDKEEKAARAYDLAALKYWGPTTTTNFPLSE
SbPLT3	87	(172)	GRQGGYDKEEKAARAYDLAALKYWGSSTTTNFPVAE
ZmPLT3	80	(161)	VYLGGYDKEEKAARAYDLAALKYWGSSTTTNFPVAE
GmPLT2	78	(198)	VYLGGYDKEEKAARAYDLAALKYWGTSTTTNFPISN
GmPLT1	82	(203)	VYLGGYDKEEKAARSYDLAALKYWGTSTTTNFPISN
OsPLT3	73	(178)	VYLGGYDKEEKAARAYDLAALKYWGPSTTTNFPVAE
GmAIL7	94	(254)	GRQGGYDKEEKAARSYDLAALKYWGPTATTNFPVSN
AtAIL6	89	(287)	VYLGGYDKEDKAARAYDLAALKYWNATATTNFPITN
AtPLT2	75	(224)	VYLGGYDKEEKAARAYDLAALKYWGPSTTTNFPITN
OsPLT3b	81	(164)	VYLGGYDKEEKAARAYDLAALKYWGPTTTTNFPVAN
AtPLT1	83	(215)	VYLGGYDKEDKAARSYDLAALKYWGPSTTTNFPITN
AtPLT3/AIL5	74	(237)	VYLGGYDKEDKAARAYDLAALKYWGPTTTTNFPISN
SbPLT3b	76	(169)	VYLGGYDKEEKAARAYDLAALKYWGATTTTNFPVSN
ZmPLT3b	72	(174)	VYLGGYDKEEKAARAYDLAALKYWGPTTTTNFPVSN
ZmANT2	97	(318)	VYLGGYDTEDKAARAYDLAALKYWGPATHVNFPVEN
AtAIL7	96	(207)	VYLGGYDKEDRAARAYDLAALKYWGSTATTNFPVSS
MtPLT1/2	84	(197)	GRQGGYDKEEKAARSYDLAALKYWGTSTTTNFPVSN
SbAIL1	91	(297)	GRQGGYDREEKAARAYDLAALKYWGPSTHINFPLSH
OsAIL1	77	(287)	VYLGGYDKEEKAARAYDLAALKYWGPTTHINFPLST
ZmAIL1	85	(305)	VYLGGYDREEKAARAYDLAALKYWGPSTHINFPLSH
OsBBM1	16	(202)	VYLGGYDKEEKAARAYDLAALKYWGTTTTTNFPVSN
AtAIL1	100	(257)	VYLGGYDEEEKAARAYDLAALKYWGPTTHLNFPLSN
AtANT	92	(317)	VYLGGYDMEEKAARAYDLAALKYWGPSTHTNFSAEN
ZmANTr	101	(182)	VYLGGYDKEDKAARAYDIAALKYWGDNATTNFPREN
AtWRI1	102	(99)	VYLGAYDSEEAAAHTYDLAALKYWGPDTILNFPAET
Consensus	50		345GGYDKE6KAARAYDLAALKYWG72T89NFP*SN

0=I or Q; 1=R or K; 2= S or T; 3= V or G; 4= Y or R; 5=L or Q; 6=E or D; 7= P or T; 8=T or H; 9=T or I; *=I, V, or L

FIG. 2C (continued)

	SEQ ID NO:		
SbBBM2	28	(113)	AVEDSEPKLEDFLGGNSFVSEH
OsBBM2	18	(108)	AVEETEPKLEDFLGGNSFVSEQ
ZmBBM2	12	(110)	AVEDSEPKLEDFLGGNSFVSDQ
SbBBM	4	(55)	SALVAEPKLEDFLGGISFSEQH
ZmBBM	10	(56)	SALVAEPKLEDFLGGISFSEQH
OsBBM	14	(61)	SALVAEPKLEDFLGGISFSEQQ
GmAIL6	88	(77)	HVPPPPPKLEDFLGDSSAVMRY
MtBBM	8	(106)	NNQQAQPKLENFLGGHSFTDHQ
GmAIL7	94	(75)	SVSHAPPKLEDFLGDSSAVMRY
MtAIL1	90	(85)	NSNEEGPKLEDFLGCYSNQNQN
GmANT	99	(97)	MVPTSSPKLEDFLGGATMGTHE
AtAIL6	89	(71)	HSQNHIPKLEDFLGDSSSIVRY
VvBBM	6	(103)	NLENQEPKLENFLGCRSFADHE
GmBBM	2	(107)	QQQQQQPKLENFLGGHSFGEHE
ZmANT2	97	(106)	MVPSSPPKLEDFLGGGNGGGQE
BnBBM2	26	(89)	NDEQDGPKLENFLGRTTTIYNT
BnBBM1	24	(89)	NDEQDGPKLENFLGRTTTIYNT
OsPLT3	73	(37)	AGAAPPPKLEDFLGGGCNGGSS
GmAIL1	86	(50)	NSNEEGPKLEDFLGCYSNSPAK
AtBBM	22	(91)	NNEQNGPKLENFLGRTTTIYNT
GmPLT2	78	(54)	HSSNEIPKVADFLGVSKSENQS
MtPLT1/2	84	(54)	HNSNEVPKVADFLGVCKSENHS
GmPLT3b	70	(68)	SIFTGGPKFEDFLGGSAATATT
SbPLT3	87	(35)	AGAAPPPKLEDFLGGGVINGES
ZmPLT3	80	(36)	AGAAPPPKLEDFLGGGVATGGP
GmPLT3a	71	(64)	SIFTGAPKFEDFLGGSSATATA
GmPLT1	82	(54)	HSSSEVPKVADFLGVSKSENES
AtPLT3/AIL5	74	(95)	SVYPGGPKLENFLGGGASTTTT
AtAIL7	96	(13)	HSQTQIPKLEDFLGDSFVRYSD
SbAIL1	91	(72)	AAEANGPKLEDFMSVTCSSNNK
OsBBM1	16	(47)	GEETAAPKLEDFLGMQVQQETA
AtPLT2	75	(58)	GEGGEVPKVADFLGVSKSGDHH
ZmAIL1	85	(76)	AAEAKGPKLEDFMSITCSNKSS
ZmANT	67	(123)	VVSSSSPKLEDFLGASASTAMA
OsAIL1	77	(66)	HAEAKDPKLEDFMSVSYSNKSS
AtPLT1	83	(52)	DEGGEVPKVADFLGVSKPDENQ
OsBBM3	20	(109)	DGVGEAPKLENFLDGNSFSDVH
MtANT	98	(110)	MSTTSAPKLENFLGNEAMGTPH
SbANT	93	(103)	QPDHHGPKLEDFLGAAAAQSQA
AtANT	92	(108)	HHQDSSPKVEDFFGTHHNNTSH
OsANT	95	(124)	VVVSASPKLEDFLGAGPAMALS
MtPLT3	79	(79)	SIFTGGHKFEDFLGSSVAPTRT
AtAIL1	100	(41)	HHDEDVPKVEDLLSNSHQTEYP
OsPLT3b	81	(42)	GPAEGAPKMEDFLGGLGGGGGA
ZmPLT3b	72	(44)	AVEESPRTVEDFLGGVGGAGAP
SbPLT3b	76	(45)	TVEESPKMVEDFLGGVGGAGAP
Consensus	51		PK123FLG

1= L or V; 2= E or A; 3= D or N

FIG. 2D

	SEQ ID NO:		
VvBBM	6	(377)	ILESSTLPIGGAAKRL
MtBBM	8	(428)	ILESSTLPIGGAAKRL
GmBBM	2	(438)	ILESTTLPIGGAAKRL
SbBBM2	28	(455)	ILESSTLPVGGAARRL
OsBBM2	18	(469)	ILESSTLPVGGAARRL
ZmBBM2	12	(448)	ILESSTLPVGGAARRL
AtPLT1	83	(350)	ILESSTLPIGGGAAKR
OsBBM3	20	(448)	ILDSSTLPVGGAARRL
GmPLT2	78	(333)	ILESNTLPIGGGAAKR
GmPLT1	82	(338)	ILESNTLPIGGGAAKR
MtPLT1/2	84	(332)	ILESNTLPIGGGAAKR
AtPLT2	75	(359)	ILESNTLPIGGGAAKR
BnBBM2	26	(379)	ILESPSLPIGSAAKRL
BnBBM1	24	(379)	ILESPSLPIGSAAKRL
SbBBM	4	(446)	ILDSSALPIGSAAKRL
ZmBBM	10	(442)	ILDSSALPIGSAAKRL
OsANT	95	(471)	ILESSTLLPGELARRK
AtAIL6	89	(421)	AIMKSALPIGGAAKRL
AtBBM	22	(379)	ILESPSLPIGSSAKRL
GmAIL7	94	(388)	AIMKSSLPVGGAAKRL
GmAIL6	88	(389)	AIMKSSLPVGGAAKRL
SbANT	93	(452)	IMASNTLLPGDLARRR
ZmANT	67	(471)	IMESSTLLPGEQVRRR
SbAIL1	91	(432)	ICASTHLIGGGDACRR
ZmAIL1	85	(440)	ICASTHLIGGGDACRR
OsBBM1	16	(337)	IIESSNLPIGTGTTRR
GmAIL1	86	(371)	ICSSSTLIAGDLAKRS
OsBBM	14	(452)	ILDSAALPVGTAAKRL
OsAIL1	77	(422)	ICSSTHLIGGDLACRR
GmANT	99	(433)	IMASSNLLAGELARRN
MtAIL1	90	(417)	ICSSSTLITGDLAKRS
GmPLT3b	70	(319)	SIANSTLPIGGLSGKN
GmPLT3a	71	(315)	SIANSTLPIGGLSGKN
AtANT	92	(452)	IMSSNTLLSGELARRN
AtAIL7	96	(341)	AVMNSSLPVGGAAAKR
SbPLT3b	76	(303)	SILNSDLPVGGGAAGR
OsPLT3b	81	(298)	SILNSDLPVGGGAATR
ZmANT2	97	(453)	IMESSTLLAVEEARKV
MtPLT3	79	(327)	SIANCSLPIGGLSNKN
ZmPLT3b	72	(308)	SILSSDLPVGGGASGR
OsPLT3	73	(312)	SIISSNLPIGSMAGNR
MtANT	98	(480)	IMASSNLLNIEQARRN
AtPLT3/AIL5	74	(371)	SIASCNLPVGGLMPKP
Consensus	52		SSTLP1GG2A334

1=I or V; 2= A, L, or G; 3= K or R; 4= L or R

FIG. 2E

	SEQ ID NO:		
AtBBM	22	(4)	MNNWLGFSLSPHDQNH
GmANT	99	(15)	NHNWLGFSLSPHMKME
BnBBM2	26	(2)	NNNWLGFSLSPYEQNH
BnBBM1	24	(2)	NNNWLGFSLSPYEQNH
VvBBM	6	(4)	MNNWLGFSLSPRELPP
OsBBM	14	(4)	MNNWLAFSLSPQDQLP
SbBBM	4	(4)	VNNWLAFSLSPQELPP
ZmBBM	10	(4)	VNNWLAFSLSPQELPP
MtANT	98	(16)	ENNWLGFSLSPQMNNI
OsBBM2	18	(4)	ANNWLGFSLSGQENPQ
ZmBBM2	12	(4)	ANNWLGFSLSGQDNPQ
SbBBM2	28	(5)	NNHWLGFSLSGQDNPQ
GmAIL1	86	(1)	MSNWLGFSLTPHLRID
MtAIL1	90	(1)	MSNWLGFSLTPHLRID
ZmANT2	97	(4)	GSNWLGFSLSPHTAME
GmAIL6	88	(4)	ATNWLSFSLSPMEMLR
GmPLT2	78	(2)	NNNWLSFPLSPTHSSL
GmPLT1	82	(2)	NNNWLSFPLSPTHSSL
MtPLT1/2	84	(2)	NNNWLSFPLSPSHSSL
GmAIL7	94	(5)	STNWLSFSLSPMDMLR
AtPLT1	83	(3)	SNNWLGFPLSPNNSSL
MtBBM	8	(3)	SMNLLGFSLSPQEQHP
AtPLT2	75	(3)	SNNWLAFPLSPTHSSL
ZmAIL1	85	(4)	NNGWLGFSLSPSAASR
OsBBM3	20	(4)	ADNWLGFSLSGQGNPQ
SbANT	93	(13)	ASSWLGFSLSPHMASA
OsANT	95	(20)	VGGWLGFSLSPHMATY
SbPLT3b	76	(10)	PHHWLSFSLSNNYHHG
OsPLT3b	81	(10)	PHHWLSFSLSNNYHHG
ZmPLT3b	72	(10)	PHHWLSFSLSNNYHHG
SbAIL1	91	(4)	NNGWLGFSLSPSAGRG
GmBBM	2	(3)	SMNLLGFSLSPQEHPS
AtPLT3/AIL5	74	(27)	HQNWLSFSLSNNNNNF
GmPLT3b	70	(13)	NNNSLAFSLSNHFPNP
GmPLT3a	71	(9)	NNNSLAFSLSNHFPNP
AtAIL1	100	(1)	MKKWLGFSLTPPLRIC
ZmANT	67	(23)	GGSWLGFSLSPHMAAT
OsPLT3	73	(8)	HYPWLNFSLAHHCEME
ZmPLT3	80	(7)	YHPWLNFSLAHHCDLE
SbPLT3	87	(6)	HYPWLNFSLAHHGDLE
OsAIL1	77	(4)	NSGWLGFSLSSSSARG
AtANT	92	(15)	TTNLLGFSLSSNMMKM
OsBBM1	16	(4)	ITNWLGFSSSSFSGAG
Consensus	53		NWLXFSLSP

X=G or S

FIG. 2F

	SEQ ID NO:		
MtBBM	8	(159)	NNSIGLSMIKTWLRNQPPPPE
BnBBM2	26	(130)	GGSLGLSMIKTWLRNQPVDNV
BnBBM1	24	(130)	GGSLGLSMIKTWLRNQPVDNV
SbBBM	4	(156)	SGSIGLSMIKNWLRSQPAPMQ
SbBBM2	28	(157)	SNTMELSMIKTWLRNNQVPQP
OsBBM	14	(156)	NGGIGLSMIKNWLRSQPAPQP
ZmBBM	10	(152)	GGGIGLSMIKNWLRSQPAPMQ
VvBBM	6	(131)	YISIGLSMIKTWLRNQPAPTH
ZmBBM2	12	(154)	SNTMELSMIKTWLRNNQVAQP
GmBBM	2	(164)	SSSIGLSMIKTWLRNQPPHSE
OsBBM3	20	(157)	GGTIELSMIKTWLRSNQSQQQ
OsBBM2	18	(154)	SNTMELSMIKTWLRNNGQVPA
OsBBM1	16	(80)	SSVVGLSMIKNWLRSQPPPAV
AtBBM	22	(131)	GGSLGLSMIKTWLSNHSVANA
Consensus	54		1LSMIK2WLR

1= G or E; 2= T or N

FIG. 2G

	SEQ ID NO:		
SbAIL1	91	(527)	AGVHQLPVFALWND
OsAIL1	77	(536)	TVHHQLPVFALWND
ZmAIL1	85	(529)	PGVHQLPMFALWND
ZmANT	67	(624)	VSIAHLPVFAAWTD
SbANT	93	(664)	VSIAHMPVFAAWTD
OsANT	95	(638)	VSIAHLPMFAAWTD
MtANT	98	(642)	LSLPQMPVFAAWTD
VvBBM	6	(629)	AVCHGTPTFTVWND
GmANT	99	(532)	ISLSHLPVFAAWTD
OsBBM	14	(681)	GVCHGAQLFSVWND
BnBBM2	26	(565)	GGGEVAPTFTVWND
BnBBM1	24	(565)	GGGEVAPTFTVWND
GmAIL1	86	(499)	GLVNQVPMFALWNE
MtAIL1	90	(561)	GLVNQVPMFALWNE
ZmANT2	97	(637)	VVVSHRPVFAAWAD
AtBBM	22	(570)	GGGEGAPTFSVWND
AtANT	92	(541)	LTLPQMPVFAAWAD
SbBBM	4	(689)	VGHGGAQLFSVWND
ZmBBM	10	(695)	VGHGGAQLFSVWND
GmPLT2	78	(540)	MQTSNGGVFTMWND
GmPLT1	82	(549)	MQTSNSGVFTMWND
GmPLT3b	70	(92)	CAPPQLPQFSTDNN
GmPLT3a	71	(88)	CAPPQLPQFSTDNN
MtPLT3	79	(105)	CAPTQLQQFSTDND
AtPLT2	75	(555)	QGSNPGGVFTMWNE
AtPLT1	83	(561)	QGSNPGGVFTMWNE
MtPLT1/2	84	(524)	ENMQTADLFTMWND
Consensus	55		PXFXXWND

X= any amino acid

FIG. 2H

	SEQ ID NO:		
GmANT	99	(210)	LQSLSLSMSPGSQSSC
AtANT	92	(194)	QQSLSLSMSPGSQSSC
GmPLT2	78	(120)	LQSLTLSMGSGKDSTC
GmPLT1	82	(121)	LQSLTLSMGSGKDSTC
MtPLT1/2	84	(122)	LQSLTLSMGSGKDSTC
MtANT	98	(250)	LHSLSLSMSPSSQSSC
MtBBM	8	(192)	VQTLSLSMSTGSQSSS
GmBBM	2	(202)	QQTLSLSMSTGSQSST
VvBBM	6	(174)	AQTLSLSMSTGSHQTG
SbBBM2	28	(221)	SQSLALSMSTGSHLPM
OsBBM2	18	(234)	SQSLALSMSTGSHSHL
ZmBBM2	12	(214)	SQSLALSMSTGSHLPM
SbANT	93	(217)	HHALALSMSSGSLSSC
ZmBBM	10	(181)	AQGLSLSMNMAGTTQG
GmAIL1	86	(150)	FQSLSLTMSPSVQNGV
OsBBM	14	(177)	AQALSLSMNMAGTTTA
BnBBM2	26	(159)	AKGLSLSMNSSTSCDN
BnBBM1	24	(159)	AKGLSLSMNSSTSCDN
SbBBM	4	(185)	VQGLSLSMNMAGATQG
OsANT	95	(241)	LHPLTLSMSSAGSQSS
MtAIL1	90	(191)	FQSLNLTMSPCVQNGV
ZmANT	67	(231)	PHPLALSMSSGTGSQS
AtPLT1	83	(126)	LQSLTLSMGTTAGNNV
AtPLT2	75	(129)	LQSLTLSMGSTGAAAA
AtBBM	22	(160)	ARGLSLSMNSSTSDSN
OsBBM3	20	(220)	GQGLALSMSTGSVAAA
ZmANT2	97	(202)	TRPLSLSMMSPGTQLS
Consensus	56		LXLSM

X = S, T or A

FIG. 2I

	SEQ ID NO:		
SbBBM	4	(529)	GWCKQEQDHAVIAAAH
OsBBM	14	(534)	GWCKQEQDHAVIAAAH
ZmBBM	10	(531)	GWCKQEQDHAVIAAAH
SbBBM2	28	(536)	GWCKPEQDAAVAAAAH
OsBBM2	18	(560)	GWCKPEQDAAVAAAAH
ZmBBM2	12	(528)	GWCKPEQDAAAAAAHS
OsBBM3	20	(522)	GWCKPEQDAVIAAGHC
MtBBM	8	(522)	LWCKQEQDSDDHSTYT
VvBBM	6	(453)	VWCKQEQDPDGTHNFQ
OsBBM1	16	(416)	AWLKQEQDSSVVTAAQ
GmBBM	2	(527)	NWCKQEQDNSDASHSL
Consensus	57		WCKXEQD

X= Q or P

FIG. 2J

	SEQ ID NO:		
OsBBM2	18	(529)	HHHGWPTIAFQQPPPLAVHYPY
SbBBM2	28	(508)	GHHAWPTIAFQQPSPLSVHYPY
ZmBBM2	12	(501)	GHHGWPTIAFQQPSPLSVHYPY
VvBBM	6	(425)	HHHGWPTVAFQQAQPFSMHYPY
SbBBM	4	(502)	YHGAWPTIAFQPSAATGLYHPY
ZmBBM	10	(500)	HGAAWPTIAFQPGAATTGLYHP
OsBBM	14	(502)	AAAAWPTIAFQAAAAPPPHAAG
Consensus	58		WPTIAFQ

FIG. 2K

	SEQ ID NO:		
SbBBM	4	(572)	MHGLGSMDNASLEHSTGSNSVVYNG
ZmBBM	10	(577)	MHGLASIDSASLEHSTGSNSVVYNG
OsBBM	14	(576)	QHGLGSIDNASLEHSTGSNSVVYNG
VvBBM	6	(487)	LHNLMSMDSSSMDHSSGSNSVIYSG
MtBBM	8	(560)	LQNIMSMDSASMDNSSGSNSVVYGG
GmBBM	2	(567)	LHPMLSMDSASIDNSSSSNSVVYDG
Consensus	59		SXGSNSVVYNG

X= S or T

FIG. 2L

	SEQ ID NO:		
SbBBM2	28	(78)	ETQDWNMRGLDY
ZmBBM2	12	(75)	ETQDWNMRGLDY
OsBBM2	18	(76)	EAQDWNMRGLDY
OsBBM3	20	(74)	ETQDWAMRGLDY
SbBBM	4	(43)	IPQDWSMRGSEL
OsBBM	14	(49)	IPQDWSMRGSEL
ZmBBM	10	(44)	IPQDWSMRGSEL
Consensus	60		QDWXMRG

X= S or N

FIG. 2M

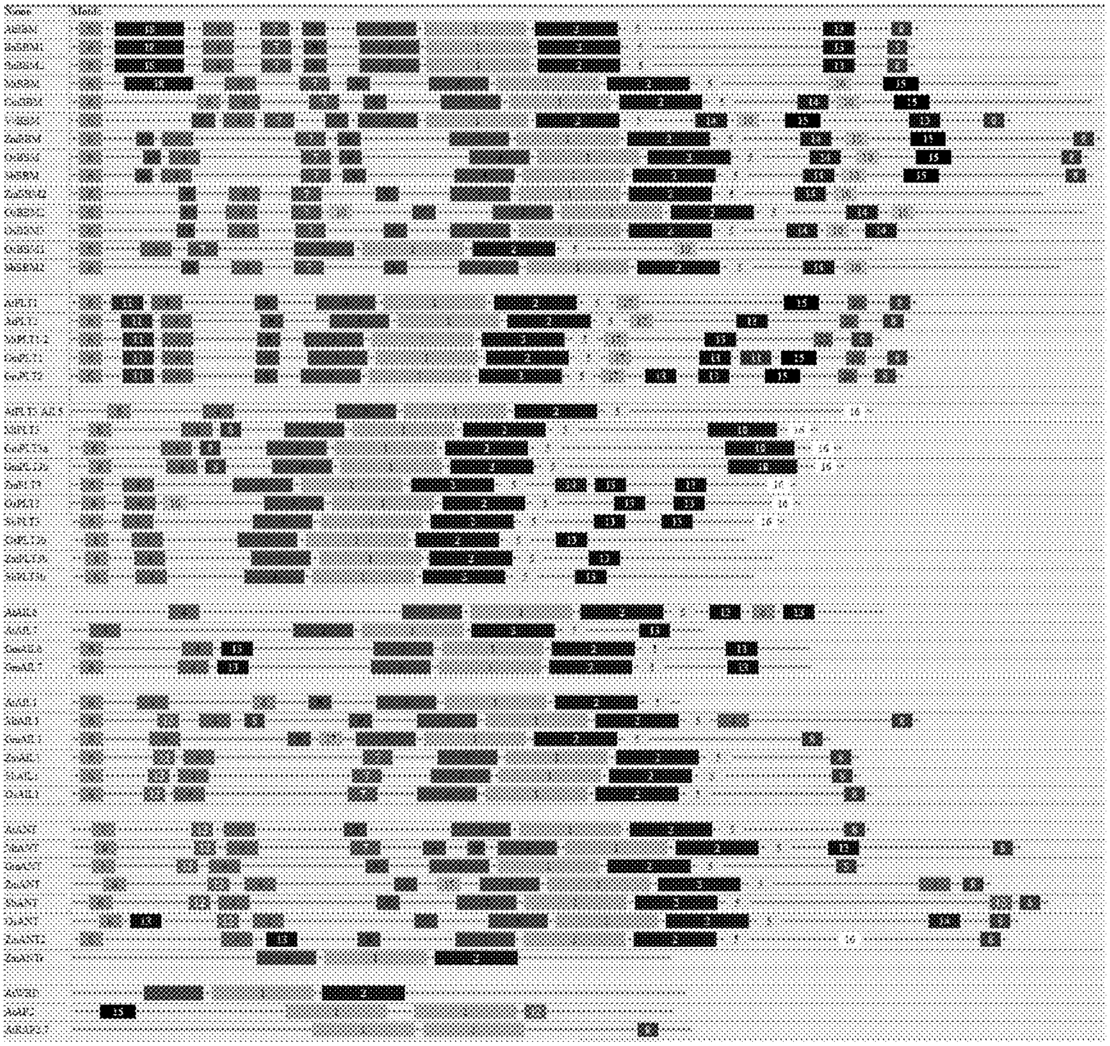
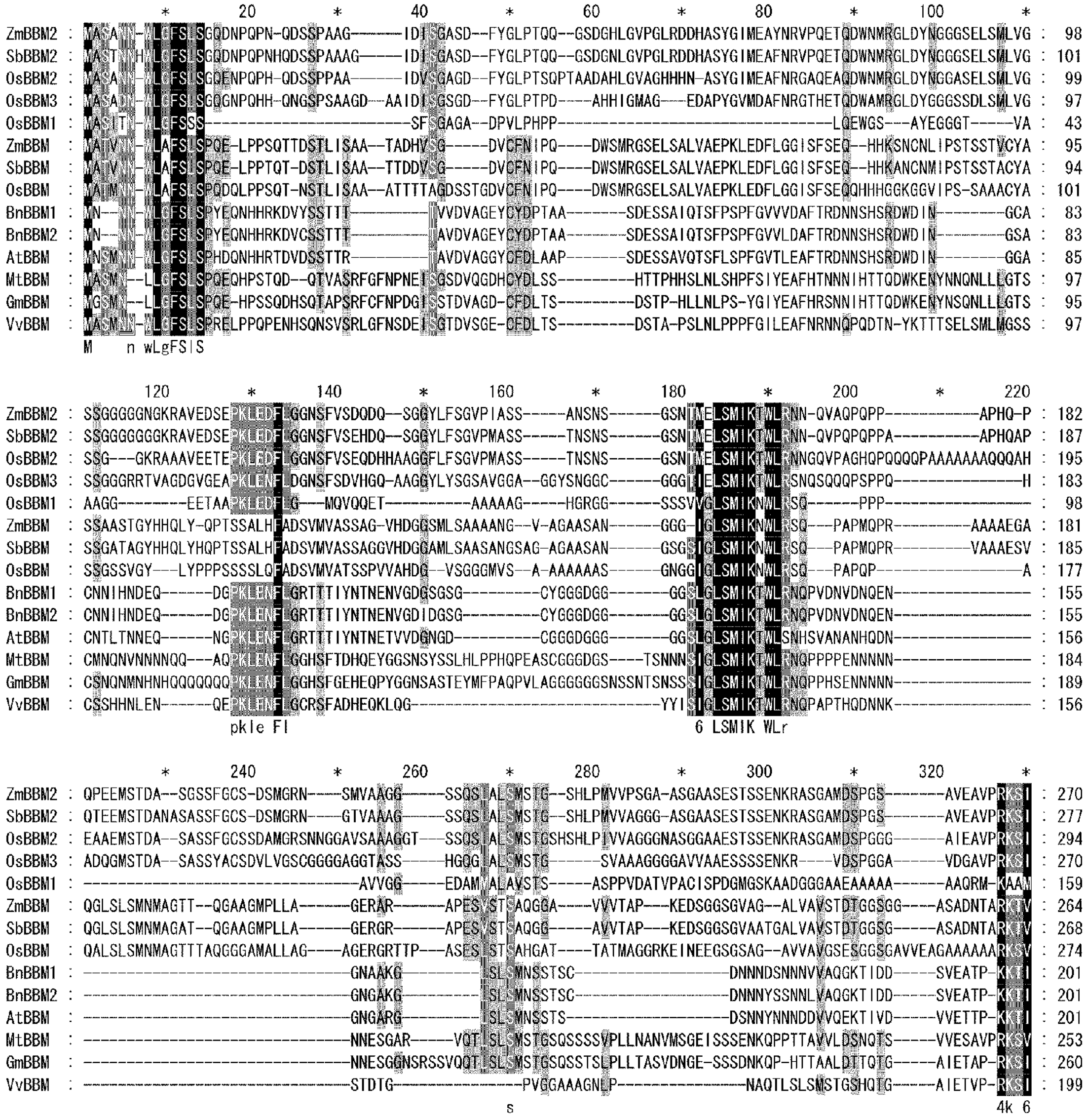


FIG. 3



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                  *        20         *        40         *        60         *        80         *       100         *
ZmBBM2 : MASANN-WLGFSLSGQDNPQPN-QDSSPAAG-------IDISGASD--FYGLPTQQ--GSDGHLGVPGLRDDHASYGIMEAYNRVPQETQDWNMRGLDYNGGGSELSMLVG :  98
SbBBM2 : MASTNNHWLGFSLSGQDNPQPNHQDSSPAAAG-----IDISGASD--FYGLPTQQ--GSDGNLGVPGLRDDHASYGIMEAFNRVPQETQDWNMRGLDYNGGGSELSMLVG : 101
OsBBM2 : MASANN-WLGFSLSGQENPQPH-QDSSPPAA------IDVSGAGD--FYGLPTSQPTAADAHLGVAGHHHN-ASYGIMEAFNRGAQEAQDWNMRGLDYNGGASELSMLVG :  99
OsBBM3 : MASADN-WLGFSLSGQGNPQHH-QNGSPSAAGD--AAIDISGSGD--FYGLPTPD----AHHIGMAG---EDAPYGVMDAFNRGTHETQDWAMRGLDYGGGSSDLSMLVG :  97
OsBBM1 : MASITN-WLGFSSS------------------------SFSGAGA--DPVLPHPP-------------------------------LQEWGS---AYEGGGT-----VA :  43
ZmBBM  : MATVNN-WLAFSLSPQE-LPPSQTTDSTLISAA--TADHVSG-----DVCFNIPQ----DWSMRGSELSALVAEPKLEDFLGGISFSEQ--HHKSNCNLIPSTSSTVCYA :  95
SbBBM  : MATVNN-WLAFSLSPQE-LPPTQT-DSTLISAA--TTDDVSG-----DVCFNIPQ----DWSMRGSELSALVAEPKLEDFLGGISFSEQ--HHKANCNMIPSTSSTACYA :  94
OsBBM  : MATMNN-WLAFSLSPQDQLPPSQT-NSTLISAA--ATTTTAGDSSTGDVCFNIPQ----DWSMRGSELSALVAEPKLEDFLGGISFSEQQHHHGGKGGVIPS-SAAACYA : 101
BnBBM1 : MN--NN-WLGFSLSPYEQNHHRKDVYSSTTT---------IVVDVAGEYCYDPTAA-------SDESSAIQTSFPSPFGVVVDAFTRDNNSHSRDWDIN--------GCA :  83
BnBBM2 : MN--NN-WLGFSLSPYEQNHHRKDVCSSTTT---------IAVDVAGEYCYDPTAA-------SDESSAIQTSFPSPFGVVLDAFTRDNNSHSRDWDIN--------GSA :  83
AtBBM  : MNSMNN-WLGFSLSPHDQNHHRTDVDSSTTR---------TAVDVAGGYCFDLAAP-------SDESSAVQTSFLSPFGVTLEAFTRDNNSHSRDWDIN--------GGA :  85
MtBBM  : MASMN--LLGFSLSPQEQHPSTQD--QTVASRFGFNPNEISGSDVQGDHCYDLSS---------HTTPHHSLNLSHPFSIYEAFHTNNNIHTTQDWKENYNNQNLLLGTS :  97
GmBBM  : MGSMN--LLGFSLSPQE-HPSSQDHSQTAPSRFCFNPDGISSTDVAGD-CFDLTS---------DSTP-HLLNLPS-YGIYEAFHRSNNIHTTQDWKENYNSQNLLLGTS :  95
VvBBM  : MASMNN-WLGFSLSPRELPPQPENHSQNSVSRLGFNSDEISGTDVSGE-CFDLTS---------DSTA-PSLNLPPPFGILEAFNRNNQPQDTN-YKTTTSELSMLMGSS :  97
         M    n wLgFSlS

              120         *       140         *       160         *       180         *       200         *       220
ZmBBM2 : SSGGGGGNGKRAVEDSEPKLEDFLGGNSFVSDQDQ--SGGYLFSGVPIASS-----ANSNS------GSNTMELSMIKTWLRNN-QVAQPQPP-----------APHQ-P : 182
SbBBM2 : SSGGGGGGGKRAVEDSEPKLEDFLGGNSFVSEHDQ--SGGYLFSGVPMASS-----TNSNS------GSNTMELSMIKTWLRNN-QVPQPQPPA----------APHQAP : 187
OsBBM2 : SSG---GKRAAAVEETEPKLEDFLGGNSFVSEQDHHAAGGFLFSGVPMASS-----TNSNS------GSNTMELSMIKTWLRNNGQVPAGHQPQQQPAAAAAAAQQQAH : 195
OsBBM3 : SSGGGRRTVAGDGVGEAPKLENFLDGNSFSDVHGQ-AAGGYLYSGSAVGGA--GGYSNGGC------GGGTIELSMIKTWLRSNQSQQQPSPPQ---------------H : 183
OsBBM1 : AAGG--------EETAAPKLEDFLG---MQVQQET----------AAAAAG-----HGRGG------SSSVVGLSMIKNWLRSQ------PPP----------------- :  98
ZmBBM  : SSAASTGYHHQLY-QPTSSALHFADSVMVASSAG-VHDGGSMLSAAAANG--V-AGAASAN------GGG-IGLSMIKNWLRSQ---PAPMQPR---------AAAAEGA : 181
SbBBM  : SSGATAGYHHQLYHQPTSSALHFADSVMVASSAGGVHDGGAMLSAASANGSAG-AGAASAN------GSGSIGLSMIKNWLRSQ---PAPMQPR---------VAAAESV : 185
OsBBM  : SSGSSVGY---LYPPPSSSSLQFADSVMVATSSPVVAHDG--VSGGGMVS--A-AAAAAAS------GNGGIGLSMIKNWLRSQ---PAPQP----------------A : 177
BnBBM1 : CNNIHNDEQ------DGPKLENFLGRTTTIYNTNENVGDGSGSG---------CYGGGDGG-------GGSLGLSMIKTWLRNQPVDNVDNQEN---------------- : 155
BnBBM2 : CNNIHNDEQ------DGPKLENFLGRTTTIYNTNENVGDIDGSG---------CYGGGDGG-------GGSLGLSMIKTWLRNQPVDNVDNQEN---------------- : 155
AtBBM  : CNTLTNNEQ------NGPKLENFLGRTTTIYNTNETVVDGNGD----------CGGGDGGG-------GGSLGLSMIKTWLSNHSVANANHQDN---------------- : 156
MtBBM  : CMNQNVNNNNQQ---AQPKLENFLGGHSFTDHQEYGGSNSYSSLHLPPHQPEASCGGGDGS----TSNNNSIGLSMIKTWLRNQPPPPENNNNN---------------- : 184
GmBBM  : CSNQNMNHNHQQQQQQPKLENFLGGHSFGEHEQPYGGNSASTEYMFPAQPVLAGGGGGGSNSSNTSNSSSIGLSMIKTWLRNQPPHSENNNNN---------------- : 189
VvBBM  : CSSHHNLEN------QEPKLENFLGCRSFADHEQKLQG----------------------------YYISIGLSMIKTWLRNQPAPTHQDNNK---------------- : 156
                          pkle Fl                                        6 LSMIK WLr

                  *       240         *       260         *       280         *       300         *       320         *
ZmBBM2 : QPEEMSTDA--SGSSFGCS-DSMGRN----SMVAAGG-----SSQSIALSMSTG--SHLPMVVPSGA-ASGAASESTSSENKRASGAMDSPGS-------AVEAVPRKSI : 270
SbBBM2 : QTEEMSTDANASASSFGCS-DSMGRN----GTVAAAG-----SSQSIALSMSTG--SHLPMVVAGGG-ASGAASESTSSENKRASGAMDSPGS-------AVEAVPRKSI : 277
OsBBM2 : EAAEMSTDA--SASSFGCSSDAMGRSNNGGAVSAAAGGT---SSQSIALSMSTGSHSHLPIVVAGGGNASGGAAESTSSENKRASGAMDSPGGG------AIEAVPRKSI : 294
OsBBM3 : ADQGMSTDA--SASSYACSDVLVGSCGGGGAGGTASS-----HGQGIALSMSTG------SVAAAGGGGAVVAAESSSSENKR----VDSPGGA------VDGAVPRKSI : 270
OsBBM1 : -------------------------------AVVGG-----EDAMVALAVSTS-----ASPPVDATVPACISPDGMGSKAADGGGAAEAAAAA------AAQRM-KAAM : 159
ZmBBM  : QGLSLSMNMAGTT--QGAAGMPLLA------GERAR------APESVSTSAQGGA----VVVTAP---KEDSGGSGVAG--ALVAVSTDTGGSGG----ASADNTARKTV : 264
SbBBM  : QGLSLSMNMAGAT--QGAAGMPLLA------GERGR------APESVSTSAQGG-----AVVTAP---KEDSGGSGVAATGALVAVSTDTGGSG-----ASADNTARKTV : 268
OsBBM  : QALSLSMNMAGTTTAQGGGAMALLAG----AGERGRTTP---ASESISTSAHGAT----TATMAGGRKEINEEGSGSAG--AVVAVGSESGGSGAVVEAGAAAAAARKSV : 274
BnBBM1 : ------------------------------GNAAKG---------ISLSMNSSTSC-----------------DNNNDSNNNVVAQGKTIDD-----SVEATP-KKTI : 201
BnBBM2 : ------------------------------GNGAKG---------ISLSMNSSTSC-----------------DNNNYSSNNLVAQGKTIDD-----SVEATP-KKTI : 201
AtBBM  : ------------------------------GNGARG---------ISLSMNSSTS------------------DSNNYNNNDDVVQEKTIVD-----VVETTP-KKTI : 201
MtBBM  : ------------------------------NNESGAR-----VQTISLSMSTGSQSSSSVPLLNANVMSGEISSSENKQPPTTAVVLDSNQTS-----VVESAVPRKSV : 253
GmBBM  : ------------------------------NNESGGNSRSSVQQTISLSMSTGSQSSTSLPLLTASVDNGE-SSSDNKQP-HTTAALDTTQTG-----AIETAP-RKSI : 260
VvBBM  : ------------------------------STDTG---------------PVGGAAAGNLP---------------NAQTLSLSMSTGSHQTG------AIETVP-RKSI : 199
                                                        s                                                          4k 6
```

FIG. 4-1

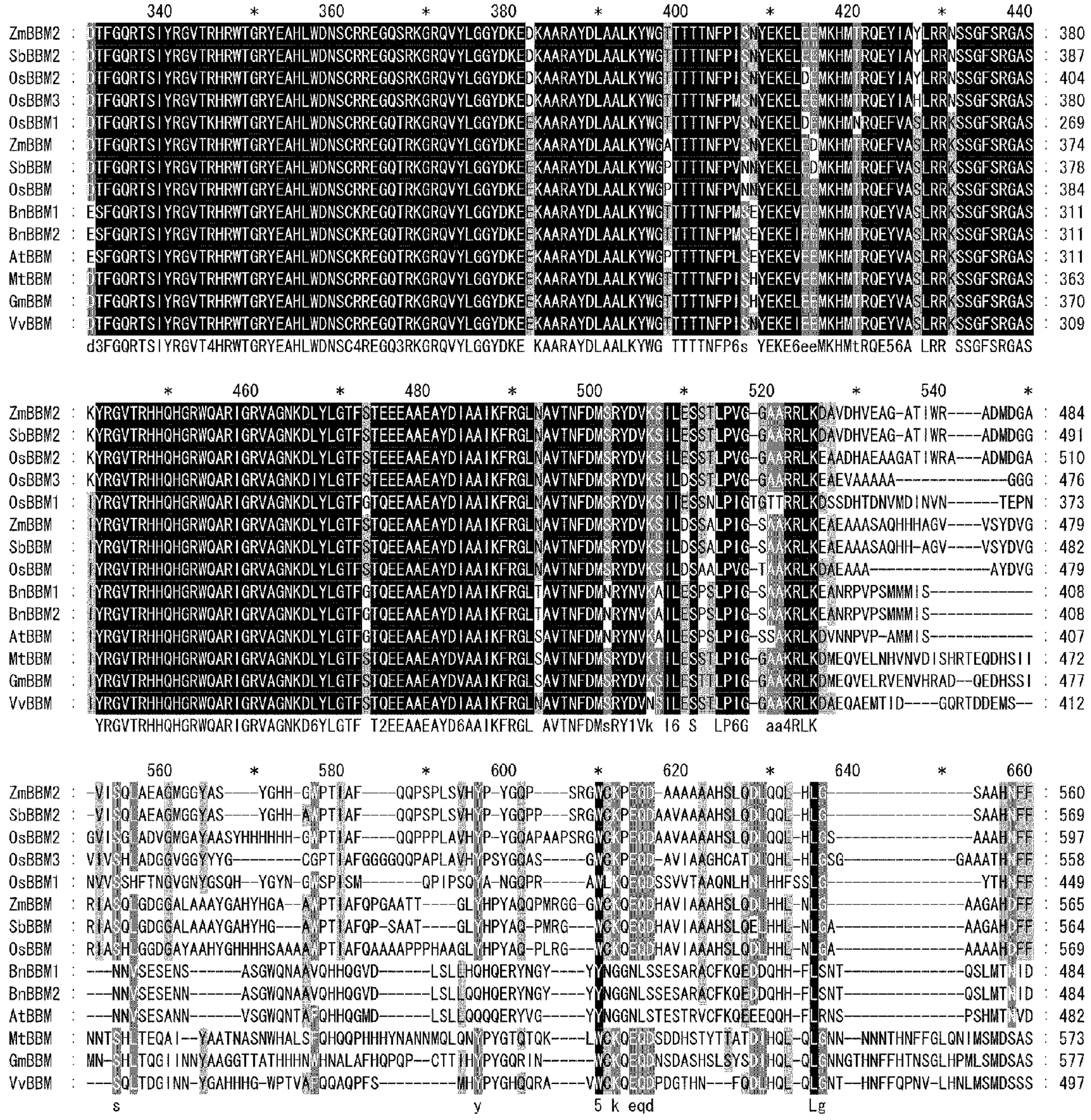
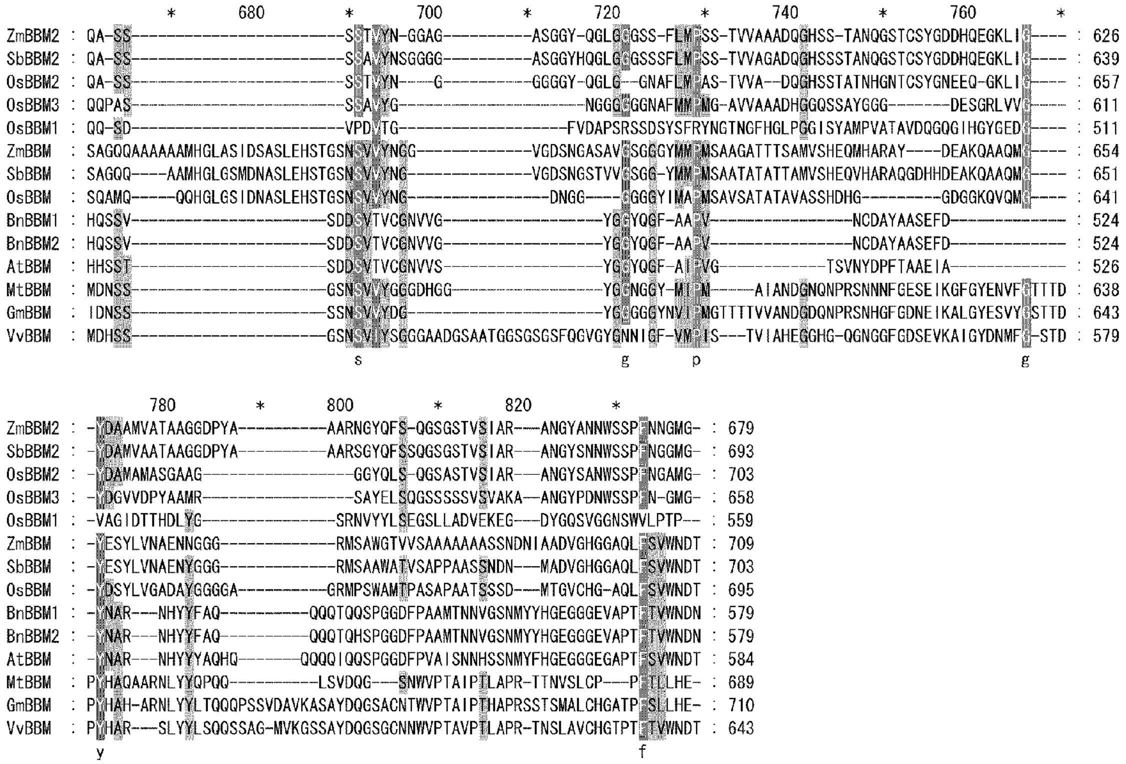

340 * 360 * 380 * 400 * 420 * 440
ZmBBM2 : DTFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQSRKGRQVYLGGYDKEDKAARAYDLAALKYWGTTTTTNFPISNYEKELEEMKHMTRQEYIAYLRRNSSGFSRGAS : 380
SbBBM2 : DTFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQSRKGRQVYLGGYDKEDKAARAYDLAALKYWGTTTTTNFPISNYEKELEEMKHMTRQEYIAYLRRNSSGFSRGAS : 387
OsBBM2 : DTFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQSRKGRQVYLGGYDKEDKAARAYDLAALKYWGTTTTTNFPISNYEKELDEMKHMTRQEYIAYLRRNSSGFSRGAS : 404
OsBBM3 : DTFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQSRKGRQVYLGGYDKEDKAARAYDLAALKYWGTTTTTNFPMSNYEKELEEMKHMTRQEYIAHLRRNSSGFSRGAS : 380
OsBBM1 : DTFGQRTSIYRGVTKHRWTGRYEAHLWDNSCRREGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGTTTTTNFPVSNYEKELDEMKHMNRQEFVASLRRKSSGFSRGAS : 269
ZmBBM : DTFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGATTTTNFPVSNYEKELEDMKHMTRQEFVASLRRKSSGFSRGAS : 374
SbBBM : DTFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGPTTTTNFPVNNYEKELEDMKHMTRQEFVASLRRKSSGFSRGAS : 378
OsBBM : DTFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGPTTTTNFPVNNYEKELEEMKHMTRQEFVASLRRKSSGFSRGAS : 384
BnBBM1 : ESFGQRTSIYRGVTRHRWTGRYEAHLWDNSCKREGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGTTTTTNFPMSEYEKEVEEMKHMTRQEYVASLRRKSSGFSRGAS : 311
BnBBM2 : ESFGQRTSIYRGVTRHRWTGRYEAHLWDNSCKREGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGTTTTTNFPMSEYEKEIEEMKHMTRQEYVASLRRKSSGFSRGAS : 311
AtBBM : ESFGQRTSIYRGVTRHRWTGRYEAHLWDNSCKREGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGPTTTTNFPLSEYEKEVEEMKHMTRQEYVASLRRKSSGFSRGAS : 311
MtBBM : DTFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGTTTTTNFPISHYEKEVEEMKHMTRQEYVASLRRKSSGFSRGAS : 363
GmBBM : DTFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGTTTTTNFPISHYEKELEEMKHMTRQEYVASLRRKSSGFSRGAS : 370
VvBBM : DTFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQTRKGRQVYLGGYDKEEKAARAYDLAALKYWGTTTTTNFPISNYEKEIEEMKHMTRQEYVASLRRKSSGFSRGAS : 309
d3FGQRTSIYRGVT4HRWTGRYEAHLWDNSC4REGQ3RKGRQVYLGGYDKE KAARAYDLAALKYWG TTTTNFP6s YEKE6eeMKHMtRQE56A LRR SSGFSRGAS
* 460 * 480 * 500 * 520 * 540 *
ZmBBM2 : KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEEAAEAYDIAAIKFRGLNAVTNFDMSRYDVKSILESSTLPVG-GAARRLKDAVDHVEAG-ATIWR----ADMDGA : 484
SbBBM2 : KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEEAAEAYDIAAIKFRGLNAVTNFDMSRYDVKSILESSTLPVG-GAARRLKDAVDHVEAG-ATIWR----ADMDGG : 491
OsBBM2 : KYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTEEEAAEAYDIAAIKFRGLNAVTNFDMSRYDVKSILESSTLPVG-GAARRLKEAADHAEAAGATIWRA---ADMDGA : 510
OsBBM3 : KYRGVTRHHQHGRWQARIGRVAGNKDIYLGTFSTEEEAAEAYDIAAIKFRGLNAVTNFDMSRYDVKSILDSSTLPVG-GAARRLKEAEVAAAAA-------------GGG : 476
OsBBM1 : IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAAEAYDIAAIKFRGLNAVTNFDMSRYDVKSIIESSNLPIGTGTTRRLKDSSDHTDNVMDINVN------TEPN : 373
ZmBBM : IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDIAAIKFRGLNAVTNFDMSRYDVKSILDSSALPIG-SAAKRLKEAEAAASAQHHHAGV----VSYDVG : 479
SbBBM : IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDIAAIKFRGLNAVTNFDMSRYDVKSILDSSALPIG-SAAKRLKEAEAAASAQHH-AGV----VSYDVG : 482
OsBBM : IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDIAAIKFRGLNAVTNFDMSRYDVKSILDSAALPVG-TAAKRLKDAEAAA--------------AYDVG : 479
BnBBM1 : IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAAEAYDIAAIKFRGLTAVTNFDMNRYNVKAILESPSLPIG-SAAKRLKEANRPVPSMMMIS------------ : 408
BnBBM2 : IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAAEAYDIAAIKFRGLTAVTNFDMNRYNVKAILESPSLPIG-SAAKRLKEANRPVPSMMMIS------------ : 408
AtBBM : IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFGTQEEAAEAYDIAAIKFRGLSAVTNFDMNRYNVKAILESPSLPIG-SSAKRLKDVNNPVP-AMMIS------------ : 407
MtBBM : IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGLSAVTNFDMSRYDVKTILESSTLPIG-GAAKRLKDMEQVELNHVNVDISHRTEQDHSII : 472
GmBBM : IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDVAAIKFRGLSAVTNFDMSRYDVKSILESTTLPIG-GAAKRLKDMEQVELRVENVHRAD--QEDHSSI : 477
VvBBM : IYRGVTRHHQHGRWQARIGRVAGNKDLYLGTFSTQEEAAEAYDIAAIKFRGLNAVTNFDMSRYDVNSILESSTLPIG-GAAKRLKDAEQAEMTID----GQRTDDEMS-- : 412
YRGVTRHHQHGRWQARIGRVAGNKD6YLGTF T2EEAAEAYD6AAIKFRGL AVTNFDMsRY1Vk I6 S LP6G aa4RLK
560 * 580 * 600 * 620 * 640 * 660
ZmBBM2 : -VISQLAEAGMGGYAS----YGHH-GWPTIAF----QQPSPLSVHYP-YGQP----SRGWCKPEQD-AAAAAAHSLQDLQQL-HLG-----------------SAAHNFF : 560
SbBBM2 : -VISQLAEAGMGGYAS----YGHH-AWPTIAF----QQPSPLSVHYP-YGQPP---SRGWCKPEQDAAVAAAAHSLQDLQQL-HLG-----------------SAAHNFF : 569
OsBBM2 : GVISGLADVGMGAYAASYHHHHHH-GWPTIAF----QQPPPLAVHYP-YGQAPAAPSRGWCKPEQDAAVAAAAHSLQDLQQL-HLS-----------------AAAHNFF : 597
OsBBM3 : VIVSHLADGGVGGYYYG--------CGPTIAFGGGGQQPAPLAVHYPSYGQAS-----GWCKPEQD-AVIAAGHCATDLQHL-HLSG---------------GAAATHNFF : 558
OsBBM1 : NVVSSHFTNGVGNYGSQH--YGYN-GWSPISM-------QPIPSQYA-NGQPR-----AWLKQEQDSSVVTAAQNLHNLHHFSSLG-----------------YTHNFF : 449
ZmBBM : RIASQLGDGGALAAAYGAHYHGA--AWPTIAFQPGAATT----GLYHPYAQQPMRGG-GWCKQEQDHAVIAAAHSLQDLHHL-NLG-----------------AAGAHDFF : 565
SbBBM : RIASQLGDGGALAAAYGAHYHG---AWPTIAFQP-SAAT----GLYHPYAQ-PMRG---WCKQEQDHAVIAAAHSLQELHHL-NLGA----------------AAGAHDFF : 564
OsBBM : RIASHLGGDGAYAAHYGHHHHSAAAAWPTIAFQAAAAPPPHAAGLYHPYAQ-PLRG---WCKQEQDHAVIAAAHSLQDLHHL-NLGA----------------AAAAHDFF : 569
BnBBM1 : ---NNVSESENS-------ASGWQNAAVQHHQGVD-------LSLLHQHQERYNGY----YYNGGNLSSESARACFKQEDDQHH-FLSNT----------------QSLMTNID : 484
BnBBM2 : ---NNVSESENN-------ASGWQNAAVQHHQGVD-------LSLLQQHQERYNGY----YYNGGNLSSESARACFKQEDDQHH-FLSNT----------------QSLMTNID : 484
AtBBM : ---NNVSESANN-------VSGWQNTAFQHHQGMD-------LSLLQQQQERYVG-----YYNGGNLSTESTRVCFKQEEEQQH-FLRNS----------------PSHMTNVD : 482
MtBBM : NNTSHLTEQAI--YAATNASNWHALSFQHQQPHHHYNANNMQLQNYPYGTQTQK-----LWCKQEQDSDDHSTYTTATDIHQL-QLGNN--NNNTHNFFGLQNIMSMDSAS : 573
GmBBM : MN-SHLTQGIINNYAAGGTTATHHHNWHNALAFHQPQP--CTTIHYPYGQRIN-------WCKQEQDNSDASHSLSYSDIHQL-QLGNNGTHNFFHTNSGLHPMLSMDSAS : 577
VvBBM : ---SQLTDGINN-YGAHHHG-WPTVAFQQAQPFS----------MHYPYGHQQRA----VWCKQEQDPDGTHN---FQDIHQL-QLGNT--HNFFQPNV-LHNLMSMDSSS : 497
s y 5 k eqd Lg

FIG. 4-2



```
                  *        680        *        700        *        720        *        740        *        760        *
ZmBBM2 : QA-SS------------------------SSTVYN-GGAG----------ASGGY-QGLGGGSS-FLMPSS-TVVAAADQGHSS-TANQGSTCSYGDDHQEGKLIG---- : 626
SbBBM2 : QA-SS------------------------SSAVYNSGGGG----------ASGGYHQGLGGGSSSFLMPSS-TVVAGADQGHSSSTANQGSTCSYGDDHQEGKLIG---- : 639
OsBBM2 : QA-SS------------------------SSTVYN----G----------GGGGY-QGLG--GNAFLMPAS-TVVA--DQGHSSTATNHGNTCSYGNEEQ-GKLIG---- : 657
OsBBM3 : QQPAS------------------------SSAVYG---------------------NGGGGGGNAFMMPMG-AVVAAADHGGQSSAYGGG-------DESGRLVVG---- : 611
OsBBM1 : QQ-SD------------------------VPDVTG-------------------FVDAPSRSSDSYSFRYNGTNGFHGLPGGISYAMPVATAVDQGQGIHGYGEDG---- : 511
ZmBBM  : SAGQQAAAAAAMHGLASIDSASLEHSTGSNSVVYNGG-------------VGDSNGASAVGSGGGYMMPMSAAGATTTSAMVSHEQMHARAY----DEAKQAAQMG---- : 654
SbBBM  : SAGQQ----AAMHGLGSMDNASLEHSTGSNSVVYNG--------------VGDSNGSTVVGSGG-YMMPMSAATATATTAMVSHEQVHARAQGDHHDEAKQAAQMG---- : 651
OsBBM  : SQAMQ-----QQHGLGSIDNASLEHSTGSNSVVYNG----------------DNGG----GGGGYIMAPMSAVSATATAVASSHDHG---------GDGGKQVQMG---- : 641
BnBBM1 : HQSSV----------------------SDDSVTVCGNVVG------------------YGGYQGF-AAPV---------------NCDAYAASEFD-------------- : 524
BnBBM2 : HQSSV----------------------SDDSVTVCGNVVG------------------YGGYQGF-AAPV---------------NCDAYAASEFD-------------- : 524
AtBBM  : HHSST----------------------SDDSVTVCGNVVS------------------YGGYQGF-AIPVG-----------TSVNYDPFTAAEIA-------------- : 526
MtBBM  : MDNSS----------------------GSNSVVYGGGDHGG-----------------YGGNGGY-MIPM-----AIANDGNQNPRSNNNFGESEIKGFGYENVFGTTTD : 638
GmBBM  : IDNSS----------------------SSNSVVYDG----------------------YGGGGGYNVIPMGTTTTVVANDGDQNPRSNHGFGDNEIKALGYESVYGSTTD : 643
VvBBM  : MDHSS----------------------GSNSVIYSGGGAADGSAATGGSGSGSFQGVGYGNNIGF-VMPIS---TVIAHEGGHG-QGNGGFGDSEVKAIGYDNMFG-STD : 579
                                      s                             g       p                                    g

                 780        *        800        *        820        *
ZmBBM2 : -YDAAMVATAAGGDPYA----------AARNGYQFS-QGSGSTVSIAR---ANGYANNWSSPFNNGMG- : 679
SbBBM2 : -YDAMVAATAAGGDPYA----------AARSGYQFSSQGSGSTVSIAR---ANGYSNNWSSPFNGGMG- : 693
OsBBM2 : -YDAMAMASGAAG-----------------GGYQLS-QGSASTVSIAR---ANGYSANWSSPFNGAMG- : 703
OsBBM3 : -YDGVVDPYAAMR-----------------SAYELSQGSSSSSVSVAKA--ANGYPDNWSSPFN-GMG- : 658
OsBBM1 : -VAGIDTTHDLYG---------------SRNVYYLSEGSLLADVEKEG---DYGQSVGGNSWVLPTP-- : 559
ZmBBM  : -YESYLVNAENNGGG-------------RMSAWGTVVSAAAAAAASSNDNIAADVGHGGAQLFSVWNDT : 709
SbBBM  : -YESYLVNAENYGGG-------------RMSAAWATVSAPPAASSNDN---MADVGHGGAQLFSVWNDT : 703
OsBBM  : -YDSYLVGADAYGGGGA----------GRMPSWAMTPASAPAATSSSD---MTGVCHG-AQLFSVWNDT : 695
BnBBM1 : -YNAR---NHYYFAQ----------QQQTQQSPGGDFPAAMTNNVGSNMYYHGEGGGEVAPTFTVWNDN : 579
BnBBM2 : -YNAR---NHYYFAQ----------QQQTQHSPGGDFPAAMTNNVGSNMYYHGEGGGEVAPTFTVWNDN : 579
AtBBM  : -YNAR---NHYYYAQHQ-------QQQQIQQSPGGDFPVAISNNHSSNMYFHGEGGGEGAPTFSVWNDT : 584
MtBBM  : PYHAQAARNLYYQPQQ----------LSVDQG---SNWVPTAIPTLAPR-TTNVSLCP---PFTLLHE- : 689
GmBBM  : PYHAH-ARNLYYLTQQQPSSVDAVKASAYDQGSACNTWVPTAIPTHAPRSSTSMALCHGATPFSLLHE- : 710
VvBBM  : PYHAR---SLYYLSQQSSAG-MVKGSSAYDQGSGCNNWVPTAVPTLAPR-TNSLAVCHGTPTFTVWNDT : 643
          y                                                            f
```

FIG. 4-3

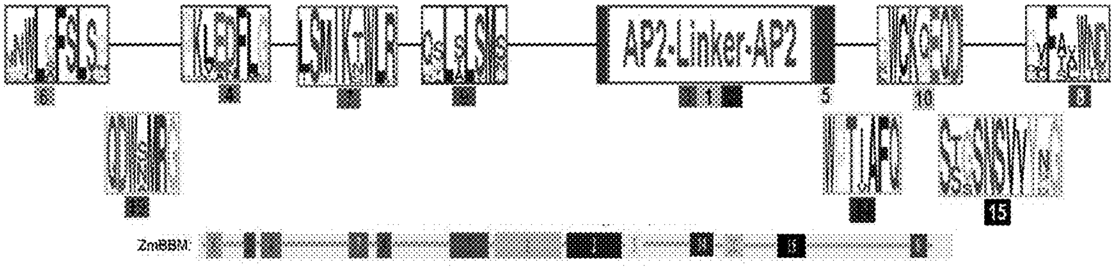


FIG. 5

METHODS AND COMPOSITIONS FOR THE INTRODUCTION AND REGULATED EXPRESSION OF GENES IN PLANTS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 61/291,257, filed on Dec. 30, 2009, the contents of which are hereby incorporated by reference in their entirety.

REFERENCE TO A SEQUENCE LISTING SUBMITTED AS A TEXT FILE VIA EFS-WEB

[0002] The official copy of the sequence listing is submitted electronically via EFS-Web as an ASCII formatted sequence listing with a file named 399843SEQLIST.TXT, created on Dec. 29, 2010, and having a size of 534 kilobytes and is filed concurrently with the specification. The sequence listing contained in this ASCII formatted document is part of the specification and is herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

[0003] The present invention is drawn to the field of plant genetics and molecular biology. More particularly, the compositions and methods are directed to the introduction and regulated expression of genes in plants.

BACKGROUND OF THE INVENTION

[0004] Current transformation technology provides an opportunity to engineer plants with desired traits. Major advances in plant transformation have occurred over the last few years. However, most transformation methods rely on the introduction of polynucleotides into embryonic tissues that are rapidly proliferating. Methods that allow for the transformation of more mature tissues would save considerable time and money. Accordingly, methods are needed in the art to increase transformation efficiencies of plants and allow for the transformation of more mature tissues.

[0005] Further, it is often necessary to reduce the activity of a transgene because the transgene may negatively affect the growth or fertility of the plant. Recombination systems can be used to excise the transgene, wherein the expression of a site-specific recombinase is regulated by an inducible promoter. Often, these systems are associated with premature excision. Accordingly, methods are needed in the art to efficiently excise transgenes with limited premature excision.

BRIEF SUMMARY OF THE INVENTION

[0006] Compositions and methods are provided for the introduction and regulated expression of genes in plants. Compositions include promoter constructs useful for regulated induction of expression of an operably linked coding sequence. In particular embodiments, the promoter construct comprises a maize rab17 promoter or an active variant or fragment thereof and an attachment B (attB) site. The modified rab17 promoter constructs find use in methods for regulating the expression of various coding sequences, including site-specific recombinases, which can minimize the premature excision of polynucleotides of interest in plants.

[0007] Further provided are methods for the transformation of plastids, such as chloroplasts, that involve the introduction of a heterologous polynucleotide encoding a cell proliferation factor, such as a babyboom (BBM) polypeptide. Novel BBM sequences are provided, along with methods of introducing the sequences into plants and plants comprising the novel BBM sequences. Methods for preparing and transforming mature embryo explants and leaf tissues are also provided.

BRIEF DESCRIPTION OF THE FIGURES

[0008] FIG. **1** provides a depiction of a phylogenetic analysis of 50 sequences with homology to maize babyboom (BBM).

[0009] FIGS. **2A-2M** show the consensus motif sequences 1-10, 14, 15, and 19, respectively, discovered in the analysis described herein, along with the alignments of the regions of various polypeptides used to generate the consensus motifs.

[0010] FIG. **3** depicts the motifs found within 50 sequences with homology to maize BBM (ZmBBM).

[0011] FIG. **4** shows an alignment of the amino acid sequence of various BBM polypeptides: maize babyboom 2 (ZmBBM2; SEQ ID NO: 12), sorghum babyboom 2 (SbBBM2; SEQ ID NO: 28), rice babyboom 2 (OsBBM2; SEQ ID NO: 18), rice babyboom 3 (OsBBM3; SEQ ID NO: 20), rice babyboom 1 (OsBBM1; SEQ ID NO: 16), maize babyboom (ZmBBM; SEQ ID NO: 10), sorghum babyboom (SbBBM; SEQ ID NO: 4), rice babyboom (OsBBM; SEQ ID NO: 14), *Brassica* babyboom 1 (BnBBM1; SEQ ID NO: 24), *Brassica* babyboom 2 (BnBBM2; SEQ ID NO: 26), *Arabidopsis* babyboom (AtBBM; SEQ ID NO: 22), *medicago* babyboom (MtBBM; SEQ ID NO: 8), soybean babyboom (GmBBM; SEQ ID NO: 2), and grape babyboom (VvBBM; SEQ ID NO: 6).

[0012] FIG. **5** provides a depiction of the motifs found in babyboom polypeptides.

DETAILED DESCRIPTION OF THE INVENTION

[0013] The presently disclosed compositions and methods are useful for the introduction and the regulated expression of genes in plants. Compositions comprise promoter constructs that provide a level of activity useful for the regulated expression of various coding sequences, including site-specific recombinases. Further provided are compositions comprising novel babyboom (BBM) polynucleotide and polypeptide sequences and plants comprising the same. Methods for the introduction of genes into plants are provided, including methods for introducing novel BBM polynucleotides and polypeptides into plants, methods for the enhancement of plastid transformation, and methods for the transformation of tissues from mature seeds.

[0014] The expression cassette having the sequence set forth in SEQ ID NO: 45, which is comprised of the maize rab17 promoter, an attB site, and the coding sequence for the site-specific recombinase FLP, is capable of expressing FLP upon induction in such a manner as to reduce premature excision. Without being bound by any theory or mechanism of action, it is believed that the presence of the attB site modifies the activity of the promoter, allowing for a tightly regulated induction of expression of an operably linked coding sequence. Therefore, compositions include promoter constructs comprising a modified maize rab17 promoter or an active variant or fragment thereof. In some of these embodiments, the promoter construct comprises the maize rab17 promoter or an active variant or fragment thereof and an attB site or a variant or fragment thereof. In some of these embodiments, the maize rab17 promoter has the sequence set forth in SEQ ID NO: 29 or an active variant or fragment thereof.

[0015] As used herein, the term "promoter" includes reference to a region of DNA involved in the recognition and binding of RNA polymerase and other proteins to initiate transcription of a coding sequence. Promoters may be naturally occurring promoters, a variant or fragment thereof, or synthetically derived. A "promoter construct" is a polynucleotide comprising a promoter and optionally, sequences that are not necessary for transcription initiation or part of the coding sequence and are located in between the promoter and the coding sequence in an expression cassette. These intervening sequences can include modulators, restriction sites, sequences of the 5'-untranslated region (5'-UTR), which is the region of a transcript that is transcribed, but is not translated into a polypeptide, and recombination sites.

[0016] The promoter in the promoter constructs is the maize rab17 promoter or an active variant or fragment thereof. The maize rab17 (responsive to abscisic acid) gene (GenBank Accession No. X15994; Vilardell et al. (1990) *Plant Mol Biol* 14:423-432; Vilardell et al. (1991) *Plant Mol Biol* 17:985-993; each of which is herein incorporated in its entirety) is expressed in late embryos, but its expression can be induced by exposure to abscisic acid or water stress. The sequence of the maize rab17 promoter corresponds to nucleotides 1-558 of GenBank Accession No. X15994, which was disclosed in Vilardell et al. (1990) Plant Mol Biol 14:423-432 and is set forth in SEQ ID NO: 126. An alternative maize rab17 promoter was disclosed in U.S. Pat. Nos. 7,253,000 and 7,491,813, each of which is herein incorporated by reference in its entirety, and is set forth in SEQ ID NO: 29. The rab17 promoter contains 5 putative abscisic acid responsive elements (ABRE) (Busk et al. (1997) *Plant J* 11:1285-1295, which is herein incorporated by reference in its entirety). The putative ABRE elements can be found at about −208 to −203 (nucleotides 304 to 309 of SEQ ID NO: 29), −162 to −157 (nucleotides 348 to 353 of SEQ ID NO: 29), −147 to −142 (nucleotides 363 to 368 of SEQ ID NO: 29), −141 to −136 (nucleotides 369 to 374 of SEQ ID NO: 29), and −96 to −91 (nucleotides 414 to 419 of SEQ ID NO: 29) in the maize rab17 promoter. The rab17 promoter also contains drought-responsive elements (DRE), of which the core sequence is identical to the DRE (drought-responsive) and CRT (cold-response elements) elements in *Arabidopsis*. The drought-responsive elements are found at −213 to −206 (nucleotides 299 to 306 of SEQ ID NO: 29) and −190 to −185 (nucleotides 322 to 327 of SEQ ID NO: 29) of the maize rab17 promoter. The CAAT and TATAA box can be found from nucleotides 395 to 398 and 479 to 484 of SEQ ID NO: 29, respectively.

[0017] In some embodiments, the maize rab17 promoter that is part of the presently disclosed promoter constructs has the sequence set forth in SEQ ID NO: 29 or an active variant or fragment thereof. In other embodiments, the maize rab17 promoter that is part of the presently disclosed promoter constructs has the sequence set forth in SEQ ID NO: 125 or 126 or an active variant or fragment thereof.

[0018] In some embodiments of the methods and compositions, the promoter constructs comprise active variants or fragments of the maize rab17 promoter. An active variant or fragment of a maize rab17 promoter (e.g., SEQ ID NO: 29, 125, 126) is a polynucleotide variant or fragment that retains the ability to initiate transcription. In some embodiments, an active fragment of a maize rab17 promoter may comprise at least about 50, 100, 150, 200, 250, 300, 350, 400, 450, or 500 contiguous nucleotides of SEQ ID NO: 29, 125, or 126, or may have at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 29, 125, or 126. In particular embodiments, an active variant or fragment of the maize rab17 promoter is one that is capable of initiating transcription in response to abscisic acid (ABA). In some of these embodiments, the promoter comprises at least one ABRE element. In particular embodiments, the promoter of the compositions and methods comprises from about −219 to about −102 of the maize rab17 promoter (corresponding to nucleotides 291 to 408 of SEQ ID NO: 29), which was shown to be sufficient to confer ABA responsiveness (Vilardell et al. (1991) *Plant Mol Biol* 17:985-993, which is herein incorporated by reference in its entirety).

[0019] In other embodiments, an active variant or fragment of the maize rab17 promoter is one that is capable of initiating transcription in response to dessication. In some of these embodiments, the promoter comprises at least one DRE element.

[0020] In particular embodiments, the active maize rab17 promoter fragment comprises from about −219 to about −80 of the maize rab17 promoter (nucleotides 291 to 430 of SEQ ID NO: 29), which comprises all of the putative DRE and ABRE elements.

[0021] Without being bound by any theory or mechanism of action, it is believed that a promoter construct (the sequence of which is set forth in SEQ ID NO: 30) comprising a maize rab17 promoter and a site-specific attachment B (attB) site has a modified level of activity in comparison to the promoter in the absence of the attB site due to the presence and/or the location of the attB site relative to the promoter. Therefore, it is believed the attB site functions as a modulator of the maize rab17 promoter. Accordingly, promoter constructs comprising a maize rab17 promoter or a fragment or variant thereof, and an attB site are provided, and in some of these embodiments, the attB site modifies the activity of the promoter. In other embodiments, the promoter construct comprises a maize rab17 promoter or a fragment or variant thereof and a modulator that modifies the activity of the rab17 promoter.

[0022] As used herein, a "modulator" refers to a polynucleotide that when present between a promoter and a coding sequence, serves to increase or decrease the activity of the promoter. Non-limiting examples of modulators include recombination sites, operators, and insulators.

[0023] Attachment sites are site-specific recombination sites found in viral and bacterial genomes that facilitate the integration or excision of the viral genome into and out of its host genome. Non-limiting examples of a viral and bacterial host system that utilize attachment sites is the lambda bacteriophage and *E. coli* system (Weisberg and Landy (1983) In Lambda II, eds. Hendrix et al. (Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.) pp. 211-250). The modulator of the promoter constructs can be an *E. coli* attachment site B (attB) site. The attB site can be naturally occurring *E. coli* attB sites or an active variants or fragments thereof or a synthetically derived sequence. Synthetically derived attB sites and active variants and fragments of naturally occurring attB sites are those that are capable of recombining with a bacteriophage lambda attachment P site, a process that is catalyzed by the bacteriophage lambda Integrase (Int) and the *E. coli* Integration Host Factor (IHF) proteins (Landy (1989) *Ann Rev Biochem* 58: 913-949, which is herein incorporated by reference in its entirety). AttB sites typically have a length of about 25 nucleotides, with a core 15-base pair sequence that is involved in the actual crossover event. Alternatively, active variants and fragments of naturally occurring attB sites are those that are capable of modulating the activity of a promoter when present within a promoter construct. Non-limiting examples of attB sites that can be used include attB1 (SEQ ID NO: 31), attB2 (SEQ ID NO: 32), attB3 (SEQ ID NO: 33), and attB4 (SEQ ID NO: 34), and variants or fragments thereof. In some embodiments, the modulator is an active variant or fragment of an attB site that is capable of modulating (i.e., increasing, decreasing) the activity of a promoter, but is not capable of recombination with an attachment P site. Non-limiting examples of such active variants of an attB site include those having the sequence set forth in SEQ ID NO: 107, 108, or 109.

[0024] In some embodiments, the distance of the modulator from the promoter impacts the ability of the modulator to modify the activity of the promoter. The modulator may be contiguous with the promoter and/or the polynucleotide of interest. In other embodiments, a linker sequence separates the promoter sequence and the modulator. As used herein, a "linker sequence" is a nucleotide sequence that functions to link one functional sequence with another without otherwise contributing to the expression or translation of a polynucleotide of interest when present in a promoter construct. Accordingly, the actual sequence of the linker sequence can vary. The linker sequence can comprise plasmid sequences, restriction sites, and/or regions of the 5'-untranslated region (5'-UTR) of the gene from which the promoter is derived. The linker sequence separating the promoter and the modulator can have a length of about 1, 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, 60, 70, 80, 90, 100, 150, 200, 250, 300, 400, 500, 1000 nucleotides or greater. In certain embodiments, a linker sequence of about 133 nucleotides separates the promoter and the modulator. In some embodiments, the linker sequence comprises a fragment of the rab17 5'-UTR. The fragment of the 5'-UTR can be about 1, 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, 60, 70, 80, 90, 100 nucleotides, or greater, in length. In certain embodiments, the promoter construct comprises a linker sequence separating the promoter and the modulator that comprises 95 nucleotides of the maize rab17 5'-UTR. In some of these embodiments, the 95 nucleotide sequence has the sequence set forth in SEQ ID NO: 35. In certain embodiments, the linker sequence between the promoter and modulator has the sequence set forth in SEQ ID NO: 36 or a variant or fragment thereof.

[0025] In some embodiments, the promoter construct comprises a linker sequence separating the modulator and the polynucleotide of interest. The length and sequence of this linker may also vary and can be about 1, 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, 60, 70, 80, 90, 100, 150, 200, 250, 300, 400, 500, 1000 nucleotides or greater in length. In certain embodiments, a linker sequence of about 61 nucleotides separates the modulator and the polynucleotide of interest. In certain embodiments, the linker sequence between the modulator and the polynucleotide of interest has the sequence set forth in SEQ ID NO: 37 or a variant or fragment thereof. In other embodiments, a linker sequence of about 25 nucleotides separates the modulator and the polynucleotide of interest. In certain embodiments, the linker sequence between the modulator and the polynucleotide of interest has the sequence set forth in SEQ ID NO: 123.

[0026] In certain embodiments, the promoter construct has the sequence set forth in SEQ ID NO: 30 or a variant or fragment thereof.

[0027] The promoter constructs can be operably linked to a polynucleotide of interest that encodes a polynucleotide or polypeptide within an expression cassette. "Operably linked" denotes a functional linkage between two or more elements. For example, an operable linkage between a polynucleotide of interest and a promoter is a functional link that allows for expression of the polynucleotide of interest. Operably linked elements may be contiguous or non-contiguous. The expression cassette can comprise other 5' or 3' regulatory elements necessary for expression.

[0028] Regulatory elements that can be included in the expression cassette 5' to the polynucleotide of interest include 5' leader sequences. Such leader sequences can act to enhance translation. Translation leaders are known in the art and include: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region) (Elroy-Stein et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:6126-6130); potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Gallie et al. (1995) *Gene* 165(2):233-238), MDMV leader (Maize Dwarf Mosaic Virus) (*Virology* 154:9-20), and human immunoglobulin heavy-chain binding protein (BiP) (Macejak et al. (1991) *Nature* 353:90-94); untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4) (Jobling et al. (1987) *Nature* 325:622-625); tobacco mosaic virus leader (TMV) (Gallie et al. (1989) in *Molecular Biology of RNA*, ed. Cech (Liss, New York), pp. 237-256); and maize chlorotic mottle virus leader (MCMV) (Lommel et al. (1991) *Virology* 81:382-385). See also, Della-Cioppa et al. (1987) *Plant Physiol.* 84:965-968. Other methods or sequences known to enhance translation can also be utilized, for example, introns, and the like.

[0029] The expression cassette may also comprise a transcriptional and/or translational termination region functional in plants. The termination region may be native with the transcriptional initiation region (i.e., promoter), may be native with the operably linked polynucleotide of interest, may be native with the plant host, or may be derived from another source (i.e., foreign to the promoter, the polynucleotide of interest, the plant host, or any combination thereof). Convenient termination regions are available from the potato proteinase inhibitor (PinII) gene or the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also Guerineau et al. (1991) *Mol. Gen. Genet.* 262:141-144; Proudfoot (1991) *Cell* 64:671-674; Sanfacon et al. (1991) *Genes Dev.* 5:141-149; Mogen et al. (1990) *Plant Cell* 2:1261-1272; Munroe et al. (1990) *Gene* 91:151-158; Ballas et al. (1989) *Nucleic Acids Res.* 17:7891-7903; and Joshi et al. (1987) *Nucleic Acid Res.* 15:9627-9639. In some embodiments, the pinII termination sequence has the sequence set forth in SEQ ID NO: 38 or an active variant or fragment thereof that is capable of terminating transcription and/or translation in a plant cell.

[0030] In certain embodiments, the expression cassette can comprise a recombination site, such as an attachment site 3' to the polynucleotide of interest. In some of these embodiments, the recombination site is a second attB site. In some of those embodiments wherein the promoter comprises a first attB site, the second attB site following the polynucleotide of interest and the modulator attB are non-identical. In some of those embodiments wherein the modulator attB site is attB1 (SEQ ID NO: 31), the second attB site 3' of the polynucleotide of interest can have the sequence set forth in SEQ ID NO: 31 (attB1), SEQ ID NO: 32 (attB2), SEQ ID NO: 33 (attB3), or SEQ ID NO: 34 (attB4), or an active variant or fragment thereof.

[0031] The recombination site 3' to the polynucleotide of interest can be 5' or 3' to the termination region when present. The recombination site can be contiguous with the polynucleotide of interest and/or the termination sequence, if present. In some embodiments, however, a linker sequence separates the polynucleotide of interest and the recombination site. The length of this linker sequence can vary, but in some embodiments, is about 1, 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, 60, 70, 80, or 90 nucleotides in length. In particular embodiments, the linker sequence separating the recombination site and the polynucleotide of interest is about 16 nucleotides. In certain embodiments, the recombination site and the polynucleotide of interest are separated by a linker sequence having the nucleotide sequence set forth in SEQ ID NO: 39, or a variant or fragment thereof. In other embodiments, the linker sequence separating the recombination site and the polynucleotide of interest is about 8 nucleotides. In certain embodiments, the recombination site and the polynucleotide of interest are separated by a linker sequence having the nucleotide sequence set forth in SEQ ID NO: 124, or a variant or fragment thereof.

[0032] In some of those embodiments wherein a termination region is present on the expression cassette and the expression cassette further comprises a recombination site 3' to the polynucleotide of interest, the termination region is 3' to the recombination site and a linker sequence separates the recombination site and the termination region. The length of this linker sequence can vary, but in some embodiments, is about 1, 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, 60, 70, 80, or 90 nucleotides in length. In particular embodiments, the linker sequence separating the recombination site and the termination region is about 14 nucleotides. In certain embodiments, the recombination site and the termination region are separated by a linker sequence having the nucleotide sequence set forth in SEQ ID NO: 40 or a variant or fragment thereof.

[0033] The expression cassettes comprise a presently disclosed promoter construct regulating the expression of a polynucleotide of interest. The polynucleotide of interest may be any polynucleotide that encodes a polynucleotide (e.g., antisense, siRNA) or encodes a polypeptide. Where appropriate, the polynucleotide(s) of interest may be optimized for increased expression in the transformed plant. That is, the polynucleotides can be synthesized using plant-preferred codons for improved expression. See, for example, Campbell and Gowri (1990) *Plant Physiol.* 92:1-11 for a discussion of host-preferred codon usage. Methods are available in the art for synthesizing plant-preferred genes. See, for example, U.S. Pat. Nos. 5,380,831, and 5,436,391, and Murray et al. (1989) *Nucleic Acids Res.* 17:477-498, herein incorporated by reference.

[0034] Additional sequence modifications are known to enhance gene expression in a cellular host. These include elimination of sequences encoding spurious polyadenylation signals, exon-intron splice site signals, transposon-like repeats, and other such well-characterized sequences that may be deleterious to gene expression. The G-C content of the sequence may be adjusted to levels average for a given cellular host, as calculated by reference to known genes expressed in the host cell. When possible, the sequence is modified to avoid predicted hairpin secondary mRNA structures.

[0035] In some embodiments, the polynucleotide of interest comprises a polynucleotide that encodes a site-specific recombinase. A site-specific recombinase, also referred to herein as a recombinase, is a polypeptide that catalyzes conservative site-specific recombination between its compatible recombination sites, and includes native polypeptides as well as derivatives, variants and/or fragments that retain activity, and native polynucleotides, derivatives, variants, and/or fragments that encode a recombinase that retains activity. The recombinase used in the methods and compositions can be a native recombinase or a biologically active fragment or variant of the recombinase. For reviews of site-specific recombinases and their recognition sites, see Sauer (1994) *Curr Op Biotechnol* 5:521-527; and Sadowski (1993) *FASEB* 7:760-767, each of which is herein incorporated by reference in its entirety.

[0036] Any recombinase system can be used in the methods and compositions. Non-limiting examples of site-specific recombinases include FLP, Cre, SSV1, lambda Int, phi C31 Int, HK022, R, Gin, Tn1721, CinH, ParA, Tn5053, Bxb1, TP907-1, U153, and other site-specific recombinases known in the art, including those described in Thomson and Ow (2006) *Genesis* 44:465-476, which is herein incorporated by reference in its entirety. Examples of site-specific recombination systems used in plants can be found in U.S. Pat. Nos. 5,929,301, 6,175,056, 6,331,661; and International Application Publication Nos. WO 99/25821, WO 99/25855, WO 99/25841, and WO 99/25840, the contents of each are herein incorporated by reference.

[0037] In some embodiments, the polynucleotide of interest encodes a recombinase from the Integrase or Resolvase families, including biologically active variants and fragments thereof. The Integrase family of recombinases has over one hundred members and includes, for example, FLP, Cre, lambda integrase, and R. For other members of the Integrase family, see, for example, Esposito et al. (1997) *Nucleic Acids Res* 25:3605-3614; and Abremski et al. (1992) *Protein Eng* 5:87-91; each of which are herein incorporated by reference in its entirety. Other recombination systems include, for example, the Streptomycete bacteriophage phi C31 (Kuhstoss et al. (1991) *J Mol Biol* 20:897-908); the SSV1 site-specific recombination system from *Sulfolobus shibatae* (Maskhelishvili et al. (1993) *Mol Gen Genet* 237:334-342); and a retroviral integrase-based integration system (Tanaka et al. (1998) *Gene* 17:67-76). In some embodiments, the recombinase does not require cofactors or a supercoiled substrate. Such recombinases include Cre, FLP, or active variants or fragments thereof.

[0038] The FLP recombinase is a protein that catalyzes a site-specific reaction that is involved in amplifying the copy number of the two-micron plasmid of *S. cerevisiae* during DNA replication. FLP recombinase catalyzes site-specific recombination between two FRT sites. The FLP protein has been cloned and expressed (Cox (1993) *Proc Natl Acad Sci USA* 80:4223-4227, which is herein incorporated by reference in its entirety). The FLP recombinase for use in the methods and compositions may be derived from the genus *Saccharomyces*. In some embodiments, a recombinase polynucleotide modified to comprise more plant-preferred codons is used. A recombinant FLP enzyme encoded by a nucleotide sequence comprising maize preferred codons (FLPm) that catalyzes site-specific recombination events is known (the polynucleotide and polypeptide sequence of which is set forth in SEQ ID NO: 41 and 42, respectively; see, e.g., U.S. Pat. No. 5,929,301, which is herein incorporated by reference in its entirety). Additional functional variants and fragments of FLP are known (Buchholz et al. (1998) *Nat Biotechnol* 16:657-662; Hartung et al. (1998) *J Biol Chem* 273:22884-22891; Saxena et al. (1997) *Biochim Biophys Acta* 1340:187-204; Hartley et al. (1980) *Nature* 286:860-864; Voziyanov et al. (2002) *Nucleic Acids Res* 30:1656-1663; Zhu & Sadowski (1995) *J Biol Chem* 270:23044-23054; and U.S. Pat. No. 7,238,854, each of which is herein incorporated by reference in its entirety).

[0039] The bacteriophage recombinase Cre catalyzes site-specific recombination between two lox sites. The Cre recombinase is known (Guo et al. (1997) *Nature* 389:40-46; Abremski et al. (1984) *J Biol Chem* 259:1509-1514; Chen et al. (1996) *Somat Cell Mol Genet* 22:477-488; Shaikh et al. (1977) *J Biol Chem* 272:5695-5702; and, Buchholz et al. (1998) *Nat Biotechnol* 16:657-662, each of which is herein incorporated by reference in its entirety). Cre polynucleotide sequences may also be synthesized using plant-preferred codons, for example such sequences (moCre; the polynucleotide and polypeptide sequence of which is set forth in SEQ ID NO: 43 and 44, respectively) are described, for example, in International Application Publication No. WO 99/25840, which is herein incorporated by reference in its entirety. Variants of the Cre recombinase are known (see, for example U.S. Pat. No. 6,890,726; Rufer & Sauer (2002) *Nucleic Acids Res* 30:2764-2772; Wierzbicki et al. (1987) *J Mol Biol* 195:785-794; Petyuk et al. (2004) *J Biol Chem* 279:37040-37048; Hartung & Kisters-Woike (1998) *J Biol Chem* 273:22884-22891; Santoro & Schultz (2002) *Proc Natl Acad Sci USA* 99:4185-4190; Koresawa et al. (2000) *J Biochem* (Tokyo) 127:367-372; and Vergunst et al. (2000) *Science* 290:979-982, each of which are herein incorporated by reference in its entirety).

[0040] In some embodiments, the polynucleotide of interest encodes a chimeric recombinase. A chimeric recombinase is a recombinant fusion protein which is capable of catalyzing site-specific recombination between recombination sites that originate from different recombination systems. For example, if the set of recombination sites comprises a FRT site and a LoxP site, a chimeric FLP/Cre recombinase or active variant or fragment thereof can be used, or both recombinases may be separately provided. Methods for the production and use of such chimeric recombinases or active variants or fragments thereof are described, for example, in International Application Publication No. WO 99/25840; and Shaikh & Sadowski (2000) *J Mol Biol* 302:27-48, each of which are herein incorporated by reference in its entirety.

[0041] In other embodiments, a variant recombinase is used. Methods for modifying the kinetics, cofactor interaction and requirements, expression, optimal conditions, and/or recognition site specificity, and screening for activity of recombinases and variants are known, see for example Miller et al. (1980) *Cell* 20:721-9; Lange-Gustafson and Nash (1984) *J Biol Chem* 259:12724-32; Christ et al. (1998) *J Mol Biol* 288:825-36; Lorbach et al. (2000) *J Mol Biol* 296:1175-81; Vergunst et al. (2000) *Science* 290:979-82; Dorgai et al. (1995) *J Mol Biol* 252:178-88; Dorgai et al. (1998) *J Mol Biol* 277:1059-70; Yagu et al. (1995) *J Mol Biol* 252:163-7; Sclimente et al. (2001) *Nucleic Acids Res* 29:5044-51; Santoro and Schultze (2002) *Proc Natl Acad Sci USA* 99:4185-90; Buchholz and Stewart (2001) *Nat Biotechnol* 19:1047-52; Voziyanov et al. (2002) *Nucleic Acids Res* 30:1656-63; Voziyanov et al. (2003) *J Mol Biol* 326:65-76; Klippel et al. (1988) *EMBO J* 7:3983-9; Arnold et al. (1999) *EMBO J* 18:1407-14; and International Application Publication Nos. WO 03/08045, WO 99/25840, and WO 99/25841; each of which is herein incorporated by reference in its entirety.

[0042] In particular embodiments, the expression cassette has the sequence set forth in SEQ ID NO: 45 or a variant or fragment thereof.

[0043] The expression cassette can be part of a vector that comprises multiple expression cassettes or multiple genes, such as a selectable marker gene. Selectable marker genes may be used to identify transformed cells or tissues. Marker genes include genes encoding antibiotic resistance, such as those encoding neomycin phosphotransferase II (NEO) and hygromycin phosphotransferase (HPT), as well as genes conferring resistance to herbicidal compounds, such as glufosinate ammonium, bromoxynil, imidazolinones, and 2,4-dichlorophenoxyacetate (2,4-D). See generally, Yarranton (1992) *Curr. Opin. Biotech.* 3:506-511; Christopherson et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:6314-6318; Yao et al. (1992) *Cell* 71:63-72; Reznikoff (1992) *Mol. Microbiol.* 6:2419-2422; Barkley et al. (1980) in *The Operon*, pp. 177-220; Hu et al. (1987) *Cell* 48:555-566; Brown et al. (1987) *Cell* 49:603-612; Figge et al. (1988) *Cell* 52:713-722; Deuschle et al. (1989) *Proc. Natl. Acad. Aci. USA* 86:5400-5404; Fuerst et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:2549-2553; Deuschle et al. (1990) *Science* 248:480-483; Gossen (1993) Ph.D. Thesis, University of Heidelberg; Reines et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:1917-1921; Labow et al. (1990) *Mol. Cell. Biol.* 10:3343-3356; Zambretti et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:3952-3956; Baim et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:5072-5076; Wyborski et al. (1991) *Nucleic Acids Res.* 19:4647-4653; Hillenand-Wissman (1989) *Topics Mol. Struc. Biol.* 10:143-162; Degenkolb et al. (1991) *Antimicrob. Agents Chemother.* 35:1591-1595; Kleinschnidt et al. (1988) *Biochemistry* 27:1094-1104; Bonin (1993) Ph.D. Thesis, University of Heidelberg; Gossen et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:5547-5551; Oliva et al. (1992) *Antimicrob. Agents Chemother.* 36:913-919; Hlavka et al. (1985) *Handbook of Experimental Pharmacology*, Vol. 78 (Springer-Verlag, Berlin); Gill et al. (1988) *Nature* 334:721-724. Such disclosures are herein incorporated by reference. The above list of selectable marker genes is not meant to be limiting. Any selectable marker gene can be used.

[0044] In some embodiments, an expression cassette comprising a presently disclosed promoter construct can further comprise a polynucleotide encoding a cell proliferation factor. As used herein, a "cell proliferation factor" is a polypeptide or a polynucleotide capable of stimulating growth of a cell or tissue, including but not limited to promoting progression through the cell cycle, inhibiting cell death, such as apoptosis, stimulating cell division, and/or stimulating embryogenesis. The polynucleotides can fall into several categories, including but not limited to, cell cycle stimulatory polynucleotides, developmental polynucleotides, anti-apoptosis polynucleotides, hormone polynucleotides, or silencing constructs targeted against cell cycle repressors or pro-apoptotic factors. The following are provided as non-limiting examples of each category and are not considered a complete list of useful polynucleotides for each category: 1) cell cycle stimulatory polynucleotides including plant viral replicase genes such as RepA, cyclins, E2F, prolifera, cdc2 and cdc25; 2) developmental polynucleotides such as Lec1, Kn1 family, WUSCHEL, Zwille, BBM, Aintegumenta (ANT), FUS3, and members of the Knotted family, such as Kn1, STM, OSH1, and SbH1; 3) anti-apoptosis polynucleotides such as CED9, Bcl2, Bcl-X(L), Bcl-W, A1, McL-1, Mac1, Boo, and Bax-inhibitors; 4) hormone polynucleotides such as IPT, TZS, and CKI-1; and 5) silencing constructs targeted against cell cycle repressors, such as Rb, CK1, prohibitin, and wee1, or stimulators of apoptosis such as APAF-1, bad, bax, CED-4, and caspase-3, and repressors of plant developmental transitions, such as Pickle and WD polycomb genes including FIE and Medea. The polynucleotides can be silenced by any known method such as antisense, RNA interference, cosuppression, chimerplasty, or transposon insertion.

[0045] The cell proliferation factors can be introduced into cells through the introduction of a polynucleotide that encodes the proliferation factor. The use of the term "polynucleotide" is not intended to limit compositions to polynucleotides comprising DNA. Polynucleotides can comprise ribonucleotides and combinations of ribonucleotides and deoxyribonucleotides. Such deoxyribonucleotides and ribonucleotides include both naturally occurring molecules and synthetic analogues. The polynucleotides also encompass all forms of sequences including, but not limited to, single-, double-, or multi-stranded forms, hairpins, stem-and-loop structures, circular plasmids, and the like. The polynucleotide encoding the cell proliferation factor may be native to the cell or heterologous. A native polypeptide or polynucleotide comprises a naturally occurring amino acid sequence or nucleotide sequence. "Heterologous" in reference to a polypeptide or a nucleotide sequence is a polypeptide or a sequence that originates from a different species, or if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention.

[0046] An "isolated" or "purified" polynucleotide or protein, or biologically active portion thereof, is substantially or essentially free from components that normally accompany or interact with the polynucleotide or protein as found in its naturally occurring environment. Thus, an isolated or purified polynucleotide or protein is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. Optimally, an "isolated" polynucleotide is free of sequences (optimally protein encoding sequences) that naturally flank the polynucleotide (i.e., sequences located at the 5' and 3' ends of the polynucleotide) in the genomic DNA of the organism from which the polynucleotide is derived. For example, in various embodiments, the isolated polynucleotide can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequence that naturally flank the polynucleotide in genomic DNA of the cell from which the polynucleotide is derived. A protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, 5%, or 1% (by dry weight) of contaminating protein. When the protein or biologically active portion thereof is recombinantly produced, optimally culture medium represents less than about 30%, 20%, 10%, 5%, or 1% (by dry weight) of chemical precursors or non-protein-of-interest chemicals.

[0047] Any of a number of cell proliferation factors can be used. In certain embodiments, those cell proliferation factors that are capable of stimulating embryogenesis are used to enhance targeted polynucleotide modification. Such cell proliferation factors are referred to herein as embryogenesis-stimulating polypeptides and they include, but are not limited to, babyboom polypeptides.

[0048] In some embodiments, the cell proliferation factor is a member of the AP2/ERF family of proteins. The AP2/ERF family of proteins is a plant-specific class of putative transcription factors that regulate a wide variety of developmental processes and are characterized by the presence of an AP2 DNA binding domain that is predicted to form an amphipathic alpha helix that binds DNA (PFAM Accession PF00847). The AP2 domain was first identified in APETALA2, an *Arabidopsis* protein that regulates meristem identity, floral organ specification, seed coat development, and floral homeotic gene expression. The AP2/ERF proteins have been subdivided into distinct subfamilies based on the presence of conserved domains. Initially, the family was divided into two subfamilies based on the number of DNA binding domains, with the ERF subfamily having one DNA binding domain, and the AP2 subfamily having 2 DNA binding domains. As more sequences were identified, the family was subsequently subdivided into five subfamilies: AP2, DREB, ERF, RAV, and others. (Sakuma et al. (2002) *Biochem Biophys Res Comm* 290:998-1009).

[0049] Members of the APETALA2 (AP2) family of proteins function in a variety of biological events, including but not limited to, development, plant regeneration, cell division, embryogenesis, and cell proliferation (see, e.g., Riechmann and Meyerowitz (1998) *Biol Chem* 379:633-646; Saleh and Pagés (2003) *Genetika* 35:37-50 and Database of *Arabidopsis* Transcription Factors at daft.cbi.pku.edu.cn). The AP2 family includes, but is not limited to, AP2, ANT, Glossy15, AtBBM, BnBBM, and maize ODP2/BBM.

[0050] Provided herein is an analysis of fifty sequences with homology to a maize BBM sequence (also referred to as maize ODP2 or ZmODP2, the polynucleotide and amino acid sequence of the maize BBM is set forth in SEQ ID NO: 9 and 10, respectively; the polynucleotide and amino acid sequence of another ZmBBM is set forth in SEQ ID NO: 121 and 122, respectively). The analysis identified three motifs (motifs 4-6; set forth in SEQ ID NOs: 51-53), along with the AP2 domains (motifs 2 and 3; SEQ ID NOs: 49 and 50) and linker sequence that bridges the AP2 domains (motif 1; SEQ ID NO: 48), that are found in all of the BBM homologues. Thus, motifs 1-6 distinguish these BBM homologues from other AP2-domain containing proteins (e.g., WRI, AP2, and RAP2.7) and these BBM homologues comprise a subgroup of AP2 family of proteins referred to herein as the BBM/PLT subgroup. In some embodiments, the cell proliferation factor that is used in the methods and compositions is a member of the BBM/PLT group of AP2 domain-containing polypeptides. In these embodiments, the cell proliferation factor comprises two AP2 domains and motifs 4-6 (SEQ ID NOs: 51-53) or a fragment or variant thereof. In some of these embodiments, the AP2 domains have the sequence set forth in SEQ ID NOs: 49 and 50 or a fragment or variant thereof, and in particular embodiments, further comprises the linker sequence of SEQ ID NO: 48 or a fragment or variant thereof. In other embodiments, the cell proliferation factor comprises at least one of motifs 4-6 or a fragment or variant thereof, along with two AP2 domains, which in some embodiments have the sequence set forth in SEQ ID NO: 49 and/or 50 or a fragment or variant thereof, and in particular embodiments have the linker sequence of SEQ ID NO: 48 or a fragment or variant thereof. Based on the phylogenetic analysis provided herein, the subgroup of BBM/PLT polypeptides can be subdivided into the BBM, AIL6/7, PLT1/2, AIL1, PLT3, and ANT groups of polypeptides.

[0051] In some embodiments, the cell proliferation factor is a babyboom (BBM) polypeptide, which is a member of the AP2 family of transcription factors. The BBM protein from *Arabidopsis* (AtBBM) is preferentially expressed in the developing embryo and seeds and has been shown to play a central role in regulating embryo-specific pathways. Overexpression of AtBBM has been shown to induce spontaneous formation of somatic embryos and cotyledon-like structures on seedlings. See, Boutiler et al. (2002) *The Plant Cell* 14:1737-1749. The maize BBM protein also induces embryogenesis and promotes transformation (See, U.S. Pat. No. 7,579,529, which is herein incorporated by reference in its entirety). Thus, BBM polypeptides stimulate proliferation, induce embryogenesis, enhance the regenerative capacity of a plant, enhance transformation, and as demonstrated herein, enhance rates of targeted polynucleotide modification. As used herein "regeneration" refers to a morphogenic response that results in the production of new tissues, organs, embryos, whole plants or parts of whole plants that are derived from a single cell or a group of cells. Regeneration may proceed indirectly via a callus phase or directly, without an intervening callus phase. "Regenerative capacity" refers to the ability of a plant cell to undergo regeneration.

[0052] In some embodiments, the babyboom polypeptide comprises two AP2 domains and at least one of motifs 7 and 10 (set forth in SEQ ID NO: 54 and 57, respectively) or a variant or fragment thereof. In certain embodiments, the AP2 domains are motifs 3 and 2 (SEQ ID NOs: 50 and 49, respectively) or a fragment or variant thereof, and in particular embodiments, the babyboom polypeptide further comprises a linker sequence between AP2 domain 1 and 2 having motif 1 (SEQ ID NO: 48) or a fragment or variant thereof. In particular embodiments, the BBM polypeptide further comprises motifs 4-6 (SEQ ID NOs 51-53) or a fragment or variant thereof. The BBM polypeptide can further comprise motifs 8 and 9 (SEQ ID NOs: 55 and 56, respectively) or a fragment or variant thereof, and in some embodiments, motif 10 (SEQ ID NO: 57) or a variant or fragment thereof. In some of these embodiments, the BBM polypeptide also comprises at least one of motif 14 (set forth in SEQ ID NO: 58), motif 15 (set forth in SEQ ID NO: 59), and motif 19 (set forth in SEQ ID NO: 60), or variants or fragments thereof. The variant of a particular amino acid motif can be an amino acid sequence having at least about 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or greater sequence identity with the motif disclosed herein. Alternatively, variants of a particular amino acid motif can be an amino acid sequence that differs from the amino acid motif by 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids.

[0053] Non-limiting examples of babyboom polynucleotides and polypeptides that can be used in the methods and compositions include the *Arabidopsis thaliana* AtBBM (SEQ ID NOs: 21 and 22), *Brassica napus* BnBBM1 (SEQ ID NOs: 23 and 24), *Brassica napus* BnBBM2 (SEQ ID NOs: 25 and 26), *Medicago truncatula* MtBBM (SEQ ID NOs: 7 and 8), *Glycine max* GmBBM (SEQ ID NOs: 1 and 2), *Vitis vinifera* VvBBM (SEQ ID NOs: 5 and 6), *Zea mays* ZmBBM (SEQ ID NOs: 9 and 10 and genomic sequence set forth in SEQ ID NO: 68; or SEQ ID NOs: 121 and 122 and genomic sequence set forth in SEQ ID NO: 116) and ZmBBM2 (SEQ ID NOs: 11 and 12), *Oryza sativa* OsBBM (polynucleotide sequences set forth in SEQ ID NOs: 13 and 120; amino acid sequence set forth in SEQ ID NO: 14; and genomic sequence set forth in SEQ ID NO: 117), OsBBM1 (SEQ ID NOs: 15 and 16), OsBBM2 (SEQ ID NOs: 17 and 18), and OsBBM3 (SEQ ID NOs: 19 and 20), *Sorghum bicolor* SbBBM (SEQ ID NOs: 3 and 4 and genomic sequence set forth in SEQ ID NO: 69) and SbBBM2 (SEQ ID NOs: 27 and 28) or active fragments or variants thereof. In particular embodiments, the cell proliferation factor is a maize BBM polypeptide (SEQ ID NO: 10, 122, or 12) or a variant or fragment thereof, or is encoded by a maize BBM polynucleotide (SEQ ID NO: 9, 68, 121, 116, or 11) or a variant or fragment thereof.

[0054] Thus, in some embodiments, a polynucleotide encoding a cell proliferation factor has a nucleotide sequence having at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the nucleotide sequence set forth in SEQ ID NO: 13, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69 or the cell proliferation factor has an amino acid sequence having at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28. In some of these embodiments, the cell proliferation factor has at least one of motifs 7 and 10 (SEQ ID NO: 54 and 57, respectively) or a variant or fragment thereof at the corresponding amino acid residue positions in the babyboom polypeptide. In other embodiments, the cell proliferation factor further comprises at least one of motif 14 (set forth in SEQ ID NO: 58), motif 15 (set forth in SEQ ID NO: 59), and motif 19 (set forth in SEQ ID NO: 60) or a variant or fragment thereof at the corresponding amino acid residue positions in the babyboom polypeptide.

[0055] In other embodiments, other cell proliferation factors, such as, Lec1, Kn1 family, WUSCHEL (e.g., WUS1, the polynucleotide and amino acid sequence of which is set forth in SEQ ID NO: 61 and 62; WUS2, the polynucleotide and amino acid sequence of which is set forth in SEQ ID NO: 63 and 64; WUS2 alt, the polynucleotide and amino acid sequence of which is set forth in SEQ ID NO: 114 and 115; WUS3, the polynucleotide and amino acid sequence of which is set forth in SEQ ID NO: 105 and 106), Zwille, and Aintegumeta (ANT), may be used alone, or in combination with a babyboom polypeptide or other cell proliferation factor. See, for example, U.S. Application Publication No. 2003/0135889, International Application Publication No. WO 03/001902, and U.S. Pat. No. 6,512,165, each of which is herein incorporated by reference. When multiple cell proliferation factors are used, or when a babyboom polypeptide is used along with any of the abovementioned polypeptides, the polynucleotides encoding each of the factors can be present on the same expression cassette or on separate expression cassettes. When two or more factors are coded for by separate expression cassettes, the expression cassettes can be provided to the plant simultaneously or sequentially.

[0056] In some embodiments, polynucleotides or polypeptides having homology to a known babyboom polynucleotide or polypeptide and/or sharing conserved functional domains can be identified by screening sequence databases using programs such as BLAST. The databases can be queried using full length sequences, or with fragments including, but not limited to, conserved domains or motifs. In some embodiments, the sequences retrieved from the search can be further characterized by alignment programs to quickly identify and compare conserved functional domains, regions of highest homology, and nucleotide and/or amino differences between sequences, including insertions, deletions, or substitutions, including those programs described in more detail elsewhere herein. The retrieved sequences can also be evaluated using a computer program to analyze and output the phylogenetic relationship between the sequences.

[0057] In other embodiments, polynucleotides or polypeptides having homology to a known babyboom polynucleotide or polypeptide or one that has been disclosed herein and/or sharing conserved functional domains can be identified using standard nucleic acid hybridization techniques, such as those described in more detail elsewhere herein. Extensive guides on nucleic acid hybridization include Tijssen (1993) Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes, Part I, Chapter 2 (Elsevier, NY); Ausubel et al., eds. (1995) Current Protocols in Molecular Biology, Chapter 2 (Greene Publishing and Wiley-Interscience, NY); and, Sambrook et al. (1989) Molecular Cloning: A Laboratory Manual (2d ed., Cold Spring Harbor Laboratory Press, Plainview, N.Y.).

[0058] Compositions further comprise isolated BBM polynucleotides and isolated BBM polypeptides and variants and fragments thereof, expression cassettes comprising the same, and plants comprising the same. Compositions can comprise isolated polynucleotides encoding GmBBM (SEQ ID NO: 1), SbBBM (SEQ ID NO: 3), MtBBM (SEQ ID NO: 7), or OsBBM2 (SEQ ID NO: 17) or an active variant or fragment thereof. Isolated polypeptides include those having SEQ ID NO: 2, 4, 8, or 18 (GmBBM, SbBBM, MtBBM, or OsBBM2, respectively) or an active variant or fragment thereof. The percent identity of the novel BBM polypeptide sequences with those known in the art is presented in Table 1.

TABLE 1

The percent sequence identity between each of 14 babyboom polypeptides.

	ZmBBM2	SbBBM2	OsBBM2	OsBBM3	OsBBM1	ZmBBM	SbBBM	OsBBM	BnBBM1	BnBBM2	AtBBM	MtBBM	GmBBM	VvBBM
ZmBBM2	100													
SbBBM2	92	100												
OsBBM2	79	77	100											
OsBBM3	64	66	67	100										
OsBBM1	50	46	46	46	100									
ZmBBM	43	44	44	47	47	100								
SbBBM	43	44	42	45	44	90	100							
OsBBM	44	44	45	46	49	69	70	100						
BnBBM1	42	41	42	41	40	45	42	43	100					
BnBBM2	43	41	42	41	39	46	44	44	97	100				
AtBBM	43	41	39	42	41	43	43	42	81	82	100			
MtBBM	41	40	40	41	43	42	43	41	47	47	47	100		
GmBBM	45	44	42	45	44	41	42	44	46	46	43	68	100	
VvBBM	51	48	50	48	50	48	47	48	49	49	48	58	62	100

[0059] By "fragment" is intended a portion of the polynucleotide or a portion of an amino acid sequence and hence protein encoded thereby. Fragments of a polynucleotide may retain the biological activity of the native polynucleotide and, for example, have promoter activity (i.e., capable of initiating transcription), or are capable of stimulating proliferation, inducing embryogenesis, or modifying the regenerative capacity of a plant. In those embodiments wherein the polynucleotide encodes a polypeptide, fragments of the polynucleotide may encode protein fragments that retain the biological activity of the native protein. Alternatively, fragments of a polynucleotide that are useful as hybridization probes generally do not retain biological activity or encode fragment proteins that retain biological activity. Thus, fragments of a nucleotide sequence may range from at least about 20, 50, 100, 150, 200, 250, 300, 400, 500 nucleotides, or greater.

[0060] A fragment of a polynucleotide that encodes a biologically active portion of a cell proliferation factor, for example, will encode at least 15, 25, 30, 50, 100, 150, 200, 250, 300, 400, 500 contiguous amino acids, or up to the total number of amino acids present in the full-length cell proliferation factor. Fragments of a cell proliferation factor polynucleotide that are useful as hybridization probes or PCR primers generally need not encode a biologically active portion of a cell proliferation factor.

[0061] "Variants" is intended to mean substantially similar sequences. For polynucleotides, a variant comprises a polynucleotide having deletions at the 5' and/or 3' end; deletion and/or addition of one or more nucleotides at one or more internal sites in the native polynucleotide; and/or substitution of one or more nucleotides at one or more sites in the native polynucleotide. As used herein, a "native" polynucleotide or polypeptide comprises a naturally occurring nucleotide sequence or amino acid sequence, respectively. For polynucleotides encoding polypeptides conservative variants include those sequences that, because of the degeneracy of the genetic code, encode the amino acid sequence the polypeptide (e.g., cell proliferation factor). Naturally occurring variants such as these can be identified with the use of well-known molecular biology techniques, such as, for example, with polymerase chain reaction (PCR) and hybridization techniques. Variant polynucleotides also include synthetically derived polynucleotides, such as those generated, for example, by using site-directed mutagenesis. Generally, variants of a particular will have at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to that particular polynucleotide as determined by sequence alignment programs and parameters.

[0062] Variants of a particular polynucleotide that encodes a polypeptide can also be evaluated by comparison of the percent sequence identity between the polypeptide encoded by a variant polynucleotide and the polypeptide encoded by the particular polynucleotide. Percent sequence identity between any two polypeptides can be calculated using sequence alignment programs and parameters. Where any given pair of polynucleotides is evaluated by comparison of the percent sequence identity shared by the two polypeptides they encode, the percent sequence identity between the two encoded polypeptides is at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity.

[0063] "Variant" protein is intended to mean a protein derived from the native protein by deletion of one or more amino acids at the N-terminal and/or C-terminal end of the native protein; deletion and/or addition of one or more amino acids at one or more internal sites in the native protein; and/or substitution of one or more amino acids at one or more sites in the native protein. Variant proteins retain the desired biological activity of the native protein. For example, variant cell proliferation factors stimulate proliferation and variant babyboom polypeptides are capable of stimulating proliferation, inducing embryogenesis, modifying the regenerative capacity of a plant, increasing the transformation efficiency in a plant, increasing or maintaining the yield in a plant under abiotic stress, producing asexually derived embryos in a plant, and/or enhancing rates of targeted polynucleotide modification. Such variants may result from, for example, genetic polymorphism or from human manipulation. Biologically active variants of a native cell proliferation factor will have at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence for the native protein as determined by sequence alignment programs and parameters. A biologically active variant of a cell proliferation factor protein may differ from that protein by as few as 1-15 amino acid residues, as few as 1-10, such as 6-10, as few as 5, as few as 4, 3, 2, or even 1 amino acid residue.

[0064] In some embodiments, variants or fragments of the BBM polypeptide have amino acid residues valine, tyrosine, and leucine at the positions corresponding to positions 311, 312, and 313, respectively, of SEQ ID NO: 4 or variants or fragments of the BBM polynucleotide encodes a polypeptide having amino acid residues valine, tyrosine, and leucine at the positions corresponding to positions 311, 312, and 313, respectively, of SEQ ID NO: 4. In certain embodiments, variants or fragments of the BBM polypeptide have amino acid residues valine, tyrosine, and leucine at the positions corresponding to positions 337, 338, and 339, respectively, of SEQ ID NO: 18 or variants or fragments of the BBM polynucleotide encodes a polypeptide having amino acid residues valine, tyrosine, and leucine at the positions corresponding to positions 337, 338, and 339, respectively, of SEQ ID NO: 18. In other embodiments, variants or fragments of the BBM polypeptide have amino acid residues methionine, alanine, and serine at the positions corresponding to positions 1, 2, and 3, respectively, of SEQ ID NO: 8 or variants or fragments of the BBM polynucleotide encodes a polypeptide having amino acid residues methionine, alanine, and serine at the positions corresponding to positions 1, 2, and 3, respectively of SEQ ID NO: 8.

[0065] The babyboom polynucleotides and polypeptides can be introduced into a plant or plant cell in order to stimulate embryogenesis, modify the regenerative capacity of the plant, increase the transformation efficiency of the plant, increase or maintain the yield in the plant under abiotic stress, and/or to enhance targeted polynucleotide modification. The babyboom polynucleotide or polypeptide can be provided to a plant simultaneously with or prior to the introduction of a polynucleotide of interest in order to facilitate transformation of the plant with the polynucleotide of interest. Further, a haploid plant cell can be provided a novel babyboom polynucleotide or polypeptide to produce a haploid plant embryo (see U.S. Pat. No. 7,579,529, which is herein incorporated by reference in its entirety).

[0066] The cell proliferation factor polynucleotide can be operably linked to a promoter active in a plant. Various promoters can be used for the regulation of the expression of the cell proliferation factor. The promoter may be selected based on the desired outcome or expression pattern (for a review of plant promoters, see Potenza et al. (2004) *In Vitro Cell Dev Biol* 40:1-22).

[0067] Constitutive promoters include, for example, the core promoter of the Rsyn7 promoter and other constitutive promoters disclosed in WO 99/43838 and U.S. Pat. No. 6,072,050; the core CaMV 35S promoter (Odell et al. (1985) *Nature* 313:810-812); rice actin (McElroy et al. (1990) *Plant Cell* 2:163-171); ubiquitin (Christensen et al. (1989) *Plant Mol. Biol.* 12:619-632 and Christensen et al. (1992) *Plant Mol. Biol.* 18:675-689); pEMU (Last et al. (1991) *Theor. Appl. Genet.* 81:581-588); MAS (Velten et al. (1984) *EMBO J.* 3:2723-2730); ALS promoter (U.S. Pat. No. 5,659,026), the *Agrobacterium* nopaline synthase (NOS) promoter (Bevan et al. (1983) *Nucl. Acids Res.* 11:369-385), and the like. Other constitutive promoters are described in, for example, U.S. Pat. Nos. 5,608,149; 5,608,144; 5,604,121; 5,569,597; 5,466,785; 5,399,680; 5,268,463; 5,608,142; and 6,177,611.

[0068] In some embodiments, an inducible promoter can be used, such as from a pathogen-inducible promoter. Such promoters include those from pathogenesis-related proteins (PR proteins), which are induced following infection by a pathogen; e.g., PR proteins, SAR proteins, beta-1,3-glucanase, chitinase, etc. See, for example, Redolfi et al. (1983) *Neth. J. Plant Pathol.* 89:245-254; Uknes et al. (1992) *Plant Cell* 4:645-656; and Van Loon (1985) *Plant Mol. Virol.* 4:111-116. See also WO 99/43819, herein incorporated by reference. Promoters that are expressed locally at or near the site of pathogen infection include, for example, Marineau et al. (1987) *Plant Mol. Biol.* 9:335-342; Matton et al. (1989) *Mol Plant-Microbe Interact* 2:325-331; Somsisch et al. (1986) *Proc. Natl. Acad. Sci. USA* 83:2427-2430; Somsisch et al. (1988) *Mol. Gen. Genet.* 2:93-98; and Yang (1996) *Proc. Natl. Acad. Sci. USA* 93:14972-14977. See also, Chen et al. (1996) *Plant J.* 10:955-966; Zhang et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:2507-2511; Warner et al. (1993) *Plant J.* 3:191-201; Siebertz et al. (1989) *Plant Cell* 1:961-968; U.S. Pat. No. 5,750,386 (nematode-inducible); and the references cited therein. Additional promoters include the inducible promoter for the maize PRms gene, whose expression is induced by the pathogen *Fusarium moniliforme* (see, for example, Cordero et al. (1992) *Physiol. Mol. Plant Path.* 41:189-200). Wound-inducible promoters include potato proteinase inhibitor (pin II) gene (Ryan (1990) *Ann. Rev. Phytopath.* 28:425-449; Duan et al. (1996) *Nat Biotechnol* 14:494-498); wun1 and wun2, U.S. Pat. No. 5,428,148; win1 and win2 (Stanford et al. (1989) *Mol. Gen. Genet.* 215:200-208); system in (McGurl et al. (1992) *Science* 225:1570-1573); WIP1 (Rohmeier et al. (1993) *Plant Mol. Biol.* 22:783-792; Eckelkamp et al. (1993) *FEBS Lett* 323:73-76); MPI gene (Corderok et al. (1994) *Plant J.* 6:141-150); and the like, herein incorporated by reference. Another inducible promoter is the maize In2-2 promoter (deVeylder et al. (2007) *Plant Cell Physiol* 38:568-577, herein incorporated by reference).

[0069] Chemical-regulated promoters can be used to modulate the expression of a gene in a plant through the application of an exogenous chemical regulator. The promoter may be a chemical-inducible promoter, where application of the chemical induces gene expression, or a chemical-repressible promoter, where application of the chemical represses gene expression. Chemical-inducible promoters are known in the art and include, but are not limited to, the maize In2-2 promoter, which is activated by benzenesulfonamide herbicide safeners (De Veylder et al. (1997) *Plant Cell Physiol.* 38:568-77), the maize GST promoter (GST-II-27, WO 93/01294), which is activated by hydrophobic electrophilic compounds that are used as pre-emergent herbicides, the PR-1 promoter (Cao et al. (2006) *Plant Cell Reports* 6:554-60), which is activated by BTH or benxo(1,2,3)thiaidazole-7-carbothioic acid s-methyl ester, the tobacco PR-1a promoter (Ono et al. (2004) *Biosci. Biotechnol. Biochem.* 68:803-7), which is activated by salicylic acid, the copper inducible ACEI promoter (Mett et al. (1993) *PNAS* 90:4567-4571), the ethanol-inducible promoter AlcA (Caddick et al. (1988) *Nature Biotechnol* 16:177-80), an estradiol-inducible promoter (Bruce et al. (2000) *Plant Cell* 12:65-79), the XVE estradiol-inducible promoter (Zao et al. (2000) *Plant J* 24:265-273), the VGE methoxyfenozide inducible promoter (Padidam et al. (2003) *Transgenic Res* 12:101-109), and the TGV dexamethasone-inducible promoter (Bohner et al. (1999) *Plant J* 19:87-95). Other chemical-regulated promoters of interest include steroid-responsive promoters (see, for example, the glucocorticoid-inducible promoter in Schena et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:10421-10425 and McNellis et al. (1998) *Plant J.* 14(2):247-257) and tetracycline-inducible and tetracycline-repressible promoters (see, for example, Gatz et al. (1991) *Mol. Gen. Genet.* 227:229-237; Gatz et al. (1992) *Plant J* 2:397-404; and U.S. Pat. Nos. 5,814,618 and 5,789,156), herein incorporated by reference.

[0070] Tissue-preferred promoters can be utilized to target enhanced expression of a sequence of interest within a particular plant tissue. Tissue-preferred promoters include Kawamata et al. (1997) *Plant Cell Physiol.* 38(7):792-803; Hansen et al. (1997) *Mol. Gen Genet.* 254(3):337-343; Russell et al. (1997) *Transgenic Res.* 6(2):157-168; Rinehart et al. (1996) *Plant Physiol.* 112(3):1331-1341; Van Camp et al. (1996) *Plant Physiol.* 112(2):525-535; Canevascini et al. (1996) *Plant Physiol.* 112(2):513-524; Lam (1994) *Results Probl. Cell Differ.* 20:181-196; and Guevara-Garcia et al. (1993) *Plant J.* 4(3):495-505.

[0071] Leaf-preferred promoters are known in the art. See, for example, Yamamoto et al. (1997) *Plant J.* 12:255-265; Kwon et al. (1994) *Plant Physiol.* 105:357-67; Yamamoto et al. (1994) *Plant Cell Physiol.* 35:773-778; Gotor et al. (1993) *Plant J.* 3:509-18; Orozco et al. (1993) *Plant Mol. Biol.* 23:1129-1138; and Matsuoka et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:9586-9590. In addition, promoter of cab and rubisco can also be used. See, for example, Simpson et al. (1958) *EMBO J* 4:2723-2729 and Timko et al. (1988) *Nature* 318:57-58.

[0072] Root-preferred promoters are known and can be selected from the many available. See, for example, Hire et al. (1992) *Plant Mol. Biol.* 20:207-218 (soybean root-specific glutamine synthase gene); Keller and Baumgartner (1991) *Plant Cell* 3:1051-1061 (root-specific control element in the GRP 1.8 gene of French bean); Sanger et al. (1990) *Plant Mol. Biol.* 14:433-443 (root-specific promoter of the mannopine synthase (MAS) gene of *Agrobacterium tumefaciens*); and Miao et al. (1991) *Plant Cell* 3:11-22 (full-length cDNA clone encoding cytosolic glutamine synthase (GS), which is expressed in roots and root nodules of soybean). See also Bogusz et al. (1990) *Plant Cell* 2:633-641, where two root-specific promoters isolated from hemoglobin genes from the nitrogen-fixing nonlegume *Parasponia andersonii* and the related non-nitrogen-fixing nonlegume *Trema tomentosa* are described. Leach and Aoyagi (1991) describe their analysis of the promoters of the highly expressed rolC and rolD root-inducing genes of *Agrobacterium rhizogenes* (see *Plant Sci* (Limerick) 79:69-76). Teeri et al. (1989) used gene fusion to lacZ to show that the *Agrobacterium* T-DNA gene encoding octopine synthase is especially active in the epidermis of the root tip and that the TR2' gene is root specific in the intact plant and stimulated by wounding in leaf tissue (see *EMBO J.* 8:343-350). The TR1' gene, fused to nptII (neomycin phosphotransferase II) showed similar characteristics. Additional root-preferred promoters include the VfENOD-GRP3 gene promoter (Kuster et al. (1995) *Plant Mol. Biol.* 29:759-772); and rolB promoter (Capana et al. (1994) *Plant Mol. Biol.* 25:681-691. See also U.S. Pat. Nos. 5,837,876; 5,750,386; 5,633,363; 5,459,252; 5,401,836; 5,110,732; and 5,023,179. Another root-preferred promoter includes the promoter of the phaseolin gene (Murai et al. (1983) *Science* 23:476-482 and Sengopta-Gopalen et al. (1988) *Proc. Natl. Acad. Sci. USA* 82:3320-3324.

[0073] Seed-preferred promoters include both those promoters active during seed development as well as promoters active during seed germination. See Thompson et al. (1989) *BioEssays* 10:108, herein incorporated by reference. Such seed-preferred promoters include, but are not limited to, Cim1 (cytokinin-induced message); cZ19B1 (maize 19 kDa zein); and milps (myo-inositol-1-phosphate synthase); (see WO 00/11177 and U.S. Pat. No. 6,225,529; herein incorporated by reference). For dicots, seed-preferred promoters include, but are not limited to, bean β-phaseolin, napin, β-conglycinin, soybean lectin, cruciferin, and the like. For monocots, seed-preferred promoters include, but are not limited to, maize 15 kDa zein, 22 kDa zein, 27 kDa gamma zein, waxy, shrunken 1, shrunken 2, globulin 1, oleosin, nuc1, etc. See also WO 00/12733, where seed-preferred promoters from end1 and end2 genes are disclosed; herein incorporated by reference.

[0074] Where low-level expression is desired, weak promoters will be used. Generally, by "weak promoter" is intended a promoter that drives expression of a coding sequence at a low level. By low level is intended at levels of about 1/1000 transcripts to about 1/100,000 transcripts to about 1/500,000 transcripts. Alternatively, it is recognized that weak promoters also encompasses promoters that are expressed in only a few cells and not in others to give a total low level of expression. Where a promoter is expressed at unacceptably high levels, portions of the promoter sequence can be deleted or modified to decrease expression levels. Such weak constitutive promoters include, for example, the core promoter of the Rsyn7 promoter (WO 99/43838 and U.S. Pat. No. 6,072,050), the core 35S CaMV promoter, and the like.

[0075] Other promoters of interest include the Rab16 promoter (Mundy et al. (1990) *PNAS* 87: 1406-1410), the *Brassica* LEA3-1 promoter (U.S. Application Publication No. US 2008/0244793), the HVA1s, Dhn8s, and Dhn4s from barley and the wsi18j, rab16Bj from rice (Xiao and Xue (2001) *Plant Cell Rep* 20:667-73), and D113 from cotton (Luo et al. (2008) *Plant Cell Rep* 27:707-717).

[0076] In some embodiments, the polynucleotide encoding a cell proliferation factor (e.g., babyboom polypeptide) is operably linked to a maize ubiquitin promoter or a maize oleosin promoter (e.g., SEQ ID NO: 65 or a variant or fragment thereof).

[0077] In some of those embodiments wherein the vector comprises a presently disclosed promoter construct operably linked to a polynucleotide encoding a site-specific recombinase and in some embodiments, a polynucleotide encoding a babyboom polypeptide, the vector can further comprise a polynucleotide encoding a Wuschel polypeptide (see International Application Publication No. WO 01/23575 and U.S. Pat. No. 7,256,322, each of which are herein incorporated by reference in its entirety). In certain embodiments, the polynucleotide encoding the Wuschel polypeptide has the sequence set forth in SEQ ID NO: 61, 63, 114, or 105 (WUS1, WUS2, WUS2 alt, or WUS3, respectively) or an active variant or fragment thereof. In particular embodiments, the Wuschel polypeptide has the sequence set forth in SEQ ID NO: 62, 64, 115, or 106 (WUS1, WUS2, WUS2 alt, or WUS3, respectively) or an active variant or fragment thereof. In some of these embodiments, the polynucleotide encoding a Wuschel polypeptide is operably linked to a promoter active in the plant, including but not limited to the maize In2-2 promoter or a nopaline synthase promoter. In some of these embodiments, the expression cassettes for the site-specific recombinase, the babyboom polypeptide, and the Wuschel polypeptide are all flanked by site-specific recombination sites that are directly repeated and are recognized by the site-specific recombinase whose expression is regulated by a presently disclosed promoter construct, such that expression of the site-specific recombinase results in the excision of the three expression cassettes.

[0078] In some embodiments, the vector comprises a promoter disclosed herein (maize Rab17 promoter with an attB1 site) operably linked to a site-specific recombinase (e.g., Cre, FLP); a second promoter operably linked to a cell proliferation factor (e.g., a babyboom polypeptide); and a third promoter operably linked to a polynucleotide of interest, such as those disclosed elsewhere herein (e.g., trait gene), or multiple polynucleotides of interest operably linked to one or more promoters; and in some embodiments, a fourth promoter operably linked to a WUS gene. In some of these embodiments, the expression cassettes for the site-specific recombinase, the cell proliferation factor, and the Wuschel polypeptide are all flanked by site-specific recombination sites that are directly repeated and are recognized by the site-specific recombinase, such that expression of the site-specific recombinase results in the excision of the three expression cassettes, leaving the polynucleotides of interest (e.g., trait genes) behind. In other embodiments, the polynucleotide of interest (e.g., trait gene) is introduced along with or following the vector comprising a presently disclosed promoter operably linked to a site-specific recombinase, and at least one cell proliferation factor (e.g., babyboom polypeptide, Wuschel polypeptide) operably linked to one or more promoters, wherein the polynucleotide of interest is present on a separate vector from the expression cassettes for the site-specific recombinase and cell proliferation factor(s). In some of these embodiments, the expression cassettes for the site-specific recombinase and cell proliferation factor(s) are flanked by recombination sites that are recognized by the site-specific recombinase. Expression of the cell proliferation factors facilitates the transformation of the polynucleotide of interest (e.g., trait gene) and expression of the site-specific recombinase results in the excision of the expression cassettes for the site-specific recombinase and cell proliferation factor(s).

[0079] The presently disclosed promoter constructs, expression cassettes, and vectors can be introduced into a host cell. By "host cell" is meant a cell, which comprises a heterologous nucleic acid sequence. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells. In some examples, host cells are monocotyledonous or dicotyledonous plant cells. In particular embodiments, the monocotyledonous host cell is a maize host cell.

[0080] An intermediate host cell may be used, for example, to increase the copy number of the cloning vector and/or to mediate transformation of a different host cell. With an increased copy number, the vector containing the nucleic acid of interest can be isolated in significant quantities for introduction into the desired plant cells. In one embodiment, plant promoters that do not cause expression of the polypeptide in bacteria are employed.

[0081] Prokaryotes most frequently are represented by various strains of *E. coli*; however, other microbial strains may also be used. Commonly used prokaryotic control sequences which are defined herein to include promoters for transcription initiation, optionally with an operator, along with ribosome binding sequences, include such commonly used promoters as the beta lactamase (penicillinase) and lactose (lac) promoter systems (Chang et al. (1977) *Nature* 198: 1056), the tryptophan (trp) promoter system (Goeddel et al. (1980) *Nucleic Acids Res.* 8:4057) and the lambda derived P

L promoter and N-gene ribosome binding site (Shimatake et al. (1981) *Nature* 292:128). The inclusion of selection markers in DNA vectors transfected in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol.

[0082] The vector is selected to allow introduction into the appropriate host cell. Bacterial vectors are typically of plasmid or phage origin. Appropriate bacterial cells are infected with phage vector particles or transfected with naked phage vector DNA. If a plasmid vector is used, the bacterial cells are transfected with the plasmid vector DNA. Expression systems for expressing a protein are available using *Bacillus* sp. and *Salmonella* (Palva et al. (1983) *Gene* 22:229-235); Mosbach et al. (1983) *Nature* 302:543-545).

[0083] Methods for expressing a polynucleotide of interest in a plant comprise introducing an expression cassette or vector. Alternatively, the method can comprise introducing a promoter construct, wherein the promoter construct is stably integrated into the genome of the plant and operably linked to a polynucleotide of interest.

[0084] "Introducing" is intended to mean presenting to the organism, such as a plant, or the cell the polynucleotide or polypeptide in such a manner that the sequence gains access to the interior of a cell of the organism or to the cell itself. The methods and compositions do not depend on a particular method for introducing a sequence into an organism or cell, only that the polynucleotide or polypeptide gains access to the interior of at least one cell of the organism. Methods for introducing polynucleotides or polypeptides into plants are known in the art including, but not limited to, stable transformation methods, transient transformation methods, virus-mediated methods, and sexual breeding.

[0085] "Stable transformation" is intended to mean that the nucleotide construct introduced into a plant integrates into a genome of the plant and is capable of being inherited by the progeny thereof. "Transient transformation" is intended to mean that a polynucleotide is introduced into the plant and does not integrate into a genome of the plant or a polypeptide is introduced into a plant.

[0086] Protocols for introducing polypeptides or polynucleotide sequences into plants may vary depending on the type of plant or plant cell, i.e., monocot or dicot, targeted for transformation. Suitable methods of introducing polypeptides and polynucleotides into plant cells include microinjection (Crossway et al. (1986) *Biotechniques* 4:320-334), electroporation (Riggs et al. (1986) *Proc. Natl. Acad. Sci. USA* 83:5602-5606, *Agrobacterium*-mediated transformation (U.S. Pat. No. 5,563,055 and U.S. Pat. No. 5,981,840), direct gene transfer (Paszkowski et al. (1984) *EMBO J.* 3:2717-2722), and ballistic particle acceleration (see, for example, U.S. Pat. No. 4,945,050; U.S. Pat. No. 5,879,918; U.S. Pat. No. 5,886,244; and, U.S. Pat. No. 5,932,782; Tomes et al. (1995) in *Plant Cell, Tissue, and Organ Culture: Fundamental Methods*, ed. Gamborg and Phillips (Springer-Verlag, Berlin); McCabe et al. (1988) *Biotechnology* 6:923-926); and Lec1 transformation (WO 00/28058). Also see Weissinger et al. (1988) *Ann. Rev. Genet.* 22:421-477; Sanford et al. (1987) *Particulate Science and Technology* 5:27-37 (onion); Christou et al. (1988) *Plant Physiol.* 87:671-674 (soybean); McCabe et al. (1988) *Bio/Technology* 6:923-926 (soybean); Finer and McMullen (1991) *In Vitro Cell Dev. Biol.* 27P:175-182 (soybean); Singh et al. (1998) *Theor. Appl. Genet.* 96:319-324 (soybean); Datta et al. (1990) *Biotechnology* 8:736-740 (rice); Klein et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:4305-4309 (maize); Klein et al. (1988) *Biotechnology* 6:559-563 (maize); U.S. Pat. Nos. 5,240,855; 5,322,783; and, 5,324,646; Klein et al. (1988) *Plant Physiol.* 91:440-444 (maize); Fromm et al. (1990) *Biotechnology* 8:833-839 (maize); Hooykaas-Van Slogteren et al. (1984) *Nature* 311: 763-764; U.S. Pat. No. 5,736,369 (cereals); Bytebier et al. (1987) *Proc. Natl. Acad. Sci. USA* 84:5345-5349 (Liliaceae); De Wet et al. (1985) in *The Experimental Manipulation of Ovule Tissues*, ed. Chapman et al. (Longman, New York), pp. 197-209 (pollen); Kaeppler et al. (1990) *Plant Cell Rep* 9:415-418 and Kaeppler et al. (1992) *Theor. Appl. Genet.* 84:560-566 (whisker-mediated transformation); D'Halluin et al. (1992) *Plant Cell* 4:1495-1505 (electroporation); Li et al. (1993) *Plant Cell Rep* 12:250-255 and Christou and Ford (1995) *Annals of Botany* 75:407-413 (rice); Osjoda et al. (1996) *Nat Biotechnol* 14:745-750 (maize via *Agrobacterium tumefaciens*); all of which are herein incorporated by reference.

[0087] In specific embodiments, the sequences can be provided to a plant using a variety of transient transformation methods. Such transient transformation methods include, but are not limited to, the introduction of the polypeptide of interest directly into the plant or the introduction of a polynucleotide encoding the polypeptide of interest into the plant. Such methods include, for example, microinjection or particle bombardment. See, for example, Crossway et al. (1986) *Mol Gen. Genet.* 202:179-185; Nomura et al. (1986) *Plant Sci.* 44:53-58; Hepler et al. (1994) *Proc. Natl. Acad. Sci.* 91:2176-2180 and Hush et al. (1994) *J Cell Sci* 107:775-784, all of which are herein incorporated by reference. Alternatively, the polynucleotide can be transiently transformed into the plant using techniques known in the art. Such techniques include viral vector system and the precipitation of the polynucleotide in a manner that precludes subsequent release of the DNA. Thus, the transcription from the particle-bound DNA can occur, but the frequency with which its released to become integrated into the genome is greatly reduced. Such methods include the use particles coated with polyethylimine (PEI; Sigma #P3143).

[0088] In other embodiments, the polynucleotide may be introduced into plants by contacting plants with a virus or viral nucleic acids. Generally, such methods involve incorporating a nucleotide construct within a viral DNA or RNA molecule. It is recognized that the cell proliferation factor may be initially synthesized as part of a viral polyprotein, which later may be processed by proteolysis in vivo or in vitro to produce the desired recombinant protein. Further, it is recognized that promoters also encompass promoters utilized for transcription by viral RNA polymerases. Methods for introducing polynucleotides into plants and expressing a protein encoded therein, involving viral DNA or RNA molecules, are known in the art. See, for example, U.S. Pat. Nos. 5,889,191, 5,889,190, 5,866,785, 5,589,367, 5,316,931, and Porta et al. (1996) *Molecular Biotechnology* 5:209-221; herein incorporated by reference.

[0089] Other methods of introducing polynucleotides into a plant can be used, including plastid transformation methods, and the methods for introducing polynucleotides into tissues from seedlings or mature seeds.

[0090] Methods are known in the art for the targeted insertion of a polynucleotide at a specific location in the plant genome. In one embodiment, the insertion of the polynucleotide at a desired genomic location is achieved using a site-specific recombination system. See, for example, WO99/

25821, WO99/25854, WO99/25840, WO99/25855, and WO99/25853, all of which are herein incorporated by reference. Briefly, the polynucleotide can be contained in a transfer cassette flanked by two non-recombinogenic recombination sites. The transfer cassette is introduced into a plant having stably incorporated into its genome a target site which is flanked by two non-recombinogenic recombination sites that correspond to the sites of the transfer cassette. An appropriate recombinase is provided and the transfer cassette is integrated at the target site. The polynucleotide of interest is thereby integrated at a specific chromosomal position in the plant genome.

[0091] In specific embodiments, methods are provided for the excision of a polynucleotide of interest from a target site in a plant, wherein the polynucleotide of interest is flanked by a first and a second recombination site that are recombinogenic with respect to one another and that are directly repeated. The method comprises introducing into the plant an expression cassette comprising a presently disclosed promoter construct (e.g., SEQ ID NO: 30 or a variant or fragment thereof) operably linked to a site-specific recombinase, expressing the recombinase, so that the recombinase recognizes and implements recombination at the recombination sites flanking the polynucleotide of interest, thereby excising the polynucleotide of interest. The expression cassette can comprise any of the linker sequences, attB sites, termination regions, etc., such as those described herein.

[0092] The terms "target site," and "target sequence," as used interchangeably herein, refer to a polynucleotide sequence present in a cell of an organism, such as a plant, that comprises at least one site-specific recombination site. The target site may be part of the organism's native genome or integrated therein or may be present on an episomal polynucleotide. The genomic target sequence may be on any region of any chromosome, and may or may not be in a region encoding a protein or RNA. The target site may be native to the cell or heterologous. In some embodiments, the heterologous target sequence may have been transgenically inserted into the organism's genome, and may be on any region of any chromosome, including an artificial or satellite chromosome, and may or may not be in a region encoding a protein or RNA. It is recognized that the cell or the organism may comprise multiple target sites, which may be located at one or multiple loci within or across chromosomes.

[0093] Alternative methods for excising a polynucleotide of interest from a target site in a plant include providing a plant comprising a target site comprising in operable linkage: a first site-specific recombination site, a first promoter, the polynucleotide of interest, a second promoter, a polynucleotide encoding a site-specific recombinase, and a second site-specific recombination site. The first and the second site-specific recombination sites are recombinogenic with respect to one another and directly repeated. The polynucleotide of interest and its operably linked promoter may precede or follow the polynucleotide encoding the site-specific recombinase and its operably linked promoter. The second promoter is one of the presently disclosed promoter constructs (e.g., SEQ ID NO: 30 or a variant or fragment thereof). The method comprises expressing the site-specific recombinase, whereby the site-specific recombinase recognizes and implements recombination at the first and the second site-specific recombination sites, thereby excising the polynucleotide of interest and the polynucleotide encoding the site-specific recombinase.

[0094] In some embodiments, the target site further comprises a third promoter operably linked to a polynucleotide encoding a Wuschel polypeptide. The three expression cassettes may be in any order, but in some embodiments, the target site comprises in operable linkage: the first site-specific recombination site, the third promoter, the polynucleotide encoding a Wuschel polypeptide, the first promoter, the polynucleotide of interest, the second promoter, the polynucleotide encoding the site-specific recombinase, and the second site-specific recombination site, wherein expression of the recombinase results in the excision of all three expression cassettes. The expression cassette can comprise any of the linker sequences, attB sites, termination regions, etc., such as those described herein.

[0095] Methods are provided to enhance the efficiency of plastid transformation, which include introducing into a plant cell a heterologous polynucleotide encoding a cell proliferation factor and expressing the heterologous polynucleotide before, during, or immediately following the transformation of the plastid of the plant cell with a polynucleotide of interest. The heterologous polynucleotide encoding a cell proliferation factor can be co-delivered with the polynucleotide of interest or the cell proliferation polynucleotide can first be introduced into the plant, followed by the introduction of the polynucleotide of interest.

[0096] As used herein, a "plastid" refers to an organelle present in plant cells that stores and manufactures chemical compounds used by the cell, such as starch, fatty acids, terpenes, and that has been derived from a proplastid. Thus, plastids of plants typically have the same genetic content. Plastids include chloroplasts, which are responsible for photosynthesis, amyloplasts, chromoplasts, statoliths, leucoplasts, elaioplasts, and proteinoplasts.

[0097] The plastid genome is circular and varies in size among plant species from about 120 to about 217 kilobase pairs (kb). The genome typically includes a large inverted repeat, which can contain up to about 76 kilobase pairs, but which is more typically in the range of about 20 to about 30 kilobase pairs. The inverted repeat present in the plastid genome of various organisms has been described (Palmer (1990) *Trends Genet* 6:115-120).

[0098] Transformation of plastids can result in a homoplasmic state, wherein essentially all of the plastids in a plant cell have the introduced DNA integrated into the plastid genome. This occurs through a selection process, whereby those cells that comprise a sufficient number of transformed plastids having an introduced selectable marker gene survive on the selection medium, and through the reproduction of the transformed plastid genomes. Plastids can be present in a plant cell at a very high copy number, with up to 50,000 copies per cell present for the chloroplast genome (Bendich (1987) BioEssays 6:279-282). Thus, through plastid transformation, plant cells can be engineered to maintain an introduced gene of interest at a very high copy number.

[0099] While plastid transformation is routine and relatively efficient in tobacco by bombardment of leaves, the application of plastid transformation technology in important crop species is not routine. For example, plastid transformation in maize and wheat has not been reported. Plastid transformation is possible in soybean, but the frequency of transformation with vectors carrying trait genes is low. Plastid transformation is possible in rice, but homoplasmic events have not been recovered.

[0100] The introduction and expression of polynucleotides encoding cell proliferation factors may be used to enhance the efficiency of plastid transformation. Any cell proliferation factor known in the art or described elsewhere herein may be used to enhance plastid transformation, including babyboom polypeptides. In certain embodiments, embryogenesis-stimulating polypeptides are used to enhance plastid transformation.

[0101] Methods are known in the art for introducing genes into the plastid genome. See, for example, Svab et al. (1990) *Proc. Natl. Acad. Sci. USA* 87: 8526-8530; Svab and Maliga (1993) *Proc. Natl. Acad. Sci. USA* 90: 913-917; Svab and Maliga (1993) *EMBO J.* 12: 601-606; and U.S. Pat. Nos. 5,451,513 and 5,545,818; each of which is herein incorporated by reference in its entirety.

[0102] One method involves the integration of a polynucleotide of interest into the plastid genome through homologous recombination. Such methods involve the introduction of a polynucleotide of interest flanked by regions of homology with regions of the plastid genome into a plant cell. Delivery of the polynucleotide of interest into the plant cell can be via any method of transformation known in the art, including those described elsewhere herein. These include, but are not limited to, particle gun delivery (Svab, Z. et al. (1990) *Proc Natl Acad Sci USA* 87:8526-8530; Svab and Maliga (1993) *Proc Natl Acad Sci USA* 90:913-917; and Staub and Maliga (1993) *EMBO J* 12:601-606; and U.S. Pat. Nos. 5,451,513 and 5,545,818; each of which is herein incorporated by reference in its entirety) and *Agrobacterium*-mediated transformation (U.S. Pat. No. 5,563,055 and U.S. Pat. No. 5,981,840). In some species, protoplasts can also be used for chloroplast transformation (O'Neill et al. (1993) *Plant J* 3:729-38; and Spoerlein et al. (1991) *Theor Appl Gen* 82:717-722; each of which is herein incorporated by reference in its entirety). Once the polynucleotide of interest flanked by the homologous regions enters the cell, the polynucleotide of interest will be integrated within the plastid genome.

[0103] The homologous regions flanking the polynucleotide of interest, and in some embodiments, its operably linked promoter, and in particular embodiments, the selectable marker gene as well, may vary in length. In some embodiments, the region of homology with the plastid genome is about 50, 75, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000 base pairs or greater in length. In most instances, the frequency of recombination and thus the frequency of obtaining plants having transformed plastids decreases with the decreasing size of the homologous regions. In those embodiments wherein the regions of homology are present in the inverted repeat regions of the plastid genome, two copies of the polynucleotide of interest are expected per transformed plastid.

[0104] In some embodiments, the polynucleotide of interest can be co-delivered with a selectable marker gene that is active in the plastid. The selectable marker gene and the polynucleotide of interest can be present on a single DNA construct or on separate constructs. A number of markers have been developed for use with plant cells, such as resistance to chloramphenicol, the aminoglycoside G418, hygromycin, or the like. Genes conferring resistance to kanamycin (NPTII or AphA6) have been used as a selectable marker for plastid transformation (Carrer et al. (1993) *Mol Gen Genetics* 241:49-56; and Huang et al. (2002) *Mol Gen Genomics* 268: 19-27; each of which is herein incorporated by reference in its entirety). Other genes which encode a product involved in chloroplast metabolism may also be used as selectable markers.

[0105] Another example of a selectable marker gene for plastid transformation is a selectable marker gene that confers resistance to a substance which inhibits protein synthesis by the plastids, such that cells which have acquired the phenotype are selected for by contacting the cells with a substance which inhibits protein synthesis by the plastids. The plastid DNA encoding the nonlethal selectable phenotype may comprise 16S ribosomal DNA mutated to confer resistance to the effects of streptomycin, or to spectinomycin, or to both antibiotics simultaneously. Expression of heterologous genes that modify non-lethal antibiotics such as streptomycin or spectinomycin by phosphorylation, adenylation or acetylation also are suitable for the selection of plastid transformation events. Another non-limiting example of a gene that confers resistance to streptomycin and spectinomycin is the bacterial aadA gene that codes for streptomycin spectinomycin adenyltransferase (Svab et al. (1993) *Proc Natl Acad Sci USA* 90:913-917). The aadA gene product allows for continued growth and greening of cells in the presence of streptomycin or spectinomycin whose chloroplasts comprise the selectable marker gene product. Cells which do not contain the selectable marker gene product are bleached. Selection for the aadA gene marker is thus based on identification of plant cells which are not bleached by the presence of streptomycin or spectinomycin, in the plant growth medium.

[0106] Other examples of selectable marker genes are those that confer resistance to an herbicide, including a photosystem II herbicide, such as a triazine herbicide, specifically the triazine herbicide atrazine. This phenotype not only provides nonlethal selection, but also provides herbicide resistance. Genes that provide resistance to plant herbicides such as glyphosate, bromoxynil, or imidazolinone may find use as a selectable marker gene. Such genes have been reported (Stalker et al. (1985) *J Biol Chem* 260:4724-4728 (glyphosate resistant EPSP); Stalker et al. (1985) *J Biol Chem* 263:6310-6314 (bromoxynil resistant nitrilase gene); and Sathasivan et al. (1990) *Nucl Acids Res* 18:2188 (AHAS imidazolinone resistance gene); each of which is herein incorporated by reference in its entirety).

[0107] The selectable marker gene and/or the polynucleotide of interest can be placed under the regulatory control of a chloroplast 5' promoter and 3' transcription termination regions, such as the tobacco 16S rRNA promoter rrn region and rps16 3' termination region. Numerous additional promoter regions may also be used to drive expression of the selectable marker gene and/or the polynucleotide of interest, including various plastid promoters and bacterial promoters which have been shown to function in plant plastids. Further, if nuclear expression of the selectable marker gene and/or the polynucleotide of interest is not desired, plastid introns can be incorporated into the selectable marker gene and/or the polynucleotide of interest. Certain classes of plastid introns can not be correctly spliced out in the nucleus, thereby preventing expression of the selectable marker gene and/or the polynucleotide of interest within the nucleus. The polynucleotide of interest and/or the heterologous polynucleotide encoding the cell proliferation factor may be optimized for expression in the chloroplast to account for differences in codon usage between the plant nucleus and this organelle. In this manner, the polynucleotide may be synthesized using chloroplast-preferred codons. See, for example, U.S. Pat. No. 5,380,831, herein incorporated by reference.

[0108] An additional method of plastid transformation occurs through the transactivation of a silent plastid-borne transgene by tissue-preferred expression of a nuclear-encoded and plastid-directed RNA polymerase. Such a system has been reported in McBride et al. (1994) *Proc. Natl. Acad. Sci. USA* 91: 7301-7305, which is herein incorporated by reference in its entirety. In these methods, the heterologous polynucleotide encoding the cell proliferation factor is introduced into the cell and expressed prior to, during, or immediately after the expression of the plastid-directed RNA polymerase.

[0109] In order to select those cells having transformed plastids, following introduction of the chloroplast transformation vectors, the treated tissue is placed on tissue culture medium containing the appropriate selection agent. After a suitable period of incubation on selection medium, transformed cells can be identified and grown to a stage that allows regeneration of the whole plants. The regeneration processes are basically identical to those used for standard nuclear transformation events. Special care must be taken to ensure that selection and regeneration conditions promote the elimination of most wild-type chloroplast genomes. The status of the proportion of wild-type to transformed chloroplast genomes can be monitored by standard molecular techniques including Southern and PCR analysis.

[0110] For tobacco and a number of other species, leaves are a preferred target for plastid transformation. In some embodiments, one or more cell proliferation factors (e.g., babyboom polypeptides) can be used to trigger a tissue culture response from leaves of maize and other species. For boosting chloroplast transformation, polynucleotides encoding cell proliferation factors under the control of inducible promoters can be introduced into the species of interest by standard nuclear transformation protocols. Events that contain the transgene can be characterized for expression of the inducible embryogenesis-stimulating polypeptides. Then, the expression of the polynucleotide encoding the cell proliferation factor is induced, thereby stimulating an embryogenic tissue culture response. For example, leaves from plants transformed with the polynucleotide(s) encoding a cell proliferation factor under the control of the tetracycline-repressor system can be placed on medium containing appropriate concentrations of doxycyline for induction of expression. The leaves can be maintained on the induction medium to allow for cell division and the initiation of embryogenic callus to take place. The plastids of the leaves can be transformed with the polynucleotide of interest, and in certain embodiments, a selectable marker gene just prior to the induction of the polynucleotide(s) encoding cell proliferation factor, during induction, or immediately after induction. Alternatively, leaf tissue can be transformed using the methods disclosed elsewhere herein. After plastid transformation, the plastid transformation events can be selected by incubating the leaves on selection medium. Following selection, the leaves or plant cells are grown on medium that stimulates callus formation.

[0111] Methods are provided for the preparation and transformation of dried mature seeds, mature embryos, and mature embryo explants. A mature embryo explant is a tissue dissected from a mature embryo, which is an embryo that has an age of at least about 18 days after pollination. Methods for preparing a mature embryo comprise dissecting a mature embryo from a mature seed and methods for preparing a mature embryo explant further comprise preparing slices (e.g., longitudinal slices) of the mature embryo. The mature embryo explant comprises at least one of the following tissues: leaf primordia, mesocotyl, shoot apical meristem, and root primordia. In some embodiments, the mature embryo explant comprises leaf primordia, mesocotyl, and root primordia. In some of these embodiments, the mature embryo explant further comprises a shoot apical meristem. The slices may be prepared using any method or suitable apparatus known in the art, including slices prepared by hand with a scalpel. In certain embodiments, each mature embryo is sliced into about 3 to 4 thin sections using a scalpel. The use of a dissecting microscope can aid in slicing of the mature embryo.

[0112] The mature seed from which the mature embryo or mature embryo explant is derived can be a seed of any plant. In some embodiments, the mature seed is from a monocot. In particular embodiments, the mature seed is from maize, rice, sorghum, barley, wheat, oats, or millet. In certain embodiments, the mature seed is from a recalcitrant plant, such as an elite maize inbred. As used herein, a “recalcitrant tissue” or “recalcitrant plant” is a tissue or a plant that has a low rate of transformation using traditional methods of transformation, such as those disclosed elsewhere herein. In some embodiments, the recalcitrant tissue or plant is unable to be transformed in the absence of the cell proliferation factor. In other embodiments, the recalcitrant tissue or plant has a rate of successful transformation of less than about 20%, less than about 15%, less than about 10%, less than about 5%, less than about 1%, less than about 0.1%, less than about 0.01%, less than about 0.001%, or less.

[0113] The mature embryo or mature embryo explant can be prepared from a dried mature seed. The dried mature seed can comprise about 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, 1%, 0.1% or less water than a mature seed that has not been dried. The dried mature seed can be imbibed with an aqueous solution for a sufficient period of time to allow the dried mature seed to soften so that the mature embryo may be dissected from the seed and in some embodiments, mature embryo explant slices prepared from the mature embryo. In some embodiments, the dried mature seed is imbibed in an aqueous solution for about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 hours or greater. In certain embodiments, the aqueous solution is water. In certain embodiments, the dried mature seed is imbibed for a sufficient period of time to induce germination of the seed. A germinated seed is one in which the radical has emerged.

[0114] Mature embryos and mature embryo explants can be transformed with a polynucleotide of interest through the provision of a cell proliferation factor (e.g., babyboom polypeptide). A heterologous polynucleotide encoding the cell proliferation factor is introduced into the mature embryo explant prior to or at the same time as the introduction of the polynucleotide of interest. The heterologous polynucleotide encoding the cell proliferation factor and the polynucleotide of interest can be provided on the same expression cassette or on separate expression cassettes.

[0115] The polynucleotides can be introduced into the mature embryo explant using any method known in the art, including but not limited to, *Agrobacterium*-mediated transformation.

[0116] In some embodiments, transformed mature embryo explants can be identified. Any method can be used to identify a plant cell or tissue comprising the polynucleotide of interest. In some examples, plant cells or tissues comprising the polynucleotide of interest are identified using one or more of the following techniques, including but not limited to PCR methods, hybridization methods such as Southern or Northern blots, restriction digest analyses, or DNA sequencing. In some embodiments, the transformed mature embryo explants can be identified by incubating the leaf mature embryo explants under conditions to allow for growth of a callus. In some embodiments, those mature embryo explants that are able to grow into a callus with significant proliferation indicate those mature embryo explains that have been transformed. In other embodiments, the transformed mature embryo explants can be identified and selected for through the introduction and expression of a selectable marker gene into the mature embryo explant.

[0117] Methods are also provided herein for the transformation of leaf tissues, which can be a leaf base. A leaf base is the tissue of a leaf above the first leaf base node. The leaf tissue can be derived from any plant. In some embodiments, the leaf tissue is derived from a monocot. In particular embodiments, the leaf tissue is derived from maize, rice, sorghum, barley, wheat, oats, or millet. In certain embodiments, the leaf tissue is derived from a recalcitrant plant, such as an elite maize inbred.

[0118] The leaf base can be from a mature leaf or a leaf from a seedling. As used herein, a "seedling" refers to a germinated seed or germinated embryo, or a plantlet generated in an in vitro system (e.g., from callus). The seedlings can be prepared by germinating seeds or dissecting mature embryos from mature seeds for germination. In some embodiments, the mature embryos are dissected from dried mature seeds that have been imbibed with an aqueous solution, as described herein.

[0119] In some embodiments, the coleoptile is removed from the leaf tissue and the leaf fragment is split longitudinally, and then horizontal slices are made to cross-dissect the leaf fragment into leaf tissue pieces. In particular embodiments, the pieces of leaf tissue are about 1 to 2 mm in length.

[0120] The leaf tissue can be transformed with a polynucleotide of interest through the provision of a cell proliferation factor (e.g., babyboom polypeptide). The polynucleotides can be introduced into the leaf tissue using any method known in the art, including but not limited to, *Agrobacterium*-mediated transformation. A heterologous polynucleotide of interest encoding the cell proliferation factor is introduced into the leaf tissue prior to or at the same time as the introduction of the polynucleotide of interest. The heterologous polynucleotide encoding the cell proliferation factor is expressed. The heterologous polynucleotide encoding the cell proliferation factor and the polynucleotide of interest can be provided on the same expression cassette or on separate expression cassettes.

[0121] In some embodiments, transformed leaf tissues can be identified. Any method can be used to identify a plant cell or tissue comprising the polynucleotide of interest. In some examples, plant cells or tissues comprising the polynucleotide of interest are identified using one or more of the following techniques, including but not limited to PCR methods, hybridization methods such as Southern or Northern blots, restriction digest analyses, or DNA sequencing. In some embodiments, the transformed leaf tissues can be identified by incubating the leaf tissues under conditions to allow for growth of a callus. In some embodiments, those leaf tissues that are able to grow a callus with significant proliferation indicate those leaf tissues that have been transformed. In other embodiments, the transformed leaf tissue can be identified and selected for through the introduction and expression of a selectable marker gene into the leaf tissue.

[0122] The cells that have been transformed may be grown into plants in accordance with conventional ways. See, for example, McCormick et al. (1986) *Plant Cell Rep* 5:81-84. These plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting hybrid having constitutive expression of the desired phenotypic characteristic identified. Two or more generations may be grown to ensure that expression of the desired phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure expression of the desired phenotypic characteristic has been achieved. In this manner, transformed seed (also referred to as "transgenic seed") having a nucleotide construct, for example, an expression cassette, stably incorporated into their genome is provided. Thus, compositions of the invention include plant cells, plant tissues, plant parts, and plants comprising the presently disclosed polynucleotides, polypeptides, promoter constructs, expression cassettes, or vectors. Likewise, the methods of the invention can be performed in plant cells, plant tissues, plant parts, and plants.

[0123] In some embodiments, the activity and/or level of the cell proliferation factor (e.g., babyboom polypeptide, Wuschel) is reduced prior to regenerating a plant from a cell or tissue having the polynucleotide of interest. In some of these embodiments, the polynucleotide encoding the cell proliferation factor is excised prior to the regeneration of a plant. In certain embodiments, the promoter and other regulatory elements that are operably linked to the heterologous polynucleotide encoding the cell proliferation factor are excised along with the cell proliferation factor coding sequence. In certain embodiments, the polynucleotide encoding the cell proliferation factor is flanked by recombination sites and an appropriate site-specific recombinase is introduced into the mature embryo explant or callus grown therefrom to excise the polynucleotide encoding the cell proliferation factor prior to regeneration of the mature embryo explant or callus into a plant. In some of those embodiments wherein both a babyboom polypeptide and a Wuschel polypeptide are provided to the plant cell, both the polynucleotide encoding the babyboom polypeptide and the polynucleotide encoding the Wuschel polypeptide are excised. The two polynucleotides can be present on the same or different expression cassettes and, therefore, can be excised in one or two different excision reactions. In some of these embodiments, the polynucleotide encoding the site-specific recombinase for excising the babyboom and Wuschel polynucleotides can be located on the same expression cassette as the babyboom and Wuschel polynucleotides and all three polynucleotides can be excised through the activity of the site-specific recombinase.

[0124] In order to control the excision of the cell proliferation factor, the expression of the site-specific recombinase that is responsible for the excision can be controlled by a late embryo promoter or an inducible promoter. In some embodiments, the late embryo promoter is GZ (Uead et al. (1994) *Mol Cell Biol* 14:4350-4359), gamma-kafarin promoter (Mishra et al. (2008) *Mol Biol Rep* 35:81-88), G1b1 promoter (Liu et al. (1998) *Plant Cell Reports* 17:650-655), ZM-LEG1

(U.S. Pat. No. 7,211,712), EEP1 (U.S. Patent Application No. US 2007/0169226), B22E (Klemsdal et al. (1991) *Mol Gen Genet* 228:9-16), or EAP1 (U.S. Pat. No. 7,321,031). In some embodiments, the inducible promoter that regulates the expression of the site-specific recombinase is a heat-shock, light-induced promoter, a drought-inducible promoter, including but not limited to Hva1 (Straub et al. (1994) *Plant Mol Biol* 26:617-630), Dhn, and WSI18 (Xiao & Xue (2001) *Plant Cell Rep* 20:667-673). In other embodiments, expression of the site-specific recombinase is regulated by the maize rab17 promoter, or one of the presently disclosed promoter constructs (e.g., maize rab17 promoter and an attB site). In some embodiments, the site-specific recombinase that excises the polynucleotide encoding the cell proliferation factor is FLP or Cre.

[0125] Any plant species can be transformed, including, but not limited to, monocots and dicots. Examples of plant species of interest include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus, B. rapa, B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor, Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense, Gossypium hirsutum*), sweet potato (*Ipomoea batatus*), cassava (*Manihot esculenta*), coffee (*Coffea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Peryea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), *macadamia* (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats (*Avena*), barley (*Hordeum*), *Arabidopsis*, switchgrass, vegetables, ornamentals, grasses, and conifers.

[0126] Vegetables include tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum.

[0127] Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*); Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). In specific embodiments, plants of the present invention are crop plants (for example, corn, alfalfa, sunflower, *Brassica*, soybean, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.). In other embodiments, corn and soybean and sugarcane plants are optimal, and in yet other embodiments corn plants are optimal.

[0128] Other plants of interest include grain plants that provide seeds of interest, oil-seed plants, and leguminous plants. Seeds of interest include grain seeds, such as corn, wheat, barley, rice, sorghum, rye, etc. Oil-seed plants include cotton, soybean, safflower, sunflower, *Brassica*, maize, alfalfa, palm, coconut, etc. Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc.

[0129] As used herein, the term plant also includes plant cells, plant protoplasts, plant cell tissue cultures from which plants can be regenerated, plant calli, plant clumps, and plant cells that are intact in plants or parts of plants such as embryos, pollen, ovules, seeds, leaves, flowers, branches, fruit, kernels, ears, cobs, husks, stalks, roots, root tips, anthers, and the like. Grain is intended to mean the mature seed produced by commercial growers for purposes other than growing or reproducing the species. Progeny, variants, and mutants of the regenerated plants are also included within the scope of the invention, provided that these parts comprise the introduced polynucleotides.

[0130] If the polynucleotide of interest is introduced into an organism, it may impart various changes in the organism, particularly plants, including, but not limited to, modification of the fatty acid composition in the plant, altering the amino acid content of the plant, altering pathogen resistance, and the like. These results can be achieved by providing expression of heterologous products, increased expression of endogenous products in plants, or suppressed expression of endogenous produces in plants.

[0131] General categories of polynucleotides of interest include, for example, those genes involved in information, such as zinc fingers, those involved in communication, such as kinases, those involved in biosynthetic pathways, and those involved in housekeeping, such as heat shock proteins. More specific categories of transgenes, for example, include sequences encoding important traits for agronomics, insect resistance, disease resistance, herbicide resistance, sterility, grain characteristics, oil, starch, carbohydrate, phytate, protein, nutrient, metabolism, digestability, kernel size, sucrose loading, and commercial products.

[0132] Traits such as oil, starch, and protein content can be genetically altered in addition to using traditional breeding methods. Modifications include increasing content of oleic acid, saturated and unsaturated oils, increasing levels of lysine and sulfur, providing essential amino acids, and also modification of starch. Protein modifications to alter amino acid levels are described in U.S. Pat. Nos. 5,703,049, 5,885,801, 5,885,802, and 5,990,389 and WO 98/20122, herein incorporated by reference.

[0133] Insect resistance genes may encode resistance to pests such as rootworm, cutworm, European Corn Borer, and the like. Such genes include, for example, *Bacillus thuringiensis* toxic protein genes (U.S. Pat. Nos. 5,366,892; 5,747,450; 5,737,514; 5,723,756; 5,593,881; and Geiser et al. (1986) *Gene* 48:109); lectins (Van Damme et al. (1994) *Plant Mol. Biol.* 24:825); and the like.

[0134] Genes encoding disease resistance traits include detoxification genes, such as against fumonosin (U.S. Pat. No. 5,792,931); avirulence (avr) and disease resistance (R) genes (Jones et al. (1994) *Science* 266:789; Martin et al. (1993) *Science* 262:1432; and Mindrinos et al. (1994) *Cell* 78:1089); and the like.

[0135] Herbicide resistance traits may include genes coding for resistance to herbicides that act to inhibit the action of acetolactate synthase (ALS), in particular the sulfonylurea-type herbicides (e.g., the S4 and/or Hra mutations in ALS), genes coding for resistance to herbicides that act to inhibit action of glutamine synthase, such as phosphinothricin or basta (e.g., the bar gene), genes providing resistance to glyphosate, such as GAT (glyphosate N-acetyltransferase; U.S. Pat. No. 6,395,485), EPSPS (enolpyruvylshikimate-3-phosphate synthase; U.S. Pat. Nos. 6,867,293, 5,188,642, 5,627,061), or GOX (glyphosate oxidoreductase; U.S. Pat. No. 5,463,175), or other such genes known in the art. The nptII gene encodes resistance to the antibiotics kanamycin and geneticin.

[0136] Sterility genes can also be encoded in an expression cassette and provide an alternative to physical detasseling. Examples of genes used in such ways include male tissue-preferred genes and genes with male sterility phenotypes such as QM, described in U.S. Pat. No. 5,583,210. Other genes include kinases and those encoding compounds toxic to either male or female gametophytic development.

[0137] Commercial traits can also be encoded on a gene or genes that could, for example increase starch for ethanol production, or provide expression of proteins.

[0138] Reduction of the activity of specific genes (also known as gene silencing, or gene suppression) is desirable for several aspects of genetic engineering in plants. Many techniques for gene silencing are well known to one of skill in the art, including but not limited to antisense technology (see, e.g., Sheehy et al. (1988) *Proc. Natl. Acad. Sci*. USA 85:8805-8809; and U.S. Pat. Nos. 5,107,065; 5,453,566; and 5,759,829); cosuppression (e.g., Taylor (1997) *Plant Cell* 9:1245; Jorgensen (1990) *Trends Biotech.* 8(12):340-344; Flavell (1994) *Proc. Natl. Acad. Sci. USA* 91:3490-3496; Finnegan et al. (1994) *Bio/Technology* 12: 883-888; and Neuhuber et al. (1994) *Mol. Gen. Genet.* 244:230-241); RNA interference (Napoli et al. (1990) *Plant Cell* 2:279-289; U.S. Pat. No. 5,034,323; Sharp (1999) *Genes Dev.* 13:139-141; Zamore et al. (2000) *Cell* 101:25-33; Javier (2003) *Nature* 425:257-263; and, Montgomery et al. (1998) *Proc. Natl. Acad. Sci. USA* 95:15502-15507), virus-induced gene silencing (Burton, et al. (2000) *Plant Cell* 12:691-705; and Baulcombe (1999) *Curr. Op. Plant Bio.* 2:109-113); target-RNA-specific ribozymes (Haseloff et al. (1988) *Nature* 334: 585-591); hairpin structures (Smith et al. (2000) *Nature* 407:319-320; WO 99/53050; WO 02/00904; and WO 98/53083); ribozymes (Steinecke et al. (1992) *EMBO J.* 11:1525; U.S. Pat. No. 4,987,071; and, Perriman et al. (1993) *Antisense Res. Dev.* 3:253); oligonucleotide mediated targeted modification (e.g., WO 03/076574 and WO 99/25853); Zn-finger targeted molecules (e.g., WO 01/52620; WO 03/048345; and WO 00/42219); and other methods or combinations of the above methods known to those of skill in the art.

[0139] The following terms are used to describe the sequence relationships between two or more polynucleotides or polypeptides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", and, (d) "percentage of sequence identity."

[0140] (a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence.

[0141] (b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two polynucleotides. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

[0142] Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent sequence identity between any two sequences can be accomplished using a mathematical algorithm. Non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller (1988) *CABIOS* 4:11-17; the local alignment algorithm of Smith et al. (1981) *Adv. Appl. Math.* 2:482; the global alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443-453; the search-for-local alignment method of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci.* 85:2444-2448; the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 872264, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877.

[0143] Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, Calif.); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the GCG Wisconsin Genetics Software Package, Version 10 (available from Accelrys Inc., 9685 Scranton Road, San Diego, Calif., USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins et al. (1988) *Gene* 73:237-244 (1988); Higgins et al. (1989) *CABIOS* 5:151-153; Corpet et al. (1988) *Nucleic Acids Res.* 16:10881-90; Huang et al. (1992) *CABIOS* 8:155-65; and Pearson et al. (1994) *Meth. Mol. Biol.* 24:307-331. The ALIGN program is based on the algorithm of Myers and Miller (1988) supra. A PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used with the ALIGN program when comparing amino acid sequences. The BLAST programs of Altschul et al (1990) *J. Mol. Biol.* 215:403 are based on the algorithm of Karlin and Altschul (1990) supra. BLAST nucleotide searches can be performed with the BLASTN program, score=100, wordlength=12, to obtain nucleotide sequences homologous to a nucleotide sequence encoding a protein of the invention. BLAST protein searches can be performed with the BLASTX program, score=50, wordlength=3, to obtain amino acid sequences homologous to a protein or polypeptide of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul et al. (1997) *Nucleic Acids Res.* 25:3389. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul et al. (1997) supra. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g., BLASTN for nucleotide sequences, BLASTX for proteins) can be used. See www.ncbi.nlm.nih.gov. Alignment may also be performed manually by inspection.

[0144] Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using GAP Version 10 using the following parameters: % identity and % similarity for a nucleotide sequence using GAP Weight of 50 and Length Weight of 3, and the nwsgapdna.cmp scoring matrix; % identity and % similarity for an amino acid sequence using GAP Weight of 8 and Length Weight of 2, and the BLOSUM62 scoring matrix; or any equivalent program thereof. By "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by GAP Version 10.

[0145] GAP uses the algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443-453, to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. GAP considers all possible alignments and gap positions and creates the alignment with the largest number of matched bases and the fewest gaps. It allows for the provision of a gap creation penalty and a gap extension penalty in units of matched bases. GAP must make a profit of gap creation penalty number of matches for each gap it inserts. If a gap extension penalty greater than zero is chosen, GAP must, in addition, make a profit for each gap inserted of the length of the gap times the gap extension penalty. Default gap creation penalty values and gap extension penalty values in Version 10 of the GCG Wisconsin Genetics Software Package for protein sequences are 8 and 2, respectively. For nucleotide sequences the default gap creation penalty is 50 while the default gap extension penalty is 3. The gap creation and gap extension penalties can be expressed as an integer selected from the group of integers consisting of from 0 to 200. Thus, for example, the gap creation and gap extension penalties can be 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65 or greater.

[0146] GAP presents one member of the family of best alignments. There may be many members of this family, but no other member has a better quality. GAP displays four figures of merit for alignments: Quality, Ratio, Identity, and Similarity. The Quality is the metric maximized in order to align the sequences. Ratio is the quality divided by the number of bases in the shorter segment. Percent Identity is the percent of the symbols that actually match. Percent Similarity is the percent of the symbols that are similar. Symbols that are across from gaps are ignored. A similarity is scored when the scoring matrix value for a pair of symbols is greater than or equal to 0.50, the similarity threshold. The scoring matrix used in Version 10 of the GCG Wisconsin Genetics Software Package is BLOSUM62 (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915).

[0147] (c) As used herein, "sequence identity" or "identity" in the context of two polynucleotides or polypeptide sequences makes reference to the residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity". Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, Calif.).

[0148] (d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

[0149] In hybridization techniques, all or part of a known polynucleotide is used as a probe that selectively hybridizes to other corresponding polynucleotides present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P, or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the babyboom polynucleotide. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, N.Y.).

[0150] For example, the entire babyboom polynucleotide, or one or more portions thereof, may be used as a probe capable of specifically hybridizing to corresponding babyboom polynucleotide and messenger RNAs. To achieve specific hybridization under a variety of conditions, such probes include sequences that are unique among babyboom polynucleotide sequences and are optimally at least about 10 nucleotides in length, and most optimally at least about 20 nucleotides in length. Such probes may be used to amplify corresponding babyboom polynucleotide from a chosen plant by PCR. This technique may be used to isolate additional coding sequences from a desired plant or as a diagnostic assay to determine the presence of coding sequences in a plant. Hybridization techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, for example, Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, N.Y.).

[0151] Hybridization of such sequences may be carried out under stringent conditions. By "stringent conditions" or "stringent hybridization conditions" is intended conditions under which a probe will hybridize to its target sequence to a detectably greater degree than to other sequences (e.g., at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences that are 100% complementary to the probe can be identified (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000 nucleotides in length, optimally less than 500 nucleotides in length.

[0152] Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C. for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C. for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37° C., and a wash in 1× to 2×SSC (20×SSC=3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55° C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37° C., and a wash in 0.5× to 1×SSC at 55 to 60° C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 0.1×SSC at 60 to 65° C. Optionally, wash buffers may comprise about 0.1% to about 1% SDS. Duration of hybridization is generally less than about 24 hours, usually about 4 to about 12 hours. The duration of the wash time will be at least a length of time sufficient to reach equilibrium.

[0153] Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl (1984) *Anal. Biochem.* 138:267-284: T_m=81.5° C.+16.6 (log M)+0.41 (% GC)-0.61 (% form)-500/L; where M is the molarity of monovalent cations, % GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1° C. for each 1% of mismatching; thus, T_m, hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with $\geqq$90% identity are sought, the T_m can be decreased 10° C. Generally, stringent conditions are selected to be about 5° C. lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4° C. lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10° C. lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20° C. lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m, those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45° C. (aqueous solution) or 32° C. (formamide solution), it is optimal to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 (Elsevier, New York); and Ausubel et al., eds. (1995) *Current Protocols in Molecular Biology, Chapter* 2 (Greene Publishing and Wiley-Interscience, New York). See Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, N.Y.).

[0154] It is to be noted that the term "a" or "an" entity refers to one or more of that entity; for example, "a polypeptide" is understood to represent one or more polypeptides. As such, the terms "a" (or "an"), "one or more," and "at least one" can be used interchangeably herein.

[0155] Throughout this specification and the claims, the words "comprise," "comprises," and "comprising" are used in a non-exclusive sense, except where the context requires otherwise.

[0156] As used herein, the term "about," when referring to a value is meant to encompass variations of, in some embodiments ±50%, in some embodiments ±20%, in some embodiments ±10%, in some embodiments ±5%, in some embodiments ±1%, in some embodiments ±0.5%, and in some embodiments ±0.1% from the specified amount, as such variations are appropriate to perform the disclosed methods or employ the disclosed compositions.

[0157] Further, when an amount, concentration, or other value or parameter is given as either a range, preferred range, or a list of upper preferable values and lower preferable values, this is to be understood as specifically disclosing all ranges formed from any pair of any upper range limit or preferred value and any lower range limit or preferred value, regardless of whether ranges are separately disclosed. Where a range of numerical values is recited herein, unless otherwise stated, the range is intended to include the endpoints thereof, and all integers and fractions within the range. It is not intended that the scope of the presently disclosed subject matter be limited to the specific values recited when defining a range.

[0158] The following examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

Example 1

A Modified Rab17 Promoter for the Regulated Expression of Genes

[0159] Gateway™ technology (Invitrogen, Carlsbad, Calif.) was used to place Gateway™ recombination sites between a promoter and a coding sequence, and between the coding sequence and a terminator. The product of a Gateway™ reaction set up in this manner leaves attB sites in those locations.

[0160] The rab17 promoter was identified as a candidate for regulating the expression of FLP recombinase for excision of polynucleotides encoding cell proliferation factors in tissue culture. It was tested for FLP/FRT excision of cell proliferation factor genes in culture. The PHP31004 plasmid was constructed, which has the following operably linked components: Rab17 Pro-attB1::FLPm-attB2::PinII+Ubi Pro-FRT1::CFP::PinII+Ubi Pro::ZmBBM::PinII-FRT1::YFP::PinII+Ubi Pro::moPAT::PinII. The sequence of the expression cassette for the FLPm gene in the PHP31004 plasmid is provided in SEQ ID NO: 46.

[0161] After excision by the FLP recombinase, the PHP31004 plasmid has the following operably linked components: Rab17 Pro-attB1::FLPm-attB2::PinII+Ubi Pro-FRT1::YFP::PinII+Ubi Pro::moPAT::PinII.

[0162] A plasmid (PHP30642) lacking the attB sites, but comprising the FLPm gene was constructed. The PHP30642 has the following operably linked components: Rab17 pro::FLPm::Gz-W64A term+Ubi pro-FRT1::CFP::PinII+Ubi-Pro::ZmBBM::PinII-FRT1::YFP::PinII+Ubi Pro::moPAT::PinII. The sequence of the expression cassette for the FLPm gene in the PHP30642 plasmid is provided in SEQ ID NO: 47.

[0163] After excision by the FLP recombinase, the PHP30642 plasmid has the following operably linked components: Rab17 pro::FLPm::Gz-W64A term+Ubi pro-FRT1::YFP::PinII+Ubi pro::moPAT::PinII. The construct lacking the attB sites resulted in frequent premature excision of the cell proliferation factor genes.

Example 2

Transformation of Maize Immature Embryos

[0164] Transformation can be accomplished by various methods known to be effective in plants, including particle-mediated delivery, *Agrobacterium*-mediated transformation, PEG-mediated delivery, and electroporation.

[0165] a. Particle-Mediated Delivery

[0166] Transformation of maize immature embryos using particle delivery is performed as follows. Media recipes follow below.

[0167] The ears are husked and surface sterilized in 30% Clorox bleach plus 0.5% Micro detergent for 20 minutes, and rinsed two times with sterile water. The immature embryos are excised and placed embryo axis side down (scutellum side up), 25 embryos per plate, on 560Y medium for 4 hours and then aligned within the 2.5-cm target zone in preparation for bombardment.

[0168] A plasmid comprising the Zm-BBM (also referred to as Zm-ODP2) coding sequence (set forth in SEQ ID NO: 9) operably linked to a promoter is constructed. This could be a weak promoter such as nos, a tissue-specific promoter, such as globulin-1 or oleosin, an inducible promoter such as In2, or a strong promoter such as ubiquitin plus a plasmid containing the selectable marker gene phosphinothricin N-acetyltransferase (PAT; Wohlleben et al. (1988) *Gene* 70:25-37) that confers resistance to the herbicide bialaphos. The plasmid DNA containing the selectable marker gene PAT and the BBM plasmid are precipitated onto 1.1 μm (average diameter) tungsten pellets using a calcium chloride ($CaCl_2$) precipitation procedure by mixing 100 μl prepared tungsten particles in water, 10 μl (1 μg) DNA in Tris EDTA buffer (1 μg total DNA), 100 μl 2.5 M $CaCl_2$, and 10 μl 0.1 M spermidine. Each reagent is added sequentially to the tungsten particle suspension, with mixing. The final mixture is sonicated briefly and allowed to incubate under constant vortexing for 10 minutes. After the precipitation period, the tubes are centrifuged briefly, liquid is removed, and the particles are washed with 500 ml 100% ethanol, followed by a 30 second centrifugation. Again, the liquid is removed, and 105 μl 100% ethanol is added to the final tungsten particle pellet. For particle gun bombardment, the tungsten/DNA particles are briefly sonicated. 10 μl of the tungsten/DNA particles is spotted onto the center of each macrocarrier, after which the spotted particles are allowed to dry about 2 minutes before bombardment.

[0169] The sample plates are bombarded at level #4 with a Biorad Helium Gun. All samples receive a single shot at 450 PSI, with a total of ten aliquots taken from each tube of prepared particles/DNA.

[0170] Following bombardment, the embryos are incubated on 560Y medium for 2 days, then transferred to 560R selection medium containing 3 mg/liter Bialaphos, and subcultured every 2 weeks. After approximately 10 weeks of selection, selection-resistant callus clones are transferred to 288J medium to initiate plant regeneration. Following somatic embryo maturation (2-4 weeks), well-developed somatic embryos are transferred to medium for germination and transferred to a lighted culture room. Approximately 7-10 days later, developing plantlets are transferred to 272V hormone-free medium in tubes for 7-10 days until plantlets are well established. Plants are then transferred to inserts in flats (equivalent to a 2.5" pot) containing potting soil and grown for 1 week in a growth chamber, subsequently grown an additional 1-2 weeks in the greenhouse, then transferred to Classic 600 pots (1.6 gallon) and grown to maturity. Plants are monitored and scored for transformation efficiency, and/or modification of regenerative capabilities.

[0171] Bombardment medium (560Y) comprises 4.0 g/l N6 basal salts (SIGMA C-1416), 1.0 ml/l Eriksson's Vitamin Mix (1000×SIGMA-1511), 0.5 mg/l thiamine HCl, 120.0 g/l sucrose, 1.0 mg/l 2,4-D, and 2.88 g/l L-proline (brought to volume with D-I H_2O following adjustment to pH 5.8 with KOH); 2.0 g/l Gelrite (added after bringing to volume with D-I H_2O); and 8.5 mg/l silver nitrate (added after sterilizing the medium and cooling to room temperature).

[0172] Selection medium (560R) comprises 4.0 g/l N6 basal salts (SIGMA C-1416), 1.0 ml/l Eriksson's Vitamin Mix (1000×SIGMA-1511), 0.5 mg/l thiamine HCl, 30.0 g/l sucrose, and 2.0 mg/l 2,4-D (brought to volume with D-I H_2O following adjustment to pH 5.8 with KOH); 3.0 g/l Gelrite (added after bringing to volume with D-I H_2O); and 0.85 mg/l silver nitrate and 3.0 mg/l bialaphos (both added after sterilizing the medium and cooling to room temperature).

[0173] Plant regeneration medium (288J) comprises 4.3 g/l MS salts (GIBCO 11117-074), 5.0 ml/l MS vitamins stock solution (0.100 g nicotinic acid, 0.02 g/l thiamine HCL, 0.10 g/l pyridoxine HCL, and 0.40 g/l glycine brought to volume with polished D-I H_2O) (Murashige and Skoog (1962) *Physiol. Plant.* 15:473), 100 mg/l myo-inositol, 0.5 mg/l zeatin, 60 g/l sucrose, and 1.0 ml/l of 0.1 mM abscisic acid (brought to volume with polished D-I H_2O after adjusting to pH 5.6); 3.0 g/l Gelrite (added after bringing to volume with D-I H_2O); and 1.0 mg/l indoleacetic acid and 3.0 mg/l bialaphos (added after sterilizing the medium and cooling to 60° C.).

[0174] Hormone-free medium (272V) comprises 4.3 g/l MS salts (GIBCO 11117-074), 5.0 ml/l MS vitamins stock solution (0.100 g/l nicotinic acid, 0.02 g/l thiamine HCL, 0.10

g/l pyridoxine HCL, and 0.40 g/l glycine brought to volume with polished D-I H_2O), 0.1 g/l myo-inositol, and 40.0 g/l sucrose (brought to volume with polished D-I H_2O after adjusting pH to 5.6); and 6 g/l bacto-agar (added after bringing to volume with polished D-I H_2O), sterilized and cooled to 60° C.

[0175] b. *Agrobacterium*-Mediated Transformation

[0176] *Agrobacterium*-mediated transformation was performed essentially as described in Djukanovic et al. (2006) *Plant Biotech J* 4:345-57. Briefly, 10-12 day old immature embryos (0.8-2.5 mm in size) were dissected from sterilized kernels and placed into liquid medium (4.0 g/L N6 Basal Salts (Sigma C-1416), 1.0 ml/L Eriksson's Vitamin Mix (Sigma E-1511), 1.0 mg/L thiamine HCl, 1.5 mg/L 2,4-D, 0.690 g/L L-proline, 68.5 g/L sucrose, 36.0 g/L glucose, pH 5.2). After embryo collection, the medium was replaced with 1 ml *Agrobacterium* at a concentration of 0.35-0.45 OD_{550}. Maize embryos were incubated with *Agrobacterium* for 5 min at room temperature, then the mixture was poured onto a media plate containing 4.0 g/L N6 Basal Salts (Sigma C-1416), 1.0 ml/L Eriksson's Vitamin Mix (Sigma E-1511), 1.0 mg/L thiamine HCl, 1.5 mg/L 2,4-D, 0.690 g/L L-proline, 30.0 g/L sucrose, 0.85 mg/L silver nitrate, 0.1 nM acetosyringone, and 3.0 g/L Gelrite, pH 5.8. Embryos were incubated axis down, in the dark for 3 days at 20° C., then incubated 4 days in the dark at 28° C., then transferred onto new media plates containing 4.0 g/L N6 Basal Salts (Sigma C-1416), 1.0 ml/L Eriksson's Vitamin Mix (Sigma E-1511), 1.0 mg/L thiamine HCl, 1.5 mg/L 2,4-D, 0.69 g/L L-proline, 30.0 g/L sucrose, 0.5 g/L MES buffer, 0.85 mg/L silver nitrate, 3.0 mg/L Bialaphos, 100 mg/L carbenicillin, and 6.0 g/L agar, pH 5.8. Embryos were subcultured every three weeks until transgenic events were identified. Somatic embryogenesis was induced by transferring a small amount of tissue onto regeneration medium (4.3 g/L MS salts (Gibco 11117), 5.0 ml/L MS Vitamins Stock Solution, 100 mg/L myo-inositol, 0.1 μM ABA, 1 mg/L IAA, 0.5 mg/L zeatin, 60.0 g/L sucrose, 1.5 mg/L Bialaphos, 100 mg/L carbenicillin, 3.0 g/L Gelrite, pH 5.6) and incubation in the dark for two weeks at 28° C. All material with visible shoots and roots were transferred onto media containing 4.3 g/L MS salts (Gibco 11117), 5.0 ml/L MS Vitamins Stock Solution, 100 mg/L myo-inositol, 40.0 g/L sucrose, 1.5 g/L Gelrite, pH 5.6, and incubated under artificial light at 28° C. One week later, plantlets were moved into glass tubes containing the same medium and grown until they were sampled and/or transplanted into soil.

Example 3

Transient Expression of BBM Enhances Transformation

[0177] Parameters of the transformation protocol can be modified to ensure that the BBM activity is transient. One such method involves precipitating the BBM-containing plasmid in a manner that allows for transcription and expression, but precludes subsequent release of the DNA, for example, by using the chemical PEI.

[0178] In one example, the BBM plasmid is precipitated onto gold particles with PEI, while the transgenic expression cassette (UBI::moPAT~GFPm::PinII; moPAT is the maize optimized PAT gene) to be integrated is precipitated onto gold particles using the standard calcium chloride method.

[0179] Briefly, gold particles were coated with PEI as follows. First, the gold particles were washed. Thirty-five mg of gold particles, 1.0 in average diameter (A.S.I. #162-0010), were weighed out in a microcentrifuge tube, and 1.2 ml absolute EtOH was added and vortexed for one minute. The tube was incubated for 15 minutes at room temperature and then centrifuged at high speed using a microfuge for 15 minutes at 4° C. The supernatant was discarded and a fresh 1.2 ml aliquot of ethanol (EtOH) was added, vortexed for one minute, centrifuged for one minute, and the supernatant again discarded (this is repeated twice). A fresh 1.2 ml aliquot of EtOH was added, and this suspension (gold particles in EtOH) was stored at −20° C. for weeks. To coat particles with polyethylimine (PEI; Sigma #P3143), 250 μl of the washed gold particle/EtOH mix was centrifuged and the EtOH discarded. The particles were washed once in 100 μl ddH_2O to remove residual ethanol, 250 μl of 0.25 mM PEI was added, followed by a pulse-sonication to suspend the particles and then the tube was plunged into a dry ice/EtOH bath to flash-freeze the suspension, which was then lyophilized overnight. At this point, dry, coated particles could be stored at −80° C. for at least 3 weeks. Before use, the particles were rinsed 3 times with 250 μl aliquots of 2.5 mM HEPES buffer, pH 7.1, with 1× pulse-sonication, and then a quick vortex before each centrifugation. The particles were then suspended in a final volume of 250 μl HEPES buffer. A 25 μl aliquot of the particles was added to fresh tubes before attaching DNA. To attach uncoated DNA, the particles were pulse-sonicated, then 1 μg of DNA (in 5 μl water) was added, followed by mixing by pipetting up and down a few times with a Pipetteman and incubated for 10 minutes. The particles were spun briefly (i.e. 10 seconds), the supernatant removed, and 60 μl EtOH added. The particles with PEI-precipitated DNA-1 were washed twice in 60 μl of EtOH. The particles were centrifuged, the supernatant discarded, and the particles were resuspended in 45 μl water. To attach the second DNA (DNA-2), precipitation using TFX-50 was used. The 45 μl of particles/DNA-1 suspension was briefly sonicated, and then 5 μl of 100 ng/μl of DNA-2 and 2.5 μl of TFX-50 were added. The solution was placed on a rotary shaker for 10 minutes, centrifuged at 10,000 g for 1 minute. The supernatant was removed, and the particles resuspended in 60 μl of EtOH. The solution was spotted onto macrocarriers and the gold particles onto which DNA-1 and DNA-2 had been sequentially attached were delivered into scutellar cells of 10 DAP Hi-II immature embryos using a standard protocol for the PDS-1000. For this experiment, the DNA-1 plasmid contained a UBI::RFP::pinII expression cassette, and DNA-2 contained a UBI::CFP::pinII expression cassette. Two days after bombardment, transient expression of both the CFP and RFP fluorescent markers was observed as numerous red & blue cells on the surface of the immature embryo. The embryos were then placed on non-selective culture medium and allowed to grow for 3 weeks before scoring for stable colonies. After this 3-week period, 10 multicellular, stably-expressing blue colonies were observed, in comparison to only one red colony. This demonstrated that PEI-precipitation could be used to effectively introduce DNA for transient expression while dramatically reducing integration of the PEI-introduced DNA and thus reducing the recovery of RFP-expressing transgenic events. In this manner, PEI-precipitation can be used to deliver transient expression of BBM and/or WUS2.

[0180] For example, the particles are first coated with UBI::BBM::pinII using PEI, then coated with UBI::moPAT~YFP using TFX-50, and then bombarded into scutellar cells on the surface of immature embryos. PEI-mediated precipitation results in a high frequency of transiently expressing cells on the surface of the immature embryo and extremely low frequencies of recovery of stable transformants (relative to the TFX-50 method). Thus, it is expected that the PEI-precipitated BBM cassette expresses transiently and stimulates a burst of embryogenic growth on the bombarded surface of the tissue (i.e. the scutellar surface), but this plasmid will not integrate. The PAT~GFP plasmid released from the Ca^{++}/gold particles is expected to integrate and express the selectable marker at a frequency that results in substantially improved recovery of transgenic events. As a control treatment, PEI-precipitated particles containing a UBI::GUS::pinII (instead of BBM) are mixed with the PAT~GFP/Ca^{++} particles. Immature embryos from both treatments are moved onto culture medium containing 3 mg/l bialaphos. After 6-8 weeks, it is expected that GFP+, bialaphos-resistant calli will be observed in the PEI/BBM treatment at a much higher frequency relative to the control treatment (PEI/GUS).

[0181] As an alternative method, the BBM plasmid is precipitated onto gold particles with PEI, and then introduced into scutellar cells on the surface of immature embryos, and subsequent transient expression of the BBM gene elicits a rapid proliferation of embryogenic growth. During this period of induced growth, the explants are treated with *Agrobacterium* using standard methods for maize (see Example 1), with T-DNA delivery into the cell introducing a transgenic expression cassette such as UBI::moPAT~GFPm::pinII After co-cultivation, explants are allowed to recover on normal culture medium, and then are moved onto culture medium containing 3 mg/l bialaphos. After 6-8 weeks, it is expected that GFP^{+}, bialaphos-resistant calli will be observed in the PEI/BBM treatment at a much higher frequency relative to the control treatment (PEI/GUS).

[0182] It may be desirable to "kick start" callus growth by transiently expressing the BBM and/or WUS2 polynucleotide products. This can be done by delivering BBM and WUS2 5'-capped polyadenylated RNA, expression cassettes containing BBM and WUS2 DNA, or BBM and/or WUS2 proteins. All of these molecules can be delivered using a biolistics particle gun. For example 5'-capped polyadenylated BBM and/or WUS2 RNA can easily be made in vitro using Ambion's mMessage mMachine kit. RNA is co-delivered along with DNA containing a polynucleotide of interest and a marker used for selection/screening such as Ubi::moPAT~GFPm::PinII. It is expected that the cells receiving the RNA will immediately begin dividing more rapidly and a large portion of these will have integrated the agronomic gene. These events can further be validated as being transgenic clonal colonies because they will also express the PAT~GFP fusion protein (and thus will display green fluorescence under appropriate illumination). Plants regenerated from these embryos can then be screened for the presence of the polynucleotide of interest.

Example 4

Excision of Genes Encoding Cell Proliferation Factors

[0183] a. Rab17::CRE

[0184] The following T-DNA was constructed: RB-Ubi pro-loxP::Rab17 pro-attB1::Cre-attB2::PinII+NOS::ZmWUS2::PinII+Ubi pro::ZmBBM::PinII-loxP::YFP::PinII+Ubi pro::moPAT::PinII-LB. As a control, a T-DNA containing Ubi pro::moPAT::PinII was constructed. These T-DNA are introduced into immature embryos (approximately 0.8-2.5 mm in length) of the maize inbred PHH5G using standard *Agrobacterium*-mediated transformation methods. Non-transformed immature embryos of this inbred swell and initiate a small volume of callus cells, but proliferation does not occur on media compositions typically used for maize tissue culture (for example, 605J media, which comprises 4.3 g/l MS salts, 0.6 g/l Shenk & Hildebrand vitamins, 100 mg/l calcium chloride, 275 mg/l ammonium sulfate, 275 mg/l ammonium sulfate, 240 mg/l potassium phosphate, 100 mg/l magnesium sulfate, 3.4 g/l potassium nitrate, 1.8 mg/l boric acid, 6 mg/l manganese sulfate, 0.15 mg/l sodium molybdate, 0.5 mg/l potassium iodide, 22 mg/l disodium EDTA, 17 mg/l ferrous sulfate, 3.4 mg/l silver nitrate, 1 g/l L-proline, 0.2 mg/l nicotinic acid, 0.4 mg/l thiamine, 0.2 mg/l pyridoxine, 0.8 mg/l glycine, 100 mg/l carbenicillin, 0.8 mg/l 2-4D, 1.2 mg/l dicamba, 0.3 g/l casein hydrosylate, 20 g/l sucrose, 0.6 g/l glucose, and 6 g/l TC agar, pH 5.8). Likewise, PHH5G immature embryos transformed with Ubi pro::moPAT::PinII alone do not produce healthy, growing callus, irrespective of whether bialaphos selection is provided. Thus, no transformed events were produced after introducing Ubi pro::moPAT::PinII alone (or with Ubi pro::moPAT::PinII+Ubi pro::YFP::PinII) In contrast, when the genes encoding cell proliferation factors (BBM and WUS2)+Ubi pro::moPAT::PinII were introduced into PHH5G immature embryos, vigorously-growing callus transformants were recovered from 45% of the treated embryos. To remove the genes encoding cell proliferation factors, the Rab17 promoter can be induced through exposure to either 20 mM abscisic acid (ABA), 20-30% sucrose, or desiccation. In this experiment, callus was placed on dry filter papers for three days to induce excision, and then transferred to regeneration medium. If callus was not treated to induce the expression of Cre recombinase, excision of the genes encoding cell proliferation factors did not occur and viable plantlets were not regenerated. However, for events that were taken through the desiccation treatment, Cre excision occurred in over 90% of single copy events (activating YFP) and subsequent regeneration was not inhibited. Transgenic plants were screened using combinations of PCR primers designed to detect the presence of the Ubi pro-loxP::YFP junction formed as a result of excision, and moPAT (not effected by excision), and the absence of Cre, WUS2 and BBM. Plants in which excision was complete were grown to maturity and were either selfed or out-crossed to wild-type plants. Transgenic progeny seed were readily identified through the yellow fluorescence phenotype and plants were easily tracked through either BASTA resistance or yellow fluorescence. PCR analysis in both the T1 and T2 generations indicated that only the excised locus was present in a single genomic copy and that no *Agrobacterium* plasmid backbone was present.

[0185] Both FLP and Cre recombinase have been successfully used to excise genes encoding cell proliferation factors before regeneration. The following two constructs represent examples of how the recombinases can be used for controlled excision:

PHP32371-FLP/FRT

[0186] RB-Ubi-FRT1::CFP::PinII-attB4+Rab17 Pro-attB1::FLP-attB2::PinII+Nos::ZmWUS2::PinII+Ubi::ZmBBM::PinII-FRT1::YFP::PinII+Ubi::moPAT::PinII-LB

[0187] The T-DNA sequence of PHP32371 is set forth in SEQ ID NO: 110.

PHP35648-Cre/LoxP

[0188] RB-Ubi-LoxP::CFP::PinII-attB4+Rab17 Pro-attb1::Cre-attB2::PinII+Nos::ZmWUS2::PinII+Ubi::ZmBBM::PinII-LoxP::YFP::PinII+Ubi::MOPAT::PinII-LB

[0189] The T-DNA sequence of PHP35648 is set forth in SEQ ID NO: 111.

[0190] For both recombinases, expression was controlled by the Rab17 promoter (Vilardell et al. (1991) *Plant Mol. Biol* 17:985-993) with the attb1 site.

[0191] For both constructs, transgenic callus events were readily recovered, and both constructs worked well for excision of the expression cassettes comprising genes encoding cell proliferation factors (see Table 2). Of the total number of calli exposed to the 3-day desiccation treatment, 61% (Cre) and 29% (FLP) of the resultant plants exhibited a normal wild-type phenotype. As confirmation of excision, PCR analysis in both the T1 and T2 generations indicated that only the excised locus was present in a single genomic copy and that no *Agrobacterium* plasmid backbone was present.

TABLE 2

Desiccation-induced excision of the recombinase, BBM & WUS expression cassettes prior to regeneration.

	# of Callus events exposed to desiccation	# of events with normal T0 plant phenotype	# of T0 plant-lets analyzed using PCR	# of single copy plants	# with a totally-excised DevGene package
PHP35648	180	110 (61%)	168	94 (56%)	81 (86%)
PHP32371	118	34 (29%)	75	51 (68%)	31 (61%)

[0192] Additional constructs that utilize Cre/LoxP were generated.

PHP46446: RB-LoxP-Rab17 Pro-attB1::Cre-attB2::PinII+Nos::Zm-WUS2::PinII::GZ-W64A Term-attB2+Ubi::ZmBBM::PinII-LoxP-LB

PHP48733: RB-LoxP-Rab17 Pro-attB1::Cre-attB2::PinII+Nos:ZmWUS2::PinII+Ubi::ZmBBM::PinII-LoxP-LB

[0193] The T-DNA sequences of PHP46446 and PHP48733 is set forth in SEQ ID NO: 112 and 113, respectively.

[0194] Introduction of PHP35648, PHP48733, or PHP46446 into PHH5G immature maize embryos via *Agrobacterium* resulted in a transformation frequency of 46%, 67%, or 37%, respectively (see Table 3).

TABLE 3

Transformation of PHH5G immature maize embryos with maize BBM and WUS2 cell proliferation factors.

Construct	No. of ears	No. of embryos	No. of callus events	Transformation frequency at callus level
PHP35648	14	589	268	45.5
PHP48733	14	584	389	66.6
PHP46446	14	547	203	37.1

[0195] The use of the PHP35648, PHP48733, PHP46446, and PHP32371 constructs (all of which comprised the Rab17 promoter (Vilardell et al. (1991) *Plant Mol. Biol* 17:985-993) with the attb1 site regulating the expression of the recombinase), did not result in frequent premature excision of the cell proliferation factor genes, similar to the results presented in Example 1 with the PHP31004 construct.

[0196] b. Tetracycline-Inducible CRE

[0197] A 35S promoter in which three tetracycline operator sequences (Top3) have been introduced in proximity to the TATA box (Gatz et al. (1992) *Plant J* 2:397-404) was operably linked to the CRE structural gene in the following T-DNA which also includes an expression cassette for the tetracycline repressor (TETR), BBM, WUS2, and moPAT, as follows:

RB-loxP-35S::Top3::CRE::PinII+Ubi pro::TETR::PinII+NOS::ZmWUS2::PinII+UBI::ZmBBM::PinII–loxP+UBI::moPAT::PinII-LB

[0198] After *Agrobacterium*-mediated transformation of 12 DAP PH581 immature embryos, followed by 6 weeks of selection on 3 mg/l bialaphos, embryos into which the control T-DNA was introduced (RB-UBI::moPAT::PinII-LB) produced transformed events at a 1% frequency. In contrast, when the above T-DNA containing ZmBBM & ZmWUS2 was transformed into immature embryos harvested from the same PH581 ears, transgenic calli were recovered at a 15% frequency. Before regenerating plantlets, callus is moved onto medium containing 0.5 mg/l tetracycline for 1 week to induce CRE-mediated excision of CRE, WUS and BBM expression cassettes. Glufosinate ammonium-resistant plants are then readily regenerated.

Example 5

Control of BBM and WUS Expression with Regulated Promoters to Increase Transformation Frequencies

[0199] a. OLE PRO::BBM

[0200] In the inbred PH581 maize line, the introduction of UBI::ZmBBM+NOS:ZmWUS2 increased transformation frequencies from <1% in the control treatment (UBI PRO::moPAT::PinII alone) to 15%. However, such strong overexpression of BBM negatively affects the regeneration of plantlets. Therefore, an oleosin promoter having high levels of expression in callus, with little to no activity during vegetative growth was used to express BBM. When OLE::ZmBBM::PinII+NOS::ZmWUS2::PinII was introduced into PH581 on a first T-DNA and UBI PRO::moPAT::PinII was introduced into the same cells on a second T-DNA, callus transformants were recovered at a 25% frequency. Normal, fertile plants were regenerated and crossed to wild-type

PH581. T1 progeny in which the cell proliferation gene locus had segregated away from the UBI PRO::moPAT::PinII locus were readily recovered.

[0201] b. Tetracycline-Inducible BBM and WUS2

[0202] A 35S promoter in which three tetracycline operator sequences have been introduced in proximity to the TATA box (Gatz et al. (1992) *Plant J* 2:397-404) is operably linked to both the BBM and WUS2 genes, and these expression cassettes are put into a T-DNA along with an expression cassette for the tetracycline repressor (TETR) as follows.

[0203] RB-35S-Top3::ZmBBM::PinII+35S-Top3::ZmWUS2::PinII+UBI::moPAT::PinII-LB

[0204] Following *Agrobacterium*-mediated transformation of Hi-II immature maize embryos, the embryos are transferred to selection medium 560R with 3 mg/l bialaphos+/−0.5 mg/l tetracycline. In the control treatment in which only the UBI::moPAT::PinII expression cassette is introduced, the transformation frequency is typically around 5-10%. For embryos in which the inducible BBM and WUS2 genes are introduced, transformation frequency is expected to be greatly increased upon the addition of tetracycline to the medium.

Example 6

Regulated Expression of BBM and WUS2 for Re-Transformation

[0205] Stable transgenic events in PHH5G are produced that express ZmBBM and ZmWUS2 in a regulated fashion, for example, having BBM and WUS2 under the control of the OLE and NOS promoters, respectively, or having them being driven by a tetracycline-inducible promoter. Immature embryos are then harvested and re-transformed using *Agrobacterium* to deliver UBI::moPAT::PinII PHH5G embryos not expressing BBM and WUS2 (i.e. wild-type control embryos) produce no transformation events. However, embryos expressing OLE PRO::ZmBBM::PinII and NOS PRO::ZmWUS2::PinII are expected to produce a much higher frequency of bialaphos-resistant events. Regulated expression of the genes encoding cell proliferation factors is expected to enhance the regeneration frequency of normal fertile plants, and the cell proliferation gene locus should readily segregate away from the newly-generated "trait" locus (represented here by the UBI::moPAT::PinII locus). Likewise, when the expression of tetracycline-inducible genes encoding cell proliferation factors are stimulated by the addition of 0.5 mg/l tetracycline, *Agrobacterium*-mediated transformation to deliver the RB-UBI::moPAT::PinII-LB T-DNA is expected to result in enhanced transformation frequencies.

Example 7

Two T-DNA Co-Transformation to Deliver Genes Encoding Cell Proliferation Factors and Trait Genes Separately

[0206] An *Agrobacterium* was modified to contain two engineered plasmids, each containing a separate T-DNA. T-DNA-1 was PHP35648 (see Example 4 for description), and T-DNA-2 (PHP41877) contained RB-attB4-UBI::moPAT::PinII+UBI-FRT1::RFP::PinII-attB1+UBI::GAT::PinII-attB2-FRT87-attB3-LB (GAT=glyphosate-N-acetyltransferase) representing the T-DNA that will contain the desired stack of trait genes). *Agrobacterium*-mediated transformation of PHH5G immature maize embryos was followed by glyphosate selection. Only embryos that have integrated T-DNA-1 grew since growth in culture for PHH5G only occurred when the ZmWUS2 and ZmBBM genes were present. Only embryos containing T-DNA-2 were glyphosate-resistant and exhibited red fluorescence. Thus, only embryos that were co-transformed with both T-DNAs grew on glyphosate.

Example 8

Identification of BBM Motifs

[0207] Fifty genes from different plant species were identified through a homology search using the maize BBM amino acid sequence (SEQ ID NO: 10) queried against annotated protein sequences (see FIG. **1**). The gene structure and sequences of these BBM homologs were manually inspected and compared with EST/cDNA alignments whenever possible. The fifty polypeptides are set forth in SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 67, and 70-104. To systematically identify possible motifs within the BBM homologs, protein sequences of these fifty homologs were submitted to the MEME web server, available on the world wide web at meme.nbcr.net/meme4_1/cgi-bin/meme.cgi, with the following specific parameters:

[0208] Number of different motifs: 20

[0209] Minimum motif width: 5

[0210] Maximum motif width: 300

[0211] Minimum number of sites: 5

[0212] Default values were applied for all other parameters. The raw results from MEME were manually compared with multiple sequence alignments generated by clustalw. Only those candidates showing good consensus with the sequence alignments were considered as motifs for further analysis.

[0213] The fifty genes were subjected to a phylogenetic analysis and a total of six subgroups were identified, including BBM, PLT3, PLT1/2, AIL6/7, AIL1, and ANT (see FIG. **1**). FIG. **3** depicts all 50 sequences with each of the motifs that were identified using the MEME web server. FIG. **2** provides the motif consensus sequences along with alignments of the various polypeptides used by the MEME web server to generate the consensus motif. With a few exceptions, motifs 1-6, as defined immediately hereinbelow, are present in all 50 genes. This includes motifs 1-3 (SEQ ID NOs 48-50, respectively), which represent the two AP2 domains and a sequence linking the two domains (linker sequence). Motif 4, with the consensus sequence of PK[L/V][E/A][D/N]FLG (SEQ ID NO: 51) is amino-terminal to the two AP2 domains. Motif 5 (SEQ ID NO: 52) flanks the two AP2 domains on the carboxy terminal end of the polypeptides. Near the amino terminus of the polypeptides is motif 6, with the consensus sequence of NWL[G/S]FSLSP (SEQ ID NO: 53).

[0214] There were motifs that were relatively specific for the BBM subgroup of the homologous sequences (referred to herein as BBM polypeptides). An alignment of the BBM polypeptides can be found in FIG. **4**. Motif 7 is found in all BBM polypeptides at the amino terminus of the polypeptide and has the consensus sequence of [G/E]LSMIK[T/N]WLR (SEQ ID NO: 54). Another motif that is present in all of the BBM polypeptides except for the polypeptides from *Brassica* and from *Arabidopsis*, is Motif 10. Motif 10 has the consensus sequence of WCK[Q/P]EQD (SEQ ID NO: 57) and is located downstream of the AP2 domains.

[0215] There are three more motifs specific to the BBM group of polypeptides, including Motif 15 (SEQ ID NO: 59) which appears only in BBM orthologs, but not in the monocot BBM2 polypeptides; a monocot specific motif (Motif 19; SEQ ID NO: 60); and a general BBM specific motif (Motif 14; SEQ ID NO: 58), which appears in BBM homologs except for the *Brassica* and legume branch.

[0216] FIG. **5** provides a summary of the motif structure of the BBM homologs. The amino terminal motifs 4 and 6 and the AP2 flanking motif 5 distinguish the BBM homologous sequences from other two AP2 domain-containing homologs, such as WRI, AP2, and RAP2.7. Therefore, motifs 1-6 can be considered as core BBM/PLT family motifs. Many subgroups of the BBM/PLT family (BBM, PLT1/2, AIL1, and ANT) also have a carboxy-terminal motif (motif 8; SEQ ID NO: 55) and the third amino terminal motif (motif 9; SEQ ID NO: 56).

[0217] The BBM polypeptides all have one additional motif (motif 7; SEQ ID NO: 54) in the amino terminus, and all but the *Brassica* and *Arabidopsis* BBM homologs have an AP2 downstream motif (motif 10; SEQ ID NO: 57). Some other BBM/PLT family members (e.g., monocot AIL1) may have a similar motif as motif 7, but none of them also have motif 9. Motif 10 appears only in BBM polypeptides. In summary, the MEME predicted motifs 1-10 can be regarded as BBM polypeptide motifs. All monocot BBM polypeptides (corn, sorghum, and rice) also have motif 14, 15, and 19 (see FIG. **3**). Some dicot BBM polypeptides and the second monocot BBM group (BBM2) have one or two of these motifs, but none have all three motifs.

Example 9

Use of Maize BBM and WUS2 to Increase Transformation in Rice

[0218] a. *Oryza sativa* L. ssp. *Indica*

[0219] Mature and immature Indica embryos were transformed using *Agrobacterium* with a T-DNA comprising the PHP46911 plasmid (control for immature embryos; see immediately hereinbelow for a description), the PHP32269 plasmid (control for mature embryos; see immediately hereinbelow for a description), or PHP35648.

PHP46911: RB-CaMV35S::Hyg::Nos term+Ubi-FRT1::Zs-yellow1::PinII-FRT87-LB PHP32269: RB-Ubi::PMI::PinII+Ubi::mo-PAT~Zs-yellow1::PinII-LB

(PMI=phosphomannose isomerase)

[0220] i. Immature Embryo Transformation

[0221] Immature embryos of proprietary Indica strain 851G were transformed using the methods disclosed in International Application Publication No. WO/1995/06722 and Hiei and Komari (2006) *Plant Cell, Tissue and Organ Culture* 85:271-283, each of which is herein incorporated by reference in its entirety. Results are shown hereinbelow in Table 4.

TABLE 4

Transformation events in *Oryza sativa* L. ssp. *Indica* 851G immature embryos infected with *Agrobacterium* containing PHP35648.

Embryo No.	No. of Pieces/Embryo	Total No. of Events/Embryo
1	2	1 (100%)
2	3	1 (100%)
3	6	3 (300%)
4	2	2 (200%)
5	3	3 (300%)
6	3	2 (200%)
7	6	2 (200%)
8	7	2 (200%)
9	11	6 (600%)
10	3	3 (300%)
11	5	3 (300%)
12	3	3 (300%)
TOTAL	54	31 (258%)

[0222] In total, infection of 12 immature Indica embryos with *Agrobacterium* containing the PHP35648 plasmid resulted in 31 transformation events, a transformation frequency of 258% events/embryo. The 31 events were derived from 54 pieces of embryo, for a transformation frequency of 57% events/embryo pieces. On the other hand, the infection of nine embryos with *Agrobacterium* containing PHP46911 resulted in only one single transformation event and an overall transformation frequency of 11%.

[0223] ii. Mature Embryo Transformation

[0224] Mature embryos of Indica strains IRV95 and 851G were transformed using the following protocol. Healthy rice seeds were dehusked and soaked in 50 ml of sterile water with a drop of Tween 20 for 5 minutes. The seeds were sterilized with 75% ethanol for 2-3 minutes, followed by a soak in 50 ml sodium hypochlorite and a drop of Tween 20 for 15-20 minutes. The seeds were rinsed and then callus was initiated in callus induction medium (4.3 g/l MS salts, 10 ml/l B5 vitamins (100×), 2 mg/l 2,4-D, 500 mg/l L-proline, 30 g/l sucrose, 0.3 g/casein hydrolysate, 3 g/l Gelrite (added after bringing to volume with D-I H_2O and adjusting pH to 5.8) under continuous light at 32° C. for 12 days.

[0225] Established callus was transformed using *Agrobacterium* by incubating the callus with the *Agrobacterium* for 10-15 minutes. The *Agrobacterium* solution was then decanted and 12-15 seeds were placed onto a filter paper disk that had been pre-moistened with 0.5 ml of AAM medium (50 ml/l AA macro elements (20×), 10 ml/l AA microelements (B5 microelements; 100×), 10 ml/l AA vitamins (B5 vitamins; 100×), 5 ml/l Fe-EDTA-B5 (200×), 1 mg/L 2,4-D, 100 ml/l amino acids, 68.5 g/l sucrose, 36 g/l glucose, 500 mg/l cas amino acid at pH 5.2) containing 50 μM acetosyringone. The seeds and pre-moistened filter papers were cultured in the dark at 21° C. for 72 hours in ACCM medium (4.3 g/l MS salts, 10 ml/l B5 vitamins (100×), 2 mg/l 2,4-D, 20 g/l sucrose, 10 g/l glucose, 0.5 g/l casein hydrolysate, 3 g/l Gelrite (added after bringing to volume with D-I H_2O and adjusting pH to 5.2) containing 200 μM acetosyringone. The calli were washed and then transferred to resting ASM medium (100 ml/l 580S major salts (10×), 10 ml/l 580S minor salts (100×), 5 ml/l 580S FeETDA-L (200×), 5 ml/l 580S vitamins (200×), 100 mg/l myo-inositol, 300 mg/l casein hydrolysate, 30 g/l maltose, 2 mg/l 2,4-D, 500 mg/l L-proline, 0.5 g/l MES buffer, 8 g/l agar (added after bringing to volume with D-I H_2O and adjusting pH to 5.8) containing 250 mg/l carbenicillin for 15 days. Following the 15 day incubation, the calli were transferred to selection medium (100 ml/l 580S major salts (10×), 10 ml/l 580S minor salts (100×), 5 ml/l 580S FeEDTA-L (200×), 5 ml/l 580S vitamins (200×), 100 mg/l myo-inositol, 300 mg/l casein hydrolysate, 30 g/l sucrose, 2 mg/l 2,4-D, 500 mg/l L-proline, 0.5 g/l MES buffer, 8 g/l agar (added after bringing to volume with D-I H_2O and adjusting pH to 5.8) with 200 mg/l carbenicillin and 2 mg/l bialaphos and subcultured every 15 days until transformation events arose.

[0226] The event was then dessicated on filter paper at 28° C. for 48 hours to excise the developmental genes. Dessicated events were identified based on the expression of Zs-yellow visualized under the microscope. The dessicated event was transferred to regeneration medium (100 ml/l N6 major salts (10×), 10 ml/l FeEDTA (100×), 10 ml/l B5 minor salts (100×), 10 ml/l B5 vitamins (100×), 1 mg/l 1-naphthalene acetic acid, 3 mg/l 6-benzyl amino purine, 30 g/L maltose, 0.3 g/l proline, 0.3 g/l vitamin assay casamino acids, 4 g/l agarose type 1, 30 mg/l glutamine (added after adjusting pH to 5.8 and sterilization) and grown at 32° C. under light. After 1-1.5 months, green shoots emerged from the callus and it was transferred to rooting medium (100 ml/l MS major salts (10×), 10 ml/l FeEDTA (100×), 10 ml/l MS minor salts (100×), 10 ml/l MS vitamins (100×), 2 mg/l indole-3-butyric acid, 15 g/l sucrose, 1 g/l vitamin assay casamino acids, 10×AA amino acid at pH 5.8). After another 15-20 days, the rooted plants are hardened in Y-medium (1.25 ml/l Stock A (9.14 g/100 ml ammonium nitrate (HIMEDIA RM5657)), 1.25 ml/l Stock B (4.03 g/100 ml sodium hydrogen phosphate (HIMEDIA 58282)), 1.25 ml/l Stock C (7.14 g/100 ml potassium sulfate (HIMEDIA 29658-4B)), 1.25 ml/l Stock D (8.86 g/100 ml calcium chloride (HIMEDIA C5080)), 1.25 ml/l Stock E (3.234 g/100 ml magnesium sulfate (HIMEDIA RM683)), 1.25 ml/l Stock F (15 mg/100 ml magnesium chloride tetrahydrate (HIMEDIA 10149), 6.74 mg/100 ml ammonium molybdate (HIMEDIA 271974), 9.34 mg/100 ml boric acid (SIGMA 136768), 0.35 mg/100 ml zinc sulfate helpta hydrate (HIMEDIA RM695), 0.31 mg/100 ml copper sulfate hepta hydrate (HIMEDIA C8027), 0.77 mg/100 ml ferric chloride hexa hydrate (SIGMA 236489), 119 mg/100 ml citric acid monohydrate (HIMEDIA C4540)) at pH 5.2.

[0227] Results are shown hereinbelow in Table 5.

TABLE 5

Transformation events in *Oryza sativa* L. ssp. Indica 851G and IRV95 mature embryo-derived callus.

Seed No	Variety	Construct	No. of infected calli	No. of events	% of events	No. of events regenerated	% of regenerated events/infected calli
1	851G	PHP35648	100	8	8.00%	5	5.00%
		PHP32269	50	1	2.00%	0	0.00%
2	851G	PHP35648	130	18	13.85%	N/A[a]	N/A
		PHP32269	50	1	2.00%	N/A	N/A
3	IRV95	PHP35648	128	20	15.63%	N/A	N/A
		PHP32269	50	1	2.00%	N/A	N/A

[a] N/A data not available;
calli are currently being dessicated, so no data on number or percentage of regenerated events are available

[0228] b. *Nipponbare* Rice (cv. *Kitake*)

[0229] Callus was initiated from mature embryos of *Oryza sativa*, var. *Nipponbare*, cv. *Kitake*, and established callus was transformed using *Agrobacterium* strain LBA4404 containing UBI::ZmBBM::PinII and NOS PRO::ZmWUS2::PinII between the T-DNA borders. Callus culture medium for rice consisted of N6 salts, Eriksson's vitamins, 0.5 mg/l thiamine, 2 mg/lo 2,4-D, 2.1 g/l proline, 30 g/l sucrose, 300 mg/l casein hydrolysate, 100 mg/l myo-inositol, and 3 g/l gelrite at pH 5.8. Five days after Agro-infection, callus was observed under an epifluorescent dissecting microscope. For calli that were transformed with UBI::ZS-GREEN::PinII alone, all the visible fluorescent foci were single cells, with a few possible 2-4 cell foci. When callus was transformed with NOS::ZmWUS2::PinII+UBI::ZmBBM::PinII+UBI::ZS-GREEN::PinII and observed 5 days later, numerous rapidly-growing, green-fluorescent, multicellular colonies were present.

Example 10

The Rice, Sorghum and Grape BBM Genes Increase Transformation Frequency in Maize

[0230] Growth assays were performed to test whether BBM genes from various species would stimulate growth in maize. For these experiments, 10-13 DAP embryos of the genotype PH581 were bombarded with a first plasmid containing a UBI PRO::moPAT~GFP::pinII expression cassette plus either a plasmid containing 35S::GUS::pinII (control treatment) or a BBM gene driven by the ubiquitin promoter. To attach the DNAs to gold particles, a 25 μl aliquot of 0.6 μm particles (0.01 mg/μl) was added to fresh tubes before attaching DNA. To attach uncoated DNA, the particles were pulse-sonicated, then 500 ng of each DNA (in 5 μl water) was added, followed by mixing (pipetting up and down a few times with a Pipetteman). Then 2.5 μl of TFX-50 was added, and the solution was placed on a rotary shaker for 10 minutes. After centrifugation at 10,000 g for 1 minute, the supernatant was removed, and the particles were resuspended in 60 μl of EtOH, followed by a 10 minute incubation. The particles were spun briefly (i.e., 10 seconds), the supernatant removed, and 60 μl EtOH added. The solution was spotted onto macrocarriers and the gold particles onto which DNA had been attached were delivered into scutellar cells of 10-13 DAP immature embryos using a standard protocol for the DuPont PDS-1000 Helium Gun. After 4-5 weeks on culture medium, the embryos were examined and the number of GFP-expressing multicellular colonies were counted.

[0231] a. OsBBM

[0232] Based on the rice BBM genomic sequence (SEQ ID NO: 117), TIGR software was used to predict intron splicing and the resultant cDNA sequence (OsBBM (MOD1) is set forth in SEQ ID NO: 118). A plasmid containing an expression cassette for the rice BBM (MOD1) gene (UBI PRO::OsBBM (MOD1)::PinII) was co-delivered with UBI::moPAT~GFP::PinII into 13 DAP PH581 immature embryos using the particle gun. When the UBI PRO::moPAT~GFP::pinII cassette was introduced with 35S::GUS, few multicellular growing sectors were observed (see Tables 6-10). When UBI::ZmBBM::PinII was introduced along with UBI::moPAT~GFP::PinII, a stimulation of growth was observed as indicated by the total number of growing multicellular colonies observed as well as the number of embryos with multiple growing colonies. Despite many conserved amino acid motifs between the encoded maize protein and the protein encoded by the predicted OsBBM (MOD1) cDNA, when the rice expression cassette UBI::OsBBM (MOD1)::PinII, was introduced along with the moPAT~GFP cassette, no stimulation of growth was observed relative to the control treatment (35S::GUS) (see Tables 6 and 7). Based on a comparison of the maize and rice MOD1 amino acid sequences, and a more careful analysis of the rice genomic sequence, it was determined that the TIGR software failed to predict the splicing around a 9-bp exon that encodes the amino acids VYL in the first AP2 domain. Upon including this 9 bp exon in a re-synthesized rice cDNA (OsBBM (MOD2); set forth in SEQ ID NO: 120), and introducing this in the expression cassette UBI::OsBBM (MOD2)::PinII, a growth stimulation similar to that observed for the maize BBM gene was observed (Table 7, 8, 9 and 10).

TABLE 6

Number of green-fluorescent multicellular colonies six weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

	GFP + Colonies/Bombarded Embryo											Total Number of Multicellular
TRT	0	1	2	3	4	5	6	7	8	9	10	Colonies
35S::GUS	44											0
UBI::ZmBBM	15	10	5	4	3	1	1			1		25
UBI::OsBBM (MOD1)	42											0
OLE::ZmBBM	14	16	6	1								14
OLE::ZmANT	44											0

TABLE 7

Number of green-fluorescent multicellular colonies five weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

	GFP + Colonies/Bombarded Embryo									Total Number of Multicellular
TRT	0	1	2	3	4	5	6	7	8	Colonies
35S::GUS	70	5	0	3						8
UBI::ZmBBM	19	24	17	7	3	1				52
UBI::OsBBM (MOD1)	70	4	2							6
UBI::OsBBM (MOD2)	28	29	11	3	1	1				45
OLE::ZmBBM	28	24	11	9	2	1	2			49
OLE::ZmANT	55	16	1	1	1					19

TABLE 8

Number of green-fluorescent multicellular colonies five weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

	Number of GFP + Colonies per Scored Embryo							Total Number of Multicellular
Treatment	0	1	2	3	4	5	6	Colonies
35S::GUS	70	5	0	3	0	0	0	8
UBI::ZmBBM	19	24	17	7	3	1	0	52
UBI::OsBBM (MOD2)	28	29	11	3	1	1	0	73
OLE::ZmBBM	28	24	11	9	2	1	2	49
OLE::ZmANT	55	16	1	1	1	0	0	19

TABLE 9

Number of green-fluorescent multicellular colonies five weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

	Number of GFP + Colonies per Scored Embryo							Total Number of Multicellular
Treatment	0	1	2	3	4	5	6	Colonies
35S::GUS	61	6	1	0	0	0	0	7
UBI::ZmBBM	21	29	12	3	2	0	0	46

TABLE 9-continued

Number of green-fluorescent multicellular colonies five weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

	Number of GFP + Colonies per Scored Embryo							Total Number of Multicellular
Treatment	0	1	2	3	4	5	6	Colonies
UBI::OsBBM (MOD2)	27	29	5	2	0	1	0	37
UBI::VvBBM	32	21	6	0	1	0	0	28
UBI::ZmBBM (genomic)	9	36	13	6	3	0	0	58

TABLE 10

Number of green-fluorescent multicellular colonies five weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

	GFP + Colonies/Scored Embryo											
TRT	0	1	2	3	4	5	6	7	8	9	10	Total Number of Multicellular Colonies
35S::GUS	80	11										11
UBI::ZmBBM	43	28	13	5	2							48
UBI::OsBBM (MOD2)	45	32	11	3								46
UBI::SbBBM (MOD1)	81	10										10

[0233] b. SbBBM

[0234] Based on the sorghum genomic BBM sequence (SEQ ID NO: 69), TIGR software was used to predict intron splicing and the resultant cDNA sequence (SbBBM (MOD1) is set forth in SEQ ID NO: 3). A plasmid containing an expression cassette for the sorghum BBM (MOD1) gene (UBI PRO::SbBBM (MOD1)::PinII) was co-delivered with UBI::moPAT~GFP::PinII into 13 DAP PH581 immature embryos using the particle gun. When the UBI PRO::moPAT~GFP::PinII cassette was introduced with 35S::GUS, few multicellular growing sectors were observed (see Table 10). Unlike UBI::ZmBBM and UBI::OsBBM (MOD2), which in this experiment produced a similar positive growth stimulation, UBI::SbBBM (MOD1)::PinII failed to simulate growth. Assuming there was some unknown defect in the SbBBM (MOD1) synthetic cDNA, the sorghum genomic BBM was cloned using PCR and sequenced to verify fidelity. In an earlier experiment, the maize genomic BBM (SEQ ID NO: 116) was placed behind the UBI promoter and when compared to the UBI::ZmBBM cDNA construct it produced a similar degree of growth stimulation (Table 9). Using the genomic sorghum clone [UBI::SbBBM (GEN)], a similar level of growth stimulation was also observed (Tables 11 and 12).

TABLE 11

Number of green-fluorescent multicellular colonies five weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

	GFP + Colonies/Scored Embryo									Total Number of Multicellular
Treatment	0	1	2	3	4	5	6	7	8	Colonies *
35S::GUS	57	3								3
UBI:VvBBM-NoVYL	57	3								3
UBI:VvBBM	36	15	4	1	1	1				22
UBI:SbBBM (Genomic)	10	19	11	11	4	3	2			50
UBI:ZmBBM	12	18	8	10	4	3	1		1	45

TABLE 12

Number of green-fluorescent multicellular colonies five weeks after bombardment with UBI::moPAT~GFP plus the plasmid indicated in each treatment.

	GFP + Colonies/Scored Embryo						Total Number of Multicellular
TRT	0	1	2	3	4	5	Colonies
35S::GUS	60						0
UBI::ZmBBM	19	18	11	7	4	1	41
UBI::SbBBM (Genomic)	20	15	14	6	5		60
UBI::VvBBM	46	11	3				14
UBI::VvBBM-No VYL	60						0

[0235] c. VvBBM

[0236] A nucleotide sequence was derived that provided good codon usage for maize, but expressed the amino acid sequence of a grape BBM (VvBBM; SEQ ID NO: 5). A plasmid containing an expression cassette for a synthetic grape BBM gene (UBI PRO::VvBBM::PinII) was co-delivered with UBI::moPAT~GFP::PinII into 10 DAP PH581 immature maize embryos using the particle gun. When the UBI PRO::moPAT~GFP::PinII cassette was introduced alone, no (Table 12) or very few (Tables 9 and 11) multicellular growing sectors were observed. When UBI::VvBBM::PinII+UBI::moPAT~GFP::PinII were co-delivered, numerous RFP+multicellular colonies were observed growing on the surface of bombarded embryo after 4 weeks. As with growth stimulation by the maize, rice and sorghum BBM genes, the growth stimulation imparted by the UBI::VvBBM::PinII cassette was manifested by an increase in the overall number of multicellular colonies, and also an increase in the number of multicellular colonies growing on single embryos (see Tables 9, 11 and 12). When a construct comprising the VvBBM sequence, in which the 9-bp sequence encoding VYL in the AP2 domain was removed, was introduced into maize, there was no observed growth stimulation (Tables 11 and 12), similar to the observations made with the rice BBM gene lacking this same exon.

[0237] d. Maize ANT Gene

[0238] The following constructs were used for comparison: OLE PRO::ZmBBM::pinII, and OLE PRO::ZmANT::pinII. The nucleotide and amino acid sequences of ZmANT are set forth in SEQ ID NOs: 66 and 67. Each of these plasmids was co-delivered with UBL:moPAT~GFP::pinII into 10 or 13 DAP PH581 immature embryos using the particle gun. When the UBI PRO::moPAT~GFP::pinII cassette was introduced alone, no (Table 6) or few multicellular growing sectors (Tables 7 and 8) were observed. When OLE::ZmBBM::pinII+UBI::moPAT~GFP::pinII were co-delivered, a substantial increase in the number of embryos with GFP+ multicellular colonies were observed growing on the surface of each bombarded embryo after 5 weeks (i.e. relative to the control treatment). In addition, the number of embryos supporting multiple GFP+colonies increased. Embryos co-bombarded with OLE::ZmANT::pinII+UBI::moPAT::pinII appeared identical (Table 6, with no multicellular colonies in either treatment) or similar to the control treatment (FIGS. **6** and **7**, with only a 2-fold increase in colony formation and numerous single GFP+ cells (indicating only transient expression but no division) and a reduced number of GFP+ colonies relative to the BBM treatment. In a second experiment with the same treatments (control with no BBM or ANT, Ole::BBM or Ole::ANT), out of 44 embryos shot per treatment, the control and ANT treatments produced no multicellular GFP+ colonies after 3 weeks while the BBM treatment produced 14 colonies.

Example 11

Expression of the Maize BBM and WUS Genes Improves Transformation in *Sorghum*

[0239] *Agrobacterium tumefaciens* LBA4404 and a super-binary vector constructed with pSB1 and pSB11 (Komari et al. (1996) *Plant J* 10:165-174; Thompson et al. (1987) *EMBO J* 6:2519-2523) can be used for sorghum transformation (Zhao (2006) In "*Agrobacterium* Protocols," vol. 1, Kan Wang, ed. Hamana Press, Totowa, N.J.; U.S. Pat. No. 6,369,298; and International Application Publication No. WO 98/49332). The super-binary vector contained a selectable marker gene, bar (Chalfie et al. (1994) *Science* 263:802-805) and a visible marker gene, such as red fluorescent protein (RFP), yellow fluorescent protein (YFP), or intron-GFP (Jefferson et al. (1986) *Proc Natl Acad Sci USA* 83:8447-8451).

[0240] Minimal AB media included 50 ml/l Stock A, 50 ml/l Stock B, 5 g/l glucose, 9 g/l Phytagar. For the *Agrobacterium* strain used in this protocol, 50 mg/l spectinomycin is added after autoclaving. Stock A included 60 g/l K_2HPO_4, and 20 g/l NaH_2PO_4, pH 7.0. Stock B is 20 g/l NH_4C1, 6 g/l $MgSO_4$ $7H_2O$, 3 g/l KCl, 0.2 g/l $CaCl_2$, and 0.5 g/l $FeSO_4$ H_2O. YP medium contained 5 g/l yeast extract, 10 g/l peptone, 5 g/l NaCl, and 15 g/l Bacto-agar. For the *Agrobacterium* stain used in this protocol, 50 mg/l spectinomycin was added after autoclaving.

[0241] PHI-I media included 4.3 g/l MS salts (GIBCO BRL catalog no. 11117-874), 0.5 mg/l nicotinic acid, 0.5 mg/l pyridoxine HCl, 1 mg/l thiamine HCl, 0.1 g/l myo-inositol, 1 g/l vitamin assay casamino acids, 1.5 mg/l 2,4-D, 68.5 g/l sucrose, 36 g/l glucose, pH 5.2. 100 μM acetosyringone is added before using.

[0242] PHI-T media included PHI-I with sucrose reduced to 20 g/l and glucose reduced to 10 g/l, 2,4-D increased to 2 mg/l, and with 0.5 g/l MES buffer, 0.7 g/l L-proline, 10 mg/l ascorbic acid, 100 μM acetosyringone and 8 g/l agar, pH 5.8 added.

[0243] PHI-U media included PHI-T without glucose and acetosyringone, and with 1.5 mg/l 2,4-D, 100 mg/l carbenicillin, and 5 mg/l PPT (glufosinate-HN4) added.

[0244] PHI-RF media included 4.3 g/L MS salts (GIBCO BRL 11117-074), 0.5 mg/L nicotinic acid, 0.1 mg/L thiamine HCl, 0.5 mg/L pyridoxine HCl, 2.0 mg/L glycine, 0.1 g/L myo-inositol, 0.49 μM cupric sulfate, 0.5 mg/L zeatin (Sigma Z-0164), 1 mg/L IAA, 26.4 μg/L ABA, 0.1 mg/L thidiazuron, 60 g/L sucrose, 3 mg/L bialaphos, 100 mg/L carbenicillin, and 8 g/L agar, pH 5.6.

[0245] PHI-Z media included 2.15 g/L MS salts, 2.5 ml/L MS vitamin mix, 20 g/L sucrose, and 3 g/L gelrite, pH 5.6

[0246] Suspension for immature embryo infection consisted of 100 μM acetosyringone in PHI-I medium (pre-warmed to room temperature). Bacteria were scraped off a working plate with a sterile bacteria loop and placed in PHI-I with 100 μM acetosyringone. The suspension was vigorously vortexed to break clumps and form a uniform suspension as determined by visual inspection. 1 ml of Agro-suspension was taken to measure optical density at 550 nm. The suspension was diluted with PHI-I plus 100 μM acetosyringone to 10^9 cfu/ml (OD at 0.7).

[0247] *Sorghum* plants were grown under greenhouse, growth chamber, or field conditions. Healthy sorghum plants were always important for a successful transformation. Immature panicles were harvested 9-13 days post-pollination depending on the growing conditions. The size of immature zygotic embryos used in transformation ranged from 0.8 to 2.5 mm in length. Immature kernels were removed from the panicles and sterilized with 50% bleach and 0.1% Tween-20 for 30 min. with vacuum, then the kernels were rinsed three times with sterile water. The kernels were kept in sterile water before isolating embryos. Embryos were aseptically dissected from each sterilized sorghum kernel and placed in a 2-ml microtube containing 2 ml PHI-I with 100 μM acetosyringone. Usually, about 100 embryos were placed in each tube.

[0248] PHI-I liquid medium was removed from the tube comprising the embryos with a 1 ml micropipettor and replaced with 1 ml of the *Agrobacterium* suspension. The tube was gently inverted a few times to mix well and incubated 5 minutes at room temperature. The *Agrobacterium* suspension was removed from the tube with a 1 ml micropipettor. The embryos were scraped from the tube using a sterile spatula. Immature embryos were transferred to a plate of PHI-T medium in a 100×15 mm Petri dish. The embryos were oriented with embryonic axis down on the surface of the medium. These embryos were incubated at 21-25° C. in the dark for 3 days. The embryos were transferred to PHI-U minus PPT with the same orientation and incubated at 28° C. in the dark for 4 days.

[0249] The embryos were transferred to PHI-U medium and incubated at 28° C. in the dark for 2-3 weeks and were subcultured every two to three weeks for about 10-20 weeks to obtain enough callus for regeneration into plants.

[0250] These calli were transferred to PHI-RF medium and incubated at 28° C. in the dark for approximately 2-3 weeks to develop shoots. When shoots formed, these cultures were moved to a lighted culture room under conditions of 16 hours light (270 μE m^{-2} sec^{-1}) and 8 hours dark at 25° C. Shoots (about 3-5 cm tall) were transferred to plastic boxes (10×9×10 cm) containing PHI-Z medium. These shoots were cultured under the same light and temperature conditions for 3-5 days. Each box contained shoots derived from a single embryo. When the plantlets reached about 8-10 cm tall with healthy roots, these plantlets were transferred to pots with Universal Mix (Strong-Lite, Seneca, Ill.61360) in the greenhouse.

[0251] Embryos were harvested from developing sorghum seed and transformed using *Agrobacterium*, delivering the PHP32371 T-DNA (see Example 4). As a control treatment, embryos were transformed with RB-Ubi::moPAT+Ubi:CFP-LB. Callus was selected on 3 mg/l bialaphos, and monitored for fluorescence to aid in identifying transgenic sectors. *Sorghum* transformation frequencies using Ubi:moPAT+Ubi:CFP averaged 0.5%. By comparison, in six experiments, a total of 393 embryos were transformed with PHP32371, producing an average transformation frequency of 18.3% (see Table 13). Callus from the first experiment (30 events from a starting total of 140 embryos) was used to test the desiccation-induced excision controlled by the Rab17 promoter, and subsequent plant regeneration. Twenty-one events were desiccated for three days on dry filter papers and then taken through the standard regeneration protocol. Fifteen of the 21 events produced a total of 81 plants, with multiple plants being regenerated for many of the individual events. Of these, 60% contained a single copy of the integrated DNA, and of the single copy events, 91% produced PCR results indicating complete excision of the genes encoding cell proliferation factors. From excised events, normal phenotype plants lacking FLP and WUS2 were readily regenerated.

TABLE 13

Transformation efficiencies after *Agrobacterium*-mediated transformation with PHP32371.

Experiment ID	Number of Embryos	Number of Transformation Events	Transformation Frequency (%)
1	140	30	21.4
2	40	3	7.5
3	60	8	13.3
4	40	7	17.5
5	61	12	19.7
6	52	12	23.1
Average			18.3

Example 12

Expression of the Maize BBM and WUS Genes Improves Transformation in Sugarcane

[0252] A developmental gene binary vector with the ZmBBM/ZmWUS2 gene cassette was compared with a standard vector containing moPAT plus either DsRED or YFP without the ZmBBM/ZmWUS2 gene cassette for transformation frequency using two *Agrobacterium* strains, AGL1 and LBA4404, in CP89-2376 and CP01-1372 sugarcane cultivars. The developmental gene binary vector contains Ubi::LoxP::CFP+Rab17Pro-attB1::Cre-attB2::PinII+Nos::Zm-WUS2::PinII+Ubi::ZmBBM::PinII-LoxP::YFP+Ubi::MOPAT::PinII. The Lox cassette containing CFP::Cre::WUS::BBM can be excised by Cre recombinase controlled by the Rab17 promoter. Callus tissues of both CP89-2376 and CP01-1372 cultivars were induced and maintained on DBC3 medium. Tissues were infected with *Agrobacterium* containing the developmental gene binary vector in 10 mM MgSO4 plus 100 uM acetosyringone and then cocultivated with liquid DBC3(M5G) medium plus 100 uM acetosyringone on the filter paper in Petri dishes at 21° C. in the dark. Three days after cocultivation, the tissues were transferred to DBC3 containing 100 mg/L cefotaxime and 150 mg/L timentin for AGL1, and DBC3 containing 100 mg/L carbenicillin for LBA4404, and incubated at 26° C. (±1° C.) in the dark or dim light for 3-7 days. Afterwards, the tissues were transferred to the same media as the previous step plus 3 or 5 mg/L bialaphos. After two months from the initiation of the experiment, transformation frequency was calculated by the number of tissues showing CFP expression divided by the number of explants infected by *Agrobacterium*. Table 14 demonstrated that AGL1 was even more efficient in transformation than LBA4404 in both CP89-2376 and CP01-1372. There was also a genotype difference in transformation frequency; CP89-2376 had much higher transformation frequencies than CP01-1372 using either of the *Agrobacterium* strains.

[0253] AGL1 containing the developmental gene vector was also used to test sugarcane germplasm screening in another set of experiments using 5 different cultivars (CP96-1252, CP01-1372, CP89-2376, CPCL97-2730 and HoCP85-845). Callus tissues of all 5 cultivars tested were induced and maintained on DBC3 medium and tissues were infected with AGL1 containing the developmental gene binary vector. The use of developmental genes dramatically increased transformation frequency in all 5 cultivars tested. Transformation frequencies in the most amenable cultivar, CP89-2376, using a standard binary vector averaged 116.7% (56/48) (Table 14). In contrast, an average transformation frequency in this cultivar from 5 experiments was >2,512.5% (>1,005 events/40 tissues infected) using the developmental gene binary vector. Similar results were obtained from the remaining 4 cultivars, CP96-1252, CP01-1372, CPCL97-2730 and HoCP85-845; transformation frequencies ranged from 62.5% to 187.5% in these 4 cultivars while no transgenic events were obtained using the standard vector without the BBM/WUS gene cassette from these cultivars.

TABLE 14

Transformation frequency in sugarcane using the developmental genes ZmBBM and ZmWUS2.

Agrobacterium	Binary	Sugarcane Cultivar				
Strain	Vector	CP96-1252	CPO1-1372	CP89-2376	CPCL97-2730	HoCP85-845
AGL1	DG[a]	n.t.[c]	37.5% (3/8)	n.t.	n.t.	n.t.
LBA4404	DG	n.t.	0% (0/8)	n.t.	n.t.	n.t.
AGL1	DG	n.t.	>1,250.0% (>100/8)	>6,250.0% (>500/8)	n.t.	n.t.
LBA4404	DG	n.t.	12.5% (1/8)	>1,500% (>120/8)	n.t.	n.t.
AGL1	DG	n.t.	n.t.	687.5% (>55/8)	n.t.	n.t.
AGL1	DG	n.t.	n.t.	>2,500% (>200/8)	175.0% (14/8)	n.t.
AGL1	DG	150.0% (12/8)	62.5% (5/8)	>625.0% (>50/8)	62.5% (6/8)	n.t.
AGL1	DG	n.t.	n.t.	>2,500% (>200/8)	n.t.	187.5% (15/8)
AGL1	Std[b]	0% (0/8)	0% (0/8)	116.7% (56/48)	0% (0/8)	0% (0/8)

Each transformation treatment had 8 pieces of callus tissues 0.4-0.5 cm in size.

DG[a]: developmental gene vector with BBM/WUS gene cassette

Std[b]: standard vector without BBM/WUS gene cassette

n.t.[c].: not tested

[0254] Transgenic callus tissues were desiccated on dry filter papers for three days to induce excision of the Lox cassette containing CFP::Cre::WUS::BBM by Cre recombinase driven by the Rab17 promoter. Excision was monitored by observing YFP expression on desiccated transgenic callus events by the presence of the UBI:loxP:YFP junction formed as a result of excision. Cre excision occurred at 83 of 87 transgenic events (95.4%) (Table 15). Plants from some transgenic events after excision are being regenerated on MSB plus 1 mg/L bialaphos and antibiotics.

TABLE 15

Excision efficiency of the BBM/WUS gene cassette in transgenic sugarcane events by desiccation.

Sugarcane Cultivar	*Agrobacterium* Strain	Binary Vector	Excision Efficiency (%)
CP89-2376	AGL1	DG[a]	93% (40/43)
CP89-2376	LBA4404	DG	100% (25/25)
CP01-1372	AGL1	DG	100% (13/13)
CP01-1372	LBA4404	DG	0% (0/1)
CP89-2376	AGL1	DG	100% (5/5)
Average			95.4% (83/87)

DG[a] developmental gene vector with BBM/WUS gene cassette

Example 13

Complementation of Separately Transformed BBM and WUS2 Genes

[0255] Nos::ZmWUS2::PinII and Rab17-attB1::CRE::PinII are integrated into the genome of an inbred maize plant. LoxP-UBI::BBM::PinII-LoxP+a trait gene operably linked to a promoter are re-transformed into the inbred as a single T-DNA. The BBM and WUS2 genes will complement each other, stimulating rapid growth only in the cells where both are present. BBM is then excised and normal fertile plants are regenerated. Later, the WUS2/CRE locus is segregated away from the genome.

Example 14

Transformation of Mature Dried Maize Seed

[0256] Cell proliferation factors can be used to increase transformation and/or recovery frequencies in recalcitrant plants and/or target tissues, such as mature seed.

[0257] A T-DNA containing an excisable construct comprising a maize BBM and a maize WUS gene was constructed:

PHP38333: RB-Ubi-LoxP::CFP::PinII-attB4+Rab17 Pro-attb1::Cre-attB2::PinII+Nos::ZmWUS2::PinII+Ubi::ZmBBM::PinII-LoxP::YFP::PinII+Ubi::moPAT::PinII-LB

[0258] As a control treatment, embryos were transformed with PHP32269: RB-Ubi::moPAT-YFP::PinII-LB.

[0259] The glycerol stock of a thymidine-auxotrophic mutant *Agrobacterium* strain LBA4404 with vector PHP38333, or the control vector were stored at −80° C. before use. A master plate was made by dipping an inoculation loop into a glycerol stock and streaking onto 12V solid medium with 50 mg/l thymidine in a 100×15 Petri dish (for

PHP38333) or onto 12S solid medium with 50 mg/l spectinomycin (for the control plasmid). Plates were incubated (inverted) at 28° C. in the dark for 2-3 days to produce single colonies. Master plates were stored at 4° C. for up to 4 weeks and are used for initiating fresh culture for transformation. Several colonies were picked from the master plates and streaked onto 810F solid medium with 50 mg/l thymidine and incubated at 28° C., in the dark for 1 day and fresh *Agrobacterium* was used for transformation.

[0260] To make the *Agrobacterium* suspension, 20 ml of 700 liquid medium with 50 mg/l thymidine was added into a 50 ml snap cap tube. A stock solution of acetosyringone (AS) was added to achieve a final concentration of 200 uM and a stock solution of Silwet L-77 was added to achieve a final concentration of 0.04%. *Agrobacterium* was collected from a 1-day culture plate and suspended in the 700 liquid medium. The tube was vortexed until the *Agrobacterium* culture clumps were completely broken up and evenly dispersed throughout the solution. One ml of the suspension was transferred to a spectrophotometer tube and the OD of the suspension was adjusted to 0.7 at 550 nm by adding either more *Agrobacterium* or more of the same suspension medium.

[0261] Maize inbred line PHN46 was used as the initial genotype for transformation tests. Dry seeds were placed in a covered glass jar, in an 80% ethanol solution with stirring for 5 min. The ethanol was decanted and a 50% bleach solution with a few drops of the surfactant Tween-20 were added and seeds in the bleach solution were stirred for 30 min and washed three times with sterile water in a sterile flow hood. Surface sterilized seed were soaked in the sterile water for approximately 24 h at room temperature, which is sufficient to trigger germination. After 24 hours, the softened seeds were sterilized once again with a 50% bleach solution for 5 min, and then washed three times with sterile water in a sterile flow hood.

[0262] Mature embryos were dissected out of the softened and sterilized kernels. Each mature embryo was sliced into 3-4 thin sections by hand using a No. 10 surgical scalpel under the dissecting microscope. Each explant contained exposed leaf primordia, mesocotyl and root primordia regions. These regions on the embryo chips were the target area for T-DNA delivery during *Agrobacterium*-mediated transformation and contain cells that are culture responsive. Sliced explants were transferred into a 6-well culture plate containing 4 ml 700 liquid medium. About 45 explants were placed into each well for *Agrobacterium* infection.

[0263] Liquid medium in the 6-well plate was removed from the explants and replaced with 4 ml of prepared *Agrobacterium* suspension. The 6-well plate was transferred into a transparent polycarbonate desiccator container. The desiccator was covered and placed on a platform shaker rotating at a speed of 100 RPM and connected to an in-house vacuum system for 30 min. After infection, the *Agrobacterium* suspension was drawn off from the wells and the explants were transferred onto solid 7101 co-cultivation medium with 50 mg/l thymidine. The infected embryo explants on the solid medium were incubated at 21° C. in the dark for 3 days. The number of infected explants was recorded to later calculate transformation efficiencies.

[0264] To evaluate T-DNA delivery efficiency, both the control vector without genes encoding cell proliferation factors and the vector with the genes encoding cell proliferation factors were used to infect embryo explants. After 3d co-cultivation, all of the chips were transferred onto 605J medium for continuous culture. T-DNA delivery was evaluated around 5 d after *Agrobacterium* infection. Transient expression of the color marker YFP (control vector) or CFP (test vector PHP38333) was a reliable indicator of the T-DNA delivery efficiency. In general, 30%-50% of the infected explants showed T-DNA delivery in the right target tissues or cells. Using an optimized infection medium and protocol, 70%-80% T-DNA delivery efficiency to the target area was achieved. Infected explants were sub-cultured to fresh medium every 3 weeks. After 6 weeks of culture, healthy, vigorously growing, embryogenic type I callus could be identified from those explants that had been infected with vector PHP38333 containing the genes encoding cell proliferation factors. These growing calli represented transformed events confirmed by the color marker (CFP) expression. Non-transformed tissues showed either no growth or very limited growth. Embryogenic type I callus were picked and transferred onto fresh culture medium to let the callus proliferate before plant regeneration (10-12 weeks). Transformation efficiency for PHP38333 at the callus level ranged from 12% to 20% calculated as the number events recovered per total number of infected explants (Table 16). Embryo explants that were infected with control vector PHP32269 also showed good T-DNA delivery based on transient YFP expression in the infected cells. However, these cells did not show significant proliferation and no healthy callus was formed during continuous culture.

TABLE 16

Transformation frequency of PHP38333 in PHN46 embryo chips.

Experiment No.	Number of Chips infected	Number of CFP(+) Events	Transformation Frequency (%)
1	137	23	16.8%
2	134	19	14.2%
3	149	20	13.4%
4	140	25	17.9%
5	148	18	12.2%
6	137	26	19.0%
7	129	27	20.9%
8	136	20	14.7%
9	137	21	15.3%
10	147	24	16.3%
Total	1393	223	16.0%

[0265] Transformed callus tissues were treated with either one of the following two desiccation methods to induce excision of the genes encoding cell proliferation factors before plant regeneration.

[0266] 1) Desiccation by natural air exchange: Transformed callus tissues were transferred to an empty 60 mm×25 mm Petri dish containing a piece of autoclaved glass filter paper and covered with a lid but not sealed. Petri dishes with callus tissues were placed into a culture box with a loose cover. The box was kept at 28° C. in the dark for 3 days.

[0267] 2) Desiccation in chambers containing a saturated salt solution: Transformed callus tissues were transferred to an empty 60 mm×25 mm Petri dish containing a piece of autoclaved glass filter paper and covered with a lid. The Petri dishes with callus tissues were placed into a container with a tight sealing cover. A glass jar containing saturated $(NH_4)_2SO_4$ salt solution without a cover was placed in the container. The container was kept at 28° C. in the dark for 3 days (as the moisture in the air inside the container was absorbed by the saturated salt solution, the callus tissue gradually lost water and experienced desiccation stress).

[0268] After 3 days of desiccation treatment, the callus tissues were transferred to 289L regeneration media for 2-3 weeks in the dark. When shoots formed with a length of about 1-2 cm, callus tissues with shoots were transferred to hormone-free 272V medium for further development of shoots and roots in the light culture room. When plantlets had formed well-developed shoots and roots, plant regeneration efficiency was evaluated. The plant regeneration frequency (number of callus producing plants out of total number of callus events for plant regeneration) varied from 45% to 75% among 10 initial experiments. At this stage, leaf samples were collected from the plantlets derived from each callus event for molecular analysis. Detailed PCR analyses were performed to determine the copy number of transgenes as well as to confirm that the genes encoding proliferation factors were excised and were not present in the regenerated transgenic plants.

[0269] Based on the molecular analysis of 316 TO plants from 162 events, about 60% of the transgenic plants contain a single copy of the transgenes. These single-copy transgenic plants showed very efficient excision of the genes encoding cell proliferation factors from the desiccation-treatment-induction (see results in Table 17). In general, plants with complete excision of genes encoding cell proliferation factors displayed normal phenotype in the tube and also in later developmental stages in the greenhouse. In contrast, TO plants in which excision did not occur (or where it was incomplete) displayed an abnormal phenotype, such as thickened roots.

[0270] Based on PCR analysis results, chimeric or incomplete excision TO plants can be eliminated and only complete-excision (free of genes encoding cell proliferation factors) events were sent to the greenhouse.

TABLE 17

Analysis of T0 plants for excision of genes encoding cell proliferation factors.

	T0 Plants	
Number of Events	Single Copy	Complete Excision
162 (Events)	103 (63.6%)	94 (91.3%)
316 (Plants)	189 (59.8%)	173 (91.5%)

Example 15

Transformation of Leaf Tissues

[0271] a. Preparation of *Agrobacterium* and Maize Leaf Explants

[0272] *Agrobacterium* suspensions were prepared as described in Example 14. Pioneer maize inbred lines PHN46, PHR03 and PHEJW were used as the initial genotypes for transformation tests. Dry seed was sterilized and imbibed overnight as described above.

[0273] Sterilized seeds were placed onto 272V solid medium for direct germination. Alternatively, mature embryos were dissected from softened and sterilized seeds and placed onto 272V solid medium for faster germination. Plates with seeds or isolated embryos were placed in a culture box and incubated at 28° C. in the dark for 3-7 days. Shoot segments of about 2-3 cm long above the first leaf base node of the seedling were excised under sterile conditions. The coleoptile was removed and the leaf fragment was split longitudinally first, then cross-dissected into smaller segments (0.5 to 2 mm). Alternatively, the 2-3 cm-long segment above the first leaf base node of the seedling was simply diced with the scalpel to produce small leaf segments. Small leaf segments were transferred into a 6-well culture plate containing 4 ml of 700 liquid medium.

[0274] Liquid medium in the 6-well plate with leaf pieces were drawn off and replaced with 4 ml prepared *Agrobacterium* suspension. The 6-well plate was transferred into a transparent polycarbonate desiccator container. The desiccator was covered and placed on a platform of the shaker with a speed of 100 RPM and connected to an in-house vacuum system for 15 min. After infection, the *Agrobacterium* suspension was drawn off from the wells and the leaf tissues were transferred onto solid 7101 co-cultivation medium with 50 mg/l thymidine and were incubated at 21° C. in the dark for 3 days.

[0275] After 3d co-cultivation, all of the leaf tissues were transferred to 13152C culture medium. T-DNA delivery was evaluated about 5 d after *Agrobacterium* infection. Transient expression of the color marker YFP (control vector) or CFP (test vector PHP38333) was a reliable indicator of the T-DNA delivery efficiency. 10%-25% of infected leaf segments showed multiple fluorescent cells along the cut edges or surface of leaf segments in all three inbred lines tested. Infected leaf tissues were sub-cultured every 2 weeks. After 6-8 weeks of culture, stable transformed callus events could be identified. The transgenic nature of these stable callus events was indicated by the expression of the fluorescent gene. Callus events with significant proliferation were subjected to desiccation treatment, and transferred onto regeneration medium for 2-4 weeks. Stable transgenic plantlets were regenerated from two tested maize inbreds, PHN46 and PHR03. Results from numerous experiments clearly demonstrated that stable transgenic plants could be produced form transformation of seedling tissue by using the vector that expresses the genes encoding cell proliferation factors. Leaf tissues infected with the control vector also showed good T-DNA delivery based on transient YFP expression, but the infected cells did not exhibit any subsequent proliferation and no stable callus events were identified from this treatment.

Example 16

The Utilization of Cell Proliferation Factors for Enhancing Chloroplast Transformation

[0276] For tobacco and a number of other species, leaves are a preferred target for chloroplast transformation. Cell proliferation factors are used to trigger a tissue culture response from leaves of maize and other species. For boosting chloroplast transformation, cell proliferation factor genes under the control of inducible promoters are introduced into the species of interest by standard nuclear transformation protocols. Events that contain the transgene are characterized for expression of the inducible cell proliferation factor genes. For example, leaves of maize from plants transformed with the cell proliferation factor genes under the control of the tetracycline-repressor system are placed on medium containing appropriate concentrations of doxycyline. The doxycyline then activates the cell proliferation factor genes and thereby induces an embryogenic tissue culture response. The leaves are maintained on this medium for about 7-21 days during which time cell division and the initiation of embryogenic callus will take place. The leaves are bombarded with chloroplast transformation vectors carrying the aadA selectable marker gene and trait gene just prior to induction of the cell proliferation genes, during induction or just after induction. One to seven days after bombardment with the chloroplast transformation vector, the tissue is placed in petri plates containing agarose-solidified media supplemented with spectinomycin. The plates are then incubated at 28° C. in the light. The tissue is transferred to fresh medium every two weeks. After about 8 weeks of incubation, green callus is observed. This tissue can be further proliferated on 13152 medium (4.3 g/l MS salts, 0.25 g/l myo-inositol, 1.0 g/l casein hydrolysate, 1 mg/l thiamine, 1 mg/l 2,4-D, 30 g/l maltose, 0.69 g/l proline, 1.2 mg/l cupric sulfate, and 3.5 g/l phytagel, pH 5.8) and the tissue analyzed for the presence of the transgene using appropriate methods including PCR and Southern analysis.

[0277] In an alternative approach, expression cassettes containing the tetracycline-inducible BBM and WUS genes are co-bombarded along with the chloroplast transformation vectors carrying the aadA gene for selection. Either leaf explants or established green tissue callus are used as the target tissue for bombardment. Tetracycline or doxycycline at a concentration of 0.5 to 2.0 mg/l is added to the culture medium (13152) after particle bombardment. Expression of BBM and WUS in cells that have received DNA stimulate callus growth rates during the period while tetracycline (or doxycycline) is present in the medium. The accelerated growth that is stimulated by BBM & WUS will result in improved recovery of homoplastic transgenic events, and the nuclear-integrated BBM/WUS genes can be removed by outcrossing T0 plants to wild-type plants and selecting BBM/WUS null plants in the T1 generation.

[0278] In another variation on the particle gun approach for delivery of BBM and WUS, a UBI::BBM::PinII and a nos::WUS2::pinII are co-delivered along with the chloroplast transformation vectors.

[0279] In another alternative approach, the cell proliferation factor genes are delivered into leaf tissue by vacuum infiltration of an *Agrobacterium* solution. The cell proliferation factor genes are under the control of strong constitutive promoters such as ubi or act or viral promoters such as 35S (Gardner et al. (1981) *Nucl Acids Res* 9:2871-2888), MMV (Dey and Maiti (1999) *Plant Mol Biol* 40:771-782), or BSV (Shenk et al. (2001) *Plant Mol Biol* 47:399-412). The cell proliferation factor genes are carried on binary vectors that facilitate transfer from the bacteria to plant cells. Following vacuum infiltration, the tissue is incubated for an appropriate period of time to allow expression of the cell proliferation factor genes in the leaf tissue. Transient expression from the cell proliferation factor genes delivered by *Agrobacterium* is expected to provide a strong boost in cell division and tissue culture response. After vacuum infiltration with *Agrobacterium*, the tissue is bombarded with a chloroplast transformation vector carrying the aadA selectable marker gene. The tissue is then transferred to media containing spectinomycin and transgenic events selected. It is expected that the *Agrobacterium*-delivered cell proliferation factor genes will not be integrated into the nuclear genome of most of the events that are recovered.

[0280] All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

[0281] Many modifications and other embodiments of the inventions set forth herein will come to mind to one skilled in the art to which these inventions pertain having the benefit of the teachings presented in the foregoing descriptions and the associated drawings. Therefore, it is to be understood that the inventions are not to be limited to the specific embodiments disclosed and that modifications and other embodiments are intended to be included within the scope of the appended claims. Although specific terms are employed herein, they are used in a generic and descriptive sense only and not for purposes of limitation.

SEQUENCE LISTING

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1               5                   10                  15

cct tct agt caa gat cac tct caa acg gca cct tct cgt ttt tgc ttc       96
Pro Ser Ser Gln Asp His Ser Gln Thr Ala Pro Ser Arg Phe Cys Phe
            20                  25                  30

aac cct gat gga atc tca agc act gat gta gca gga gac tgc ttt gat      144
Asn Pro Asp Gly Ile Ser Ser Thr Asp Val Ala Gly Asp Cys Phe Asp
        35                  40                  45
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ctc act tct gac tca act cct cat tta ctc aac ctt ccc tct tac ggc      192
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    50                  55                  60

ata tac gaa gct ttt cat agg agc aac aat att cac acc act caa gat      240
Ile Tyr Glu Ala Phe His Arg Ser Asn Asn Ile His Thr Thr Gln Asp
65                  70                  75                  80

tgg aag gag aac tac aac agc caa aac ttg cta ttg gga act tca tgc      288
Trp Lys Glu Asn Tyr Asn Ser Gln Asn Leu Leu Leu Gly Thr Ser Cys
                85                  90                  95

agc aac caa aac atg aac cac aac cat cag caa caa caa caa caa cag      336
Ser Asn Gln Asn Met Asn His Asn His Gln Gln Gln Gln Gln Gln Gln
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cca aag ctt gaa aac ttc ctc ggt gga cac tca ttt ggt gaa cat gag      384
Pro Lys Leu Glu Asn Phe Leu Gly Gly His Ser Phe Gly Glu His Glu
        115                 120                 125

caa ccc tac ggt ggt aac tca gcc tct aca gaa tac atg ttc ccg gct      432
Gln Pro Tyr Gly Gly Asn Ser Ala Ser Thr Glu Tyr Met Phe Pro Ala
    130                 135                 140

cag ccg gta ttg gcc ggt ggc ggc ggc ggt ggt agc aat agc agc aac      480
Gln Pro Val Leu Ala Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser Asn
145                 150                 155                 160

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Thr Ser Asn Ser Ser Ser Ile Gly Leu Ser Met Ile Lys Thr Trp Leu
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agg aac caa cca cca cac tca gaa aac aac aat aac aac aac aat gaa      576
Arg Asn Gln Pro Pro His Ser Glu Asn Asn Asn Asn Asn Asn Asn Glu
            180                 185                 190

agt ggt ggc aat agt aga agc agt gtg cag cag act cta tca ctt tcc      624
Ser Gly Gly Asn Ser Arg Ser Ser Val Gln Gln Thr Leu Ser Leu Ser
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atg agt act ggt tca caa tca agc aca tca cta ccc ctt ctc act gct      672
Met Ser Thr Gly Ser Gln Ser Ser Thr Ser Leu Pro Leu Leu Thr Ala
    210                 215                 220

agt gtg gat aat gga gag agt tct tct gat aac aaa caa cca cat acc      720
Ser Val Asp Asn Gly Glu Ser Ser Ser Asp Asn Lys Gln Pro His Thr
225                 230                 235                 240

acg gct gca ctt gat aca acc caa acc gga gcc att gaa act gca ccc      768
Thr Ala Ala Leu Asp Thr Thr Gln Thr Gly Ala Ile Glu Thr Ala Pro
                245                 250                 255

aga aag tcc att gac act ttt gga cag aga act tct atc tac cgt ggt      816
Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly
            260                 265                 270

gta aca agg cat agg tgg acg ggg agg tat gag gct cac ctg tgg gat      864
Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp
        275                 280                 285

aat agt tgt aga aga gag gga caa act cgc aaa gga agg caa gtt tac      912
Asn Ser Cys Arg Arg Glu Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr
    290                 295                 300

ttg gga ggt tat gac aaa gaa gaa aag gca gct aga gcc tac gat ttg      960
Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu
305                 310                 315                 320

gca gca cta aaa tac tgg gga aca act acg aca aca aat ttt cca att     1008
Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr Thr Asn Phe Pro Ile
                325                 330                 335

agc cac tat gag aaa gag ttg gaa gaa atg aag cac atg act agg caa     1056
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gca tcc att tat cga ggt gtg acg aga cac cat caa cat gga aga tgg     1152
Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp
    370                 375                 380

caa gcg agg att gga aga gtt gct ggc aac aag gat ctc tac ttg gga     1200
Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly
385                 390                 395                 400

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Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala
                405                 410                 415

atc aaa ttc aga gga cta agt gct gtt aca aac ttt gac atg agc aga     1296
Ile Lys Phe Arg Gly Leu Ser Ala Val Thr Asn Phe Asp Met Ser Arg
            420                 425                 430

tat gac gtg aaa agc ata ctt gag agc acc act ttg cca att ggt ggt     1344
Tyr Asp Val Lys Ser Ile Leu Glu Ser Thr Thr Leu Pro Ile Gly Gly
        435                 440                 445

gct gca aag cgt ttg aag gat atg gag cag gtg gaa ctg agg gtg gag     1392
Ala Ala Lys Arg Leu Lys Asp Met Glu Gln Val Glu Leu Arg Val Glu
    450                 455                 460

aat gtt cat aga gca gat caa gaa gat cat agt agc atc atg aac tct     1440
Asn Val His Arg Ala Asp Gln Glu Asp His Ser Ser Ile Met Asn Ser
465                 470                 475                 480

cac tta act caa gga atc att aac aac tat gca gca gga gga aca aca     1488
His Leu Thr Gln Gly Ile Ile Asn Asn Tyr Ala Ala Gly Gly Thr Thr
                485                 490                 495

gcg act cat cat cat aac tgg cac aat gct ctt gca ttc cac caa cct     1536
Ala Thr His His His Asn Trp His Asn Ala Leu Ala Phe His Gln Pro
            500                 505                 510

caa cct tgc acc acc ata cac tac cct tat gga caa aga att aat tgg     1584
Gln Pro Cys Thr Thr Ile His Tyr Pro Tyr Gly Gln Arg Ile Asn Trp
        515                 520                 525

tgc aag caa gaa caa gac aac tct gat gcc tct cac tct ttg tct tat     1632
Cys Lys Gln Glu Gln Asp Asn Ser Asp Ala Ser His Ser Leu Ser Tyr
    530                 535                 540

tca gat att cat caa cta cag cta ggg aac aat ggc aca cac aac ttc     1680
Ser Asp Ile His Gln Leu Gln Leu Gly Asn Asn Gly Thr His Asn Phe
545                 550                 555                 560

ttt cac aca aat tca ggg ttg cac cct atg tta agc atg gat tct gct     1728
Phe His Thr Asn Ser Gly Leu His Pro Met Leu Ser Met Asp Ser Ala
                565                 570                 575

tcc att gac aat agc tct tca tct aac tct gtt gtt tat gat ggt tat     1776
Ser Ile Asp Asn Ser Ser Ser Ser Asn Ser Val Val Tyr Asp Gly Tyr
            580                 585                 590

gga ggt ggt ggg ggc tat aat gtg att cct atg ggg act act act act     1824
Gly Gly Gly Gly Gly Tyr Asn Val Ile Pro Met Gly Thr Thr Thr Thr
        595                 600                 605

gtt gtt gca aat gat ggt gat caa aat cca aga agc aat cat ggt ttt     1872
Val Val Ala Asn Asp Gly Asp Gln Asn Pro Arg Ser Asn His Gly Phe
    610                 615                 620

ggt gat aat gag ata aag gca ctt ggt tat gaa agt gtg tat ggt tct     1920
Gly Asp Asn Glu Ile Lys Ala Leu Gly Tyr Glu Ser Val Tyr Gly Ser
625                 630                 635                 640

aca act gat cct tat cat gca cat gca agg aac ttg tat tat ctt act     1968
Thr Thr Asp Pro Tyr His Ala His Ala Arg Asn Leu Tyr Tyr Leu Thr
                645                 650                 655
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caa cag caa cca tct tct gtt gat gca gtg aag gct agt gca tat gat     2016
Gln Gln Gln Pro Ser Ser Val Asp Ala Val Lys Ala Ser Ala Tyr Asp
            660                 665                 670

caa gga tct gca tgc aat act tgg gtt cca act gct att cca act cat     2064
Gln Gly Ser Ala Cys Asn Thr Trp Val Pro Thr Ala Ile Pro Thr His
        675                 680                 685

gca cca agg tct agt act agt atg gct ctc tgc cat ggt gct acg ccc     2112
Ala Pro Arg Ser Ser Thr Ser Met Ala Leu Cys His Gly Ala Thr Pro
    690                 695                 700

ttc tct tta ttg cat gaa tag                                         2133
Phe Ser Leu Leu His Glu
705                 710


<210> SEQ ID NO 2
<211> LENGTH: 710
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 2

Met Gly Ser Met Asn Leu Leu Gly Phe Ser Leu Ser Pro Gln Glu His
1               5                   10                  15

Pro Ser Ser Gln Asp His Ser Gln Thr Ala Pro Ser Arg Phe Cys Phe
            20                  25                  30

Asn Pro Asp Gly Ile Ser Ser Thr Asp Val Ala Gly Asp Cys Phe Asp
        35                  40                  45

Leu Thr Ser Asp Ser Thr Pro His Leu Leu Asn Leu Pro Ser Tyr Gly
    50                  55                  60

Ile Tyr Glu Ala Phe His Arg Ser Asn Asn Ile His Thr Thr Gln Asp
65                  70                  75                  80

Trp Lys Glu Asn Tyr Asn Ser Gln Asn Leu Leu Leu Gly Thr Ser Cys
                85                  90                  95

Ser Asn Gln Asn Met Asn His Asn His Gln Gln Gln Gln Gln Gln Gln
            100                 105                 110

Pro Lys Leu Glu Asn Phe Leu Gly Gly His Ser Phe Gly Glu His Glu
        115                 120                 125

Gln Pro Tyr Gly Gly Asn Ser Ala Ser Thr Glu Tyr Met Phe Pro Ala
    130                 135                 140

Gln Pro Val Leu Ala Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser Asn
145                 150                 155                 160

Thr Ser Asn Ser Ser Ser Ile Gly Leu Ser Met Ile Lys Thr Trp Leu
                165                 170                 175

Arg Asn Gln Pro Pro His Ser Glu Asn Asn Asn Asn Asn Asn Asn Glu
            180                 185                 190

Ser Gly Gly Asn Ser Arg Ser Ser Val Gln Gln Thr Leu Ser Leu Ser
        195                 200                 205

Met Ser Thr Gly Ser Gln Ser Ser Thr Ser Leu Pro Leu Leu Thr Ala
    210                 215                 220

Ser Val Asp Asn Gly Glu Ser Ser Ser Asp Asn Lys Gln Pro His Thr
225                 230                 235                 240

Thr Ala Ala Leu Asp Thr Thr Gln Thr Gly Ala Ile Glu Thr Ala Pro
                245                 250                 255

Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly
            260                 265                 270
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Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp
        275                 280                 285

Asn Ser Cys Arg Arg Glu Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr
    290                 295                 300

Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu
305                 310                 315                 320

Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr Thr Asn Phe Pro Ile
                325                 330                 335

Ser His Tyr Glu Lys Glu Leu Glu Glu Met Lys His Met Thr Arg Gln
            340                 345                 350

Glu Tyr Val Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly
        355                 360                 365

Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp
    370                 375                 380

Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly
385                 390                 395                 400

Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala
                405                 410                 415

Ile Lys Phe Arg Gly Leu Ser Ala Val Thr Asn Phe Asp Met Ser Arg
            420                 425                 430

Tyr Asp Val Lys Ser Ile Leu Glu Ser Thr Thr Leu Pro Ile Gly Gly
        435                 440                 445

Ala Ala Lys Arg Leu Lys Asp Met Glu Gln Val Glu Leu Arg Val Glu
    450                 455                 460

Asn Val His Arg Ala Asp Gln Glu Asp His Ser Ser Ile Met Asn Ser
465                 470                 475                 480

His Leu Thr Gln Gly Ile Ile Asn Asn Tyr Ala Ala Gly Gly Thr Thr
                485                 490                 495

Ala Thr His His His Asn Trp His Asn Ala Leu Ala Phe His Gln Pro
            500                 505                 510

Gln Pro Cys Thr Thr Ile His Tyr Pro Tyr Gly Gln Arg Ile Asn Trp
        515                 520                 525

Cys Lys Gln Glu Gln Asp Asn Ser Asp Ala Ser His Ser Leu Ser Tyr
    530                 535                 540

Ser Asp Ile His Gln Leu Gln Leu Gly Asn Asn Gly Thr His Asn Phe
545                 550                 555                 560

Phe His Thr Asn Ser Gly Leu His Pro Met Leu Ser Met Asp Ser Ala
                565                 570                 575

Ser Ile Asp Asn Ser Ser Ser Ser Asn Ser Val Val Tyr Asp Gly Tyr
            580                 585                 590

Gly Gly Gly Gly Gly Tyr Asn Val Ile Pro Met Gly Thr Thr Thr Thr
        595                 600                 605

Val Val Ala Asn Asp Gly Asp Gln Asn Pro Arg Ser Asn His Gly Phe
    610                 615                 620

Gly Asp Asn Glu Ile Lys Ala Leu Gly Tyr Glu Ser Val Tyr Gly Ser
625                 630                 635                 640

Thr Thr Asp Pro Tyr His Ala His Ala Arg Asn Leu Tyr Tyr Leu Thr
                645                 650                 655

Gln Gln Gln Pro Ser Ser Val Asp Ala Val Lys Ala Ser Ala Tyr Asp
            660                 665                 670

Gln Gly Ser Ala Cys Asn Thr Trp Val Pro Thr Ala Ile Pro Thr His
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        675                 680                 685

Ala Pro Arg Ser Ser Thr Ser Met Ala Leu Cys His Gly Ala Thr Pro
    690                 695                 700

Phe Ser Leu Leu His Glu
705                 710


<210> SEQ ID NO 3
<211> LENGTH: 2112
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(2112)

<400> SEQUENCE: 3

atg gct act gtg aac aac tgg ctc gct ttc tcc ctc tcc ccg cag gag           48
Met Ala Thr Val Asn Asn Trp Leu Ala Phe Ser Leu Ser Pro Gln Glu
1               5                   10                  15

ctg ccg ccc acc cag acg gac tcc acc ctc atc tct gcc gcc acc acc           96
Leu Pro Pro Thr Gln Thr Asp Ser Thr Leu Ile Ser Ala Ala Thr Thr
            20                  25                  30

gac gat gtc tcc ggc gat gtc tgc ttc aac atc ccc caa gat tgg agc          144
Asp Asp Val Ser Gly Asp Val Cys Phe Asn Ile Pro Gln Asp Trp Ser
        35                  40                  45

atg agg gga tcc gag ctt tcg gcg ctc gtc gcc gag ccg aag ctg gag          192
Met Arg Gly Ser Glu Leu Ser Ala Leu Val Ala Glu Pro Lys Leu Glu
    50                  55                  60

gac ttc ctc ggc gga atc tcc ttc tcc gag cag cac cac aag gcc aac          240
Asp Phe Leu Gly Gly Ile Ser Phe Ser Glu Gln His His Lys Ala Asn
65                  70                  75                  80

tgc aac atg atc ccc agc act agc agc aca gct tgc tac gcg agc tcg          288
Cys Asn Met Ile Pro Ser Thr Ser Ser Thr Ala Cys Tyr Ala Ser Ser
                85                  90                  95

ggt gct acc gcc ggc tac cat cac cag ctg tac cac cag ccc acc agc          336
Gly Ala Thr Ala Gly Tyr His His Gln Leu Tyr His Gln Pro Thr Ser
            100                 105                 110

tcc gcg ctc cac ttc gct gac tcc gtc atg gtg gcc tcc tcg gcc ggc          384
Ser Ala Leu His Phe Ala Asp Ser Val Met Val Ala Ser Ser Ala Gly
        115                 120                 125

ggc gtc cac gac gga ggt gcc atg ctc agc gcg gcc agc gct aat ggt          432
Gly Val His Asp Gly Gly Ala Met Leu Ser Ala Ala Ser Ala Asn Gly
    130                 135                 140

agc gct ggc gct ggc gct gcc agt gcc aat ggc agc ggc agc atc ggg          480
Ser Ala Gly Ala Gly Ala Ala Ser Ala Asn Gly Ser Gly Ser Ile Gly
145                 150                 155                 160

ctg tcc atg atc aag aac tgg ctg cgg agc caa cca gct ccc atg cag          528
Leu Ser Met Ile Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Met Gln
                165                 170                 175

ccg agg gtg gcg gcg gct gag agc gtg cag ggg ctc tct ttg tcc atg          576
Pro Arg Val Ala Ala Ala Glu Ser Val Gln Gly Leu Ser Leu Ser Met
            180                 185                 190

aac atg gcg ggg gcg acg caa ggc gcc gct ggc atg cca ctt ctt gct          624
Asn Met Ala Gly Ala Thr Gln Gly Ala Ala Gly Met Pro Leu Leu Ala
        195                 200                 205

gga gag cgc ggc cgg gcg ccc gag agt gtc tcg acg tcg gca cag ggt          672
Gly Glu Arg Gly Arg Ala Pro Glu Ser Val Ser Thr Ser Ala Gln Gly
    210                 215                 220

gga gcc gtc gtc acg gct cca aag gag gat agc ggt ggc agc ggt gtt          720
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Gly Ala Val Val Thr Ala Pro Lys Glu Asp Ser Gly Gly Ser Gly Val
225                 230                 235                 240

gcc gcc acc ggc gcc cta gta gcc gtg agc acg gac acg ggt ggc agc      768
Ala Ala Thr Gly Ala Leu Val Ala Val Ser Thr Asp Thr Gly Gly Ser
                245                 250                 255

ggc gcg tcg gct gac aac acg gca agg aag acg gtg gac acg ttc ggg      816
Gly Ala Ser Ala Asp Asn Thr Ala Arg Lys Thr Val Asp Thr Phe Gly
            260                 265                 270

cag cgc acg tcg att tac cgt ggc gtg aca agg cat aga tgg act ggg      864
Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly
        275                 280                 285

aga tat gaa gca cat ctg tgg gac aac agt tgc aga agg gaa gga caa      912
Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln
    290                 295                 300

act cgc aag ggt cgt caa gtc tat tta ggt ggc tat gat aaa gag gag      960
Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu
305                 310                 315                 320

aaa gct gct agg gct tat gat ctg gct gct ctt aag tac tgg ggt ccc     1008
Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro
                325                 330                 335

acg aca aca aca aat ttt cca gtg aat aac tac gaa aag gag ctg gag     1056
Thr Thr Thr Thr Asn Phe Pro Val Asn Asn Tyr Glu Lys Glu Leu Glu
            340                 345                 350

gat atg aag cac atg aca agg cag gag ttt gta gcg tct ctg aga agg     1104
Asp Met Lys His Met Thr Arg Gln Glu Phe Val Ala Ser Leu Arg Arg
        355                 360                 365

aag agc agt ggt ttc tcc aga ggt gca tcc att tac agg gga gtg act     1152
Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr
    370                 375                 380

agg cat cac cag cat gga aga tgg caa gca cgg att gga cga gtt gca     1200
Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala
385                 390                 395                 400

ggg aac aag gat ctc tac ttg ggc acc ttc agc acg cag gag gag gca     1248
Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala
                405                 410                 415

gcg gag gca tac gac att gcg gcg atc aag ttc cgc ggc ctc aac gcc     1296
Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala
            420                 425                 430

gtc aca aac ttc gac atg agc cgc tac gac gtc aag agc atc ctg gac     1344
Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser Ile Leu Asp
        435                 440                 445

agc agt gcg ctc ccc atc ggc agc gcc gcc aag cgt ctc aag gag gcc     1392
Ser Ser Ala Leu Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Glu Ala
    450                 455                 460

gag gcc gcc gcg tcc gca cag cac cat gcc ggc gtg gtg agc tac gac     1440
Glu Ala Ala Ala Ser Ala Gln His His Ala Gly Val Val Ser Tyr Asp
465                 470                 475                 480

gtc ggc cgc ata gcc tca cag ctc ggc gac ggc ggc gcc ctg gcg gcg     1488
Val Gly Arg Ile Ala Ser Gln Leu Gly Asp Gly Gly Ala Leu Ala Ala
                485                 490                 495

gcg tac ggc gcg cac tac cat ggc gcc tgg ccg acc atc gcg ttc cag     1536
Ala Tyr Gly Ala His Tyr His Gly Ala Trp Pro Thr Ile Ala Phe Gln
            500                 505                 510

ccg agc gcg gcc acg ggc ctg tac cac ccg tac gcg cag ccg atg cgc     1584
Pro Ser Ala Ala Thr Gly Leu Tyr His Pro Tyr Ala Gln Pro Met Arg
        515                 520                 525

ggg tgg tgc aag cag gag cag gac cac gcg gtg atc gcg gcc gcg cac     1632
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Gly Trp Cys Lys Gln Glu Gln Asp His Ala Val Ile Ala Ala Ala His
    530                 535                 540

agc ctg cag gag ctc cac cac ctg aac ctg ggt gct gcc gcc ggc gcg     1680
Ser Leu Gln Glu Leu His His Leu Asn Leu Gly Ala Ala Ala Gly Ala
545                 550                 555                 560

cac gac ttc ttc tcg gcg ggg cag cag gcg gcg atg cac ggc ctg ggt     1728
His Asp Phe Phe Ser Ala Gly Gln Gln Ala Ala Met His Gly Leu Gly
            565                 570                 575

agc atg gac aat gca tca ctc gag cac agc acc ggc tcc aac tcc gtc     1776
Ser Met Asp Asn Ala Ser Leu Glu His Ser Thr Gly Ser Asn Ser Val
            580                 585                 590

gtg tac aac ggt gtt ggt gat agc aac ggc agc acc gtc gtc ggc agt     1824
Val Tyr Asn Gly Val Gly Asp Ser Asn Gly Ser Thr Val Val Gly Ser
        595                 600                 605

ggt ggc tac atg atg cct atg agc gct gcc acg gcg acg gct acc acg     1872
Gly Gly Tyr Met Met Pro Met Ser Ala Ala Thr Ala Thr Ala Thr Thr
    610                 615                 620

gca atg gtg agc cac gag cag gtg cat gca cgg gca cag ggt gat cac     1920
Ala Met Val Ser His Glu Gln Val His Ala Arg Ala Gln Gly Asp His
625                 630                 635                 640

cac gac gaa gcc aag cag gct gct cag atg ggg tac gag agc tac ctg     1968
His Asp Glu Ala Lys Gln Ala Ala Gln Met Gly Tyr Glu Ser Tyr Leu
            645                 650                 655

gtg aac gca gag aac tat ggc ggc ggg agg atg tct gcg gcc tgg gcg     2016
Val Asn Ala Glu Asn Tyr Gly Gly Gly Arg Met Ser Ala Ala Trp Ala
            660                 665                 670

act gtc tca gcg cca ccg gcg gca agc agc aac gat aac atg gcg gac     2064
Thr Val Ser Ala Pro Pro Ala Ala Ser Ser Asn Asp Asn Met Ala Asp
        675                 680                 685

gtc ggc cat ggc ggc gca cag ctc ttc agt gtc tgg aac gat act taa     2112
Val Gly His Gly Gly Ala Gln Leu Phe Ser Val Trp Asn Asp Thr
    690                 695                 700


<210> SEQ ID NO 4
<211> LENGTH: 703
<212> TYPE: PRT
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 4

Met Ala Thr Val Asn Asn Trp Leu Ala Phe Ser Leu Ser Pro Gln Glu
1               5                   10                  15

Leu Pro Pro Thr Gln Thr Asp Ser Thr Leu Ile Ser Ala Ala Thr Thr
            20                  25                  30

Asp Asp Val Ser Gly Asp Val Cys Phe Asn Ile Pro Gln Asp Trp Ser
        35                  40                  45

Met Arg Gly Ser Glu Leu Ser Ala Leu Val Ala Glu Pro Lys Leu Glu
    50                  55                  60

Asp Phe Leu Gly Gly Ile Ser Phe Ser Glu Gln His His Lys Ala Asn
65                  70                  75                  80

Cys Asn Met Ile Pro Ser Thr Ser Ser Thr Ala Cys Tyr Ala Ser Ser
                85                  90                  95

Gly Ala Thr Ala Gly Tyr His His Gln Leu Tyr His Gln Pro Thr Ser
            100                 105                 110

Ser Ala Leu His Phe Ala Asp Ser Val Met Val Ala Ser Ser Ala Gly
        115                 120                 125

Gly Val His Asp Gly Gly Ala Met Leu Ser Ala Ala Ser Ala Asn Gly
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    130                 135                 140

Ser Ala Gly Ala Gly Ala Ala Ser Ala Asn Gly Ser Gly Ser Ile Gly
145                 150                 155                 160

Leu Ser Met Ile Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Met Gln
                165                 170                 175

Pro Arg Val Ala Ala Ala Glu Ser Val Gln Gly Leu Ser Leu Ser Met
            180                 185                 190

Asn Met Ala Gly Ala Thr Gln Gly Ala Ala Gly Met Pro Leu Leu Ala
        195                 200                 205

Gly Glu Arg Gly Arg Ala Pro Glu Ser Val Ser Thr Ser Ala Gln Gly
    210                 215                 220

Gly Ala Val Val Thr Ala Pro Lys Glu Asp Ser Gly Gly Ser Gly Val
225                 230                 235                 240

Ala Ala Thr Gly Ala Leu Val Ala Val Ser Thr Asp Thr Gly Gly Ser
                245                 250                 255

Gly Ala Ser Ala Asp Asn Thr Ala Arg Lys Thr Val Asp Thr Phe Gly
            260                 265                 270

Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly
        275                 280                 285

Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln
    290                 295                 300

Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu
305                 310                 315                 320

Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro
                325                 330                 335

Thr Thr Thr Thr Asn Phe Pro Val Asn Asn Tyr Glu Lys Glu Leu Glu
            340                 345                 350

Asp Met Lys His Met Thr Arg Gln Glu Phe Val Ala Ser Leu Arg Arg
        355                 360                 365

Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr
    370                 375                 380

Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala
385                 390                 395                 400

Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala
                405                 410                 415

Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala
            420                 425                 430

Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser Ile Leu Asp
        435                 440                 445

Ser Ser Ala Leu Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Glu Ala
    450                 455                 460

Glu Ala Ala Ala Ser Ala Gln His His Ala Gly Val Val Ser Tyr Asp
465                 470                 475                 480

Val Gly Arg Ile Ala Ser Gln Leu Gly Asp Gly Gly Ala Leu Ala Ala
                485                 490                 495

Ala Tyr Gly Ala His Tyr His Gly Ala Trp Pro Thr Ile Ala Phe Gln
            500                 505                 510

Pro Ser Ala Ala Thr Gly Leu Tyr His Pro Tyr Ala Gln Pro Met Arg
        515                 520                 525

Gly Trp Cys Lys Gln Glu Gln Asp His Ala Val Ile Ala Ala Ala His
    530                 535                 540
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Ser Leu Gln Glu Leu His His Leu Asn Leu Gly Ala Ala Ala Gly Ala
545                 550                 555                 560

His Asp Phe Phe Ser Ala Gly Gln Gln Ala Ala Met His Gly Leu Gly
                565                 570                 575

Ser Met Asp Asn Ala Ser Leu Glu His Ser Thr Gly Ser Asn Ser Val
            580                 585                 590

Val Tyr Asn Gly Val Gly Asp Ser Asn Gly Ser Thr Val Val Gly Ser
        595                 600                 605

Gly Gly Tyr Met Met Pro Met Ser Ala Ala Thr Ala Thr Ala Thr Thr
    610                 615                 620

Ala Met Val Ser His Glu Gln Val His Ala Arg Ala Gln Gly Asp His
625                 630                 635                 640

His Asp Glu Ala Lys Gln Ala Ala Gln Met Gly Tyr Glu Ser Tyr Leu
                645                 650                 655

Val Asn Ala Glu Asn Tyr Gly Gly Gly Arg Met Ser Ala Ala Trp Ala
            660                 665                 670

Thr Val Ser Ala Pro Pro Ala Ala Ser Ser Asn Asp Asn Met Ala Asp
        675                 680                 685

Val Gly His Gly Gly Ala Gln Leu Phe Ser Val Trp Asn Asp Thr
    690                 695                 700


<210> SEQ ID NO 5
<211> LENGTH: 1932
<212> TYPE: DNA
<213> ORGANISM: Vitis vinifera
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(1932)

<400> SEQUENCE: 5

atg gct tcc atg aac aac tgg ttg ggt ttc tct ttg tcc cct cga gaa         48
Met Ala Ser Met Asn Asn Trp Leu Gly Phe Ser Leu Ser Pro Arg Glu
1               5                   10                  15

ctt cca cca cag cct gaa aat cac tca cag aac agt gtc tct aga ctt         96
Leu Pro Pro Gln Pro Glu Asn His Ser Gln Asn Ser Val Ser Arg Leu
            20                  25                  30

ggt ttc aac tct gat gaa atc tct ggg act gat gtg tca ggt gag tgt        144
Gly Phe Asn Ser Asp Glu Ile Ser Gly Thr Asp Val Ser Gly Glu Cys
        35                  40                  45

ttt gat ctc act tca gat tcc act gct ccc tct ctc aac ctc cct ccc        192
Phe Asp Leu Thr Ser Asp Ser Thr Ala Pro Ser Leu Asn Leu Pro Pro
    50                  55                  60

cct ttt ggg ata ctt gaa gca ttc aac agg aat aat cag ccc caa gat        240
Pro Phe Gly Ile Leu Glu Ala Phe Asn Arg Asn Asn Gln Pro Gln Asp
65                  70                  75                  80

act aac tac aaa acc acc act tct gag ctc tcc atg ctc atg ggt agt        288
Thr Asn Tyr Lys Thr Thr Thr Ser Glu Leu Ser Met Leu Met Gly Ser
                85                  90                  95

tca tgc agt agt cat cat aac ctc gaa aac caa gaa ccc aaa ctt gaa        336
Ser Cys Ser Ser His His Asn Leu Glu Asn Gln Glu Pro Lys Leu Glu
            100                 105                 110

aat ttc ctg ggc tgc cgc tct ttt gct gat cat gag cag aaa ctt caa        384
Asn Phe Leu Gly Cys Arg Ser Phe Ala Asp His Glu Gln Lys Leu Gln
        115                 120                 125

ggg tac tac att tcc att ggt tta tcc atg atc aag aca tgg ctg cgg        432
Gly Tyr Tyr Ile Ser Ile Gly Leu Ser Met Ile Lys Thr Trp Leu Arg
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    130                 135                 140

aac caa cct gca ccc acc cat cag gat aac aac aag agt act gat act      480
Asn Gln Pro Ala Pro Thr His Gln Asp Asn Asn Lys Ser Thr Asp Thr
145                 150                 155                 160

ggg cct gtc ggt gga gcc gcc gct ggg aac cta ccc aat gca cag acc      528
Gly Pro Val Gly Gly Ala Ala Ala Gly Asn Leu Pro Asn Ala Gln Thr
                165                 170                 175

tta tcg ttg tcc atg agc acc ggc tcg cac cag acc ggt gcc att gaa      576
Leu Ser Leu Ser Met Ser Thr Gly Ser His Gln Thr Gly Ala Ile Glu
            180                 185                 190

acg gtg cca agg aag tcc att gat aca ttt gga cag agg aca tcc ata      624
Thr Val Pro Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Ile
        195                 200                 205

tac cgt ggt gta aca agg cat aga tgg acg ggt aga tat gag gct cat      672
Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His
    210                 215                 220

cta tgg gac aac agt tgc aga aga gaa gga caa act cga aag gga agg      720
Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Thr Arg Lys Gly Arg
225                 230                 235                 240

caa gtt tat tta ggt ggt tat gac aaa gaa gaa aag gca gct agg gct      768
Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala
                245                 250                 255

tac gat tta gca gca ctg aag tat tgg ggt acc acc acc aca aca aat      816
Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr Thr Asn
            260                 265                 270

ttc cct att agc aac tat gaa aaa gag ata gag gag atg aag cac atg      864
Phe Pro Ile Ser Asn Tyr Glu Lys Glu Ile Glu Glu Met Lys His Met
        275                 280                 285

aca agg cag gag tac gta gca tct ctg cga agg aag agt agc ggg ttt      912
Thr Arg Gln Glu Tyr Val Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe
    290                 295                 300

tct cgt gga gca tcc ata tat aga gga gtg acc aga cac cat cag cat      960
Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His
305                 310                 315                 320

ggg aga tgg cag gca agg att gga aga gtc gca ggc aac aaa gat ctt     1008
Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu
                325                 330                 335

tac ttg gga act ttc agc acc caa gag gaa gca gca gag gcc tat gac     1056
Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp
            340                 345                 350

att gct gcc att aag ttt cga gga ttg aat gcg gtg acc aac ttt gat     1104
Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp
        355                 360                 365

atg agt aga tat gat gtt aat agc att cta gag agc agt acc ttg ccg     1152
Met Ser Arg Tyr Asp Val Asn Ser Ile Leu Glu Ser Ser Thr Leu Pro
    370                 375                 380

att ggt gga gct gca aag cgg ttg aaa gat gct gag cag gct gaa atg     1200
Ile Gly Gly Ala Ala Lys Arg Leu Lys Asp Ala Glu Gln Ala Glu Met
385                 390                 395                 400

act ata gat gga cag agg aca gac gat gag atg agc tca cag ctg act     1248
Thr Ile Asp Gly Gln Arg Thr Asp Asp Glu Met Ser Ser Gln Leu Thr
                405                 410                 415

gat gga atc aac aac tat gga gca cac cac cat ggc tgg cct act gtt     1296
Asp Gly Ile Asn Asn Tyr Gly Ala His His His Gly Trp Pro Thr Val
            420                 425                 430

gca ttc caa caa gct cag cca ttt agc atg cac tac cct tat ggc cat     1344
Ala Phe Gln Gln Ala Gln Pro Phe Ser Met His Tyr Pro Tyr Gly His
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                              -continued
        435                 440                 445

cag cag agg gct gtt tgg tgt aag caa gag caa gac cct gat ggc aca     1392
Gln Gln Arg Ala Val Trp Cys Lys Gln Glu Gln Asp Pro Asp Gly Thr
    450                 455                 460

cac aac ttt caa gat ctt cac caa cta caa ttg gga aac act cac aac     1440
His Asn Phe Gln Asp Leu His Gln Leu Gln Leu Gly Asn Thr His Asn
465                 470                 475                 480

ttc ttc cag cct aat gtt ctg cac aac ctc atg agc atg gac tct tct     1488
Phe Phe Gln Pro Asn Val Leu His Asn Leu Met Ser Met Asp Ser Ser
                485                 490                 495

tca atg gac cat agc tca ggc tcc aat tca gtc atc tat agc ggt ggt     1536
Ser Met Asp His Ser Ser Gly Ser Asn Ser Val Ile Tyr Ser Gly Gly
            500                 505                 510

gga gcc gct gat ggc agc gct gca act ggc ggc agt ggc agt ggg agc     1584
Gly Ala Ala Asp Gly Ser Ala Ala Thr Gly Gly Ser Gly Ser Gly Ser
        515                 520                 525

ttc caa ggg gta ggt tat ggg aac aac att ggc ttt gtg atg ccc ata     1632
Phe Gln Gly Val Gly Tyr Gly Asn Asn Ile Gly Phe Val Met Pro Ile
    530                 535                 540

agc acc gtc atc gct cat gaa ggc ggc cat ggc cag gga aat ggt ggc     1680
Ser Thr Val Ile Ala His Glu Gly Gly His Gly Gln Gly Asn Gly Gly
545                 550                 555                 560

ttt gga gat agc gaa gtg aag gcg att ggt tac gac aac atg ttt gga     1728
Phe Gly Asp Ser Glu Val Lys Ala Ile Gly Tyr Asp Asn Met Phe Gly
                565                 570                 575

tcg aca gat cct tac cat gct agg agc ttg tac tat ctt tca cag caa     1776
Ser Thr Asp Pro Tyr His Ala Arg Ser Leu Tyr Tyr Leu Ser Gln Gln
            580                 585                 590

tca tct gca ggc atg gtg aag ggc agt agt gca tat gat cag ggg tca     1824
Ser Ser Ala Gly Met Val Lys Gly Ser Ser Ala Tyr Asp Gln Gly Ser
        595                 600                 605

ggg tgt aac aac tgg gtt cca act gca gtt cca acc cta gct cca agg     1872
Gly Cys Asn Asn Trp Val Pro Thr Ala Val Pro Thr Leu Ala Pro Arg
    610                 615                 620

act aac agc ttg gca gta tgc cat gga aca cct aca ttc aca gta tgg     1920
Thr Asn Ser Leu Ala Val Cys His Gly Thr Pro Thr Phe Thr Val Trp
625                 630                 635                 640

aat gat aca taa                                                     1932
Asn Asp Thr


<210> SEQ ID NO 6
<211> LENGTH: 643
<212> TYPE: PRT
<213> ORGANISM: Vitis vinifera

<400> SEQUENCE: 6

Met Ala Ser Met Asn Asn Trp Leu Gly Phe Ser Leu Ser Pro Arg Glu
1               5                   10                  15

Leu Pro Pro Gln Pro Glu Asn His Ser Gln Asn Ser Val Ser Arg Leu
            20                  25                  30

Gly Phe Asn Ser Asp Glu Ile Ser Gly Thr Asp Val Ser Gly Glu Cys
        35                  40                  45

Phe Asp Leu Thr Ser Asp Ser Thr Ala Pro Ser Leu Asn Leu Pro Pro
    50                  55                  60

Pro Phe Gly Ile Leu Glu Ala Phe Asn Arg Asn Asn Gln Pro Gln Asp
65                  70                  75                  80
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Thr Asn Tyr Lys Thr Thr Thr Ser Glu Leu Ser Met Leu Met Gly Ser
                85                  90                  95

Ser Cys Ser Ser His His Asn Leu Glu Asn Gln Glu Pro Lys Leu Glu
            100                 105                 110

Asn Phe Leu Gly Cys Arg Ser Phe Ala Asp His Glu Gln Lys Leu Gln
        115                 120                 125

Gly Tyr Tyr Ile Ser Ile Gly Leu Ser Met Ile Lys Thr Trp Leu Arg
    130                 135                 140

Asn Gln Pro Ala Pro Thr His Gln Asp Asn Asn Lys Ser Thr Asp Thr
145                 150                 155                 160

Gly Pro Val Gly Gly Ala Ala Ala Gly Asn Leu Pro Asn Ala Gln Thr
                165                 170                 175

Leu Ser Leu Ser Met Ser Thr Gly Ser His Gln Thr Gly Ala Ile Glu
            180                 185                 190

Thr Val Pro Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Ile
        195                 200                 205

Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His
    210                 215                 220

Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Thr Arg Lys Gly Arg
225                 230                 235                 240

Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala
                245                 250                 255

Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr Thr Asn
            260                 265                 270

Phe Pro Ile Ser Asn Tyr Glu Lys Glu Ile Glu Glu Met Lys His Met
        275                 280                 285

Thr Arg Gln Glu Tyr Val Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe
    290                 295                 300

Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His
305                 310                 315                 320

Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu
                325                 330                 335

Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp
            340                 345                 350

Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp
        355                 360                 365

Met Ser Arg Tyr Asp Val Asn Ser Ile Leu Glu Ser Ser Thr Leu Pro
    370                 375                 380

Ile Gly Gly Ala Ala Lys Arg Leu Lys Asp Ala Glu Gln Ala Glu Met
385                 390                 395                 400

Thr Ile Asp Gly Gln Arg Thr Asp Asp Glu Met Ser Ser Gln Leu Thr
                405                 410                 415

Asp Gly Ile Asn Asn Tyr Gly Ala His His His Gly Trp Pro Thr Val
            420                 425                 430

Ala Phe Gln Gln Ala Gln Pro Phe Ser Met His Tyr Pro Tyr Gly His
        435                 440                 445

Gln Gln Arg Ala Val Trp Cys Lys Gln Glu Gln Asp Pro Asp Gly Thr
    450                 455                 460

His Asn Phe Gln Asp Leu His Gln Leu Gln Leu Gly Asn Thr His Asn
465                 470                 475                 480

Phe Phe Gln Pro Asn Val Leu His Asn Leu Met Ser Met Asp Ser Ser
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                485                 490                 495

Ser Met Asp His Ser Ser Gly Ser Asn Ser Val Ile Tyr Ser Gly Gly
            500                 505                 510

Gly Ala Ala Asp Gly Ser Ala Ala Thr Gly Gly Ser Gly Ser Gly Ser
        515                 520                 525

Phe Gln Gly Val Gly Tyr Gly Asn Asn Ile Gly Phe Val Met Pro Ile
    530                 535                 540

Ser Thr Val Ile Ala His Glu Gly Gly His Gly Gln Gly Asn Gly Gly
545                 550                 555                 560

Phe Gly Asp Ser Glu Val Lys Ala Ile Gly Tyr Asp Asn Met Phe Gly
                565                 570                 575

Ser Thr Asp Pro Tyr His Ala Arg Ser Leu Tyr Tyr Leu Ser Gln Gln
            580                 585                 590

Ser Ser Ala Gly Met Val Lys Gly Ser Ser Ala Tyr Asp Gln Gly Ser
        595                 600                 605

Gly Cys Asn Asn Trp Val Pro Thr Ala Val Pro Thr Leu Ala Pro Arg
    610                 615                 620

Thr Asn Ser Leu Ala Val Cys His Gly Thr Pro Thr Phe Thr Val Trp
625                 630                 635                 640

Asn Asp Thr


<210> SEQ ID NO 7
<211> LENGTH: 2070
<212> TYPE: DNA
<213> ORGANISM: Medicago truncatula
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(2070)

<400> SEQUENCE: 7

atg gcc tct atg aac ttg tta ggt ttc tct cta tct cca caa gaa caa         48
Met Ala Ser Met Asn Leu Leu Gly Phe Ser Leu Ser Pro Gln Glu Gln
1               5                   10                  15

cat cca tca aca caa gat caa acg gtg gct tcc cgt ttt ggg ttc aac         96
His Pro Ser Thr Gln Asp Gln Thr Val Ala Ser Arg Phe Gly Phe Asn
            20                  25                  30

cct aat gaa atc tca ggc tct gat gtt caa gga gat cac tgc tat gat        144
Pro Asn Glu Ile Ser Gly Ser Asp Val Gln Gly Asp His Cys Tyr Asp
        35                  40                  45

ctc tct tct cac aca act cct cat cat tca ctc aac ctt tct cat cct        192
Leu Ser Ser His Thr Thr Pro His His Ser Leu Asn Leu Ser His Pro
    50                  55                  60

ttt tcc att tat gaa gct ttc cac aca aat aac aac att cac acc act        240
Phe Ser Ile Tyr Glu Ala Phe His Thr Asn Asn Asn Ile His Thr Thr
65                  70                  75                  80

caa gat tgg aag gag aac tac aac aac caa aac cta cta ttg gga aca        288
Gln Asp Trp Lys Glu Asn Tyr Asn Asn Gln Asn Leu Leu Leu Gly Thr
                85                  90                  95

tca tgc atg aac caa aat gtg aac aac aac aac caa caa gca caa cca        336
Ser Cys Met Asn Gln Asn Val Asn Asn Asn Asn Gln Gln Ala Gln Pro
            100                 105                 110

aag cta gaa aac ttc ctc ggt gga cac tct ttc acc gac cat caa gaa        384
Lys Leu Glu Asn Phe Leu Gly Gly His Ser Phe Thr Asp His Gln Glu
        115                 120                 125

tac ggt ggt agc aac tca tac tct tca tta cac ctc cca cct cat cag        432
Tyr Gly Gly Ser Asn Ser Tyr Ser Ser Leu His Leu Pro Pro His Gln
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    130                 135                 140

ccg gaa gca tcc tgt ggc ggt ggt gat ggt agt aca agt aac aat aac      480
Pro Glu Ala Ser Cys Gly Gly Gly Asp Gly Ser Thr Ser Asn Asn Asn
145                 150                 155                 160

tca ata ggt tta tct atg ata aaa aca tgg ctc aga aac caa cca cca      528
Ser Ile Gly Leu Ser Met Ile Lys Thr Trp Leu Arg Asn Gln Pro Pro
                165                 170                 175

cca cca gaa aac aac aac aat aac aac aat gaa agt ggt gca cgt gtg      576
Pro Pro Glu Asn Asn Asn Asn Asn Asn Asn Glu Ser Gly Ala Arg Val
            180                 185                 190

cag aca cta tca ctt tct atg agt act ggc tca cag tca agt tca tct      624
Gln Thr Leu Ser Leu Ser Met Ser Thr Gly Ser Gln Ser Ser Ser Ser
        195                 200                 205

gtg cct ctt ctc aat gca aat gtg atg agt ggt gag att tcc tca tcg      672
Val Pro Leu Leu Asn Ala Asn Val Met Ser Gly Glu Ile Ser Ser Ser
    210                 215                 220

gaa aac aaa caa cca ccc aca act gca gtt gta ctt gat agc aac caa      720
Glu Asn Lys Gln Pro Pro Thr Thr Ala Val Val Leu Asp Ser Asn Gln
225                 230                 235                 240

aca agt gtc gtt gaa agt gct gtg cct aga aaa tcc gtt gat aca ttt      768
Thr Ser Val Val Glu Ser Ala Val Pro Arg Lys Ser Val Asp Thr Phe
                245                 250                 255

gga caa aga act tcc att tac cgt ggt gta aca agg cat aga tgg aca      816
Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr
            260                 265                 270

ggg aga tat gaa gct cac ctt tgg gat aat agt tgt aga aga gag ggg      864
Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly
        275                 280                 285

cag act cgc aaa gga agg caa gtt tac ttg gga ggt tat gac aaa gaa      912
Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu
    290                 295                 300

gaa aaa gca gct aga gcc tat gat ttg gca gca cta aaa tat tgg gga      960
Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly
305                 310                 315                 320

aca act act aca aca aat ttt cca att agc cat tat gaa aaa gaa gtg     1008
Thr Thr Thr Thr Thr Asn Phe Pro Ile Ser His Tyr Glu Lys Glu Val
                325                 330                 335

gaa gaa atg aag cat atg aca agg caa gag tac gtt gcg tca ttg aga     1056
Glu Glu Met Lys His Met Thr Arg Gln Glu Tyr Val Ala Ser Leu Arg
            340                 345                 350

agg aaa agt agt ggt ttt tca cga ggt gca tcc att tac cga gga gta     1104
Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val
        355                 360                 365

aca aga cat cat caa cat ggt aga tgg caa gct agg att gga aga gtt     1152
Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val
    370                 375                 380

gca ggc aac aaa gat ctc tac cta gga act ttc agc act caa gaa gag     1200
Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu
385                 390                 395                 400

gca gca gag gca tat gat gtg gca gca ata aaa ttc aga gga ctg agt     1248
Ala Ala Glu Ala Tyr Asp Val Ala Ala Ile Lys Phe Arg Gly Leu Ser
                405                 410                 415

gca gtt aca aac ttt gac atg agc aga tat gat gtc aaa acc ata ctt     1296
Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Thr Ile Leu
            420                 425                 430

gag agc agc aca tta cca att ggt ggt gct gca aag cgt tta aaa gac     1344
Glu Ser Ser Thr Leu Pro Ile Gly Gly Ala Ala Lys Arg Leu Lys Asp
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        435                 440                 445

atg gag caa gtt gaa ttg aat cat gtg aat gtt gat att agc cat aga     1392
Met Glu Gln Val Glu Leu Asn His Val Asn Val Asp Ile Ser His Arg
    450                 455                 460

act gaa caa gat cat agc atc atc aac aac act tcc cat tta aca gaa     1440
Thr Glu Gln Asp His Ser Ile Ile Asn Asn Thr Ser His Leu Thr Glu
465                 470                 475                 480

caa gcc atc tat gca gca aca aat gca tct aat tgg cat gca ctt tca     1488
Gln Ala Ile Tyr Ala Ala Thr Asn Ala Ser Asn Trp His Ala Leu Ser
                485                 490                 495

ttc caa cat caa caa cca cat cat cat tac aat gcc aac aac atg cag     1536
Phe Gln His Gln Gln Pro His His His Tyr Asn Ala Asn Asn Met Gln
            500                 505                 510

tta cag aat tat cct tat gga act caa act caa aag ctt tgg tgc aaa     1584
Leu Gln Asn Tyr Pro Tyr Gly Thr Gln Thr Gln Lys Leu Trp Cys Lys
        515                 520                 525

caa gaa caa gat tct gat gat cat agt act tat act act gct act gat     1632
Gln Glu Gln Asp Ser Asp Asp His Ser Thr Tyr Thr Thr Ala Thr Asp
    530                 535                 540

att cat caa cta cag tta ggg aat aat aat aac aat act cac aat ttc     1680
Ile His Gln Leu Gln Leu Gly Asn Asn Asn Asn Asn Thr His Asn Phe
545                 550                 555                 560

ttt ggt tta caa aat atc atg agt atg gat tct gct tcc atg gat aat     1728
Phe Gly Leu Gln Asn Ile Met Ser Met Asp Ser Ala Ser Met Asp Asn
                565                 570                 575

agt tct gga tct aat tct gtt gtt tat ggt ggt gga gat cat ggt ggt     1776
Ser Ser Gly Ser Asn Ser Val Val Tyr Gly Gly Gly Asp His Gly Gly
            580                 585                 590

tat gga gga aat ggt gga tat atg att cca atg gct att gca aat gat     1824
Tyr Gly Gly Asn Gly Gly Tyr Met Ile Pro Met Ala Ile Ala Asn Asp
        595                 600                 605

ggt aac caa aat cca aga agc aac aac aat ttt ggt gag agt gag att     1872
Gly Asn Gln Asn Pro Arg Ser Asn Asn Asn Phe Gly Glu Ser Glu Ile
    610                 615                 620

aaa gga ttt ggt tat gaa aat gtt ttt ggg act act act gat cct tat     1920
Lys Gly Phe Gly Tyr Glu Asn Val Phe Gly Thr Thr Thr Asp Pro Tyr
625                 630                 635                 640

cat gca cag gca gca agg aac ttg tac tat cag cca caa caa tta tct     1968
His Ala Gln Ala Ala Arg Asn Leu Tyr Tyr Gln Pro Gln Gln Leu Ser
                645                 650                 655

gtt gat caa gga tca aat tgg gtt cca act gct att cca aca ctt gct     2016
Val Asp Gln Gly Ser Asn Trp Val Pro Thr Ala Ile Pro Thr Leu Ala
            660                 665                 670

cca agg act acc aat gtc tct cta tgt cct cct ttc act ttg ttg cat     2064
Pro Arg Thr Thr Asn Val Ser Leu Cys Pro Pro Phe Thr Leu Leu His
        675                 680                 685

gaa tag                                                             2070
Glu


<210> SEQ ID NO 8
<211> LENGTH: 689
<212> TYPE: PRT
<213> ORGANISM: Medicago truncatula

<400> SEQUENCE: 8

Met Ala Ser Met Asn Leu Leu Gly Phe Ser Leu Ser Pro Gln Glu Gln
1               5                   10                  15
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His Pro Ser Thr Gln Asp Gln Thr Val Ala Ser Arg Phe Gly Phe Asn
            20                  25                  30

Pro Asn Glu Ile Ser Gly Ser Asp Val Gln Gly Asp His Cys Tyr Asp
        35                  40                  45

Leu Ser Ser His Thr Thr Pro His His Ser Leu Asn Leu Ser His Pro
    50                  55                  60

Phe Ser Ile Tyr Glu Ala Phe His Thr Asn Asn Asn Ile His Thr Thr
65                  70                  75                  80

Gln Asp Trp Lys Glu Asn Tyr Asn Asn Gln Asn Leu Leu Leu Gly Thr
                85                  90                  95

Ser Cys Met Asn Gln Asn Val Asn Asn Asn Asn Gln Gln Ala Gln Pro
            100                 105                 110

Lys Leu Glu Asn Phe Leu Gly Gly His Ser Phe Thr Asp His Gln Glu
        115                 120                 125

Tyr Gly Gly Ser Asn Ser Tyr Ser Ser Leu His Leu Pro Pro His Gln
    130                 135                 140

Pro Glu Ala Ser Cys Gly Gly Gly Asp Gly Ser Thr Ser Asn Asn Asn
145                 150                 155                 160

Ser Ile Gly Leu Ser Met Ile Lys Thr Trp Leu Arg Asn Gln Pro Pro
                165                 170                 175

Pro Pro Glu Asn Asn Asn Asn Asn Asn Asn Glu Ser Gly Ala Arg Val
            180                 185                 190

Gln Thr Leu Ser Leu Ser Met Ser Thr Gly Ser Gln Ser Ser Ser Ser
        195                 200                 205

Val Pro Leu Leu Asn Ala Asn Val Met Ser Gly Glu Ile Ser Ser Ser
    210                 215                 220

Glu Asn Lys Gln Pro Pro Thr Thr Ala Val Val Leu Asp Ser Asn Gln
225                 230                 235                 240

Thr Ser Val Val Glu Ser Ala Val Pro Arg Lys Ser Val Asp Thr Phe
                245                 250                 255

Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr
            260                 265                 270

Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly
        275                 280                 285

Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu
    290                 295                 300

Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly
305                 310                 315                 320

Thr Thr Thr Thr Thr Asn Phe Pro Ile Ser His Tyr Glu Lys Glu Val
                325                 330                 335

Glu Glu Met Lys His Met Thr Arg Gln Glu Tyr Val Ala Ser Leu Arg
            340                 345                 350

Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val
        355                 360                 365

Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val
    370                 375                 380

Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu
385                 390                 395                 400

Ala Ala Glu Ala Tyr Asp Val Ala Ala Ile Lys Phe Arg Gly Leu Ser
                405                 410                 415

Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Thr Ile Leu
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            420                 425                 430

Glu Ser Ser Thr Leu Pro Ile Gly Gly Ala Ala Lys Arg Leu Lys Asp
        435                 440                 445

Met Glu Gln Val Glu Leu Asn His Val Asn Val Asp Ile Ser His Arg
    450                 455                 460

Thr Glu Gln Asp His Ser Ile Ile Asn Asn Thr Ser His Leu Thr Glu
465                 470                 475                 480

Gln Ala Ile Tyr Ala Ala Thr Asn Ala Ser Asn Trp His Ala Leu Ser
                485                 490                 495

Phe Gln His Gln Gln Pro His His His Tyr Asn Ala Asn Asn Met Gln
            500                 505                 510

Leu Gln Asn Tyr Pro Tyr Gly Thr Gln Thr Gln Lys Leu Trp Cys Lys
        515                 520                 525

Gln Glu Gln Asp Ser Asp Asp His Ser Thr Tyr Thr Thr Ala Thr Asp
    530                 535                 540

Ile His Gln Leu Gln Leu Gly Asn Asn Asn Asn Asn Thr His Asn Phe
545                 550                 555                 560

Phe Gly Leu Gln Asn Ile Met Ser Met Asp Ser Ala Ser Met Asp Asn
                565                 570                 575

Ser Ser Gly Ser Asn Ser Val Val Tyr Gly Gly Gly Asp His Gly Gly
            580                 585                 590

Tyr Gly Gly Asn Gly Gly Tyr Met Ile Pro Met Ala Ile Ala Asn Asp
        595                 600                 605

Gly Asn Gln Asn Pro Arg Ser Asn Asn Asn Phe Gly Glu Ser Glu Ile
    610                 615                 620

Lys Gly Phe Gly Tyr Glu Asn Val Phe Gly Thr Thr Thr Asp Pro Tyr
625                 630                 635                 640

His Ala Gln Ala Ala Arg Asn Leu Tyr Tyr Gln Pro Gln Gln Leu Ser
                645                 650                 655

Val Asp Gln Gly Ser Asn Trp Val Pro Thr Ala Ile Pro Thr Leu Ala
            660                 665                 670

Pro Arg Thr Thr Asn Val Ser Leu Cys Pro Pro Phe Thr Leu Leu His
        675                 680                 685

Glu


<210> SEQ ID NO 9
<211> LENGTH: 2130
<212> TYPE: DNA
<213> ORGANISM: Zea mays
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(2130)

<400> SEQUENCE: 9

atg gcc act gtg aac aac tgg ctc gct ttc tcc ctc tcc ccg cag gag           48
Met Ala Thr Val Asn Asn Trp Leu Ala Phe Ser Leu Ser Pro Gln Glu
1               5                   10                  15

ctg ccg ccc tcc cag acg acg gac tcc acg ctc atc tcg gcc gcc acc           96
Leu Pro Pro Ser Gln Thr Thr Asp Ser Thr Leu Ile Ser Ala Ala Thr
            20                  25                  30

gcc gac cat gtc tcc ggc gat gtc tgc ttc aac atc ccc caa gat tgg          144
Ala Asp His Val Ser Gly Asp Val Cys Phe Asn Ile Pro Gln Asp Trp
        35                  40                  45

agc atg agg gga tca gag ctt tcg gcg ctc gtc gcg gag ccg aag ctg          192
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Ser Met Arg Gly Ser Glu Leu Ser Ala Leu Val Ala Glu Pro Lys Leu
    50                  55                  60

gag gac ttc ctc ggc ggc atc tcc ttc tcc gag cag cat cac aag tcc      240
Glu Asp Phe Leu Gly Gly Ile Ser Phe Ser Glu Gln His His Lys Ser
65                  70                  75                  80

aac tgc aac ttg ata ccc agc act agc agc aca gtt tgc tac gcg agc      288
Asn Cys Asn Leu Ile Pro Ser Thr Ser Ser Thr Val Cys Tyr Ala Ser
                85                  90                  95

tca gct gct agc acc ggc tac cat cac cag ctg tac cag ccc acc agc      336
Ser Ala Ala Ser Thr Gly Tyr His His Gln Leu Tyr Gln Pro Thr Ser
            100                 105                 110

tcc gcg ctc cac ttc gcg gac tcc gtc atg gtg gcc tcc tcg gcc ggt      384
Ser Ala Leu His Phe Ala Asp Ser Val Met Val Ala Ser Ser Ala Gly
        115                 120                 125

gtc cac gac ggc ggt tcc atg ctc agc gcg gcc gcc gct aac ggt gtc      432
Val His Asp Gly Gly Ser Met Leu Ser Ala Ala Ala Ala Asn Gly Val
    130                 135                 140

gct ggc gct gcc agt gcc aac ggc ggc ggc atc ggg ctg tcc atg atc      480
Ala Gly Ala Ala Ser Ala Asn Gly Gly Gly Ile Gly Leu Ser Met Ile
145                 150                 155                 160

aag aac tgg ctg cgg agc caa ccg gcg ccc atg cag ccg agg gcg gcg      528
Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Met Gln Pro Arg Ala Ala
                165                 170                 175

gcg gct gag ggc gcg cag ggg ctc tct ttg tcc atg aac atg gcg ggg      576
Ala Ala Glu Gly Ala Gln Gly Leu Ser Leu Ser Met Asn Met Ala Gly
            180                 185                 190

acg acc caa ggc gct gct ggc atg cca ctt ctc gct gga gag cgc gca      624
Thr Thr Gln Gly Ala Ala Gly Met Pro Leu Leu Ala Gly Glu Arg Ala
        195                 200                 205

cgg gcg ccc gag agt gta tcg acg tca gca cag ggt ggt gcc gtc gtc      672
Arg Ala Pro Glu Ser Val Ser Thr Ser Ala Gln Gly Gly Ala Val Val
    210                 215                 220

gtc acg gcg ccg aag gag gat agc ggt ggc agc ggt gtt gcc ggt gct      720
Val Thr Ala Pro Lys Glu Asp Ser Gly Gly Ser Gly Val Ala Gly Ala
225                 230                 235                 240

cta gta gcc gtg agc acg gac acg ggt ggc agc ggc ggc gcg tcg gct      768
Leu Val Ala Val Ser Thr Asp Thr Gly Gly Ser Gly Gly Ala Ser Ala
                245                 250                 255

gac aac acg gca agg aag acg gtg gac acg ttc ggg cag cgc acg tcg      816
Asp Asn Thr Ala Arg Lys Thr Val Asp Thr Phe Gly Gln Arg Thr Ser
            260                 265                 270

att tac cgt ggc gtg aca agg cat aga tgg act ggg aga tat gag gca      864
Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala
        275                 280                 285

cat ctt tgg gat aac agt tgc aga agg gaa gga caa act cgt aag ggt      912
His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Thr Arg Lys Gly
    290                 295                 300

cgt caa gtc tat tta ggt ggc tat gat aaa gag gag aaa gct gct agg      960
Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg
305                 310                 315                 320

gct tat gat ctt gct gct ctg aag tac tgg ggt gcc aca aca aca aca     1008
Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Ala Thr Thr Thr Thr
                325                 330                 335

aat ttt cca gtg agt aac tac gaa aag gag ctc gag gac atg aag cac     1056
Asn Phe Pro Val Ser Asn Tyr Glu Lys Glu Leu Glu Asp Met Lys His
            340                 345                 350

atg aca agg cag gag ttt gta gcg tct ctg aga agg aag agc agt ggt     1104
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Met Thr Arg Gln Glu Phe Val Ala Ser Leu Arg Arg Lys Ser Ser Gly
        355                 360                 365

ttc tcc aga ggt gca tcc att tac agg gga gtg act agg cat cac caa     1152
Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln
    370                 375                 380

cat gga aga tgg caa gca cgg att gga cga gtt gca ggg aac aag gat     1200
His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp
385                 390                 395                 400

ctt tac ttg ggc acc ttc agc acc cag gag gag gca gcg gag gcg tac     1248
Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr
                405                 410                 415

gac atc gcg gcg atc aag ttc cgc ggc ctc aac gcc gtc acc aac ttc     1296
Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe
            420                 425                 430

gac atg agc cgc tac gac gtg aag agc atc ctg gac agc agc gcc ctc     1344
Asp Met Ser Arg Tyr Asp Val Lys Ser Ile Leu Asp Ser Ser Ala Leu
        435                 440                 445

ccc atc ggc agc gcc gcc aag cgt ctc aag gag gcc gag gcc gca gcg     1392
Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Glu Ala Glu Ala Ala Ala
    450                 455                 460

tcc gcg cag cac cac cac gcc ggc gtg gtg agc tac gac gtc ggc cgc     1440
Ser Ala Gln His His His Ala Gly Val Val Ser Tyr Asp Val Gly Arg
465                 470                 475                 480

atc gcc tcg cag ctc ggc gac ggc gga gcc cta gcg gcg gcg tac ggc     1488
Ile Ala Ser Gln Leu Gly Asp Gly Gly Ala Leu Ala Ala Ala Tyr Gly
                485                 490                 495

gcg cac tac cac ggc gcc gcc tgg ccg acc atc gcg ttc cag ccg ggc     1536
Ala His Tyr His Gly Ala Ala Trp Pro Thr Ile Ala Phe Gln Pro Gly
            500                 505                 510

gcc gcc acc aca ggc ctg tac cac ccg tac gcg cag cag cca atg cgc     1584
Ala Ala Thr Thr Gly Leu Tyr His Pro Tyr Ala Gln Gln Pro Met Arg
        515                 520                 525

ggc ggc ggg tgg tgc aag cag gag cag gac cac gcg gtg atc gcg gcc     1632
Gly Gly Gly Trp Cys Lys Gln Glu Gln Asp His Ala Val Ile Ala Ala
    530                 535                 540

gcg cac agc ctg cag gac ctc cac cac ttg aac ctg ggc gcg gcc ggc     1680
Ala His Ser Leu Gln Asp Leu His His Leu Asn Leu Gly Ala Ala Gly
545                 550                 555                 560

gcg cac gac ttt ttc tcg gca ggg cag cag gcc gcc gcc gca gct gcg     1728
Ala His Asp Phe Phe Ser Ala Gly Gln Gln Ala Ala Ala Ala Ala Ala
                565                 570                 575

atg cac ggc ctg gct agc atc gac agt gcg tcg ctc gag cac agc acc     1776
Met His Gly Leu Ala Ser Ile Asp Ser Ala Ser Leu Glu His Ser Thr
            580                 585                 590

ggc tcc aac tcc gtc gtc tac aac ggc ggg gtc ggc gat agc aac ggc     1824
Gly Ser Asn Ser Val Val Tyr Asn Gly Gly Val Gly Asp Ser Asn Gly
        595                 600                 605

gcc agc gcc gtt ggc agc ggc ggt ggc tac atg atg ccg atg agc gct     1872
Ala Ser Ala Val Gly Ser Gly Gly Gly Tyr Met Met Pro Met Ser Ala
    610                 615                 620

gcc gga gca acc act aca tcg gca atg gtg agc cac gag cag atg cat     1920
Ala Gly Ala Thr Thr Thr Ser Ala Met Val Ser His Glu Gln Met His
625                 630                 635                 640

gca cgg gcc tac gac gaa gcc aag cag gct gct cag atg ggg tac gag     1968
Ala Arg Ala Tyr Asp Glu Ala Lys Gln Ala Ala Gln Met Gly Tyr Glu
                645                 650                 655

agc tac ctg gtg aac gcg gag aac aat ggt ggc gga agg atg tct gca     2016
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Ser Tyr Leu Val Asn Ala Glu Asn Asn Gly Gly Gly Arg Met Ser Ala
            660                 665                 670

tgg ggg acc gtc gtc tct gca gcc gcg gcg gca gca gca agc agc aac      2064
Trp Gly Thr Val Val Ser Ala Ala Ala Ala Ala Ala Ala Ser Ser Asn
        675                 680                 685

gac aac att gcc gcc gac gtc ggc cat ggc ggc gcg cag ctc ttc agt      2112
Asp Asn Ile Ala Ala Asp Val Gly His Gly Gly Ala Gln Leu Phe Ser
    690                 695                 700

gtc tgg aac gac act taa                                              2130
Val Trp Asn Asp Thr
705


<210> SEQ ID NO 10
<211> LENGTH: 709
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 10

Met Ala Thr Val Asn Asn Trp Leu Ala Phe Ser Leu Ser Pro Gln Glu
1               5                   10                  15

Leu Pro Pro Ser Gln Thr Thr Asp Ser Thr Leu Ile Ser Ala Ala Thr
            20                  25                  30

Ala Asp His Val Ser Gly Asp Val Cys Phe Asn Ile Pro Gln Asp Trp
        35                  40                  45

Ser Met Arg Gly Ser Glu Leu Ser Ala Leu Val Ala Glu Pro Lys Leu
    50                  55                  60

Glu Asp Phe Leu Gly Gly Ile Ser Phe Ser Glu Gln His His Lys Ser
65                  70                  75                  80

Asn Cys Asn Leu Ile Pro Ser Thr Ser Ser Thr Val Cys Tyr Ala Ser
                85                  90                  95

Ser Ala Ala Ser Thr Gly Tyr His His Gln Leu Tyr Gln Pro Thr Ser
            100                 105                 110

Ser Ala Leu His Phe Ala Asp Ser Val Met Val Ala Ser Ser Ala Gly
        115                 120                 125

Val His Asp Gly Gly Ser Met Leu Ser Ala Ala Ala Ala Asn Gly Val
    130                 135                 140

Ala Gly Ala Ala Ser Ala Asn Gly Gly Gly Ile Gly Leu Ser Met Ile
145                 150                 155                 160

Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Met Gln Pro Arg Ala Ala
                165                 170                 175

Ala Ala Glu Gly Ala Gln Gly Leu Ser Leu Ser Met Asn Met Ala Gly
            180                 185                 190

Thr Thr Gln Gly Ala Ala Gly Met Pro Leu Leu Ala Gly Glu Arg Ala
        195                 200                 205

Arg Ala Pro Glu Ser Val Ser Thr Ser Ala Gln Gly Gly Ala Val Val
    210                 215                 220

Val Thr Ala Pro Lys Glu Asp Ser Gly Gly Ser Gly Val Ala Gly Ala
225                 230                 235                 240

Leu Val Ala Val Ser Thr Asp Thr Gly Gly Ser Gly Gly Ala Ser Ala
                245                 250                 255

Asp Asn Thr Ala Arg Lys Thr Val Asp Thr Phe Gly Gln Arg Thr Ser
            260                 265                 270

Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala
        275                 280                 285
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His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Thr Arg Lys Gly
    290                 295                 300

Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg
305                 310                 315                 320

Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Ala Thr Thr Thr Thr
                325                 330                 335

Asn Phe Pro Val Ser Asn Tyr Glu Lys Glu Leu Glu Asp Met Lys His
            340                 345                 350

Met Thr Arg Gln Glu Phe Val Ala Ser Leu Arg Arg Lys Ser Ser Gly
        355                 360                 365

Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln
    370                 375                 380

His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp
385                 390                 395                 400

Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr
                405                 410                 415

Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe
            420                 425                 430

Asp Met Ser Arg Tyr Asp Val Lys Ser Ile Leu Asp Ser Ser Ala Leu
        435                 440                 445

Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Glu Ala Glu Ala Ala Ala
    450                 455                 460

Ser Ala Gln His His His Ala Gly Val Val Ser Tyr Asp Val Gly Arg
465                 470                 475                 480

Ile Ala Ser Gln Leu Gly Asp Gly Gly Ala Leu Ala Ala Ala Tyr Gly
                485                 490                 495

Ala His Tyr His Gly Ala Ala Trp Pro Thr Ile Ala Phe Gln Pro Gly
            500                 505                 510

Ala Ala Thr Thr Gly Leu Tyr His Pro Tyr Ala Gln Gln Pro Met Arg
        515                 520                 525

Gly Gly Gly Trp Cys Lys Gln Glu Gln Asp His Ala Val Ile Ala Ala
    530                 535                 540

Ala His Ser Leu Gln Asp Leu His His Leu Asn Leu Gly Ala Ala Gly
545                 550                 555                 560

Ala His Asp Phe Phe Ser Ala Gly Gln Gln Ala Ala Ala Ala Ala Ala
                565                 570                 575

Met His Gly Leu Ala Ser Ile Asp Ser Ala Ser Leu Glu His Ser Thr
            580                 585                 590

Gly Ser Asn Ser Val Val Tyr Asn Gly Gly Val Gly Asp Ser Asn Gly
        595                 600                 605

Ala Ser Ala Val Gly Ser Gly Gly Gly Tyr Met Met Pro Met Ser Ala
    610                 615                 620

Ala Gly Ala Thr Thr Thr Ser Ala Met Val Ser His Glu Gln Met His
625                 630                 635                 640

Ala Arg Ala Tyr Asp Glu Ala Lys Gln Ala Ala Gln Met Gly Tyr Glu
                645                 650                 655

Ser Tyr Leu Val Asn Ala Glu Asn Asn Gly Gly Gly Arg Met Ser Ala
            660                 665                 670

Trp Gly Thr Val Val Ser Ala Ala Ala Ala Ala Ala Ala Ser Ser Asn
        675                 680                 685
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Asp Asn Ile Ala Ala Asp Val Gly His Gly Gly Ala Gln Leu Phe Ser
    690                 695                 700

Val Trp Asn Asp Thr
705


<210> SEQ ID NO 11
<211> LENGTH: 2040
<212> TYPE: DNA
<213> ORGANISM: Zea mays
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(2040)

<400> SEQUENCE: 11

atg gct tca gcg aac aac tgg ctg ggc ttc tcg ctc tcg ggc cag gat       48
Met Ala Ser Ala Asn Asn Trp Leu Gly Phe Ser Leu Ser Gly Gln Asp
1               5                   10                  15

aac ccg cag cct aac cag gat agc tcg cct gcc gcc ggt atc gac atc       96
Asn Pro Gln Pro Asn Gln Asp Ser Ser Pro Ala Ala Gly Ile Asp Ile
            20                  25                  30

tcc ggc gcc agc gac ttc tat ggc ctg ccc acg cag cag ggc tcc gac      144
Ser Gly Ala Ser Asp Phe Tyr Gly Leu Pro Thr Gln Gln Gly Ser Asp
        35                  40                  45

ggg cat ctc ggc gtg ccg ggc ctg cgg gac gat cac gct tct tat ggt      192
Gly His Leu Gly Val Pro Gly Leu Arg Asp Asp His Ala Ser Tyr Gly
    50                  55                  60

atc atg gag gcc tac aac agg gtt cct caa gaa acc caa gat tgg aac      240
Ile Met Glu Ala Tyr Asn Arg Val Pro Gln Glu Thr Gln Asp Trp Asn
65                  70                  75                  80

atg agg ggc ttg gac tac aac ggc ggt ggc tcg gag ctc tcg atg ctt      288
Met Arg Gly Leu Asp Tyr Asn Gly Gly Gly Ser Glu Leu Ser Met Leu
                85                  90                  95

gtg ggg tcc agc ggc ggc ggc ggg ggc aac ggc aag agg gcc gtg gaa      336
Val Gly Ser Ser Gly Gly Gly Gly Gly Asn Gly Lys Arg Ala Val Glu
            100                 105                 110

gac agc gag ccc aag ctc gaa gat ttc ctc ggc ggc aac tcg ttc gtc      384
Asp Ser Glu Pro Lys Leu Glu Asp Phe Leu Gly Gly Asn Ser Phe Val
        115                 120                 125

tcc gat caa gat cag tcc ggc ggt tac ctg ttc tct gga gtc ccg ata      432
Ser Asp Gln Asp Gln Ser Gly Gly Tyr Leu Phe Ser Gly Val Pro Ile
    130                 135                 140

gcc agc agc gcc aat agc aac agc ggg agc aac acc atg gag ctc tcc      480
Ala Ser Ser Ala Asn Ser Asn Ser Gly Ser Asn Thr Met Glu Leu Ser
145                 150                 155                 160

atg atc aag acc tgg cta cgg aac aac cag gtg gcc cag ccc cag ccg      528
Met Ile Lys Thr Trp Leu Arg Asn Asn Gln Val Ala Gln Pro Gln Pro
                165                 170                 175

cca gct cca cat cag ccg cag cct gag gaa atg agc acc gac gcc agc      576
Pro Ala Pro His Gln Pro Gln Pro Glu Glu Met Ser Thr Asp Ala Ser
            180                 185                 190

ggc agc agc ttt gga tgc tcg gat tcg atg gga agg aac agc atg gtg      624
Gly Ser Ser Phe Gly Cys Ser Asp Ser Met Gly Arg Asn Ser Met Val
        195                 200                 205

gcg gct ggt ggg agc tcg cag agc ctg gcg ctc tcg atg agc acg ggc      672
Ala Ala Gly Gly Ser Ser Gln Ser Leu Ala Leu Ser Met Ser Thr Gly
    210                 215                 220

tcg cac ctg ccc atg gtt gtg ccc agc ggc gcc gcc agc gga gcg gcc      720
Ser His Leu Pro Met Val Val Pro Ser Gly Ala Ala Ser Gly Ala Ala
225                 230                 235                 240
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tcg gag agc aca tcg tcg gag aac aag cga gcg agc ggt gcc atg gat      768
Ser Glu Ser Thr Ser Ser Glu Asn Lys Arg Ala Ser Gly Ala Met Asp
                245                 250                 255

tcg ccc ggc agc gcg gta gaa gcc gta ccg agg aag tcc atc gac acg      816
Ser Pro Gly Ser Ala Val Glu Ala Val Pro Arg Lys Ser Ile Asp Thr
            260                 265                 270

ttc ggg caa agg acc tct ata tat cga ggt gta aca agg cat aga tgg      864
Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp
        275                 280                 285

aca ggg cgg tat gag gct cat cta tgg gat aat agt tgt aga agg gaa      912
Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu
    290                 295                 300

ggg cag agt cgc aag ggt agg caa gtt tac ctt ggt ggc tat gac aag      960
Gly Gln Ser Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys
305                 310                 315                 320

gag gac aag gca gca agg gct tat gat ttg gca gct ctc aag tat tgg     1008
Glu Asp Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp
                325                 330                 335

ggc act acg aca aca aca aat ttc cct ata agc aac tac gaa aag gag     1056
Gly Thr Thr Thr Thr Thr Asn Phe Pro Ile Ser Asn Tyr Glu Lys Glu
            340                 345                 350

cta gaa gaa atg aaa cat atg act aga cag gag tac att gca tac cta     1104
Leu Glu Glu Met Lys His Met Thr Arg Gln Glu Tyr Ile Ala Tyr Leu
        355                 360                 365

aga aga aat agc agt gga ttt tct cgt ggg gcg tca aag tat cgt gga     1152
Arg Arg Asn Ser Ser Gly Phe Ser Arg Gly Ala Ser Lys Tyr Arg Gly
    370                 375                 380

gta act aga cat cat cag cat ggg aga tgg caa gca agg ata ggg aga     1200
Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg
385                 390                 395                 400

gtt gca gga aac aag gat ctc tac ttg ggc aca ttc agc acc gag gag     1248
Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Glu Glu
                405                 410                 415

gag gcg gcg gag gcc tac gac atc gcc gcg atc aag ttc cgc ggt ctc     1296
Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu
            420                 425                 430

aac gcc gtc acc aac ttc gac atg agc cgc tac gac gtg aag agc atc     1344
Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser Ile
        435                 440                 445

ctc gag agc agc aca ctg cct gtc ggc ggt gcg gcc agg cgc ctc aag     1392
Leu Glu Ser Ser Thr Leu Pro Val Gly Gly Ala Ala Arg Arg Leu Lys
    450                 455                 460

gac gcc gtg gac cac gtg gag gcc ggc gcc acc atc tgg cgc gcc gac     1440
Asp Ala Val Asp His Val Glu Ala Gly Ala Thr Ile Trp Arg Ala Asp
465                 470                 475                 480

atg gac ggc gcc gtg atc tcc cag ctg gcc gaa gcc ggg atg ggc ggc     1488
Met Asp Gly Ala Val Ile Ser Gln Leu Ala Glu Ala Gly Met Gly Gly
                485                 490                 495

tac gcc tcg tac ggc cac cac ggc tgg ccg acc atc gcg ttc cag cag     1536
Tyr Ala Ser Tyr Gly His His Gly Trp Pro Thr Ile Ala Phe Gln Gln
            500                 505                 510

ccg tcg ccg ctc tcc gtc cac tac ccg tac ggc cag ccg tcc cgc ggg     1584
Pro Ser Pro Leu Ser Val His Tyr Pro Tyr Gly Gln Pro Ser Arg Gly
        515                 520                 525

tgg tgc aaa ccc gag cag gac gcg gcc gcc gcc gcg gcg cac agc ctg     1632
Trp Cys Lys Pro Glu Gln Asp Ala Ala Ala Ala Ala Ala His Ser Leu
    530                 535                 540
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cag gac ctc cag cag ctg cac ctc ggc agc gcg gcc cac aac ttc ttc     1680
Gln Asp Leu Gln Gln Leu His Leu Gly Ser Ala Ala His Asn Phe Phe
545                 550                 555                 560

cag gcg tcg tcg agc tcc aca gtc tac aac ggc ggc gcc ggc gcc agt     1728
Gln Ala Ser Ser Ser Ser Thr Val Tyr Asn Gly Gly Ala Gly Ala Ser
                565                 570                 575

ggt ggg tac cag ggc ctc ggt ggt ggc agc tct ttc ctc atg ccg tcg     1776
Gly Gly Tyr Gln Gly Leu Gly Gly Gly Ser Ser Phe Leu Met Pro Ser
            580                 585                 590

agc act gtc gtg gcg gcg gcc gac cag ggg cac agc agc acg gcc aac     1824
Ser Thr Val Val Ala Ala Ala Asp Gln Gly His Ser Ser Thr Ala Asn
        595                 600                 605

cag ggg agc acg tgc agc tac ggg gac gac cac cag gag ggg aag ctc     1872
Gln Gly Ser Thr Cys Ser Tyr Gly Asp Asp His Gln Glu Gly Lys Leu
    610                 615                 620

atc ggt tac gac gcc gcc atg gtg gcg acc gca gct ggt gga gac ccg     1920
Ile Gly Tyr Asp Ala Ala Met Val Ala Thr Ala Ala Gly Gly Asp Pro
625                 630                 635                 640

tac gct gcg gcg agg aac ggg tac cag ttc tcg cag ggc tcg gga tcc     1968
Tyr Ala Ala Ala Arg Asn Gly Tyr Gln Phe Ser Gln Gly Ser Gly Ser
                645                 650                 655

acg gtg agc atc gcg agg gcg aac ggg tac gct aac aac tgg agc tct     2016
Thr Val Ser Ile Ala Arg Ala Asn Gly Tyr Ala Asn Asn Trp Ser Ser
            660                 665                 670

cct ttc aac aac ggc atg ggg tga                                     2040
Pro Phe Asn Asn Gly Met Gly
        675


<210> SEQ ID NO 12
<211> LENGTH: 679
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 12

Met Ala Ser Ala Asn Asn Trp Leu Gly Phe Ser Leu Ser Gly Gln Asp
1               5                   10                  15

Asn Pro Gln Pro Asn Gln Asp Ser Ser Pro Ala Ala Gly Ile Asp Ile
            20                  25                  30

Ser Gly Ala Ser Asp Phe Tyr Gly Leu Pro Thr Gln Gln Gly Ser Asp
        35                  40                  45

Gly His Leu Gly Val Pro Gly Leu Arg Asp Asp His Ala Ser Tyr Gly
    50                  55                  60

Ile Met Glu Ala Tyr Asn Arg Val Pro Gln Glu Thr Gln Asp Trp Asn
65                  70                  75                  80

Met Arg Gly Leu Asp Tyr Asn Gly Gly Gly Ser Glu Leu Ser Met Leu
                85                  90                  95

Val Gly Ser Ser Gly Gly Gly Gly Gly Asn Gly Lys Arg Ala Val Glu
            100                 105                 110

Asp Ser Glu Pro Lys Leu Glu Asp Phe Leu Gly Gly Asn Ser Phe Val
        115                 120                 125

Ser Asp Gln Asp Gln Ser Gly Gly Tyr Leu Phe Ser Gly Val Pro Ile
    130                 135                 140

Ala Ser Ser Ala Asn Ser Asn Ser Gly Ser Asn Thr Met Glu Leu Ser
145                 150                 155                 160

Met Ile Lys Thr Trp Leu Arg Asn Asn Gln Val Ala Gln Pro Gln Pro
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                165                 170                 175

Pro Ala Pro His Gln Pro Gln Pro Glu Glu Met Ser Thr Asp Ala Ser
            180                 185                 190

Gly Ser Ser Phe Gly Cys Ser Asp Ser Met Gly Arg Asn Ser Met Val
        195                 200                 205

Ala Ala Gly Gly Ser Ser Gln Ser Leu Ala Leu Ser Met Ser Thr Gly
    210                 215                 220

Ser His Leu Pro Met Val Val Pro Ser Gly Ala Ala Ser Gly Ala Ala
225                 230                 235                 240

Ser Glu Ser Thr Ser Ser Glu Asn Lys Arg Ala Ser Gly Ala Met Asp
                245                 250                 255

Ser Pro Gly Ser Ala Val Glu Ala Val Pro Arg Lys Ser Ile Asp Thr
            260                 265                 270

Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp
        275                 280                 285

Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu
    290                 295                 300

Gly Gln Ser Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys
305                 310                 315                 320

Glu Asp Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp
                325                 330                 335

Gly Thr Thr Thr Thr Thr Asn Phe Pro Ile Ser Asn Tyr Glu Lys Glu
            340                 345                 350

Leu Glu Glu Met Lys His Met Thr Arg Gln Glu Tyr Ile Ala Tyr Leu
        355                 360                 365

Arg Arg Asn Ser Ser Gly Phe Ser Arg Gly Ala Ser Lys Tyr Arg Gly
    370                 375                 380

Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg
385                 390                 395                 400

Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Glu Glu
                405                 410                 415

Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu
            420                 425                 430

Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser Ile
        435                 440                 445

Leu Glu Ser Ser Thr Leu Pro Val Gly Gly Ala Ala Arg Arg Leu Lys
    450                 455                 460

Asp Ala Val Asp His Val Glu Ala Gly Ala Thr Ile Trp Arg Ala Asp
465                 470                 475                 480

Met Asp Gly Ala Val Ile Ser Gln Leu Ala Glu Ala Gly Met Gly Gly
                485                 490                 495

Tyr Ala Ser Tyr Gly His His Gly Trp Pro Thr Ile Ala Phe Gln Gln
            500                 505                 510

Pro Ser Pro Leu Ser Val His Tyr Pro Tyr Gly Gln Pro Ser Arg Gly
        515                 520                 525

Trp Cys Lys Pro Glu Gln Asp Ala Ala Ala Ala Ala Ala His Ser Leu
    530                 535                 540

Gln Asp Leu Gln Gln Leu His Leu Gly Ser Ala Ala His Asn Phe Phe
545                 550                 555                 560

Gln Ala Ser Ser Ser Ser Thr Val Tyr Asn Gly Gly Ala Gly Ala Ser
                565                 570                 575
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Gly Gly Tyr Gln Gly Leu Gly Gly Gly Ser Ser Phe Leu Met Pro Ser
            580                 585                 590

Ser Thr Val Val Ala Ala Ala Asp Gln Gly His Ser Ser Thr Ala Asn
        595                 600                 605

Gln Gly Ser Thr Cys Ser Tyr Gly Asp Asp His Gln Glu Gly Lys Leu
    610                 615                 620

Ile Gly Tyr Asp Ala Ala Met Val Ala Thr Ala Ala Gly Gly Asp Pro
625                 630                 635                 640

Tyr Ala Ala Ala Arg Asn Gly Tyr Gln Phe Ser Gln Gly Ser Gly Ser
                645                 650                 655

Thr Val Ser Ile Ala Arg Ala Asn Gly Tyr Ala Asn Asn Trp Ser Ser
            660                 665                 670

Pro Phe Asn Asn Gly Met Gly
        675


<210> SEQ ID NO 13
<211> LENGTH: 2088
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(2088)

<400> SEQUENCE: 13

atg gcc acc atg aac aac tgg ctg gcc ttc tcc ctc tcc ccg cag gat       48
Met Ala Thr Met Asn Asn Trp Leu Ala Phe Ser Leu Ser Pro Gln Asp
1               5                   10                  15

cag ctc ccg ccg tct cag acc aac tcc act ctc atc tcc gcc gcc gcc       96
Gln Leu Pro Pro Ser Gln Thr Asn Ser Thr Leu Ile Ser Ala Ala Ala
            20                  25                  30

acc acc acc acc gcc ggc gac tcc tcc acc ggc gac gtc tgc ttc aac      144
Thr Thr Thr Thr Ala Gly Asp Ser Ser Thr Gly Asp Val Cys Phe Asn
        35                  40                  45

atc ccc caa gat tgg agc atg agg gga tcg gag ctc tcg gcg ctc gtc      192
Ile Pro Gln Asp Trp Ser Met Arg Gly Ser Glu Leu Ser Ala Leu Val
    50                  55                  60

gcc gag ccg aag ctg gag gac ttc ctc ggc ggc atc tcc ttc tcg gag      240
Ala Glu Pro Lys Leu Glu Asp Phe Leu Gly Gly Ile Ser Phe Ser Glu
65                  70                  75                  80

cag cag cat cat cac ggc ggc aag ggc ggc gtg atc ccg agc agc gcc      288
Gln Gln His His His Gly Gly Lys Gly Gly Val Ile Pro Ser Ser Ala
                85                  90                  95

gcc gct tgc tac gcg agc tcc ggc agc agc gtc ggc tac ctg tac cct      336
Ala Ala Cys Tyr Ala Ser Ser Gly Ser Ser Val Gly Tyr Leu Tyr Pro
            100                 105                 110

cct cca agc tca tcc tcg ctc cag ttc gcc gac tcc gtc atg gtg gcc      384
Pro Pro Ser Ser Ser Ser Leu Gln Phe Ala Asp Ser Val Met Val Ala
        115                 120                 125

acc tcc tcg ccc gtc gtc gcc cac gac ggc gtc agc ggc ggc ggc atg      432
Thr Ser Ser Pro Val Val Ala His Asp Gly Val Ser Gly Gly Gly Met
    130                 135                 140

gtg agc gcc gcc gcc gcc gcg gcg gcc agt ggc aac ggc ggc att ggc      480
Val Ser Ala Ala Ala Ala Ala Ala Ala Ser Gly Asn Gly Gly Ile Gly
145                 150                 155                 160

ctg tcc atg atc aag aac tgg ctc cgg agc cag ccg gcg ccg cag ccg      528
Leu Ser Met Ile Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Gln Pro
                165                 170                 175
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gcg cag gcg ctg tct ctg tcc atg aac atg gcg ggg acg acg acg gcg       576
Ala Gln Ala Leu Ser Leu Ser Met Asn Met Ala Gly Thr Thr Thr Ala
            180                 185                 190

cag ggc ggc ggc gcc atg gcg ctc ctc gcc ggc gca ggg gag cga ggc       624
Gln Gly Gly Gly Ala Met Ala Leu Leu Ala Gly Ala Gly Glu Arg Gly
        195                 200                 205

cgg acg acg ccc gcg tca gag agc ctg tcc acg tcg gcg cac gga gcg       672
Arg Thr Thr Pro Ala Ser Glu Ser Leu Ser Thr Ser Ala His Gly Ala
    210                 215                 220

acg acg gcg acg atg gct ggt ggt cgc aag gag att aac gag gaa ggc       720
Thr Thr Ala Thr Met Ala Gly Gly Arg Lys Glu Ile Asn Glu Glu Gly
225                 230                 235                 240

agc ggc agc gcc ggc gcc gtg gtt gcc gtc ggc tcg gag tca ggc ggc       768
Ser Gly Ser Ala Gly Ala Val Val Ala Val Gly Ser Glu Ser Gly Gly
                245                 250                 255

agc ggc gcc gtg gtg gag gcc ggc gcg gcg gcg gcg gcg gcg agg aag       816
Ser Gly Ala Val Val Glu Ala Gly Ala Ala Ala Ala Ala Ala Arg Lys
            260                 265                 270

tcc gtc gac acg ttc ggc cag aga aca tcg atc tac cgc ggc gtg aca       864
Ser Val Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr
        275                 280                 285

agg cat aga tgg aca ggg agg tat gag gct cat ctt tgg gac aac agc       912
Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser
    290                 295                 300

tgc aga aga gag ggc caa act cgc aag ggt cgt caa gtc tat cta ggt       960
Cys Arg Arg Glu Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly
305                 310                 315                 320

ggt tat gac aaa gag gaa aaa gct gct aga gct tat gat ttg gct gct      1008
Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala
                325                 330                 335

ctc aaa tac tgg ggc ccg acg acg acg aca aat ttt ccg gta aat aac      1056
Leu Lys Tyr Trp Gly Pro Thr Thr Thr Thr Asn Phe Pro Val Asn Asn
            340                 345                 350

tat gaa aag gag ctg gag gag atg aag cac atg aca agg cag gag ttc      1104
Tyr Glu Lys Glu Leu Glu Glu Met Lys His Met Thr Arg Gln Glu Phe
        355                 360                 365

gta gcc tct ttg aga agg aag agc agt ggt ttc tcc aga ggt gca tcc      1152
Val Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser
    370                 375                 380

att tac cgt gga gta act agg cat cac cag cat ggg aga tgg caa gca      1200
Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala
385                 390                 395                 400

agg ata gga aga gtt gca ggg aac aag gac ctc tac ttg ggc acc ttc      1248
Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe
                405                 410                 415

agc acg cag gag gag gcg gcg gag gcg tac gac atc gcg gcg atc aag      1296
Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys
            420                 425                 430

ttc cgg ggg ctc aac gcc gtc acc aac ttc gac atg agc cgc tac gac      1344
Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp
        435                 440                 445

gtc aag agc atc ctc gac agc gct gcc ctc ccc gtc ggc acc gcc gcc      1392
Val Lys Ser Ile Leu Asp Ser Ala Ala Leu Pro Val Gly Thr Ala Ala
    450                 455                 460

aag cgc ctc aag gac gcc gag gcc gcc gcc gcc tac gac gtc ggc cgc      1440
Lys Arg Leu Lys Asp Ala Glu Ala Ala Ala Ala Tyr Asp Val Gly Arg
465                 470                 475                 480
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atc gcc tcg cac ctc ggc ggc gac ggc gcc tac gcc gcg cat tac ggc     1488
Ile Ala Ser His Leu Gly Gly Asp Gly Ala Tyr Ala Ala His Tyr Gly
                485                 490                 495

cac cac cac cac tcg gcc gcc gcc gcc tgg ccg acc atc gcg ttc cag     1536
His His His His Ser Ala Ala Ala Ala Trp Pro Thr Ile Ala Phe Gln
            500                 505                 510

gcg gcg gcg gcg ccg ccg ccg cac gcc gcc ggg ctt tac cac ccg tac     1584
Ala Ala Ala Ala Pro Pro Pro His Ala Ala Gly Leu Tyr His Pro Tyr
        515                 520                 525

gcg cag ccg ctg cgt ggg tgg tgc aag cag gag cag gac cac gcc gtg     1632
Ala Gln Pro Leu Arg Gly Trp Cys Lys Gln Glu Gln Asp His Ala Val
    530                 535                 540

atc gcg gcg gcg cac agc ctg cag gat ctc cac cac ctc aac ctc ggc     1680
Ile Ala Ala Ala His Ser Leu Gln Asp Leu His His Leu Asn Leu Gly
545                 550                 555                 560

gcc gcc gcc gcc gcg cat gac ttc ttc tcg cag gcg atg cag cag cag     1728
Ala Ala Ala Ala Ala His Asp Phe Phe Ser Gln Ala Met Gln Gln Gln
                565                 570                 575

cac ggc ctc ggc agc atc gac aac gcg tcg ctc gag cac agc acc ggc     1776
His Gly Leu Gly Ser Ile Asp Asn Ala Ser Leu Glu His Ser Thr Gly
            580                 585                 590

tcc aac tcc gtc gtc tac aac ggc gac aat ggc ggc gga ggc ggc ggc     1824
Ser Asn Ser Val Val Tyr Asn Gly Asp Asn Gly Gly Gly Gly Gly Gly
        595                 600                 605

tac atc atg gcg ccg atg agc gcc gtg tcg gcc acg gcc acc gcg gtg     1872
Tyr Ile Met Ala Pro Met Ser Ala Val Ser Ala Thr Ala Thr Ala Val
    610                 615                 620

gcg agc agc cac gat cac ggc ggc gac ggc ggg aag cag gtg cag atg     1920
Ala Ser Ser His Asp His Gly Gly Asp Gly Gly Lys Gln Val Gln Met
625                 630                 635                 640

ggg tac gac agc tac ctc gtc ggc gca gac gcc tac ggc ggc ggc ggc     1968
Gly Tyr Asp Ser Tyr Leu Val Gly Ala Asp Ala Tyr Gly Gly Gly Gly
                645                 650                 655

gcc ggg agg atg cca tcc tgg gcg atg acg ccg gcg tcg gcg ccg gcc     2016
Ala Gly Arg Met Pro Ser Trp Ala Met Thr Pro Ala Ser Ala Pro Ala
            660                 665                 670

gcc acg agc agc agc gac atg acc gga gtc tgc cat ggc gca cag ctc     2064
Ala Thr Ser Ser Ser Asp Met Thr Gly Val Cys His Gly Ala Gln Leu
        675                 680                 685

ttc agc gtc tgg aac gac aca taa                                     2088
Phe Ser Val Trp Asn Asp Thr
    690                 695


<210> SEQ ID NO 14
<211> LENGTH: 695
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 14

Met Ala Thr Met Asn Asn Trp Leu Ala Phe Ser Leu Ser Pro Gln Asp
1               5                   10                  15

Gln Leu Pro Pro Ser Gln Thr Asn Ser Thr Leu Ile Ser Ala Ala Ala
            20                  25                  30

Thr Thr Thr Thr Ala Gly Asp Ser Ser Thr Gly Asp Val Cys Phe Asn
        35                  40                  45

Ile Pro Gln Asp Trp Ser Met Arg Gly Ser Glu Leu Ser Ala Leu Val
    50                  55                  60
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Ala Glu Pro Lys Leu Glu Asp Phe Leu Gly Gly Ile Ser Phe Ser Glu
65                  70                  75                  80

Gln Gln His His His Gly Gly Lys Gly Gly Val Ile Pro Ser Ser Ala
                85                  90                  95

Ala Ala Cys Tyr Ala Ser Ser Gly Ser Ser Val Gly Tyr Leu Tyr Pro
            100                 105                 110

Pro Pro Ser Ser Ser Ser Leu Gln Phe Ala Asp Ser Val Met Val Ala
        115                 120                 125

Thr Ser Ser Pro Val Val Ala His Asp Gly Val Ser Gly Gly Gly Met
    130                 135                 140

Val Ser Ala Ala Ala Ala Ala Ala Ala Ser Gly Asn Gly Gly Ile Gly
145                 150                 155                 160

Leu Ser Met Ile Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Gln Pro
                165                 170                 175

Ala Gln Ala Leu Ser Leu Ser Met Asn Met Ala Gly Thr Thr Thr Ala
            180                 185                 190

Gln Gly Gly Gly Ala Met Ala Leu Leu Ala Gly Ala Gly Glu Arg Gly
        195                 200                 205

Arg Thr Thr Pro Ala Ser Glu Ser Leu Ser Thr Ser Ala His Gly Ala
    210                 215                 220

Thr Thr Ala Thr Met Ala Gly Gly Arg Lys Glu Ile Asn Glu Glu Gly
225                 230                 235                 240

Ser Gly Ser Ala Gly Ala Val Val Ala Val Gly Ser Glu Ser Gly Gly
                245                 250                 255

Ser Gly Ala Val Val Glu Ala Gly Ala Ala Ala Ala Ala Ala Arg Lys
            260                 265                 270

Ser Val Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr
        275                 280                 285

Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser
    290                 295                 300

Cys Arg Arg Glu Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly
305                 310                 315                 320

Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala
                325                 330                 335

Leu Lys Tyr Trp Gly Pro Thr Thr Thr Thr Asn Phe Pro Val Asn Asn
            340                 345                 350

Tyr Glu Lys Glu Leu Glu Glu Met Lys His Met Thr Arg Gln Glu Phe
        355                 360                 365

Val Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser
    370                 375                 380

Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala
385                 390                 395                 400

Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe
                405                 410                 415

Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys
            420                 425                 430

Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp
        435                 440                 445

Val Lys Ser Ile Leu Asp Ser Ala Ala Leu Pro Val Gly Thr Ala Ala
    450                 455                 460
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Lys Arg Leu Lys Asp Ala Glu Ala Ala Ala Ala Tyr Asp Val Gly Arg
465                 470                 475                 480

Ile Ala Ser His Leu Gly Gly Asp Gly Ala Tyr Ala Ala His Tyr Gly
                485                 490                 495

His His His His Ser Ala Ala Ala Ala Trp Pro Thr Ile Ala Phe Gln
            500                 505                 510

Ala Ala Ala Ala Pro Pro Pro His Ala Ala Gly Leu Tyr His Pro Tyr
        515                 520                 525

Ala Gln Pro Leu Arg Gly Trp Cys Lys Gln Glu Gln Asp His Ala Val
    530                 535                 540

Ile Ala Ala Ala His Ser Leu Gln Asp Leu His His Leu Asn Leu Gly
545                 550                 555                 560

Ala Ala Ala Ala Ala His Asp Phe Phe Ser Gln Ala Met Gln Gln Gln
                565                 570                 575

His Gly Leu Gly Ser Ile Asp Asn Ala Ser Leu Glu His Ser Thr Gly
            580                 585                 590

Ser Asn Ser Val Val Tyr Asn Gly Asp Asn Gly Gly Gly Gly Gly Gly
        595                 600                 605

Tyr Ile Met Ala Pro Met Ser Ala Val Ser Ala Thr Ala Thr Ala Val
    610                 615                 620

Ala Ser Ser His Asp His Gly Gly Asp Gly Gly Lys Gln Val Gln Met
625                 630                 635                 640

Gly Tyr Asp Ser Tyr Leu Val Gly Ala Asp Ala Tyr Gly Gly Gly Gly
                645                 650                 655

Ala Gly Arg Met Pro Ser Trp Ala Met Thr Pro Ala Ser Ala Pro Ala
            660                 665                 670

Ala Thr Ser Ser Ser Asp Met Thr Gly Val Cys His Gly Ala Gln Leu
        675                 680                 685

Phe Ser Val Trp Asn Asp Thr
    690                 695


<210> SEQ ID NO 15
<211> LENGTH: 1680
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(1680)

<400> SEQUENCE: 15

atg gcc tcc atc acc aac tgg ctc ggc ttc tcc tcc tcc tcc ttc tcc       48
Met Ala Ser Ile Thr Asn Trp Leu Gly Phe Ser Ser Ser Ser Phe Ser
1               5                   10                  15

ggc gcc ggc gcc gac ccc gtc ctg ccc cac ccg ccg ctg caa gag tgg       96
Gly Ala Gly Ala Asp Pro Val Leu Pro His Pro Pro Leu Gln Glu Trp
            20                  25                  30

ggg agc gct tat gag ggc ggc ggc acg gtg gcg gcc gcc ggc ggg gag      144
Gly Ser Ala Tyr Glu Gly Gly Gly Thr Val Ala Ala Ala Gly Gly Glu
        35                  40                  45

gag acg gcg gcg ccg aag ctg gag gac ttc ctc ggc atg cag gtg cag      192
Glu Thr Ala Ala Pro Lys Leu Glu Asp Phe Leu Gly Met Gln Val Gln
    50                  55                  60

cag gag acg gcc gcc gcg gcg gcg ggg cac ggc cgt gga ggc agc tcg      240
Gln Glu Thr Ala Ala Ala Ala Ala Gly His Gly Arg Gly Gly Ser Ser
65                  70                  75                  80
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tcg gtc gtt ggg ctg tcc atg atc aag aac tgg cta cgc agc cag ccg      288
Ser Val Val Gly Leu Ser Met Ile Lys Asn Trp Leu Arg Ser Gln Pro
                85                  90                  95

ccg ccc gcg gtg gtt ggg gga gaa gac gct atg atg gcg ctc gcg gtg      336
Pro Pro Ala Val Val Gly Gly Glu Asp Ala Met Met Ala Leu Ala Val
            100                 105                 110

tcg acg tcg gcg tcg ccg ccg gtg gac gcg acg gtg ccg gcc tgc att      384
Ser Thr Ser Ala Ser Pro Pro Val Asp Ala Thr Val Pro Ala Cys Ile
        115                 120                 125

tcg ccg gat ggg atg ggg tcg aag gcg gcc gac ggc ggc ggc gcg gcc      432
Ser Pro Asp Gly Met Gly Ser Lys Ala Ala Asp Gly Gly Gly Ala Ala
    130                 135                 140

gag gcg gcg gcg gcg gcg gcg gcg cag agg atg aag gcg gcc atg gac      480
Glu Ala Ala Ala Ala Ala Ala Ala Gln Arg Met Lys Ala Ala Met Asp
145                 150                 155                 160

acg ttc ggg cag cgg acg tcc atc tac cgg ggt gtc acc aag cac agg      528
Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Lys His Arg
                165                 170                 175

tgg aca gga agg tat gaa gcc cat ctt tgg gat aac agc tgc aga aga      576
Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg
            180                 185                 190

gaa ggt cag act cgc aaa ggc aga caa gta tat ctt gga gga tat gat      624
Glu Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp
        195                 200                 205

aag gaa gaa aaa gct gct agg gct tat gat ttg gct gcc ctt aaa tac      672
Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr
    210                 215                 220

tgg ggc act aca acg acg acg aat ttt ccg gta agc aac tac gaa aaa      720
Trp Gly Thr Thr Thr Thr Thr Asn Phe Pro Val Ser Asn Tyr Glu Lys
225                 230                 235                 240

gag ttg gat gaa atg aag cac atg aat agg cag gaa ttt gtt gca tcc      768
Glu Leu Asp Glu Met Lys His Met Asn Arg Gln Glu Phe Val Ala Ser
                245                 250                 255

ctt aga aga aaa agc agt gga ttt tca cgt ggt gct tcc ata tat cgt      816
Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg
            260                 265                 270

ggt gtt aca aga cac cat cag cat gga agg tgg caa gca agg ata gga      864
Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly
        275                 280                 285

cgg gtg gca gga aac aag gat ctg tat ttg ggc aca ttt ggc acc caa      912
Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln
    290                 295                 300

gag gaa gct gca gag gca tat gat atc gct gca atc aaa ttc cgt ggt      960
Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly
305                 310                 315                 320

ctc aat gct gtg aca aac ttt gac atg agc cgg tac gat gtc aag agc     1008
Leu Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser
                325                 330                 335

atc att gaa agc agc aat ctc cca att ggt act gga acc acc cgg cga     1056
Ile Ile Glu Ser Ser Asn Leu Pro Ile Gly Thr Gly Thr Thr Arg Arg
            340                 345                 350

ttg aag gac tcc tct gat cac act gat aat gtc atg gac atc aat gtc     1104
Leu Lys Asp Ser Ser Asp His Thr Asp Asn Val Met Asp Ile Asn Val
        355                 360                 365

aat acc gaa ccc aat aat gtg gta tca tcc cac ttc acc aat ggg gtt     1152
Asn Thr Glu Pro Asn Asn Val Val Ser Ser His Phe Thr Asn Gly Val
    370                 375                 380
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ggc aac tat ggt tcg cag cat tat ggt tac aat gga tgg tcg cca att     1200
Gly Asn Tyr Gly Ser Gln His Tyr Gly Tyr Asn Gly Trp Ser Pro Ile
385                 390                 395                 400

agc atg cag ccg atc ccc tcg cag tac gcc aac ggc cag ccc agg gca     1248
Ser Met Gln Pro Ile Pro Ser Gln Tyr Ala Asn Gly Gln Pro Arg Ala
                405                 410                 415

tgg ttg aaa caa gag cag gac agc tct gtg gtt aca gcg gcg cag aac     1296
Trp Leu Lys Gln Glu Gln Asp Ser Ser Val Val Thr Ala Ala Gln Asn
            420                 425                 430

ctg cac aat cta cat cat ttt agt tcc ttg ggc tac acc cac aac ttc     1344
Leu His Asn Leu His His Phe Ser Ser Leu Gly Tyr Thr His Asn Phe
        435                 440                 445

ttc cag caa tct gat gtt cca gac gtc aca ggt ttc gtt gat gcg cct     1392
Phe Gln Gln Ser Asp Val Pro Asp Val Thr Gly Phe Val Asp Ala Pro
    450                 455                 460

tcg agg tcc agt gac tca tac tcc ttc agg tac aat gga aca aat ggc     1440
Ser Arg Ser Ser Asp Ser Tyr Ser Phe Arg Tyr Asn Gly Thr Asn Gly
465                 470                 475                 480

ttt cat ggt ctc ccg ggt gga atc agc tat gct atg ccg gtt gcg aca     1488
Phe His Gly Leu Pro Gly Gly Ile Ser Tyr Ala Met Pro Val Ala Thr
                485                 490                 495

gcg gtg gac caa ggt cag ggc atc cat ggc tat gga gaa gat ggt gtg     1536
Ala Val Asp Gln Gly Gln Gly Ile His Gly Tyr Gly Glu Asp Gly Val
            500                 505                 510

gca ggc att gac acc aca cat gac ctg tat ggc agc cgt aat gtg tac     1584
Ala Gly Ile Asp Thr Thr His Asp Leu Tyr Gly Ser Arg Asn Val Tyr
        515                 520                 525

tac ctt tcc gag ggt tcg ctt ctt gcc gat gtc gaa aaa gaa ggc gac     1632
Tyr Leu Ser Glu Gly Ser Leu Leu Ala Asp Val Glu Lys Glu Gly Asp
    530                 535                 540

tat ggc caa tct gtg ggg ggc aac agc tgg gtt ttg ccg aca ccg tag     1680
Tyr Gly Gln Ser Val Gly Gly Asn Ser Trp Val Leu Pro Thr Pro
545                 550                 555


<210> SEQ ID NO 16
<211> LENGTH: 559
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 16

Met Ala Ser Ile Thr Asn Trp Leu Gly Phe Ser Ser Ser Ser Phe Ser
1               5                   10                  15

Gly Ala Gly Ala Asp Pro Val Leu Pro His Pro Pro Leu Gln Glu Trp
            20                  25                  30

Gly Ser Ala Tyr Glu Gly Gly Gly Thr Val Ala Ala Ala Gly Gly Glu
        35                  40                  45

Glu Thr Ala Ala Pro Lys Leu Glu Asp Phe Leu Gly Met Gln Val Gln
    50                  55                  60

Gln Glu Thr Ala Ala Ala Ala Ala Gly His Gly Arg Gly Gly Ser Ser
65                  70                  75                  80

Ser Val Val Gly Leu Ser Met Ile Lys Asn Trp Leu Arg Ser Gln Pro
                85                  90                  95

Pro Pro Ala Val Val Gly Gly Glu Asp Ala Met Met Ala Leu Ala Val
            100                 105                 110

Ser Thr Ser Ala Ser Pro Pro Val Asp Ala Thr Val Pro Ala Cys Ile
        115                 120                 125
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Ser Pro Asp Gly Met Gly Ser Lys Ala Ala Asp Gly Gly Gly Ala Ala
    130                 135                 140

Glu Ala Ala Ala Ala Ala Ala Ala Gln Arg Met Lys Ala Ala Met Asp
145                 150                 155                 160

Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Lys His Arg
                165                 170                 175

Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg
            180                 185                 190

Glu Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp
        195                 200                 205

Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr
    210                 215                 220

Trp Gly Thr Thr Thr Thr Thr Asn Phe Pro Val Ser Asn Tyr Glu Lys
225                 230                 235                 240

Glu Leu Asp Glu Met Lys His Met Asn Arg Gln Glu Phe Val Ala Ser
                245                 250                 255

Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg
            260                 265                 270

Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly
        275                 280                 285

Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln
    290                 295                 300

Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly
305                 310                 315                 320

Leu Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser
                325                 330                 335

Ile Ile Glu Ser Ser Asn Leu Pro Ile Gly Thr Gly Thr Thr Arg Arg
            340                 345                 350

Leu Lys Asp Ser Ser Asp His Thr Asp Asn Val Met Asp Ile Asn Val
        355                 360                 365

Asn Thr Glu Pro Asn Asn Val Val Ser Ser His Phe Thr Asn Gly Val
    370                 375                 380

Gly Asn Tyr Gly Ser Gln His Tyr Gly Tyr Asn Gly Trp Ser Pro Ile
385                 390                 395                 400

Ser Met Gln Pro Ile Pro Ser Gln Tyr Ala Asn Gly Gln Pro Arg Ala
                405                 410                 415

Trp Leu Lys Gln Glu Gln Asp Ser Ser Val Val Thr Ala Ala Gln Asn
            420                 425                 430

Leu His Asn Leu His His Phe Ser Ser Leu Gly Tyr Thr His Asn Phe
        435                 440                 445

Phe Gln Gln Ser Asp Val Pro Asp Val Thr Gly Phe Val Asp Ala Pro
    450                 455                 460

Ser Arg Ser Ser Asp Ser Tyr Ser Phe Arg Tyr Asn Gly Thr Asn Gly
465                 470                 475                 480

Phe His Gly Leu Pro Gly Gly Ile Ser Tyr Ala Met Pro Val Ala Thr
                485                 490                 495

Ala Val Asp Gln Gly Gln Gly Ile His Gly Tyr Gly Glu Asp Gly Val
            500                 505                 510

Ala Gly Ile Asp Thr Thr His Asp Leu Tyr Gly Ser Arg Asn Val Tyr
        515                 520                 525

Tyr Leu Ser Glu Gly Ser Leu Leu Ala Asp Val Glu Lys Glu Gly Asp
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    530                 535                 540

Tyr Gly Gln Ser Val Gly Gly Asn Ser Trp Val Leu Pro Thr Pro
545                 550                 555


<210> SEQ ID NO 17
<211> LENGTH: 2112
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(2112)

<400> SEQUENCE: 17

atg gct tct gca aac aac tgg ctg ggc ttc tcg ctc tcc ggc caa gag       48
Met Ala Ser Ala Asn Asn Trp Leu Gly Phe Ser Leu Ser Gly Gln Glu
1               5                   10                  15

aat ccg cag cct cac cag gat agc tcg cct ccg gca gcc atc gac gtc       96
Asn Pro Gln Pro His Gln Asp Ser Ser Pro Pro Ala Ala Ile Asp Val
            20                  25                  30

tcc ggc gcc ggc gac ttc tat ggc ctg ccg acg tcg cag ccg acg gcg      144
Ser Gly Ala Gly Asp Phe Tyr Gly Leu Pro Thr Ser Gln Pro Thr Ala
        35                  40                  45

gcc gac gcg cac ctc ggc gtg gcg ggg cat cat cac aac gcc tcg tat      192
Ala Asp Ala His Leu Gly Val Ala Gly His His His Asn Ala Ser Tyr
    50                  55                  60

ggc atc atg gag gcc ttc aat agg gga gct caa gag gca caa gat tgg      240
Gly Ile Met Glu Ala Phe Asn Arg Gly Ala Gln Glu Ala Gln Asp Trp
65                  70                  75                  80

aac atg agg ggg ctg gac tac aac ggc ggc gcc tcg gag ctg tcg atg      288
Asn Met Arg Gly Leu Asp Tyr Asn Gly Gly Ala Ser Glu Leu Ser Met
                85                  90                  95

ctc gtc ggc tcc agc ggc ggc aag agg gcg gcg gcg gtg gag gag acc      336
Leu Val Gly Ser Ser Gly Gly Lys Arg Ala Ala Ala Val Glu Glu Thr
            100                 105                 110

gag ccg aag ctg gag gac ttc ctc ggc ggc aac tcg ttc gtc tcc gag      384
Glu Pro Lys Leu Glu Asp Phe Leu Gly Gly Asn Ser Phe Val Ser Glu
        115                 120                 125

caa gat cat cac gcg gcg ggg ggc ttc ctc ttc tcc ggc gtc ccg atg      432
Gln Asp His His Ala Ala Gly Gly Phe Leu Phe Ser Gly Val Pro Met
    130                 135                 140

gcc agc agc acc aac agc aac agc ggg agc aac act atg gag ctc tcc      480
Ala Ser Ser Thr Asn Ser Asn Ser Gly Ser Asn Thr Met Glu Leu Ser
145                 150                 155                 160

atg atc aag acc tgg ctc cgg aac aac ggc cag gtg ccc gcc ggc cac      528
Met Ile Lys Thr Trp Leu Arg Asn Asn Gly Gln Val Pro Ala Gly His
                165                 170                 175

cag ccg cag cag cag cag ccg gcg gcc gcg gcc gcc gcc gcg cag cag      576
Gln Pro Gln Gln Gln Gln Pro Ala Ala Ala Ala Ala Ala Ala Gln Gln
            180                 185                 190

cag gcg cac gag gcg gcg gag atg agc acc gac gcg agc gcg agc agc      624
Gln Ala His Glu Ala Ala Glu Met Ser Thr Asp Ala Ser Ala Ser Ser
        195                 200                 205

ttc ggg tgc tcc tcc gac gcg atg ggg agg agt aac aac ggc ggc gcg      672
Phe Gly Cys Ser Ser Asp Ala Met Gly Arg Ser Asn Asn Gly Gly Ala
    210                 215                 220

gtc tcg gcg gcg gcc ggc ggg acg agc tcg cag agc ctg gcg ctc tcg      720
Val Ser Ala Ala Ala Gly Gly Thr Ser Ser Gln Ser Leu Ala Leu Ser
225                 230                 235                 240
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atg agc acg ggc tcg cac tcg cac ctg cct atc gtc gtc gcc ggc ggc      768
Met Ser Thr Gly Ser His Ser His Leu Pro Ile Val Val Ala Gly Gly
                245                 250                 255

ggg aac gcc agc ggc gga gcg gcc gag agc aca tcg tcg gag aac aag      816
Gly Asn Ala Ser Gly Gly Ala Ala Glu Ser Thr Ser Ser Glu Asn Lys
            260                 265                 270

cgg gcc agc ggc gcc atg gat tcg ccg ggc ggt ggc gcg ata gag gcc      864
Arg Ala Ser Gly Ala Met Asp Ser Pro Gly Gly Gly Ala Ile Glu Ala
        275                 280                 285

gtg ccg agg aag tcc atc gac acg ttc ggg caa agg acc tcg ata tat      912
Val Pro Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr
    290                 295                 300

cga ggt gta aca agg cat aga tgg aca ggg cga tat gag gct cat ctc      960
Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu
305                 310                 315                 320

tgg gat aat agc tgt aga aga gaa ggg cag agt cgc aag ggt agg caa     1008
Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Ser Arg Lys Gly Arg Gln
                325                 330                 335

gtt tat ctt ggt ggc tat gac aag gag gat aaa gca gcg aga gct tat     1056
Val Tyr Leu Gly Gly Tyr Asp Lys Glu Asp Lys Ala Ala Arg Ala Tyr
            340                 345                 350

gat ttg gca gct ctg aag tat tgg ggc aca aca aca aca aca aat ttc     1104
Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr Thr Asn Phe
        355                 360                 365

cca ata agt aac tat gaa aaa gag cta gat gaa atg aaa cat atg acc     1152
Pro Ile Ser Asn Tyr Glu Lys Glu Leu Asp Glu Met Lys His Met Thr
    370                 375                 380

agg cag gag tat att gca tac cta aga agg aat agc agt gga ttt tct     1200
Arg Gln Glu Tyr Ile Ala Tyr Leu Arg Arg Asn Ser Ser Gly Phe Ser
385                 390                 395                 400

cgt ggt gca tcg aaa tat cgt ggt gta acc agg cac cat cag cat ggg     1248
Arg Gly Ala Ser Lys Tyr Arg Gly Val Thr Arg His His Gln His Gly
                405                 410                 415

aga tgg caa gca agg ata ggg agg gtt gca gga aac aag gac ctc tac     1296
Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr
            420                 425                 430

tta ggc acc ttc agc acc gag gag gag gcg gcg gag gcg tac gac atc     1344
Leu Gly Thr Phe Ser Thr Glu Glu Glu Ala Ala Glu Ala Tyr Asp Ile
        435                 440                 445

gcg gcg atc aag ttc cgg ggg ctc aac gcc gtc acc aac ttt gac atg     1392
Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Met
    450                 455                 460

agc cgc tac gac gtc aag agc atc ctg gag agc agc acg ctg ccg gtg     1440
Ser Arg Tyr Asp Val Lys Ser Ile Leu Glu Ser Ser Thr Leu Pro Val
465                 470                 475                 480

ggc ggc gcg gcg agg cgg ctg aag gag gcg gcg gac cac gcg gag gcg     1488
Gly Gly Ala Ala Arg Arg Leu Lys Glu Ala Ala Asp His Ala Glu Ala
                485                 490                 495

gcc ggc gcc acc atc tgg cgc gcc gcc gac atg gac ggc gcc ggc gtc     1536
Ala Gly Ala Thr Ile Trp Arg Ala Ala Asp Met Asp Gly Ala Gly Val
            500                 505                 510

atc tcc ggc ctg gcc gac gtc ggg atg ggc gcc tac gcc gcc tcg tac     1584
Ile Ser Gly Leu Ala Asp Val Gly Met Gly Ala Tyr Ala Ala Ser Tyr
        515                 520                 525

cac cac cac cac cac cac ggc tgg ccg acc atc gcg ttc cag cag ccg     1632
His His His His His His Gly Trp Pro Thr Ile Ala Phe Gln Gln Pro
    530                 535                 540
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ccg ccg ctc gcc gtg cac tac ccg tac ggc cag gcg ccg gcg gcg ccg     1680
Pro Pro Leu Ala Val His Tyr Pro Tyr Gly Gln Ala Pro Ala Ala Pro
545                 550                 555                 560

tcg cgc ggg tgg tgc aag ccc gag cag gac gcc gcc gtc gct gcc gcc     1728
Ser Arg Gly Trp Cys Lys Pro Glu Gln Asp Ala Ala Val Ala Ala Ala
                565                 570                 575

gcg cac agc ctc cag gac ctc cag cag ctg cac ctc ggc agc gcc gcc     1776
Ala His Ser Leu Gln Asp Leu Gln Gln Leu His Leu Gly Ser Ala Ala
            580                 585                 590

gcc cac aac ttc ttc cag gcg tcg tcg agc tcg acg gtc tac aac ggc     1824
Ala His Asn Phe Phe Gln Ala Ser Ser Ser Ser Thr Val Tyr Asn Gly
        595                 600                 605

ggc ggc ggc ggg tac cag ggc ctc ggt ggc aac gcc ttc ttg atg ccg     1872
Gly Gly Gly Gly Tyr Gln Gly Leu Gly Gly Asn Ala Phe Leu Met Pro
    610                 615                 620

gcg agc acc gtc gtg gcc gac cag ggg cac agc agc acg gcc acc aac     1920
Ala Ser Thr Val Val Ala Asp Gln Gly His Ser Ser Thr Ala Thr Asn
625                 630                 635                 640

cat gga aac acc tgc agc tac ggc aac gag gag cag ggg aag ctc atc     1968
His Gly Asn Thr Cys Ser Tyr Gly Asn Glu Glu Gln Gly Lys Leu Ile
                645                 650                 655

ggg tac gac gcc atg gcg atg gcg agc ggc gcc gcc ggc ggc ggg tac     2016
Gly Tyr Asp Ala Met Ala Met Ala Ser Gly Ala Ala Gly Gly Gly Tyr
            660                 665                 670

cag ctg tcg cag ggc tcg gcg tcg acg gtg agc atc gcg agg gcg aac     2064
Gln Leu Ser Gln Gly Ser Ala Ser Thr Val Ser Ile Ala Arg Ala Asn
        675                 680                 685

ggc tac tcg gcc aac tgg agc tcg cct ttc aat ggc gcc atg gga tga     2112
Gly Tyr Ser Ala Asn Trp Ser Ser Pro Phe Asn Gly Ala Met Gly
    690                 695                 700


<210> SEQ ID NO 18
<211> LENGTH: 703
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 18

Met Ala Ser Ala Asn Asn Trp Leu Gly Phe Ser Leu Ser Gly Gln Glu
1               5                   10                  15

Asn Pro Gln Pro His Gln Asp Ser Ser Pro Pro Ala Ala Ile Asp Val
            20                  25                  30

Ser Gly Ala Gly Asp Phe Tyr Gly Leu Pro Thr Ser Gln Pro Thr Ala
        35                  40                  45

Ala Asp Ala His Leu Gly Val Ala Gly His His His Asn Ala Ser Tyr
    50                  55                  60

Gly Ile Met Glu Ala Phe Asn Arg Gly Ala Gln Glu Ala Gln Asp Trp
65                  70                  75                  80

Asn Met Arg Gly Leu Asp Tyr Asn Gly Gly Ala Ser Glu Leu Ser Met
                85                  90                  95

Leu Val Gly Ser Ser Gly Gly Lys Arg Ala Ala Ala Val Glu Glu Thr
            100                 105                 110

Glu Pro Lys Leu Glu Asp Phe Leu Gly Gly Asn Ser Phe Val Ser Glu
        115                 120                 125

Gln Asp His His Ala Ala Gly Gly Phe Leu Phe Ser Gly Val Pro Met
    130                 135                 140

Ala Ser Ser Thr Asn Ser Asn Ser Gly Ser Asn Thr Met Glu Leu Ser
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145                 150                 155                 160

Met Ile Lys Thr Trp Leu Arg Asn Asn Gly Gln Val Pro Ala Gly His
                165                 170                 175

Gln Pro Gln Gln Gln Gln Pro Ala Ala Ala Ala Ala Ala Ala Gln Gln
            180                 185                 190

Gln Ala His Glu Ala Ala Glu Met Ser Thr Asp Ala Ser Ala Ser Ser
        195                 200                 205

Phe Gly Cys Ser Ser Asp Ala Met Gly Arg Ser Asn Asn Gly Gly Ala
    210                 215                 220

Val Ser Ala Ala Ala Gly Gly Thr Ser Ser Gln Ser Leu Ala Leu Ser
225                 230                 235                 240

Met Ser Thr Gly Ser His Ser His Leu Pro Ile Val Val Ala Gly Gly
                245                 250                 255

Gly Asn Ala Ser Gly Gly Ala Ala Glu Ser Thr Ser Ser Glu Asn Lys
            260                 265                 270

Arg Ala Ser Gly Ala Met Asp Ser Pro Gly Gly Gly Ala Ile Glu Ala
        275                 280                 285

Val Pro Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr
    290                 295                 300

Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu
305                 310                 315                 320

Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Ser Arg Lys Gly Arg Gln
                325                 330                 335

Val Tyr Leu Gly Gly Tyr Asp Lys Glu Asp Lys Ala Ala Arg Ala Tyr
            340                 345                 350

Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr Thr Asn Phe
        355                 360                 365

Pro Ile Ser Asn Tyr Glu Lys Glu Leu Asp Glu Met Lys His Met Thr
    370                 375                 380

Arg Gln Glu Tyr Ile Ala Tyr Leu Arg Arg Asn Ser Ser Gly Phe Ser
385                 390                 395                 400

Arg Gly Ala Ser Lys Tyr Arg Gly Val Thr Arg His His Gln His Gly
                405                 410                 415

Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr
            420                 425                 430

Leu Gly Thr Phe Ser Thr Glu Glu Glu Ala Ala Glu Ala Tyr Asp Ile
        435                 440                 445

Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Met
    450                 455                 460

Ser Arg Tyr Asp Val Lys Ser Ile Leu Glu Ser Ser Thr Leu Pro Val
465                 470                 475                 480

Gly Gly Ala Ala Arg Arg Leu Lys Glu Ala Ala Asp His Ala Glu Ala
                485                 490                 495

Ala Gly Ala Thr Ile Trp Arg Ala Ala Asp Met Asp Gly Ala Gly Val
            500                 505                 510

Ile Ser Gly Leu Ala Asp Val Gly Met Gly Ala Tyr Ala Ala Ser Tyr
        515                 520                 525

His His His His His His Gly Trp Pro Thr Ile Ala Phe Gln Gln Pro
    530                 535                 540

Pro Pro Leu Ala Val His Tyr Pro Tyr Gly Gln Ala Pro Ala Ala Pro
545                 550                 555                 560
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Ser Arg Gly Trp Cys Lys Pro Glu Gln Asp Ala Ala Val Ala Ala Ala
                565                 570                 575

Ala His Ser Leu Gln Asp Leu Gln Gln Leu His Leu Gly Ser Ala Ala
            580                 585                 590

Ala His Asn Phe Phe Gln Ala Ser Ser Ser Thr Val Tyr Asn Gly
        595                 600                 605

Gly Gly Gly Gly Tyr Gln Gly Leu Gly Gly Asn Ala Phe Leu Met Pro
    610                 615                 620

Ala Ser Thr Val Val Ala Asp Gln Gly His Ser Ser Thr Ala Thr Asn
625                 630                 635                 640

His Gly Asn Thr Cys Ser Tyr Gly Asn Glu Glu Gln Gly Lys Leu Ile
                645                 650                 655

Gly Tyr Asp Ala Met Ala Met Ala Ser Gly Ala Ala Gly Gly Gly Tyr
            660                 665                 670

Gln Leu Ser Gln Gly Ser Ala Ser Thr Val Ser Ile Ala Arg Ala Asn
        675                 680                 685

Gly Tyr Ser Ala Asn Trp Ser Ser Pro Phe Asn Gly Ala Met Gly
    690                 695                 700


<210> SEQ ID NO 19
<211> LENGTH: 1977
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(1977)

<400> SEQUENCE: 19

atg gct tct gca gat aac tgg cta ggc ttc tcg ctc tcc ggc caa ggc       48
Met Ala Ser Ala Asp Asn Trp Leu Gly Phe Ser Leu Ser Gly Gln Gly
1               5                   10                  15

aac cca cag cat cac cag aac ggc tcg ccg tct gcc gcc ggc gac gcc       96
Asn Pro Gln His His Gln Asn Gly Ser Pro Ser Ala Ala Gly Asp Ala
            20                  25                  30

gcc atc gac atc tcc ggc tca ggc gac ttc tat ggt ctg cca acg ccg      144
Ala Ile Asp Ile Ser Gly Ser Gly Asp Phe Tyr Gly Leu Pro Thr Pro
        35                  40                  45

gac gca cac cac atc ggc atg gcg ggc gaa gac gcg ccc tat ggc gtc      192
Asp Ala His His Ile Gly Met Ala Gly Glu Asp Ala Pro Tyr Gly Val
    50                  55                  60

atg gat gct ttc aac aga ggc acc cat gaa acc caa gat tgg gcg atg      240
Met Asp Ala Phe Asn Arg Gly Thr His Glu Thr Gln Asp Trp Ala Met
65                  70                  75                  80

agg ggt ttg gac tac ggc ggc ggc tcc tcc gac ctc tcg atg ctc gtc      288
Arg Gly Leu Asp Tyr Gly Gly Gly Ser Ser Asp Leu Ser Met Leu Val
                85                  90                  95

ggc tcg agc ggc ggc ggg agg agg acg gtg gcc ggc gac ggc gtc ggc      336
Gly Ser Ser Gly Gly Gly Arg Arg Thr Val Ala Gly Asp Gly Val Gly
            100                 105                 110

gag gcg ccg aag ctg gag aac ttc ctc gac ggc aac tca ttc tcc gac      384
Glu Ala Pro Lys Leu Glu Asn Phe Leu Asp Gly Asn Ser Phe Ser Asp
        115                 120                 125

gtg cac ggc caa gcc gcc ggc ggg tac ctc tac tcc gga agc gct gtc      432
Val His Gly Gln Ala Ala Gly Gly Tyr Leu Tyr Ser Gly Ser Ala Val
    130                 135                 140

ggc ggc gcc ggt ggt tac agt aac ggc gga tgc ggc ggc gga acc ata      480
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Gly Gly Ala Gly Gly Tyr Ser Asn Gly Gly Cys Gly Gly Gly Thr Ile
145                 150                 155                 160

gag ctg tcc atg atc aag acg tgg ctc cgg agc aac cag tcg cag cag      528
Glu Leu Ser Met Ile Lys Thr Trp Leu Arg Ser Asn Gln Ser Gln Gln
                165                 170                 175

cag cca tcg ccg ccg cag cac gct gat cag ggc atg agc acc gac gcc      576
Gln Pro Ser Pro Pro Gln His Ala Asp Gln Gly Met Ser Thr Asp Ala
            180                 185                 190

agc gcg agc agc tac gcg tgc tcc gac gtg ctg gtg ggg agc tgc ggc      624
Ser Ala Ser Ser Tyr Ala Cys Ser Asp Val Leu Val Gly Ser Cys Gly
        195                 200                 205

ggc ggc ggc gcc ggg ggc acg gcg agc tcg cat ggg cag ggc ctg gcg      672
Gly Gly Gly Ala Gly Gly Thr Ala Ser Ser His Gly Gln Gly Leu Ala
    210                 215                 220

ctg tcg atg agc acg ggg tcg gtg gcc gcc gcc gga ggg ggc ggc gcc      720
Leu Ser Met Ser Thr Gly Ser Val Ala Ala Ala Gly Gly Gly Gly Ala
225                 230                 235                 240

gtc gtc gcg gcc gag agc tcg tcg tcg gag aac aag cgg gtg gat tcg      768
Val Val Ala Ala Glu Ser Ser Ser Ser Glu Asn Lys Arg Val Asp Ser
                245                 250                 255

ccg ggc ggc gcc gtg gac ggc gcc gtc ccg agg aaa tcc atc gac acc      816
Pro Gly Gly Ala Val Asp Gly Ala Val Pro Arg Lys Ser Ile Asp Thr
            260                 265                 270

ttc ggg caa agg acg tct ata tac cga ggt gta aca agg cat aga tgg      864
Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp
        275                 280                 285

aca gga aga tat gaa gct cat ctg tgg gat aat agc tgt agg aga gaa      912
Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu
    290                 295                 300

ggc caa agt cgc aag ggg aga cag gtt tat ttg ggc ggt tat gac aaa      960
Gly Gln Ser Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys
305                 310                 315                 320

gaa gat aag gcg gct cgg gct tat gat ttg gca gct cta aaa tac tgg     1008
Glu Asp Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp
                325                 330                 335

ggc acg acc aca aca aca aat ttc cca atg agt aat tat gaa aag gag     1056
Gly Thr Thr Thr Thr Thr Asn Phe Pro Met Ser Asn Tyr Glu Lys Glu
            340                 345                 350

cta gag gaa atg aaa cac atg acc agg cag gag tac att gca cat ctt     1104
Leu Glu Glu Met Lys His Met Thr Arg Gln Glu Tyr Ile Ala His Leu
        355                 360                 365

aga agg aat agc agt gga ttt tct cgt ggt gca tcc aaa tat cgt ggt     1152
Arg Arg Asn Ser Ser Gly Phe Ser Arg Gly Ala Ser Lys Tyr Arg Gly
    370                 375                 380

gtt act agg cat cat cag cat ggg aga tgg cag gca agg ata ggg cga     1200
Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg
385                 390                 395                 400

gtt gca ggc aac aag gat atc tac cta ggc acc ttc agc acc gag gag     1248
Val Ala Gly Asn Lys Asp Ile Tyr Leu Gly Thr Phe Ser Thr Glu Glu
                405                 410                 415

gag gcc gcc gag gcg tac gac atc gcc gcc atc aag ttc cgc ggg ctc     1296
Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu
            420                 425                 430

aac gcc gtc acc aac ttc gac atg agc cgg tac gac gtc aag agc atc     1344
Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser Ile
        435                 440                 445

ctg gac agc agc acg ctg ccg gtc ggc ggc gcg gcg cgg cgg ctc aag     1392
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Leu Asp Ser Ser Thr Leu Pro Val Gly Gly Ala Ala Arg Arg Leu Lys
    450                 455                 460

gag gcg gag gtc gcc gcc gcc gcc gcg ggc ggc ggc gtg atc gtc tcc     1440
Glu Ala Glu Val Ala Ala Ala Ala Ala Gly Gly Gly Val Ile Val Ser
465                 470                 475                 480

cac ctg gcc gac ggc ggt gtg ggt ggg tac tac tac ggg tgc ggc ccg     1488
His Leu Ala Asp Gly Gly Val Gly Gly Tyr Tyr Tyr Gly Cys Gly Pro
                485                 490                 495

acc atc gcg ttc ggc ggc ggc ggc cag cag ccg gcg ccg ctc gcc gtg     1536
Thr Ile Ala Phe Gly Gly Gly Gly Gln Gln Pro Ala Pro Leu Ala Val
            500                 505                 510

cac tac ccg tcg tac ggc cag gcc agc ggg tgg tgc aag ccg gag cag     1584
His Tyr Pro Ser Tyr Gly Gln Ala Ser Gly Trp Cys Lys Pro Glu Gln
        515                 520                 525

gac gcg gtg atc gcg gcc ggg cac tgc gcg acg gac ctc cag cac ctg     1632
Asp Ala Val Ile Ala Ala Gly His Cys Ala Thr Asp Leu Gln His Leu
    530                 535                 540

cac ctc ggg agc ggc ggc gcc gcc gcc acc cac aac ttc ttc cag cag     1680
His Leu Gly Ser Gly Gly Ala Ala Ala Thr His Asn Phe Phe Gln Gln
545                 550                 555                 560

ccg gcg tca agc tcg gcc gtc tac ggc aac ggc ggc ggc ggc ggc ggc     1728
Pro Ala Ser Ser Ser Ala Val Tyr Gly Asn Gly Gly Gly Gly Gly Gly
                565                 570                 575

aac gcg ttc atg atg ccg atg ggc gcc gtg gtg gcc gcc gcc gat cac     1776
Asn Ala Phe Met Met Pro Met Gly Ala Val Val Ala Ala Ala Asp His
            580                 585                 590

ggc ggg cag agc agc gcc tac ggc ggt ggc gac gag agc ggg agg ctc     1824
Gly Gly Gln Ser Ser Ala Tyr Gly Gly Gly Asp Glu Ser Gly Arg Leu
        595                 600                 605

gtc gtg ggg tac gac ggc gtc gtc gac ccg tac gcg gcc atg aga agc     1872
Val Val Gly Tyr Asp Gly Val Val Asp Pro Tyr Ala Ala Met Arg Ser
    610                 615                 620

gcg tac gag ctc tcg cag ggc tcg tcg tcg tcg tcg gtg agc gtc gcg     1920
Ala Tyr Glu Leu Ser Gln Gly Ser Ser Ser Ser Ser Val Ser Val Ala
625                 630                 635                 640

aag gcg gcg aac ggg tac ccg gac aac tgg agc tcg ccg ttc aac ggc     1968
Lys Ala Ala Asn Gly Tyr Pro Asp Asn Trp Ser Ser Pro Phe Asn Gly
                645                 650                 655

atg gga tga                                                         1977
Met Gly


<210> SEQ ID NO 20
<211> LENGTH: 658
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 20

Met Ala Ser Ala Asp Asn Trp Leu Gly Phe Ser Leu Ser Gly Gln Gly
1               5                   10                  15

Asn Pro Gln His His Gln Asn Gly Ser Pro Ser Ala Ala Gly Asp Ala
            20                  25                  30

Ala Ile Asp Ile Ser Gly Ser Gly Asp Phe Tyr Gly Leu Pro Thr Pro
        35                  40                  45

Asp Ala His His Ile Gly Met Ala Gly Glu Asp Ala Pro Tyr Gly Val
    50                  55                  60

Met Asp Ala Phe Asn Arg Gly Thr His Glu Thr Gln Asp Trp Ala Met
65                  70                  75                  80
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Arg Gly Leu Asp Tyr Gly Gly Gly Ser Ser Asp Leu Ser Met Leu Val
                85                  90                  95

Gly Ser Ser Gly Gly Gly Arg Arg Thr Val Ala Gly Asp Gly Val Gly
            100                 105                 110

Glu Ala Pro Lys Leu Glu Asn Phe Leu Asp Gly Asn Ser Phe Ser Asp
        115                 120                 125

Val His Gly Gln Ala Ala Gly Gly Tyr Leu Tyr Ser Gly Ser Ala Val
    130                 135                 140

Gly Gly Ala Gly Gly Tyr Ser Asn Gly Gly Cys Gly Gly Gly Thr Ile
145                 150                 155                 160

Glu Leu Ser Met Ile Lys Thr Trp Leu Arg Ser Asn Gln Ser Gln Gln
                165                 170                 175

Gln Pro Ser Pro Pro Gln His Ala Asp Gln Gly Met Ser Thr Asp Ala
            180                 185                 190

Ser Ala Ser Ser Tyr Ala Cys Ser Asp Val Leu Val Gly Ser Cys Gly
        195                 200                 205

Gly Gly Gly Ala Gly Gly Thr Ala Ser Ser His Gly Gln Gly Leu Ala
    210                 215                 220

Leu Ser Met Ser Thr Gly Ser Val Ala Ala Ala Gly Gly Gly Gly Ala
225                 230                 235                 240

Val Val Ala Ala Glu Ser Ser Ser Ser Glu Asn Lys Arg Val Asp Ser
                245                 250                 255

Pro Gly Gly Ala Val Asp Gly Ala Val Pro Arg Lys Ser Ile Asp Thr
            260                 265                 270

Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp
        275                 280                 285

Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu
    290                 295                 300

Gly Gln Ser Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys
305                 310                 315                 320

Glu Asp Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp
                325                 330                 335

Gly Thr Thr Thr Thr Thr Asn Phe Pro Met Ser Asn Tyr Glu Lys Glu
            340                 345                 350

Leu Glu Glu Met Lys His Met Thr Arg Gln Glu Tyr Ile Ala His Leu
        355                 360                 365

Arg Arg Asn Ser Ser Gly Phe Ser Arg Gly Ala Ser Lys Tyr Arg Gly
    370                 375                 380

Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg
385                 390                 395                 400

Val Ala Gly Asn Lys Asp Ile Tyr Leu Gly Thr Phe Ser Thr Glu Glu
                405                 410                 415

Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu
            420                 425                 430

Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser Ile
        435                 440                 445

Leu Asp Ser Ser Thr Leu Pro Val Gly Gly Ala Ala Arg Arg Leu Lys
    450                 455                 460

Glu Ala Glu Val Ala Ala Ala Ala Ala Gly Gly Gly Val Ile Val Ser
465                 470                 475                 480
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```
His Leu Ala Asp Gly Gly Val Gly Gly Tyr Tyr Tyr Gly Cys Gly Pro
                485                 490                 495

Thr Ile Ala Phe Gly Gly Gly Gly Gln Gln Pro Ala Pro Leu Ala Val
            500                 505                 510

His Tyr Pro Ser Tyr Gly Gln Ala Ser Gly Trp Cys Lys Pro Glu Gln
        515                 520                 525

Asp Ala Val Ile Ala Ala Gly His Cys Ala Thr Asp Leu Gln His Leu
    530                 535                 540

His Leu Gly Ser Gly Gly Ala Ala Ala Thr His Asn Phe Phe Gln Gln
545                 550                 555                 560

Pro Ala Ser Ser Ser Ala Val Tyr Gly Asn Gly Gly Gly Gly Gly Gly
                565                 570                 575

Asn Ala Phe Met Met Pro Met Gly Ala Val Val Ala Ala Ala Asp His
            580                 585                 590

Gly Gly Gln Ser Ser Ala Tyr Gly Gly Gly Asp Glu Ser Gly Arg Leu
        595                 600                 605

Val Val Gly Tyr Asp Gly Val Val Asp Pro Tyr Ala Ala Met Arg Ser
    610                 615                 620

Ala Tyr Glu Leu Ser Gln Gly Ser Ser Ser Ser Ser Val Ser Val Ala
625                 630                 635                 640

Lys Ala Ala Asn Gly Tyr Pro Asp Asn Trp Ser Ser Pro Phe Asn Gly
                645                 650                 655

Met Gly


<210> SEQ ID NO 21
<211> LENGTH: 1755
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(1755)

<400> SEQUENCE: 21

atg aac tcg atg aat aac tgg tta ggc ttc tct ctc tct cct cat gat       48
Met Asn Ser Met Asn Asn Trp Leu Gly Phe Ser Leu Ser Pro His Asp
1               5                   10                  15

caa aat cat cac cgt acg gat gtt gac tcc tcc acc acc aga acc gcc       96
Gln Asn His His Arg Thr Asp Val Asp Ser Ser Thr Thr Arg Thr Ala
            20                  25                  30

gta gat gtt gcc gga ggg tac tgt ttt gat ctg gcc gct ccc tcc gat      144
Val Asp Val Ala Gly Gly Tyr Cys Phe Asp Leu Ala Ala Pro Ser Asp
        35                  40                  45

gaa tct tct gcc gtt caa aca tct ttt ctt tct cct ttc ggt gtc acc      192
Glu Ser Ser Ala Val Gln Thr Ser Phe Leu Ser Pro Phe Gly Val Thr
    50                  55                  60

ctc gaa gct ttc acc aga gac aat aat agt cac tcc cga gat tgg gac      240
Leu Glu Ala Phe Thr Arg Asp Asn Asn Ser His Ser Arg Asp Trp Asp
65                  70                  75                  80

atc aat ggt ggt gca tgc aat aca tta acc aat aac gaa caa aat gga      288
Ile Asn Gly Gly Ala Cys Asn Thr Leu Thr Asn Asn Glu Gln Asn Gly
                85                  90                  95

cca aag ctt gag aat ttc ctc ggc cgc acc acc acg att tac aat acc      336
Pro Lys Leu Glu Asn Phe Leu Gly Arg Thr Thr Thr Ile Tyr Asn Thr
            100                 105                 110

aac gag acc gtt gta gat gga aat ggc gat tgt gga gga gga gac ggt      384
Asn Glu Thr Val Val Asp Gly Asn Gly Asp Cys Gly Gly Gly Asp Gly
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        115                 120                 125

ggt ggt ggc ggc tca cta ggc ctt tcg atg ata aaa aca tgg ctg agt      432
Gly Gly Gly Gly Ser Leu Gly Leu Ser Met Ile Lys Thr Trp Leu Ser
    130                 135                 140

aat cat tcg gtt gct aat gct aat cat caa gac aat ggt aac ggt gca      480
Asn His Ser Val Ala Asn Ala Asn His Gln Asp Asn Gly Asn Gly Ala
145                 150                 155                 160

cga ggc ttg tcc ctc tct atg aat tca tct act agt gat agc aac aac      528
Arg Gly Leu Ser Leu Ser Met Asn Ser Ser Thr Ser Asp Ser Asn Asn
                165                 170                 175

tac aac aac aat gat gat gtc gtc caa gag aag act att gtt gat gtc      576
Tyr Asn Asn Asn Asp Asp Val Val Gln Glu Lys Thr Ile Val Asp Val
            180                 185                 190

gta gaa act aca ccg aag aaa act att gag agt ttt gga caa agg acg      624
Val Glu Thr Thr Pro Lys Lys Thr Ile Glu Ser Phe Gly Gln Arg Thr
        195                 200                 205

tct ata tac cgc ggt gtt aca agg cat cgg tgg aca ggt aga tac gag      672
Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
    210                 215                 220

gca cat tta tgg gac aat agt tgc aaa aga gaa ggc cag act cgc aaa      720
Ala His Leu Trp Asp Asn Ser Cys Lys Arg Glu Gly Gln Thr Arg Lys
225                 230                 235                 240

gga aga caa gtt tat ctg gga ggt tat gac aaa gaa gaa aaa gca gct      768
Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala
                245                 250                 255

agg gct tac gat tta gcc gca cta aag tat tgg gga ccc acc act act      816
Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Thr Thr Thr
            260                 265                 270

act aac ttc ccc ttg agt gaa tat gag aaa gag gta gaa gag atg aag      864
Thr Asn Phe Pro Leu Ser Glu Tyr Glu Lys Glu Val Glu Glu Met Lys
        275                 280                 285

cac atg acg agg caa gag tat gtt gcc tct ctg cgc agg aaa agt agt      912
His Met Thr Arg Gln Glu Tyr Val Ala Ser Leu Arg Arg Lys Ser Ser
    290                 295                 300

ggt ttc tct cgt ggt gca tcg att tat cga gga gta aca agg cat cac      960
Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His
305                 310                 315                 320

caa cat gga agg tgg caa gct agg atc gga aga gtc gcc ggt aac aaa     1008
Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys
                325                 330                 335

gac ctc tac ttg gga act ttc ggc aca cag gaa gag gct gct gag gct     1056
Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu Ala
            340                 345                 350

tat gac att gca gcc att aaa ttc aga gga tta agc gca gtg act aac     1104
Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Ser Ala Val Thr Asn
        355                 360                 365

ttc gac atg aac aga tac aat gtt aaa gca atc ctc gag agc ccg agt     1152
Phe Asp Met Asn Arg Tyr Asn Val Lys Ala Ile Leu Glu Ser Pro Ser
    370                 375                 380

cta cct att ggt agt tct gcg aaa cgt ctc aag gac gtt aac aat ccg     1200
Leu Pro Ile Gly Ser Ser Ala Lys Arg Leu Lys Asp Val Asn Asn Pro
385                 390                 395                 400

gtt cca gct atg atg att agt aat aac gtt tca gag agt gca aat aat     1248
Val Pro Ala Met Met Ile Ser Asn Asn Val Ser Glu Ser Ala Asn Asn
                405                 410                 415

gtt agc ggt tgg caa aac act gcg ttt cag cat cat cag gga atg gat     1296
Val Ser Gly Trp Gln Asn Thr Ala Phe Gln His His Gln Gly Met Asp
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            420                 425                 430

ttg agc tta ttg cag caa cag cag gag agg tac gtt ggt tat tac aat      1344
Leu Ser Leu Leu Gln Gln Gln Gln Glu Arg Tyr Val Gly Tyr Tyr Asn
        435                 440                 445

gga gga aac ttg tct acc gag agt act agg gtt tgt ttc aaa caa gag      1392
Gly Gly Asn Leu Ser Thr Glu Ser Thr Arg Val Cys Phe Lys Gln Glu
    450                 455                 460

gag gaa caa caa cac ttc ttg aga aac tcg ccg agt cac atg act aat      1440
Glu Glu Gln Gln His Phe Leu Arg Asn Ser Pro Ser His Met Thr Asn
465                 470                 475                 480

gtt gat cat cat agc tcg acc tct gat gat tct gtt acc gtt tgt gga      1488
Val Asp His His Ser Ser Thr Ser Asp Asp Ser Val Thr Val Cys Gly
                485                 490                 495

aat gtt gtt agt tat ggt ggt tat caa gga ttc gca atc cct gtt gga      1536
Asn Val Val Ser Tyr Gly Gly Tyr Gln Gly Phe Ala Ile Pro Val Gly
            500                 505                 510

aca tcg gtt aat tac gat ccc ttt act gct gct gag att gct tac aac      1584
Thr Ser Val Asn Tyr Asp Pro Phe Thr Ala Ala Glu Ile Ala Tyr Asn
        515                 520                 525

gca aga aat cat tat tac tat gct cag cat cag caa caa cag cag att      1632
Ala Arg Asn His Tyr Tyr Tyr Ala Gln His Gln Gln Gln Gln Gln Ile
    530                 535                 540

cag cag tcg ccg gga gga gat ttt ccg gtg gcg att tcg aat aac cat      1680
Gln Gln Ser Pro Gly Gly Asp Phe Pro Val Ala Ile Ser Asn Asn His
545                 550                 555                 560

agc tct aac atg tac ttt cac ggg gaa ggt ggt gga gaa ggg gct cca      1728
Ser Ser Asn Met Tyr Phe His Gly Glu Gly Gly Gly Glu Gly Ala Pro
                565                 570                 575

acg ttt tca gtt tgg aac gac act tag                                  1755
Thr Phe Ser Val Trp Asn Asp Thr
            580


<210> SEQ ID NO 22
<211> LENGTH: 584
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 22

Met Asn Ser Met Asn Asn Trp Leu Gly Phe Ser Leu Ser Pro His Asp
1               5                   10                  15

Gln Asn His His Arg Thr Asp Val Asp Ser Ser Thr Thr Arg Thr Ala
            20                  25                  30

Val Asp Val Ala Gly Gly Tyr Cys Phe Asp Leu Ala Ala Pro Ser Asp
        35                  40                  45

Glu Ser Ser Ala Val Gln Thr Ser Phe Leu Ser Pro Phe Gly Val Thr
    50                  55                  60

Leu Glu Ala Phe Thr Arg Asp Asn Asn Ser His Ser Arg Asp Trp Asp
65                  70                  75                  80

Ile Asn Gly Gly Ala Cys Asn Thr Leu Thr Asn Asn Glu Gln Asn Gly
                85                  90                  95

Pro Lys Leu Glu Asn Phe Leu Gly Arg Thr Thr Thr Ile Tyr Asn Thr
            100                 105                 110

Asn Glu Thr Val Val Asp Gly Asn Gly Asp Cys Gly Gly Gly Asp Gly
        115                 120                 125

Gly Gly Gly Gly Ser Leu Gly Leu Ser Met Ile Lys Thr Trp Leu Ser
    130                 135                 140
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Asn His Ser Val Ala Asn Ala Asn His Gln Asp Asn Gly Asn Gly Ala
145                 150                 155                 160

Arg Gly Leu Ser Leu Ser Met Asn Ser Ser Thr Ser Asp Ser Asn Asn
                165                 170                 175

Tyr Asn Asn Asn Asp Asp Val Val Gln Glu Lys Thr Ile Val Asp Val
            180                 185                 190

Val Glu Thr Thr Pro Lys Lys Thr Ile Glu Ser Phe Gly Gln Arg Thr
        195                 200                 205

Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
    210                 215                 220

Ala His Leu Trp Asp Asn Ser Cys Lys Arg Glu Gly Gln Thr Arg Lys
225                 230                 235                 240

Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala
                245                 250                 255

Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Thr Thr Thr
            260                 265                 270

Thr Asn Phe Pro Leu Ser Glu Tyr Glu Lys Glu Val Glu Glu Met Lys
        275                 280                 285

His Met Thr Arg Gln Glu Tyr Val Ala Ser Leu Arg Arg Lys Ser Ser
    290                 295                 300

Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His
305                 310                 315                 320

Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys
                325                 330                 335

Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu Ala
            340                 345                 350

Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Ser Ala Val Thr Asn
        355                 360                 365

Phe Asp Met Asn Arg Tyr Asn Val Lys Ala Ile Leu Glu Ser Pro Ser
    370                 375                 380

Leu Pro Ile Gly Ser Ser Ala Lys Arg Leu Lys Asp Val Asn Asn Pro
385                 390                 395                 400

Val Pro Ala Met Met Ile Ser Asn Asn Val Ser Glu Ser Ala Asn Asn
                405                 410                 415

Val Ser Gly Trp Gln Asn Thr Ala Phe Gln His His Gln Gly Met Asp
            420                 425                 430

Leu Ser Leu Leu Gln Gln Gln Gln Glu Arg Tyr Val Gly Tyr Tyr Asn
        435                 440                 445

Gly Gly Asn Leu Ser Thr Glu Ser Thr Arg Val Cys Phe Lys Gln Glu
    450                 455                 460

Glu Glu Gln Gln His Phe Leu Arg Asn Ser Pro Ser His Met Thr Asn
465                 470                 475                 480

Val Asp His His Ser Ser Thr Ser Asp Asp Ser Val Thr Val Cys Gly
                485                 490                 495

Asn Val Val Ser Tyr Gly Gly Tyr Gln Gly Phe Ala Ile Pro Val Gly
            500                 505                 510

Thr Ser Val Asn Tyr Asp Pro Phe Thr Ala Ala Glu Ile Ala Tyr Asn
        515                 520                 525

Ala Arg Asn His Tyr Tyr Tyr Ala Gln His Gln Gln Gln Gln Gln Ile
    530                 535                 540
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Gln Gln Ser Pro Gly Gly Asp Phe Pro Val Ala Ile Ser Asn Asn His
545                 550                 555                 560

Ser Ser Asn Met Tyr Phe His Gly Glu Gly Gly Gly Glu Gly Ala Pro
                565                 570                 575

Thr Phe Ser Val Trp Asn Asp Thr
            580


<210> SEQ ID NO 23
<211> LENGTH: 1740
<212> TYPE: DNA
<213> ORGANISM: Brassica napus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(1740)

<400> SEQUENCE: 23

atg aat aat aac tgg tta ggc ttt tct ctc tct cct tat gaa caa aat       48
Met Asn Asn Asn Trp Leu Gly Phe Ser Leu Ser Pro Tyr Glu Gln Asn
1               5                   10                  15

cac cat cgt aag gac gtc tac tct tcc acc acc aca acc gtc gta gat       96
His His Arg Lys Asp Val Tyr Ser Ser Thr Thr Thr Thr Val Val Asp
            20                  25                  30

gtc gcc gga gag tac tgt tac gat ccg acc gct gcc tcc gat gag tct      144
Val Ala Gly Glu Tyr Cys Tyr Asp Pro Thr Ala Ala Ser Asp Glu Ser
        35                  40                  45

tca gcc atc caa aca tcg ttt cct tct ccc ttt ggt gtc gtc gtc gat      192
Ser Ala Ile Gln Thr Ser Phe Pro Ser Pro Phe Gly Val Val Val Asp
    50                  55                  60

gct ttc acc aga gac aac aat agt cac tcc cga gat tgg gac atc aat      240
Ala Phe Thr Arg Asp Asn Asn Ser His Ser Arg Asp Trp Asp Ile Asn
65                  70                  75                  80

ggt tgt gca tgc aat aac atc cac aac gat gag caa gat gga cca aag      288
Gly Cys Ala Cys Asn Asn Ile His Asn Asp Glu Gln Asp Gly Pro Lys
                85                  90                  95

ctt gag aat ttc ctt ggc cgc acc acc acg att tac aac acc aac gaa      336
Leu Glu Asn Phe Leu Gly Arg Thr Thr Thr Ile Tyr Asn Thr Asn Glu
            100                 105                 110

aac gtt gga gat gga agt gga agt ggc tgt tat gga gga gga gac ggt      384
Asn Val Gly Asp Gly Ser Gly Ser Gly Cys Tyr Gly Gly Gly Asp Gly
        115                 120                 125

ggt ggt ggc tca cta gga ctt tcg atg ata aag aca tgg ctg aga aat      432
Gly Gly Gly Ser Leu Gly Leu Ser Met Ile Lys Thr Trp Leu Arg Asn
    130                 135                 140

caa ccc gtg gat aat gtt gat aat caa gaa aat ggc aat gct gca aaa      480
Gln Pro Val Asp Asn Val Asp Asn Gln Glu Asn Gly Asn Ala Ala Lys
145                 150                 155                 160

ggc ctg tcc ctc tca atg aac tca tct act tct tgt gat aac aac aac      528
Gly Leu Ser Leu Ser Met Asn Ser Ser Thr Ser Cys Asp Asn Asn Asn
                165                 170                 175

gac agc aat aac aac gtt gtt gcc caa ggg aag act att gat gat agc      576
Asp Ser Asn Asn Asn Val Val Ala Gln Gly Lys Thr Ile Asp Asp Ser
            180                 185                 190

gtt gaa gct aca ccg aag aaa act att gag agt ttt gga cag agg acg      624
Val Glu Ala Thr Pro Lys Lys Thr Ile Glu Ser Phe Gly Gln Arg Thr
        195                 200                 205

tct ata tac cgc ggt gtt aca agg cat cgg tgg aca gga aga tat gag      672
Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
    210                 215                 220
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gca cat tta tgg gat aat agt tgt aaa aga gaa ggc caa acg cgc aaa       720
Ala His Leu Trp Asp Asn Ser Cys Lys Arg Glu Gly Gln Thr Arg Lys
225                 230                 235                 240

gga aga caa gtt tat ttg gga ggt tat gac aaa gaa gaa aaa gca gct       768
Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala
                245                 250                 255

agg gct tat gat tta gcc gca ctc aag tat tgg gga acc acc act act       816
Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr
            260                 265                 270

act aac ttc ccc atg agc gaa tat gaa aaa gag gta gaa gag atg aag       864
Thr Asn Phe Pro Met Ser Glu Tyr Glu Lys Glu Val Glu Glu Met Lys
        275                 280                 285

cac atg aca agg caa gag tat gtt gcc tca ctg cgc agg aaa agt agt       912
His Met Thr Arg Gln Glu Tyr Val Ala Ser Leu Arg Arg Lys Ser Ser
    290                 295                 300

ggt ttc tct cgt ggt gca tcg att tat cgt gga gta aca aga cat cac       960
Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His
305                 310                 315                 320

caa cat gga aga tgg caa gct agg ata gga aga gtc gcc ggt aac aaa      1008
Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys
                325                 330                 335

gac ctc tac ttg gga act ttt ggc aca caa gaa gaa gct gca gag gca      1056
Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu Ala
            340                 345                 350

tac gac att gcg gcc atc aaa ttc aga gga tta acc gca gtg act aac      1104
Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Thr Ala Val Thr Asn
        355                 360                 365

ttc gac atg aac aga tac aac gtt aaa gca atc ctc gaa agc cct agt      1152
Phe Asp Met Asn Arg Tyr Asn Val Lys Ala Ile Leu Glu Ser Pro Ser
    370                 375                 380

ctt cct att ggt agc gcc gca aaa cgt ctc aag gag gct aac cgt ccg      1200
Leu Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Glu Ala Asn Arg Pro
385                 390                 395                 400

gtt cca agt atg atg atg atc agt aat aac gtt tca gag agt gag aat      1248
Val Pro Ser Met Met Met Ile Ser Asn Asn Val Ser Glu Ser Glu Asn
                405                 410                 415

agt gct agc ggt tgg caa aac gct gcg gtt cag cat cat cag gga gta      1296
Ser Ala Ser Gly Trp Gln Asn Ala Ala Val Gln His His Gln Gly Val
            420                 425                 430

gat ttg agc tta ttg cac caa cat caa gag agg tac aat ggt tat tat      1344
Asp Leu Ser Leu Leu His Gln His Gln Glu Arg Tyr Asn Gly Tyr Tyr
        435                 440                 445

tac aat gga gga aac ttg tct tcg gag agt gct agg gct tgt ttc aaa      1392
Tyr Asn Gly Gly Asn Leu Ser Ser Glu Ser Ala Arg Ala Cys Phe Lys
    450                 455                 460

caa gag gat gat caa cac cat ttc ttg agc aac acg cag agc ctc atg      1440
Gln Glu Asp Asp Gln His His Phe Leu Ser Asn Thr Gln Ser Leu Met
465                 470                 475                 480

act aat atc gat cat caa agt tct gtt tcg gat gat tcg gtt act gtt      1488
Thr Asn Ile Asp His Gln Ser Ser Val Ser Asp Asp Ser Val Thr Val
                485                 490                 495

tgt gga aat gtt gtt ggt tat ggt ggt tat caa gga ttt gca gcc ccg      1536
Cys Gly Asn Val Val Gly Tyr Gly Gly Tyr Gln Gly Phe Ala Ala Pro
            500                 505                 510

gtt aac tgc gat gcc tac gct gct agt gag ttt gat tat aac gca aga      1584
Val Asn Cys Asp Ala Tyr Ala Ala Ser Glu Phe Asp Tyr Asn Ala Arg
        515                 520                 525
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aac cat tat tac ttt gct cag cag cag cag acc cag cag tcg cca ggt     1632
Asn His Tyr Tyr Phe Ala Gln Gln Gln Gln Thr Gln Gln Ser Pro Gly
    530                 535                 540

gga gat ttt ccc gcg gca atg acg aat aat gtt ggc tct aat atg tat     1680
Gly Asp Phe Pro Ala Ala Met Thr Asn Asn Val Gly Ser Asn Met Tyr
545                 550                 555                 560

tac cat ggg gaa ggt ggt gga gaa gtt gct cca aca ttt aca gtt tgg     1728
Tyr His Gly Glu Gly Gly Gly Glu Val Ala Pro Thr Phe Thr Val Trp
                565                 570                 575

aac gac aat tag                                                     1740
Asn Asp Asn


<210> SEQ ID NO 24
<211> LENGTH: 579
<212> TYPE: PRT
<213> ORGANISM: Brassica napus

<400> SEQUENCE: 24

Met Asn Asn Asn Trp Leu Gly Phe Ser Leu Ser Pro Tyr Glu Gln Asn
1               5                   10                  15

His His Arg Lys Asp Val Tyr Ser Ser Thr Thr Thr Thr Val Val Asp
            20                  25                  30

Val Ala Gly Glu Tyr Cys Tyr Asp Pro Thr Ala Ala Ser Asp Glu Ser
        35                  40                  45

Ser Ala Ile Gln Thr Ser Phe Pro Ser Pro Phe Gly Val Val Val Asp
    50                  55                  60

Ala Phe Thr Arg Asp Asn Asn Ser His Ser Arg Asp Trp Asp Ile Asn
65                  70                  75                  80

Gly Cys Ala Cys Asn Asn Ile His Asn Asp Glu Gln Asp Gly Pro Lys
                85                  90                  95

Leu Glu Asn Phe Leu Gly Arg Thr Thr Thr Ile Tyr Asn Thr Asn Glu
            100                 105                 110

Asn Val Gly Asp Gly Ser Gly Ser Gly Cys Tyr Gly Gly Gly Asp Gly
        115                 120                 125

Gly Gly Gly Ser Leu Gly Leu Ser Met Ile Lys Thr Trp Leu Arg Asn
    130                 135                 140

Gln Pro Val Asp Asn Val Asp Asn Gln Glu Asn Gly Asn Ala Ala Lys
145                 150                 155                 160

Gly Leu Ser Leu Ser Met Asn Ser Ser Thr Ser Cys Asp Asn Asn Asn
                165                 170                 175

Asp Ser Asn Asn Asn Val Val Ala Gln Gly Lys Thr Ile Asp Asp Ser
            180                 185                 190

Val Glu Ala Thr Pro Lys Lys Thr Ile Glu Ser Phe Gly Gln Arg Thr
        195                 200                 205

Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
    210                 215                 220

Ala His Leu Trp Asp Asn Ser Cys Lys Arg Glu Gly Gln Thr Arg Lys
225                 230                 235                 240

Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala
                245                 250                 255

Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr
            260                 265                 270

Thr Asn Phe Pro Met Ser Glu Tyr Glu Lys Glu Val Glu Glu Met Lys
        275                 280                 285
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His Met Thr Arg Gln Glu Tyr Val Ala Ser Leu Arg Arg Lys Ser Ser
    290                 295                 300

Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His
305                 310                 315                 320

Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys
                325                 330                 335

Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu Ala
            340                 345                 350

Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Thr Ala Val Thr Asn
        355                 360                 365

Phe Asp Met Asn Arg Tyr Asn Val Lys Ala Ile Leu Glu Ser Pro Ser
    370                 375                 380

Leu Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Glu Ala Asn Arg Pro
385                 390                 395                 400

Val Pro Ser Met Met Met Ile Ser Asn Asn Val Ser Glu Ser Glu Asn
                405                 410                 415

Ser Ala Ser Gly Trp Gln Asn Ala Ala Val Gln His His Gln Gly Val
            420                 425                 430

Asp Leu Ser Leu Leu His Gln His Gln Glu Arg Tyr Asn Gly Tyr Tyr
        435                 440                 445

Tyr Asn Gly Gly Asn Leu Ser Ser Glu Ser Ala Arg Ala Cys Phe Lys
    450                 455                 460

Gln Glu Asp Asp Gln His His Phe Leu Ser Asn Thr Gln Ser Leu Met
465                 470                 475                 480

Thr Asn Ile Asp His Gln Ser Ser Val Ser Asp Asp Ser Val Thr Val
                485                 490                 495

Cys Gly Asn Val Val Gly Tyr Gly Gly Tyr Gln Gly Phe Ala Ala Pro
            500                 505                 510

Val Asn Cys Asp Ala Tyr Ala Ala Ser Glu Phe Asp Tyr Asn Ala Arg
        515                 520                 525

Asn His Tyr Tyr Phe Ala Gln Gln Gln Gln Thr Gln Gln Ser Pro Gly
    530                 535                 540

Gly Asp Phe Pro Ala Ala Met Thr Asn Asn Val Gly Ser Asn Met Tyr
545                 550                 555                 560

Tyr His Gly Glu Gly Gly Gly Glu Val Ala Pro Thr Phe Thr Val Trp
                565                 570                 575

Asn Asp Asn


<210> SEQ ID NO 25
<211> LENGTH: 1740
<212> TYPE: DNA
<213> ORGANISM: Brassica napus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(1740)

<400> SEQUENCE: 25

atg aat aat aac tgg tta ggc ttt tct ctc tct cct tat gaa caa aat       48
Met Asn Asn Asn Trp Leu Gly Phe Ser Leu Ser Pro Tyr Glu Gln Asn
1               5                   10                  15

cac cat cgt aag gac gtc tgc tct tcc acc acc aca acc gcc gta gat       96
His His Arg Lys Asp Val Cys Ser Ser Thr Thr Thr Thr Ala Val Asp
            20                  25                  30
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gtc gcc gga gag tac tgt tac gat ccg acc gct gcc tcc gat gag tct      144
Val Ala Gly Glu Tyr Cys Tyr Asp Pro Thr Ala Ala Ser Asp Glu Ser
        35                  40                  45

tca gcc atc caa aca tcg ttt cct tct ccc ttt ggt gtc gtc ctc gat      192
Ser Ala Ile Gln Thr Ser Phe Pro Ser Pro Phe Gly Val Val Leu Asp
    50                  55                  60

gct ttc acc aga gac aac aat agt cac tcc cga gat tgg gac atc aat      240
Ala Phe Thr Arg Asp Asn Asn Ser His Ser Arg Asp Trp Asp Ile Asn
65                  70                  75                  80

ggt agt gca tgt aat aac atc cac aat gat gag caa gat gga cca aaa      288
Gly Ser Ala Cys Asn Asn Ile His Asn Asp Glu Gln Asp Gly Pro Lys
                85                  90                  95

ctt gag aat ttc ctt ggc cgc acc acc acg att tac aac acc aac gaa      336
Leu Glu Asn Phe Leu Gly Arg Thr Thr Thr Ile Tyr Asn Thr Asn Glu
            100                 105                 110

aac gtt gga gat atc gat gga agt ggg tgt tat gga gga gga gac ggt      384
Asn Val Gly Asp Ile Asp Gly Ser Gly Cys Tyr Gly Gly Gly Asp Gly
        115                 120                 125

ggt ggt ggc tca cta gga ctt tcg atg ata aag aca tgg ctg aga aat      432
Gly Gly Gly Ser Leu Gly Leu Ser Met Ile Lys Thr Trp Leu Arg Asn
    130                 135                 140

caa ccc gtg gat aat gtt gat aat caa gaa aat ggc aat ggt gca aaa      480
Gln Pro Val Asp Asn Val Asp Asn Gln Glu Asn Gly Asn Gly Ala Lys
145                 150                 155                 160

ggc ctg tcc ctc tca atg aac tca tct act tct tgt gat aac aac aac      528
Gly Leu Ser Leu Ser Met Asn Ser Ser Thr Ser Cys Asp Asn Asn Asn
                165                 170                 175

tac agc agt aac aac ctt gtt gcc caa ggg aag act att gat gat agc      576
Tyr Ser Ser Asn Asn Leu Val Ala Gln Gly Lys Thr Ile Asp Asp Ser
            180                 185                 190

gtt gaa gct aca ccg aag aaa act att gag agt ttt gga cag agg acg      624
Val Glu Ala Thr Pro Lys Lys Thr Ile Glu Ser Phe Gly Gln Arg Thr
        195                 200                 205

tct ata tac cgc ggt gtt aca agg cat cgg tgg aca gga aga tat gag      672
Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
    210                 215                 220

gca cat tta tgg gat aat agt tgt aaa cga gaa ggc caa acg cgc aaa      720
Ala His Leu Trp Asp Asn Ser Cys Lys Arg Glu Gly Gln Thr Arg Lys
225                 230                 235                 240

gga aga caa gtt tat ttg gga ggt tat gac aaa gaa gaa aaa gca gct      768
Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala
                245                 250                 255

agg gct tat gat tta gcc gca ctc aag tat tgg gga acc acc act act      816
Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr
            260                 265                 270

act aac ttc ccc atg agc gaa tat gag aaa gag ata gaa gag atg aag      864
Thr Asn Phe Pro Met Ser Glu Tyr Glu Lys Glu Ile Glu Glu Met Lys
        275                 280                 285

cac atg aca agg caa gag tat gtt gcc tca ctt cgc agg aaa agt agt      912
His Met Thr Arg Gln Glu Tyr Val Ala Ser Leu Arg Arg Lys Ser Ser
    290                 295                 300

ggt ttc tct cgt ggt gca tcg att tat cgt gga gta aca aga cat cac      960
Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His
305                 310                 315                 320

caa cat gga aga tgg caa gct agg ata gga aga gtc gcc ggt aac aaa     1008
Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys
                325                 330                 335
```

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```
gac ctc tac ttg gga act ttt ggc aca caa gaa gaa gct gca gag gca         1056
Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu Ala
            340                 345                 350

tac gac att gcg gcc atc aaa ttc aga gga tta acc gca gtg act aac         1104
Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Thr Ala Val Thr Asn
        355                 360                 365

ttc gac atg aac aga tac aac gtt aaa gca atc ctc gaa agc cct agt         1152
Phe Asp Met Asn Arg Tyr Asn Val Lys Ala Ile Leu Glu Ser Pro Ser
    370                 375                 380

ctt cct att ggt agc gcc gca aaa cgt ctc aag gag gct aac cgt ccg         1200
Leu Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Glu Ala Asn Arg Pro
385                 390                 395                 400

gtt cca agt atg atg atg atc agt aat aac gtt tca gag agt gag aat         1248
Val Pro Ser Met Met Met Ile Ser Asn Asn Val Ser Glu Ser Glu Asn
                405                 410                 415

aat gct agc ggt tgg caa aac gct gcg gtt cag cat cat cag gga gta         1296
Asn Ala Ser Gly Trp Gln Asn Ala Ala Val Gln His His Gln Gly Val
            420                 425                 430

gat ttg agc tta ttg cag caa cat caa gag agg tac aat ggt tat tat         1344
Asp Leu Ser Leu Leu Gln Gln His Gln Glu Arg Tyr Asn Gly Tyr Tyr
        435                 440                 445

tac aat gga gga aac ttg tct tcg gag agt gct agg gct tgt ttc aaa         1392
Tyr Asn Gly Gly Asn Leu Ser Ser Glu Ser Ala Arg Ala Cys Phe Lys
    450                 455                 460

caa gag gat gat caa cac cat ttc ttg agc aac acg cag agc ctc atg         1440
Gln Glu Asp Asp Gln His His Phe Leu Ser Asn Thr Gln Ser Leu Met
465                 470                 475                 480

act aat atc gat cat caa agt tct gtt tca gat gat tcg gtt act gtt         1488
Thr Asn Ile Asp His Gln Ser Ser Val Ser Asp Asp Ser Val Thr Val
                485                 490                 495

tgt gga aat gtt gtt ggt tat ggt ggt tat caa gga ttt gca gcc ccg         1536
Cys Gly Asn Val Val Gly Tyr Gly Gly Tyr Gln Gly Phe Ala Ala Pro
            500                 505                 510

gtt aac tgc gat gcc tac gct gct agt gag ttt gac tat aac gca aga         1584
Val Asn Cys Asp Ala Tyr Ala Ala Ser Glu Phe Asp Tyr Asn Ala Arg
        515                 520                 525

aac cat tat tac ttt gct cag cag cag cag acc cag cat tcg cca gga         1632
Asn His Tyr Tyr Phe Ala Gln Gln Gln Gln Thr Gln His Ser Pro Gly
    530                 535                 540

gga gat ttt ccc gcg gca atg acg aat aat gtt ggc tct aat atg tat         1680
Gly Asp Phe Pro Ala Ala Met Thr Asn Asn Val Gly Ser Asn Met Tyr
545                 550                 555                 560

tac cat ggg gaa ggt ggt gga gaa gtt gct cca aca ttt aca gtt tgg         1728
Tyr His Gly Glu Gly Gly Gly Glu Val Ala Pro Thr Phe Thr Val Trp
                565                 570                 575

aac gac aat tag                                                     1740
Asn Asp Asn


<210> SEQ ID NO 26
<211> LENGTH: 579
<212> TYPE: PRT
<213> ORGANISM: Brassica napus

<400> SEQUENCE: 26

Met Asn Asn Asn Trp Leu Gly Phe Ser Leu Ser Pro Tyr Glu Gln Asn
1               5                   10                  15

His His Arg Lys Asp Val Cys Ser Ser Thr Thr Thr Thr Ala Val Asp
            20                  25                  30
```

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Val Ala Gly Glu Tyr Cys Tyr Asp Pro Thr Ala Ala Ser Asp Glu Ser
        35                  40                  45

Ser Ala Ile Gln Thr Ser Phe Pro Ser Pro Phe Gly Val Val Leu Asp
    50                  55                  60

Ala Phe Thr Arg Asp Asn Asn Ser His Ser Arg Asp Trp Asp Ile Asn
65                  70                  75                  80

Gly Ser Ala Cys Asn Asn Ile His Asn Asp Glu Gln Asp Gly Pro Lys
                85                  90                  95

Leu Glu Asn Phe Leu Gly Arg Thr Thr Thr Ile Tyr Asn Thr Asn Glu
            100                 105                 110

Asn Val Gly Asp Ile Asp Gly Ser Gly Cys Tyr Gly Gly Asp Gly
        115                 120                 125

Gly Gly Gly Ser Leu Gly Leu Ser Met Ile Lys Thr Trp Leu Arg Asn
    130                 135                 140

Gln Pro Val Asp Asn Val Asp Asn Gln Glu Asn Gly Asn Gly Ala Lys
145                 150                 155                 160

Gly Leu Ser Leu Ser Met Asn Ser Ser Thr Ser Cys Asp Asn Asn Asn
                165                 170                 175

Tyr Ser Ser Asn Asn Leu Val Ala Gln Gly Lys Thr Ile Asp Asp Ser
            180                 185                 190

Val Glu Ala Thr Pro Lys Lys Thr Ile Glu Ser Phe Gly Gln Arg Thr
        195                 200                 205

Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
    210                 215                 220

Ala His Leu Trp Asp Asn Ser Cys Lys Arg Glu Gly Gln Thr Arg Lys
225                 230                 235                 240

Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala
                245                 250                 255

Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr
            260                 265                 270

Thr Asn Phe Pro Met Ser Glu Tyr Glu Lys Glu Ile Glu Glu Met Lys
        275                 280                 285

His Met Thr Arg Gln Glu Tyr Val Ala Ser Leu Arg Arg Lys Ser Ser
    290                 295                 300

Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His
305                 310                 315                 320

Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys
                325                 330                 335

Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu Ala
            340                 345                 350

Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Thr Ala Val Thr Asn
        355                 360                 365

Phe Asp Met Asn Arg Tyr Asn Val Lys Ala Ile Leu Glu Ser Pro Ser
    370                 375                 380

Leu Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Glu Ala Asn Arg Pro
385                 390                 395                 400

Val Pro Ser Met Met Met Ile Ser Asn Asn Val Ser Glu Ser Glu Asn
                405                 410                 415

Asn Ala Ser Gly Trp Gln Asn Ala Ala Val Gln His His Gln Gly Val
            420                 425                 430
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```
Asp Leu Ser Leu Leu Gln Gln His Gln Glu Arg Tyr Asn Gly Tyr Tyr
        435                 440                 445

Tyr Asn Gly Gly Asn Leu Ser Ser Glu Ser Ala Arg Ala Cys Phe Lys
    450                 455                 460

Gln Glu Asp Asp Gln His His Phe Leu Ser Asn Thr Gln Ser Leu Met
465                 470                 475                 480

Thr Asn Ile Asp His Gln Ser Ser Val Ser Asp Asp Ser Val Thr Val
                485                 490                 495

Cys Gly Asn Val Val Gly Tyr Gly Gly Tyr Gln Gly Phe Ala Ala Pro
            500                 505                 510

Val Asn Cys Asp Ala Tyr Ala Ala Ser Glu Phe Asp Tyr Asn Ala Arg
        515                 520                 525

Asn His Tyr Tyr Phe Ala Gln Gln Gln Gln Thr Gln His Ser Pro Gly
    530                 535                 540

Gly Asp Phe Pro Ala Ala Met Thr Asn Asn Val Gly Ser Asn Met Tyr
545                 550                 555                 560

Tyr His Gly Glu Gly Gly Gly Glu Val Ala Pro Thr Phe Thr Val Trp
                565                 570                 575

Asn Asp Asn


<210> SEQ ID NO 27
<211> LENGTH: 2082
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(2082)

<400> SEQUENCE: 27

atg gct tcg acg aac aac cac tgg ctg ggt ttc tcg ctc tcg ggc cag       48
Met Ala Ser Thr Asn Asn His Trp Leu Gly Phe Ser Leu Ser Gly Gln
1               5                   10                  15

gat aac ccg cag cct aat cat cag gac agc tcg cct gcc gcc gcc ggc       96
Asp Asn Pro Gln Pro Asn His Gln Asp Ser Ser Pro Ala Ala Ala Gly
            20                  25                  30

atc gac atc tcc ggc gcc agc gac ttc tat ggc ttg ccc acg cag cag      144
Ile Asp Ile Ser Gly Ala Ser Asp Phe Tyr Gly Leu Pro Thr Gln Gln
        35                  40                  45

ggc tcc gac ggg aat ctc ggc gtg ccg ggc ctg cgg gac gat cac gct      192
Gly Ser Asp Gly Asn Leu Gly Val Pro Gly Leu Arg Asp Asp His Ala
    50                  55                  60

tct tat ggc atc atg gag gcc ttc aac agg gtt cct caa gaa acc caa      240
Ser Tyr Gly Ile Met Glu Ala Phe Asn Arg Val Pro Gln Glu Thr Gln
65                  70                  75                  80

gat tgg aac atg agg gga ttg gac tac aac ggc ggt ggc tcg gaa ctc      288
Asp Trp Asn Met Arg Gly Leu Asp Tyr Asn Gly Gly Gly Ser Glu Leu
                85                  90                  95

tcg atg ctt gtg ggg tcc agc ggc ggc ggc ggg ggc ggc ggc aag agg      336
Ser Met Leu Val Gly Ser Ser Gly Gly Gly Gly Gly Gly Gly Lys Arg
            100                 105                 110

gcc gtg gaa gac agc gag ccc aag ctc gaa gat ttc ctc ggc ggc aac      384
Ala Val Glu Asp Ser Glu Pro Lys Leu Glu Asp Phe Leu Gly Gly Asn
        115                 120                 125

tcg ttc gtc tcc gag cat gat cag tcc ggc ggt tac ctg ttc tct gga      432
Ser Phe Val Ser Glu His Asp Gln Ser Gly Gly Tyr Leu Phe Ser Gly
    130                 135                 140
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gtc ccg atg gcc agc agc acc aac agc aac agc ggg agc aac acc atg       480
Val Pro Met Ala Ser Ser Thr Asn Ser Asn Ser Gly Ser Asn Thr Met
145                 150                 155                 160

gag ctc tcc atg atc aag acc tgg ctc cgg aac aac cag gtg ccc cag       528
Glu Leu Ser Met Ile Lys Thr Trp Leu Arg Asn Asn Gln Val Pro Gln
                165                 170                 175

ccg cag ccg cca gca gct ccg cat cag gcg ccg cag act gag gag atg       576
Pro Gln Pro Pro Ala Ala Pro His Gln Ala Pro Gln Thr Glu Glu Met
            180                 185                 190

agc acc gac gcc aac gcc agc gcc agc agc ttt ggc tgc tcg gat tcg       624
Ser Thr Asp Ala Asn Ala Ser Ala Ser Ser Phe Gly Cys Ser Asp Ser
        195                 200                 205

atg ggg agg aac ggc acg gtg gcg gct gct ggg agc tcc cag agc ctg       672
Met Gly Arg Asn Gly Thr Val Ala Ala Ala Gly Ser Ser Gln Ser Leu
    210                 215                 220

gcg ctc tcg atg agc acg ggc tcg cac ctg ccg atg gtt gtg gcc ggc       720
Ala Leu Ser Met Ser Thr Gly Ser His Leu Pro Met Val Val Ala Gly
225                 230                 235                 240

ggc ggc gcc agc gga gcg gcc tcg gag agc acg tca tcg gag aac aag       768
Gly Gly Ala Ser Gly Ala Ala Ser Glu Ser Thr Ser Ser Glu Asn Lys
                245                 250                 255

cga gcg agc ggc gcc atg gat tcg ccc ggc agc gcg gta gaa gcc gtc       816
Arg Ala Ser Gly Ala Met Asp Ser Pro Gly Ser Ala Val Glu Ala Val
            260                 265                 270

ccg agg aag tcc atc gac acg ttc ggg caa agg acc tct ata tat cga       864
Pro Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg
        275                 280                 285

ggt gta aca aga cat aga tgg aca ggg cga tat gag gct cat cta tgg       912
Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp
    290                 295                 300

gat aat agt tgt aga aga gaa ggg cag agt cgc aag ggt agg caa gtt       960
Asp Asn Ser Cys Arg Arg Glu Gly Gln Ser Arg Lys Gly Arg Gln Val
305                 310                 315                 320

tac ctt ggt ggc tat gac aag gaa gac aag gca gca agg gct tat gat      1008
Tyr Leu Gly Gly Tyr Asp Lys Glu Asp Lys Ala Ala Arg Ala Tyr Asp
                325                 330                 335

ttg gca gct ctc aag tat tgg ggc act act aca aca aca aat ttc cct      1056
Leu Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr Thr Asn Phe Pro
            340                 345                 350

ata agc aac tat gaa aag gag cta gag gaa atg aaa cat atg act agg      1104
Ile Ser Asn Tyr Glu Lys Glu Leu Glu Glu Met Lys His Met Thr Arg
        355                 360                 365

cag gag tat att gca tac cta aga aga aat agc agt gga ttt tct cgt      1152
Gln Glu Tyr Ile Ala Tyr Leu Arg Arg Asn Ser Ser Gly Phe Ser Arg
    370                 375                 380

ggc gca tca aaa tat cgt gga gta act aga cat cat cag cat ggg aga      1200
Gly Ala Ser Lys Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg
385                 390                 395                 400

tgg caa gca agg ata ggg aga gtt gca gga aac aag gat ctc tac ttg      1248
Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu
                405                 410                 415

ggc aca ttc agc acc gag gag gag gcg gcg gag gcc tac gac atc gcc      1296
Gly Thr Phe Ser Thr Glu Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala
            420                 425                 430

gcg atc aag ttc cgc ggt ctg aac gcc gtc acc aac ttc gac atg agc      1344
Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Met Ser
        435                 440                 445
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cgc tac gac gtc aag agc atc ctc gag agc agc acg ctg cct gtc ggc     1392
Arg Tyr Asp Val Lys Ser Ile Leu Glu Ser Ser Thr Leu Pro Val Gly
    450                 455                 460

ggc gcg gcc agg cgc ctc aag gat gcc gtg gac cac gtg gag gcc ggc     1440
Gly Ala Ala Arg Arg Leu Lys Asp Ala Val Asp His Val Glu Ala Gly
465                 470                 475                 480

gcc acc atc tgg cgc gcc gac atg gac ggc ggc gtg atc tcc cag ctc     1488
Ala Thr Ile Trp Arg Ala Asp Met Asp Gly Gly Val Ile Ser Gln Leu
                485                 490                 495

gcc gaa gcc ggg atg ggc ggc tac gcc tcg tac ggg cac cac gcc tgg     1536
Ala Glu Ala Gly Met Gly Gly Tyr Ala Ser Tyr Gly His His Ala Trp
            500                 505                 510

ccg acc atc gcg ttc cag cag ccg tcg ccg ctc tcc gtc cac tac ccg     1584
Pro Thr Ile Ala Phe Gln Gln Pro Ser Pro Leu Ser Val His Tyr Pro
        515                 520                 525

tac ggg cag ccg ccg tcc cgc ggg tgg tgc aag ccc gag cag gac gcg     1632
Tyr Gly Gln Pro Pro Ser Arg Gly Trp Cys Lys Pro Glu Gln Asp Ala
    530                 535                 540

gcc gtc gcc gcc gcc gcg cac agc ctg cag gac ctc cag cag ctg cac     1680
Ala Val Ala Ala Ala Ala His Ser Leu Gln Asp Leu Gln Gln Leu His
545                 550                 555                 560

ctc ggc agc gcg gca cac aac ttc ttc cag gcg tcg tcg agc tcg gca     1728
Leu Gly Ser Ala Ala His Asn Phe Phe Gln Ala Ser Ser Ser Ser Ala
                565                 570                 575

gtc tac aac agc ggc ggc ggc ggc gct agc ggc ggg tac cac cag ggc     1776
Val Tyr Asn Ser Gly Gly Gly Gly Ala Ser Gly Gly Tyr His Gln Gly
            580                 585                 590

ctc ggt ggc ggc agc agc tcc ttc ctc atg ccg tcg agc act gtc gtg     1824
Leu Gly Gly Gly Ser Ser Ser Phe Leu Met Pro Ser Ser Thr Val Val
        595                 600                 605

gcg ggg gcc gac cag ggg cac agc agc agc acg gcc aac cag ggg agc     1872
Ala Gly Ala Asp Gln Gly His Ser Ser Ser Thr Ala Asn Gln Gly Ser
    610                 615                 620

acg tgc agc tac ggg gac gat cac cag gaa ggg aag ctc atc ggg tac     1920
Thr Cys Ser Tyr Gly Asp Asp His Gln Glu Gly Lys Leu Ile Gly Tyr
625                 630                 635                 640

gac gcc atg gtg gcg gcg acc gca gcc ggc ggg gac ccg tac gcc gcg     1968
Asp Ala Met Val Ala Ala Thr Ala Ala Gly Gly Asp Pro Tyr Ala Ala
                645                 650                 655

gcg agg agc ggg tac cag ttc tcg tcg cag ggc tcg gga tcc acg gtg     2016
Ala Arg Ser Gly Tyr Gln Phe Ser Ser Gln Gly Ser Gly Ser Thr Val
            660                 665                 670

agc atc gcg agg gcg aac ggg tac tct aac aac tgg agc tct cct ttc     2064
Ser Ile Ala Arg Ala Asn Gly Tyr Ser Asn Asn Trp Ser Ser Pro Phe
        675                 680                 685

aac ggc ggc atg ggg tga                                             2082
Asn Gly Gly Met Gly
    690


<210> SEQ ID NO 28
<211> LENGTH: 693
<212> TYPE: PRT
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 28

Met Ala Ser Thr Asn Asn His Trp Leu Gly Phe Ser Leu Ser Gly Gln
1               5                   10                  15

Asp Asn Pro Gln Pro Asn His Gln Asp Ser Ser Pro Ala Ala Ala Gly
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            20                  25                  30

Ile Asp Ile Ser Gly Ala Ser Asp Phe Tyr Gly Leu Pro Thr Gln Gln
        35                  40                  45

Gly Ser Asp Gly Asn Leu Gly Val Pro Gly Leu Arg Asp Asp His Ala
    50                  55                  60

Ser Tyr Gly Ile Met Glu Ala Phe Asn Arg Val Pro Gln Glu Thr Gln
65                  70                  75                  80

Asp Trp Asn Met Arg Gly Leu Asp Tyr Asn Gly Gly Gly Ser Glu Leu
                85                  90                  95

Ser Met Leu Val Gly Ser Ser Gly Gly Gly Gly Gly Gly Gly Lys Arg
            100                 105                 110

Ala Val Glu Asp Ser Glu Pro Lys Leu Glu Asp Phe Leu Gly Gly Asn
        115                 120                 125

Ser Phe Val Ser Glu His Asp Gln Ser Gly Gly Tyr Leu Phe Ser Gly
    130                 135                 140

Val Pro Met Ala Ser Ser Thr Asn Ser Asn Ser Gly Ser Asn Thr Met
145                 150                 155                 160

Glu Leu Ser Met Ile Lys Thr Trp Leu Arg Asn Asn Gln Val Pro Gln
                165                 170                 175

Pro Gln Pro Pro Ala Ala Pro His Gln Ala Pro Gln Thr Glu Glu Met
            180                 185                 190

Ser Thr Asp Ala Asn Ala Ser Ala Ser Ser Phe Gly Cys Ser Asp Ser
        195                 200                 205

Met Gly Arg Asn Gly Thr Val Ala Ala Ala Gly Ser Ser Gln Ser Leu
    210                 215                 220

Ala Leu Ser Met Ser Thr Gly Ser His Leu Pro Met Val Val Ala Gly
225                 230                 235                 240

Gly Gly Ala Ser Gly Ala Ala Ser Glu Ser Thr Ser Ser Glu Asn Lys
                245                 250                 255

Arg Ala Ser Gly Ala Met Asp Ser Pro Gly Ser Ala Val Glu Ala Val
            260                 265                 270

Pro Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg
        275                 280                 285

Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp
    290                 295                 300

Asp Asn Ser Cys Arg Arg Glu Gly Gln Ser Arg Lys Gly Arg Gln Val
305                 310                 315                 320

Tyr Leu Gly Gly Tyr Asp Lys Glu Asp Lys Ala Ala Arg Ala Tyr Asp
                325                 330                 335

Leu Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr Thr Thr Asn Phe Pro
            340                 345                 350

Ile Ser Asn Tyr Glu Lys Glu Leu Glu Glu Met Lys His Met Thr Arg
        355                 360                 365

Gln Glu Tyr Ile Ala Tyr Leu Arg Arg Asn Ser Ser Gly Phe Ser Arg
    370                 375                 380

Gly Ala Ser Lys Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg
385                 390                 395                 400

Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu
                405                 410                 415

Gly Thr Phe Ser Thr Glu Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala
            420                 425                 430
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```
Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Met Ser
        435                 440                 445

Arg Tyr Asp Val Lys Ser Ile Leu Glu Ser Ser Thr Leu Pro Val Gly
    450                 455                 460

Gly Ala Ala Arg Arg Leu Lys Asp Ala Val Asp His Val Glu Ala Gly
465                 470                 475                 480

Ala Thr Ile Trp Arg Ala Asp Met Asp Gly Gly Val Ile Ser Gln Leu
                485                 490                 495

Ala Glu Ala Gly Met Gly Gly Tyr Ala Ser Tyr Gly His His Ala Trp
            500                 505                 510

Pro Thr Ile Ala Phe Gln Gln Pro Ser Pro Leu Ser Val His Tyr Pro
        515                 520                 525

Tyr Gly Gln Pro Pro Ser Arg Gly Trp Cys Lys Pro Glu Gln Asp Ala
    530                 535                 540

Ala Val Ala Ala Ala Ala His Ser Leu Gln Asp Leu Gln Gln Leu His
545                 550                 555                 560

Leu Gly Ser Ala Ala His Asn Phe Phe Gln Ala Ser Ser Ser Ser Ala
                565                 570                 575

Val Tyr Asn Ser Gly Gly Gly Gly Ala Ser Gly Gly Tyr His Gln Gly
            580                 585                 590

Leu Gly Gly Gly Ser Ser Ser Phe Leu Met Pro Ser Ser Thr Val Val
        595                 600                 605

Ala Gly Ala Asp Gln Gly His Ser Ser Ser Thr Ala Asn Gln Gly Ser
    610                 615                 620

Thr Cys Ser Tyr Gly Asp Asp His Gln Glu Gly Lys Leu Ile Gly Tyr
625                 630                 635                 640

Asp Ala Met Val Ala Ala Thr Ala Ala Gly Gly Asp Pro Tyr Ala Ala
                645                 650                 655

Ala Arg Ser Gly Tyr Gln Phe Ser Ser Gln Gly Ser Gly Ser Thr Val
            660                 665                 670

Ser Ile Ala Arg Ala Asn Gly Tyr Ser Asn Asn Trp Ser Ser Pro Phe
        675                 680                 685

Asn Gly Gly Met Gly
    690


<210> SEQ ID NO 29
<211> LENGTH: 508
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 29

ctatagtatt ttaaaattgc attaacaaac atgtcctaat tggtactcct gagatactat      60

accctcctgt tttaaaatag ttggcattat cgaattatca ttttactttt taatgttttc     120

tcttctttta atatatttta tgaattttaa tgtattttaa aatgttatgc agttcgctct     180

ggacttttct gctgcgccta cacttgggtg tactgggcct aaattcagcc tgaccgaccg     240

cctgcattga ataatggatg agcaccggta aaatccgcgt acccaacttt cgagaagaac     300

cgagacgtgg cgggccgggc caccgacgca cggcaccagc gactgcacac gtcccgccgg     360

cgtacgtgta cgtgctgttc cctcactggc cgcccaatcc actcatgcat gcccacgtac     420

acccctgccg tggcgcgccc agatcctaat cctttcgccg ttctgcactt ctgctgccta     480
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taaatggcgg catcgaccgt cacctgct                                       508


<210> SEQ ID NO 30
<211> LENGTH: 665
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Promoter construct comprising Zea mays Rab17
      promoter and attB1 site

<400> SEQUENCE: 30

ctatagtatt ttaaaattgc attaacaaac atgtcctaat tggtactcct gagatactat     60

accctcctgt tttaaaatag ttggcattat cgaattatca ttttactttt taatgttttc    120

tcttctttta atatatttta tgaattttaa tgtattttaa aatgttatgc agttcgctct    180

ggacttttct gctgcgccta cacttgggtg tactgggcct aaattcagcc tgaccgaccg    240

cctgcattga ataatggatg agcaccggta aaatccgcgt acccaacttt cgagaagaac    300

cgagacgtgg cgggccgggc caccgacgca cggcaccagc gactgcacac gtcccgccgg    360

cgtacgtgta cgtgctgttc cctcactggc cgcccaatcc actcatgcat gcccacgtac    420

acccctgccg tggcgcgccc agatcctaat cctttcgccg ttctgcactt ctgctgccta    480

taaatggcgg catcgaccgt cacctgcttc accaccggcg agccacatcg agaacacgat    540

cgagcacaca agcacgaaga ctcgtttagg agaaaccaca aaccaccaag ccgtgcaagc    600

accaagcttg gtcacccggt ccgggcctag aaggccagct tcaagtttgt acaaaaaagc    660

aggct                                                                665


<210> SEQ ID NO 31
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: attachment B1 site

<400> SEQUENCE: 31

caagtttgta caaaaaagca ggct                                            24


<210> SEQ ID NO 32
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: attachment B2 site

<400> SEQUENCE: 32

acccagcttt cttgtacaaa gtgg                                            24


<210> SEQ ID NO 33
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: attachment B3 site

<400> SEQUENCE: 33

acaactttgt ataataaagt tg                                              22


<210> SEQ ID NO 34
<211> LENGTH: 22
```

```
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: attachment B4 site

<400> SEQUENCE: 34

acaactttgt atagaaaagt tg                                               22


<210> SEQ ID NO 35
<211> LENGTH: 95
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 35

tcaccaccgg cgagccacat cgagaacacg atcgagcaca caagcacgaa gactcgttta      60

ggagaaacca caaaccacca agccgtgcaa gcacc                                 95


<210> SEQ ID NO 36
<211> LENGTH: 133
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid linker sequence

<400> SEQUENCE: 36

tcaccaccgg cgagccacat cgagaacacg atcgagcaca caagcacgaa gactcgttta      60

ggagaaacca caaaccacca agccgtgcaa gcaccaagct tggtcacccg gtccgggcct     120

agaaggccag ctt                                                        133


<210> SEQ ID NO 37
<211> LENGTH: 61
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid linker sequence

<400> SEQUENCE: 37

tcgaaggaga tagaaccaat tctctaagga aatacttaac catggtcgac tggatccaac      60

a                                                                      61


<210> SEQ ID NO 38
<211> LENGTH: 318
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PinII terminator

<400> SEQUENCE: 38

agacttgtcc atcttctgga ttggccaact taattaatgt atgaaataaa aggatgcaca      60

catagtgaca tgctaatcac tataatgtgg gcatcaaagt tgtgtgttat gtgtaattac     120

tagttatctg aataaaagag aaagagatca tccatatttc ttatcctaaa tgaatgtcac     180

gtgtctttat aattctttga tgaaccagat gcatttcatt aaccaaatcc atatacatat     240

aaatattaat catatataat taatatcaat tgggttagca aaacaaatct agtctaggtg     300

tgttttgcga attgcggc                                                   318


<210> SEQ ID NO 39
<211> LENGTH: 16
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid linker sequence

<400> SEQUENCE: 39

gtttcgagat atctag                                                   16


<210> SEQ ID NO 40
<211> LENGTH: 14
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid linker sequence

<400> SEQUENCE: 40

ccgttaacgg atcc                                                     14


<210> SEQ ID NO 41
<211> LENGTH: 1272
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Maize optimized FLP coding sequence
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(1272)

<400> SEQUENCE: 41

atg ccc cag ttc gac atc ctc tgc aag acc ccc ccc aag gtg ctc gtg       48
Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val
1               5                   10                  15

agg cag ttc gtg gag agg ttc gag agg ccc tcc ggc gag aag atc gcc       96
Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala
            20                  25                  30

ctc tgc gcc gcc gag ctc acc tac ctc tgc tgg atg atc acc cac aac      144
Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn
        35                  40                  45

ggc acc gcc att aag agg gcc acc ttc atg tca tac aac acc atc atc      192
Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
    50                  55                  60

tcc aac tcc ctc tcc ttc gac atc gtg aac aag tcc ctc cag ttc aaa      240
Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
65                  70                  75                  80

tac aag acc cag aag gcc acc atc ctc gag gcc tcc ctc aag aag ctc      288
Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
                85                  90                  95

atc ccc gcc tgg gag ttc acc atc atc ccc tac tac ggc cag aag cac      336
Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
            100                 105                 110

cag tcc gac atc acc gac atc gtg tca tcc ctc cag ctt cag ttc gag      384
Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
        115                 120                 125

tcc tcc gag gag gct gac aag ggc aac tcc cac tcc aag aag atg ctg      432
Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
    130                 135                 140

aag gcc ctc ctc tcc gag ggc gag tcc atc tgg gag atc acc gag aag      480
Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
145                 150                 155                 160

atc ctc aac tcc ttc gag tac acc tcc agg ttc act aag acc aag acc      528
Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
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            165                 170                 175

ctc tac cag ttc ctc ttc ctc gcc acc ttc atc aac tgc ggc agg ttc      576
Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
            180                 185                 190

tca gac atc aag aac gtg gac ccc aag tcc ttc aag ctc gtg cag aac      624
Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
        195                 200                 205

aag tac ctc ggc gtg atc atc cag tgc ctc gtg acc gag acc aag acc      672
Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
    210                 215                 220

tcc gtg tcc agg cac atc tac ttc ttc tcc gct cgc ggc agg atc gac      720
Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
225                 230                 235                 240

ccc ctc gtg tac ctc gac gag ttc ctc agg aac tca gag ccc gtg ctc      768
Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu
                245                 250                 255

aag agg gtg aac agg acc ggc aac tcc tcc tcc aac aag cag gag tac      816
Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr
            260                 265                 270

cag ctc ctc aag gac aac ctc gtg agg tcc tac aac aag gcc ctc aag      864
Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys
        275                 280                 285

aag aac gcc ccc tac tcc atc ttc gcc atc aag aac ggc ccc aag tcc      912
Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser
    290                 295                 300

cac atc ggt agg cac ctc atg acc tcc ttc ctc tca atg aag ggc ctc      960
His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
305                 310                 315                 320

acc gag ctc acc aac gtg gtg ggc aac tgg tcc gac aag agg gcc tcc     1008
Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
                325                 330                 335

gcc gtg gcc agg acc acc tac acc cac cag atc acc gcc atc ccc gac     1056
Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
            340                 345                 350

cac tac ttc gcc ctc gtg tca agg tac tac gcc tac gac ccc atc tcc     1104
His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser
        355                 360                 365

aag gag atg atc gcc ctc aag gac gag act aac ccc atc gag gag tgg     1152
Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp
    370                 375                 380

cag cac atc gag cag ctc aag ggc tcc gcc gag ggc tcc atc agg tac     1200
Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
385                 390                 395                 400

ccc gcc tgg aac ggc atc atc tcc cag gag gtg ctc gac tac ctc tcc     1248
Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser
                405                 410                 415

tcc tac atc aac agg agg atc tga                                     1272
Ser Tyr Ile Asn Arg Arg Ile
            420


<210> SEQ ID NO 42
<211> LENGTH: 423
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: FLP

<400> SEQUENCE: 42
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Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val
1               5                   10                  15

Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala
            20                  25                  30

Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn
        35                  40                  45

Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
    50                  55                  60

Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
65                  70                  75                  80

Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
                85                  90                  95

Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
            100                 105                 110

Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
        115                 120                 125

Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
    130                 135                 140

Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
145                 150                 155                 160

Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
                165                 170                 175

Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
            180                 185                 190

Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
        195                 200                 205

Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
    210                 215                 220

Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
225                 230                 235                 240

Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu
                245                 250                 255

Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr
            260                 265                 270

Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys
        275                 280                 285

Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser
    290                 295                 300

His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
305                 310                 315                 320

Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
                325                 330                 335

Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
            340                 345                 350

His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser
        355                 360                 365

Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp
    370                 375                 380

Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
385                 390                 395                 400

Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser
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                405                 410                 415

Ser Tyr Ile Asn Arg Arg Ile
            420


<210> SEQ ID NO 43
<211> LENGTH: 1032
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Maize optimized Cre coding sequence
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(1032)

<400> SEQUENCE: 43

atg tcc aac ctg ctc acg gtt cac cag aac ctt ccg gct ctt cca gtg           48
Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1               5                   10                  15

gac gcg acg tcc gat gaa gtc agg aag aac ctc atg gac atg ttc cgc           96
Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
            20                  25                  30

gac agg caa gcg ttc agc gag cac acc tgg aag atg ctg ctc tcc gtc          144
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
        35                  40                  45

tgc cgc tcc tgg gct gca tgg tgc aag ctg aac aac agg aag tgg ttc          192
Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
    50                  55                  60

ccc gct gag ccc gag gac gtg agg gat tac ctt ctg tac ctg caa gct          240
Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65                  70                  75                  80

cgc ggg ctg gca gtg aag acc atc cag caa cac ctt gga caa ctg aac          288
Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
                85                  90                  95

atg ctt cac agg cgc tcc ggc ctc ccg cgc ccc agc gac tcg aac gcc          336
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
            100                 105                 110

gtg agc ctc gtc atg cgc cgc atc agg aag gaa aac gtc gat gcc ggc          384
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
        115                 120                 125

gaa agg gca aag cag gcc ctc gcg ttc gag agg acc gat ttc gac cag          432
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130                 135                 140

gtc cgc agc ctg atg gag aac agc gac agg tgc cag gac att agg aac          480
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

ctg gcg ttc ctc gga att gca tac aac acg ctc ctc agg atc gcg gaa          528
Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
                165                 170                 175

att gcc cgc att cgc gtg aag gac att agc cgc acc gac ggc ggc agg          576
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

atg ctt atc cac att ggc agg acc aag acg ctc gtt tcc acc gca ggc          624
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

gtc gaa aag gcc ctc agc ctc gga gtg acc aag ctc gtc gaa cgc tgg          672
Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

atc tcc gtg tcc ggc gtc gcg gac gac cca aac aac tac ctc ttc tgc          720
Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
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225                 230                 235                 240

cgc gtc cgc aag aac ggg gtg gct gcc cct agc gcc acc agc caa ctc      768
Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
                245                 250                 255

agc acg agg gcc ttg gaa ggt att ttc gag gcc acc cac cgc ctg atc      816
Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
            260                 265                 270

tac ggc gcg aag gat gac agc ggt caa cgc tac ctc gca tgg tcc ggg      864
Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275                 280                 285

cac tcc gcc cgc gtt gga gct gct agg gac atg gcc cgc gcc ggt gtt      912
His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

tcc atc ccc gaa atc atg cag gcg ggt gga tgg acg aac gtg aac att      960
Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305                 310                 315                 320

gtc atg aac tac att cgc aac ctt gac agc gag acg ggc gca atg gtt     1008
Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

cgc ctc ctg gaa gat ggt gac tga                                     1032
Arg Leu Leu Glu Asp Gly Asp
            340


<210> SEQ ID NO 44
<211> LENGTH: 343
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cre

<400> SEQUENCE: 44

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1               5                   10                  15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
            20                  25                  30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
        35                  40                  45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
    50                  55                  60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65                  70                  75                  80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
                85                  90                  95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
            100                 105                 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
        115                 120                 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
                165                 170                 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190
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Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
                245                 250                 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
            260                 265                 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Gly Asp
            340
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<210> SEQ ID NO 45
<211> LENGTH: 1198
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Expression cassette comprising Zea mays rab17
      promoter, attB1 site, and FLPm coding sequence

<400> SEQUENCE: 45

ctatagtatt ttaaaattgc attaacaaac atgtcctaat tggtactcct gagatactat     60

accctcctgt tttaaaatag ttggcattat cgaattatca ttttactttt taatgttttc    120

tcttctttta atatatttta tgaattttaa tgtattttaa aatgttatgc agttcgctct    180

ggacttttct gctgcgccta cacttgggtg tactgggcct aaattcagcc tgaccgaccg    240

cctgcattga ataatggatg agcaccggta aaatccgcgt acccaacttt cgagaagaac    300

cgagacgtgg cgggccgggc caccgacgca cggcaccagc gactgcacac gtcccgccgg    360

cgtacgtgta cgtgctgttc cctcactggc cgcccaatcc actcatgcat gcccacgtac    420

acccctgccg tggcgcgccc agatcctaat cctttcgccg ttctgcactt ctgctgccta    480

taaatggcgg catcgaccgt cacctgcttc accaccggcg agccacatcg agaacacgat    540

cgagcacaca agcacgaaga ctcgtttagg agaaaccaca aaccaccaag ccgtgcaagc    600

accaagcttg gtcacccggt ccgggcctag aaggccagct tcaagtttgt acaaaaaagc    660

aggcttcgaa ggagatagaa ccaattctct aaggaaatac ttaaccatgg tcgactggat    720

ccaacaatgc cccagttcga catcctctgc aagacccccc ccaaggtgct cgtgaggcag    780

ttcgtggaga ggttcgagag gccctccggc gagaagatcg ccctctgcgc cgccgagctc    840

acctacctct gctggatgat cacccacaac ggcaccgcca ttaagagggc caccttcatg    900

tcatacaaca ccatcatctc caactccctc tccttcgaca tcgtgaacaa gtccctccag    960

ttcaaataca agacccagaa ggccaccatc ctcgaggcct ccctcaagaa gctcatcccc   1020

gcctgggagt tcaccatcat cccctactac ggccagaagc accagtccga catcaccgac   1080
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atcgtgtcat ccctccagct tcagttcgag tcctccgagg aggctgacaa gggcaactcc 1140

cactccaaga agatgctgaa ggccctcctc tccgagggcg agtccatctg ggagatca 1198

<210> SEQ ID NO 46
<211> LENGTH: 2370
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid PHP31004

<400> SEQUENCE: 46

ctatagtatt ttaaaattgc attaacaaac atgtcctaat tggtactcct gagatactat 60

accctcctgt tttaaaatag ttggcattat cgaattatca ttttactttt taatgttttc 120

tcttctttta atatatttta tgaattttaa tgtattttaa aatgttatgc agttcgctct 180

ggacttttct gctgcgccta cacttgggtg tactgggcct aaattcagcc tgaccgaccg 240

cctgcattga ataatggatg agcaccggta aaatccgcgt acccaacttt cgagaagaac 300

cgagacgtgg cgggccgggc caccgacgca cggcaccagc gactgcacac gtcccgccgg 360

cgtacgtgta cgtgctgttc cctcactggc cgcccaatcc actcatgcat gcccacgtac 420

acccctgccg tggcgcgccc agatcctaat cctttcgccg ttctgcactt ctgctgccta 480

taaatggcgg catcgaccgt cacctgcttc accaccggcg agccacatcg agaacacgat 540

cgagcacaca agcacgaaga ctcgtttagg agaaaccaca aaccaccaag ccgtgcaagc 600

accaagcttg gtcacccggt ccgggcctag aaggccagct tcaagtttgt acaaaaaagc 660

aggcttcgaa ggagatagaa ccaattctct aaggaaatac ttaaccatgg tcgactggat 720

ccaacaatgc cccagttcga catcctctgc aagacccccc ccaaggtgct cgtgaggcag 780

ttcgtggaga ggttcgagag gccctccggc gagaagatcg ccctctgcgc cgccgagctc 840

acctacctct gctggatgat cacccacaac ggcaccgcca ttaagagggc caccttcatg 900

tcatacaaca ccatcatctc caactccctc tccttcgaca tcgtgaacaa gtccctccag 960

ttcaaataca agacccagaa ggccaccatc ctcgaggcct ccctcaagaa gctcatcccc 1020

gcctgggagt tcaccatcat cccctactac ggccagaagc accagtccga catcaccgac 1080

atcgtgtcat ccctccagct tcagttcgag tcctccgagg aggctgacaa gggcaactcc 1140

cactccaaga agatgctgaa ggccctcctc tccgagggcg agtccatctg ggagatcacc 1200

gagaagatcc tcaactcctt cgagtacacc tccaggttca ctaagaccaa gaccctctac 1260

cagttcctct tcctcgccac cttcatcaac tgcggcaggt tctcagacat caagaacgtg 1320

gaccccaagt ccttcaagct cgtgcagaac aagtacctcg gcgtgatcat ccagtgcctc 1380

gtgaccgaga ccaagacctc cgtgtccagg cacatctact tcttctccgc tcgcggcagg 1440

atcgaccccc tcgtgtacct cgacgagttc ctcaggaact cagagcccgt gctcaagagg 1500

gtgaacagga ccggcaactc ctcctccaac aagcaggagt accagctcct caaggacaac 1560

ctcgtgaggt cctacaacaa ggccctcaag aagaacgccc cctactccat cttcgccatc 1620

aagaacggcc ccaagtccca catcggtagg cacctcatga cctccttcct ctcaatgaag 1680

ggcctcaccg agctcaccaa cgtggtgggc aactggtccg acaagagggc ctccgccgtg 1740

gccaggacca cctacaccca ccagatcacc gccatccccg accactactt cgccctcgtg 1800

tcaaggtact acgcctacga ccccatctcc aaggagatga tcgccctcaa ggacgagact 1860

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aaccccatcg aggagtggca gcacatcgag cagctcaagg gctccgccga gggctccatc 1920

aggtaccccg cctggaacgg catcatctcc caggaggtgc tcgactacct ctcctcctac 1980

atcaacagga ggatctgagt ttcgagatat ctagacccag ctttcttgta caaagtggcc 2040

gttaacggat ccagacttgt ccatcttctg gattggccaa cttaattaat gtatgaaata 2100

aaaggatgca cacatagtga catgctaatc actataatgt gggcatcaaa gttgtgtgtt 2160

atgtgtaatt actagttatc tgaataaaag agaaagagat catccatatt tcttatccta 2220

aatgaatgtc acgtgtcttt ataattcttt gatgaaccag atgcatttca ttaaccaaat 2280

ccatatacat ataaatatta atcatatata attaatatca attgggttag caaaacaaat 2340

ctagtctagg tgtgttttgc gaattgcggc 2370

<210> SEQ ID NO 47
<211> LENGTH: 2383
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid PHP30642

<400> SEQUENCE: 47

ctatagtatt ttaaaattgc attaacaaac atgtcctaat tggtactcct gagatactat 60

accctcctgt tttaaaatag ttggcattat cgaattatca ttttactttt taatgttttc 120

tcttctttta atatatttta tgaattttaa tgtattttaa aatgttatgc agttcgctct 180

ggacttttct gctgcgccta cacttgggtg tactgggcct aaattcagcc tgaccgaccg 240

cctgcattga ataatggatg agcaccggta aaatccgcgt acccaacttt cgagaagaac 300

cgagacgtgg cgggccgggc caccgacgca cggcaccagc gactgcacac gtcccgccgg 360

cgtacgtgta cgtgctgttc cctcactggc cgcccaatcc actcatgcat gcccacgtac 420

acccctgccg tggcgcgccc agatcctaat cctttcgccg ttctgcactt ctgctgccta 480

taaatggcgg catcgaccgt cacctgcttc accaccggcg agccacatcg agaacacgat 540

cgagcacaca agcacgaaga ctcgtttagg agaaaccaca aaccaccaag ccgtgcaagc 600

accatggatc caacaatgcc ccagttcgac atcctctgca agaccccccc caaggtgctc 660

gtgaggcagt tcgtggagag gttcgagagg ccctccggcg agaagatcgc cctctgcgcc 720

gccgagctca cctacctctg ctggatgatc acccacaacg gcaccgccat taagagggcc 780

accttcatgt catacaacac catcatctcc aactccctct ccttcgacat cgtgaacaag 840

tccctccagt tcaaatacaa gacccagaag gccaccatcc tcgaggcctc cctcaagaag 900

ctcatccccg cctgggagtt caccatcatc ccctactacg gccagaagca ccagtccgac 960

atcaccgaca tcgtgtcatc cctccagctt cagttcgagt cctccgagga ggctgacaag 1020

ggcaactccc actccaagaa gatgctgaag gccctcctct ccgagggcga gtccatctgg 1080

gagatcaccg agaagatcct caactccttc gagtacacct ccaggttcac taagaccaag 1140

accctctacc agttcctctt cctcgccacc ttcatcaact gcggcaggtt ctcagacatc 1200

aagaacgtgg accccaagtc cttcaagctc gtgcagaaca agtacctcgg cgtgatcatc 1260

cagtgcctcg tgaccgagac caagacctcc gtgtccaggc acatctactt cttctccgct 1320

cgcggcagga tcgaccccct cgtgtacctc gacgagttcc tcaggaactc agagcccgtg 1380

ctcaagaggg tgaacaggac cggcaactcc tcctccaaca agcaggagta ccagctcctc 1440

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aaggacaacc tcgtgaggtc ctacaacaag gccctcaaga agaacgcccc ctactccatc 1500

ttcgccatca agaacggccc caagtcccac atcggtaggc acctcatgac ctccttcctc 1560

tcaatgaagg gcctcaccga gctcaccaac gtggtgggca actggtccga caagagggcc 1620

tccgccgtgg ccaggaccac ctacacccac cagatcaccg ccatccccga ccactacttc 1680

gccctcgtgt caaggtacta cgcctacgac cccatctcca aggagatgat cgccctcaag 1740

gacgagacta accccatcga ggagtggcag cacatcgagc agctcaaggg ctccgccgag 1800

ggctccatca ggtaccccgc ctggaacggc atcatctccc aggaggtgct cgactacctc 1860

tcctcctaca tcaacaggag gatctgagtt ctagttcgaa tgtgagttga tccccggcgg 1920

tgtcccccac tgaagaaact atgtgctgta gtatagccgc tggctagcta gctagttgag 1980

tcatttagcg gcgatgattg agtaataatg tgtcacgcat caccatgcat gggtggcagt 2040

ctcagtgtga gcaatgacct gaatgaacaa ttgaaatgaa aagaaaaaag tattgttcca 2100

aattaaacgt tttaaccttt taataggttt atacaataat tgatatatgt tttctgtata 2160

tgtctaattt gttatcatcc atttagatat agacgaaaaa aaatctaaga actaaaacaa 2220

atgctaattt gaaatgaagg gagtatatat tgggataatg tcgatgagat ccctcgtaat 2280

atcaccgaca tcacacgtgt ccagttaatg tatcagtgat acgtgtattc acatttgttg 2340

cgcgtaggcg tacccaacaa ttttgatcga ctatcagaaa gtc 2383

<210> SEQ ID NO 48
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence motif 1
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 10
<223> OTHER INFORMATION: Xaa = His or Asn
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 16
<223> OTHER INFORMATION: Xaa = Phe or Tyr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 17
<223> OTHER INFORMATION: Xaa = Val or Ile
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 19
<223> OTHER INFORMATION: Xaa = Ser or His

<400> SEQUENCE: 48

Tyr Glu Lys Glu Leu Glu Glu Met Lys Xaa Met Thr Arg Gln Glu Xaa
1   5   10   15

Xaa Ala Xaa Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala
            20   25   30

<210> SEQ ID NO 49
<211> LENGTH: 63
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence motif 2
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa = Ile or Met

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<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 36
<223> OTHER INFORMATION: Xaa = Gln or Glu
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 45
<223> OTHER INFORMATION: Xaa = Ile or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 60
<223> OTHER INFORMATION: Xaa = Asp or Glu
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 61
<223> OTHER INFORMATION: Xaa = Met or Ile
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (62)...(62)
<223> OTHER INFORMATION: Xaa = Ser or Asn

<400> SEQUENCE: 49

Ser Xaa Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln
1               5                   10                  15

Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr
            20                  25                  30

Phe Ser Thr Xaa Glu Glu Ala Ala Glu Ala Tyr Asp Xaa Ala Ala Ile
        35                  40                  45

Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Xaa Xaa Xaa Arg
    50                  55                  60


<210> SEQ ID NO 50
<211> LENGTH: 68
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence motif 3
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa = Ile or Gln
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 26
<223> OTHER INFORMATION: Xaa = Arg or Lys
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 30, 59
<223> OTHER INFORMATION: Xaa = Ser or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 33
<223> OTHER INFORMATION: Xaa = Val or Gly
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 34
<223> OTHER INFORMATION: Xaa = Tyr or Arg
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (35)...(35)
<223> OTHER INFORMATION: Xaa = Leu or Gln
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (42)...(42)
<223> OTHER INFORMATION: Xaa = Glu or Asp
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (58)...(58)
<223> OTHER INFORMATION: Xaa = Pro or Thr
<220> FEATURE:
<221> NAME/KEY: VARIANT
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<222> LOCATION: (61)...(61)
<223> OTHER INFORMATION: Xaa = Thr or His
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (62)...(62)
<223> OTHER INFORMATION: Xaa = Thr or Ile
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (66)...(66)
<223> OTHER INFORMATION: Xaa = Ile, Val, or Leu

<400> SEQUENCE: 50

Ser Xaa Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
1               5                   10                  15

Ala His Leu Trp Asp Asn Ser Cys Arg Xaa Glu Gly Gln Xaa Arg Lys
            20                  25                  30

Xaa Xaa Xaa Gly Gly Tyr Asp Lys Glu Xaa Lys Ala Ala Arg Ala Tyr
        35                  40                  45

Asp Leu Ala Ala Leu Lys Tyr Trp Gly Xaa Xaa Thr Xaa Xaa Asn Phe
    50                  55                  60

Pro Xaa Ser Asn
65


<210> SEQ ID NO 51
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence motif 4
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 3
<223> OTHER INFORMATION: Xaa = Leu or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa = Glu or Ala
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 5
<223> OTHER INFORMATION: Xaa = Asp or Asn

<400> SEQUENCE: 51

Pro Lys Xaa Xaa Xaa Phe Leu Gly
1               5


<210> SEQ ID NO 52
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence motif 5
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 6
<223> OTHER INFORMATION: Xaa = Ile or Val
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 9
<223> OTHER INFORMATION: Xaa = Ala or Leu
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 11, 12
<223> OTHER INFORMATION: Xaa = Lys or Arg
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 13
<223> OTHER INFORMATION: Xaa = Leu or Arg
```

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```
<400> SEQUENCE: 52

Ser Ser Thr Leu Pro Xaa Gly Gly Xaa Ala Xaa Xaa Xaa
1               5                   10


<210> SEQ ID NO 53
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence motif 6
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa = Gly or Ser

<400> SEQUENCE: 53

Asn Trp Leu Xaa Phe Ser Leu Ser Pro
1               5


<210> SEQ ID NO 54
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence motif 7
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 1
<223> OTHER INFORMATION: Xaa = Gly or Glu
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 7
<223> OTHER INFORMATION: Xaa = Thr or Asn

<400> SEQUENCE: 54

Xaa Leu Ser Met Ile Lys Xaa Trp Leu Arg
1               5                   10


<210> SEQ ID NO 55
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence motif 8
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2, 4, 5
<223> OTHER INFORMATION: Xaa = Any Amino Acid

<400> SEQUENCE: 55

Pro Xaa Phe Xaa Xaa Trp Asn Asp
1               5


<210> SEQ ID NO 56
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence motif 9
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa = Ser, Thr, or Ala

<400> SEQUENCE: 56

Leu Xaa Leu Ser Met
```

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```
1               5


<210> SEQ ID NO 57
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence motif 10
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa = Gln or Pro

<400> SEQUENCE: 57

Trp Cys Lys Xaa Glu Gln Asp
1               5


<210> SEQ ID NO 58
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence motif 14

<400> SEQUENCE: 58

Trp Pro Thr Ile Ala Phe Gln
1               5


<210> SEQ ID NO 59
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence motif 15
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 2
<223> OTHER INFORMATION: Xaa = Ser or Thr

<400> SEQUENCE: 59

Ser Xaa Gly Ser Asn Ser Val Val Tyr Asn Gly
1               5                   10


<210> SEQ ID NO 60
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus sequence motif 19
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 4
<223> OTHER INFORMATION: Xaa = Ser or Asn

<400> SEQUENCE: 60

Gln Asp Trp Xaa Met Arg Gly
1               5


<210> SEQ ID NO 61
<211> LENGTH: 975
<212> TYPE: DNA
<213> ORGANISM: Zea mays
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(975)

<400> SEQUENCE: 61
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```
atg gag acg cca cag cag caa tcc gcc gcc gcc gcc gcc gcc gcc gcc       48
Met Glu Thr Pro Gln Gln Gln Ser Ala Ala Ala Ala Ala Ala Ala Ala
1               5                   10                  15

cac ggg cag gac gac ggc ggg tcg ccg ccg atg tcg ccg gcc tcc gcc       96
His Gly Gln Asp Asp Gly Gly Ser Pro Pro Met Ser Pro Ala Ser Ala
            20                  25                  30

gcg gcg gcg gcg ctg gcg aac gcg cgg tgg aac ccg acc aag gag cag      144
Ala Ala Ala Ala Leu Ala Asn Ala Arg Trp Asn Pro Thr Lys Glu Gln
        35                  40                  45

gtg gcc gtg ctg gag ggg ctg tac gag cac ggc ctg cgc acc ccc agc      192
Val Ala Val Leu Glu Gly Leu Tyr Glu His Gly Leu Arg Thr Pro Ser
    50                  55                  60

gcg gag cag ata cag cag atc acg ggc agg ctg cgg gag cac ggc gcc      240
Ala Glu Gln Ile Gln Gln Ile Thr Gly Arg Leu Arg Glu His Gly Ala
65                  70                  75                  80

atc gag ggc aag aac gtc ttc tac tgg ttc cag aac cac aag gcc cgc      288
Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala Arg
                85                  90                  95

cag cgc cag agg cag aag cag gac agc ttc gcc tac ttc agc agg ctc      336
Gln Arg Gln Arg Gln Lys Gln Asp Ser Phe Ala Tyr Phe Ser Arg Leu
            100                 105                 110

ctc cgc cgg ccc ccg ccg ctg ccc gtg ctc tcc atg ccc ccc gcg cca      384
Leu Arg Arg Pro Pro Pro Leu Pro Val Leu Ser Met Pro Pro Ala Pro
        115                 120                 125

ccg tac cat cac gcc cgc gtc ccg gcg ccg ccc gcg ata ccg atg ccg      432
Pro Tyr His His Ala Arg Val Pro Ala Pro Pro Ala Ile Pro Met Pro
    130                 135                 140

atg gcg ccg ccg ccg ccc gct gca tgc aac gac aac ggc ggc gcg cgt      480
Met Ala Pro Pro Pro Pro Ala Ala Cys Asn Asp Asn Gly Gly Ala Arg
145                 150                 155                 160

gtg atc tac agg aac cca ttc tac gtg gct gcg ccg cag gcg ccc cct      528
Val Ile Tyr Arg Asn Pro Phe Tyr Val Ala Ala Pro Gln Ala Pro Pro
                165                 170                 175

gca aat gcc gcc tac tac tac cca cag cca cag cag cag cag cag cag      576
Ala Asn Ala Ala Tyr Tyr Tyr Pro Gln Pro Gln Gln Gln Gln Gln Gln
            180                 185                 190

cag gtg aca gtc atg tac cag tac ccg aga atg gag gta gcc ggc cag      624
Gln Val Thr Val Met Tyr Gln Tyr Pro Arg Met Glu Val Ala Gly Gln
        195                 200                 205

gac aag atg atg acc agg gcc gcg gcg cac cag cag cag cag cac aac      672
Asp Lys Met Met Thr Arg Ala Ala Ala His Gln Gln Gln Gln His Asn
    210                 215                 220

ggc gcc ggg caa caa ccg gga cgc gcc ggc cac ccc agc cgc gag acg      720
Gly Ala Gly Gln Gln Pro Gly Arg Ala Gly His Pro Ser Arg Glu Thr
225                 230                 235                 240

ctc cag ctg ttc ccg ctc cag ccc acc ttc gtg ctg cgg cac gac aag      768
Leu Gln Leu Phe Pro Leu Gln Pro Thr Phe Val Leu Arg His Asp Lys
                245                 250                 255

ggg cgc gcc gcc aac ggc agt aat aac gac tcc ctg acg tcg acg tcg      816
Gly Arg Ala Ala Asn Gly Ser Asn Asn Asp Ser Leu Thr Ser Thr Ser
            260                 265                 270

acg gcg act gcg aca gcg aca gcg aca gcg aca gcg tcc gct tcc atc      864
Thr Ala Thr Ala Thr Ala Thr Ala Thr Ala Thr Ala Ser Ala Ser Ile
        275                 280                 285

tcc gag gac tcg gat ggc ctg gag agc ggc agc tcc ggc aag ggc gtc      912
Ser Glu Asp Ser Asp Gly Leu Glu Ser Gly Ser Ser Gly Lys Gly Val
    290                 295                 300
```

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```
gag gag gcg ccc gcg ctg ccg ttc tat gac ttc ttc ggg ctc cag tcc       960
Glu Glu Ala Pro Ala Leu Pro Phe Tyr Asp Phe Phe Gly Leu Gln Ser
305                 310                 315                 320

tcc gga ggc cgc tga                                                   975
Ser Gly Gly Arg


<210> SEQ ID NO 62
<211> LENGTH: 324
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 62

Met Glu Thr Pro Gln Gln Gln Ser Ala Ala Ala Ala Ala Ala Ala Ala
1               5                   10                  15

His Gly Gln Asp Asp Gly Gly Ser Pro Pro Met Ser Pro Ala Ser Ala
            20                  25                  30

Ala Ala Ala Ala Leu Ala Asn Ala Arg Trp Asn Pro Thr Lys Glu Gln
        35                  40                  45

Val Ala Val Leu Glu Gly Leu Tyr Glu His Gly Leu Arg Thr Pro Ser
    50                  55                  60

Ala Glu Gln Ile Gln Gln Ile Thr Gly Arg Leu Arg Glu His Gly Ala
65                  70                  75                  80

Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln Asn His Lys Ala Arg
                85                  90                  95

Gln Arg Gln Arg Gln Lys Gln Asp Ser Phe Ala Tyr Phe Ser Arg Leu
            100                 105                 110

Leu Arg Arg Pro Pro Pro Leu Pro Val Leu Ser Met Pro Pro Ala Pro
        115                 120                 125

Pro Tyr His His Ala Arg Val Pro Ala Pro Pro Ala Ile Pro Met Pro
    130                 135                 140

Met Ala Pro Pro Pro Pro Ala Ala Cys Asn Asp Asn Gly Gly Ala Arg
145                 150                 155                 160

Val Ile Tyr Arg Asn Pro Phe Tyr Val Ala Ala Pro Gln Ala Pro Pro
                165                 170                 175

Ala Asn Ala Ala Tyr Tyr Tyr Pro Gln Pro Gln Gln Gln Gln Gln Gln
            180                 185                 190

Gln Val Thr Val Met Tyr Gln Tyr Pro Arg Met Glu Val Ala Gly Gln
        195                 200                 205

Asp Lys Met Met Thr Arg Ala Ala Ala His Gln Gln Gln Gln His Asn
    210                 215                 220

Gly Ala Gly Gln Gln Pro Gly Arg Ala Gly His Pro Ser Arg Glu Thr
225                 230                 235                 240

Leu Gln Leu Phe Pro Leu Gln Pro Thr Phe Val Leu Arg His Asp Lys
                245                 250                 255

Gly Arg Ala Ala Asn Gly Ser Asn Asn Asp Ser Leu Thr Ser Thr Ser
            260                 265                 270

Thr Ala Thr Ala Thr Ala Thr Ala Thr Ala Thr Ala Ser Ala Ser Ile
        275                 280                 285

Ser Glu Asp Ser Asp Gly Leu Glu Ser Gly Ser Ser Gly Lys Gly Val
    290                 295                 300

Glu Glu Ala Pro Ala Leu Pro Phe Tyr Asp Phe Phe Gly Leu Gln Ser
305                 310                 315                 320
```

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```
Ser Gly Gly Arg


<210> SEQ ID NO 63
<211> LENGTH: 909
<212> TYPE: DNA
<213> ORGANISM: Zea mays
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(909)

<400> SEQUENCE: 63

atg gcg gcc aat gcg ggc ggc ggt gga gcg gga gga ggc agc ggc agc       48
Met Ala Ala Asn Ala Gly Gly Gly Gly Ala Gly Gly Gly Ser Gly Ser
1               5                   10                  15

ggc agc gtg gct gcg ccg gcg gtg tgc cgc ccc agc ggc tcg cgg tgg       96
Gly Ser Val Ala Ala Pro Ala Val Cys Arg Pro Ser Gly Ser Arg Trp
            20                  25                  30

acg ccg acg ccg gag cag atc agg atg ctg aag gag ctc tac tac ggc      144
Thr Pro Thr Pro Glu Gln Ile Arg Met Leu Lys Glu Leu Tyr Tyr Gly
        35                  40                  45

tgc ggc atc cgg tcg ccc agc tcg gag cag atc cag cgc atc acc gcc      192
Cys Gly Ile Arg Ser Pro Ser Ser Glu Gln Ile Gln Arg Ile Thr Ala
    50                  55                  60

atg ctg cgg cag cac ggc aag atc gag ggc aag aac gtc ttc tac tgg      240
Met Leu Arg Gln His Gly Lys Ile Glu Gly Lys Asn Val Phe Tyr Trp
65                  70                  75                  80

ttc cag aac cac aag gcc cgc gag cgc cag aag cgc cgc ctc acc agc      288
Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Arg Arg Leu Thr Ser
                85                  90                  95

ctc gac gtc aac gtg ccc gcc gcc ggc gcg gcc gac gcc acc acc agc      336
Leu Asp Val Asn Val Pro Ala Ala Gly Ala Ala Asp Ala Thr Thr Ser
            100                 105                 110

caa ctc ggc gtc ctc tcg ctg tcg tcg ccg ccg cct tca ggc gcg gcg      384
Gln Leu Gly Val Leu Ser Leu Ser Ser Pro Pro Pro Ser Gly Ala Ala
        115                 120                 125

cct ccc tcg ccc acc ctc ggc ttc tac gcc gcc ggc aat ggc ggc gga      432
Pro Pro Ser Pro Thr Leu Gly Phe Tyr Ala Ala Gly Asn Gly Gly Gly
    130                 135                 140

tcg gct gtg ctg ctg gac acg agt tcc gac tgg ggc agc agc ggc gct      480
Ser Ala Val Leu Leu Asp Thr Ser Ser Asp Trp Gly Ser Ser Gly Ala
145                 150                 155                 160

gcc atg gcc acc gag aca tgc ttc ctg cag gac tac atg ggc gtg acg      528
Ala Met Ala Thr Glu Thr Cys Phe Leu Gln Asp Tyr Met Gly Val Thr
                165                 170                 175

gac acg ggc agc tcg tcg cag tgg cca cgc ttc tcg tcg tcg gac acg      576
Asp Thr Gly Ser Ser Ser Gln Trp Pro Arg Phe Ser Ser Ser Asp Thr
            180                 185                 190

ata atg gcg gcg gcc gcg gcg cgg gcg gcg acg acg cgg gcg ccc gag      624
Ile Met Ala Ala Ala Ala Ala Arg Ala Ala Thr Thr Arg Ala Pro Glu
        195                 200                 205

acg ctc cct ctc ttc ccg acc tgc ggc gac gac ggc ggc agc ggt agc      672
Thr Leu Pro Leu Phe Pro Thr Cys Gly Asp Asp Gly Gly Ser Gly Ser
    210                 215                 220

agc agc tac ttg ccg ttc tgg ggt gcc gcg tcc aca act gcc ggc gcc      720
Ser Ser Tyr Leu Pro Phe Trp Gly Ala Ala Ser Thr Thr Ala Gly Ala
225                 230                 235                 240

act tct tcc gtt gcg atc cag cag caa cac cag ctg cag gag cag tac      768
Thr Ser Ser Val Ala Ile Gln Gln Gln His Gln Leu Gln Glu Gln Tyr
                245                 250                 255
```

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```
agc ttt tac agc aac agc aac agc acc cag ctg gcc ggc acc ggc aac       816
Ser Phe Tyr Ser Asn Ser Asn Ser Thr Gln Leu Ala Gly Thr Gly Asn
            260                 265                 270

caa gac gta tcg gca aca gca gca gca gcc gcc gcc ctg gag ctg agc       864
Gln Asp Val Ser Ala Thr Ala Ala Ala Ala Ala Ala Leu Glu Leu Ser
        275                 280                 285

ctc agc tca tgg tgc tcc cct tac cct gct gca ggg agt atg tga           909
Leu Ser Ser Trp Cys Ser Pro Tyr Pro Ala Ala Gly Ser Met
    290                 295                 300


<210> SEQ ID NO 64
<211> LENGTH: 302
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 64

Met Ala Ala Asn Ala Gly Gly Gly Gly Ala Gly Gly Gly Ser Gly Ser
1               5                   10                  15

Gly Ser Val Ala Ala Pro Ala Val Cys Arg Pro Ser Gly Ser Arg Trp
            20                  25                  30

Thr Pro Thr Pro Glu Gln Ile Arg Met Leu Lys Glu Leu Tyr Tyr Gly
        35                  40                  45

Cys Gly Ile Arg Ser Pro Ser Ser Glu Gln Ile Gln Arg Ile Thr Ala
    50                  55                  60

Met Leu Arg Gln His Gly Lys Ile Glu Gly Lys Asn Val Phe Tyr Trp
65                  70                  75                  80

Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Arg Arg Leu Thr Ser
                85                  90                  95

Leu Asp Val Asn Val Pro Ala Ala Gly Ala Ala Asp Ala Thr Thr Ser
            100                 105                 110

Gln Leu Gly Val Leu Ser Leu Ser Ser Pro Pro Pro Ser Gly Ala Ala
        115                 120                 125

Pro Pro Ser Pro Thr Leu Gly Phe Tyr Ala Ala Gly Asn Gly Gly Gly
    130                 135                 140

Ser Ala Val Leu Leu Asp Thr Ser Ser Asp Trp Gly Ser Ser Gly Ala
145                 150                 155                 160

Ala Met Ala Thr Glu Thr Cys Phe Leu Gln Asp Tyr Met Gly Val Thr
                165                 170                 175

Asp Thr Gly Ser Ser Ser Gln Trp Pro Arg Phe Ser Ser Ser Asp Thr
            180                 185                 190

Ile Met Ala Ala Ala Ala Ala Arg Ala Ala Thr Thr Arg Ala Pro Glu
        195                 200                 205

Thr Leu Pro Leu Phe Pro Thr Cys Gly Asp Asp Gly Gly Ser Gly Ser
    210                 215                 220

Ser Ser Tyr Leu Pro Phe Trp Gly Ala Ala Ser Thr Thr Ala Gly Ala
225                 230                 235                 240

Thr Ser Ser Val Ala Ile Gln Gln Gln His Gln Leu Gln Glu Gln Tyr
                245                 250                 255

Ser Phe Tyr Ser Asn Ser Asn Ser Thr Gln Leu Ala Gly Thr Gly Asn
            260                 265                 270

Gln Asp Val Ser Ala Thr Ala Ala Ala Ala Ala Ala Leu Glu Leu Ser
        275                 280                 285

Leu Ser Ser Trp Cys Ser Pro Tyr Pro Ala Ala Gly Ser Met
```

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```
    290                 295                 300


<210> SEQ ID NO 65
<211> LENGTH: 961
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 65

gatccgattg actatctcat tcctccaaac ccaaacacct caaatatatc tgctatcggg      60

attggcattc ctgtatccct acgcccgtgt accccctgtt tagagaacct cccaaggtat     120

aagatggcga agattattgt tgtcttgtct ttcatcatat atcgagtctt tccctaggat     180

attattattg gcaatgagca ttacacggtt aatcgattga gagaacatgc atctcacctt     240

cagcaaataa ttacgataat ccatatttta cgcttcgtaa cttctcatga gtttcgatat     300

acaaatttgt tttctggaca ccctaccatt catcctcttc ggagaagaga ggaagtgtcc     360

tcaatttaaa tatgttgtca tgctgtagtt cttcacccaa tctcaacagg taccaagcac     420

attgtttcca caaattatat tttagtcaca ataaatctat attattatta atatactaaa     480

actatactga cgctcagatg cttttactag ttcttgctag tatgtgatgt aggtctacgt     540

ggaccagaaa atagtgagac acggaagaca aaagaagtaa aagaggcccg gactacggcc     600

cacatgagat tcggccccgc cacctccggc aaccagcggc cgatccaacg gaagtgcgcg     660

cacacacaca acctcgtata tatcgccgcg cggaagcggc gcgaccgagg aagccttgtc     720

ctcgacaccc cctacacagg tgtcgcgctg cccccgacac gagtcccgca tgcgtcccac     780

gcggccgcgc cagatcccgc ctccgcgcgt tgccacgccc tctataaaca cccagctctc     840

cctcgccctc atctacctca ctcgtagtcg tagctcaagc atcagcggca gcggcagcgg     900

caggagctct gggcagcgtg cgcacgtggg gtacctagct cgctctgcta gcctacctta     960

a                                                                      961


<210> SEQ ID NO 66
<211> LENGTH: 1917
<212> TYPE: DNA
<213> ORGANISM: Zea mays
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(1917)

<400> SEQUENCE: 66

atg acc agc aac agc agc cag aac atg agc agc tgc agc acc ggc gga       48
Met Thr Ser Asn Ser Ser Gln Asn Met Ser Ser Cys Ser Thr Gly Gly
1               5                   10                  15

agc gac gcg gcg gtc ggc ggc ggc agc tgg ctc ggc ttc tcg ctg tcg       96
Ser Asp Ala Ala Val Gly Gly Gly Ser Trp Leu Gly Phe Ser Leu Ser
            20                  25                  30

cct cac atg gcg gcg acc atg gac ggc gcg gcc gac ggc gtt ccg gtg      144
Pro His Met Ala Ala Thr Met Asp Gly Ala Ala Asp Gly Val Pro Val
        35                  40                  45

cag cac cac cac cac gaa ggc ctc ttc tac cct ccc gtc gtc agc tcc      192
Gln His His His His Glu Gly Leu Phe Tyr Pro Pro Val Val Ser Ser
    50                  55                  60

tcg ccc gcg ccc ttc tgc tac gct ctc ggc ggc ggc caa gat ggc ctc      240
Ser Pro Ala Pro Phe Cys Tyr Ala Leu Gly Gly Gly Gln Asp Gly Leu
65                  70                  75                  80

gcc acg gcg gcc gcc aat ggt ggc ggg ggg ttc tac ccc ggg ctc tcc      288
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Ala Thr Ala Ala Ala Asn Gly Gly Gly Gly Phe Tyr Pro Gly Leu Ser
                85                  90                  95

tct atg ccg ctc aag tcc gac ggc tcc cta tgc atc ctg gag gcc ctc      336
Ser Met Pro Leu Lys Ser Asp Gly Ser Leu Cys Ile Leu Glu Ala Leu
            100                 105                 110

cac agg agc gag caa gaa cgg cac ggg gtg gtg gtg tcg tcg tcg tcg      384
His Arg Ser Glu Gln Glu Arg His Gly Val Val Val Ser Ser Ser Ser
        115                 120                 125

ccc aaa ctg gag gat ttc ttg ggc gcg agc gcg agc acg gcg atg gcg      432
Pro Lys Leu Glu Asp Phe Leu Gly Ala Ser Ala Ser Thr Ala Met Ala
    130                 135                 140

ctg agc ttg gac agc tcc agc ttc tac tac ggc tgc ggc cac ggc cac      480
Leu Ser Leu Asp Ser Ser Ser Phe Tyr Tyr Gly Cys Gly His Gly His
145                 150                 155                 160

ggc cac gac caa ggc ggg tac ctg cag cca atg cag tgc gcg gtg atg      528
Gly His Asp Gln Gly Gly Tyr Leu Gln Pro Met Gln Cys Ala Val Met
                165                 170                 175

ccc ggc tcg ggc ggg cac gac gtg tac ggc ggc ggg cac gcg cag atg      576
Pro Gly Ser Gly Gly His Asp Val Tyr Gly Gly Gly His Ala Gln Met
            180                 185                 190

gtg gac gag cag tcc gcc gcg gca atg gcg gcg agc tgg ttc tcc gcc      624
Val Asp Glu Gln Ser Ala Ala Ala Met Ala Ala Ser Trp Phe Ser Ala
        195                 200                 205

cgc ggc aat ggc ggc tac gac gtc gac ggc gcc ggc gcc ggc gcc atc      672
Arg Gly Asn Gly Gly Tyr Asp Val Asp Gly Ala Gly Ala Gly Ala Ile
    210                 215                 220

gtg ccg ttg cag ggc cac ccg cac ccg ctc gcc ctc tcc atg agc tcc      720
Val Pro Leu Gln Gly His Pro His Pro Leu Ala Leu Ser Met Ser Ser
225                 230                 235                 240

ggg acg ggg tcc cag tcc agc agc gtc acc atg caa gtc ggc agc gcc      768
Gly Thr Gly Ser Gln Ser Ser Ser Val Thr Met Gln Val Gly Ser Ala
                245                 250                 255

cac gcc gac gcc gtc acc gag tac atc gcc atg gac ggg agc aag aag      816
His Ala Asp Ala Val Thr Glu Tyr Ile Ala Met Asp Gly Ser Lys Lys
            260                 265                 270

cgc ggc gcc ggc aac ggc gct agt gcc ggg cag aag cag ccc acc atc      864
Arg Gly Ala Gly Asn Gly Ala Ser Ala Gly Gln Lys Gln Pro Thr Ile
        275                 280                 285

cac cgc aag acc atc gac aca ttc ggg cag cgc acg tcg cag tac cgc      912
His Arg Lys Thr Ile Asp Thr Phe Gly Gln Arg Thr Ser Gln Tyr Arg
    290                 295                 300

ggc gtc acc agg cat agg tgg acg ggg agg tat gag gcg cac ctc tgg      960
Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp
305                 310                 315                 320

gac aac agc tgc agg aag gaa ggg cag acc cgg aaa ggc cgg caa gtt     1008
Asp Asn Ser Cys Arg Lys Glu Gly Gln Thr Arg Lys Gly Arg Gln Val
                325                 330                 335

tat ctc ggc ggg tat gac gtg gag gag aag gcc gcg agg gca tat gac     1056
Tyr Leu Gly Gly Tyr Asp Val Glu Glu Lys Ala Ala Arg Ala Tyr Asp
            340                 345                 350

ctg gcg gcg ctc aag tac tgg ggg acg tcc acg cac gtg aat ttc ccg     1104
Leu Ala Ala Leu Lys Tyr Trp Gly Thr Ser Thr His Val Asn Phe Pro
        355                 360                 365

gtg gag gac tac agg gaa gag ctg gag gag atg aag aac atg acc aga     1152
Val Glu Asp Tyr Arg Glu Glu Leu Glu Glu Met Lys Asn Met Thr Arg
    370                 375                 380

cag gag tac gtc gct cac ctg aga agg aaa agc agc ggc ttc tcg cgc     1200
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Gln Glu Tyr Val Ala His Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg
385                 390                 395                 400

ggc gct tcg atc tac cgg gga gtc acc agg cat cac cag cac ggg cgg     1248
Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg
                405                 410                 415

tgg cag gcg cgc atc ggc cgc gtc tcg ggc aac aag gac ctc tac ctc     1296
Trp Gln Ala Arg Ile Gly Arg Val Ser Gly Asn Lys Asp Leu Tyr Leu
            420                 425                 430

gga acg ttc agc acc cag gag gag gcg gcg gag gcg tac gac gtg gcc     1344
Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala
        435                 440                 445

gcg atc aag ttc cgc ggc ctc agc gcg gtc acc aac ttc gac atc acg     1392
Ala Ile Lys Phe Arg Gly Leu Ser Ala Val Thr Asn Phe Asp Ile Thr
    450                 455                 460

cgg tac gac gtg gac aag atc atg gag agc agc acg ctg ctc ccg ggc     1440
Arg Tyr Asp Val Asp Lys Ile Met Glu Ser Ser Thr Leu Leu Pro Gly
465                 470                 475                 480

gag cag gtc cgg cgc agg aag gaa ggc gcc gac gcc gcg gtc tcg gag     1488
Glu Gln Val Arg Arg Arg Lys Glu Gly Ala Asp Ala Ala Val Ser Glu
                485                 490                 495

gcc gcc gcc gcg ctg gtg cag gcc ggc aac tgc atg acg gac acc tgg     1536
Ala Ala Ala Ala Leu Val Gln Ala Gly Asn Cys Met Thr Asp Thr Trp
            500                 505                 510

aag atc cag gcg gcg ctg ccg gct gcc gcg cgg gcc gac gag cgc ggc     1584
Lys Ile Gln Ala Ala Leu Pro Ala Ala Ala Arg Ala Asp Glu Arg Gly
        515                 520                 525

gcc ggc cag cag cag cgt cag gac ttg ctg tcg agc gag gcc ttc tcg     1632
Ala Gly Gln Gln Gln Arg Gln Asp Leu Leu Ser Ser Glu Ala Phe Ser
    530                 535                 540

ctg ctc cac gac atc gtg tcc gtc gac gcc gct gct ggt aca ggg aca     1680
Leu Leu His Asp Ile Val Ser Val Asp Ala Ala Ala Gly Thr Gly Thr
545                 550                 555                 560

ggg ggc atg tcg aac gcg tcc tcg tcg ctg gcc ccc agc gtg agc aac     1728
Gly Gly Met Ser Asn Ala Ser Ser Ser Leu Ala Pro Ser Val Ser Asn
                565                 570                 575

tcc cgg gag cag agc ccg gac cgg ggc ggc gcc agc ctc gcc atg ctc     1776
Ser Arg Glu Gln Ser Pro Asp Arg Gly Gly Ala Ser Leu Ala Met Leu
            580                 585                 590

ttc gcc aag ccc gcc gcg gcg ccc aag ctg gct tgc ccg ctg ccg ctg     1824
Phe Ala Lys Pro Ala Ala Ala Pro Lys Leu Ala Cys Pro Leu Pro Leu
        595                 600                 605

ggg tcc tgg gtg tcg ccg tcc gcg gtg tcc gcc agg ccg ccc ggc gtg     1872
Gly Ser Trp Val Ser Pro Ser Ala Val Ser Ala Arg Pro Pro Gly Val
    610                 615                 620

tca atc gcg cac ctg ccg gtg ttc gcc gcg tgg acc gac gca tga         1917
Ser Ile Ala His Leu Pro Val Phe Ala Ala Trp Thr Asp Ala
625                 630                 635


<210> SEQ ID NO 67
<211> LENGTH: 638
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 67

Met Thr Ser Asn Ser Ser Gln Asn Met Ser Ser Cys Ser Thr Gly Gly
1               5                   10                  15

Ser Asp Ala Ala Val Gly Gly Gly Ser Trp Leu Gly Phe Ser Leu Ser
            20                  25                  30
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Pro His Met Ala Ala Thr Met Asp Gly Ala Ala Asp Gly Val Pro Val
        35                  40                  45

Gln His His His His Glu Gly Leu Phe Tyr Pro Pro Val Val Ser Ser
    50                  55                  60

Ser Pro Ala Pro Phe Cys Tyr Ala Leu Gly Gly Gly Gln Asp Gly Leu
65                  70                  75                  80

Ala Thr Ala Ala Ala Asn Gly Gly Gly Gly Phe Tyr Pro Gly Leu Ser
                85                  90                  95

Ser Met Pro Leu Lys Ser Asp Gly Ser Leu Cys Ile Leu Glu Ala Leu
            100                 105                 110

His Arg Ser Glu Gln Glu Arg His Gly Val Val Val Ser Ser Ser Ser
        115                 120                 125

Pro Lys Leu Glu Asp Phe Leu Gly Ala Ser Ala Ser Thr Ala Met Ala
    130                 135                 140

Leu Ser Leu Asp Ser Ser Ser Phe Tyr Tyr Gly Cys Gly His Gly His
145                 150                 155                 160

Gly His Asp Gln Gly Gly Tyr Leu Gln Pro Met Gln Cys Ala Val Met
                165                 170                 175

Pro Gly Ser Gly Gly His Asp Val Tyr Gly Gly Gly His Ala Gln Met
            180                 185                 190

Val Asp Glu Gln Ser Ala Ala Ala Met Ala Ala Ser Trp Phe Ser Ala
        195                 200                 205

Arg Gly Asn Gly Gly Tyr Asp Val Asp Gly Ala Gly Ala Gly Ala Ile
    210                 215                 220

Val Pro Leu Gln Gly His Pro His Pro Leu Ala Leu Ser Met Ser Ser
225                 230                 235                 240

Gly Thr Gly Ser Gln Ser Ser Ser Val Thr Met Gln Val Gly Ser Ala
                245                 250                 255

His Ala Asp Ala Val Thr Glu Tyr Ile Ala Met Asp Gly Ser Lys Lys
            260                 265                 270

Arg Gly Ala Gly Asn Gly Ala Ser Ala Gly Gln Lys Gln Pro Thr Ile
        275                 280                 285

His Arg Lys Thr Ile Asp Thr Phe Gly Gln Arg Thr Ser Gln Tyr Arg
    290                 295                 300

Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp
305                 310                 315                 320

Asp Asn Ser Cys Arg Lys Glu Gly Gln Thr Arg Lys Gly Arg Gln Val
                325                 330                 335

Tyr Leu Gly Gly Tyr Asp Val Glu Glu Lys Ala Ala Arg Ala Tyr Asp
            340                 345                 350

Leu Ala Ala Leu Lys Tyr Trp Gly Thr Ser Thr His Val Asn Phe Pro
        355                 360                 365

Val Glu Asp Tyr Arg Glu Glu Leu Glu Glu Met Lys Asn Met Thr Arg
    370                 375                 380

Gln Glu Tyr Val Ala His Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg
385                 390                 395                 400

Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg
                405                 410                 415

Trp Gln Ala Arg Ile Gly Arg Val Ser Gly Asn Lys Asp Leu Tyr Leu
            420                 425                 430
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Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala
        435                 440                 445

Ala Ile Lys Phe Arg Gly Leu Ser Ala Val Thr Asn Phe Asp Ile Thr
    450                 455                 460

Arg Tyr Asp Val Asp Lys Ile Met Glu Ser Ser Thr Leu Leu Pro Gly
465                 470                 475                 480

Glu Gln Val Arg Arg Arg Lys Glu Gly Ala Asp Ala Ala Val Ser Glu
                485                 490                 495

Ala Ala Ala Ala Leu Val Gln Ala Gly Asn Cys Met Thr Asp Thr Trp
            500                 505                 510

Lys Ile Gln Ala Ala Leu Pro Ala Ala Ala Arg Ala Asp Glu Arg Gly
        515                 520                 525

Ala Gly Gln Gln Gln Arg Gln Asp Leu Leu Ser Ser Glu Ala Phe Ser
    530                 535                 540

Leu Leu His Asp Ile Val Ser Val Asp Ala Ala Ala Gly Thr Gly Thr
545                 550                 555                 560

Gly Gly Met Ser Asn Ala Ser Ser Ser Leu Ala Pro Ser Val Ser Asn
                565                 570                 575

Ser Arg Glu Gln Ser Pro Asp Arg Gly Gly Ala Ser Leu Ala Met Leu
            580                 585                 590

Phe Ala Lys Pro Ala Ala Ala Pro Lys Leu Ala Cys Pro Leu Pro Leu
        595                 600                 605

Gly Ser Trp Val Ser Pro Ser Ala Val Ser Ala Arg Pro Pro Gly Val
    610                 615                 620

Ser Ile Ala His Leu Pro Val Phe Ala Ala Trp Thr Asp Ala
625                 630                 635


<210> SEQ ID NO 68
<211> LENGTH: 2260
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 68

cttccctaac ctttgcactg tccaaaatgg cttcctgatc ccctcacttc ctcgaatcaa      60

tctaagaaga aactcaagcc gcaaccatta ggggcagatt aattgctgca ctttcagata     120

atcaaccatg gccactgtga acaactggct cgctttctcc ctctccccgc aggagctgcc     180

gccctcccag acgacggact ccacactcat ctcggccgcc accgccgacc atgtctccgg     240

cgatgtctgc ttcaacatcc cccaagattg gagcatgagg ggatcagagc tttcggcgct     300

cgtcgcggag ccgaagctgg aggacttcct cggcggcatc tccttctccg agcagcatca     360

caaggccaac tgcaacatga tacccagcac tagcagcaca gtttgctacg cgagctcagg     420

tgctagcacc ggctaccatc accagctgta ccaccagccc accagctcag cgctccactt     480

cgcggactcc gtaatggtgg cctcctcggc cggtgtccac gacggcggtg ccatgctcag     540

cgcggccgcc gctaacggtg tcgctggcgc tgccagtgcc aacggcggcg gcatcgggct     600

gtccatgatt aagaactggc tgcggagcca accggcgccc atgcagccga gggtggcggc     660

ggctgagggc gcgcaggggc tctctttgtc catgaacatg gcggggacga cccaaggcgc     720

tgctggcatg ccacttctcg ctggagagcg cgcacgggcg cccgagagtg tatcgacgtc     780

agcacagggt ggagccgtcg tcgtcacggc gccgaaggag gatagcggtg gcagcggtgt     840

tgccggcgct ctagtagccg tgagcacgga cacgggtggc agcggcggcg cgtcggctga     900
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caacacggca aggaagacgg tggacacgtt cgggcagcgc acgtcgattt accgtggcgt 960

gacaaggcat agatggactg ggagatatga ggcacatctt tgggataaca gttgcagaag 1020

ggaagggcaa actcgtaagg gtcgtcaagt ctatttaggt ggctatgata aagaggagaa 1080

agctgctagg gcttatgatc ttgctgctct gaagtactgg ggtgccacaa caacaacaaa 1140

ttttccagtg agtaactacg aaaaggagct cgaggacatg aagcacatga caaggcagga 1200

gtttgtagcg tctctgagaa ggaagagcag tggtttctcc agaggtgcat ccatttacag 1260

gggagtgact aggcatcacc aacatggaag atggcaagca cggattggac gagttgcagg 1320

gaacaaggat ctttacttgg gcaccttcag cacccaggag gaggcagcgg aggcgtacga 1380

catcgcggcg atcaagttcc gcggcctcaa cgccgtcacc aacttcgaca tgagccgcta 1440

cgacgtgaag agcatcctgg acagcagcgc cctccccatc ggcagcgccg ccaagcgcct 1500

caaggaggcc gaggccgcag cgtccgcgca gcaccaccac gccggcgtgg tgagctacga 1560

cgtcggccgc atcgcctcgc agctcggcga cggcggagcc ctggcggcgg cgtacggcgc 1620

gcactaccac ggcgccgcct ggccgaccat cgcgttccag ccgggcgccg ccagcacagg 1680

cctgtaccac ccgtacgcgc agcagccaat gcgcggcggc gggtggtgca agcaggagca 1740

ggaccacgcg gtgatcgcgg ccgcgcacag cctgcaggac ctccaccacc tgaacctggg 1800

cgcggccggc gcgcacgact tttctcggc agggcagcag gccgccgccg ctgcgatgca 1860

cggcctgggt agcatcgaca gtgcgtcgct cgagcacagc accggctcca actccgtcgt 1920

ctacaacggc ggggtcggcg acagcaacgg cgccagcgcc gtcggcggca gtggcggtgg 1980

ctacatgatg ccgatgagcg ctgccggagc aaccactaca tcggcaatgg tgagccacga 2040

gcaggtgcat gcacgggcct acgacgaagc caagcaggct gctcagatgg ggtacgagag 2100

ctacctggtg aacgcggaga acaatggtgg cggaaggatg tctgcatggg ggactgtcgt 2160

gtctgcagcc gcggcggcag cagcaagcag caacgacaac atggccgccg acgtcggcca 2220

tggcggcgcg cagctcttca gtgtctggaa cgacacttaa 2260

<210> SEQ ID NO 69
<211> LENGTH: 3766
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 69

atggctactg tgaacaactg gctcgctttc tccctctccc cgcaggagct gccgcccacc 60

cagacggact ccaccctcat ctctgccgcc accaccgacg atgtctccgg cgatgtctgc 120

ttcaacatcc cccaaggtat gcatctatcg atcgatatat gtacgtacag tgcgcatata 180

tatatatatc tgcagtttgt ggtacgaata ctgattgaag ctagcatgaa atgtcgtttg 240

ttctttcaga ttggagcatg aggggatccg agctttcggc gctcgtcgcc gagccgaagc 300

tggaggactt cctcggcgga atctccttct ccgagcagca ccacaaggcc aactgcaaca 360

tgatccccag cactagcagc acagcttgct acgcgagctc gggtgctacc gccggctacc 420

atcaccagct gtaccaccag cccaccagct ccgcgctcca cttcgctgac tccgtcatgg 480

tggcctcctc ggccggcggc gtccacgacg gaggtgccat gctcagcgcg gccagcgcta 540

atggtagcgc tggcgctggc gctgccagtg ccaatggcag cggcagcatc gggctgtcca 600

tgatcaagaa ctggctgcgg agccaaccag ctcccatgca gccgagggtg gcggcggctg 660

-continued

agagcgtgca ggggctctct ttgtccatga acatggcggg ggcgacgcaa ggcgccgctg 720

gcatgccact tcttgctgga gagcgcggcc gggcgcccga gagtgtctcg acgtcggcac 780

agggtggagc cgtcgtcacg gctccaaagg aggatagcgg tggcagcggt gttgccgcca 840

ccggcgccct agtagccgtg agcacggaca cgggtggcag cggcgcgtcg gctgacaaca 900

cggcaaggaa gacggtggac acgttcgggc agcgcacgtc gatttaccgt ggcgtgacaa 960

ggtaataagg gtccggtatt acaatgaatc gtcacttcgt cagagaacta aactagcaca 1020

aatcagcaat gaatcaagta atatcatgaa atttagaaaa gccgttagca atgcaaggag 1080

ctatcattat agatttgatt gcatctagac agttctgaat taaatgagta gggcaatgtg 1140

tagcctttga tgatctcgct gattattagg agtgccattt gtattggcta tgattgtggt 1200

atatacagca gtagacaatt aacaaaaggc taccactttc gaattatttt aggcatagat 1260

ggactgggag atatgaagca catctgtggg acaacagttg cagaagggaa ggacaaactc 1320

gcaagggtcg tcaaggtacc aatataatgc aatacaccgt atttaaatat atatgctttt 1380

ctgtaattaa gtttatactt tcacaaaact gacattactt cgcattatca tttttggatt 1440

gtcgtcgtca tgattggcgg gattgaaatg aactattgaa tctacagtct atttaggtaa 1500

gcgatttcac ttggttatta atttgggacc aactacttaa tccagtttgt ttttccccta 1560

taaccattat tttttcatct gtgttctcaa ctcttacttt tccatcttgt tccactgata 1620

ggtggctatg ataaagagga gaaagctgct agggcttatg atctggctgc tcttaagtac 1680

tggggtccca cgacaacaac aaattttcca gtatgtatat gtagaatgca gttttacttc 1740

actgaagatc ataccttttgc tatgtctcaa atgccgttca ttagttagtg gatctgaagt 1800

gaaggttctg taatttttgt taactatgta cattgctgga attgtactta aagtcatttg 1860

tttttgtata tctaggtgaa taactacgaa aaggagctgg aggatatgaa gcacatgaca 1920

aggcaggagt ttgtagcgtc tctgagaagg tcggtcgaac agcattgatt aatcaatgcc 1980

aactctattg aataaacatc tactctgtta attgttaaag tttgagagaa agatctgcat 2040

gttagatctt aatagaccac tgtatatgaa tgcaggaaga gcagtggttt ctccagaggt 2100

gcatccattt acaggggagt gactaggtat gaattcatat aatggcgtca acaaacacac 2160

atacactttg attgaggagg cgaatgcacg catggattga atgtgaatgg tgttttactt 2220

gaactatgta attataggca tcaccagcat ggaagatggc aagcacggat tggacgagtt 2280

gcagggaaca aggatctcta cttgggcacc ttcagtaagt atcagagatg ttttctcatt 2340

gtatatagag gagtacttct atatgtatat atacattcag ttattcacca cacaaaagca 2400

aattgcagtc aactaataac aatctcaacg caatgagaag caagtgttac agctgatagt 2460

acacatttgt agaccttctg catatggatg ttatatatga tgactattaa aaatgtgacc 2520

attgcatcaa gtcatgcaaa gttgcattgc agtagtacat acattactta gtgcatgctc 2580

ctcaagtggc tttttcaaac ctgatcccat gtctggcgct attgttgtct cccattcacc 2640

cgtgcatcag gtcaaaatag tactatgcct caataagaaa cacatgagca tgcactggca 2700

gcagcagact aatcaagttc tatcatttac taataaacta attaggctac agcatccaaa 2760

agattctacc cattaagcca caactgttca tgcatgcatt cataaaccag gataccacca 2820

tgcatgcgtg caccgtgttc gtgcttggaa tattgagctg agccgagtgc acccttgcgt 2880

ggatgcaggc acgcaggagg aggcagcgga ggcatacgac attgcggcga tcaagttccg 2940

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cggcctcaac gccgtcacaa acttcgacat gagccgctac gacgtcaaga gcatcctgga   3000

cagcagtgcg ctccccatcg gcagcgccgc caagcgtctc aaggaggccg aggccgccgc   3060

gtccgcacag caccatgccg gcgtggtgag ctacgacgtc ggccgcatag cctcacagct   3120

cggcgacggc ggcgccctgg cggcggcgta cggcgcgcac taccatggcg cctggccgac   3180

catcgcgttc cagccgagcg cggccacggg cctgtaccac ccgtacgcgc agccgatgcg   3240

cgggtggtgc aagcaggagc aggaccacgc ggtgatcgcg gccgcgcaca gcctgcagga   3300

gctccaccac ctgaacctgg gtgctgccgc cggcgcgcac gacttcttct cggcggggca   3360

gcaggcggcg atgcacggcc tgggtagcat ggacaatgca tcactcgagc acagcaccgg   3420

ctccaactcc gtcgtgtaca acggtgttgg tgatagcaac ggcagcaccg tcgtcggcag   3480

tggtggctac atgatgccta tgagcgctgc cacggcgacg gctaccacgg caatggtgag   3540

ccacgagcag gtgcatgcac gggcacaggg tgatcaccac gacgaagcca agcaggctgc   3600

tcagatgggg tacgagagct acctggtgaa cgcagagaac tatggcggcg ggaggatgtc   3660

tgcggcctgg gcgactgtct cagcgccacc ggcggcaagc agcaacgata acatggcgga   3720

cgtcggccat ggcggcgcac agctcttcag tgtctggaac gatact                 3766


<210> SEQ ID NO 70
<211> LENGTH: 530
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 70

Met Asp Ser Ser Ser Ser Ser Pro Pro Asn Ser Thr Asn Asn Asn Ser
1               5                   10                  15

Leu Ala Phe Ser Leu Ser Asn His Phe Pro Asn Pro Ser Ser Ser Pro
            20                  25                  30

Leu Ser Leu Phe His Ser Phe Thr Tyr Pro Ser Leu Ser Leu Thr Gly
        35                  40                  45

Ser Asn Thr Val Asp Ala Pro Pro Glu Pro Thr Ala Gly Ala Gly Pro
    50                  55                  60

Thr Asn Leu Ser Ile Phe Thr Gly Gly Pro Lys Phe Glu Asp Phe Leu
65                  70                  75                  80

Gly Gly Ser Ala Ala Thr Ala Thr Thr Val Ala Cys Ala Pro Pro Gln
                85                  90                  95

Leu Pro Gln Phe Ser Thr Asp Asn Asn Asn His Leu Tyr Asp Ser Glu
            100                 105                 110

Leu Lys Ser Thr Ile Ala Ala Cys Phe Pro Arg Ala Leu Ala Ala Glu
        115                 120                 125

Gln Ser Thr Glu Pro Gln Lys Pro Ser Pro Lys Lys Thr Val Asp Thr
    130                 135                 140

Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp
145                 150                 155                 160

Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu
                165                 170                 175

Gly Gln Ser Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys
            180                 185                 190

Glu Asp Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp
        195                 200                 205
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Gly Pro Thr Thr Thr Thr Asn Phe Pro Ile Ser Asn Tyr Glu Lys Glu
    210                 215                 220

Leu Glu Glu Met Lys Asn Met Thr Arg Gln Glu Phe Val Ala Ser Leu
225                 230                 235                 240

Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly
                245                 250                 255

Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg
            260                 265                 270

Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu
        275                 280                 285

Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu
    290                 295                 300

Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser Ile
305                 310                 315                 320

Ala Asn Ser Thr Leu Pro Ile Gly Gly Leu Ser Gly Lys Asn Lys Asn
                325                 330                 335

Ser Thr Asp Ser Ala Ser Glu Ser Lys Ser His Glu Pro Ser Gln Ser
            340                 345                 350

Asp Gly Asp Pro Ser Ser Ala Ser Ser Val Thr Phe Ala Ser Gln Gln
        355                 360                 365

Gln Pro Ser Ser Ser Asn Leu Ser Phe Ala Ile Pro Ile Lys Gln Asp
    370                 375                 380

Pro Ser Asp Tyr Trp Ser Ile Leu Gly Tyr His Asn Thr Pro Leu Asp
385                 390                 395                 400

Asn Ser Gly Ile Arg Asn Thr Thr Ser Thr Val Thr Thr Thr Thr Phe
                405                 410                 415

Pro Ser Ser Asn Asn Gly Thr Ala Ser Ser Leu Thr Pro Phe Asn Met
            420                 425                 430

Glu Phe Ser Ser Ala Pro Ser Ser Thr Gly Ser Asp Asn Asn Ala Ala
        435                 440                 445

Phe Phe Ser Gly Gly Gly Ile Phe Val Gln Gln Gln Thr Ser His Gly
    450                 455                 460

His Gly Asn Ala Ser Ser Gly Ser Ser Ser Ser Ser Leu Ser Cys Ser
465                 470                 475                 480

Ile Pro Phe Ala Thr Pro Ile Phe Ser Leu Asn Ser Asn Thr Ser Tyr
                485                 490                 495

Glu Ser Ser Ala Gly Tyr Gly Asn Trp Ile Gly Pro Thr Leu His Thr
            500                 505                 510

Phe Gln Ser His Ala Lys Pro Ser Leu Phe Gln Thr Pro Ile Phe Gly
        515                 520                 525

Met Glu
    530


<210> SEQ ID NO 71
<211> LENGTH: 528
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 71

Met Asp Ser Cys Ser Ser Pro Pro Asn Asn Asn Ser Leu Ala Phe Ser
1               5                   10                  15

Leu Ser Asn His Phe Pro Asn Pro Ser Ser Ser Pro Leu Ser Leu Phe
            20                  25                  30
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His Ser Phe Thr Tyr Pro Ser Leu Ser Leu Thr Gly Ser His Thr Ala
        35                  40                  45

Asp Ala Pro Pro Glu Pro Ile Ala Gly Gly Gly Ala Thr Asn Leu Ser
    50                  55                  60

Ile Phe Thr Gly Ala Pro Lys Phe Glu Asp Phe Leu Gly Gly Ser Ser
65                  70                  75                  80

Ala Thr Ala Thr Ala Thr Thr Cys Ala Pro Pro Gln Leu Pro Gln Phe
                85                  90                  95

Ser Thr Asp Asn Asn Asn His Leu Tyr Asp Ser Glu Leu Lys Thr Thr
            100                 105                 110

Ile Ala Ala Cys Phe Pro Arg Ala Phe Ala Ala Glu Pro Thr Thr Glu
        115                 120                 125

Pro Gln Lys Pro Ser Pro Lys Lys Thr Val Asp Thr Phe Gly Gln Arg
    130                 135                 140

Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr
145                 150                 155                 160

Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Ser Arg
                165                 170                 175

Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Asp Lys Ala
            180                 185                 190

Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Thr Thr
        195                 200                 205

Thr Thr Asn Phe Pro Ile Ser Asn Tyr Glu Lys Glu Leu Glu Glu Met
    210                 215                 220

Lys Asn Met Thr Arg Gln Glu Phe Val Ala Ser Leu Arg Arg Lys Ser
225                 230                 235                 240

Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His
                245                 250                 255

His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn
            260                 265                 270

Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu
        275                 280                 285

Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr
    290                 295                 300

Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser Ile Ala Asn Ser Thr
305                 310                 315                 320

Leu Pro Ile Gly Gly Leu Ser Gly Lys Asn Lys Asn Ser Thr Asp Ser
                325                 330                 335

Ala Ser Glu Ser Lys Ser His Glu Ala Ser Arg Ser Asp Glu Arg Asp
            340                 345                 350

Pro Ser Ala Ala Ser Ser Val Thr Phe Ala Ser Gln Gln Gln Pro Ser
        355                 360                 365

Ser Ser Thr Leu Ser Phe Ala Ile Pro Ile Lys Gln Asp Pro Ser Asp
    370                 375                 380

Tyr Trp Ser Ile Leu Gly Tyr His Asn Ser Pro Leu Asp Asn Thr Gly
385                 390                 395                 400

Ile Arg Asn Thr Thr Ser Val Thr Ala Thr Ser Phe Pro Ser Ser Asn
                405                 410                 415

Asn Gly Thr Thr Ser Ser Leu Thr Pro Phe His Met Glu Phe Ser Asn
            420                 425                 430
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Ala Pro Thr Ser Thr Gly Ser Asp Asn Asp Ala Ala Phe Phe Ser Gly
        435                 440                 445

Gly Gly Ile Phe Val Gln Gln Gln Ser Gly His Gly Asn Gly His Gly
    450                 455                 460

Ser Gly Ser Ser Gly Ser Ser Ser Ser Ser Leu Ser Cys Ser Ile Pro
465                 470                 475                 480

Phe Ala Thr Pro Ile Phe Ser Leu Asn Ser Asn Thr Ser Tyr Glu Asn
                485                 490                 495

Ser Ala Gly Tyr Gly Asn Trp Ile Gly Pro Thr Leu His Thr Phe Gln
            500                 505                 510

Ser His Ala Lys Pro Ser Leu Phe Gln Thr Pro Ile Phe Gly Met Glu
        515                 520                 525


<210> SEQ ID NO 72
<211> LENGTH: 488
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 72

Met Asp Met Asp Met Ser Ser Ala Tyr Pro His His Trp Leu Ser Phe
1               5                   10                  15

Ser Leu Ser Asn Asn Tyr His His Gly Leu Leu Glu Ala Phe Ser Asn
            20                  25                  30

Ser Ser Gly Thr Pro Leu Gly Asp Glu Gln Gly Ala Val Glu Glu Ser
        35                  40                  45

Pro Arg Thr Val Glu Asp Phe Leu Gly Gly Val Gly Gly Ala Gly Ala
    50                  55                  60

Pro Pro Gln Pro Ala Ala Ala Ala Asp Gln Asp His Gln Leu Val Cys
65                  70                  75                  80

Gly Glu Leu Gly Ser Ile Thr Ala Arg Phe Leu Arg His Tyr Pro Ala
                85                  90                  95

Ala Pro Ala Gly Thr Thr Val Glu Asn Pro Gly Ala Val Thr Val Ala
            100                 105                 110

Ala Met Ser Ser Thr Asp Val Ala Gly Ala Glu Ser Asp Gln Ala Arg
        115                 120                 125

Arg Pro Ala Glu Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val
    130                 135                 140

Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn
145                 150                 155                 160

Ser Cys Arg Arg Glu Gly Gln Ser Arg Lys Gly Arg Gln Val Tyr Leu
                165                 170                 175

Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala
            180                 185                 190

Ala Leu Lys Tyr Trp Gly Pro Thr Thr Thr Thr Asn Phe Pro Val Ser
        195                 200                 205

Asn Tyr Glu Lys Glu Leu Glu Glu Met Lys Ser Met Thr Arg Gln Glu
    210                 215                 220

Phe Ile Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala
225                 230                 235                 240

Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln
                245                 250                 255

Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr
            260                 265                 270
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Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile
275 280 285

Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr
290 295 300

Asp Val Glu Ser Ile Leu Ser Ser Asp Leu Pro Val Gly Gly Gly Ala
305 310 315 320

Ser Gly Arg Ala Pro Ala Lys Phe Pro Leu Asp Ser Leu Gln Pro Gly
325 330 335

Ser Ala Ala Ala Met Met Leu Ala Gly Ala Ala Ala Ala Ser Gln Ala
340 345 350

Thr Met Pro Pro Ser Glu Lys Asp Tyr Trp Ser Leu Leu Ala Leu His
355 360 365

Tyr Gln Gln Gln Gln Glu Gln Glu Arg Gln Phe Pro Ala Ser Ala Tyr
370 375 380

Glu Ala Tyr Gly Ser Gly Gly Val Asn Val Asp Phe Thr Met Gly Thr
385 390 395 400

Ser Ser Gly Asn Asn Asn Asn Asn Thr Gly Ser Gly Val Met Trp Gly
405 410 415

Ala Thr Thr Gly Ala Val Val Val Gly Gln Gln Asp Ser Ser Gly Lys
420 425 430

Gln Gly Asn Gly Tyr Ala Ser Asn Ile Pro Tyr Ala Ala Ala Ala Met
435 440 445

Val Ser Gly Ser Ala Gly Tyr Glu Gly Ser Thr Gly Asp Asn Gly Thr
450 455 460

Trp Val Thr Thr Thr Thr Ser Ser Asn Thr Gly Thr Ala Pro His Tyr
465 470 475 480

Tyr Asn Tyr Leu Phe Gly Met Glu
485

<210> SEQ ID NO 73
<211> LENGTH: 495
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 73

Met Asp Met Asp Thr Ser His His Tyr Pro Trp Leu Asn Phe Ser Leu
1 5 10 15

Ala His His Cys Glu Met Glu Glu Glu Glu Arg Gly Ala Ala Ala Glu
20 25 30

Leu Ala Ala Ile Ala Gly Ala Ala Pro Pro Pro Lys Leu Glu Asp Phe
35 40 45

Leu Gly Gly Gly Cys Asn Gly Gly Ser Ser Gly Gly Ala Cys Pro Pro
50 55 60

Val Gln Thr Thr Ala Pro Thr Ala Ala Glu Leu Tyr Glu Ser Glu Leu
65 70 75 80

Lys Phe Leu Ala Ala Gly Phe Gln Leu Ser Gly Ala Ala Gly Ala Ala
85 90 95

Pro Pro Val Pro Ala Leu Leu Pro Ala Ala Ala Leu Glu Gln Thr Asp
100 105 110

Glu Thr Lys Gln Leu Ala Leu Pro Pro Gln Ala Ala Val Ala Pro Pro
115 120 125

Pro Glu Gln Lys Lys Ala Val Asp Ser Phe Gly Gln Arg Thr Ser Ile

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    130                 135                 140

Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His
145                 150                 155                 160

Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Ser Arg Lys Gly Arg
                165                 170                 175

Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala
            180                 185                 190

Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Ser Thr Thr Thr Asn
        195                 200                 205

Phe Pro Val Ala Glu Tyr Glu Lys Glu Leu Glu Glu Met Lys His Met
    210                 215                 220

Thr Arg Gln Glu Phe Val Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe
225                 230                 235                 240

Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His
                245                 250                 255

Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu
            260                 265                 270

Tyr Leu Gly Thr Phe Gly Thr Glu Glu Glu Ala Ala Glu Ala Tyr Asp
        275                 280                 285

Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Glu
    290                 295                 300

Ile Gly Arg Tyr Asn Val Glu Ser Ile Ile Ser Ser Asn Leu Pro Ile
305                 310                 315                 320

Gly Ser Met Ala Gly Asn Arg Ser Thr Lys Ala Gly Leu Glu Leu Ala
                325                 330                 335

Pro Ser Ser Ser Ala Asp Ala Ile Ala Ala Thr Glu Ala Asn His Thr
            340                 345                 350

Gly Val Ala Pro Pro Ser Thr Leu Ala Phe Thr Ala Leu Pro Met Lys
        355                 360                 365

Tyr Asp Gln Ala Asp Tyr Leu Ser Tyr Leu Ala Leu Gln His His Gln
    370                 375                 380

Gln Gly Asn Leu Gln Gly Leu Gly Phe Gly Leu Tyr Ser Ser Gly Val
385                 390                 395                 400

Asn Leu Asp Phe Ala Asn Ala Asn Gly Asn Gly Ala Met Ser Asn Cys
                405                 410                 415

Tyr Thr Asn Val Ser Leu His Glu Gln Gln Gln Gln His Gln His Gln
            420                 425                 430

His Gln Gln Glu Gln Gln Gln Asp Gln Gln Asp Asp Gln Ser Gln Ser
        435                 440                 445

Ser Asn Asn Ser Cys Gly Ser Ile Pro Phe Ala Thr Pro Ile Ala Phe
    450                 455                 460

Ser Gly Ser Tyr Glu Ser Ser Met Thr Ala Ala Gly Thr Phe Gly Tyr
465                 470                 475                 480

Tyr Pro Asn Val Ala Ala Phe Gln Thr Pro Ile Phe Gly Met Glu
                485                 490                 495
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<210> SEQ ID NO 74
<211> LENGTH: 558
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 74

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Met Lys Asn Asn Asn Asn Lys Ser Ser Ser Ser Ser Ser Tyr Asp Ser
1               5                   10                  15

Ser Leu Ser Pro Ser Ser Ser Ser Ser Ser His Gln Asn Trp Leu Ser
            20                  25                  30

Phe Ser Leu Ser Asn Asn Asn Asn Asn Phe Asn Ser Ser Ser Asn Pro
        35                  40                  45

Asn Leu Thr Ser Ser Thr Ser Asp His His His Pro His Pro Ser His
    50                  55                  60

Leu Ser Leu Phe Gln Ala Phe Ser Thr Ser Pro Val Glu Arg Gln Asp
65                  70                  75                  80

Gly Ser Pro Gly Val Ser Pro Ser Asp Ala Thr Ala Val Leu Ser Val
                85                  90                  95

Tyr Pro Gly Gly Pro Lys Leu Glu Asn Phe Leu Gly Gly Gly Ala Ser
            100                 105                 110

Thr Thr Thr Thr Arg Pro Met Gln Gln Val Gln Ser Leu Gly Gly Val
        115                 120                 125

Val Phe Ser Ser Asp Leu Gln Pro Pro Leu His Pro Pro Ser Ala Ala
    130                 135                 140

Glu Ile Tyr Asp Ser Glu Leu Lys Ser Ile Ala Ala Ser Phe Leu Gly
145                 150                 155                 160

Asn Tyr Ser Gly Gly His Ser Ser Glu Val Ser Ser Val His Lys Gln
                165                 170                 175

Gln Pro Asn Pro Leu Ala Val Ser Glu Ala Ser Pro Thr Pro Lys Lys
            180                 185                 190

Asn Val Glu Ser Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr
        195                 200                 205

Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser
    210                 215                 220

Cys Arg Arg Glu Gly Gln Ser Arg Lys Gly Arg Gln Val Tyr Leu Gly
225                 230                 235                 240

Gly Tyr Asp Lys Glu Asp Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala
                245                 250                 255

Leu Lys Tyr Trp Gly Pro Thr Thr Thr Thr Asn Phe Pro Ile Ser Asn
            260                 265                 270

Tyr Glu Ser Glu Leu Glu Glu Met Lys His Met Thr Arg Gln Glu Phe
        275                 280                 285

Val Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser
    290                 295                 300

Met Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala
305                 310                 315                 320

Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe
                325                 330                 335

Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys
            340                 345                 350

Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Ile Ser Arg Tyr Asp
        355                 360                 365

Val Lys Ser Ile Ala Ser Cys Asn Leu Pro Val Gly Gly Leu Met Pro
    370                 375                 380

Lys Pro Ser Pro Ala Thr Ala Ala Ala Asp Lys Thr Val Asp Leu Ser
385                 390                 395                 400

Pro Ser Asp Ser Pro Ser Leu Thr Thr Pro Ser Leu Thr Phe Asn Val
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                405                 410                 415

Ala Thr Pro Val Asn Asp His Gly Gly Thr Phe Tyr His Thr Gly Ile
            420                 425                 430

Pro Ile Lys Pro Asp Pro Ala Asp His Tyr Trp Ser Asn Ile Phe Gly
        435                 440                 445

Phe Gln Ala Asn Pro Lys Ala Glu Met Arg Pro Leu Ala Asn Phe Gly
    450                 455                 460

Ser Asp Leu His Asn Pro Ser Pro Gly Tyr Ala Ile Met Pro Val Met
465                 470                 475                 480

Gln Glu Gly Glu Asn Asn Phe Gly Gly Ser Phe Val Gly Ser Asp Gly
                485                 490                 495

Tyr Asn Asn His Ser Ala Ala Ser Asn Pro Val Ser Ala Ile Pro Leu
            500                 505                 510

Ser Ser Thr Thr Thr Met Ser Asn Gly Asn Glu Gly Tyr Gly Gly Asn
        515                 520                 525

Ile Asn Trp Ile Asn Asn Asn Ile Ser Ser Ser Tyr Gln Thr Ala Lys
    530                 535                 540

Ser Asn Leu Ser Val Leu His Thr Pro Val Phe Gly Leu Glu
545                 550                 555


<210> SEQ ID NO 75
<211> LENGTH: 568
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 75

Met Asn Ser Asn Asn Trp Leu Ala Phe Pro Leu Ser Pro Thr His Ser
1               5                   10                  15

Ser Leu Pro Pro His Ile His Ser Ser Gln Asn Ser His Phe Asn Leu
            20                  25                  30

Gly Leu Val Asn Asp Asn Ile Asp Asn Pro Phe Gln Asn Gln Gly Trp
        35                  40                  45

Asn Met Ile Asn Pro His Gly Gly Gly Gly Glu Gly Gly Glu Val Pro
    50                  55                  60

Lys Val Ala Asp Phe Leu Gly Val Ser Lys Ser Gly Asp His His Thr
65                  70                  75                  80

Asp His Asn Leu Val Pro Tyr Asn Asp Ile His Gln Thr Asn Ala Ser
                85                  90                  95

Asp Tyr Tyr Phe Gln Thr Asn Ser Leu Leu Pro Thr Val Val Thr Cys
            100                 105                 110

Ala Ser Asn Ala Pro Asn Asn Tyr Glu Leu Gln Glu Ser Ala His Asn
        115                 120                 125

Leu Gln Ser Leu Thr Leu Ser Met Gly Ser Thr Gly Ala Ala Ala Ala
    130                 135                 140

Glu Val Ala Thr Val Lys Ala Ser Pro Ala Glu Thr Ser Ala Asp Asn
145                 150                 155                 160

Ser Ser Ser Thr Thr Asn Thr Ser Gly Gly Ala Ile Val Glu Ala Thr
                165                 170                 175

Pro Arg Arg Thr Leu Glu Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg
            180                 185                 190

Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp
        195                 200                 205
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Asp Asn Ser Cys Arg Arg Glu Gly Gln Ser Arg Lys Gly Arg Gln Val
    210                 215                 220

Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp
225                 230                 235                 240

Leu Ala Ala Leu Lys Tyr Trp Gly Pro Ser Thr Thr Thr Asn Phe Pro
                245                 250                 255

Ile Thr Asn Tyr Glu Lys Glu Val Glu Glu Met Lys Asn Met Thr Arg
            260                 265                 270

Gln Glu Phe Val Ala Ser Ile Arg Arg Lys Ser Ser Gly Phe Ser Arg
        275                 280                 285

Gly Ala Ser Met Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg
    290                 295                 300

Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu
305                 310                 315                 320

Gly Thr Phe Ser Thr Glu Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala
                325                 330                 335

Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Glu Ile Asn
            340                 345                 350

Arg Tyr Asp Val Lys Ala Ile Leu Glu Ser Asn Thr Leu Pro Ile Gly
        355                 360                 365

Gly Gly Ala Ala Lys Arg Leu Lys Glu Ala Gln Ala Leu Glu Ser Ser
    370                 375                 380

Arg Lys Arg Glu Glu Met Ile Ala Leu Gly Ser Asn Phe His Gln Tyr
385                 390                 395                 400

Gly Ala Ala Ser Gly Ser Ser Ser Val Ala Ser Ser Ser Arg Leu Gln
                405                 410                 415

Leu Gln Pro Tyr Pro Leu Ser Ile Gln Gln Pro Phe Glu His Leu His
            420                 425                 430

His His Gln Pro Leu Leu Thr Leu Gln Asn Asn Asn Asp Ile Ser Gln
        435                 440                 445

Tyr His Asp Ser Phe Ser Tyr Ile Gln Thr Gln Leu His Leu His Gln
    450                 455                 460

Gln Gln Thr Asn Asn Tyr Leu Gln Ser Ser Ser His Thr Ser Gln Leu
465                 470                 475                 480

Tyr Asn Ala Tyr Leu Gln Ser Asn Pro Gly Leu Leu His Gly Phe Val
                485                 490                 495

Ser Asp Asn Asn Asn Thr Ser Gly Phe Leu Gly Asn Asn Gly Ile Gly
            500                 505                 510

Ile Gly Ser Ser Ser Thr Val Gly Ser Ser Ala Glu Glu Glu Phe Pro
        515                 520                 525

Ala Val Lys Val Asp Tyr Asp Met Pro Pro Ser Gly Gly Ala Thr Gly
    530                 535                 540

Tyr Gly Gly Trp Asn Ser Gly Glu Ser Ala Gln Gly Ser Asn Pro Gly
545                 550                 555                 560

Gly Val Phe Thr Met Trp Asn Glu
                565


<210> SEQ ID NO 76
<211> LENGTH: 474
<212> TYPE: PRT
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 76
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Met Asp Met Asp Met Ser Ser Ala Tyr Pro His His Trp Leu Ser Phe
1               5                   10                  15

Ser Leu Ser Asn Asn Tyr His His Gly Leu Leu Glu Ala Phe Ser Asn
            20                  25                  30

Ser Ser Ser Ala Ala Pro Leu Gly Asp Glu Gln Gly Thr Val Glu Glu
        35                  40                  45

Ser Pro Lys Met Val Glu Asp Phe Leu Gly Gly Val Gly Gly Ala Gly
    50                  55                  60

Ala Pro Pro Ala Ala Ala Thr Ala Ala Glu Asp His Gln Leu Val Cys
65                  70                  75                  80

Gly Glu Leu Gly Ser Ile Thr Ala Gly Phe Leu Arg His Tyr Pro Ala
                85                  90                  95

Pro Gly Thr Thr Val Glu Asn Pro Gly Ala Val Thr Val Ala Ala Met
            100                 105                 110

Ser Thr Asp Val Ala Glu Ser Asp Gln Ala Arg Arg Pro Ala Glu Thr
        115                 120                 125

Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp
    130                 135                 140

Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu
145                 150                 155                 160

Gly Gln Ser Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys
                165                 170                 175

Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp
            180                 185                 190

Gly Ala Thr Thr Thr Thr Asn Phe Pro Val Ser Asn Tyr Glu Lys Glu
        195                 200                 205

Leu Glu Glu Met Lys Ser Met Thr Arg Gln Glu Phe Ile Ala Ser Leu
    210                 215                 220

Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly
225                 230                 235                 240

Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg
                245                 250                 255

Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu
            260                 265                 270

Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu
        275                 280                 285

Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Asp Ser Ile
    290                 295                 300

Leu Asn Ser Asp Leu Pro Val Gly Gly Gly Ala Ala Gly Arg Ala Ser
305                 310                 315                 320

Lys Phe Pro Leu Asp Ser Leu Gln Pro Gly Ser Ala Ala Ala Met Ile
                325                 330                 335

Ala Gly Ala Ala Ser Gln Ala Met Pro Pro Ser Glu Lys Asp Tyr Trp
            340                 345                 350

Ser Leu Leu Ala Leu His Tyr Gln Gln Gln Gln Gln Gln Gln Gln Phe
        355                 360                 365

Pro Ala Ser Ala Tyr Glu Ala Tyr Gly Ser Gly Val Asn Val Asp Phe
    370                 375                 380

Thr Met Gly Thr Ser Ser His Ser Ser Ser Asn Thr Gly Ser Gly Val
385                 390                 395                 400
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```
Met Trp Gly Thr Thr Thr Gly Ala Met Gly Gln Gln Asp Ser Ser Ser
                405                 410                 415

Ser Lys Gln Gly Asn Gly Tyr Ala Ser Asn Ile Pro Tyr Ala Ala Ala
            420                 425                 430

Ala Ala Ala Met Val Ser Gly Ser Ala Gly Tyr Glu Gly Ser Thr Gly
        435                 440                 445

Asn Asn Gly Thr Trp Val Thr Ser Ser Thr Ser Thr Ser Thr Ala Pro
    450                 455                 460

Gln Tyr Tyr Asn Tyr Leu Phe Gly Met Glu
465                 470


<210> SEQ ID NO 77
<211> LENGTH: 549
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 77

Met Asp Met Asn Ser Gly Trp Leu Gly Phe Ser Leu Ser Ser Ser Ser
1               5                   10                  15

Ala Arg Gly Tyr Gly Asp Gly Cys Gly Glu Gly Asn Gly Gly Gly Asp
            20                  25                  30

Gly Asp Gly Ser Cys Ser Ser Pro Val Ala Ala Ser Pro Leu Val Ala
        35                  40                  45

Met Pro Leu His Ser Asp Gly Ser Val His Tyr Asp Ala Pro Asp Trp
    50                  55                  60

Arg His Ala Glu Ala Lys Asp Pro Lys Leu Glu Asp Phe Met Ser Val
65                  70                  75                  80

Ser Tyr Ser Asn Lys Ser Ser Ser Asn Leu Tyr Gly Ser Ser Ser Ser
                85                  90                  95

Ser Ser Cys Gly His Ala Asp Gln Ile Lys Tyr His His Val His Asp
            100                 105                 110

Val Gln Ala Phe Ser Thr Pro Tyr Phe Tyr Gly His Gly Gly Ser Gly
        115                 120                 125

Val Gly Ile Asp Ile Asn Met Asn Ala Pro Pro Ala Gly Cys Thr Gly
    130                 135                 140

Val Leu Pro Asp His Arg Pro Pro Pro Pro Gln Gln Asp His Ile Phe
145                 150                 155                 160

Leu Pro Pro His Gly Gln Tyr Phe Leu Gly Pro Pro Asn Pro Met Ala
                165                 170                 175

Pro Ala Pro Met Tyr Asn Ala Gly Gly Gly Gly Gly Gly Val Val Asp
            180                 185                 190

Gly Ser Met Ser Ile Ser Gly Ile Lys Ser Trp Leu Arg Gln Ala Met
        195                 200                 205

Tyr Val Pro Glu Arg Ser Ala Ala Ala Leu Ser Leu Ser Val Pro Ala
    210                 215                 220

Ala Pro Pro Ser Glu Ala Pro Leu Pro Pro Ala Ala Met Pro Val Val
225                 230                 235                 240

Arg Lys Pro Ala Gln Thr Phe Gly Gln Arg Thr Ser Gln Phe Arg Gly
                245                 250                 255

Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp
            260                 265                 270

Asn Thr Cys Arg Lys Glu Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr
        275                 280                 285
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Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu
    290                 295                 300

Ala Ala Leu Lys Tyr Trp Gly Pro Thr Thr His Ile Asn Phe Pro Leu
305                 310                 315                 320

Ser Thr Tyr Glu Lys Glu Leu Glu Glu Met Lys His Met Thr Arg Gln
                325                 330                 335

Glu Phe Ile Ala His Leu Arg Arg Asn Ser Ser Gly Phe Ser Arg Gly
            340                 345                 350

Ala Ser Met Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp
        355                 360                 365

Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly
    370                 375                 380

Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala
385                 390                 395                 400

Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Ile Ser Lys
                405                 410                 415

Tyr Asp Val Lys Arg Ile Cys Ser Ser Thr His Leu Ile Gly Gly Asp
            420                 425                 430

Leu Ala Cys Arg Arg Ser Pro Thr Arg Met Leu Pro Pro Asp Ala Pro
        435                 440                 445

Ala Gly Ala Ala Gly Val Asp Val Val Val Ala Pro Gly Asp His Gln
    450                 455                 460

Gln Ile Ser Ala Gly Gly Gly Gly Ala Ser Asp Asn Ser Asp Thr Ala
465                 470                 475                 480

Ser Asp Gly His Arg Gly Ala His Leu Leu His Gly Leu Gln Tyr Ala
                485                 490                 495

His Ala Met Lys Phe Glu Ala Gly Glu Ser Ser Gly Gly Gly Gly Gly
            500                 505                 510

Asp Gly Ala Thr Thr Asn Trp Met Ala Ala Ala Ala Ala Ala Ala Arg
        515                 520                 525

Pro Val Ala Gly Ile Pro Thr Thr Val His His Gln Leu Pro Val Phe
    530                 535                 540

Ala Leu Trp Asn Asp
545


<210> SEQ ID NO 78
<211> LENGTH: 553
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 78

Met Asn Asn Asn Trp Leu Ser Phe Pro Leu Ser Pro Thr His Ser Ser
1               5                   10                  15

Leu Pro Ala His Asp Leu Gln Ala Thr Gln Tyr His Gln Phe Ser Leu
            20                  25                  30

Gly Leu Val Asn Glu Asn Met Asp Asn Pro Phe Gln Asn His Asp Trp
        35                  40                  45

Asn Leu Ile Asn Thr His Ser Ser Asn Glu Ile Pro Lys Val Ala Asp
    50                  55                  60

Phe Leu Gly Val Ser Lys Ser Glu Asn Gln Ser Asp Leu Ala Ala Leu
65                  70                  75                  80

Asn Glu Ile His Ser Asn Asp Ser Asp Tyr Leu Phe Thr Asn Asn Ser
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                85                  90                  95

Leu Val Pro Met Gln Asn Pro Val Leu Asp Thr Pro Ser Asn Glu Tyr
            100                 105                 110

Gln Glu Asn Ala Asn Ser Asn Leu Gln Ser Leu Thr Leu Ser Met Gly
        115                 120                 125

Ser Gly Lys Asp Ser Thr Cys Glu Thr Ser Gly Glu Asn Ser Thr Asn
    130                 135                 140

Thr Thr Val Glu Val Ala Pro Arg Arg Thr Leu Asp Thr Phe Gly Gln
145                 150                 155                 160

Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg
                165                 170                 175

Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Ser
            180                 185                 190

Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys
        195                 200                 205

Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Ser
    210                 215                 220

Thr Thr Thr Asn Phe Pro Ile Ser Asn Tyr Glu Lys Glu Leu Asp Glu
225                 230                 235                 240

Met Lys His Met Thr Arg Gln Glu Phe Val Ala Ala Ile Arg Arg Lys
                245                 250                 255

Ser Ser Gly Phe Ser Arg Gly Ala Ser Met Tyr Arg Gly Val Thr Arg
            260                 265                 270

His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly
        275                 280                 285

Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Glu Glu Glu Ala Ala
    290                 295                 300

Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val
305                 310                 315                 320

Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ala Ile Leu Glu Ser
                325                 330                 335

Asn Thr Leu Pro Ile Gly Gly Gly Ala Ala Lys Arg Leu Lys Glu Ala
            340                 345                 350

Gln Ala Leu Glu Ser Ser Arg Lys Arg Glu Glu Met Ile Ala Leu Gly
        355                 360                 365

Ser Ser Ser Thr Phe Gln Tyr Gly Thr Ser Ala Ser Ser Ser Arg Leu
    370                 375                 380

His Ala Tyr Pro Leu Met Gln His His His Gln Phe Glu Gln Pro Gln
385                 390                 395                 400

Pro Leu Leu Thr Leu Gln Asn His Asp Ile Ser Ser Ser His Phe Ser
                405                 410                 415

His Gln Gln Asp Pro Leu His His Gln Gly Tyr Ile Gln Thr Gln Leu
            420                 425                 430

Gln Leu His Gln Gln Ser Gly Ala Ser Ser Tyr Ser Phe Gln Asn Asn
        435                 440                 445

Ala Gln Phe Tyr Asn Gly Tyr Leu Gln Asn His Pro Ala Leu Leu Gln
    450                 455                 460

Gly Met Met Asn Met Gly Ser Ser Ser Ser Ser Ser Ser Val Leu Glu
465                 470                 475                 480

Asn Asn Asn Ser Asn Asn Asn Asn Asn Asn Val Gly Gly Phe Val Gly
                485                 490                 495
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Ser Gly Phe Gly Met Ala Ser Asn Ala Thr Ala Gly Asn Thr Val Gly
            500                 505                 510

Thr Ala Glu Glu Leu Gly Leu Val Lys Val Asp Tyr Asp Met Pro Ala
        515                 520                 525

Gly Gly Tyr Gly Gly Trp Ser Ala Ala Asp Ser Met Gln Thr Ser Asn
    530                 535                 540

Gly Gly Val Phe Thr Met Trp Asn Asp
545                 550


<210> SEQ ID NO 79
<211> LENGTH: 509
<212> TYPE: PRT
<213> ORGANISM: Medicago truncatula

<400> SEQUENCE: 79

Met Asp Lys Ser Ser Ser Ser Pro Pro Thr Asn Thr Asn Asn Thr Ser
1               5                   10                  15

Leu Ala Phe Ser Leu Ser Asn Asn Asn Phe Pro Asn Pro Ser His Ser
            20                  25                  30

Ser Ser Ser His Leu Ser Leu Phe His Ser Phe Thr Pro Tyr Pro Ser
        35                  40                  45

Ser Ile Ile Pro Pro Ser Leu Thr Leu Thr Gly Ser Asn Asn Pro Val
    50                  55                  60

Glu Ala Ser Pro Glu Ala Thr Asp Gly Gly Thr Thr Asn Leu Ser Ile
65                  70                  75                  80

Phe Thr Gly Gly His Lys Phe Glu Asp Phe Leu Gly Ser Ser Val Ala
                85                  90                  95

Pro Thr Arg Thr Ala Ala Ala Thr Cys Ala Pro Thr Gln Leu Gln Gln
            100                 105                 110

Phe Ser Thr Asp Asn Asp Val Tyr Asn Ser Glu Leu Lys Lys Thr Ile
        115                 120                 125

Ala Ala Cys Phe Pro Gly Gly Tyr Pro Thr Glu Pro Asn Ser Glu Pro
    130                 135                 140

Gln Lys Pro Ser Pro Lys Lys Thr Val Asp Thr Phe Gly Gln Arg Thr
145                 150                 155                 160

Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
                165                 170                 175

Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Ser Arg Lys
            180                 185                 190

Gly Arg Gln Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala Tyr
        195                 200                 205

Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Thr Thr Thr Thr Asn Phe
    210                 215                 220

Pro Ile Ser Asn Tyr Glu Lys Glu Ile Asp Asp Met Lys Asn Met Thr
225                 230                 235                 240

Arg Gln Glu Phe Val Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser
                245                 250                 255

Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly
            260                 265                 270

Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr
        275                 280                 285

Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Ile
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    290                 295                 300

Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Met
305                 310                 315                 320

Ser Arg Tyr Asp Val Lys Ser Ile Ala Asn Cys Ser Leu Pro Ile Gly
                325                 330                 335

Gly Leu Ser Asn Lys Asn Asn Lys Asn Ser Thr Asp Cys Val Ser Glu
            340                 345                 350

Thr Lys Ile Asn Glu Pro Ile Gln Ser Asp Glu Ile Asp His Pro Ser
        355                 360                 365

Ser Thr Ser Ser Ala Thr Thr Leu Ser Phe Ala Leu Pro Ile Lys Gln
    370                 375                 380

Asp Pro Ser Thr Asp Tyr Trp Ser Asn Ile Leu Gly Phe His Asn Asn
385                 390                 395                 400

Pro Ser Ala Val Thr Thr Thr Thr Ile Pro Phe Asn Met Asp Phe Ser
                405                 410                 415

Ala His Val Pro Ser Asn Thr Asn Ser Asp Asn Pro His Asn Ala Ala
            420                 425                 430

Phe Phe Ser Gly Ser Gly Ile Phe Val Gln Gln Gln Asn Met Asn Gly
        435                 440                 445

Ser Ser Gly Ser Asn Ser Ser Ser Ser Ser Ser Ala Ser Thr Ser Ser
    450                 455                 460

Ile Pro Phe Ala Thr Pro Ile Phe Ser Leu Asn Ser Asn Ser Ser Ser
465                 470                 475                 480

Tyr Gly Asn Gly Asn Asn Trp Ile Gly His Thr Phe Gln Thr His Ala
                485                 490                 495

Lys Pro Ser Leu Phe Gln Thr Pro Ile Phe Gly Met Glu
            500                 505
```

<210> SEQ ID NO 80
<211> LENGTH: 492
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 80

```
Met Asp Thr Ser His His Tyr His Pro Trp Leu Asn Phe Ser Leu Ala
1               5                   10                  15

His His Cys Asp Leu Glu Glu Glu Glu Arg Gly Ala Ala Ala Glu Leu
            20                  25                  30

Ala Ala Ile Ala Gly Ala Ala Pro Pro Pro Lys Leu Glu Asp Phe Leu
        35                  40                  45

Gly Gly Gly Val Ala Thr Gly Gly Pro Glu Ala Val Ala Pro Ala Glu
    50                  55                  60

Met Tyr Asp Ser Asp Leu Lys Phe Ile Ala Ala Ala Gly Phe Leu Gly
65                  70                  75                  80

Gly Ser Ala Ala Ala Ala Ala Thr Ser Pro Leu Ser Ser Leu Asp Gln
                85                  90                  95

Ala Gly Ser Lys Leu Ala Leu Pro Ala Ala Ala Ala Ala Pro Ala Pro
            100                 105                 110

Glu Gln Arg Lys Ala Val Asp Ser Phe Gly Gln Arg Thr Ser Ile Tyr
        115                 120                 125

Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu
    130                 135                 140
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Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Ser Arg Lys Gly Arg Gln
145                 150                 155                 160

Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala Tyr
                165                 170                 175

Asp Leu Ala Ala Leu Lys Tyr Trp Gly Ser Ser Thr Thr Thr Asn Phe
            180                 185                 190

Pro Val Ala Glu Tyr Glu Lys Glu Val Glu Glu Met Lys Asn Met Thr
        195                 200                 205

Arg Gln Glu Phe Val Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser
    210                 215                 220

Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly
225                 230                 235                 240

Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr
                245                 250                 255

Leu Gly Thr Phe Ser Thr Glu Glu Glu Ala Ala Glu Ala Tyr Asp Ile
            260                 265                 270

Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Glu Ile
        275                 280                 285

Ser Arg Tyr Asn Val Glu Thr Ile Met Ser Ser Asn Leu Pro Val Ala
    290                 295                 300

Ser Met Ser Ser Ser Ala Ala Ala Ala Ala Gly Gly Arg Ser Ser Lys
305                 310                 315                 320

Ala Leu Glu Ser Pro Pro Ser Gly Ser Leu Asp Gly Gly Gly Gly Met
                325                 330                 335

Pro Val Val Glu Ala Ser Thr Ala Pro Pro Leu Phe Ile Pro Val Lys
            340                 345                 350

Tyr Asp Gln Gln Gln Gln Glu Tyr Leu Ser Met Leu Ala Leu Gln Gln
        355                 360                 365

His His Gln Gln Gln Gln Ala Gly Asn Leu Leu Gln Gly Pro Leu Val
    370                 375                 380

Gly Phe Gly Gly Leu Tyr Ser Ser Gly Val Asn Leu Asp Phe Ala Asn
385                 390                 395                 400

Ser His Gly Thr Ala Ala Pro Ser Ser Met Ala His His Cys Tyr Ala
                405                 410                 415

Asn Gly Thr Ala Ser Ala Ser His Glu His Gln His Gln Met Gln Gln
            420                 425                 430

Gly Gly Glu Asn Glu Thr Gln Pro Gln Pro Gln Gln Ser Ser Ser Ser
        435                 440                 445

Cys Ser Ser Leu Pro Phe Ala Thr Pro Val Ala Phe Asn Gly Ser Tyr
    450                 455                 460

Glu Ser Ser Ile Thr Ala Ala Gly Pro Phe Gly Tyr Ser Tyr Pro Asn
465                 470                 475                 480

Val Ala Ala Phe Gln Thr Pro Ile Tyr Gly Met Glu
                485                 490


<210> SEQ ID NO 81
<211> LENGTH: 469
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 81

Met Asp Met Asp Met Ser Ser Ala Tyr Pro His His Trp Leu Ser Phe
1               5                   10                  15
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```
Ser Leu Ser Asn Asn Tyr His His Gly Leu Leu Glu Ala Leu Ser Thr
            20                  25                  30

Thr Ser Ala Pro Pro Leu Gly Glu Glu Gly Pro Ala Glu Gly Ala Pro
    35                  40                  45

Lys Met Glu Asp Phe Leu Gly Gly Leu Gly Gly Gly Gly Gly Ala Val
    50                  55                  60

Ala Ala Ala Pro Ala Ala Ala Pro Glu Asp Gln Leu Ser Cys Gly Glu
65                  70                  75                  80

Leu Gly Ser Ile Ala Ala Gly Phe Leu Arg Arg Tyr Pro Ala Pro Glu
                85                  90                  95

Asn Ala Gly Gly Val Thr Ile Ala Met Ala Thr Asp Ala Ala Ala Glu
            100                 105                 110

Leu Ala Asp Pro Ala Arg Arg Thr Ala Glu Thr Phe Gly Gln Arg Thr
    115                 120                 125

Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
    130                 135                 140

Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Ser Arg Lys
145                 150                 155                 160

Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala
                165                 170                 175

Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Thr Thr Thr
            180                 185                 190

Thr Asn Phe Pro Val Ala Asn Tyr Glu Thr Glu Leu Glu Glu Met Lys
    195                 200                 205

Ser Met Thr Arg Gln Glu Phe Ile Ala Ser Leu Arg Arg Lys Ser Ser
    210                 215                 220

Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His
225                 230                 235                 240

Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys
                245                 250                 255

Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala
            260                 265                 270

Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn
    275                 280                 285

Phe Asp Met Ser Arg Tyr Asp Val Asp Ser Ile Leu Asn Ser Asp Leu
    290                 295                 300

Pro Val Gly Gly Gly Ala Ala Thr Arg Ala Ser Lys Phe Pro Ser Asp
305                 310                 315                 320

Pro Ser Leu Pro Leu Pro Ser Pro Ala Met Pro Pro Ser Glu Lys Asp
                325                 330                 335

Tyr Trp Ser Leu Leu Ala Leu His Tyr His His His Gln Gln Gln Gln
            340                 345                 350

Gln Gln Gln Gln Phe Pro Ala Ser Ala Phe Asp Thr Tyr Gly Cys Ser
    355                 360                 365

Ser Gly Val Asn Val Asp Phe Thr Met Gly Thr Ser Ser His Ser Gly
    370                 375                 380

Ser Asn Ser Asn Ser Ser Ser Ser Ser Ala Ile Trp Gly Thr Ala Ala
385                 390                 395                 400

Gly Ala Ala Met Gly Arg Gln Gln Asn Gly Gly Ser Ser Asn Lys Gln
                405                 410                 415
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```
Ser Asn Ser Tyr Ser Gly Asn Asn Ile Pro Tyr Ala Ala Ala Ala Ala
            420                 425                 430

Met Thr Ser Gly Ser Ala Leu Tyr Gly Gly Ser Thr Gly Ser Asn Gly
        435                 440                 445

Thr Trp Val Ala Ser Asn Thr Ser Thr Ala Pro His Phe Tyr Asn Tyr
    450                 455                 460

Leu Phe Gly Met Glu
465


<210> SEQ ID NO 82
<211> LENGTH: 562
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 82

Met Asn Asn Asn Trp Leu Ser Phe Pro Leu Ser Pro Thr His Ser Ser
1               5                   10                  15

Leu Pro Ala His Asp Leu Gln Ala Thr Gln Tyr His Gln Phe Ser Leu
            20                  25                  30

Gly Leu Val Asn Glu Asn Met Glu Asn Pro Phe Gln Asn His Asp Trp
        35                  40                  45

Ser Leu Ile Asn Thr His Ser Ser Ser Glu Val Pro Lys Val Ala Asp
    50                  55                  60

Phe Leu Gly Val Ser Lys Ser Glu Asn Glu Ser Asp Leu Ala Ala Ser
65                  70                  75                  80

Leu Asn Glu Ile Gln Ser Asn Asp Ser Asp Tyr Leu Phe Thr Asn Asn
                85                  90                  95

Ser Leu Val Pro Met Gln Asn Pro Ala Val Asp Thr Pro Ser Asn Glu
            100                 105                 110

Tyr Gln Glu Asn Ala Asn Ser Ser Leu Gln Ser Leu Thr Leu Ser Met
        115                 120                 125

Gly Ser Gly Lys Asp Ser Thr Cys Glu Thr Ser Gly Asp Asn Ser Thr
    130                 135                 140

Asn Thr Thr Thr Thr Thr Thr Val Glu Ala Ala Pro Arg Arg Thr Leu
145                 150                 155                 160

Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His
                165                 170                 175

Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg
            180                 185                 190

Arg Glu Gly Gln Ser Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr
        195                 200                 205

Asp Lys Glu Glu Lys Ala Ala Arg Ser Tyr Asp Leu Ala Ala Leu Lys
    210                 215                 220

Tyr Trp Gly Thr Ser Thr Thr Thr Asn Phe Pro Ile Ser Asn Tyr Glu
225                 230                 235                 240

Lys Glu Leu Asp Glu Met Lys His Met Thr Arg Gln Glu Phe Val Ala
                245                 250                 255

Ala Ile Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Met Tyr
            260                 265                 270

Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile
        275                 280                 285

Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr
    290                 295                 300
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```
Glu Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg
305                 310                 315                 320

Gly Leu Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys
                325                 330                 335

Ala Ile Leu Glu Ser Asn Thr Leu Pro Ile Gly Gly Gly Ala Ala Lys
            340                 345                 350

Arg Leu Lys Glu Ala Gln Ala Leu Glu Ser Ser Arg Lys Arg Glu Glu
        355                 360                 365

Met Ile Ala Leu Gly Ser Ser Thr Phe Gln Tyr Gly Thr Thr Ser Ser
    370                 375                 380

Asn Ser Arg Leu His Ala Tyr Pro Leu Met Gln His His His Gln Phe
385                 390                 395                 400

Glu Gln Pro Gln Pro Leu Leu Thr Leu Gln Asn His Asp Ile Ser Ser
                405                 410                 415

His Phe Ser His Gln Gln Asp Pro Leu His Gln Gly Tyr Ile Gln Thr
            420                 425                 430

Gln Leu Gln Leu His Gln Gln Gln Ser Gly Gly Ser Ser Ser Tyr Ser
        435                 440                 445

Phe Gln Asn Asn Asn Ile Asn Asn Ala Gln Phe Tyr Asn Gly Tyr Asn
    450                 455                 460

Leu Gln Asn His Pro Ala Leu Leu Gln Gly Met Ile Asn Met Gly Ser
465                 470                 475                 480

Ser Ser Ser Ser Ser Val Leu Glu Asn Asn Asn Ser Asn Asn Asn Asn
                485                 490                 495

Val Gly Gly Phe Val Gly Ser Gly Phe Gly Met Ala Ser Asn Ala Thr
            500                 505                 510

Ser Gly Asn Thr Val Gly Thr Ala Glu Glu Leu Gly Leu Val Lys Val
        515                 520                 525

Asp Tyr Asp Met Pro Thr Gly Gly Tyr Gly Gly Trp Ser Ala Ala Ala
    530                 535                 540

Ala Ala Glu Ser Met Gln Thr Ser Asn Ser Gly Val Phe Thr Met Trp
545                 550                 555                 560

Asn Asp


<210> SEQ ID NO 83
<211> LENGTH: 574
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 83

Met Asn Ser Asn Asn Trp Leu Gly Phe Pro Leu Ser Pro Asn Asn Ser
1               5                   10                  15

Ser Leu Pro Pro His Glu Tyr Asn Leu Gly Leu Val Ser Asp His Met
            20                  25                  30

Asp Asn Pro Phe Gln Thr Gln Glu Trp Asn Met Ile Asn Pro His Gly
        35                  40                  45

Gly Gly Gly Asp Glu Gly Gly Glu Val Pro Lys Val Ala Asp Phe Leu
    50                  55                  60

Gly Val Ser Lys Pro Asp Glu Asn Gln Ser Asn His Leu Val Ala Tyr
65                  70                  75                  80

Asn Asp Ser Asp Tyr Tyr Phe His Thr Asn Ser Leu Met Pro Ser Val
                85                  90                  95
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```
Gln Ser Asn Asp Val Val Val Ala Ala Cys Asp Ser Asn Thr Pro Asn
            100                 105                 110

Asn Ser Ser Tyr His Glu Leu Gln Glu Ser Ala His Asn Leu Gln Ser
        115                 120                 125

Leu Thr Leu Ser Met Gly Thr Thr Ala Gly Asn Asn Val Val Asp Lys
    130                 135                 140

Ala Ser Pro Ser Glu Thr Thr Gly Asp Asn Ala Ser Gly Gly Ala Leu
145                 150                 155                 160

Ala Val Val Glu Thr Ala Thr Pro Arg Arg Ala Leu Asp Thr Phe Gly
                165                 170                 175

Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly
            180                 185                 190

Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln
        195                 200                 205

Ser Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Asp
    210                 215                 220

Lys Ala Ala Arg Ser Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro
225                 230                 235                 240

Ser Thr Thr Thr Asn Phe Pro Ile Thr Asn Tyr Glu Lys Glu Val Glu
                245                 250                 255

Glu Met Lys His Met Thr Arg Gln Glu Phe Val Ala Ala Ile Arg Arg
            260                 265                 270

Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Met Tyr Arg Gly Val Thr
        275                 280                 285

Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala
    290                 295                 300

Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Glu Glu Glu Ala
305                 310                 315                 320

Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala
                325                 330                 335

Val Thr Asn Phe Glu Ile Asn Arg Tyr Asp Val Lys Ala Ile Leu Glu
            340                 345                 350

Ser Ser Thr Leu Pro Ile Gly Gly Gly Ala Ala Lys Arg Leu Lys Glu
        355                 360                 365

Ala Gln Ala Leu Glu Ser Ser Arg Lys Arg Glu Ala Glu Met Ile Ala
    370                 375                 380

Leu Gly Ser Ser Phe Gln Tyr Gly Gly Gly Ser Ser Thr Gly Ser Gly
385                 390                 395                 400

Ser Thr Ser Ser Arg Leu Gln Leu Gln Pro Tyr Pro Leu Ser Ile Gln
                405                 410                 415

Gln Pro Leu Glu Pro Phe Leu Ser Leu Gln Asn Asn Asp Ile Ser His
            420                 425                 430

Tyr Asn Asn Asn Asn Ala His Asp Ser Ser Ser Phe Asn His His Ser
        435                 440                 445

Tyr Ile Gln Thr Gln Leu His Leu His Gln Gln Thr Asn Asn Tyr Leu
    450                 455                 460

Gln Gln Gln Ser Ser Gln Asn Ser Gln Gln Leu Tyr Asn Ala Tyr Leu
465                 470                 475                 480

His Ser Asn Pro Ala Leu Leu His Gly Leu Val Ser Thr Ser Ile Val
                485                 490                 495
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```
Asp Asn Asn Asn Asn Asn Gly Gly Ser Ser Gly Ser Tyr Asn Thr Ala
            500                 505                 510

Ala Phe Leu Gly Asn His Gly Ile Gly Ile Gly Ser Ser Ser Thr Val
        515                 520                 525

Gly Ser Thr Glu Glu Phe Pro Thr Val Lys Thr Asp Tyr Asp Met Pro
    530                 535                 540

Ser Ser Asp Gly Thr Gly Gly Tyr Ser Gly Trp Thr Ser Glu Ser Val
545                 550                 555                 560

Gln Gly Ser Asn Pro Gly Gly Val Phe Thr Met Trp Asn Glu
                565                 570


<210> SEQ ID NO 84
<211> LENGTH: 543
<212> TYPE: PRT
<213> ORGANISM: Medicago truncatula

<400> SEQUENCE: 84

Met Asn Asn Asn Trp Leu Ser Phe Pro Leu Ser Pro Ser His Ser Ser
1               5                   10                  15

Leu Pro Ser Asn Asp Leu Gln Ala Thr Gln Tyr His His Phe Pro Leu
            20                  25                  30

Gly Leu Val Asn Asp Asn Met Glu Asn Pro Phe Gln Asn His Asp Trp
        35                  40                  45

Asn Leu Met Asn Thr His Asn Ser Asn Glu Val Pro Lys Val Ala Asp
    50                  55                  60

Phe Leu Gly Val Cys Lys Ser Glu Asn His Ser Asp Leu Ala Thr Pro
65                  70                  75                  80

Asn Glu Ile Gln Ser Asn Asp Ser Asp Tyr Leu Phe Thr Asn Asn Asn
                85                  90                  95

Thr Leu Met Pro Met Gln Asn Gln Met Val Thr Thr Cys Thr Asn Glu
            100                 105                 110

Tyr Gln Glu Lys Ala Ser Asn Ser Asn Leu Gln Ser Leu Thr Leu Ser
        115                 120                 125

Met Gly Ser Gly Lys Asp Ser Thr Cys Glu Thr Ser Gly Glu Asn Ser
    130                 135                 140

Thr Asn Thr Val Glu Val Ala Val Pro Lys Arg Thr Ser Glu Thr Phe
145                 150                 155                 160

Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr Lys His Arg Trp Thr
                165                 170                 175

Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly
            180                 185                 190

Gln Ser Arg Lys Gly Arg Gln Gly Gly Tyr Asp Lys Glu Glu Lys Ala
        195                 200                 205

Ala Arg Ser Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Ser Thr
    210                 215                 220

Thr Thr Asn Phe Pro Val Ser Asn Tyr Glu Lys Glu Ile Asp Glu Met
225                 230                 235                 240

Lys His Met Thr Arg Gln Glu Phe Val Ala Ser Ile Arg Arg Lys Ser
                245                 250                 255

Ser Gly Phe Ser Arg Gly Ala Ser Met Tyr Arg Gly Val Thr Arg His
            260                 265                 270

His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn
        275                 280                 285
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```
Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Glu Glu Glu Ala Ala Glu
    290                 295                 300

Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr
305                 310                 315                 320

Asn Phe Asp Met Thr Arg Tyr Asp Val Lys Ala Ile Leu Glu Ser Asn
                325                 330                 335

Thr Leu Pro Ile Gly Gly Gly Ala Ala Lys Arg Leu Lys Glu Ala Gln
            340                 345                 350

Ala Leu Glu Thr Ser Arg Lys Arg Glu Glu Met Leu Ala Leu Asn Ser
        355                 360                 365

Ser Ser Phe Gln Tyr Gly Thr Ser Ser Ser Ser Asn Thr Arg Leu Gln
    370                 375                 380

Pro Tyr Pro Leu Met Gln Tyr His His Gln Phe Glu Gln Pro Gln Pro
385                 390                 395                 400

Leu Leu Thr Leu Gln Asn Asn His Glu Ser Leu Asn Ser Gln Gln Phe
                405                 410                 415

Ser Gln His Gln Gly Gly Gly Tyr Phe Gln Thr Gln Leu Glu Leu Cys
            420                 425                 430

Gln Gln Gln Asn Gln Gln Pro Ser Gln Asn Ser Asn Ile Gly Ser Phe
        435                 440                 445

Tyr Asn Gly Tyr Tyr Gln Asn His Pro Gly Leu Phe Gln Met Asn Asn
    450                 455                 460

Ile Gly Ser Ser Ser Ser Ser Ser Val Met Gly Asn Asn Gly Gly Gly
465                 470                 475                 480

Ser Ser Gly Ile Tyr Ser Asn Ser Gly Gly Leu Ile Ser Asn Asn Ala
                485                 490                 495

Val Glu Glu Phe Val Pro Val Lys Val Asp Tyr Asp Met Gln Gly Asp
            500                 505                 510

Gly Ser Gly Phe Gly Gly Trp Ser Ala Ala Gly Glu Asn Met Gln Thr
        515                 520                 525

Ala Asp Leu Phe Thr Met Trp Asn Asp Tyr Glu Thr Arg Glu Asn
    530                 535                 540


<210> SEQ ID NO 85
<211> LENGTH: 543
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 85

Met Asp Met Asn Asn Gly Trp Leu Gly Phe Ser Leu Ser Pro Ser Ala
1               5                   10                  15

Ala Ser Arg Gly Gly Tyr Gly Tyr Gly Asp Gly Gly Gly Gly Ala Ser
            20                  25                  30

Ala Ser Ala Cys Gly Asp Gly Glu Gly Ser Cys Pro Ser Pro Ala Ala
        35                  40                  45

Ala Ala Ser Pro Leu Pro Leu Val Ala Met Pro Leu Asp Asp Ser Leu
    50                  55                  60

His Tyr Ser Ser Ala Pro Asp Trp Arg His Gly Ala Ala Glu Ala Lys
65                  70                  75                  80

Gly Pro Lys Leu Glu Asp Phe Met Ser Ile Thr Cys Ser Asn Lys Ser
                85                  90                  95

Ser Gly Arg Ser Leu Tyr Asp Ser Cys Gly His His Asp Asp Glu Gln
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            100                 105                 110

Ala Ser Lys Tyr His Glu Val His Gly Ile His Pro Leu Ser Cys Gly
        115                 120                 125

Ser Tyr Tyr His Gly Cys Ile Ser Ser Gly Gly Gly Gly Gly Gly Gly
    130                 135                 140

Ile Gly Leu Gly Ile Asn Met Asn Ala Pro Pro Cys Thr Gly Gly Phe
145                 150                 155                 160

Pro Asp His Gln His His Gln Phe Val Pro Ser Ser His His Gly Gln
                165                 170                 175

Tyr Phe Leu Gly Ala Pro Ala Ala Ser Ala Gly Pro Pro Ala Gly Ala
            180                 185                 190

Ala Met Pro Met Tyr Asn Ala Gly Gly Gly Ser Val Val Gly Gly Ser
        195                 200                 205

Met Ser Ile Ser Gly Ile Lys Ser Trp Leu Arg Glu Ala Met Tyr Val
    210                 215                 220

Pro Pro Glu Arg Pro Ala Ala Ala Ala Leu Ser Leu Ala Val Thr Asp
225                 230                 235                 240

Asp Val Pro Pro Ala Glu Pro Pro Gln Leu Leu Pro Ala Pro Leu Pro
                245                 250                 255

Val His Arg Lys Pro Ala Gln Thr Phe Gly Gln Arg Thr Ser Gln Phe
            260                 265                 270

Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu
        275                 280                 285

Trp Asp Asn Thr Cys Arg Lys Glu Gly Gln Thr Arg Lys Gly Arg Gln
    290                 295                 300

Val Tyr Leu Gly Gly Tyr Asp Arg Glu Glu Lys Ala Ala Arg Ala Tyr
305                 310                 315                 320

Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Ser Thr His Ile Asn Phe
                325                 330                 335

Pro Leu Ser His Tyr Glu Lys Glu Leu Glu Glu Met Lys His Met Ser
            340                 345                 350

Arg Gln Glu Phe Ile Ala His Leu Arg Arg Asn Ser Ser Gly Phe Ser
        355                 360                 365

Arg Gly Ala Ser Met Tyr Arg Gly Val Thr Arg His His Gln His Gly
    370                 375                 380

Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr
385                 390                 395                 400

Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Ile
                405                 410                 415

Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Ile
            420                 425                 430

Ser Lys Tyr Asp Val Lys Arg Ile Cys Ala Ser Thr His Leu Ile Gly
        435                 440                 445

Gly Gly Asp Ala Cys Arg Arg Ser Pro Thr Arg Pro Pro Asp Ala Ala
    450                 455                 460

Pro Ala Leu Ala Gly Gly Ala Asp Arg Ser Ser Asp Ala Pro Gly Asp
465                 470                 475                 480

Gln Ala Ala Ser Asp Asn Ser Asp Thr Ser Asp Gly His Arg Gly Ala
                485                 490                 495

His Leu Leu His Gly Leu Gln Tyr Gly His Pro Met Lys Leu Glu Ala
            500                 505                 510
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```
Gly Glu Gly Ser Ser Trp Met Ala Ala Ala Ala Ala Ala Arg Pro Val
        515                 520                 525

Pro Gly Val His Gln Leu Pro Met Phe Ala Leu Trp Asn Asp Cys
    530                 535                 540


<210> SEQ ID NO 86
<211> LENGTH: 512
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 86

Met Ser Asn Trp Leu Gly Phe Ser Leu Thr Pro His Leu Arg Ile Asp
1               5                   10                  15

Glu Glu Phe Glu Arg Glu Asn Gln Glu Arg Gly Gly Gly Ile Ile Leu
            20                  25                  30

Phe Glu Lys Lys Lys Thr Lys Trp Arg Tyr Asp Ser Ala Ile Gly Gly
        35                  40                  45

Gly Asn Ser Asn Glu Glu Gly Pro Lys Leu Glu Asp Phe Leu Gly Cys
    50                  55                  60

Tyr Ser Asn Ser Pro Ala Lys Val Phe Cys Gln Asp Ser Gln Pro Asp
65                  70                  75                  80

Gln Asn Gln Ser Gln Asn Asn Val Ser Lys Ile Asn Ile Glu Thr Gly
                85                  90                  95

Asp Asn Leu Thr Asn Pro Ser Ser Leu Leu His Ser Phe His Ala Tyr
            100                 105                 110

Asn Asp Asn Ser His Ala Leu Ile Pro Thr Asn Gly Met Tyr Lys Ser
        115                 120                 125

Trp Leu Ala Gln Thr Gln Phe Ser Ser Asp Gly Lys Pro Ser Asn Glu
    130                 135                 140

Ala Asn Gly Cys Asn Phe Gln Ser Leu Ser Leu Thr Met Ser Pro Ser
145                 150                 155                 160

Val Gln Asn Gly Val Gly Ala Ile Ser Ser Val Gln Val Asn Glu Asp
                165                 170                 175

Ser Arg Lys Arg Val Met Ala Lys Ser His Ala Arg Glu Pro Val Pro
            180                 185                 190

Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Gln Tyr Arg Gly
        195                 200                 205

Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp
    210                 215                 220

Asn Ser Cys Arg Lys Glu Gly Gln Thr Arg Lys Gly Arg Gln Gly Gly
225                 230                 235                 240

Tyr Asp Lys Glu Glu Lys Ala Ala Lys Ala Tyr Asp Leu Ala Ala Leu
                245                 250                 255

Lys Tyr Trp Gly Pro Thr Thr His Ile Asn Phe Pro Leu Ser Thr Tyr
            260                 265                 270

Glu Lys Glu Leu Glu Glu Met Lys His Met Thr Arg Gln Glu Phe Val
        275                 280                 285

Ala Asn Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Val
    290                 295                 300

Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg
305                 310                 315                 320

Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser
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                325                 330                 335

Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe
            340                 345                 350

Arg Gly Thr Ser Ala Val Thr Asn Phe Asp Ile Ser Arg Tyr Asp Val
        355                 360                 365

Lys Arg Ile Cys Ser Ser Ser Thr Leu Ile Ala Gly Asp Leu Ala Lys
    370                 375                 380

Arg Ser Pro Lys Glu Ser Pro Ala Pro Pro Pro Pro Leu Ala Ile Thr
385                 390                 395                 400

Asp Gly Glu His Ser Asp Glu Leu Ser Asn Met Met Trp Asn Ala Asn
                405                 410                 415

Asn Ser Asp Glu Gln Ala Gln Asn Glu Ser Gly Gly Ala Glu Phe Asn
            420                 425                 430

Asn Asn Val Thr Glu Ser Ser Ser Ser Gln Gln Val Ser Pro Ser Ser
        435                 440                 445

Asn Lys Asp Ala Leu Asn Pro Gln Ser Pro Asn Glu Phe Gly Val Ser
    450                 455                 460

Gly Ala Asp Tyr Gly His Gly Tyr Phe Thr Leu Asp Gly Pro Lys Tyr
465                 470                 475                 480

Asp Asp Gly Asn Asn Glu Asn Asp His Met Ser Thr Asn Arg Leu Gly
                485                 490                 495

Asn Leu Gly Leu Val Asn Gln Val Pro Met Phe Ala Leu Trp Asn Glu
            500                 505                 510


<210> SEQ ID NO 87
<211> LENGTH: 485
<212> TYPE: PRT
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 87

Met Asp Thr Ser His His Tyr Pro Trp Leu Asn Phe Ser Leu Ala His
1               5                   10                  15

His Gly Asp Leu Glu Glu Glu Glu Arg Gly Ala Ala Ala Glu Leu Ala
            20                  25                  30

Ala Ile Ala Gly Ala Ala Pro Pro Pro Lys Leu Glu Asp Phe Leu Gly
        35                  40                  45

Gly Gly Val Ile Asn Gly Glu Ser Ala Arg Ser Gly Gly Gly Val Pro
    50                  55                  60

Val Ala Ala Pro Glu Val Ser Ala Pro Ala Glu Met Tyr Asp Ser Asp
65                  70                  75                  80

Leu Lys Phe Ile Ala Ala Ala Gly Phe Leu Gly Gly Gly Ser Ala Ala
                85                  90                  95

Gly Pro Val Ala Thr Ser Pro Leu Ser Ser Leu Asp Gln Ala Asp Pro
            100                 105                 110

Lys Leu Ala Leu Pro Ala Ala Ala Ala Ala Ala Pro Ala Pro Glu Gln
        115                 120                 125

Arg Lys Ala Val Asp Ser Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly
    130                 135                 140

Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp
145                 150                 155                 160

Asn Ser Cys Arg Arg Glu Gly Gln Ser Arg Lys Gly Arg Gln Gly Gly
                165                 170                 175
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Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu
            180                 185                 190

Lys Tyr Trp Gly Ser Ser Thr Thr Thr Asn Phe Pro Val Ala Glu Tyr
        195                 200                 205

Glu Lys Glu Leu Glu Glu Met Lys Thr Met Thr Arg Gln Glu Phe Val
    210                 215                 220

Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile
225                 230                 235                 240

Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg
                245                 250                 255

Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser
            260                 265                 270

Thr Glu Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe
        275                 280                 285

Arg Gly Leu Asn Ala Val Thr Asn Phe Glu Ile Ser Arg Tyr Asn Val
    290                 295                 300

Glu Ser Ile Met Asn Ser Asn Ile Pro Met Gly Ser Met Ser Ala Gly
305                 310                 315                 320

Gly Arg Ser Asn Lys Ala Leu Glu Ser Pro Pro Ser Gly Ser Pro Asp
                325                 330                 335

Ala Met Pro Val Glu Ala Ser Thr Ala Pro Leu Phe Ala Ala Leu Pro
            340                 345                 350

Val Lys Tyr Asp Gln Gln Gln Gln Asp Tyr Leu Ser Met Leu Ala Leu
        355                 360                 365

Gln His His Gln Gln Gly Asn Leu Gln Gly Leu Gly Phe Gly Leu Tyr
    370                 375                 380

Ser Ser Gly Val Asn Leu Asp Phe Ala Asn Ser His Ser Thr Ala Ser
385                 390                 395                 400

Ser Met Thr His Cys Tyr Val Asn Gly Gly Thr Val Ser Ser His Glu
                405                 410                 415

Gln His Gln His His Gln Gln Leu Gln Asp His Gln Gln Gln Gly Glu
            420                 425                 430

Ser Glu Thr Gln Gln Ser Ser Asn Ser Cys Ser Ser Leu Pro Phe Ala
        435                 440                 445

Thr Pro Ile Ala Phe Asn Gly Ser Tyr Glu Ser Ser Met Thr Ala Ala
    450                 455                 460

Gly Pro Phe Gly Tyr Ser Tyr Pro Asn Val Ala Ala Phe Gln Thr Pro
465                 470                 475                 480

Ile Tyr Gly Met Glu
                485


<210> SEQ ID NO 88
<211> LENGTH: 507
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 88

Met Ala Arg Ala Thr Asn Trp Leu Ser Phe Ser Leu Ser Pro Met Glu
1               5                   10                  15

Met Leu Arg Thr Ser Glu Pro Gln Phe Leu Gln Tyr Asp Ala Ala Ser
            20                  25                  30

Ala Thr Ser Ser His His Tyr Tyr Leu Asp Asn Leu Tyr Thr Asn Gly
        35                  40                  45
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Trp Gly Asn Gly Ser Leu Lys Phe Glu Gln Asn Leu Asn His Ser Asp
    50                  55                  60

Val Ser Phe Val Glu Ser Ser Ser Gln Ser Val Gly His Val Pro Pro
65                  70                  75                  80

Pro Pro Pro Lys Leu Glu Asp Phe Leu Gly Asp Ser Ser Ala Val Met
                85                  90                  95

Arg Tyr Ser Asp Ser Gln Thr Glu Thr Gln Asp Ser Ser Leu Thr His
            100                 105                 110

Ile Tyr Asp His His His His His His His His His Gly Ser Thr Ser
        115                 120                 125

Tyr Phe Gly Gly Asp Gln Gln Asp Leu Lys Ala Ile Thr Gly Phe Gln
    130                 135                 140

Ala Phe Ser Thr Asn Ser Gly Ser Glu Val Asp Asp Ser Ala Ser Ile
145                 150                 155                 160

Gly Lys Ala Gln Ala Ser Glu Phe Gly Thr His Ser Ile Glu Ser Ser
                165                 170                 175

Gly Asn Glu Phe Ala Ala Phe Ser Gly Gly Thr Thr Gly Thr Leu Ser
            180                 185                 190

Leu Ala Val Ala Leu Ser Ser Glu Lys Ala Val Val Ala Ala Glu Ser
        195                 200                 205

Asn Ser Ser Lys Lys Ile Val Asp Thr Phe Gly Gln Arg Thr Ser Ile
    210                 215                 220

Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His
225                 230                 235                 240

Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Ala Arg Lys Gly Arg
                245                 250                 255

Gln Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu
            260                 265                 270

Ala Ala Leu Lys Tyr Trp Gly Pro Thr Ala Thr Thr Asn Phe Pro Val
        275                 280                 285

Ser Asn Tyr Ser Lys Glu Val Glu Glu Met Lys His Val Thr Lys Gln
    290                 295                 300

Glu Phe Ile Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly
305                 310                 315                 320

Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln Gln Gly Arg Trp
                325                 330                 335

Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly
            340                 345                 350

Thr Phe Ala Thr Glu Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala
        355                 360                 365

Ile Lys Phe Arg Gly Ala Asn Ala Val Thr Asn Phe Glu Met Asn Arg
    370                 375                 380

Tyr Asp Val Glu Ala Ile Met Lys Ser Ser Leu Pro Val Gly Gly Ala
385                 390                 395                 400

Ala Lys Arg Leu Arg Leu Ser Leu Glu Ser Glu Gln Lys Ala Pro Pro
                405                 410                 415

Val Asn Ser Ser Ser Gln Gln Gln Asn Pro Gln Cys Gly Asn Val Ser
            420                 425                 430

Gly Ser Ile Asn Phe Ser Ala Ile His Gln Pro Ile Ala Ser Ile Pro
        435                 440                 445
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Cys Gly Ile Pro Phe Asp Ser Thr Thr Ala Tyr Tyr Pro His Asn Leu
    450                 455                 460

Phe Gln His Phe His Pro Thr Asn Ala Gly Ala Ala Ala Ser Ala Val
465                 470                 475                 480

Thr Ser Ala Asn Ala Thr Ala Leu Thr Ala Leu Pro Ala Ser Ala Ala
                485                 490                 495

Thr Glu Phe Phe Ile Trp Pro His Gln Ser Tyr
        500                 505


<210> SEQ ID NO 89
<211> LENGTH: 569
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 89

Met Glu Met Leu Arg Ser Ser Asp Gln Ser Gln Phe Val Ser Tyr Asp
1               5                   10                  15

Ala Ser Ser Ala Ala Ser Ser Ser Pro Tyr Leu Leu Asp Asn Phe Tyr
            20                  25                  30

Gly Trp Ser Asn Gln Lys Pro Gln Glu Phe Phe Lys Glu Glu Ala Gln
        35                  40                  45

Leu Ala Ala Ala Ala Ser Met Ala Asp Ser Thr Ile Leu Thr Thr Phe
    50                  55                  60

Val Asp Pro Gln Ser His His Ser Gln Asn His Ile Pro Lys Leu Glu
65                  70                  75                  80

Asp Phe Leu Gly Asp Ser Ser Ser Ile Val Arg Tyr Ser Asp Asn Ser
                85                  90                  95

Gln Thr Asp Thr Gln Asp Ser Ser Leu Thr Gln Ile Tyr Asp Pro Arg
            100                 105                 110

His His His Asn Gln Thr Gly Phe Tyr Ser Asp His His Asp Phe Lys
        115                 120                 125

Thr Met Ala Gly Phe Gln Ser Ala Phe Ser Thr Asn Ser Gly Ser Glu
    130                 135                 140

Val Asp Asp Ser Ala Ser Ile Gly Arg Thr His Leu Ala Gly Asp Tyr
145                 150                 155                 160

Leu Gly His Val Val Glu Ser Ser Gly Pro Glu Leu Gly Phe His Gly
                165                 170                 175

Gly Ser Thr Gly Ala Leu Ser Leu Gly Val Asn Val Asn Asn Asn Thr
            180                 185                 190

Asn His Arg Asn Asp Asn Asp Asn His Tyr Arg Gly Asn Asn Asn Gly
        195                 200                 205

Glu Arg Ile Asn Asn Asn Asn Asn Asn Asp Asn Glu Lys Thr Asp Ser
    210                 215                 220

Glu Lys Glu Lys Ala Val Val Ala Val Glu Thr Ser Asp Cys Ser Asn
225                 230                 235                 240

Lys Lys Ile Ala Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly
                245                 250                 255

Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp
            260                 265                 270

Asn Ser Cys Arg Arg Glu Gly Gln Ala Arg Lys Gly Arg Gln Val Tyr
        275                 280                 285

Leu Gly Gly Tyr Asp Lys Glu Asp Lys Ala Ala Arg Ala Tyr Asp Leu
    290                 295                 300
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Ala Ala Leu Lys Tyr Trp Asn Ala Thr Ala Thr Thr Asn Phe Pro Ile
305                 310                 315                 320

Thr Asn Tyr Ser Lys Glu Val Glu Glu Met Lys His Met Thr Lys Gln
                325                 330                 335

Glu Phe Ile Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly
            340                 345                 350

Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln Gln Gly Arg Trp
        355                 360                 365

Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly
    370                 375                 380

Thr Phe Ala Thr Glu Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala
385                 390                 395                 400

Ile Lys Phe Arg Gly Ile Asn Ala Val Thr Asn Phe Glu Met Asn Arg
                405                 410                 415

Tyr Asp Val Glu Ala Ile Met Lys Ser Ala Leu Pro Ile Gly Gly Ala
            420                 425                 430

Ala Lys Arg Leu Lys Leu Ser Leu Glu Ala Ala Ala Ser Ser Glu Gln
        435                 440                 445

Lys Pro Ile Leu Gly His His Gln Leu His His Phe Gln Gln Gln Gln
    450                 455                 460

Gln Gln Gln Gln Leu Gln Leu Gln Ser Ser Pro Asn His Ser Ser Ile
465                 470                 475                 480

Asn Phe Ala Leu Cys Pro Asn Ser Ala Val Gln Ser Gln Gln Ile Ile
                485                 490                 495

Pro Cys Gly Ile Pro Phe Glu Ala Ala Ala Leu Tyr His His His Gln
            500                 505                 510

Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Asn Phe Phe Gln
        515                 520                 525

His Phe Pro Ala Asn Ala Ala Ser Asp Ser Thr Gly Ser Asn Asn Asn
    530                 535                 540

Ser Asn Val Gln Gly Thr Met Gly Leu Met Ala Pro Asn Pro Ala Glu
545                 550                 555                 560

Phe Phe Leu Trp Pro Asn Gln Ser Tyr
                565


<210> SEQ ID NO 90
<211> LENGTH: 574
<212> TYPE: PRT
<213> ORGANISM: Medicago truncatula

<400> SEQUENCE: 90

Met Ser Asn Trp Leu Gly Phe Ser Leu Thr Pro His Leu Arg Ile Asp
1               5                   10                  15

Glu Glu Phe Gly Thr Glu Asn Gln Asn Gln Asn Gln Asn His Val Ala
            20                  25                  30

Glu Gly Ser Glu Ile Gly Arg Asn Tyr Val Thr Pro Ser Ser His Pro
        35                  40                  45

His Pro His His Leu Ser Ile Met Pro Leu Arg Ser Asp Gly Ser Leu
    50                  55                  60

Cys Val Ser Asp Ser Phe Thr Pro Gln Glu Trp Arg Tyr Glu Asn Ala
65                  70                  75                  80

Ile Thr Asp Gly Asn Ser Asn Glu Glu Gly Pro Lys Leu Glu Asp Phe
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                85                  90                  95

Leu Gly Cys Tyr Ser Asn Gln Asn Gln Asn Ser Thr Thr Thr Ser Thr
            100                 105                 110

Met Ser Lys Ile Asn Val Asn Val Ser Pro Ser Phe Cys Thr Asn Asn
        115                 120                 125

Asn Pro Glu Ile Asp Thr Arg Glu Asn Leu Thr Asn Gln Ser Leu Ile
    130                 135                 140

His Ser Phe His Ala Tyr Asn Asp His Ser Asn Asn Asn His His Ala
145                 150                 155                 160

Leu Ile His Asp Asn Ser Met Tyr Lys Ser Trp Met Thr Gln Thr Gln
                165                 170                 175

Phe Ser Ser Glu Gly Lys Thr Thr Ser Ser Asp Gly Asn Gly Phe Gln
            180                 185                 190

Ser Leu Asn Leu Thr Met Ser Pro Cys Val Gln Asn Gly Val Gly Gly
        195                 200                 205

Gly Val Gly Ser Ala Ile Ser Asn Val Gln Val Asn Glu Asp Pro Arg
    210                 215                 220

Lys Arg Ser Leu Ser Lys Ser Asn Ala Arg Glu Pro Val Pro Arg Lys
225                 230                 235                 240

Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Gln Tyr Arg Gly Val Thr
                245                 250                 255

Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser
            260                 265                 270

Cys Arg Lys Glu Gly Gln Thr Arg Lys Gly Arg Gln Gly Gly Tyr Asp
        275                 280                 285

Lys Glu Glu Lys Ala Ala Lys Ala Tyr Asp Leu Ala Ala Leu Lys Tyr
    290                 295                 300

Trp Gly Pro Thr Thr His Ile Asn Phe Pro Leu Ser Thr Tyr Asp Lys
305                 310                 315                 320

Glu Leu Glu Glu Met Lys His Met Thr Arg Gln Glu Phe Val Ala Asn
                325                 330                 335

Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Val Tyr Arg
            340                 345                 350

Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly
        355                 360                 365

Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln
    370                 375                 380

Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly
385                 390                 395                 400

Thr Ser Ala Val Thr Asn Phe Asp Ile Ser Arg Tyr Asp Val Lys Arg
                405                 410                 415

Ile Cys Ser Ser Ser Thr Leu Ile Thr Gly Asp Leu Ala Lys Arg Ser
            420                 425                 430

Pro Lys Asp Ser Thr Pro Pro Ala Thr Thr Ala Glu Asp Phe Asn Ser
        435                 440                 445

Cys Gly Ser Ser Ser Thr Leu Ser Gln Pro Pro Pro Leu Thr Ile Thr
    450                 455                 460

Asp Gly Glu Gln His Ser Asp Glu Leu Ser Asn Met Val Trp Asn Ser
465                 470                 475                 480

Asn Asn Asp Glu Gln Lys Pro Gln Asn Gly Thr Asn Ile Thr Glu Ser
                485                 490                 495
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Ser Gln His Gly Ser Pro Ser Asn Lys Asn Glu Met Asn Pro Gln Ser
            500                 505                 510

Pro Lys Cys Ser Leu Gly Leu Pro Asn Glu Phe Gly Val Ser Gly Ala
        515                 520                 525

Asp Tyr Gly His Gly Tyr Phe Thr Leu His Gly Pro Lys Phe Asp Asp
    530                 535                 540

Gly Ser Asn Glu Asn Asp His Met Asn Asn Asn Arg Leu Gly Asn Leu
545                 550                 555                 560

Gly Leu Val Asn Gln Val Pro Met Phe Ala Leu Trp Asn Glu
            565                 570


<210> SEQ ID NO 91
<211> LENGTH: 541
<212> TYPE: PRT
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 91

Met Asp Met Asn Asn Gly Trp Leu Gly Phe Ser Leu Ser Pro Ser Ala
1               5                   10                  15

Gly Arg Gly Gly Tyr Gly Asp Gly Gly Ala Ser Ala Ser Gly Asp Gly
            20                  25                  30

Gly Asp Gly Ser Cys Ser Ser Pro Ala Ala Ala Ala Ser Pro Val Pro
        35                  40                  45

Leu Val Ala Met Pro Leu Gln Pro Asp Gly Ser Leu His Tyr Thr Ser
    50                  55                  60

Ala Pro Asp Trp Arg His Gly Ala Ala Glu Ala Asn Gly Pro Lys Leu
65                  70                  75                  80

Glu Asp Phe Met Ser Val Thr Cys Ser Ser Asn Asn Lys Arg Ser Ser
                85                  90                  95

Ser Ser Ser Ser Phe Tyr Asp Arg Cys Ser His Ala Glu Gln Ala Asn
            100                 105                 110

Lys Tyr His Glu Val His Asp Leu Gln Pro Leu Ser Cys Gly Ser Tyr
        115                 120                 125

Tyr His Gly Ser Ser Gly Gly Gly Gly Asn Gly Ile Ala Leu Gly Ile
    130                 135                 140

Asn Met Asn Ala Pro Pro Cys Ser Gly Gly Gly Phe Pro Asp His His
145                 150                 155                 160

His His His Gln Phe Val Ser Ser His His Gly Gln Tyr Phe Leu Gly
                165                 170                 175

Ala Pro Leu Asn Ala Ser Pro Pro Gly Ala Val Pro Met Tyr Ser Ala
            180                 185                 190

Gly Gly Gly Gly Val Gly Gly Ser Met Ser Ile Ser Gly Ile Lys Ser
        195                 200                 205

Trp Leu Arg Glu Ala Met Tyr Val Pro Pro Glu Arg Pro Val Ala Ala
    210                 215                 220

Ala Ala Ala Leu Ser Leu Ala Val Thr Asp Asp Val Gly Ala Glu Pro
225                 230                 235                 240

Pro Gln Leu Leu Pro Ala Ala Pro Met Pro Pro Val His Arg Lys Pro
                245                 250                 255

Ala Gln Thr Phe Gly Gln Arg Thr Ser Gln Phe Arg Gly Val Thr Arg
            260                 265                 270

His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Thr Cys
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        275                 280                 285

Arg Lys Glu Gly Gln Thr Arg Lys Gly Arg Gln Gly Gly Tyr Asp Arg
    290                 295                 300

Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp
305                 310                 315                 320

Gly Pro Ser Thr His Ile Asn Phe Pro Leu Ser His Tyr Glu Lys Glu
                325                 330                 335

Leu Glu Glu Met Lys His Met Ser Arg Gln Glu Phe Ile Ala His Leu
            340                 345                 350

Arg Arg Asn Ser Ser Gly Phe Ser Arg Gly Ala Ser Met Tyr Arg Gly
        355                 360                 365

Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg
    370                 375                 380

Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu
385                 390                 395                 400

Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu
                405                 410                 415

Asn Ala Val Thr Asn Phe Asp Ile Ser Lys Tyr Asp Val Lys Arg Ile
            420                 425                 430

Cys Ala Ser Thr His Leu Ile Gly Gly Gly Asp Ala Cys Arg Arg Ser
        435                 440                 445

Pro Thr Gln Pro Pro Asp Ala Pro Ala Leu Ala Ile Asp Ala Ala Gly
    450                 455                 460

Ala Asp Arg Ser Ser Asp Ala Pro Gly Gly Gly Asp Gln Ala Val Ser
465                 470                 475                 480

Asp Asn Ser Asp Thr Ser Ala Gly His Arg Gly Ala His Leu Leu His
                485                 490                 495

Gly Leu Gln Tyr Gly His Pro Met Lys Leu Glu Ala Gly Glu Gly Ser
            500                 505                 510

Ser Trp Met Ala Ala Ala Thr Ala Ala Ala Ala Arg Pro Val Ala Gly
        515                 520                 525

Val His Gln Leu Pro Val Phe Ala Leu Trp Asn Asp Cys
    530                 535                 540


<210> SEQ ID NO 92
<211> LENGTH: 555
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 92

Met Lys Ser Phe Cys Asp Asn Asp Asp Asn Asn His Ser Asn Thr Thr
1               5                   10                  15

Asn Leu Leu Gly Phe Ser Leu Ser Ser Asn Met Met Lys Met Gly Gly
            20                  25                  30

Arg Gly Gly Arg Glu Ala Ile Tyr Ser Ser Ser Thr Ser Ser Ala Ala
        35                  40                  45

Thr Ser Ser Ser Ser Val Pro Pro Gln Leu Val Val Gly Asp Asn Thr
    50                  55                  60

Ser Asn Phe Gly Val Cys Tyr Gly Ser Asn Pro Asn Gly Gly Ile Tyr
65                  70                  75                  80

Ser His Met Ser Val Met Pro Leu Arg Ser Asp Gly Ser Leu Cys Leu
                85                  90                  95
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Met Glu Ala Leu Asn Arg Ser Ser His Ser Asn His His Gln Asp Ser
            100                 105                 110

Ser Pro Lys Val Glu Asp Phe Phe Gly Thr His His Asn Asn Thr Ser
        115                 120                 125

His Lys Glu Ala Met Asp Leu Ser Leu Asp Ser Leu Phe Tyr Asn Thr
    130                 135                 140

Thr His Glu Pro Asn Thr Thr Thr Asn Phe Gln Glu Phe Phe Ser Phe
145                 150                 155                 160

Pro Gln Thr Arg Asn His Glu Glu Glu Thr Arg Asn Tyr Gly Asn Asp
                165                 170                 175

Pro Ser Leu Thr His Gly Gly Ser Phe Asn Val Gly Val Tyr Gly Glu
            180                 185                 190

Phe Gln Gln Ser Leu Ser Leu Ser Met Ser Pro Gly Ser Gln Ser Ser
        195                 200                 205

Cys Ile Thr Gly Ser His His His Gln Gln Asn Gln Asn Gln Asn His
    210                 215                 220

Gln Ser Gln Asn His Gln Gln Ile Ser Glu Ala Leu Val Glu Thr Ser
225                 230                 235                 240

Val Gly Phe Glu Thr Thr Thr Met Ala Ala Ala Lys Lys Lys Arg Gly
                245                 250                 255

Gln Glu Asp Val Val Val Val Gly Gln Lys Gln Ile Val His Arg Lys
            260                 265                 270

Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Gln Tyr Arg Gly Val Thr
        275                 280                 285

Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser
    290                 295                 300

Phe Lys Lys Glu Gly His Ser Arg Lys Gly Arg Gln Val Tyr Leu Gly
305                 310                 315                 320

Gly Tyr Asp Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala
                325                 330                 335

Leu Lys Tyr Trp Gly Pro Ser Thr His Thr Asn Phe Ser Ala Glu Asn
            340                 345                 350

Tyr Gln Lys Glu Ile Glu Asp Met Lys Asn Met Thr Arg Gln Glu Tyr
        355                 360                 365

Val Ala His Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser
    370                 375                 380

Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala
385                 390                 395                 400

Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe
                405                 410                 415

Gly Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala Ile Lys
            420                 425                 430

Phe Arg Gly Thr Asn Ala Val Thr Asn Phe Asp Ile Thr Arg Tyr Asp
        435                 440                 445

Val Asp Arg Ile Met Ser Ser Asn Thr Leu Leu Ser Gly Glu Leu Ala
    450                 455                 460

Arg Arg Asn Asn Asn Ser Ile Val Val Arg Asn Thr Glu Asp Gln Thr
465                 470                 475                 480

Ala Leu Asn Ala Val Val Glu Gly Gly Ser Asn Lys Glu Val Ser Thr
                485                 490                 495

Pro Glu Arg Leu Leu Ser Phe Pro Ala Ile Phe Ala Leu Pro Gln Val
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            500                 505                 510

Asn Gln Lys Met Phe Gly Ser Asn Met Gly Gly Asn Met Ser Pro Trp
        515                 520                 525

Thr Ser Asn Pro Asn Ala Glu Leu Lys Thr Val Ala Leu Thr Leu Pro
    530                 535                 540

Gln Met Pro Val Phe Ala Ala Trp Ala Asp Ser
545                 550                 555


<210> SEQ ID NO 93
<211> LENGTH: 678
<212> TYPE: PRT
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 93

Met Thr Asn Asn Asn Gly Asn Gly Thr Asn Ala Ala Ala Ser Ser Trp
1               5                   10                  15

Leu Gly Phe Ser Leu Ser Pro His Met Ala Ser Ala Met Asp Glu His
            20                  25                  30

His His Val Gln Gln Gln Gln Gln His His His His His Ser Leu Phe
        35                  40                  45

Phe Pro Ser Val Thr Ala Ala Ala Ala Ala Ala Tyr Gly Leu Gly Gly
    50                  55                  60

Ser Asp Gly Gly Val Ala Thr Ser Ala Ser Pro Tyr Tyr Thr Pro Gln
65                  70                  75                  80

Leu Ala Ser Met Pro Leu Lys Ser Asp Gly Ser Leu Cys Ile Met Glu
                85                  90                  95

Ala Leu Arg Arg Ser Asp Gln Pro Asp His His Gly Pro Lys Leu Glu
            100                 105                 110

Asp Phe Leu Gly Ala Ala Ala Ala Gln Ser Gln Ala Met Ala Leu Ser
        115                 120                 125

Leu Gln Asp Asn Pro Ala Ala Ala Ala Ser Ser Phe Tyr Tyr Tyr Gly
    130                 135                 140

Asn Gly Gly Gly Gly Gly Ser Gly His Gln His His Gly Gly Phe Leu
145                 150                 155                 160

Gln Pro Cys Ala Asp Leu Tyr Gly Gly Pro Ser Glu Ala Ser Leu Val
                165                 170                 175

Ala Asp Asp Asp Glu Ala Ala Ala Ala Ala Thr Ala Met Ala Ser Trp
            180                 185                 190

Val Ala Ala Arg Ala Gly Glu Ser Gly Gly Val Leu Ser Ala Ala Ala
        195                 200                 205

Ala Ala Ala Gly His Gln His His His His Ala Leu Ala Leu Ser Met
    210                 215                 220

Ser Ser Gly Ser Leu Ser Ser Cys Val Thr Ala His Pro Gly Ala Ala
225                 230                 235                 240

Ala Ala Asp Tyr Gly Val Val Ala Ala Thr Ala Ser Ala Ser Leu Asp
                245                 250                 255

Gly Gly Arg Lys Arg Gly Gly Ala Ala Gly Gln Lys Gln Pro Val His
            260                 265                 270

His Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Gln Tyr Arg
        275                 280                 285

Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp
    290                 295                 300
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Asp Asn Ser Cys Lys Lys Glu Gly Gln Thr Arg Lys Gly Arg Gln Gly
305                 310                 315                 320

Gly Tyr Asp Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala
                325                 330                 335

Leu Lys Tyr Trp Gly Pro Ser Thr His Ile Asn Phe Pro Leu Glu Asp
            340                 345                 350

Tyr Gln Glu Glu Leu Glu Glu Met Lys Asn Met Thr Arg Gln Glu Tyr
        355                 360                 365

Val Ala His Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser
    370                 375                 380

Met Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala
385                 390                 395                 400

Arg Ile Gly Arg Val Ser Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe
                405                 410                 415

Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys
            420                 425                 430

Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Ile Thr Arg Tyr Asp
        435                 440                 445

Val Asp Lys Ile Met Ala Ser Asn Thr Leu Leu Pro Gly Asp Leu Ala
    450                 455                 460

Arg Arg Arg Lys Asp Asp Asp Pro Ala Ala Val Ile Ala Gly Ala Asp
465                 470                 475                 480

Ala Ser Asn Gly Gly Gly Val Thr Thr Ala Ala Ala Ala Ala Ala Leu
                485                 490                 495

Val Gln Gln Ala Ala Ala Ala Ala Ala Ala Gly Ala Gly Gly Asn His
            500                 505                 510

Ser Ala Ser Ser Ser Glu Thr Trp Ile Lys Val Ala Ala Ala Ala Ala
        515                 520                 525

Leu Gln Ala Ala Gly Ala Ala Pro Arg Asp Gly Asn His His His His
    530                 535                 540

His His Asp Val Leu Ser Gly Glu Ala Phe Ser Val Leu His Asp Leu
545                 550                 555                 560

Val Val Thr Ala Ala Asp Gly Gly Asn Gly Asn Gly Asn Gly Gly His
                565                 570                 575

His His His His Val His Asn Ser Ala Ala Thr Ala Gln His Met Ser
            580                 585                 590

Met Ser Ser Ala Ser Ser Leu Val Thr Ser Leu Gly Asn Ser Arg Glu
        595                 600                 605

Gly Ser Pro Asp Arg Gly Gly Gly Leu Ser Met Leu Phe Ser Lys Pro
    610                 615                 620

Pro Ala Pro Ala Pro Ala Ala Ser Ala His Ala Ala Asn Lys Pro Met
625                 630                 635                 640

Ser Pro Leu Met Pro Leu Gly Ser Trp Ala Ser Thr Ala Ala Ala Ser
                645                 650                 655

Ala Arg Ala Ala Ala Ala Ala Val Ser Ile Ala His Met Pro Val Phe
            660                 665                 670

Ala Ala Trp Thr Asp Ala
        675

<210> SEQ ID NO 94
<211> LENGTH: 509
<212> TYPE: PRT
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<213> ORGANISM: Glycine max

<400> SEQUENCE: 94

Met Ala Arg Ala Ser Thr Asn Trp Leu Ser Phe Ser Leu Ser Pro Met
1               5                   10                  15

Asp Met Leu Arg Thr Pro Glu Pro Gln Phe Val Gln Tyr Asp Ala Ala
            20                  25                  30

Ser Asp Thr Ser Ser His His Tyr Tyr Leu Asp Asn Leu Tyr Thr Asn
        35                  40                  45

Gly Trp Gly Asn Gly Ser Leu Lys Phe Glu Gln Asn Leu Asn His Ser
    50                  55                  60

Asp Val Ser Phe Val Gln Ser Ser Ser Gln Ser Val Ser His Ala Pro
65                  70                  75                  80

Pro Lys Leu Glu Asp Phe Leu Gly Asp Ser Ser Ala Val Met Arg Tyr
                85                  90                  95

Ser Asp Ser Gln Thr Glu Thr Gln Asp Ser Ser Leu Thr His Ile Tyr
            100                 105                 110

Asp His His His His His His His Gly Ser Ser Ala Tyr Phe Gly Gly
        115                 120                 125

Asp His Gln Asp Leu Lys Ala Ile Thr Gly Phe Gln Ala Phe Ser Thr
    130                 135                 140

Asn Ser Gly Ser Glu Val Asp Asp Ser Ala Ser Ile Gly Lys Ala Gln
145                 150                 155                 160

Gly Ser Glu Phe Gly Thr His Ser Ile Glu Ser Ser Val Asn Glu Phe
                165                 170                 175

Ala Ala Phe Ser Gly Gly Thr Asn Thr Gly Gly Thr Leu Ser Leu Ala
            180                 185                 190

Val Ala Gln Ser Ser Glu Lys Ala Val Ala Ala Ala Ala Glu Ser Asp
        195                 200                 205

Arg Ser Lys Lys Val Val Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr
    210                 215                 220

Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu
225                 230                 235                 240

Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Ala Arg Lys Gly Arg Gln
                245                 250                 255

Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ser Tyr Asp Leu Ala
            260                 265                 270

Ala Leu Lys Tyr Trp Gly Pro Thr Ala Thr Thr Asn Phe Pro Val Ser
        275                 280                 285

Asn Tyr Ser Lys Glu Val Glu Glu Met Lys His Val Thr Lys Gln Glu
    290                 295                 300

Phe Ile Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala
305                 310                 315                 320

Ser Ile Tyr Arg Gly Val Thr Arg His His Gln Gln Gly Arg Trp Gln
                325                 330                 335

Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr
            340                 345                 350

Phe Ala Thr Glu Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile
        355                 360                 365

Lys Phe Arg Gly Ala Asn Ala Val Thr Asn Phe Glu Met Asn Arg Tyr
    370                 375                 380
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Asp Val Glu Ala Ile Met Lys Ser Ser Leu Pro Val Gly Gly Ala Ala
385                 390                 395                 400

Lys Arg Leu Lys Leu Ser Leu Glu Ser Glu Gln Lys Ala Leu Pro Val
                405                 410                 415

Ser Ser Ser Ser Ser Ser Ser Gln Gln Gln Asn Pro Gln Cys Gly Asn
            420                 425                 430

Val Ser Ala Ser Ile Asn Phe Ser Ser Ile His Gln Pro Ile Ala Ser
        435                 440                 445

Ile Pro Cys Gly Ile Pro Phe Asp Ser Thr Thr Ala Tyr Tyr His His
    450                 455                 460

Asn Leu Phe Gln His Phe His Pro Thr Asn Ala Gly Thr Ala Ala Ser
465                 470                 475                 480

Ala Val Thr Ser Ala Asn Ala Asn Ala Leu Thr Ala Leu Pro Pro Thr
                485                 490                 495

Ala Ala Ala Glu Phe Phe Ile Trp Pro His Gln Ser Tyr
            500                 505


<210> SEQ ID NO 95
<211> LENGTH: 652
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 95

Met Ala Ser Gly Asn Ser Ser Ser Ser Ser Gly Ser Met Ala Ala Thr
1               5                   10                  15

Ala Gly Gly Val Gly Gly Trp Leu Gly Phe Ser Leu Ser Pro His Met
            20                  25                  30

Ala Thr Tyr Cys Ala Gly Gly Val Asp Asp Val Gly His His His His
        35                  40                  45

His His Val His Gln His Gln Gln Gln His Gly Gly Gly Leu Phe Tyr
    50                  55                  60

Asn Pro Ala Ala Val Ala Ser Ser Phe Tyr Tyr Gly Gly Gly His Asp
65                  70                  75                  80

Ala Val Val Thr Ser Ala Ala Gly Gly Gly Ser Tyr Tyr Gly Ala Gly
                85                  90                  95

Phe Ser Ser Met Pro Leu Lys Ser Asp Gly Ser Leu Cys Ile Met Glu
            100                 105                 110

Ala Leu Arg Gly Gly Asp Gln Glu Gln Gln Gly Val Val Val Ser Ala
        115                 120                 125

Ser Pro Lys Leu Glu Asp Phe Leu Gly Ala Gly Pro Ala Met Ala Leu
    130                 135                 140

Ser Leu Asp Asn Ser Ala Phe Tyr Tyr Gly Gly His Gly His His Gln
145                 150                 155                 160

Gly His Ala Gln Asp Gly Gly Ala Val Gly Gly Asp Pro His His Gly
                165                 170                 175

Gly Gly Gly Phe Leu Gln Cys Ala Val Ile Pro Gly Ala Gly Ala Gly
            180                 185                 190

His Asp Ala Ala Leu Val His Asp Gln Ser Ala Ala Ala Val Ala Ala
        195                 200                 205

Gly Trp Ala Ala Met His Gly Gly Gly Tyr Asp Ile Ala Asn Ala Ala
    210                 215                 220

Ala Asp Asp Val Cys Ala Ala Gly Pro Ile Ile Pro Thr Gly Gly His
225                 230                 235                 240
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Leu His Pro Leu Thr Leu Ser Met Ser Ser Ala Gly Ser Gln Ser Ser
                245                 250                 255

Cys Val Thr Val Gln Ala Ala Ala Ala Gly Glu Pro Tyr Met Ala Met
            260                 265                 270

Asp Ala Val Ser Lys Lys Arg Gly Gly Ala Asp Arg Ala Gly Gln Lys
        275                 280                 285

Gln Pro Val His Arg Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser
    290                 295                 300

Gln Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala
305                 310                 315                 320

His Leu Trp Asp Asn Ser Cys Lys Lys Glu Gly Gln Thr Arg Lys Gly
                325                 330                 335

Arg Gln Gly Gly Tyr Asp Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp
            340                 345                 350

Leu Ala Ala Leu Lys Tyr Trp Gly Pro Ser Thr His Ile Asn Phe Pro
        355                 360                 365

Leu Glu Asp Tyr Gln Glu Glu Leu Glu Glu Met Lys Asn Met Ser Arg
    370                 375                 380

Gln Glu Tyr Val Ala His Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg
385                 390                 395                 400

Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg
                405                 410                 415

Trp Gln Ala Arg Ile Gly Arg Val Ser Gly Asn Lys Asp Leu Tyr Leu
            420                 425                 430

Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala
        435                 440                 445

Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Ile Thr
    450                 455                 460

Arg Tyr Asp Val Asp Lys Ile Leu Glu Ser Ser Thr Leu Leu Pro Gly
465                 470                 475                 480

Glu Leu Ala Arg Arg Lys Gly Lys Val Gly Asp Gly Gly Gly Ala Ala
                485                 490                 495

Ala Val Ala Asp Ala Ala Ala Ala Leu Val Gln Ala Gly Asn Val Ala
            500                 505                 510

Glu Trp Lys Met Ala Thr Ala Ala Ala Leu Pro Ala Ala Ala Arg Thr
        515                 520                 525

Glu Gln Gln Gln Gln His Gly His Gly Gly His Gln His His Asp Leu
    530                 535                 540

Leu Pro Ser Asp Ala Phe Ser Val Leu Gln Asp Ile Val Ser Thr Val
545                 550                 555                 560

Asp Ala Ala Gly Ala Pro Pro Arg Ala Pro His Met Ser Met Ala Ala
                565                 570                 575

Thr Ser Leu Gly Asn Ser Arg Glu Gln Ser Pro Asp Arg Gly Val Gly
            580                 585                 590

Gly Gly Gly Gly Gly Gly Val Leu Ala Thr Leu Phe Ala Lys Pro Ala
        595                 600                 605

Ala Ala Ser Lys Leu Tyr Ser Pro Val Pro Leu Asn Thr Trp Ala Ser
    610                 615                 620

Pro Ser Pro Ala Val Ser Ser Val Pro Ala Arg Ala Gly Val Ser Ile
625                 630                 635                 640
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Ala His Leu Pro Met Phe Ala Ala Trp Thr Asp Ala
                645                 650


<210> SEQ ID NO 96
<211> LENGTH: 440
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 96

Met Ala Asp Ser Thr Thr Leu Ser Thr Phe Phe Asp His Ser Gln Thr
1               5                   10                  15

Gln Ile Pro Lys Leu Glu Asp Phe Leu Gly Asp Ser Phe Val Arg Tyr
            20                  25                  30

Ser Asp Asn Gln Thr Glu Thr Gln Asp Ser Ser Ser Leu Thr Pro Phe
        35                  40                  45

Tyr Asp Pro Arg His Arg Thr Val Ala Glu Gly Val Thr Gly Phe Phe
    50                  55                  60

Ser Asp His His Gln Pro Asp Phe Lys Thr Ile Asn Ser Gly Pro Glu
65                  70                  75                  80

Ile Phe Asp Asp Ser Thr Thr Ser Asn Ile Gly Gly Thr His Leu Ser
                85                  90                  95

Ser His Val Val Glu Ser Ser Thr Thr Ala Lys Leu Gly Phe Asn Gly
            100                 105                 110

Asp Cys Thr Thr Thr Gly Gly Val Leu Ser Leu Gly Val Asn Asn Thr
        115                 120                 125

Ser Asp Gln Pro Leu Ser Cys Asn Asn Gly Glu Arg Gly Gly Asn Ser
    130                 135                 140

Asn Lys Lys Lys Thr Val Ser Lys Lys Glu Thr Ser Asp Asp Ser Lys
145                 150                 155                 160

Lys Lys Ile Val Glu Thr Leu Gly Gln Arg Thr Ser Ile Tyr Arg Gly
                165                 170                 175

Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp
            180                 185                 190

Asn Ser Cys Arg Arg Glu Gly Gln Ala Arg Lys Gly Arg Gln Val Tyr
        195                 200                 205

Leu Gly Gly Tyr Asp Lys Glu Asp Arg Ala Ala Arg Ala Tyr Asp Leu
    210                 215                 220

Ala Ala Leu Lys Tyr Trp Gly Ser Thr Ala Thr Thr Asn Phe Pro Val
225                 230                 235                 240

Ser Ser Tyr Ser Lys Glu Leu Glu Glu Met Asn His Met Thr Lys Gln
                245                 250                 255

Glu Phe Ile Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly
            260                 265                 270

Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln Gln Gly Arg Trp
        275                 280                 285

Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly
    290                 295                 300

Thr Phe Ala Thr Glu Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala
305                 310                 315                 320

Ile Lys Phe Arg Gly Ile Asn Ala Val Thr Asn Phe Glu Met Asn Arg
                325                 330                 335

Tyr Asp Ile Glu Ala Val Met Asn Ser Ser Leu Pro Val Gly Gly Ala
            340                 345                 350
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Ala Ala Lys Arg His Lys Leu Lys Leu Ala Leu Glu Ser Pro Ser Ser
        355                 360                 365

Ser Ser Ser Asp His Asn Leu Gln Gln Gln Gln Leu Leu Pro Ser Ser
    370                 375                 380

Ser Pro Ser Asp Gln Asn Pro Asn Ser Ile Pro Cys Gly Ile Pro Phe
385                 390                 395                 400

Glu Pro Ser Val Leu Tyr Tyr His Gln Asn Phe Phe Gln His Tyr Pro
                405                 410                 415

Leu Val Ser Asp Ser Thr Ile Gln Ala Pro Met Asn Gln Ala Glu Phe
            420                 425                 430

Phe Leu Trp Pro Asn Gln Ser Tyr
        435                 440


<210> SEQ ID NO 97
<211> LENGTH: 651
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 97

Met Ala Asn Gly Ser Asn Trp Leu Gly Phe Ser Leu Ser Pro His Thr
1               5                   10                  15

Ala Met Glu Val Pro Ser Val Ser Glu Pro Ala Ser Thr His His Ala
            20                  25                  30

Pro Pro Pro Pro Ser Ser Ser Thr Thr Ile Ser Ser Ser Ser Thr Asn
        35                  40                  45

Asn Thr Ile Ser Ser Asn Phe Leu Phe Ser Pro Met Ala Ser Pro Tyr
    50                  55                  60

Pro Gly Tyr Tyr Cys Val Gly Gly Ala Tyr Gly Asp Gly Thr Ser Ala
65                  70                  75                  80

Ala Gly Val Tyr Tyr Ser His Leu Pro Ala Met Pro Asn Lys Ser Asp
                85                  90                  95

Asp Gly Thr Leu Cys Asn Met Glu Gly Met Val Pro Ser Ser Pro Pro
            100                 105                 110

Lys Leu Glu Asp Phe Leu Gly Gly Gly Asn Gly Gly Gly Gln Glu Thr
        115                 120                 125

Ala Thr Tyr Tyr Ser His Gln Gln Gln Gly Gln Glu Glu Gly Ala Ser
    130                 135                 140

Arg Asp Tyr Arg Gln Tyr His Tyr Gln His Gln Gln Leu Val Pro Tyr
145                 150                 155                 160

Asn Phe Gln Pro Leu Thr Glu Ala Glu Met Leu Gln Glu Gly Ala Ala
                165                 170                 175

Pro Met Glu Glu Ala Met Ala Ala Ala Lys Asn Phe Leu Leu Ala Ser
            180                 185                 190

Tyr Gly Ala Cys Tyr Ser Asn Glu Glu Thr Arg Pro Leu Ser Leu Ser
        195                 200                 205

Met Met Ser Pro Gly Thr Gln Leu Ser Ser Cys Val Ser Ala Ala Pro
    210                 215                 220

Gln Gln Gln His Gln Met Ala Ala Thr Val Ala Thr Ala Ala Thr Ala
225                 230                 235                 240

Ala Ala Ala Leu Gly Arg Ser Asn Gly Asp Gly Glu Gln Cys Val Gly
                245                 250                 255

Arg Lys Arg Ser Thr Gly Lys Gly Gly His Lys Gln Thr Val His Arg
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            260                 265                 270

Lys Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Arg Tyr Arg Gly Val
        275                 280                 285

Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn
    290                 295                 300

Ser Cys Arg Lys Asp Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu
305                 310                 315                 320

Gly Gly Tyr Asp Thr Glu Asp Lys Ala Ala Arg Ala Tyr Asp Leu Ala
                325                 330                 335

Ala Leu Lys Tyr Trp Gly Pro Ala Thr His Val Asn Phe Pro Val Glu
            340                 345                 350

Asn Tyr Arg Asp Glu Leu Glu Glu Met Lys Gly Met Thr Arg Gln Glu
        355                 360                 365

Phe Val Ala His Leu Arg Arg Arg Ser Ser Gly Phe Ser Arg Gly Ala
    370                 375                 380

Ser Ile Tyr Arg Gly Val Thr Arg His His Gln Gln Gly Arg Trp Gln
385                 390                 395                 400

Ser Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr
                405                 410                 415

Phe Thr Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile
            420                 425                 430

Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Ile Ala Arg Tyr
        435                 440                 445

Asp Val Asp Lys Ile Met Glu Ser Ser Thr Leu Leu Ala Val Glu Glu
    450                 455                 460

Ala Arg Lys Val Lys Ala Val Glu Ala Ala Ser Ser Ala Pro Met Thr
465                 470                 475                 480

His Thr His Ser Gly Gly Lys Glu Gln Leu Asn Ala Thr Thr Ala Glu
                485                 490                 495

Glu Thr Ser Ser Ala Gly Trp Arg Met Val Leu His Gly Ser Pro His
            500                 505                 510

Gln Leu Glu Ala Ala Arg Cys Pro Glu Ala Ala Asp Leu Gln Ser Ala
        515                 520                 525

Ile Met Asn Asn Asp Ser His Pro Arg Pro Ser Leu His Gly Ile Ala
    530                 535                 540

Gly Leu Asp Ile Glu Cys Ala Val His Asp His His Asp His Leu Asp
545                 550                 555                 560

Val Pro Ala Gly Ser Arg Thr Thr Ala Ala Gly Ser Ile Asn Phe Ser
                565                 570                 575

Asn Ser Ser Ser Gln Val Thr Ser Leu Gly Asn Ser Arg Glu Gly Ser
            580                 585                 590

Pro Glu Arg Leu Gly Leu Ala Met Met Tyr Gly Lys Gln Pro Ser Ser
        595                 600                 605

Ala Val Ser Leu Ala Ala Thr Met Ser Pro Trp Thr Pro Val Ala Ala
    610                 615                 620

Gln Thr Val Ala His Val Leu Lys Gln Gln Pro Asn Val Val Val Ser
625                 630                 635                 640

His Arg Pro Val Phe Ala Ala Trp Ala Asp Ala
                645                 650

<210> SEQ ID NO 98
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<211> LENGTH: 656
<212> TYPE: PRT
<213> ORGANISM: Medicago truncatula

<400> SEQUENCE: 98

Met Lys Arg Met Glu Asn Asn Asp Asp Ser Val Asp Ile Asn Asn Glu
1               5                   10                  15

Asn Asn Trp Leu Gly Phe Ser Leu Ser Pro Gln Met Asn Asn Ile Gly
            20                  25                  30

Val Ser Ser His Thr His His His Ser Leu Pro Ser Ala Thr Ala Thr
        35                  40                  45

Ala Ser Glu Val Val Pro Leu Gln Ala Ser Phe Tyr His Ser Ser Pro
    50                  55                  60

Leu Ser Asn Phe Cys Tyr Ser Tyr Gly Leu Glu His Glu Asn Ala Gly
65                  70                  75                  80

Leu Tyr Ser Leu Leu Pro Ile Met Pro Leu Lys Ser Asp Gly Ser Leu
                85                  90                  95

Phe Glu Met Glu Ala Leu Ser Arg Ser Gln Thr Gln Ala Met Ser Thr
            100                 105                 110

Thr Ser Ala Pro Lys Leu Glu Asn Phe Leu Gly Asn Glu Ala Met Gly
        115                 120                 125

Thr Pro His Tyr Ala Cys Ser Ser Thr Val Thr Glu Thr Met Pro Leu
    130                 135                 140

Ser Leu Asp Ser Met Phe Gln Asn Gln Ile Gln Gln Asn Met Asn Met
145                 150                 155                 160

Asn Asn Gln Gln His Leu Ser Tyr Tyr Asn Ser Thr Leu Arg Asn His
                165                 170                 175

Glu Leu Met Leu Glu Gly Ser Lys Gln Ser Gln Thr Ser Ser Gly Asn
            180                 185                 190

Phe His Gln Ser Asn Met Gly Glu Asp His Gly Leu Ser Gly Leu Lys
        195                 200                 205

Asn Trp Val Leu Arg Asn Phe Pro Ala Ser His Gly His Asp Gln Ser
    210                 215                 220

Lys Met Ile Val Pro Val Val Glu Glu Asn Glu Gly Glu Cys Gly Ser
225                 230                 235                 240

Asn Ile Gly Ser Met Ala Tyr Gly Asp Leu His Ser Leu Ser Leu Ser
                245                 250                 255

Met Ser Pro Ser Ser Gln Ser Ser Cys Val Thr Thr Ser Gln Asn Met
            260                 265                 270

Ser Ser Ala Val Val Glu Asn Ser Val Ala Met Asp Thr Lys Lys Arg
        275                 280                 285

Gly Ser Glu Lys Phe Glu Gln Lys Gln Ile Val His Arg Lys Ser Ile
    290                 295                 300

Asp Thr Phe Gly Gln Arg Thr Ser Gln Tyr Arg Gly Val Thr Arg His
305                 310                 315                 320

Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser Cys Lys
                325                 330                 335

Lys Glu Gly Gln Ser Arg Lys Gly Arg Gln Gly Gly Tyr Asp Met Glu
            340                 345                 350

Glu Lys Ala Ala Arg Ala Tyr Asp Gln Ala Ala Leu Lys Tyr Trp Gly
        355                 360                 365

Pro Ser Thr His Ile Asn Phe Pro Leu Glu Asn Tyr Gln Asn Gln Leu
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    370                 375                 380

Glu Glu Met Lys Asn Met Thr Arg Gln Glu Tyr Val Ala His Leu Arg
385                 390                 395                 400

Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Met Tyr Arg Gly Val
                405                 410                 415

Thr Ser Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg
            420                 425                 430

Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu
        435                 440                 445

Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Ala
    450                 455                 460

Asn Ala Val Thr Asn Phe Asp Ile Ile Lys Tyr Asp Val Glu Lys Ile
465                 470                 475                 480

Met Ala Ser Ser Asn Leu Leu Asn Ile Glu Gln Ala Arg Arg Asn Lys
                485                 490                 495

Glu Val Val Asp Ile Ser Ser Thr Gln Tyr Ile Asp Gln Asn Lys Pro
            500                 505                 510

Ser Ser Ala Tyr Asp Asn Asn Ser Thr Gln Glu Ala Ile Ser Met Gln
        515                 520                 525

Lys Ser Met Val Leu Tyr Gln Ser Ser Gln His Gln Gln Leu Gln Gln
    530                 535                 540

Asn Gln Pro Arg Phe Glu Asn Glu Arg Thr His Gln Thr Phe Ser Ser
545                 550                 555                 560

Val Ser Leu Asp Asn Met Phe His Gln Glu Val Val Glu Glu Ala Ser
                565                 570                 575

Lys Met Arg Thr His Val Ser Asn Ala Ser Ser Leu Ala Thr Ser Leu
            580                 585                 590

Ser Ser Ser Arg Glu Gly Thr Pro Asp Arg Thr Ser Leu Gln Asn Leu
        595                 600                 605

Ser Gly Ile Met Pro Ser Thr Ala Ser Lys Leu Leu Val Thr Ser Ala
    610                 615                 620

Pro Asn Ser Asn Leu Asn Ser Trp Asp Pro Ser Gln His Leu Arg Pro
625                 630                 635                 640

Ser Leu Ser Leu Pro Gln Met Pro Val Phe Ala Ala Trp Thr Asp Ala
                645                 650                 655


<210> SEQ ID NO 99
<211> LENGTH: 546
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 99

Met Lys Arg Met Asn Glu Ser Asn Asn Thr Asp Asp Gly Asn Asn His
1               5                   10                  15

Asn Trp Leu Gly Phe Ser Leu Ser Pro His Met Lys Met Glu Val Thr
            20                  25                  30

Ser Ala Ala Thr Val Ser Asp Asn Asn Val Pro Thr Thr Phe Tyr Met
        35                  40                  45

Ser Pro Ser His Met Ser Asn Ser Gly Met Cys Tyr Ser Val Gly Glu
    50                  55                  60

Asn Gly Asn Phe His Ser Pro Leu Thr Val Met Pro Leu Lys Ser Asp
65                  70                  75                  80
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Gly Ser Leu Gly Ile Leu Glu Ala Leu Asn Arg Ser Gln Thr Gln Val
                85                  90                  95

Met Val Pro Thr Ser Ser Pro Lys Leu Glu Asp Phe Leu Gly Gly Ala
            100                 105                 110

Thr Met Gly Thr His Glu Tyr Gly Asn His Glu Arg Gly Leu Ser Leu
        115                 120                 125

Asp Ser Ile Tyr Tyr Asn Ser Gln Asn Ala Glu Ala Gln Pro Asn Arg
    130                 135                 140

Asn Leu Leu Ser His Pro Phe Arg Gln Gln Gly His Ala Pro Ser Glu
145                 150                 155                 160

Glu Glu Ala Thr Lys Glu Thr His Val Ser Val Met Pro Gln Met Thr
                165                 170                 175

Gly Gly Gly Leu Gln Asn Trp Ile Leu Glu Gln Gln Met Asn Cys Gly
            180                 185                 190

Ile Trp Asn Glu Arg Ser Gly Val Ser Val Gly Thr Val Gly Cys Gly
        195                 200                 205

Glu Leu Gln Ser Leu Ser Leu Ser Met Ser Pro Gly Ser Gln Ser Ser
    210                 215                 220

Cys Val Thr Ala Pro Ser Gly Thr Asp Ser Val Ala Val Asp Ala Lys
225                 230                 235                 240

Lys Arg Gly His Ala Lys Leu Gly Gln Lys Gln Pro Val His Arg Lys
                245                 250                 255

Ser Ile Asp Thr Phe Gly Gln Arg Thr Ser Gln Tyr Arg Gly Val Thr
            260                 265                 270

Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser
        275                 280                 285

Cys Lys Lys Glu Gly Gln Thr Arg Lys Gly Arg Gln Gly Gly Tyr Asp
    290                 295                 300

Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr
305                 310                 315                 320

Trp Gly Pro Ser Thr His Ile Asn Phe Ser Ile Glu Asn Tyr Gln Val
                325                 330                 335

Gln Leu Glu Glu Met Lys Asn Met Ser Arg Gln Glu Tyr Val Ala His
            340                 345                 350

Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg
        355                 360                 365

Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly
    370                 375                 380

Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln
385                 390                 395                 400

Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly
                405                 410                 415

Ala Asn Ala Val Thr Asn Phe Asp Ile Ser Arg Tyr Asp Val Glu Arg
            420                 425                 430

Ile Met Ala Ser Ser Asn Leu Leu Ala Gly Glu Leu Ala Arg Arg Asn
        435                 440                 445

Lys Asp Asn Asp Pro Arg Asn Glu Ala Ile Asp Tyr Asn Lys Ser Val
    450                 455                 460

Phe Lys Gln Glu Thr Thr Met Lys Met Ile Arg Ser Gly Arg Cys Leu
465                 470                 475                 480

Ser Ser Ser Arg Glu Ala Ser Pro Glu Lys Met Gly Pro Ser Leu Leu
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                485                 490                 495

Phe Pro Lys Pro Pro Pro Met Glu Thr Lys Ile Val Asn Pro Ile Gly
            500                 505                 510

Thr Ser Val Thr Ser Trp Leu Pro Ser Pro Thr Val Gln Met Arg Pro
        515                 520                 525

Ser Pro Ala Ile Ser Leu Ser His Leu Pro Val Phe Ala Ala Trp Thr
    530                 535                 540

Asp Thr
545


<210> SEQ ID NO 100
<211> LENGTH: 415
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 100

Met Lys Lys Trp Leu Gly Phe Ser Leu Thr Pro Pro Leu Arg Ile Cys
1               5                   10                  15

Asn Ser Glu Glu Glu Glu Leu Arg His Asp Gly Ser Asp Val Trp Arg
            20                  25                  30

Tyr Asp Ile Asn Phe Asp His His His His Asp Glu Asp Val Pro Lys
        35                  40                  45

Val Glu Asp Leu Leu Ser Asn Ser His Gln Thr Glu Tyr Pro Ile Asn
    50                  55                  60

His Asn Gln Thr Asn Val Asn Cys Thr Thr Val Val Asn Arg Leu Asn
65                  70                  75                  80

Pro Pro Gly Tyr Leu Leu His Asp Gln Thr Val Val Thr Pro His Tyr
                85                  90                  95

Pro Asn Leu Asp Pro Asn Leu Ser Asn Asp Tyr Gly Gly Phe Glu Arg
            100                 105                 110

Val Gly Ser Val Ser Val Phe Lys Ser Trp Leu Glu Gln Gly Thr Pro
        115                 120                 125

Ala Phe Pro Leu Ser Ser His Tyr Val Thr Glu Glu Ala Gly Thr Ser
    130                 135                 140

Asn Asn Ile Ser His Phe Ser Asn Glu Glu Thr Gly Tyr Asn Thr Asn
145                 150                 155                 160

Gly Ser Met Leu Ser Leu Ala Leu Ser His Gly Ala Cys Ser Asp Leu
                165                 170                 175

Ile Asn Glu Ser Asn Val Ser Ala Arg Val Glu Glu Pro Val Lys Val
            180                 185                 190

Asp Glu Lys Arg Lys Arg Leu Val Val Lys Pro Gln Val Lys Glu Ser
        195                 200                 205

Val Pro Arg Lys Ser Val Asp Ser Tyr Gly Gln Arg Thr Ser Gln Tyr
    210                 215                 220

Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu
225                 230                 235                 240

Trp Asp Asn Ser Cys Lys Lys Glu Gly Gln Thr Arg Arg Gly Arg Gln
                245                 250                 255

Val Tyr Leu Gly Gly Tyr Asp Glu Glu Glu Lys Ala Ala Arg Ala Tyr
            260                 265                 270

Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Thr Thr His Leu Asn Phe
        275                 280                 285
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```
Pro Leu Ser Asn Tyr Glu Lys Glu Ile Glu Glu Leu Asn Asn Met Asn
    290                 295                 300

Arg Gln Glu Phe Val Ala Met Leu Arg Arg Asn Ser Ser Gly Phe Ser
305                 310                 315                 320

Arg Gly Ala Ser Val Tyr Arg Gly Val Thr Arg His His Gln His Gly
                325                 330                 335

Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr
            340                 345                 350

Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Ile
        355                 360                 365

Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Ile
    370                 375                 380

Asn Arg Tyr Asp Val Lys Arg Ile Cys Ser Ser Ser Thr Ile Val Asp
385                 390                 395                 400

Ser Asp Gln Ala Lys His Ser Pro Thr Ser Ser Gly Ala Gly His
                405                 410                 415


<210> SEQ ID NO 101
<211> LENGTH: 428
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 101

Met Ser Pro Pro Thr Asn Gly Ala Ile Ser Leu Ala Tyr Ala Pro Ser
1               5                   10                  15

Met Met Leu Gly Ala Gly Ala Leu Thr Asn Pro Pro Leu Leu Pro Phe
            20                  25                  30

Asp Gly Phe Thr Asp Glu Asp Phe Leu Ala Ser Ala Asp Ala Ala Leu
        35                  40                  45

Leu Gly Glu Ala Gly Thr Asp Gln Thr Leu Leu Leu Leu Pro Ser Cys
    50                  55                  60

Pro Gly Ala Asn Cys Cys Gly Gly Ser Ser Ser Asp Gln Gly Leu Gly
65                  70                  75                  80

Ala Leu Ala Cys Glu Val Thr Thr Ala Gly Ser Phe Ser Leu Leu Gly
                85                  90                  95

Gln Pro Ala Pro Gly Gln Val Ser Trp Glu Val Thr Thr Ala Val Ala
            100                 105                 110

Ala Asp Arg Asn Thr Phe Ser Arg Ala Arg Asp Pro Ala Pro Ser Pro
        115                 120                 125

Pro Pro Ser Pro Ala Leu Pro Leu Val Gln Thr Thr Ser Gln Ser Gln
    130                 135                 140

Arg Thr Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg
145                 150                 155                 160

Tyr Glu Ala His Leu Trp Asp Asn Thr Cys Arg Lys Glu Gly Gln Lys
                165                 170                 175

Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Asp Lys
            180                 185                 190

Ala Ala Arg Ala Tyr Asp Ile Ala Ala Leu Lys Tyr Trp Gly Asp Asn
        195                 200                 205

Ala Thr Thr Asn Phe Pro Arg Glu Asn Tyr Ile Arg Glu Ile Gln Asp
    210                 215                 220

Met Gln Asn Met Asn Arg Arg Asp Val Val Ala Ser Leu Arg Arg Lys
225                 230                 235                 240
```

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```
Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Lys
                245                 250                 255

His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly
            260                 265                 270

Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ala Thr Glu Gln Glu Ala Ala
        275                 280                 285

Glu Ala Tyr Asp Ile Ala Ala Leu Lys Phe Arg Gly Glu Asn Ala Val
    290                 295                 300

Thr Asn Phe Glu Pro Ser Arg Tyr Asn Leu Leu Ala Ile Ala Gln Arg
305                 310                 315                 320

Asp Ile Pro Ile Leu Gly Arg Lys Leu Ile Gln Lys Pro Ala Pro Glu
                325                 330                 335

Ala Glu Asp Gln Ala Ala Leu Ser Ala Arg Ser Phe Ser Gln Ser Gln
            340                 345                 350

Gln Ser Ser Asn Ser Leu Pro Pro Tyr Phe Leu Thr Asn Leu Leu Gln
        355                 360                 365

Pro Leu Pro Ser Gln His Ser Leu Ala Gln Ala Leu Pro Ser Tyr Asn
    370                 375                 380

Asn Leu Gly Phe Gly Glu Pro Ser Leu Tyr Trp Pro Cys Pro Cys Gly
385                 390                 395                 400

Asp Pro Gly Glu Gln Lys Val Gln Leu Gly Ser Lys Leu Glu Ile Val
                405                 410                 415

Asp Gly Leu Val Gln Leu Ala Asn Ser Ala Ala Asn
            420                 425
```

<210> SEQ ID NO 102
<211> LENGTH: 438
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 102

```
Met Lys Lys Arg Leu Thr Thr Ser Thr Cys Ser Ser Ser Pro Ser Ser
1               5                   10                  15

Ser Val Ser Ser Ser Thr Thr Thr Ser Ser Pro Ile Gln Ser Glu Ala
            20                  25                  30

Pro Arg Pro Lys Arg Ala Lys Arg Ala Lys Lys Ser Ser Pro Ser Gly
        35                  40                  45

Asp Lys Ser His Asn Pro Thr Ser Pro Ala Ser Thr Arg Arg Ser Ser
    50                  55                  60

Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Phe Glu Ala
65                  70                  75                  80

His Leu Trp Asp Lys Ser Ser Trp Asn Ser Ile Gln Asn Lys Lys Gly
                85                  90                  95

Lys Gln Val Tyr Leu Gly Ala Tyr Asp Ser Glu Glu Ala Ala Ala His
            100                 105                 110

Thr Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Asp Thr Ile Leu
        115                 120                 125

Asn Phe Pro Ala Glu Thr Tyr Thr Lys Glu Leu Glu Glu Met Gln Arg
    130                 135                 140

Val Thr Lys Glu Glu Tyr Leu Ala Ser Leu Arg Arg Gln Ser Ser Gly
145                 150                 155                 160

Phe Ser Arg Gly Val Ser Lys Tyr Arg Gly Val Ala Arg His His His
```

-continued

```
                165                 170                 175

Asn Gly Arg Trp Glu Ala Arg Ile Gly Arg Val Phe Gly Asn Lys Tyr
            180                 185                 190

Leu Tyr Leu Gly Thr Tyr Asn Thr Gln Glu Glu Ala Ala Ala Ala Tyr
        195                 200                 205

Asp Met Ala Ala Ile Glu Tyr Arg Gly Ala Asn Ala Val Thr Asn Phe
    210                 215                 220

Asp Ile Ser Asn Tyr Ile Asp Arg Leu Lys Lys Lys Gly Val Phe Pro
225                 230                 235                 240

Phe Pro Val Asn Gln Ala Asn His Gln Glu Gly Ile Leu Val Glu Ala
                245                 250                 255

Lys Gln Glu Val Glu Thr Arg Glu Ala Lys Glu Glu Pro Arg Glu Glu
            260                 265                 270

Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Glu Lys
        275                 280                 285

Glu Glu Glu Lys Ala Glu Gln Gln Glu Ala Glu Ile Val Gly Tyr Ser
    290                 295                 300

Glu Glu Ala Ala Val Val Asn Cys Cys Ile Asp Ser Ser Thr Ile Met
305                 310                 315                 320

Glu Met Asp Arg Cys Gly Asp Asn Asn Glu Leu Ala Trp Asn Phe Cys
                325                 330                 335

Met Met Asp Thr Gly Phe Ser Pro Phe Leu Thr Asp Gln Asn Leu Ala
            340                 345                 350

Asn Glu Asn Pro Ile Glu Tyr Pro Glu Leu Phe Asn Glu Leu Ala Phe
        355                 360                 365

Glu Asp Asn Ile Asp Phe Met Phe Asp Asp Gly Lys His Glu Cys Leu
    370                 375                 380

Asn Leu Glu Asn Leu Asp Cys Cys Val Val Gly Arg Glu Ser Pro Pro
385                 390                 395                 400

Ser Ser Ser Ser Pro Leu Ser Cys Leu Ser Thr Asp Ser Ala Ser Ser
                405                 410                 415

Thr Thr Thr Thr Thr Thr Ser Val Ser Cys Asn Tyr Leu Phe Gln Gly
            420                 425                 430

Leu Phe Val Gly Ser Glu
        435


<210> SEQ ID NO 103
<211> LENGTH: 432
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 103

Met Trp Asp Leu Asn Asp Ala Pro His Gln Thr Gln Arg Glu Glu Glu
1               5                   10                  15

Ser Glu Glu Phe Cys Tyr Ser Ser Pro Ser Lys Arg Val Gly Ser Phe
            20                  25                  30

Ser Asn Ser Ser Ser Ser Ala Val Val Ile Glu Asp Gly Ser Asp Asp
        35                  40                  45

Asp Glu Leu Asn Arg Val Arg Pro Asn Asn Pro Leu Val Thr His Gln
    50                  55                  60

Phe Phe Pro Glu Met Asp Ser Asn Gly Gly Gly Val Ala Ser Gly Phe
65                  70                  75                  80
```

-continued

```
Pro Arg Ala His Trp Phe Gly Val Lys Phe Cys Gln Ser Asp Leu Ala
                85                  90                  95

Thr Gly Ser Ser Ala Gly Lys Ala Thr Asn Val Ala Ala Ala Val Val
            100                 105                 110

Glu Pro Ala Gln Pro Leu Lys Lys Ser Arg Arg Gly Pro Arg Ser Arg
        115                 120                 125

Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr Gly Arg Trp
    130                 135                 140

Glu Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu Gly Gly Phe
145                 150                 155                 160

Asp Thr Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys
                165                 170                 175

Phe Arg Gly Val Glu Ala Asp Ile Asn Phe Asn Ile Asp Asp Tyr Asp
            180                 185                 190

Asp Asp Leu Lys Gln Met Thr Asn Leu Thr Lys Glu Glu Phe Val His
        195                 200                 205

Val Leu Arg Arg Gln Ser Thr Gly Phe Pro Arg Gly Ser Ser Lys Tyr
    210                 215                 220

Arg Gly Val Thr Leu His Lys Cys Gly Arg Trp Glu Ala Arg Met Gly
225                 230                 235                 240

Gln Phe Leu Gly Lys Lys Tyr Val Tyr Leu Gly Leu Phe Asp Thr Glu
                245                 250                 255

Val Glu Ala Ala Arg Ala Tyr Asp Lys Ala Ala Ile Lys Cys Asn Gly
            260                 265                 270

Lys Asp Ala Val Thr Asn Phe Asp Pro Ser Ile Tyr Asp Glu Glu Leu
        275                 280                 285

Asn Ala Glu Ser Ser Gly Asn Pro Thr Thr Pro Gln Asp His Asn Leu
    290                 295                 300

Asp Leu Ser Leu Gly Asn Ser Ala Asn Ser Lys His Lys Ser Gln Asp
305                 310                 315                 320

Met Arg Leu Arg Met Asn Gln Gln Gln Gln Asp Ser Leu His Ser Asn
                325                 330                 335

Glu Val Leu Gly Leu Gly Gln Thr Gly Met Leu Asn His Thr Pro Asn
            340                 345                 350

Ser Asn His Gln Phe Pro Gly Ser Ser Asn Ile Gly Ser Gly Gly Gly
        355                 360                 365

Phe Ser Leu Phe Pro Ala Ala Glu Asn His Arg Phe Asp Gly Arg Ala
    370                 375                 380

Ser Thr Asn Gln Val Leu Thr Asn Ala Ala Ala Ser Ser Gly Phe Ser
385                 390                 395                 400

Pro His His His Asn Gln Ile Phe Asn Ser Thr Ser Thr Pro His Gln
                405                 410                 415

Asn Trp Leu Gln Thr Asn Gly Phe Gln Pro Pro Leu Met Arg Pro Ser
            420                 425                 430


<210> SEQ ID NO 104
<211> LENGTH: 449
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 104

Met Leu Asp Leu Asn Leu Asn Ala Asp Ser Pro Glu Ser Thr Gln Tyr
1               5                   10                  15
```

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```
Gly Gly Asp Ser Tyr Leu Asp Arg Gln Thr Ser Asp Asn Ser Ala Gly
            20                  25                  30

Asn Arg Val Glu Glu Ser Gly Thr Ser Thr Ser Ser Val Ile Asn Ala
        35                  40                  45

Asp Gly Asp Glu Asp Ser Cys Ser Thr Arg Ala Phe Thr Leu Ser Phe
    50                  55                  60

Asp Ile Leu Lys Val Gly Ser Ser Ser Gly Gly Asp Glu Ser Pro Ala
65                  70                  75                  80

Ala Ser Ala Ser Val Thr Lys Glu Phe Phe Pro Val Ser Gly Asp Cys
                85                  90                  95

Gly His Leu Arg Asp Val Glu Gly Ser Ser Ser Ser Arg Asn Trp Ile
            100                 105                 110

Asp Leu Ser Phe Asp Arg Ile Gly Asp Gly Glu Thr Lys Leu Val Thr
        115                 120                 125

Pro Val Pro Thr Pro Ala Pro Val Pro Ala Gln Val Lys Lys Ser Arg
    130                 135                 140

Arg Gly Pro Arg Ser Arg Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr
145                 150                 155                 160

Arg Arg Thr Gly Arg Trp Glu Ser His Ile Trp Asp Cys Gly Lys Gln
                165                 170                 175

Val Tyr Leu Gly Gly Phe Asp Thr Ala His Ala Ala Ala Arg Ala Tyr
            180                 185                 190

Asp Arg Ala Ala Ile Lys Phe Arg Gly Val Asp Ala Asp Ile Asn Phe
        195                 200                 205

Thr Leu Gly Asp Tyr Glu Glu Asp Met Lys Gln Val Gln Asn Leu Ser
    210                 215                 220

Lys Glu Glu Phe Val His Ile Leu Arg Arg Gln Ser Thr Gly Phe Ser
225                 230                 235                 240

Arg Gly Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg
                245                 250                 255

Trp Glu Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Ala Tyr Asp Lys
            260                 265                 270

Ala Ala Ile Asn Thr Asn Gly Arg Glu Ala Val Thr Asn Phe Glu Met
        275                 280                 285

Ser Ser Tyr Gln Asn Glu Ile Asn Ser Glu Ser Asn Asn Ser Glu Ile
    290                 295                 300

Asp Leu Asn Leu Gly Ile Ser Leu Ser Thr Gly Asn Ala Pro Lys Gln
305                 310                 315                 320

Asn Gly Arg Leu Phe His Phe Pro Ser Asn Thr Tyr Glu Thr Gln Arg
                325                 330                 335

Gly Val Ser Leu Arg Ile Asp Asn Glu Tyr Met Gly Lys Pro Val Asn
            340                 345                 350

Thr Pro Leu Pro Tyr Gly Ser Ser Asp His Arg Leu Tyr Trp Asn Gly
        355                 360                 365

Ala Cys Pro Ser Tyr Asn Asn Pro Ala Glu Gly Arg Ala Thr Glu Lys
    370                 375                 380

Arg Ser Glu Ala Glu Gly Met Met Ser Asn Trp Gly Trp Gln Arg Pro
385                 390                 395                 400

Gly Gln Thr Ser Ala Val Arg Pro Gln Pro Pro Gly Pro Gln Pro Pro
                405                 410                 415
```

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```
Pro Leu Phe Ser Val Ala Ala Ala Ser Ser Gly Phe Ser His Phe Arg
            420                 425                 430

Pro Gln Pro Pro Asn Asp Asn Ala Thr Arg Gly Tyr Phe Tyr Pro His
        435                 440                 445

Pro


<210> SEQ ID NO 105
<211> LENGTH: 663
<212> TYPE: DNA
<213> ORGANISM: Zea mays
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(663)

<400> SEQUENCE: 105

atg gag gcg ctg agc ggg cgg gta ggc gtc aag tgc ggg cgg tgg aac       48
Met Glu Ala Leu Ser Gly Arg Val Gly Val Lys Cys Gly Arg Trp Asn
1               5                   10                  15

cct acg gcg gag cag gtg aag gtc ctg acg gag ctc ttc cgc gcg ggg       96
Pro Thr Ala Glu Gln Val Lys Val Leu Thr Glu Leu Phe Arg Ala Gly
            20                  25                  30

ctg cgg acg ccc agc acg gag cag atc cag cgc atc tcc acc cac ctc      144
Leu Arg Thr Pro Ser Thr Glu Gln Ile Gln Arg Ile Ser Thr His Leu
        35                  40                  45

agc gcc ttc ggc aag gtg gag agc aag aac gtc ttc tac tgg ttc cag      192
Ser Ala Phe Gly Lys Val Glu Ser Lys Asn Val Phe Tyr Trp Phe Gln
    50                  55                  60

aac cac aag gcc cgc gag cgc cac cac cac aag aag cgc cgc cgc ggc      240
Asn His Lys Ala Arg Glu Arg His His His Lys Lys Arg Arg Arg Gly
65                  70                  75                  80

gcg tcg tcg tcc tcc ccc gac agc ggc agc ggc agg gga agc aac aac      288
Ala Ser Ser Ser Ser Pro Asp Ser Gly Ser Gly Arg Gly Ser Asn Asn
                85                  90                  95

gag gaa gac ggc cgt ggt gcc gcc tcg cag tcg cac gac gcc gac gcc      336
Glu Glu Asp Gly Arg Gly Ala Ala Ser Gln Ser His Asp Ala Asp Ala
            100                 105                 110

gac gcc gac ctc gtg ctg caa ccg cca gag agc aag cgg gag gcc aga      384
Asp Ala Asp Leu Val Leu Gln Pro Pro Glu Ser Lys Arg Glu Ala Arg
        115                 120                 125

agc tat ggc cac cat cac cgg ctc gtg aca tgc tac gtc agg gac gtg      432
Ser Tyr Gly His His His Arg Leu Val Thr Cys Tyr Val Arg Asp Val
    130                 135                 140

gtg gag cag cag gag gcg tcg ccg tcg tgg gag cgg ccg acg agg gag      480
Val Glu Gln Gln Glu Ala Ser Pro Ser Trp Glu Arg Pro Thr Arg Glu
145                 150                 155                 160

gtg gag acg cta gag ctc ttc ccc ctc aag tcg tac ggc gac ctc gag      528
Val Glu Thr Leu Glu Leu Phe Pro Leu Lys Ser Tyr Gly Asp Leu Glu
                165                 170                 175

gcg gcg gag aag gtc cgg tcg tac gtc aga ggc atc gcc gcc acc agc      576
Ala Ala Glu Lys Val Arg Ser Tyr Val Arg Gly Ile Ala Ala Thr Ser
            180                 185                 190

gag cag tgc agg gag ttg tcc ttc ttc gac gtc tcc gcc ggc cgg gat      624
Glu Gln Cys Arg Glu Leu Ser Phe Phe Asp Val Ser Ala Gly Arg Asp
        195                 200                 205

ccg ccg ctc gag ctc agg ctc tgc agc ttc ggt ccc tag                  663
Pro Pro Leu Glu Leu Arg Leu Cys Ser Phe Gly Pro
    210                 215                 220
```

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<210> SEQ ID NO 106
<211> LENGTH: 220
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 106

Met Glu Ala Leu Ser Gly Arg Val Gly Val Lys Cys Gly Arg Trp Asn
1               5                   10                  15

Pro Thr Ala Glu Gln Val Lys Val Leu Thr Glu Leu Phe Arg Ala Gly
            20                  25                  30

Leu Arg Thr Pro Ser Thr Glu Gln Ile Gln Arg Ile Ser Thr His Leu
        35                  40                  45

Ser Ala Phe Gly Lys Val Glu Ser Lys Asn Val Phe Tyr Trp Phe Gln
    50                  55                  60

Asn His Lys Ala Arg Glu Arg His His His Lys Lys Arg Arg Arg Gly
65                  70                  75                  80

Ala Ser Ser Ser Ser Pro Asp Ser Gly Ser Gly Arg Gly Ser Asn Asn
                85                  90                  95

Glu Glu Asp Gly Arg Gly Ala Ala Ser Gln Ser His Asp Ala Asp Ala
            100                 105                 110

Asp Ala Asp Leu Val Leu Gln Pro Pro Glu Ser Lys Arg Glu Ala Arg
        115                 120                 125

Ser Tyr Gly His His His Arg Leu Val Thr Cys Tyr Val Arg Asp Val
    130                 135                 140

Val Glu Gln Gln Glu Ala Ser Pro Ser Trp Glu Arg Pro Thr Arg Glu
145                 150                 155                 160

Val Glu Thr Leu Glu Leu Phe Pro Leu Lys Ser Tyr Gly Asp Leu Glu
                165                 170                 175

Ala Ala Glu Lys Val Arg Ser Tyr Val Arg Gly Ile Ala Ala Thr Ser
            180                 185                 190

Glu Gln Cys Arg Glu Leu Ser Phe Phe Asp Val Ser Ala Gly Arg Asp
        195                 200                 205

Pro Pro Leu Glu Leu Arg Leu Cys Ser Phe Gly Pro
    210                 215                 220


<210> SEQ ID NO 107
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: attB1 variant

<400> SEQUENCE: 107

caagttcgta caaaaaagca ggct                                            24


<210> SEQ ID NO 108
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: attB1 variant

<400> SEQUENCE: 108

caagtttgta caaaaaggac tct                                             23


<210> SEQ ID NO 109
<211> LENGTH: 24
```

-continued

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: attB1 variant

<400> SEQUENCE: 109

caagtgcata caaaaaggac tgct 24

<210> SEQ ID NO 110
<211> LENGTH: 17747
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PHP32371
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4310)...(4817)
<223> OTHER INFORMATION: Rab17 promoter
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4818)...(4912)
<223> OTHER INFORMATION: Rab17 5' UTR
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4951)...(4974)
<223> OTHER INFORMATION: attB1
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5036)...(6496)
<223> OTHER INFORMATION: FLP
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6513)...(6536)
<223> OTHER INFORMATION: attB2
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6551)...(6868)
<223> OTHER INFORMATION: PinII term

<400> SEQUENCE: 110

gtttacccgc caatatatcc tgtcaaacac tgatagttta aactgaaggc gggaaacgac 60

aatctgatca tgagcggaga attaagggag tcacgttatg acccccgccg atgacgcggg 120

acaagccgtt ttacgtttgg aactgacaga accgcaacgt tgaaggagcc actcagcaag 180

ctggtacgat tgtaatacga ctcactatag ggcgaattga gcgctgttta aacgctcttc 240

aactggaaga gcggttacca gagctggtca cctttgtcca ccaagatgga actgcggccg 300

ctcattaatt aagtcaggcg cgcctctagt tgaagacacg ttcatgtctt catcgtaaga 360

agacactcag tagtcttcgg ccagaatggc catctggatt cagcaggcct agaaggccat 420

ttaaatcctg aggatctggt cttcctaagg acccgggata tcgctatcaa ctttgtatag 480

aaaagttggg ccgaattcga gctcggtacg gccagaatgg cccggaccgg gttaccgaat 540

tcgagctcgg taccctggga tccggtgcgg gcctcttcgc tattacgcca gctggcgaaa 600

gggggatgtg ctgcaaggcg attaagttgg gtaacgccag ggttttccca gtcacgacgt 660

tgtaaaacga cggccagtgc caagctcaga tcagcttgca tgcctgcagt gcagcgtgac 720

ccggtcgtgc ccctctctag agataatgag cattgcatgt ctaagttata aaaaattacc 780

acatattttt tttgtcacac ttgtttgaag tgcagtttat ctatctttat acatatattt 840

aaactttact ctacgaataa tataatctat agtactacaa taatatcagt gttttagaga 900

atcatataaa tgaacagtta gacatggtct aaaggacaat tgagtatttt gacaacagga 960

ctctacagtt ttatcttttt agtgtgcatg tgttctcctt tttttttgca aatagcttca 1020

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```
cctatataat acttcatcca ttttattagt acatccattt agggtttagg gttaatggtt   1080

tttatagact aatttttta gtacatctat tttattctat tttagcctct aaattaagaa   1140

aactaaaact ctattttagt ttttttattt aataatttag atataaaata gaataaaata   1200

aagtgactaa aaattaaaca aatacccttt aagaaattaa aaaaactaag gaaacatttt   1260

tcttgtttcg agtagataat gccagcctgt taaacgccgt cgacgagtct aacggacacc   1320

aaccagcgaa ccagcagcgt cgcgtcgggc caagcgaagc agacggcacg gcatctctgt   1380

cgctgcctct ggacccctct cgagagttcc gctccaccgt tggacttgct ccgctgtcgg   1440

catccagaaa ttgcgtggcg gagcggcaga cgtgagccgg cacggcaggc ggcctcctcc   1500

tcctctcacg gcacggcagc tacgggggat tcctttccca ccgctccttc gctttccctt   1560

cctcgcccgc cgtaataaat agacaccccc tccacacct ctttccccaa cctcgtgttg   1620

ttcggagcgc acacacacac aaccagatct cccccaaatc cacccgtcgg cacctccgct   1680

tcaaggtacg ccgctcgtcc tccccccccc cccctctcta ccttctctag atcggcgttc   1740

cggtccatgg ttagggcccg gtagttctac ttctgttcat gtttgtgtta gatccgtgtt   1800

tgtgttagat ccgtgctgct agcgttcgta cacggatgcg acctgtacgt cagacacgtt   1860

ctgattgcta acttgccagt gtttctcttt ggggaatcct gggatggctc tagccgttcc   1920

gcagacggga tcgatttcat gatttttttt gtttcgttgc atagggtttg gtttgccctt   1980

ttcctttatt tcaatatatg ccgtgcactt gtttgtcggg tcatcttttc atgctttttt   2040

ttgtcttggt tgtgatgatg tggtctggtt gggcggtcgt tctagatcgg agtagaattc   2100

tgtttcaaac tacctggtgg atttattaat tttggatctg tatgtgtgtg ccatacatat   2160

tcatagttac gaattgaaga tgatggatgg aaatatcgat ctaggatagg tatacatgtt   2220

gatgcgggtt ttactgatgc atatacagag atgctttttg ttcgcttggt tgtgatgatg   2280

tggtgtggtt gggcggtcgt tcattcgttc tagatcggag tagaatactg tttcaaacta   2340

cctggtgtat ttattaattt tggaactgta tgtgtgtgtc atacatcttc atagttacga   2400

gtttaagatg gatggaaata tcgatctagg ataggtatac atgttgatgt gggttttact   2460

gatgcatata catgatggca tatgcagcat ctattcatat gctctaacct tgagtaccta   2520

tctattataa taaacaagta tgttttataa ttattttgat cttgatatac ttggatgatg   2580

gcatatgcag cagctatatg tggatttttt tagccctgcc ttcatacgct atttatttgc   2640

ttggtactgt ttcttttgtc gatgctcacc ctgttgtttg gtgttacttc tgcaggtcga   2700

ctctagagga tccaccatgg ctagcgaagt tcctattccg aagttcctat tctctagaaa   2760

gtataggaac ttcagatctg ccctgtccaa caagttcatc ggcgacgaca tgaagatgac   2820

ctaccacatg gacggctgcg tgaacggcca ctacttcacc gtgaagggcg agggcagcgg   2880

caagccctac gagggcaccc agacctccac cttcaaggtg accatggcca acggcggccc   2940

cctggccttc tccttcgaca tcctgtccac cgtgttcatg tacggcaacc gctgcttcac   3000

cgcctacccc accagcatgc ccgactactt caagcaggcc ttccccgacg gcatgtccta   3060

cgagagaacc ttcacctacg aggacggcgg cgtggccacc gccagctggg agatcagcct   3120

gaagggcaac tgcttcgagc acaagtccac cttccacggc gtgaacttcc ccgccgacgg   3180

ccccgtgatg gccaagaaga ccaccggctg ggacccctcc ttcgagaaga tgaccgtgtg   3240

cgacggcatc ttgaagggcg acgtgaccgc cttcctgatg ctgcagggcg gcggcaacta   3300
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cagatgccag ttccacacct cctacaagac caagaagccc gtgaccatgc cccccaacca 3360

cgtggtggag caccgcatcg ccagaaccga cctggacaag ggcggcaaca gcgtgcagct 3420

gaccgagcac gccgtggccc acatcacctc cgtggtgccc ttctgaagcg gccgcaacct 3480

agacttgtcc atcttctgga ttggccaact taattaatgt atgaaataaa aggatgcaca 3540

catagtgaca tgctaatcac tataatgtgg gcatcaaagt tgtgtgttat gtgtaattac 3600

tagttatctg aataaaagag aaagagatca tccatatttc ttatcctaaa tgaatgtcac 3660

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cacgactttt tctcggcagg gcagcaggcc gccgccgctg cgatgcacgg cctgggtagc 9300

atcgacagtg cgtcgctcga gcacagcacc ggctccaact ccgtcgtcta caacggcggg 9360

gtcggcgaca gcaacggcgc cagcgccgtc ggcggcagtg gcggtggcta catgatgccg 9420

atgagcgctg ccggagcaac cactacatcg gcaatggtga gccacgagca ggtgcatgca 9480

cgggcctacg acgaagccaa gcaggctgct cagatggggt acgagagcta cctggtgaac 9540

gcggagaaca atggtggcgg aaggatgtct gcatggggga ctgtcgtgtc tgcagccgcg 9600

gcggcagcag caagcagcaa cgacaacatg gccgccgacg tcgggcatgg cggcgcgcag 9660

ctcttcagtg tctggaacga cacttaagcg tacgtgccgg cctggctctc cgaaagggcg 9720

tattccagca cactggcggc cgttactaga cccaacctag acttgtccat cttctggatt 9780

ggccaactta attaatgtat gaaataaaag gatgcacaca tagtgacatg ctaatcacta 9840

taatgtgggc atcaaagttg tgtgttatgt gtaattacta gttatctgaa taaaagagaa 9900

agagatcatc catatttctt atcctaaatg aatgtcacgt gtctttataa ttctttgatg 9960

aaccagatgc atttcattaa ccaaatccat atacatataa atattaatca tatataatta 10020

atatcaattg ggttagcaaa acaaatctag tctaggtgtg ttttgcgaat tagcttggtc 10080

acccggtccg ggcctagaag gccagcttcg gccgccccgg gcaactttat tatacaaagt 10140

tgatagatcg aataacttcg tatagcatac attatacgaa gttatcctga gctgattccg 10200

atgacttcgt aggttcctag ctcaagccgc tcgtgtccaa gcgtcactta cgattagcta 10260

atgattacgg catctaggac cgactagcta actaactagt acgtagaatt gtagaattaa 10320

ttcattccga ttaatcgtgg cctcttgctc ttcaggatga agagctatgt ttaaacgtgc 10380

aagcgctact agacaattca gtacattaaa aacgtccgca atgtgttatt aagttgtcta 10440

agcgtcaatt tgtttacacc acaatatatc ctgccac 10477

<210> SEQ ID NO 114
<211> LENGTH: 978
<212> TYPE: DNA
<213> ORGANISM: Zea mays
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(978)

<400> SEQUENCE: 114

atg gcg gcc aat gcg ggc ggc ggt gga gcg gga gga ggc agc ggc agc 48
Met Ala Ala Asn Ala Gly Gly Gly Gly Ala Gly Gly Gly Ser Gly Ser

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1               5                   10                  15

ggc agc gtg gct gcg ccg gcg gtg tgc cgc ccc agc ggc tcg cgg tgg       96
Gly Ser Val Ala Ala Pro Ala Val Cys Arg Pro Ser Gly Ser Arg Trp
            20                  25                  30

acg ccg acg ccg gag cag atc agg atg ctg aag gag ctc tac tac ggc      144
Thr Pro Thr Pro Glu Gln Ile Arg Met Leu Lys Glu Leu Tyr Tyr Gly
        35                  40                  45

tgc ggc atc cgg tcg ccc agc tcg gag cag atc cag cgc atc acc gcc      192
Cys Gly Ile Arg Ser Pro Ser Ser Glu Gln Ile Gln Arg Ile Thr Ala
    50                  55                  60

atg ctg cgg cag cac ggc aag atc gag ggc aag aac gtc ttc tac tgg      240
Met Leu Arg Gln His Gly Lys Ile Glu Gly Lys Asn Val Phe Tyr Trp
65                  70                  75                  80

ttc cag aac cac aag gcc cgc gag cgc cag aag cgc cgc ctc acc agc      288
Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Arg Arg Leu Thr Ser
                85                  90                  95

ctc gac gtc aac gtg ccc gcc gcc ggc gcg gcc gac gcc acc acc agc      336
Leu Asp Val Asn Val Pro Ala Ala Gly Ala Ala Asp Ala Thr Thr Ser
            100                 105                 110

caa ctc ggc gtc ctc tcg ctg tcg tcg ccg cct tca ggc gcg gcg cct      384
Gln Leu Gly Val Leu Ser Leu Ser Ser Pro Pro Ser Gly Ala Ala Pro
        115                 120                 125

ccc tcg ccc acc ctc ggc ttc tac gcc gcc ggc aat ggc ggc gga tcg      432
Pro Ser Pro Thr Leu Gly Phe Tyr Ala Ala Gly Asn Gly Gly Gly Ser
    130                 135                 140

gct ggg ctg ctg gac acg agt tcc gac tgg ggc agc agc ggc gct gct      480
Ala Gly Leu Leu Asp Thr Ser Ser Asp Trp Gly Ser Ser Gly Ala Ala
145                 150                 155                 160

atg gcc acc gag aca tgc ttc ctg cag gac tac atg ggc gtg acg gac      528
Met Ala Thr Glu Thr Cys Phe Leu Gln Asp Tyr Met Gly Val Thr Asp
                165                 170                 175

acg ggc agc tcg tcg cag tgg cca tgc ttc tcg tcg tcg gac acg ata      576
Thr Gly Ser Ser Ser Gln Trp Pro Cys Phe Ser Ser Ser Asp Thr Ile
            180                 185                 190

atg gcg gcg gcg gcg gcc gcg gcg cgg gtg gcg acg acg cgg gcg ccc      624
Met Ala Ala Ala Ala Ala Ala Ala Arg Val Ala Thr Thr Arg Ala Pro
        195                 200                 205

gag aca ctc cct ctc ttc ccg acc tgc ggc gac gac gac gac gac gac      672
Glu Thr Leu Pro Leu Phe Pro Thr Cys Gly Asp Asp Asp Asp Asp Asp
    210                 215                 220

agc cag ccc ccg ccg cgg ccg cgg cac gca gtc cca gtc ccg gca ggc      720
Ser Gln Pro Pro Pro Arg Pro Arg His Ala Val Pro Val Pro Ala Gly
225                 230                 235                 240

gag acc atc cgc ggc ggc ggc ggc agc agc agc agc tac ttg ccg ttc      768
Glu Thr Ile Arg Gly Gly Gly Gly Ser Ser Ser Ser Tyr Leu Pro Phe
                245                 250                 255

tgg ggt gcc ggt gcc gcg tcc aca act gcc ggc gcc act tct tcc gtt      816
Trp Gly Ala Gly Ala Ala Ser Thr Thr Ala Gly Ala Thr Ser Ser Val
            260                 265                 270

gcg atc cag cag caa cac cag ctg cag gag cag tac agc ttt tac agc      864
Ala Ile Gln Gln Gln His Gln Leu Gln Glu Gln Tyr Ser Phe Tyr Ser
        275                 280                 285

aac agc acc cag ctg gcc ggc acc ggc agc caa gac gta tcg gct tca      912
Asn Ser Thr Gln Leu Ala Gly Thr Gly Ser Gln Asp Val Ser Ala Ser
    290                 295                 300

gcg gcc gcc ctg gag ctg agc ctc agc tca tgg tgc tcc cct tac cct      960
Ala Ala Ala Leu Glu Leu Ser Leu Ser Ser Trp Cys Ser Pro Tyr Pro
```

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305                 310                 315                 320

gct gca ggg agc atg tga                                              978
Ala Ala Gly Ser Met
                325


<210> SEQ ID NO 115
<211> LENGTH: 325
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 115

Met Ala Ala Asn Ala Gly Gly Gly Gly Ala Gly Gly Gly Ser Gly Ser
1               5                   10                  15

Gly Ser Val Ala Ala Pro Ala Val Cys Arg Pro Ser Gly Ser Arg Trp
            20                  25                  30

Thr Pro Thr Pro Glu Gln Ile Arg Met Leu Lys Glu Leu Tyr Tyr Gly
        35                  40                  45

Cys Gly Ile Arg Ser Pro Ser Ser Glu Gln Ile Gln Arg Ile Thr Ala
    50                  55                  60

Met Leu Arg Gln His Gly Lys Ile Glu Gly Lys Asn Val Phe Tyr Trp
65                  70                  75                  80

Phe Gln Asn His Lys Ala Arg Glu Arg Gln Lys Arg Arg Leu Thr Ser
                85                  90                  95

Leu Asp Val Asn Val Pro Ala Ala Gly Ala Ala Asp Ala Thr Thr Ser
            100                 105                 110

Gln Leu Gly Val Leu Ser Leu Ser Ser Pro Pro Ser Gly Ala Ala Pro
        115                 120                 125

Pro Ser Pro Thr Leu Gly Phe Tyr Ala Ala Gly Asn Gly Gly Gly Ser
    130                 135                 140

Ala Gly Leu Leu Asp Thr Ser Ser Asp Trp Gly Ser Ser Gly Ala Ala
145                 150                 155                 160

Met Ala Thr Glu Thr Cys Phe Leu Gln Asp Tyr Met Gly Val Thr Asp
                165                 170                 175

Thr Gly Ser Ser Ser Gln Trp Pro Cys Phe Ser Ser Ser Asp Thr Ile
            180                 185                 190

Met Ala Ala Ala Ala Ala Ala Ala Arg Val Ala Thr Thr Arg Ala Pro
        195                 200                 205

Glu Thr Leu Pro Leu Phe Pro Thr Cys Gly Asp Asp Asp Asp Asp Asp
    210                 215                 220

Ser Gln Pro Pro Pro Arg Pro Arg His Ala Val Pro Val Pro Ala Gly
225                 230                 235                 240

Glu Thr Ile Arg Gly Gly Gly Gly Ser Ser Ser Ser Tyr Leu Pro Phe
                245                 250                 255

Trp Gly Ala Gly Ala Ala Ser Thr Thr Ala Gly Ala Thr Ser Ser Val
            260                 265                 270

Ala Ile Gln Gln Gln His Gln Leu Gln Glu Gln Tyr Ser Phe Tyr Ser
        275                 280                 285

Asn Ser Thr Gln Leu Ala Gly Thr Gly Ser Gln Asp Val Ser Ala Ser
    290                 295                 300

Ala Ala Ala Leu Glu Leu Ser Leu Ser Ser Trp Cys Ser Pro Tyr Pro
305                 310                 315                 320

Ala Ala Gly Ser Met
                325
```

<210> SEQ ID NO 116
<211> LENGTH: 3727
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 116

atggccactg tgaacaactg gctcgctttc tccctctccc cgcaggagct gccgccctcc 60

cagacgacgg actccacact catctcggcc gccaccgccg accatgtctc cggcgatgtc 120

tgcttcaaca tcccccaaga ttggagcatg aggggatcag agctttcggc gctcgtcgcg 180

gagccgaagc tggaggactt cctcggcggc atctccttct ccgagcagca tcacaaggcc 240

aactgcaaca tgatacccag cactagcagc acagtttgct acgcgagctc aggtgctagc 300

accggctacc atcaccagct gtaccaccag cccaccagct cagcgctcca cttcgcggac 360

tccgtaatgg tggcctcctc ggccggtgtc cacgacggcg gtgccatgct cagcgcggcc 420

gccgctaacg gtgtcgctgg cgctgccagt gccaacggcg gcggcatcgg gctgtccatg 480

atcaagaact ggctgcggag ccaaccggcg cccatgcagc cgagggcggc ggcggctgag 540

ggcgcgcagg ggctctcttt gtccatgaac atggcgggga cgacccaagg cgctgctggc 600

atgccacttc tcgctggaga gcgcgcacgg gcgcccgaga gtgtatcgac gtcagcacag 660

ggtggtgccg tcgtcgtcac ggcgccgaag gaggatagcg gtggcagcgg tgttgccggt 720

gctctagtag ccgtgagcac ggacacgggt ggcagcggcg gcgcgtcggc tgacaacacg 780

gcaaggaaga cggtggacac gttcgggcag cgcacgtcga tttaccgtgg cgtgacaagg 840

taagggggtg gatgaatcaa gtaatcatga aattttgaaa agccattggt aatccaagga 900

actgtcatga tagatttgat tgcatctaga catagttccg atcgaatcaa atgagtaggc 960

caatgtttag cctttgggga tctcgctgat tattaggagt accattgtat tgggcatggt 1020

tgtggtatag tagtagacaa ttaacaaaaa agctaccact tttcaattat tttaggcata 1080

gatggactgg gagatatgag gcacatcttt gggataacag ttgcagaagg gaaggacaaa 1140

ctcgtaaggg tcgtcaaggt atacaaatat aatgcaacat actgtcatta aatatgcttt 1200

ttctgtaagt tttatatttc accaatgatg ttgttattgt taactgacat tgcttcacac 1260

tatcaatttt ggattcggcg caatgatttg tgggattgaa atcaaatctt aaatctacag 1320

tctatttagg tacgcgattt ctctccaact acttaatgca gttcgtttct ccctataacc 1380

atattctttt tcatctcaaa tctcactcga ctcttttttt ttatcttgta ccattgatag 1440

gtggctatga taaagaggag aaagctgcta gggcttatga tcttgctgct ctgaagtact 1500

ggggtcccac aacaacaaca aatttcccag tatgtatatg tagcatccag ttttacttta 1560

ctgaagttca tatctcgtta tgggctataa atatgtatca aatgatgtcc attagctagt 1620

gatctggagt gaaggttcta tagtaaagta aacgctgtgt gcggagtgca gtagcgggag 1680

gtctctcttc tattttctaa gaaaaatgga cattgctgaa attgtactta aagtcgttta 1740

ttttattttt ttgtatttcc aggtgagtaa ctacgaaaag gagctcgagg acatgaagca 1800

catgacaagg caggagtttg tagcgtctct gagaaggtcg gtctaacagc attgattaat 1860

cagtaccacc tctactgaat aaaatctgct gctatttgtt aaattttgag cgaggtcaac 1920

tgcatatttg atcttattag accactgtat atgaatgcag gaagagcagt ggtttctcca 1980

gaggtgcatc catttacagg ggagtgacta ggtatgaatt catatagcta agaacttaac 2040

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atcaacaaaa acacacatac acttgggttg atgtggcaga tgcatgcatg gattgaaaat   2100

gtgtgcatgt tgttttactt gaactcgatc tctgtattta taggcatcac caacatggaa   2160

gatggcaagc acggattgga cgagttgcag ggaacaagga tctttacttg ggcaccttca   2220

gtaagtagca aacaaatatg tttttgcatt gtatatagag tacccttgaa tatataaatt   2280

caccacatat acaagcaagt tacagtcaac taacacaatc tcaacgcaac gagaaagcaa   2340

gtgttccagc tgatagtaca catttgtaga ccagccgcat atggttgttt tgtatgcatg   2400

atgactatta aaaatgtgac catcgcatta agtcatgcaa agttgcattg cagtagtaca   2460

ttgcttagtg catgctcctc aagtggcttt tttcaaacct gatcccatgt ctggtgctat   2520

tgttgtctcc cattcacccg tgcatcaggt caaaatagta ccatgcctga ataagaaaaa   2580

caaaacgagc atgcactggc agcagcagac taataaacaa agttccagca tttactaata   2640

aactaattag gctacagcat ccaaaagatt cttccaatta agccacaact gttcatgcat   2700

acatgggtat gccacccagg ataccatgca tgcaccgtgc acgacgaaag cgaaacgctc   2760

gttctcggaa tattagaact gacgaagccg agtgcaacct tctgtcgtgg atgcaggcac   2820

ccaggaggag gcagcggagg cgtacgacat cgcggcgatc aagttccgcg gcctaaacgc   2880

cgtcaccaac ttcgacatga gccgctacga cgtgaagagc atcctggaca gcagcgccct   2940

ccccatcggc agcgccgcca agcgcctcaa ggaggccgag gccgcagcgt ccgcgcagca   3000

ccaccacgcc ggcgtggtga gttacgacgt cggccgcatc gcctcgcagc tcggcgacgg   3060

cggagccctg gcggcggcgt acggcgcgca ctaccacggc gccgcctggc cgaccatcgc   3120

gttccagccg ggcgccgcca ccacaggcct gtaccacccg tacgcgcagc agccaatgcg   3180

cggcggcggg tggtgcaagc aggagcagga ccacgcggtg atcgcggccg cgcacagcct   3240

gcaggacctc caccacctga acctgggcgc ggccggcgcg cacgactttt tctcggcagg   3300

gcagcaggcc gccgccgctg cgatgcacgg cctgggtagc atcgacagtg cgtcgctcga   3360

gcacagcacc ggctccaact ccgtcgtcta caacggcggg gtcggcgaca gcaacggcgc   3420

cagcgccgtc ggcggcagtg gcggtggcta catgatgccg atgagcgctg ccggagcaac   3480

cactacatcg gcaatggtga gccacgagca ggtgcatgca cgggcctacg acgaagccaa   3540

gcaggctgct cagatggggt acgagagcta cctggtgaac gcggagaaca atggtggcgg   3600

aaggatgtct gcatggggga ctgtcgtgtc tgcagccgcg gcggcagcag caagcagcaa   3660

cgacaacatg gccgccgacg tcggccatgg cggcgcgcag ctcttcagtg tctggaacga   3720

cacttaa                                                             3727
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<210> SEQ ID NO 117
<211> LENGTH: 4325
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 117

atgcatatct atcttatata aatatctacc agtgatactg ttgcttagtg ctccaaacct     60

ctcttgacct cttcttcttc ttctcagtta gcttagctta agcttcccct aaccttgagc    120

tcaccacaac aatggcgact tgatctaaca gagcttaacc aagtagcaaa tcatacatat    180

aaccatagct taattcgcat tgaatcttgt cttgttcagt gtgaatcatc aaccatggcc    240

accatgaaca actggctggc cttctccctc tccccgcagg atcagctccc gccgtctcag    300
```

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```
accaactcca ctctcatctc cgccgccgcc accaccacca ccgccggcga ctcctccacc    360

ggcgacgtct gcttcaacat cccccaaggt aattaagctc accaatcgat gcatgcattc    420

atgagctaga tatagctagt gttggttggg atttgaagag acatgcatgt ttgattgatt    480

gatttgatgt gcagattgga gcatgagggg atcggagctc tcggcgctcg tcgccgagcc    540

gaagctggag gacttcctcg gcggcatctc cttctcggag cagcagcatc atcacggcgg    600

caagggcggc gtgatcccga gcagcgccgc cgcttgctac gcgagctccg gcagcagcgt    660

cggctacctg taccctcctc caagctcatc ctcgctccag ttcgccgact ccgtcatggt    720

ggccacctcc tcgcccgtcg tcgcccacga cggcgtcagc ggcggcggca tggtgagcgc    780

cgccgccgcc gcggcggcca gtggcaacgg cggcattggc ctgtccatga tcaagaactg    840

gctccggagc cagccggcgc cgcagccggc gcaggcgctg tctctgtcca tgaacatggc    900

ggggacgacg acggcgcagg gcggcggcgc catggcgctc ctcgccggcg caggggagcg    960

aggccggacg acgcccgcgt cagagagcct gtccacgtcg gcgcacggag cgacgacggc   1020

gacgatggct ggtggtcgca aggagattaa cgaggaaggc agcggcagcg ccggcgccgt   1080

ggttgccgtc ggctcggagt caggcggcag cggcgccgtg gtggaggccg gcgcggcggc   1140

ggcggcggcg aggaagtccg tcgacacgtt cggccagaga acatcgatct accgcggcgt   1200

gacaaggtat ttagggtgca attaattaat catctatcta tattttgctc aaaaaagttc   1260

atctactagc tagcttagca caaatcatca tcagtgtaat catatatatt ctttgatgat   1320

ttaactgtgt tgcatgaatt cattcctatt tgatgtttgt gatttggatc ccatttttcta   1380

ggatagctat ataggtgata gattgatcat tagatttgta ggatttatca ttatgtcatt   1440

attatgtggg acatgattgt tgtgattaac aaagttgtaa tatcttttgg tttggttata   1500

ggcatagatg gacagggagg tatgaggctc atctttggga caacagctgc agaagagagg   1560

gccaaactcg caagggtcgt caaggtaggc taactagtgc catttaaatc gattaattgt   1620

tttttatgc tccaatggcg attgatactg atcttgtttc tttttctaat gatcatttcg   1680

ggatcgaatg atcttcctct gtttgatcga acttggcttt tgaatctaca gtctatctag   1740

gtgagtgaga ttccttgaac ctagatgttc tgtttgcgat gcatgtatat attcggtaga   1800

ttgaattatt tgctgatctt tgctttcttg aagtttaatg atcttataaa ttgtaatgct   1860

gataggtggt tatgacaaag aggaaaaagc tgctagagct tatgatttgg ctgctctcaa   1920

atactggggc ccgacgacga cgacaaattt tccggtgtgt ttataattaa tatacagatt   1980

gtgtcacatt gttattttct cactctttta tttgatactg atctagtgta atgatgatta   2040

ctaaaactgt acttaaaggc aatggtttct gtatttttca ggtaaataac tatgaaaagg   2100

agctggagga gatgaagcac atgacaaggc aggagttcgt agcctctttg agaaggttgg   2160

tctctacaat caagatatcc atactatact aattaatttc cttttagatt tatagtaatt   2220

tatctatcgc attgaagtta attaattatc tgatgcttac tgatactaac aaatactgtt   2280

ccttatatgt gcaggaagag cagtggtttc tccagaggtg catccattta ccgtggagta   2340

actaggtaca tatatatatg catcattgta caattaattt ttttaatttt tttagggtaa   2400

aaaatgaaga ctgtgatata gatccattaa tttgatcttg tgtacttgta aatataggca   2460

tcaccagcat gggagatggc aagcaaggat aggaagagtt gcagggaaca aggacctcta   2520

cttgggcacc ttcagtaagt acaaatattc atatttatac tgcaaaacca tataaatcca   2580
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tattaataag tatgtccttt ctcattgagt atacaaaata tcatattttc ttggcaagta   2640

caatttattc attcagggca aaatagtagt agtaagaaag aggggtgact cttcaaagaa   2700

cacagagctt acttaagcct gtaactaatt aattaaacta aaaatgtgat ctgcaagtca   2760

tgtcaagttg cattacacca ctaatatata tactctgtgc atgcttgcat gctctcctca   2820

tgtggctagc taccttttca aaccttccat gtctggtgct actcctgtct ccattcacca   2880

ctgcacctgg tcaagatcct cactaattaa gaaacaataa tgcattattt gcagtaaata   2940

atttaactag tgttaatcac attctttgca acacaaacta atcaccaatt aagctagcta   3000

gctagccaaa atgataatct tgcttgcatg cgctaatggt gtgtgtgatg atggtggtgt   3060

cacgcatgca ggcacgcagg aggaggcggc ggaggcgtac gacatcgcgg cgatcaagtt   3120

ccgggggctc aacgccgtca ccaacttcga catgagccgc tacgacgtca agagcatcct   3180

cgacagcgct gccctccccg tcggcaccgc cgccaagcgc ctcaaggacg ccgaggccgc   3240

cgccgcctac gacgtcggcc gcatcgcctc gcacctcggc ggcgacggcg cctacgccgc   3300

gcattacggc caccaccacc actcggccgc cgccgcctgg ccgaccatcg cgttccaggc   3360

ggcggcggcg ccgccgccgc acgccgccgg gctttaccac ccgtacgcgc agccgctgcg   3420

tgggtggtgc aagcaggagc aggaccacgc cgtgatcgcg gcggcgcaca gcctgcagga   3480

tctccaccac ctcaacctcg gcgccgccgc cgccgcgcat gacttcttct cgcaggcgat   3540

gcagcagcag cacggcctcg gcagcatcga caacgcgtcg ctcgagcaca gcaccggctc   3600

caactccgtc gtctacaacg gcgacaatgg cggcggaggc ggcggctaca tcatggcgcc   3660

gatgagcgcc gtgtcggcca cggccaccgc ggtggcgagc agccacgatc acggcggcga   3720

cggcgggaag caggtgcaga tggggtacga cagctacctc gtcggcgcag acgcctacgg   3780

cggcggcggc gccgggagga tgccatcctg ggcgatgacg ccggcgtcgg cgccggccgc   3840

cacgagcagc agcgacatga ccggagtctg ccatggcgca cagctcttca gcgtctggaa   3900

cgacacataa aaaaaaaact aggttagcca gcttaattag cagggtaaac cactgacaca   3960

attaagccat acttaaatta gggttcatga gatgaccatt aagcaggtta ttatcattaa   4020

tgatgtttaa tttctcaatt agtacttagc tcaaaaggag gggatttctt ctgaaggatg   4080

gtgatggctt gtgaaattga acctggtgtt cttgccatga tttttttttc acaagctgcc   4140

attttggggt tcaggttcag aaggatcctg attattatta accagccata tatatataga   4200

agggtagaaa tggaggtatc ctgcttgtaa attggggcaa tggtagctag agttgatgca   4260

atgaccatgc ttcatgtgat gagaactaat tgtcttcctc tgatcaaatt aagcaggaag   4320

attaa                                                              4325
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<210> SEQ ID NO 118
<211> LENGTH: 2079
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(2079)

<400> SEQUENCE: 118

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atg gcc act atg aac aac tgg ctc gcc ttc tcg ctc tcg ccg cag gac        48
Met Ala Thr Met Asn Asn Trp Leu Ala Phe Ser Leu Ser Pro Gln Asp
1               5                   10                  15
```

-continued

```
caa ctc cca ccg tcg cag acc aat agc act ctc atc tcc gct gct gca       96
Gln Leu Pro Pro Ser Gln Thr Asn Ser Thr Leu Ile Ser Ala Ala Ala
            20                  25                  30

acc acc aca acc gca ggc gat tcg tca acg ggc gac gtc tgc ttc aac      144
Thr Thr Thr Thr Ala Gly Asp Ser Ser Thr Gly Asp Val Cys Phe Asn
        35                  40                  45

atc cct caa gac tgg tcc atg cgc gga agc gag ctt agc gct ctc gtc      192
Ile Pro Gln Asp Trp Ser Met Arg Gly Ser Glu Leu Ser Ala Leu Val
    50                  55                  60

gcg gag ccc aag ttg gag gat ttc ttg gga ggc atc tcc ttc tcg gag      240
Ala Glu Pro Lys Leu Glu Asp Phe Leu Gly Gly Ile Ser Phe Ser Glu
65                  70                  75                  80

caa cag cat cat cac ggc gga aag ggc ggt gtt atc cca agc tct gct      288
Gln Gln His His His Gly Gly Lys Gly Gly Val Ile Pro Ser Ser Ala
                85                  90                  95

gcc gca tgc tat gca agc tcc ggc tcc agc gtg ggc tac ctc tac cct      336
Ala Ala Cys Tyr Ala Ser Ser Gly Ser Ser Val Gly Tyr Leu Tyr Pro
            100                 105                 110

ccg cct tca tcc tcg tca ctt cag ttt gca gac agc gtg atg gtc gca      384
Pro Pro Ser Ser Ser Ser Leu Gln Phe Ala Asp Ser Val Met Val Ala
        115                 120                 125

acc tca tct cca gtg gtt gcg cac gat ggc gtg agc ggt ggc ggt atg      432
Thr Ser Ser Pro Val Val Ala His Asp Gly Val Ser Gly Gly Gly Met
    130                 135                 140

gtc tca gca gca gcg gct gca gca gct tcg ggt aat ggc ggg att ggc      480
Val Ser Ala Ala Ala Ala Ala Ala Ala Ser Gly Asn Gly Gly Ile Gly
145                 150                 155                 160

ctc tcc atg atc aag aac tgg ctc agg agc caa ccg gct ccg caa cct      528
Leu Ser Met Ile Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Gln Pro
                165                 170                 175

gcg caa gca ctc agc ctg tcg atg aac atg gct ggt act act acc gct      576
Ala Gln Ala Leu Ser Leu Ser Met Asn Met Ala Gly Thr Thr Thr Ala
            180                 185                 190

caa ggt gga ggc gca atg gca ctt ctc gca ggc gct ggc gaa aga gga      624
Gln Gly Gly Gly Ala Met Ala Leu Leu Ala Gly Ala Gly Glu Arg Gly
        195                 200                 205

agg acc aca cca gca tcc gag agc ctc tct act tcc gcg cac gga gcc      672
Arg Thr Thr Pro Ala Ser Glu Ser Leu Ser Thr Ser Ala His Gly Ala
    210                 215                 220

acc acg gct aca atg gct ggc ggg agg aaa gag atc aac gag gaa gga      720
Thr Thr Ala Thr Met Ala Gly Gly Arg Lys Glu Ile Asn Glu Glu Gly
225                 230                 235                 240

tct gga tcc gct ggt gcc gtg gtt gca gtt ggc tca gaa tca ggt gga      768
Ser Gly Ser Ala Gly Ala Val Val Ala Val Gly Ser Glu Ser Gly Gly
                245                 250                 255

tcc ggc gct gtt gtt gaa gct ggt gcc gct gcg gca gcg gct cgg aag      816
Ser Gly Ala Val Val Glu Ala Gly Ala Ala Ala Ala Ala Ala Arg Lys
            260                 265                 270

agc gtt gat act ttc ggc caa aga acg agc atc tac aga ggc gtt act      864
Ser Val Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr
        275                 280                 285

cgg cac cgc tgg acc ggc agg tac gag gca cac ttg tgg gac aac agc      912
Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser
    290                 295                 300

tgt cgc cgc gag ggc caa act agg aag gga aga cag gga gga tat gac      960
Cys Arg Arg Glu Gly Gln Thr Arg Lys Gly Arg Gln Gly Gly Tyr Asp
305                 310                 315                 320
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aaa gag gag aag gct gcc aga gcg tac gac ctg gcc gcg ttg aag tac      1008
Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr
                325                 330                 335

tgg ggt cca aca acg acg acc aac ttc ccg gtg aac aac tac gag aag      1056
Trp Gly Pro Thr Thr Thr Thr Asn Phe Pro Val Asn Asn Tyr Glu Lys
            340                 345                 350

gag ctg gaa gag atg aag cac atg acg cgg cag gag ttc gtc gct tct      1104
Glu Leu Glu Glu Met Lys His Met Thr Arg Gln Glu Phe Val Ala Ser
        355                 360                 365

ctc agg cgc aag tca tct ggt ttc tcc aga ggt gcg tcg atc tat aga      1152
Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg
    370                 375                 380

gga gtt acc cgc cac cac cag cac gga agg tgg cag gca aga atc ggg      1200
Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly
385                 390                 395                 400

aga gtc gcc ggt aac aag gac ctg tac ttg gga acc ttc tcg act cag      1248
Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln
                405                 410                 415

gag gag gca gcg gaa gcg tat gac att gcg gcg atc aag ttc cgc ggt      1296
Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly
            420                 425                 430

ctc aat gcc gtg acc aac ttc gac atg tca cgc tat gat gtc aag tcg      1344
Leu Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser
        435                 440                 445

att ctg gat agc gct gcg ttg cct gtg gga acc gct gcc aaa cgc ctc      1392
Ile Leu Asp Ser Ala Ala Leu Pro Val Gly Thr Ala Ala Lys Arg Leu
    450                 455                 460

aag gac gcg gaa gca gct gcc gcg tac gat gtt ggc agg att gcc tca      1440
Lys Asp Ala Glu Ala Ala Ala Ala Tyr Asp Val Gly Arg Ile Ala Ser
465                 470                 475                 480

cat ctc ggt gga gat gga gct tac gct gcc cac tac ggg cat cat cac      1488
His Leu Gly Gly Asp Gly Ala Tyr Ala Ala His Tyr Gly His His His
                485                 490                 495

cac tct gca gcc gca gct tgg cct aca ata gca ttc caa gcg gca gcg      1536
His Ser Ala Ala Ala Ala Trp Pro Thr Ile Ala Phe Gln Ala Ala Ala
            500                 505                 510

gct cct cct cca cac gct gct ggt ctt tac cat ccg tac gcg caa cct      1584
Ala Pro Pro Pro His Ala Ala Gly Leu Tyr His Pro Tyr Ala Gln Pro
        515                 520                 525

ctc cgc ggt tgg tgt aag cag gaa caa gat cat gcg gtg att gcg gct      1632
Leu Arg Gly Trp Cys Lys Gln Glu Gln Asp His Ala Val Ile Ala Ala
    530                 535                 540

gca cac agc ttg caa gat ctg cat cac ctc aat ctg gga gcc gca gca      1680
Ala His Ser Leu Gln Asp Leu His His Leu Asn Leu Gly Ala Ala Ala
545                 550                 555                 560

gct gcc cat gac ttc ttc tca caa gcc atg cag cag cag cat ggc ctg      1728
Ala Ala His Asp Phe Phe Ser Gln Ala Met Gln Gln Gln His Gly Leu
                565                 570                 575

ggc agc ata gac aat gcg tct ctg gag cac tcc acc gga tcg aac tcg      1776
Gly Ser Ile Asp Asn Ala Ser Leu Glu His Ser Thr Gly Ser Asn Ser
            580                 585                 590

gtg gtg tac aat gga gac aac ggc gga gga ggt gga ggt tac atc atg      1824
Val Val Tyr Asn Gly Asp Asn Gly Gly Gly Gly Gly Gly Tyr Ile Met
        595                 600                 605

gca cct atg tca gcg gtc tct gct acc gct acg gcg gtg gcc tca tcc      1872
Ala Pro Met Ser Ala Val Ser Ala Thr Ala Thr Ala Val Ala Ser Ser
    610                 615                 620
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cac gac cac ggt gga gac ggc ggc aag cag gtc caa atg ggc tac gac     1920
His Asp His Gly Gly Asp Gly Gly Lys Gln Val Gln Met Gly Tyr Asp
625                 630                 635                 640

tcc tac ctt gtg gga gct gac gct tac ggc gga gga gga gct ggt cgc     1968
Ser Tyr Leu Val Gly Ala Asp Ala Tyr Gly Gly Gly Gly Ala Gly Arg
                645                 650                 655

atg cct agc tgg gcc atg acg cct gct tct gct cct gcg gct acg agc     2016
Met Pro Ser Trp Ala Met Thr Pro Ala Ser Ala Pro Ala Ala Thr Ser
            660                 665                 670

tcg tcg gat atg aca gga gtg tgt cat ggc gcc caa ctg ttc tcg gtg     2064
Ser Ser Asp Met Thr Gly Val Cys His Gly Ala Gln Leu Phe Ser Val
        675                 680                 685

tgg aat gat aca tag                                                 2079
Trp Asn Asp Thr
    690


<210> SEQ ID NO 119
<211> LENGTH: 692
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 119

Met Ala Thr Met Asn Asn Trp Leu Ala Phe Ser Leu Ser Pro Gln Asp
1               5                   10                  15

Gln Leu Pro Pro Ser Gln Thr Asn Ser Thr Leu Ile Ser Ala Ala Ala
            20                  25                  30

Thr Thr Thr Thr Ala Gly Asp Ser Ser Thr Gly Asp Val Cys Phe Asn
        35                  40                  45

Ile Pro Gln Asp Trp Ser Met Arg Gly Ser Glu Leu Ser Ala Leu Val
    50                  55                  60

Ala Glu Pro Lys Leu Glu Asp Phe Leu Gly Gly Ile Ser Phe Ser Glu
65                  70                  75                  80

Gln Gln His His His Gly Gly Lys Gly Gly Val Ile Pro Ser Ser Ala
                85                  90                  95

Ala Ala Cys Tyr Ala Ser Ser Gly Ser Ser Val Gly Tyr Leu Tyr Pro
            100                 105                 110

Pro Pro Ser Ser Ser Ser Leu Gln Phe Ala Asp Ser Val Met Val Ala
        115                 120                 125

Thr Ser Ser Pro Val Val Ala His Asp Gly Val Ser Gly Gly Gly Met
    130                 135                 140

Val Ser Ala Ala Ala Ala Ala Ala Ala Ser Gly Asn Gly Gly Ile Gly
145                 150                 155                 160

Leu Ser Met Ile Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Gln Pro
                165                 170                 175

Ala Gln Ala Leu Ser Leu Ser Met Asn Met Ala Gly Thr Thr Thr Ala
            180                 185                 190

Gln Gly Gly Gly Ala Met Ala Leu Leu Ala Gly Ala Gly Glu Arg Gly
        195                 200                 205

Arg Thr Thr Pro Ala Ser Glu Ser Leu Ser Thr Ser Ala His Gly Ala
    210                 215                 220

Thr Thr Ala Thr Met Ala Gly Gly Arg Lys Glu Ile Asn Glu Glu Gly
225                 230                 235                 240

Ser Gly Ser Ala Gly Ala Val Val Ala Val Gly Ser Glu Ser Gly Gly
                245                 250                 255
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Ser Gly Ala Val Val Glu Ala Gly Ala Ala Ala Ala Ala Ala Arg Lys
            260                 265                 270

Ser Val Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr
        275                 280                 285

Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser
    290                 295                 300

Cys Arg Arg Glu Gly Gln Thr Arg Lys Gly Arg Gln Gly Gly Tyr Asp
305                 310                 315                 320

Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr
                325                 330                 335

Trp Gly Pro Thr Thr Thr Thr Asn Phe Pro Val Asn Asn Tyr Glu Lys
            340                 345                 350

Glu Leu Glu Glu Met Lys His Met Thr Arg Gln Glu Phe Val Ala Ser
        355                 360                 365

Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg
    370                 375                 380

Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg Ile Gly
385                 390                 395                 400

Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln
                405                 410                 415

Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly
            420                 425                 430

Leu Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp Val Lys Ser
        435                 440                 445

Ile Leu Asp Ser Ala Ala Leu Pro Val Gly Thr Ala Ala Lys Arg Leu
    450                 455                 460

Lys Asp Ala Glu Ala Ala Ala Ala Tyr Asp Val Gly Arg Ile Ala Ser
465                 470                 475                 480

His Leu Gly Gly Asp Gly Ala Tyr Ala Ala His Tyr Gly His His His
                485                 490                 495

His Ser Ala Ala Ala Ala Trp Pro Thr Ile Ala Phe Gln Ala Ala Ala
            500                 505                 510

Ala Pro Pro Pro His Ala Ala Gly Leu Tyr His Pro Tyr Ala Gln Pro
        515                 520                 525

Leu Arg Gly Trp Cys Lys Gln Glu Gln Asp His Ala Val Ile Ala Ala
    530                 535                 540

Ala His Ser Leu Gln Asp Leu His His Leu Asn Leu Gly Ala Ala Ala
545                 550                 555                 560

Ala Ala His Asp Phe Phe Ser Gln Ala Met Gln Gln Gln His Gly Leu
                565                 570                 575

Gly Ser Ile Asp Asn Ala Ser Leu Glu His Ser Thr Gly Ser Asn Ser
            580                 585                 590

Val Val Tyr Asn Gly Asp Asn Gly Gly Gly Gly Gly Tyr Ile Met
        595                 600                 605

Ala Pro Met Ser Ala Val Ser Ala Thr Ala Thr Ala Val Ala Ser Ser
    610                 615                 620

His Asp His Gly Gly Asp Gly Gly Lys Gln Val Gln Met Gly Tyr Asp
625                 630                 635                 640

Ser Tyr Leu Val Gly Ala Asp Ala Tyr Gly Gly Gly Gly Ala Gly Arg
                645                 650                 655

Met Pro Ser Trp Ala Met Thr Pro Ala Ser Ala Pro Ala Ala Thr Ser
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            660                 665                 670

Ser Ser Asp Met Thr Gly Val Cys His Gly Ala Gln Leu Phe Ser Val
        675                 680                 685

Trp Asn Asp Thr
    690


<210> SEQ ID NO 120
<211> LENGTH: 2088
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(2088)

<400> SEQUENCE: 120

atg gcc act atg aac aac tgg ctc gcc ttc tcg ctc tcg ccg cag gac       48
Met Ala Thr Met Asn Asn Trp Leu Ala Phe Ser Leu Ser Pro Gln Asp
1           5                       10                      15

caa ctc cca ccg tcg cag acc aat agc act ctc atc tcc gct gct gca       96
Gln Leu Pro Pro Ser Gln Thr Asn Ser Thr Leu Ile Ser Ala Ala Ala
            20                  25                  30

acc acc aca acc gca ggc gat tcg tca acg ggc gac gtc tgc ttc aac      144
Thr Thr Thr Thr Ala Gly Asp Ser Ser Thr Gly Asp Val Cys Phe Asn
        35                  40                  45

atc cct caa gac tgg tcc atg cgc gga agc gag ctt agc gct ctc gtc      192
Ile Pro Gln Asp Trp Ser Met Arg Gly Ser Glu Leu Ser Ala Leu Val
    50                  55                  60

gcg gag ccc aag ttg gag gat ttc ttg gga ggc atc tcc ttc tcg gag      240
Ala Glu Pro Lys Leu Glu Asp Phe Leu Gly Gly Ile Ser Phe Ser Glu
65                  70                  75                  80

caa cag cat cat cac ggc gga aag ggc ggt gtt atc cca agc tct gct      288
Gln Gln His His His Gly Gly Lys Gly Gly Val Ile Pro Ser Ser Ala
                85                  90                  95

gcc gca tgc tat gca agc tcc ggc tcc agc gtg ggc tac ctc tac cct      336
Ala Ala Cys Tyr Ala Ser Ser Gly Ser Ser Val Gly Tyr Leu Tyr Pro
            100                 105                 110

ccg cct tca tcc tcg tca ctt cag ttt gca gac agc gtg atg gtc gca      384
Pro Pro Ser Ser Ser Ser Leu Gln Phe Ala Asp Ser Val Met Val Ala
        115                 120                 125

acc tca tct cca gtg gtt gcg cac gat ggc gtg agc ggt ggc ggt atg      432
Thr Ser Ser Pro Val Val Ala His Asp Gly Val Ser Gly Gly Gly Met
    130                 135                 140

gtc tca gca gca gcg gct gca gca gct tcg ggt aat ggc ggg att ggc      480
Val Ser Ala Ala Ala Ala Ala Ala Ala Ser Gly Asn Gly Gly Ile Gly
145                 150                 155                 160

ctc tcc atg atc aag aac tgg ctc agg agc caa ccg gct ccg caa cct      528
Leu Ser Met Ile Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Gln Pro
                165                 170                 175

gcg caa gca ctc agc ctg tcg atg aac atg gct ggt act act acc gct      576
Ala Gln Ala Leu Ser Leu Ser Met Asn Met Ala Gly Thr Thr Thr Ala
            180                 185                 190

caa ggt gga ggc gca atg gca ctt ctc gca ggc gct ggc gaa aga gga      624
Gln Gly Gly Gly Ala Met Ala Leu Leu Ala Gly Ala Gly Glu Arg Gly
        195                 200                 205

agg acc aca cca gca tcc gag agc ctc tct act tcc gcg cac gga gcc      672
Arg Thr Thr Pro Ala Ser Glu Ser Leu Ser Thr Ser Ala His Gly Ala
    210                 215                 220

acc acg gct aca atg gct ggc ggg agg aaa gag atc aac gag gaa gga      720
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Thr Thr Ala Thr Met Ala Gly Gly Arg Lys Glu Ile Asn Glu Glu Gly
225                 230                 235                 240

tct gga tcc gct ggt gcc gtg gtt gca gtt ggc tca gaa tca ggt gga      768
Ser Gly Ser Ala Gly Ala Val Val Ala Val Gly Ser Glu Ser Gly Gly
                245                 250                 255

tcc ggc gct gtt gtt gaa gct ggt gcc gct gcg gca gcg gct cgg aag      816
Ser Gly Ala Val Val Glu Ala Gly Ala Ala Ala Ala Ala Ala Arg Lys
            260                 265                 270

agc gtt gat act ttc ggc caa aga acg agc atc tac aga ggc gtt act      864
Ser Val Asp Thr Phe Gly Gln Arg Thr Ser Ile Tyr Arg Gly Val Thr
        275                 280                 285

cgg cac cgc tgg acc ggc agg tac gag gca cac ttg tgg gac aac agc      912
Arg His Arg Trp Thr Gly Arg Tyr Glu Ala His Leu Trp Asp Asn Ser
    290                 295                 300

tgt cgc cgc gag ggc caa act agg aag gga aga cag gtc tat cta gga      960
Cys Arg Arg Glu Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly
305                 310                 315                 320

gga tat gac aaa gag gag aag gct gcc aga gcg tac gac ctg gcc gcg     1008
Gly Tyr Asp Lys Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala
                325                 330                 335

ttg aag tac tgg ggt cca aca acg acg acc aac ttc ccg gtg aac aac     1056
Leu Lys Tyr Trp Gly Pro Thr Thr Thr Thr Asn Phe Pro Val Asn Asn
            340                 345                 350

tac gag aag gag ctg gaa gag atg aag cac atg acg cgg cag gag ttc     1104
Tyr Glu Lys Glu Leu Glu Glu Met Lys His Met Thr Arg Gln Glu Phe
        355                 360                 365

gtc gct tct ctc agg cgc aag tca tct ggt ttc tcc aga ggt gcg tcg     1152
Val Ala Ser Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser
    370                 375                 380

atc tat aga gga gtt acc cgc cac cac cag cac gga agg tgg cag gca     1200
Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala
385                 390                 395                 400

aga atc ggg aga gtc gcc ggt aac aag gac ctg tac ttg gga acc ttc     1248
Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe
                405                 410                 415

tcg act cag gag gag gca gcg gaa gcg tat gac att gcg gcg atc aag     1296
Ser Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Ile Ala Ala Ile Lys
            420                 425                 430

ttc cgc ggt ctc aat gcc gtg acc aac ttc gac atg tca cgc tat gat     1344
Phe Arg Gly Leu Asn Ala Val Thr Asn Phe Asp Met Ser Arg Tyr Asp
        435                 440                 445

gtc aag tcg att ctg gat agc gct gcg ttg cct gtg gga acc gct gcc     1392
Val Lys Ser Ile Leu Asp Ser Ala Ala Leu Pro Val Gly Thr Ala Ala
    450                 455                 460

aaa cgc ctc aag gac gcg gaa gca gct gcc gcg tac gat gtt ggc agg     1440
Lys Arg Leu Lys Asp Ala Glu Ala Ala Ala Ala Tyr Asp Val Gly Arg
465                 470                 475                 480

att gcc tca cat ctc ggt gga gat gga gct tac gct gcc cac tac ggg     1488
Ile Ala Ser His Leu Gly Gly Asp Gly Ala Tyr Ala Ala His Tyr Gly
                485                 490                 495

cat cat cac cac tct gca gcc gca gct tgg cct aca ata gca ttc caa     1536
His His His His Ser Ala Ala Ala Ala Trp Pro Thr Ile Ala Phe Gln
            500                 505                 510

gcg gca gcg gct cct cct cca cac gct gct ggt ctt tac cat ccg tac     1584
Ala Ala Ala Ala Pro Pro Pro His Ala Ala Gly Leu Tyr His Pro Tyr
        515                 520                 525

gcg caa cct ctc cgc ggt tgg tgt aag cag gaa caa gat cat gcg gtg     1632
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Ala Gln Pro Leu Arg Gly Trp Cys Lys Gln Glu Gln Asp His Ala Val
    530                 535                 540

att gcg gct gca cac agc ttg caa gat ctg cat cac ctc aat ctg gga     1680
Ile Ala Ala Ala His Ser Leu Gln Asp Leu His His Leu Asn Leu Gly
545                 550                 555                 560

gcc gca gca gct gcc cat gac ttc ttc tca caa gcc atg cag cag cag     1728
Ala Ala Ala Ala Ala His Asp Phe Phe Ser Gln Ala Met Gln Gln Gln
                565                 570                 575

cat ggc ctg ggc agc ata gac aat gcg tct ctg gag cac tcc acc gga     1776
His Gly Leu Gly Ser Ile Asp Asn Ala Ser Leu Glu His Ser Thr Gly
            580                 585                 590

tcg aac tcg gtg gtg tac aat gga gac aac ggc gga gga ggt gga ggt     1824
Ser Asn Ser Val Val Tyr Asn Gly Asp Asn Gly Gly Gly Gly Gly Gly
        595                 600                 605

tac atc atg gca cct atg tca gcg gtc tct gct acc gct acg gcg gtg     1872
Tyr Ile Met Ala Pro Met Ser Ala Val Ser Ala Thr Ala Thr Ala Val
    610                 615                 620

gcc tca tcc cac gac cac ggt gga gac ggc ggc aag cag gtc caa atg     1920
Ala Ser Ser His Asp His Gly Gly Asp Gly Gly Lys Gln Val Gln Met
625                 630                 635                 640

ggc tac gac tcc tac ctt gtg gga gct gac gct tac ggc gga gga gga     1968
Gly Tyr Asp Ser Tyr Leu Val Gly Ala Asp Ala Tyr Gly Gly Gly Gly
                645                 650                 655

gct ggt cgc atg cct agc tgg gcc atg acg cct gct tct gct cct gcg     2016
Ala Gly Arg Met Pro Ser Trp Ala Met Thr Pro Ala Ser Ala Pro Ala
            660                 665                 670

gct acg agc tcg tcg gat atg aca gga gtg tgt cat ggc gcc caa ctg     2064
Ala Thr Ser Ser Ser Asp Met Thr Gly Val Cys His Gly Ala Gln Leu
        675                 680                 685

ttc tcg gtg tgg aat gat aca tag                                     2088
Phe Ser Val Trp Asn Asp Thr
    690                 695


<210> SEQ ID NO 121
<211> LENGTH: 2133
<212> TYPE: DNA
<213> ORGANISM: Zea mays
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(2133)

<400> SEQUENCE: 121

atg gcc act gtg aac aac tgg ctc gct ttc tcc ctc tcc ccg cag gag       48
Met Ala Thr Val Asn Asn Trp Leu Ala Phe Ser Leu Ser Pro Gln Glu
1               5                   10                  15

ctg ccg ccc tcc cag acg acg gac tcc aca ctc atc tcg gcc gcc acc       96
Leu Pro Pro Ser Gln Thr Thr Asp Ser Thr Leu Ile Ser Ala Ala Thr
            20                  25                  30

gcc gac cat gtc tcc ggc gat gtc tgc ttc aac atc ccc caa gat tgg      144
Ala Asp His Val Ser Gly Asp Val Cys Phe Asn Ile Pro Gln Asp Trp
        35                  40                  45

agc atg agg gga tca gag ctt tcg gcg ctc gtc gcg gag ccg aag ctg      192
Ser Met Arg Gly Ser Glu Leu Ser Ala Leu Val Ala Glu Pro Lys Leu
    50                  55                  60

gag gac ttc ctc ggc ggc atc tcc ttc tcc gag cag cat cac aag gcc      240
Glu Asp Phe Leu Gly Gly Ile Ser Phe Ser Glu Gln His His Lys Ala
65                  70                  75                  80

aac tgc aac atg ata ccc agc act agc agc aca gtt tgc tac gcg agc      288
Asn Cys Asn Met Ile Pro Ser Thr Ser Ser Thr Val Cys Tyr Ala Ser
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                85                  90                  95

tca ggt gct agc acc ggc tac cat cac cag ctg tac cac cag ccc acc      336
Ser Gly Ala Ser Thr Gly Tyr His His Gln Leu Tyr His Gln Pro Thr
            100                 105                 110

agc tca gcg ctc cac ttc gcg gac tcc gta atg gtg gcc tcc tcg gcc      384
Ser Ser Ala Leu His Phe Ala Asp Ser Val Met Val Ala Ser Ser Ala
        115                 120                 125

ggt gtc cac gac ggc ggt gcc atg ctc agc gcg gcc gcc gct aac ggt      432
Gly Val His Asp Gly Gly Ala Met Leu Ser Ala Ala Ala Ala Asn Gly
    130                 135                 140

gtc gct ggc gct gcc agt gcc aac ggc ggc ggc atc ggg ctg tcc atg      480
Val Ala Gly Ala Ala Ser Ala Asn Gly Gly Gly Ile Gly Leu Ser Met
145                 150                 155                 160

att aag aac tgg ctg cgg agc caa ccg gcg ccc atg cag ccg agg gtg      528
Ile Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Met Gln Pro Arg Val
                165                 170                 175

gcg gcg gct gag ggc gcg cag ggg ctc tct ttg tcc atg aac atg gcg      576
Ala Ala Ala Glu Gly Ala Gln Gly Leu Ser Leu Ser Met Asn Met Ala
            180                 185                 190

ggg acg acc caa ggc gct gct ggc atg cca ctt ctc gct gga gag cgc      624
Gly Thr Thr Gln Gly Ala Ala Gly Met Pro Leu Leu Ala Gly Glu Arg
        195                 200                 205

gca cgg gcg ccc gag agt gta tcg acg tca gca cag ggt gga gcc gtc      672
Ala Arg Ala Pro Glu Ser Val Ser Thr Ser Ala Gln Gly Gly Ala Val
    210                 215                 220

gtc gtc acg gcg ccg aag gag gat agc ggt ggc agc ggt gtt gcc ggc      720
Val Val Thr Ala Pro Lys Glu Asp Ser Gly Gly Ser Gly Val Ala Gly
225                 230                 235                 240

gct cta gta gcc gtg agc acg gac acg ggt ggc agc ggc ggc gcg tcg      768
Ala Leu Val Ala Val Ser Thr Asp Thr Gly Gly Ser Gly Gly Ala Ser
                245                 250                 255

gct gac aac acg gca agg aag acg gtg gac acg ttc ggg cag cgc acg      816
Ala Asp Asn Thr Ala Arg Lys Thr Val Asp Thr Phe Gly Gln Arg Thr
            260                 265                 270

tcg att tac cgt ggc gtg aca agg cat aga tgg act ggg aga tat gag      864
Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
        275                 280                 285

gca cat ctt tgg gat aac agt tgc aga agg gaa ggg caa act cgt aag      912
Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Thr Arg Lys
    290                 295                 300

ggt cgt caa gtc tat tta ggt ggc tat gat aaa gag gag aaa gct gct      960
Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala
305                 310                 315                 320

agg gct tat gat ctt gct gct ctg aag tac tgg ggt gcc aca aca aca     1008
Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Ala Thr Thr Thr
                325                 330                 335

aca aat ttt cca gtg agt aac tac gaa aag gag ctc gag gac atg aag     1056
Thr Asn Phe Pro Val Ser Asn Tyr Glu Lys Glu Leu Glu Asp Met Lys
            340                 345                 350

cac atg aca agg cag gag ttt gta gcg tct ctg aga agg aag agc agt     1104
His Met Thr Arg Gln Glu Phe Val Ala Ser Leu Arg Arg Lys Ser Ser
        355                 360                 365

ggt ttc tcc aga ggt gca tcc att tac agg gga gtg act agg cat cac     1152
Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His
    370                 375                 380

caa cat gga aga tgg caa gca cgg att gga cga gtt gca ggg aac aag     1200
Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys
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385                 390                 395                 400

gat ctt tac ttg ggc acc ttc agc acc cag gag gag gca gcg gag gcg      1248
Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala
                405                 410                 415

tac gac atc gcg gcg atc aag ttc cgc ggc ctc aac gcc gtc acc aac      1296
Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn
            420                 425                 430

ttc gac atg agc cgc tac gac gtg aag agc atc ctg gac agc agc gcc      1344
Phe Asp Met Ser Arg Tyr Asp Val Lys Ser Ile Leu Asp Ser Ser Ala
        435                 440                 445

ctc ccc atc ggc agc gcc gcc aag cgc ctc aag gag gcc gag gcc gca      1392
Leu Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Glu Ala Glu Ala Ala
    450                 455                 460

gcg tcc gcg cag cac cac cac gcc ggc gtg gtg agc tac gac gtc ggc      1440
Ala Ser Ala Gln His His His Ala Gly Val Val Ser Tyr Asp Val Gly
465                 470                 475                 480

cgc atc gcc tcg cag ctc ggc gac ggc gga gcc ctg gcg gcg gcg tac      1488
Arg Ile Ala Ser Gln Leu Gly Asp Gly Gly Ala Leu Ala Ala Ala Tyr
                485                 490                 495

ggc gcg cac tac cac ggc gcc gcc tgg ccg acc atc gcg ttc cag ccg      1536
Gly Ala His Tyr His Gly Ala Ala Trp Pro Thr Ile Ala Phe Gln Pro
            500                 505                 510

ggc gcc gcc agc aca ggc ctg tac cac ccg tac gcg cag cag cca atg      1584
Gly Ala Ala Ser Thr Gly Leu Tyr His Pro Tyr Ala Gln Gln Pro Met
        515                 520                 525

cgc ggc ggc ggg tgg tgc aag cag gag cag gac cac gcg gtg atc gcg      1632
Arg Gly Gly Gly Trp Cys Lys Gln Glu Gln Asp His Ala Val Ile Ala
    530                 535                 540

gcc gcg cac agc ctg cag gac ctc cac cac ctg aac ctg ggc gcg gcc      1680
Ala Ala His Ser Leu Gln Asp Leu His His Leu Asn Leu Gly Ala Ala
545                 550                 555                 560

ggc gcg cac gac ttt ttc tcg gca ggg cag cag gcc gcc gcc gct gcg      1728
Gly Ala His Asp Phe Phe Ser Ala Gly Gln Gln Ala Ala Ala Ala Ala
                565                 570                 575

atg cac ggc ctg ggt agc atc gac agt gcg tcg ctc gag cac agc acc      1776
Met His Gly Leu Gly Ser Ile Asp Ser Ala Ser Leu Glu His Ser Thr
            580                 585                 590

ggc tcc aac tcc gtc gtc tac aac ggc ggg gtc ggc gac agc aac ggc      1824
Gly Ser Asn Ser Val Val Tyr Asn Gly Gly Val Gly Asp Ser Asn Gly
        595                 600                 605

gcc agc gcc gtc ggc ggc agt ggc ggt ggc tac atg atg ccg atg agc      1872
Ala Ser Ala Val Gly Gly Ser Gly Gly Gly Tyr Met Met Pro Met Ser
    610                 615                 620

gct gcc gga gca acc act aca tcg gca atg gtg agc cac gag cag gtg      1920
Ala Ala Gly Ala Thr Thr Thr Ser Ala Met Val Ser His Glu Gln Val
625                 630                 635                 640

cat gca cgg gcc tac gac gaa gcc aag cag gct gct cag atg ggg tac      1968
His Ala Arg Ala Tyr Asp Glu Ala Lys Gln Ala Ala Gln Met Gly Tyr
                645                 650                 655

gag agc tac ctg gtg aac gcg gag aac aat ggt ggc gga agg atg tct      2016
Glu Ser Tyr Leu Val Asn Ala Glu Asn Asn Gly Gly Gly Arg Met Ser
            660                 665                 670

gca tgg ggg act gtc gtg tct gca gcc gcg gcg gca gca gca agc agc      2064
Ala Trp Gly Thr Val Val Ser Ala Ala Ala Ala Ala Ala Ala Ser Ser
        675                 680                 685

aac gac aac atg gcc gcc gac gtc ggc cat ggc ggc gcg cag ctc ttc      2112
Asn Asp Asn Met Ala Ala Asp Val Gly His Gly Gly Ala Gln Leu Phe
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    690                 695                 700

agt gtc tgg aac gac act taa                                         2133
Ser Val Trp Asn Asp Thr
705                 710


<210> SEQ ID NO 122
<211> LENGTH: 710
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 122

Met Ala Thr Val Asn Asn Trp Leu Ala Phe Ser Leu Ser Pro Gln Glu
1               5                   10                  15

Leu Pro Pro Ser Gln Thr Thr Asp Ser Thr Leu Ile Ser Ala Ala Thr
            20                  25                  30

Ala Asp His Val Ser Gly Asp Val Cys Phe Asn Ile Pro Gln Asp Trp
        35                  40                  45

Ser Met Arg Gly Ser Glu Leu Ser Ala Leu Val Ala Glu Pro Lys Leu
    50                  55                  60

Glu Asp Phe Leu Gly Gly Ile Ser Phe Ser Glu Gln His His Lys Ala
65                  70                  75                  80

Asn Cys Asn Met Ile Pro Ser Thr Ser Ser Thr Val Cys Tyr Ala Ser
                85                  90                  95

Ser Gly Ala Ser Thr Gly Tyr His His Gln Leu Tyr His Gln Pro Thr
            100                 105                 110

Ser Ser Ala Leu His Phe Ala Asp Ser Val Met Val Ala Ser Ser Ala
        115                 120                 125

Gly Val His Asp Gly Gly Ala Met Leu Ser Ala Ala Ala Ala Asn Gly
    130                 135                 140

Val Ala Gly Ala Ala Ser Ala Asn Gly Gly Gly Ile Gly Leu Ser Met
145                 150                 155                 160

Ile Lys Asn Trp Leu Arg Ser Gln Pro Ala Pro Met Gln Pro Arg Val
                165                 170                 175

Ala Ala Ala Glu Gly Ala Gln Gly Leu Ser Leu Ser Met Asn Met Ala
            180                 185                 190

Gly Thr Thr Gln Gly Ala Ala Gly Met Pro Leu Leu Ala Gly Glu Arg
        195                 200                 205

Ala Arg Ala Pro Glu Ser Val Ser Thr Ser Ala Gln Gly Gly Ala Val
    210                 215                 220

Val Val Thr Ala Pro Lys Glu Asp Ser Gly Gly Ser Gly Val Ala Gly
225                 230                 235                 240

Ala Leu Val Ala Val Ser Thr Asp Thr Gly Gly Ser Gly Gly Ala Ser
                245                 250                 255

Ala Asp Asn Thr Ala Arg Lys Thr Val Asp Thr Phe Gly Gln Arg Thr
            260                 265                 270

Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
        275                 280                 285

Ala His Leu Trp Asp Asn Ser Cys Arg Arg Glu Gly Gln Thr Arg Lys
    290                 295                 300

Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala
305                 310                 315                 320

Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Ala Thr Thr Thr
                325                 330                 335
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Thr Asn Phe Pro Val Ser Asn Tyr Glu Lys Glu Leu Glu Asp Met Lys
            340                 345                 350

His Met Thr Arg Gln Glu Phe Val Ala Ser Leu Arg Arg Lys Ser Ser
        355                 360                 365

Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His
    370                 375                 380

Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys
385                 390                 395                 400

Asp Leu Tyr Leu Gly Thr Phe Ser Thr Gln Glu Glu Ala Ala Glu Ala
                405                 410                 415

Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Asn Ala Val Thr Asn
            420                 425                 430

Phe Asp Met Ser Arg Tyr Asp Val Lys Ser Ile Leu Asp Ser Ser Ala
        435                 440                 445

Leu Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Glu Ala Glu Ala Ala
    450                 455                 460

Ala Ser Ala Gln His His His Ala Gly Val Val Ser Tyr Asp Val Gly
465                 470                 475                 480

Arg Ile Ala Ser Gln Leu Gly Asp Gly Gly Ala Leu Ala Ala Ala Tyr
                485                 490                 495

Gly Ala His Tyr His Gly Ala Ala Trp Pro Thr Ile Ala Phe Gln Pro
            500                 505                 510

Gly Ala Ala Ser Thr Gly Leu Tyr His Pro Tyr Ala Gln Gln Pro Met
        515                 520                 525

Arg Gly Gly Gly Trp Cys Lys Gln Glu Gln Asp His Ala Val Ile Ala
    530                 535                 540

Ala Ala His Ser Leu Gln Asp Leu His His Leu Asn Leu Gly Ala Ala
545                 550                 555                 560

Gly Ala His Asp Phe Phe Ser Ala Gly Gln Gln Ala Ala Ala Ala Ala
                565                 570                 575

Met His Gly Leu Gly Ser Ile Asp Ser Ala Ser Leu Glu His Ser Thr
            580                 585                 590

Gly Ser Asn Ser Val Val Tyr Asn Gly Gly Val Gly Asp Ser Asn Gly
        595                 600                 605

Ala Ser Ala Val Gly Gly Ser Gly Gly Gly Tyr Met Met Pro Met Ser
    610                 615                 620

Ala Ala Gly Ala Thr Thr Thr Ser Ala Met Val Ser His Glu Gln Val
625                 630                 635                 640

His Ala Arg Ala Tyr Asp Glu Ala Lys Gln Ala Ala Gln Met Gly Tyr
                645                 650                 655

Glu Ser Tyr Leu Val Asn Ala Glu Asn Asn Gly Gly Gly Arg Met Ser
            660                 665                 670

Ala Trp Gly Thr Val Val Ser Ala Ala Ala Ala Ala Ala Ala Ser Ser
        675                 680                 685

Asn Asp Asn Met Ala Ala Asp Val Gly His Gly Gly Ala Gln Leu Phe
    690                 695                 700

Ser Val Trp Asn Asp Thr
705                 710

<210> SEQ ID NO 123
<211> LENGTH: 25
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid linker sequence

<400> SEQUENCE: 123

tcgaaggaga tagaaccgat ccacc                                            25


<210> SEQ ID NO 124
<211> LENGTH: 8
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid linker sequence

<400> SEQUENCE: 124

tgagctag                                                                8


<210> SEQ ID NO 125
<211> LENGTH: 508
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 125

ctatagtatt ttaaaattgc attaacaaac atgtcctaat tggtactcct gagatactat     60

accctcctgt tttaaaatag ttggcattat cgaattatca ttttactttt taatgttttc    120

tcttctttta atatatttta tgaattttaa tgtattttaa aatgttatgc agttcgctct    180

ggacttttct cgtgcgccta cacttgggtg tactgggcct aaattcagcc tgaccgaccg    240

cctgcattga ataatggatg agcaccggta aaatccgcgt acccaacttt cgagaagaac    300

cgagacgtgg cgggccgggc caccgacgca cggcaccagc gactgcacac gtcccgccgg    360

cgtacgtgta cgtgctgttc cctcactggc cgcccaatcc actcatgcat gcccacgtac    420

acccctgccg tggcgcgccc agatcctaat cctttcgccg ttctgcactt ctgctgccta    480

taaatggcgg catcgaccgt cacctgct                                       508


<210> SEQ ID NO 126
<211> LENGTH: 558
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 126

gtactgtaat atttatatta tatataatta taaactataa tatttcaaaa ctatagtatt     60

ttaaaattgc attaacaaac atgtcctaat tggtactcct gagatactat accctcctgt    120

tttaaaatag ttggcattat cgaattatca ttttactttt taatgttttc tcttctttta    180

atatatttta tgaattttaa tgtattttaa aatgttatgc agttcgctct ggacttttct    240

cgtgcgccta cacttgggtg tactgggcct aaattcagcc tgaccgaccg cctgcattga    300

ataatggatg agcaccggta aaatccgcgt acccaacttt cgagaagaac cgagacgtgg    360

cgggccgggc caccgacgca cggcaccagc gactgcacac gtcccgccgg cgtacgtgta    420

cgtgctgttc cctcactggc cgcccaatcc actcatgcat gcccacgtac acccctgccg    480

tggcgcgccc agatcctaat cctttcgccg ttctgcactt ctgctgccta taaatggcgg    540

catcgaccgt cacctgct                                                  558
```

That which is claimed:

1. A promoter construct comprising a promoter followed by a first attachment B (attB) site, wherein the promoter is selected from the group consisting of:

- a) a promoter comprising a nucleotide sequence having the sequence set forth in SEQ ID NO: 29;
- b) a promoter comprising a nucleotide sequence having at least 70% sequence identity to the sequence set forth in SEQ ID NO: 29; and
- c) a promoter comprising at least 50 contiguous nucleotides of the sequence set forth in SEQ ID NO: 29; and

wherein said first attB site has the nucleotide sequence set forth in SEQ ID NO: 31.

2. The promoter construct of claim **1**, wherein said first attB site modulates the activity of said promoter.

3. The promoter construct of claim **1**, wherein said promoter comprises the sequence set forth in nucleotides 291-430 of SEQ ID NO: 29 or a sequence having at least 70% sequence identity to the sequence set forth in nucleotides 291-430 of SEQ ID NO: 29.

4. The promoter construct of claim **1**, wherein said promoter construct further comprises a linker sequence that separates said promoter and said first attB site.

5. The promoter construct of claim **4**, wherein said linker sequence that separates said promoter and said first attB site is about 133 nucleotides in length.

6. The promoter construct of claim **4**, wherein said linker sequence that separates said promoter and said first attB site comprises nucleotides of a maize rab17 5' untranslated region (5'-UTR).

7. The promoter construct of claim **6**, wherein said linker sequence that separates said promoter and said first attB site comprises the nucleotide sequence set forth in SEQ ID NO: 35.

8. The promoter construct of claim **4**, wherein said linker sequence that separates said promoter and said first attB site has the sequence set forth in SEQ ID NO: 36 or a nucleotide sequence having at least 70% sequence identity to the sequence set forth in SEQ ID NO: 36.

9. An expression cassette comprising the promoter construct of claim **1** operably linked to a polynucleotide of interest.

10. The expression cassette of claim **9**, wherein said polynucleotide of interest is a nucleotide sequence encoding a site-specific recombinase.

11. The expression cassette of claim **10**, wherein said site-specific recombinase is selected from the group consisting of FLP, Cre, SSV1, lambda Int, phi C31 Int, HK022, R, Gin, Tn1721, CinH, ParA, Tn5053, Bxb1, TP907-1, and U153.

12. The expression cassette of claim **9**, further comprising a polynucleotide encoding a babyboom polypeptide operably linked to a second promoter, wherein said second promoter is active in a plant.

13. The expression cassette of claim **12**, wherein said babyboom polypeptide comprises at least two AP2 domains and at least one of the following amino acid sequences:

- the amino acid sequence set forth in SEQ ID NO: 54 or an amino acid sequence that differs from the amino acid sequence set forth in SEQ ID NO: 54 by one amino acid; and
- b) the amino acid sequence set forth in SEQ ID NO: 57 or an amino acid sequence that differs from the amino acid sequence sit forth in SEQ ID NO: 57 by one amino acid.

14. The expression cassette of claim **12**, wherein said polynucleotide encoding said babyboom polypeptide has a nucleotide sequence selected from the group consisting of:

- a) the nucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69;
- b) a nucleotide sequence having at least 70% sequence identity to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69;
- c) a nucleotide sequence encoding a polypeptide haying the amino acid sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28; and
- d) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28.

15. The expression cassette of claim **12**, wherein said second promoter is a maize ubiquitin promoter or a maize oleosin promoter.

16. The expression cassette of claim **12**, wherein said expression cassette further comprises a polynucleotide encoding a Wuschel polypeptide operably linked to a third promoter, wherein said third promoter is active in a plant.

17. The expression cassette of claim **16**, wherein said polynucleotide encoding said Wuschel polypeptide has a nucleotide sequence selected from the group consisting of:

- a) the nucleotide sequence set forth in SEQ ID NO: 61, 63, 114, or 105; and
- b) a nucleotide sequence having at least 70% sequence identity to SEQ ID NO: 61, 63, 114, or 105;
- c) a nucleotide sequence encoding a polypeptide having the amino acid sequence set forth in SEQ ID NO: 62, 64, 115, or 106; and
- d) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 70% sequence identity to SEQ ID NO: 62, 64, 115, or 106.

18. The expression cassette of claim **16**, wherein said third promoter is a maize In2-2 promoter or a nopaline synthase promoter.

19. A host cell comprising the expression cassette of claim **9**.

20. A plant cell comprising the expression cassette of claim **9**.

21. A transgenic seed of a plant comprising the plant cell of claim **20**, wherein said seed comprises said expression cassette.

22. A plant cell comprising an expression cassette comprising a promoter construct according to claim **1** operably linked to a polynucleotide encoding a site-specific recombinase, wherein said plant cell further comprises a polynucleotide of interest flanked by a first and a second recombination site, wherein said first and second recombination sites are recombinogenic with respect to one another and are directly repeated, and wherein said site-specific recombinase can recognize and implement recombination at said first and said second recombination sites, thereby excising said polynucleotide of interest.

23. A method for expressing a polynucleotide of interest in a plant cell, said method comprising introducing into said plant cell an expression cassette, wherein said expression cassette is the expression cassette according to claim **9**.

24. A method for excising a polynucleotide of interest front a target site in a plant cell, wherein said target site comprises a first site-specific recombination site, said polynucleotide of interest, and a second site-specific recombination site, wherein said first and said second site-specific recombination sites are recombinogenic with respect to one another and are directly repeated, said method comprising:

a) introducing into said plant cell an expression cassette comprising a first promoter operably linked to a polynucleotide encoding a site-specific recombinase, wherein said first promoter comprises the promoter construct of claim **1**; and

b) expressing said polynucleotide encoding said site-specific recombinase, wherein said site-specific recombinase recognizes and implements recombination at said first and said second site-specific recombination sites, thereby excising said polynucleotide of interest.

25. The method of claim **24**, wherein said target site comprises in operable linkage: said first recombination site, a second promoter, a polynucleotide sequence encoding a Wuschel polypeptide, a third promoter, a polynucleotide encoding a babyboom polypeptide, and said second recombination site, wherein said polynucleotide encoding said Wuschel polypeptide and its operably linked second promoter can follow or precede said polynucleotide encoding said babyboom polypeptide and its operably linked third promoter in the target site.

26. A method for excising a polynucleotide of interest from a target site in a plant cell, wherein said target site comprises in operable linkage: a first site-specific recombination site, a first promoter, said polynucleotide of interest, a second promoter, a polynucleotide encoding a site-specific recombinase, and a second site-specific recombination site; wherein said first and said second site-specific recombination sites are recombinogenic with respect to one another and are directly repeated; wherein said second promoter comprises the promoter construct of claim **1**, wherein the polynucleotide, of interest and its operably linked first promoter can follow or precede the polynucleotide encoding the site-specific recombinase and its operably linked second promoter in the target site; said method comprising expressing said polynucleotide encoding said site-specific recombinase; wherein said site-specific recombinase recognizes and implements recombination at said first and said second site-specific recombination sites, thereby excising said polynucleotide of interest and said polynucleotide encoding said site-specific recombinase.

27. The method of claim **26**, wherein said first promoter is a maize ubiquitin promoter or a maize oleosin promoter.

28. The method of claim **26**, wherein said target, site further comprises a third promoter operably linked to a polynucleotide, encoding a Wuschel polypeptide, wherein the target site comprises in operable linkage: said first site-specific recombination site, said third promoter, said polynucleotide encoding a Wuschel polypeptide, said first promoter, said polynucleotide of interest, said second promoter, said polynucleotide encoding said site-specific recombinase, and said second site-specific recombination site, wherein the polynucleotide encoding the Wuschel polypeptide and its operably linked third promoter, the polynucleotide of interest and its operably linked first promoter, and the polynucleotide encoding the site-specific recombinase and its operably linked second promoter can be in any order at the target site.

29. The method of claim **28**, wherein the target site comprises in the following order: said first site-specific recombination site, said third promoter, said polynucleotide encoding a Wuschel polypeptide, said first promoter, said polynucleotide of interest, said second promoter, said polynucleotide encoding said site-specific recombinase, and said second site-specific recombination site.

30. The method of claim **26**, wherein said site-specific recombinase is selected from the group consisting of FLP, Cre, SSV1, lambda Int, phi C31 Int, HK022, R, Gin, Tn1721, CinH, ParA, Tn5053, Bxb1, TP907-1, and U153.

31. The method of claim **26**, wherein said polynucleotide of interest is a polynucleotide encoding a cell proliferation factor.

32. The method of claim **31**, wherein said cell proliferation factor comprises a babyboom polypeptide.

33. The method of claim **32**, wherein said babyboom polypeptide comprises at least two AP2 domains and at least one of the following amino acid sequences:

a) the amino acid sequence set forth in SEQ ID NO: 54 or an amino acid sequence that differs from the amino acid sequence set forth in SEQ ID NO: 54 by one amino acid; and

b) the amino acid sequence set forth in SEQ ID NO: 57 or an amino acid sequence that differs from the amino acid sequence set forth in SEQ ID NO: 57 by one amino acid.

34. The method of claim **32**, wherein said polynucleotide encoding said babyboom polypeptide has a nucleotide sequence selected from the group consisting of:

a) the nucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69;

b) a nucleotide sequence having at least 70% sequence identity to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 68, 116, 117, 120, 121, or 69;

c) a nucleotide sequence encoding a polypeptide having the amino acid sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28; and

d) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 122, or 28.

35. A method for transforming a plastid of a plant cell with a polynucleotide of interest, said method comprising:

a) introducing into a plant cell a heterologous polynucleotide encoding a cell proliferation factor;

b) expressing said heterologous polynucleotide encoding said cell proliferation factor; and

c) introducing into a plastid of said plant cell a vector comprising said polynucleotide of interest, wherein the heterologous polynucleotide encoding said cell proliferation factor is expressed prior to, during, or following the introduction into said plastid of said vector comprising said polynucleotide of interest.

36. The method of claim **35**, wherein said cell proliferation factor is a babyboom polypeptide.

37. The method of claim **35**, wherein said heterologous polynucleotide encoding said cell proliferation factor is operably linked to a promoter, and wherein said promoter is part of a tetracycline-repressor system, and expressing said heterologous polynucleotide comprises providing to said plant cell doxycycline.

38. The method of claim **35**, wherein said plastid is a chloroplast, amyloplast, or chromoplast.

39. A method for introducing a polynucleotide of interest into a mature embryo explain of a mature seed, said method comprising:

a) dissecting a mature embryo from a mature seed;

b) making slices of said mature embryo to prepare said mature embryo explant, wherein said mature embryo explain comprises at least one of the tissues selected from the group consisting of leaf primordia, mesocotyl, shoot apical meristem, and root primordia; and

c) introducing into said mature embryo explant:

i) a heterologous polynucleotide encoding a cell proliferation factor and expressing said heterologous polynucleotide encoding said cell proliferation factor; and

ii) a polynucleotide of interest.

40. The method of claim **39**, wherein said mature embryo explant comprises leaf primordia, mesocotyl, and root primordia.

41. The method of claim **39**, wherein said cell proliferation factor comprises a babyboom polypeptide.

42. A method for introducing a polynucleotide of interest into a leaf tissue and regenerating a plant therefrom, said method comprising:

a) excising a leaf segment from a leaf above the first leaf base node;

b) dissecting said leaf fragment into leaf tissue;

d) introducing into said leaf tissue:

i) a heterologous polynucleotide encoding a cell proliferation factor flanked by recombination sites;

ii) an expression cassette comprising the promoter construct according to claim **1** operably linked to a polynucleotide encoding a site-specific recombinase that is capable of recognizing and implementing recombination at said recombination sites; and

iii) a polynucleotide of interest;

e) expressing said heterologous polynucleotide encoding said cell proliferation factor;

f) incubating said leaf tissue under conditions to allow for growth of a callus;

g) expressing said polynucleotide encoding said site-specific recombinase, thereby excising said heterologous polynucleotide encoding said cell proliferation factor;

h) regenerating a plant from said callus.

43. The method of claim **42**, wherein said cell proliferation factor comprises a bah boom polypeptide.

44. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

a) the amino acid sequence set forth in SEQ ID NO: 2, 4, 8, or 18; and

b) an amino acid sequence having at least 75% sequence identity to the sequence set forth in SEQ ID NO: 2, wherein said polypeptide has BBM activity;

c) an amino acid sequence having at least 75% sequence identity to the sequence set forth in SEQ ID NO: 4, wherein said amino acid sequence has amino acid residues valine, tyrosine, and leucine at the positions corresponding to positions 311, 312, and 313, respectively of SEQ ID NO: 4, wherein said polypeptide has BBM activity;

d) an amino acid sequence having at least 75% sequence identity to the sequence set forth in SEQ ID NO; 8, wherein said amino acid sequence has amino acid residues methionine, alanine, and serine at the positions corresponding to positions 1, 2, and 3, respectively, of SEQ ID NO: 8, wherein said polypeptide has BBM activity; and

e) an amino acid sequence having at least 75% sequence identity to the sequence set forth in SEQ ID NO: 18, wherein said amino acid sequence has amino acid residues valine, tyrosine, and leucine at the positions corresponding to positions 337, 338, and 339, respectively, of SEQ ID NO: 18, wherein said polypeptide has BBM activity.

45. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

a) a nucleotide sequence comprising the sequence set forth in SEQ ID NO: 1, 3, 7, or 17;

b) a nucleotide sequence having at least 75% sequence identity to the sequence set forth in SEQ ID NO: 1, wherein said nucleotide sequence encodes a polypeptide having BBM activity;

c) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 2, 4, 8, or 18; and

d) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 75% sequence identity to the amino acid sequence set forth in SEQ ID NO: 2, wherein said polypeptide has BBM activity;

e) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 75% sequence identity to the sequence set forth in SEQ ID NO: 4, wherein said amino acid sequence has amino acid residues valine, tyrosine, and leucine at the positions corresponding to positions 311, 312, and 313, respectively of SEQ ID NO: 4, wherein said polypeptide has BBM activity;

f) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 75% sequence identity to the sequence set forth in SEQ ID NO; 8, Wherein said amino acid sequence has amino acid residues methionine, alanine, and serine at the positions corresponding to positions 1, 2, and 3, respectively, of SEQ ID NO: 8, wherein said polypeptide has BBM activity; and

g) a nucleotide sequence encoding a polypeptide having an amino acid sequence having at least 75% sequence identity to the sequence set forth in SEQ ID NO: 18, wherein said amino acid sequence has amino acid residues valine, tyrosine, and leucine at the positions corresponding to positions 337, 338, and 339, respectively, of SEQ ID NO: 18, wherein said polypeptide has BBM activity;

h) the complement of any one of the nucleotide sequences of a), b), c), d), e), f), or g).

46. An expression cassette comprising the isolated polynucleotide of claim **45**, wherein said polynucleotide is operably linked to a promoter that drives expression in a plant.

47. A plant comprising a heterologous polynucleotide operably linked to a promoter that drives expression in the plant, wherein said polynucleotide is selected from the group consisting of:

a) a polynucleotide comprising the nucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 17, or 27; or a complement thereof;

b) a polynucleotide comprising a nucleotide sequence having at least 75% sequence identity to the sequence set forth in SEQ ID NO: 1, 3, 5, 17, or 27;

wherein said nucleotide sequence encodes a polypeptide having BBM activity;

c) a polynucleotide encoding the amino acid sequence set forth in SEQ ID NO: 2, 4, 6, 8, 18, or 28;

d) a polynucleotide encoding an amino acid sequence having at least 75% sequence identity to the sequence set forth in SEQ ID NO; 8, wherein said amino acid sequence has amino acid residues methionine, alanine, and serine at the positions corresponding to positions 1, 2, and 3, respectively, of SEQ ID NO: 8, wherein said polynucleotide encodes a polypeptide having BBM activity; and

e) a polynucleotide encoding an amino acid sequence having at least 75% sequence identity to the amino acid sequence set forth in SEQ ID NO: 2, 4, 6, 18, or 28; wherein said polynucleotide encodes a polypeptide having BBM activity.

48. A method of increasing the activity of a polypeptide in a plant comprising providing to said plant a polypeptide selected from the group consisting of:

a) the polypeptide comprising the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 18, or 28;

b) the polypeptide having at least 75% sequence identity to SEQ ID NO: 2, 4, 6, 18, or 28, wherein said polypeptide has BBM activity; and

c) the polypeptide having an amino acid sequence having at least 75% sequence identity to the sequence set forth in SEQ ID NO; 8, wherein said amino acid, sequence has amino acid residues methionine, alanine, and serine at the positions corresponding to positions 1, 2, and 3, respectively, of SEQ ID NO: 8, wherein said polypeptide has BBM activity; and

wherein increasing the activity of said polypeptide produces a phenotype in the plant selected from the group consisting of:

a) produces asexually derived embryos in the plant;

b) modifies the regenerative capacity of the plant;

c) increases the transformation efficiency in the plant;

d) increases or maintains the yield in the plant under abiotic stress; and

e) induces embryogenesis.

49. The method of claim **48**, wherein providing the polypeptide comprises introducing into said plant a heterologous polynucleotide selected from the group consisting of:

a) the polynucleotide comprising SEQ ID NO: 1, 3, 5, 7, 17, or 27;

b) the polynucleotide encoding the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 18, or 28;

c) the polynucleotide having at least 75% sequence identity to SEQ ID NO: 1, 3, 5, 17, or 27, wherein said polynucleotide encodes a polypeptide having BBM activity;

d) the polynucleotide encoding an amino acid sequence having at least 75% sequence identity to SEQ ID NO: 2, 4, 6, 18, or 28, wherein said polynucleotide encodes a polypeptide having BBM activity; and

e) the polynucleotide encoding an amino acid sequence having at least 75% sequence identity to the sequence set forth in SEQ ID NO; 8, wherein said amino acid sequence has amino acid residues methionine, alanine, and serine at the positions corresponding to positions 1, 2, and 3, respectively, of SEQ ID NO: 8, wherein said polynucleotide encodes a polypeptide having BBM activity.

50. A method of transforming a plant cell comprising:

(a) transforming a plant cell with a polynucleotide of interest and a heterologous polynucleotide comprising a first nucleotide sequence selected from the group consisting of:

a) a nucleotide sequence comprising SEQ ID NO: 1, 3, 5, 7, 17, or 27;

b) a nucleotide sequence encoding the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 18, or 28;

c) a nucleotide sequence having at least 75% sequence identity to SEQ ID NO: 1, 3, 5, 17, or 27, wherein said nucleotide sequence encodes a polypeptide having BBM activity;

d) a nucleotide sequence encoding an amino acid sequence having at least 75% sequence identity to SEQ ID NO: 2, 4, 6, 18, or 28, wherein said nucleotide sequence encodes a polypeptide having BBM activity; and

e) a nucleotide sequence encoding an amino acid sequence having at least 75% sequence identity to the sequence set forth in SEQ ID NO; 8, wherein said amino acid sequence has amino acid residues methionine, alanine, and serine at the positions corresponding to positions 1, 2, and 3, respectively, of SEQ ID NO: 8, wherein said nucleotide sequence encodes a polypeptide having BBM activity.

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