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Zhang et al.

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(54) **PLANTS WITH ALTERED PHYTOCHROMES**

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 740 days.

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(22) Filed: **Mar. 14, 2013**

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Related U.S. Application Data

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(51) **Int. Cl.**

C12N 15/29	(2006.01)
C12N 15/82	(2006.01)
C07K 14/415	(2006.01)

(52) **U.S. Cl.**

CPC ***C12N 15/8269*** (2013.01); ***C07K 14/415*** (2013.01); ***C12N 15/8261*** (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

Polynucleotides encoding polypeptides that increase the light sensitivity of plants were identified. Introduction of the polynucleotides into plants produces plants having altered characteristics, such as decreased height, decreased diameter, decreased petiole length, decreased internode length, decreased hypocotyl length, increased hyponasty or enhanced germination.

21 Claims, 18 Drawing Sheets

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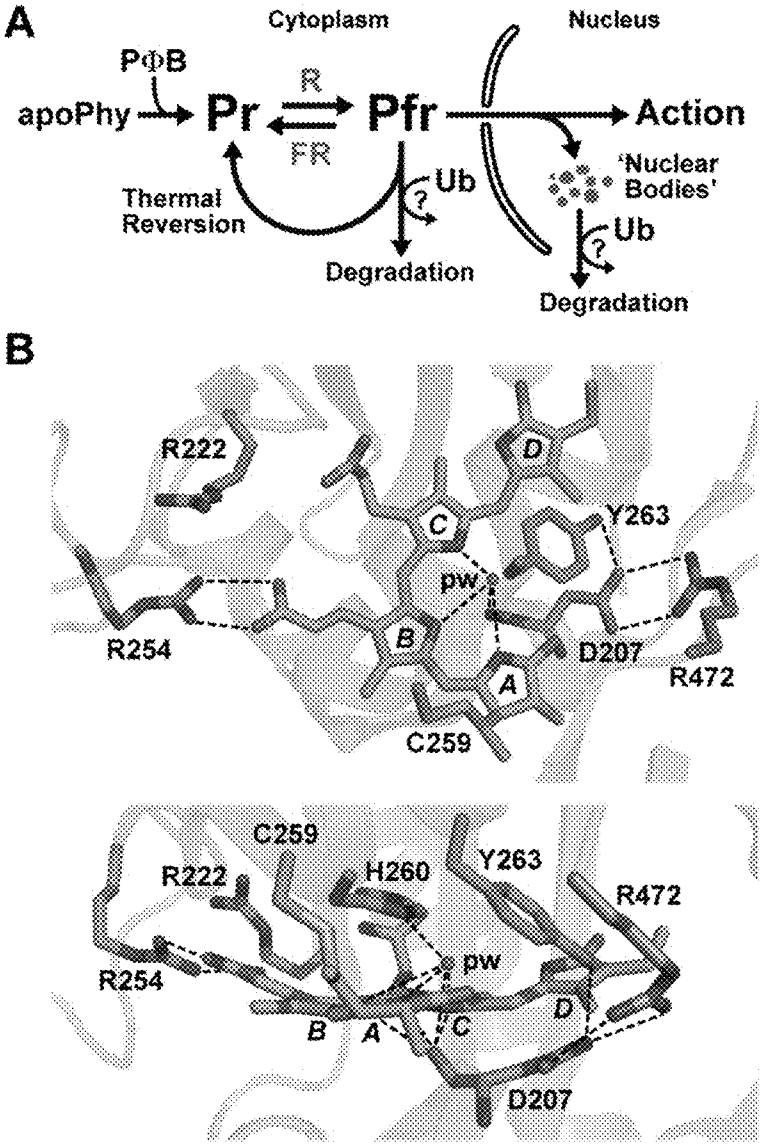

A
Cytoplasm
Nucleus
PΦB
apoPhy
Pr
R
FR
Pfr
Action
'Nuclear Bodies'
Ub
Thermal Reversion
Degradation
Ub
Degradation
B
R222
D
C
Y263
pw
R254
B
D207
R472
A
C259
C259
R222
H260
Y263
R472
pw
R254
B
A
C
D
D207

FIGURE 1

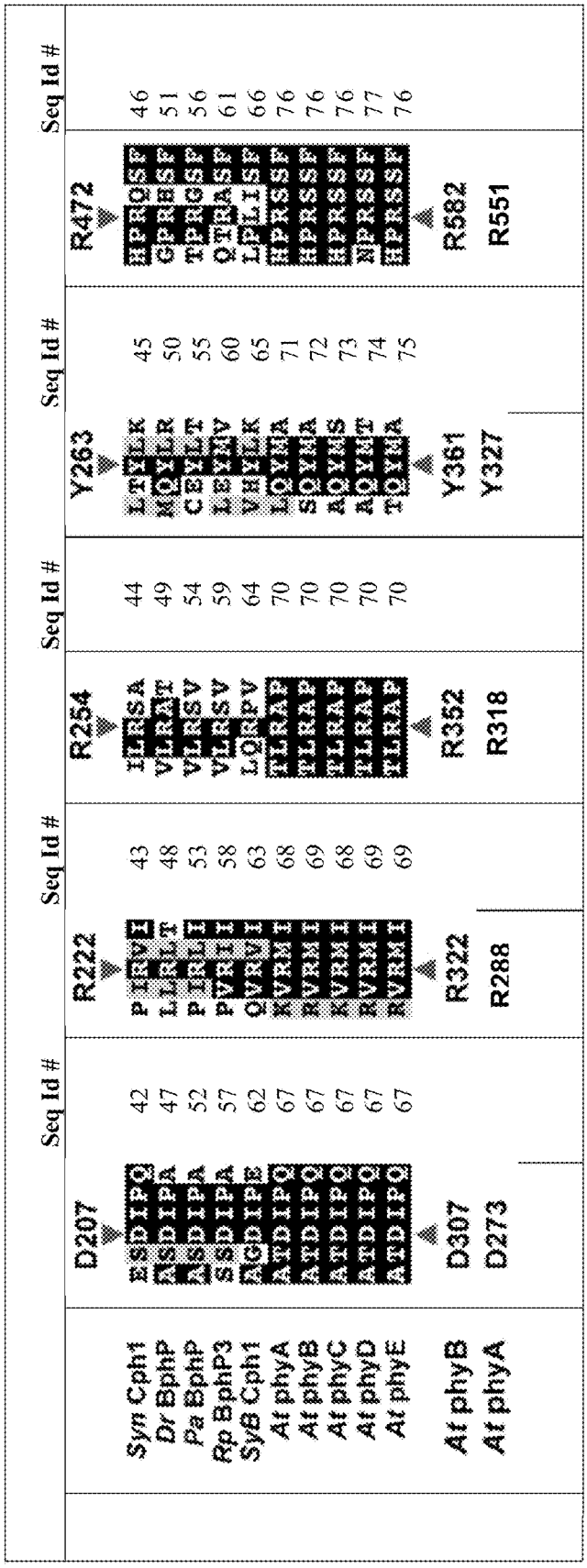

C
Seq Id #
Seq Id #
Seq Id #
Seq Id #
D207
R222
R254
Y263
R472
Syn Cph1
Dr BphP
Pa BphP
Rp BphP3
SyB Cph1
At phyA
At phyB
At phyC
At phyD
At phyE
At phyB
At phyA
D307
D273
R322
R288
R352
R318
Y361
Y327
R582
R551

FIGURE 1

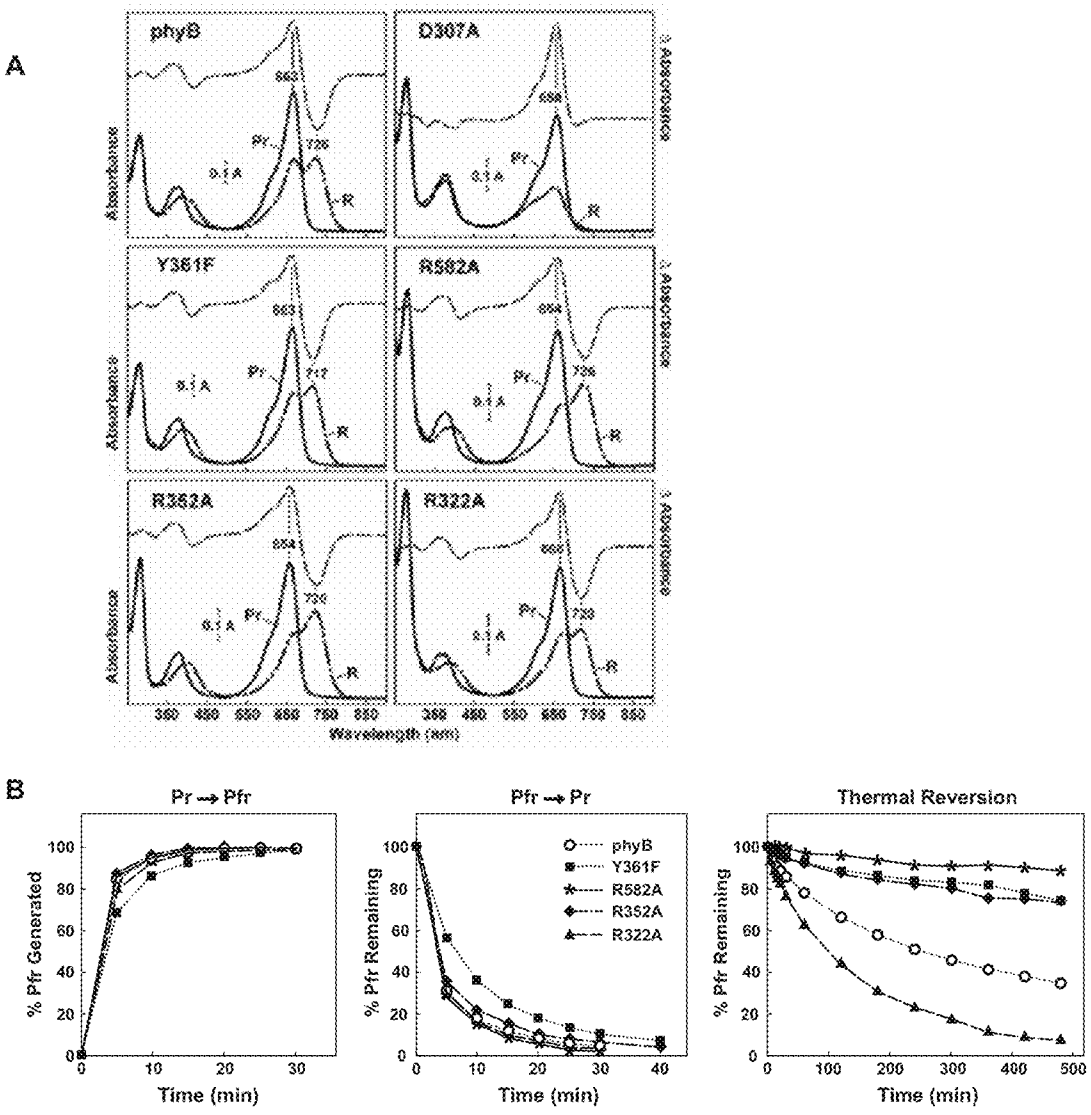

A
phyB
D307A
Y361F
R582A
R352A
R322A
Absorbance
Δ Absorbance
Pr
Pfr
R
Wavelength (nm)
B
Pr → Pfr
Pfr → Pr
Thermal Reversion
% Pfr Generated
% Pfr Remaining
Time (min)
phyB
Y361F
R582A
R352A
R322A

FIGURE 2

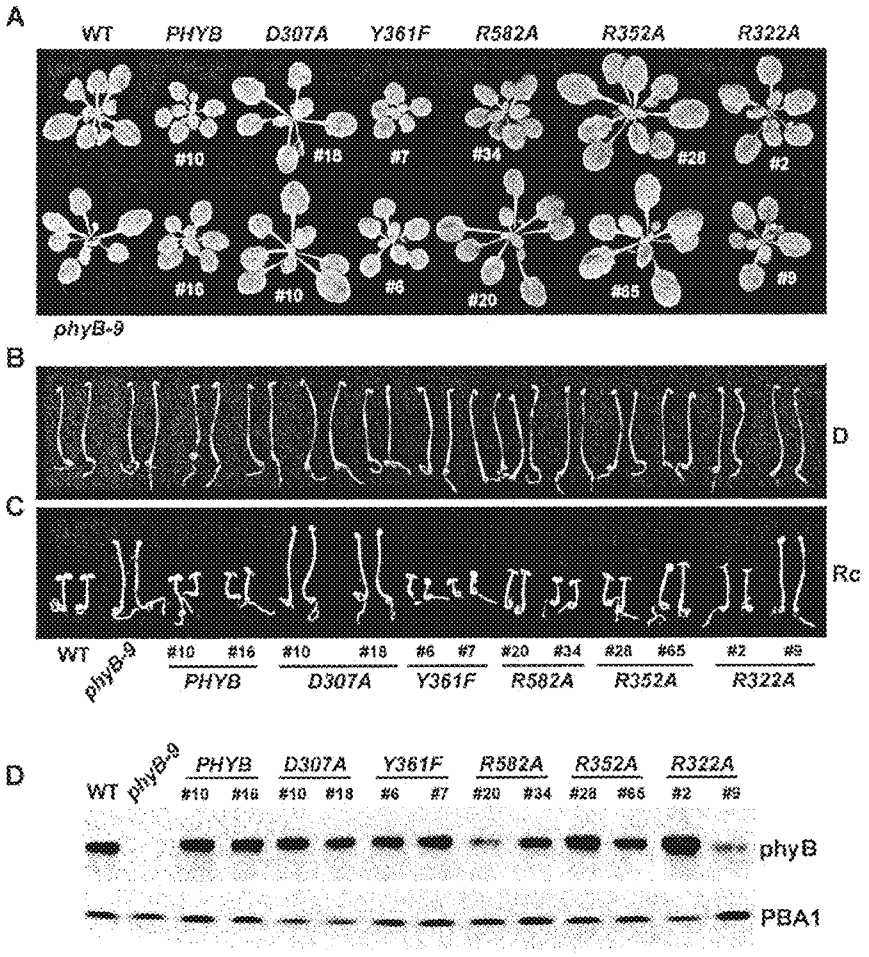

A
WT
PHYB
D307A
Y361F
R582A
R352A
R322A
#10
#16
#10
#18
#7
#34
#28
#2
#16
#10
#10
#6
#20
#65
#9
phyB-9
B
D
C
Rc
WT
phyB-9
#10 #16
PHYB
#10 #18
D307A
#6 #7
Y361F
#20 #34
R582A
#28 #65
R352A
#2 #9
R322A
D
WT
phyB-9
PHYB
D307A
Y361F
R582A
R352A
R322A
#10 #16 #10 #18 #6 #7 #20 #34 #28 #65 #2 #9
phyB
PBA1

FIGURE 3

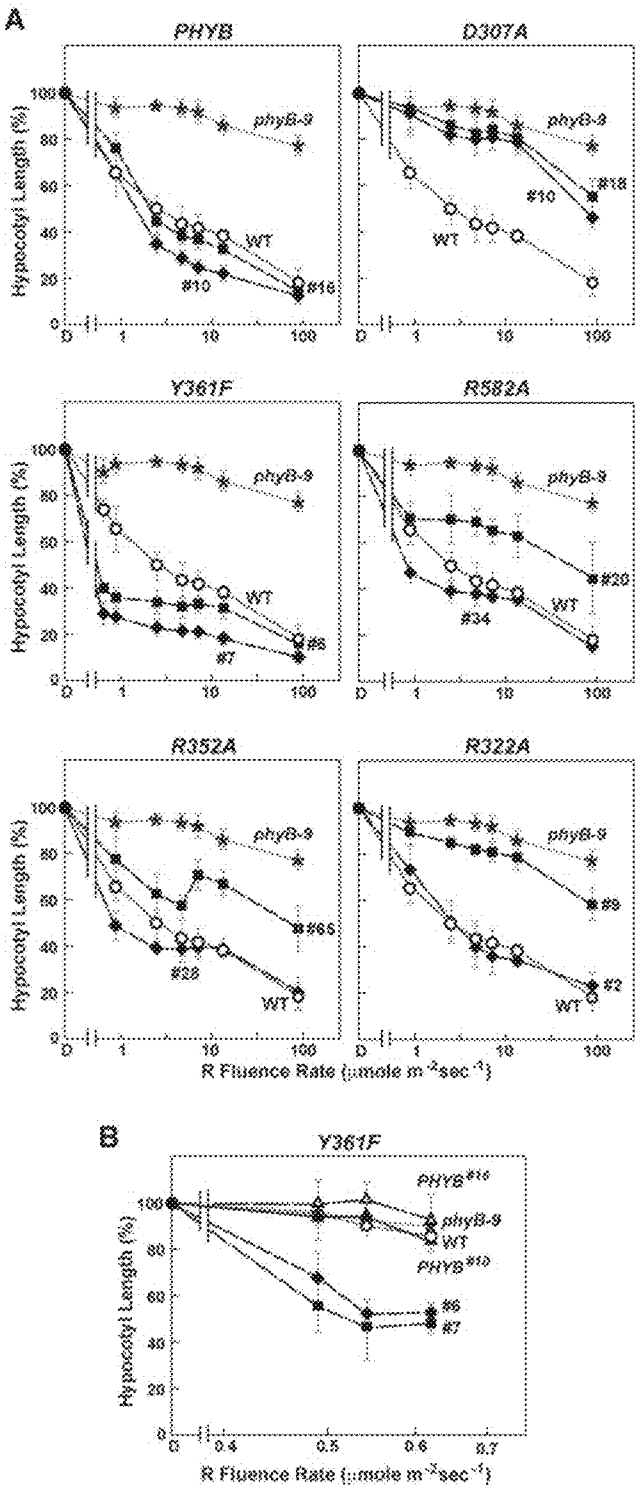

A
PHYB
D307A
Y361F
R582A
R352A
R322A
phyB-9
WT
#10
#16
#18
#20
#34
#5
#7
#56
#28
#9
#2
Hypocotyl Length (%)
R Fluence Rate (μmole m⁻²sec⁻¹)
B
Y361F
PHYB#16
PHYB#10
#6
#7
0.4
0.5
0.6
0.7

FIGURE 4

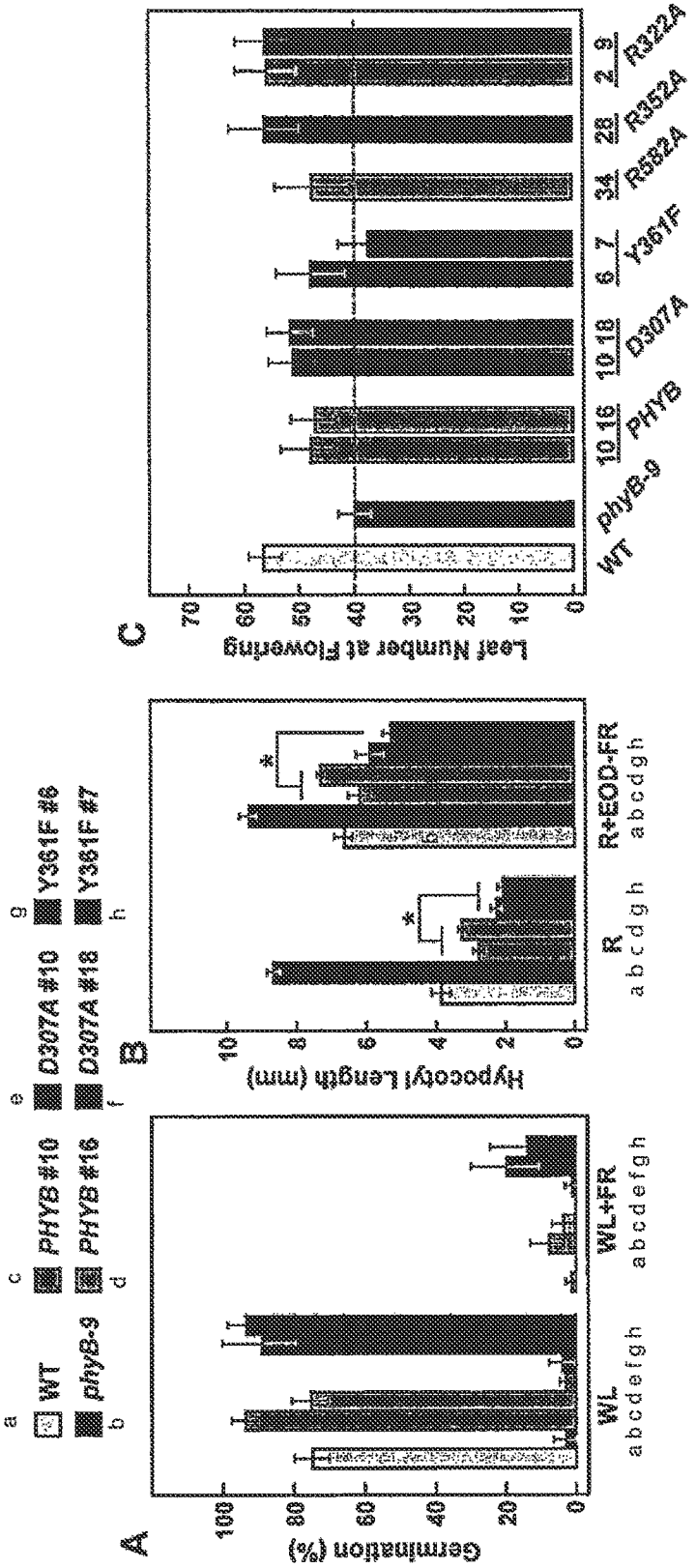

A
B
C
Germination (%)
Hypocotyl Length (mm)
Leaf Number at Flowering
WT
phyB-9
PHYB
D307A
Y361F
R582A
R352A
R322A
WL
R
R+EOD-FR
WL+FR

FIGURE 5

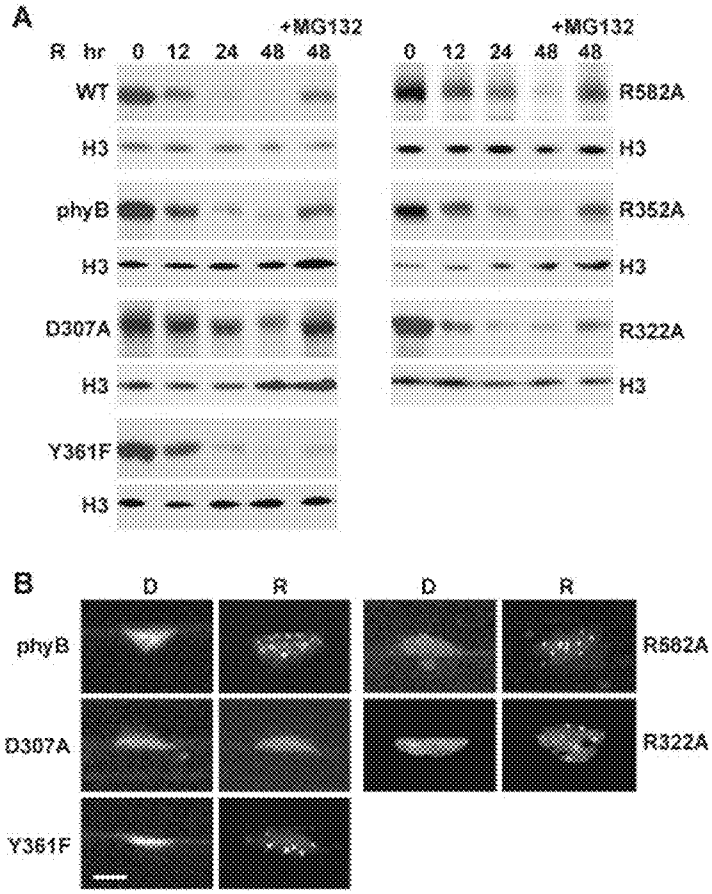

A
+MG132
+MG132
R hr 0 12 24 48 48
0 12 24 48 48
WT
H3
phyB
H3
D307A
H3
Y361F
H3
R582A
H3
R352A
H3
R322A
H3
B
D
R
D
R
phyB
D307A
Y361F
R582A
R322A

FIGURE 6

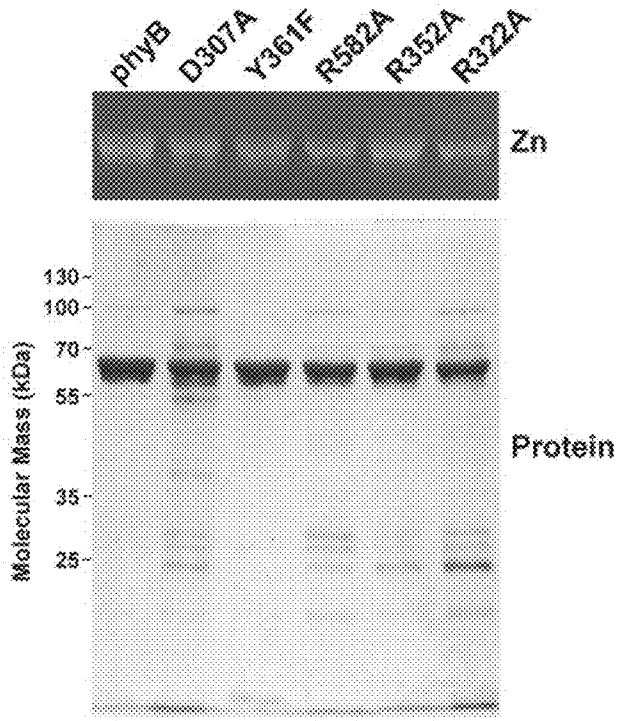

phyB
D307A
Y361F
R582A
R352A
R322A
Zn
130
100
70
55
35
25
Molecular Mass (kDa)
Protein

FIGURE 7

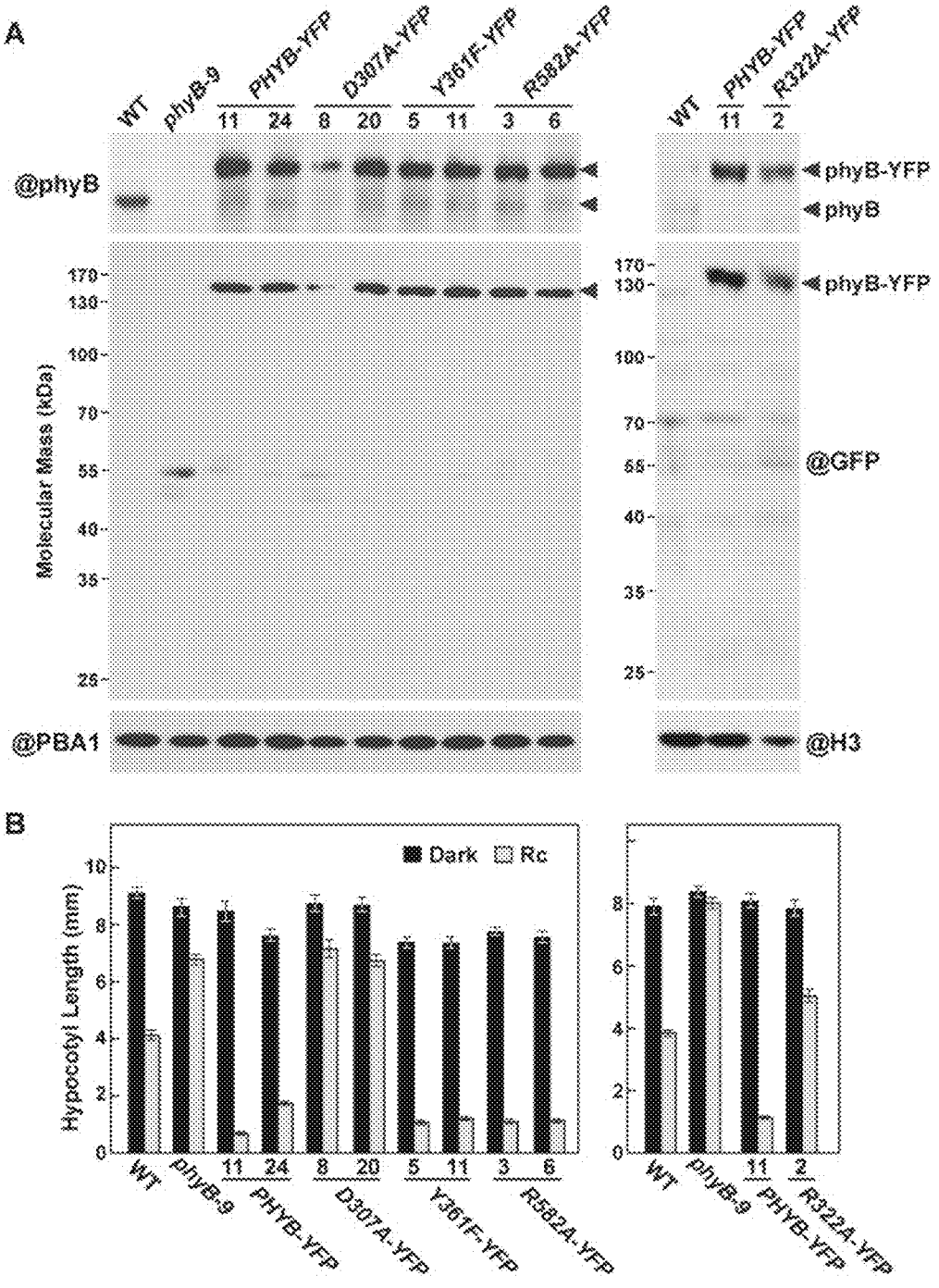
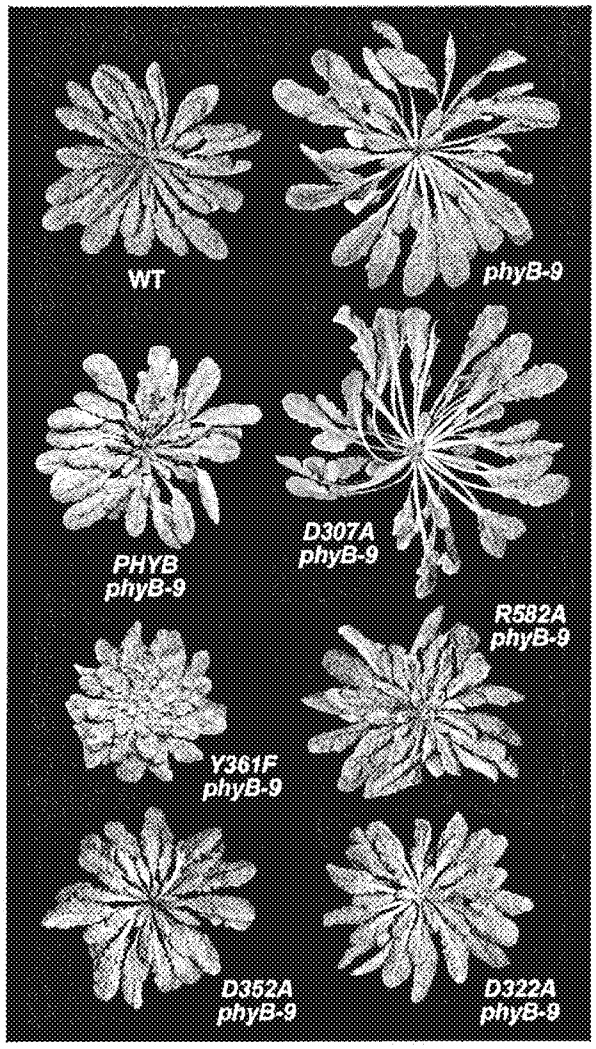

A
WT
phyB-9
PHYB-YFP
D307A-YFP
Y361F-YFP
R582A-YFP
R322A-YFP
11
24
8
20
5
11
3
6
2
@phyB
phyB-YFP
phyB
@GFP
@PBA1
@H3
Molecular Mass (kDa)
170
130
100
70
55
40
35
25
180
65
B
Dark
Rc
Hypocotyl Length (mm)
0
2
4
6
8
10

FIGURE 8


WT
phyB-9
PHYB
phyB-9
D307A
phyB-9
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phyB-9
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phyB-9
D352A
phyB-9
D322A
phyB-9

FIGURE 9

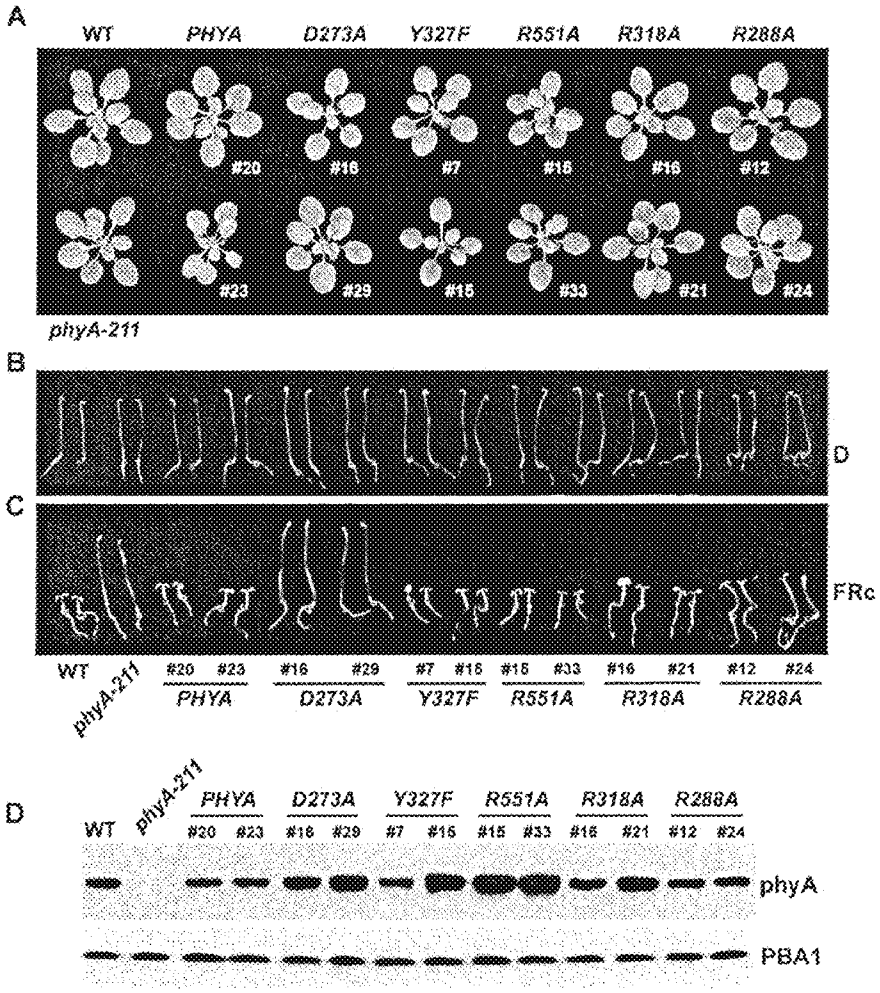
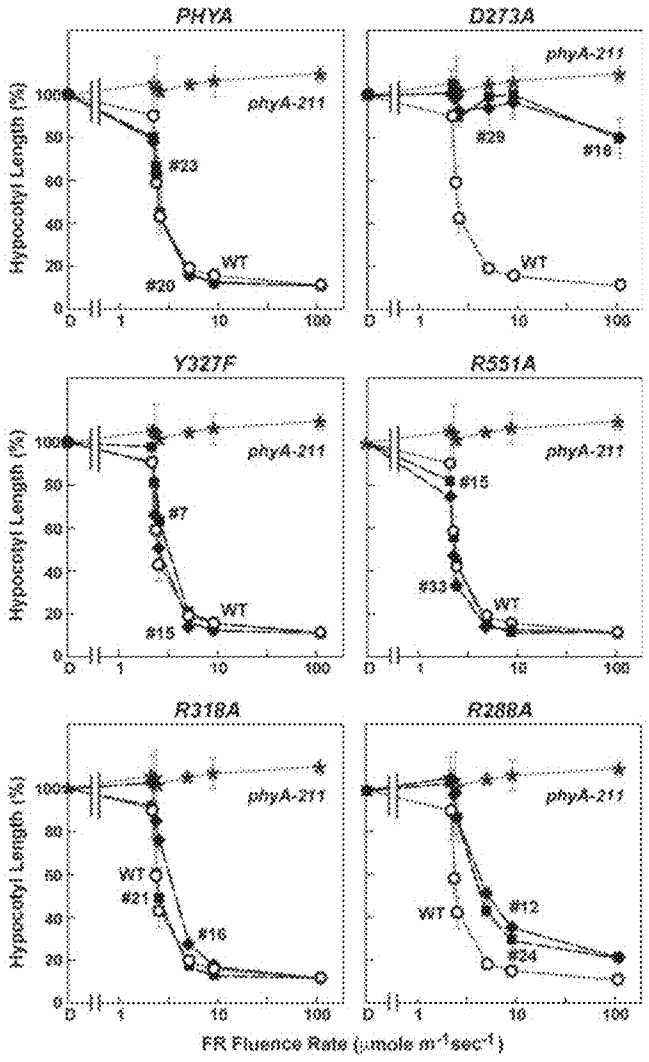

A
WT
PHYA
D273A
Y327F
R551A
R318A
R288A
#20
#16
#7
#15
#16
#12
#23
#29
#15
#33
#21
#24
phyA-211
B
D
C
FRc
WT
phyA-211
#20 #23
PHYA
#16 #29
D273A
#7 #15
Y327F
#15 #33
R551A
#16 #21
R318A
#12 #24
R288A
D
WT
phyA-211
PHYA
#20 #23
D273A
#16 #29
Y327F
#7 #15
R551A
#15 #33
R318A
#16 #21
R288A
#12 #24
phyA
PBA1

FIGURE 10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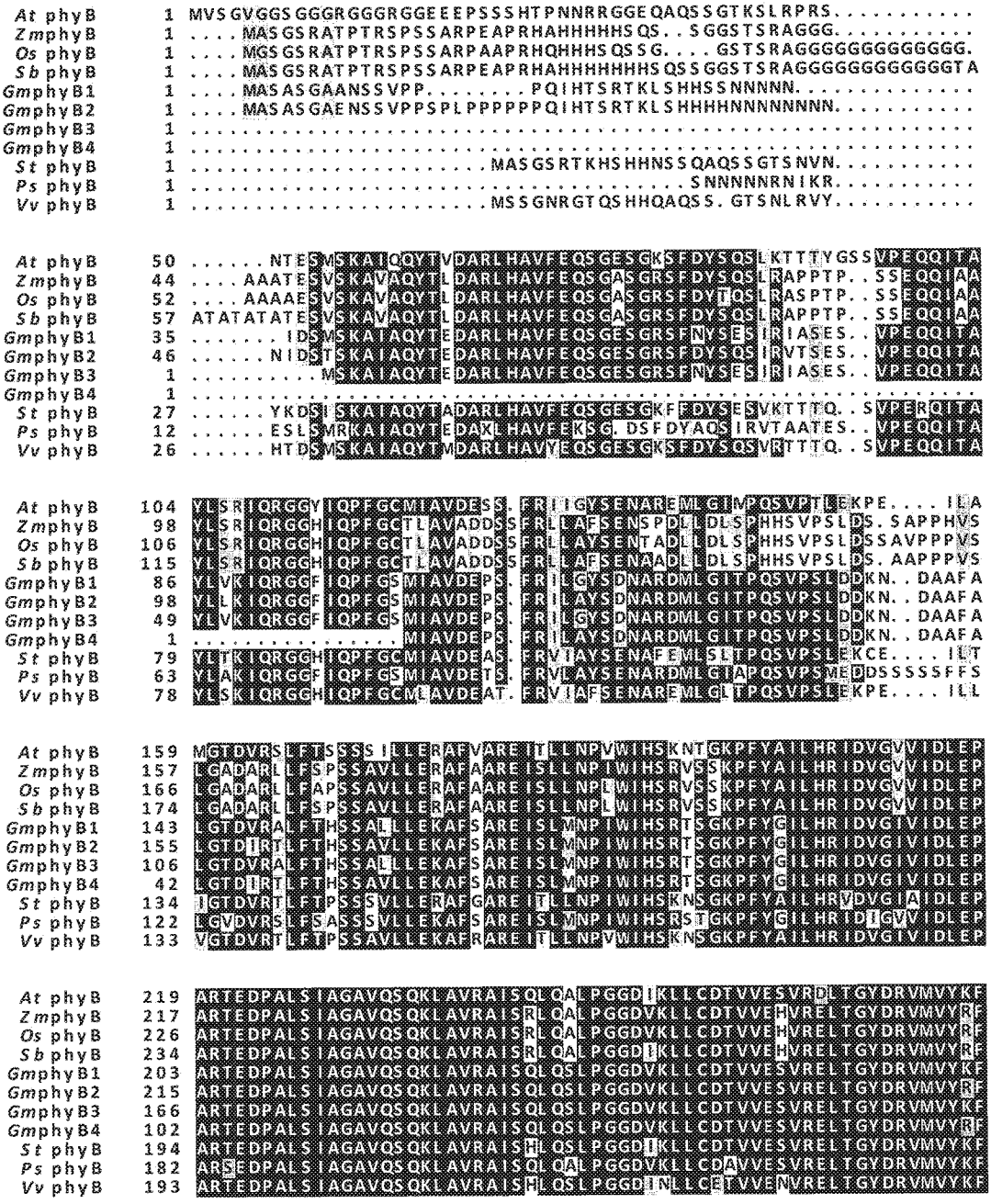
D273A
Y327F
R551A
R318A
R288A
phyA-211
WT
#23
#20
#29
#18
#7
#15
#33
#21
#16
#12
#24
Hypocotyl Length (%)
FR Fluence Rate (μmole m⁻¹sec⁻¹)

FIGURE 11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ZmphyB 1 ....MASGSRATPTRSPSSARPEAPRHAHHHHHSQS..SGGSTSRAGGG.....
Os phyB 1 ....MGSGSRATPTRSPSSARPAAPRHQHHHSQSSG....GSTSRAGGGGGGGGGGGG.
Sb phyB 1 ....MASGSRATPTRSPSSARPEAPRHAHHHHHHHSQSSGGSTSRAGGGGGGGGGGGGGTA
GmphyB1 1 ....MASASGAANSSVPP.....PQIHTSRTKLSHHSSNNNNN.....
GmphyB2 1 ....MASASGAENSSVPPSPLPPPPPPQIHTSRTKLSHHHHNNNNNNNN.....
GmphyB3 1 .....
GmphyB4 1 .....
St phyB 1 .....MASGSRTKHSHHNSSQAQSSGTSNVN.....
Ps phyB 1 .....SNNNNNRNIKR.....
Vv phyB 1 .....MSSGNRGTQSHHQAQSS.GTSNLRVY.....
At phyB 50 .....NTESMSKAIAQQYTVDARLHAVFEQSGESGKSFDYSQSLKTTTYGSSVPEQQITA
ZmphyB 44 ....AAATESVSKAVAQYTLDARLHAVFEQSGASGRSFDYSQSLRAPPTP..SSEQQIAA
Os phyB 52 ....AAAAESVSKAVAQYTLDARLHAVFEQSGASGRSFDYTQSLRASPTP..SSEQQIAA
Sb phyB 57 ATATATATESVSKAVAQYTLDARLHAVFEQSGASGRSFDYSQSLRAPPTP..SSEQQIAA
GmphyB1 35 .....IDSMSKAIAQYTEDARLHAVFEQSGESGRSFNYSESIRIASES..VPEQQITA
GmphyB2 46 .....NIDSTSKAIAQYTEDARLHAVFEQSGESGRSFDYSQSIRVTSES..VPEQQITA
GmphyB3 1 .....MSKAIAQYTEDARLHAVFEQSGESGRSFNYSESIRIASES..VPEQQITA
GmphyB4 1 .....
St phyB 27 .....YKDSISKAIAQYTADARLHAVFEQSGESGKFFDYSESVKTTTQ..SVPERQITA
Ps phyB 12 .....ESLSMRKAIAQYTEDAXLHAVFEKSG.DSFDYAQSIRVTAATES..VPEQQITA
Vv phyB 26 .....HTDSMSKAIAQYTMDARLHAVYEQSGESGKSFDYSQSVRTTTQ..SVPEQQITA
At phyB 104 YLSRIQRGGYIQPFGCMIAVDESS.FRIIGYSENAREMLGIMPQSVPTLEKPE....ILA
ZmphyB 98 YLSRIQRGGHIQPFGCTLAVADDSSFRLLAFSENSPDLLDLSPHHSVPSLDS.SAPPHVS
Os phyB 106 YLSRIQRGGHIQPFGCTLAVADDSSFRLLAYSENTADLLDLSPHHSVPSLDSSAVPPPVS
Sb phyB 115 YLSRIQRGGHIQPFGCTLAVADDSSFRLLAFSENAADLLDLSPHHSVPSLDS.AAPPPVS
GmphyB1 86 YLVKIQRGGFIQPFGSMIAVDEPS.FRILGYSDNARDMLGITPQSVPSLDDKN..DAAFA
GmphyB2 98 YLLKIQRGGFIQPFGSMIAVDEPS.FRILAYSDNARDMLGITPQSVPSLDDKN..DAAFA
GmphyB3 49 YLVKIQRGGFIQPFGSMIAVDEPS.FRILGYSDNARDMLGITPQSVPSLDDKN..DAAFA
GmphyB4 1 .....MIAVDEPS.FRILAYSDNARDMLGITPQSVPSLDDKN..DAAFA
St phyB 79 YLTKIQRGGHIQPFGCMIAVDEAS.FRVIAYSENAFEMLSLTPQSVPSLEKCE....ILT
Ps phyB 63 YLAKIQRGGFIQPFGSMIAVDETS.FRVLAYSENARDMLGIAPQSVPSMEPDSSSSSFFS
Vv phyB 78 YLSKIQRGGHIQPFGCMLAVDEAT.FRVIAFSENAREMLGLTPQSVPSLEKPE....ILL
At phyB 159 MGTDVRSLFTSSSSILLERAFVARETTLLNPVWIHSKNTGKPFYAILHRIDVGVVIDLEP
ZmphyB 157 LGADARLLFSPSSAVLLERAFAARETSLLNPTWIHSRVSSKPFYAILHRIDVGVVIDLEP
Os phyB 166 LGADARLLFAPSSAVLLERAFAARETSLLNPLWIHSRVSSKPFYAILHRIDVGVVIDLEP
Sb phyB 174 LGADARLLFSPSSAVLLERAFAARETSLLNPLWIHSRVSSKPFYAILHRIDVGVVIDLEP
GmphyB1 143 LGTDVRALFTHSSALLLEKAFSARETSLMNPIWIHSRTSGKPFYGILHRIDVGIVIDLEP
GmphyB2 155 LGTDIRTLFTHSSAVLLEKAFSARETSLMNPIWIHSRTSGKPFYGILHRIDVGIVIDLEP
GmphyB3 106 LGTDVRALFTHSSALLLEKAFSARETSLMNPIWIHSRTSGKPFYGILHRIDVGIVIDLEP
GmphyB4 42 LGTDIRTLFTHSSAVLLEKAFSARETSLMNPIWIHSRTSGKPFYGILHRIDVGIVIDLEP
St phyB 134 IGTDVRTLFTPSSSVLLERAFGARETTLLNPIWIHSKNSGKPFYAILHRVDVGIAIDLEP
Ps phyB 122 LGVDVRSLFSASSSVLLEKAFSARETSLMNPIWIHSRSTGKPFYGILHRIDIGVVIDLEP
Vv phyB 133 VGTDVRTLFTPSSAVLLEKAFRARETTLLNPVWIHSKNSGKPFYAILHRIDVGIVIDLEP
At phyB 219 ARTEDPALSIAGAVQSQKLAVRAISQLQALPGGDIKLLCDTVVESVRDLTGYDRVMVYKF
ZmphyB 217 ARTEDPALSIAGAVQSQKLAVRAISRLQALPGGDVKLLCDTVVEHVRELTGYDRVMVYRF
Os phyB 226 ARTEDPALSIAGAVQSQKLAVRAISRLQALPGGDVKLLCDTVVEHVRELTGYDRVMVYRF
Sb phyB 234 ARTEDPALSIAGAVQSQKLAVRAISRLQALPGGDIKLLCDTVVEHVRELTGYDRVMVYRF
GmphyB1 203 ARTEDPALSIAGAVQSQKLAVRAISQLQSLPGGDVKLLCDTVVESVRELTGYDRVMVYKF
GmphyB2 215 ARTEDPALSIAGAVQSQKLAVRAISQLQSLPGGDVKLLCDTVVESVRELTGYDRVMVYRF
GmphyB3 166 ARTEDPALSIAGAVQSQKLAVRAISQLQSLPGGDVKLLCDTVVESVRELTGYDRVMVYKF
GmphyB4 102 ARTEDPALSIAGAVQSQKLAVRAISQLQSLPGGDVKLLCDTVVESVRELTGYDRVMVYRF
St phyB 194 ARTEDPALSIAGAVQSQKLAVRAISHLQSLPGGDIKLLCDTVVESVRELTGYDRVMVYKF
Ps phyB 182 ARSEDPALSIAGAVQSQKLAVRAISQLQALPGGDVKLLCDAVVESVRELTGYDRVMVYKF
Vv phyB 193 ARTEDPALSIAGAVQSQKLAVRAISHLQSLPGGDINLLCETVVENVRELTGYDRVMVYKF

FIG. 12A

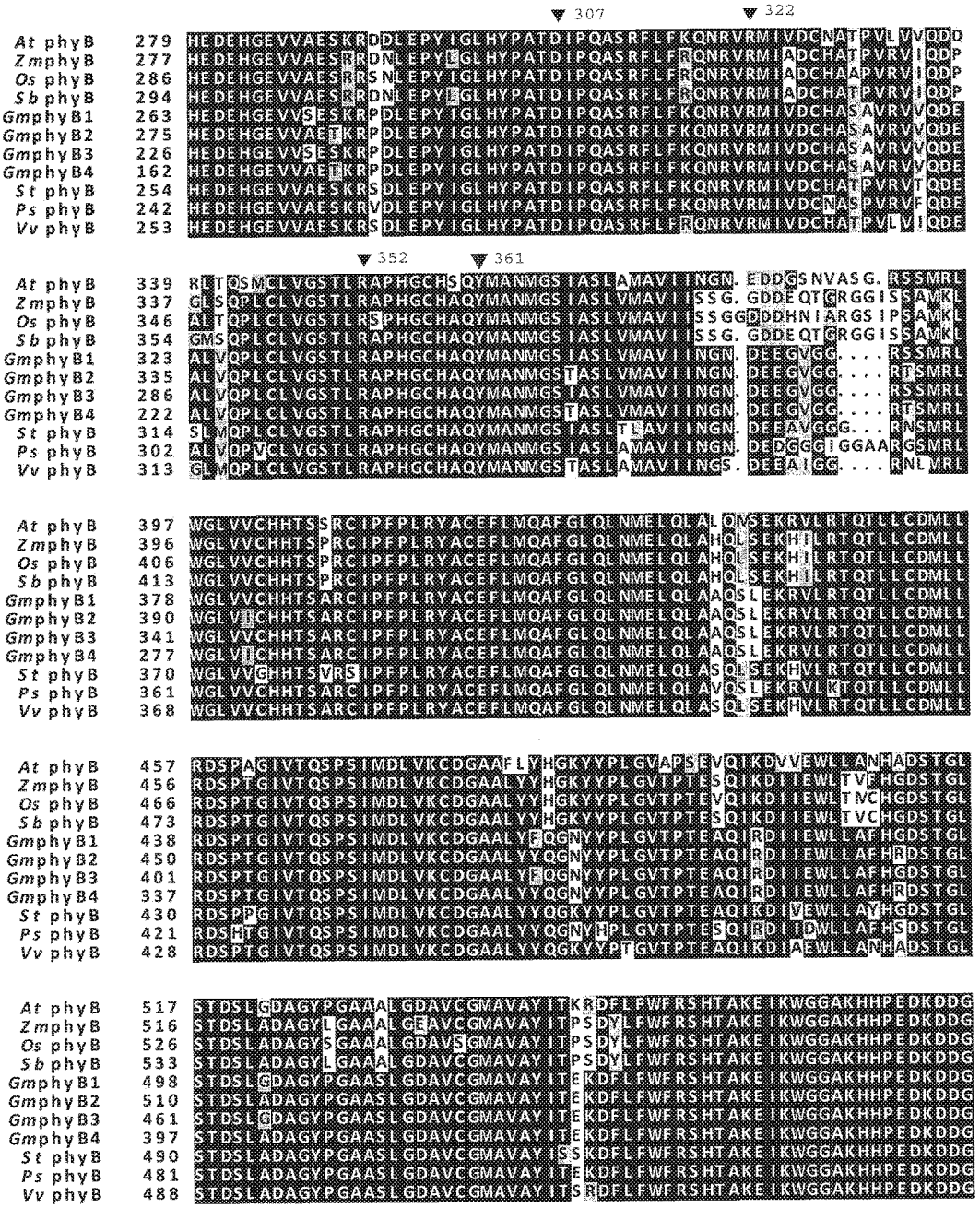

307
322
352
361
At phyB 279
Zmphy B 277
Os phyB 286
Sb phyB 294
Gmphy B1 263
Gmphy B2 275
Gmphy B3 226
Gmphy B4 162
St phyB 254
Ps phyB 242
Vv phyB 253
At phyB 339
Zmphy B 337
Os phyB 346
Sb phyB 354
Gmphy B1 323
Gmphy B2 335
Gmphy B3 286
Gmphy B4 222
St phyB 314
Ps phyB 302
Vv phyB 313
At phyB 397
Zmphy B 396
Os phyB 406
Sb phyB 413
Gmphy B1 378
Gmphy B2 390
Gmphy B3 341
Gmphy B4 277
St phyB 370
Ps phyB 361
Vv phyB 368
At phyB 457
Zmphy B 456
Os phyB 466
Sb phyB 473
Gmphy B1 438
Gmphy B2 450
Gmphy B3 401
Gmphy B4 337
St phyB 430
Ps phyB 421
Vv phyB 428
At phyB 517
Zmphy B 516
Os phyB 526
Sb phyB 533
Gmphy B1 498
Gmphy B2 510
Gmphy B3 461
Gmphy B4 397
St phyB 490
Ps phyB 481
Vv phyB 488

FIG. 12B

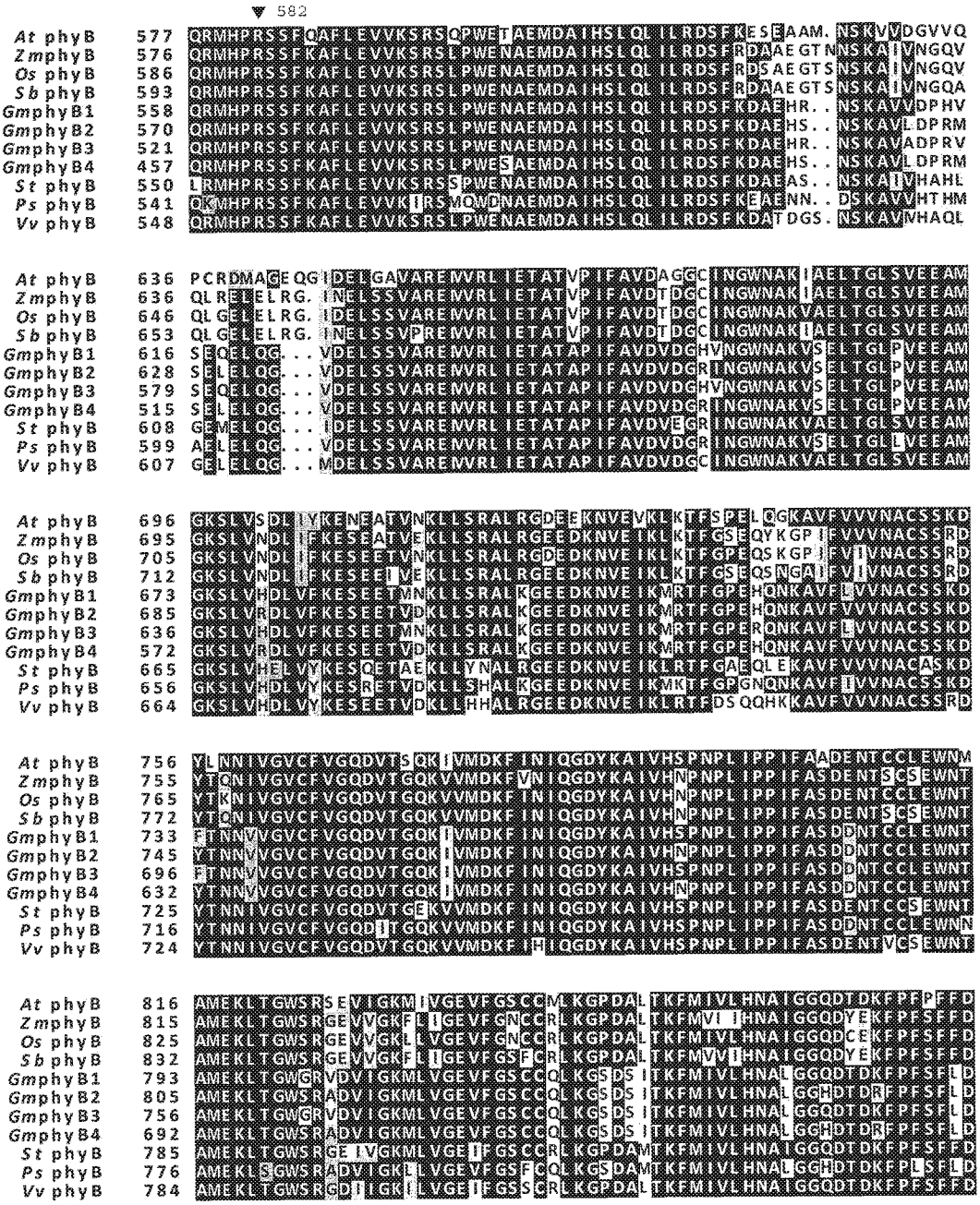
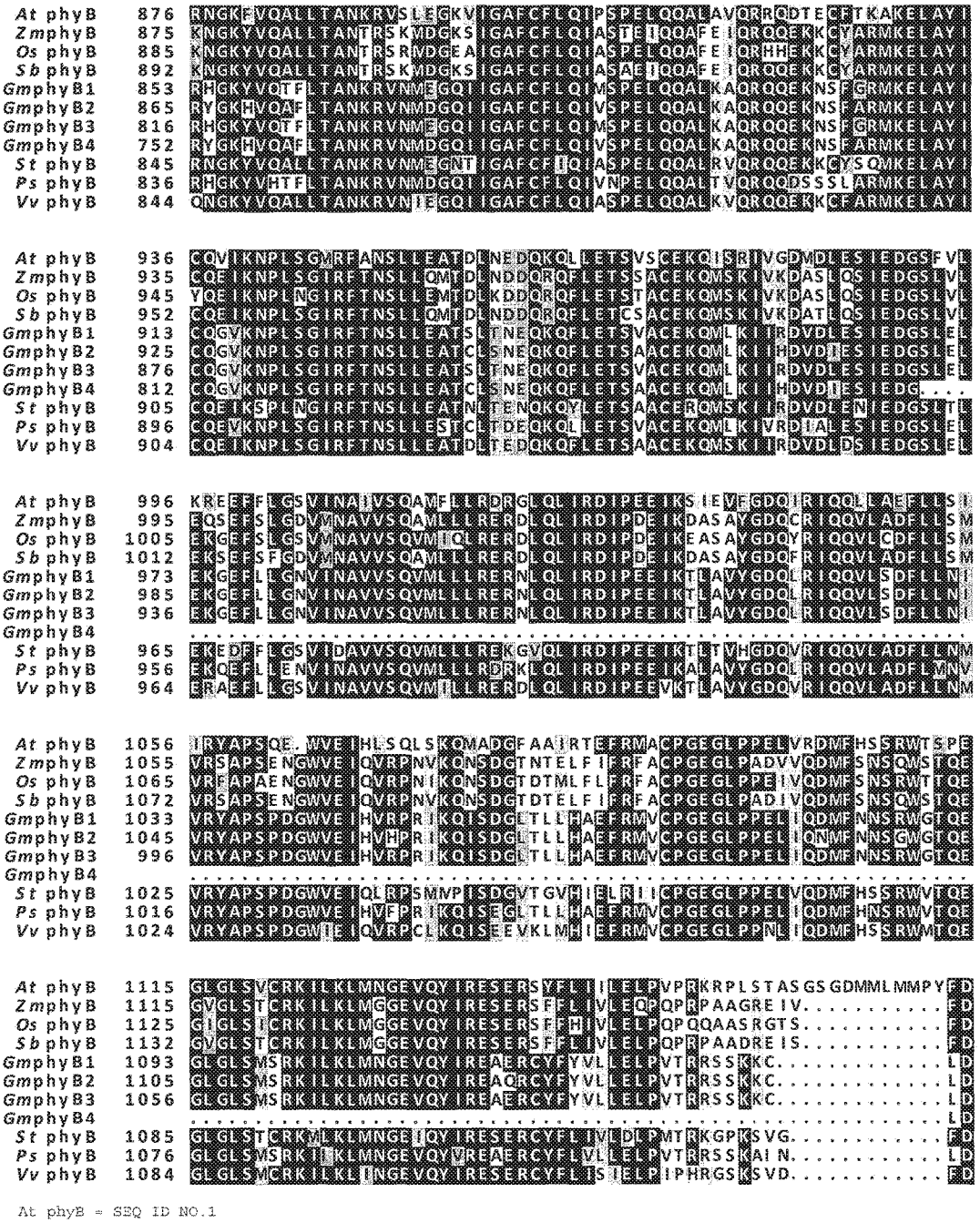

582
At phyB 577 QRMHPRSSFQAFLEVVKSRSQPWETAEMDAIHSLQLILRDSFKESEAAM.NSKVVDGVVQ
Zmphy B 576 QRMHPRSSFKAFLEVVKSRSLPWENAEMDAIHSLQLILRDSFRDAAEGTNNSKAIVNGQV
Os phyB 586 QRMHPRSSFKAFLEVVKSRSLPWENAEMDAIHSLQLILRDSFRDSAEGTSNSKAIVNGQV
Sb phyB 593 QRMHPRSSFKAFLEVVKSRSLPWENAEMDAIHSLQLILRDSFRDAAEGTSNSKAIVNGQA
GmphyB1 558 QRMHPRSSFKAFLEVVKSRSLPWENAEMDAIHSLQLILRDSFKDAEHR..NSKAVVDPHV
GmphyB2 570 QRMHPRSSFKAFLEVVKSRSLPWENAEMDAIHSLQLILRDSFKDAEHS..NSKAVLDPRM
GmphyB3 521 QRMHPRSSFKAFLEVVKSRSLPWENAEMDAIHSLQLILRDSFKDAEHR..NSKAVADPRV
GmphyB4 457 QRMHPRSSFKAFLEVVKSRSLPWESAEMDAIHSLQLILRDSFKDAEHS..NSKAVLDPRM
St phyB 550 LRMHPRSSFKAFLEVVKSRSSPWENAEMDAIHSLQLILRDSFKDAEAS..NSKAIVHAHL
Ps phyB 541 QKMHPRSSFKAFLEVVKIRSMQWDNAEMDAIHSLQLILRDSFKEAENN..DSKAVVHTHM
Vv phyB 548 QRMHPRSSFKAFLEVVKSRSLPWENAEMDAIHSLQLILRDSFKDATDGS.NSKAVVHAQL
At phyB 636 PCRDMAGEQGIDELGAVAREMVRLIETATVPIFAVDAGGCINGWNAKIAELTGLSVEEAM
Zmphy B 636 QLRELELRG.INELSSVAREMVRLIETATVPIFAVDTDGCINGWNAKIAELTGLSVEEAM
Os phyB 646 QLGELELRG.IDELSSVAREMVRLIETATVPIFAVDTDGCINGWNAKVAELTGLSVEEAM
Sb phyB 653 QLGELELRG.INELSSVPREMVRLIETATVPIFAVDTDGCINGWNAKIAELTGLSVEEAM
GmphyB1 616 SEQELQG...VDELSSVAREMVRLIETATAPIFAVDVDGHVNGWNAKVSELTGLPVEEAM
GmphyB2 628 SELELQG...VDELSSVAREMVRLIETATAPIFAVDVDGRINGWNAKVSELTGLPVEEAM
GmphyB3 579 SEQELQG...VDELSSVAREMVRLIETATAPIFAVDVDGHVNGWNAKVSELTGLPVEEAM
GmphyB4 515 SELELQG...VDELSSVAREMVRLIETATAPIFAVDVDGRINGWNAKVSELTGLPVEEAM
St phyB 608 GEMELQG...IDELSSVAREMVRLIETATAPIFAVDVEGRINGWNAKVAELTGLSVEEAM
Ps phyB 599 AELELQG...VDELSSVAREMVRLIETATAPIFAVDVDGRINGWNAKVSELTGLLVEEAM
Vv phyB 607 GELELQG...MDELSSVAREMVRLIETATAPIFAVDVDGCINGWNAKVAELTGLSVEEAM
At phyB 696 GKSLVSDLIYKENEATVNKLLSRALRGDEEKNVEVKLKTFSPELQGKAVFVVVNACSSKD
Zmphy B 695 GKSLVNDLIFKESEATVEKLLSRALRGEEDKNVEIKLKTFGSEQYKGPIFVVVNACSSRD
Os phyB 705 GKSLVNDLIFKESEETVNKLLSRALRGDEDKNVEIKLKTFGPEQSKGPIFVIVNACSSRD
Sb phyB 712 GKSLVNDLIFKESEEIVEKLLSRALRGEEDKNVEIKLKTFGSEQSNGAIFVIVNACSSRD
GmphyB1 673 GKSLVHDLVFKESEETMNKLLSRALKGEEDKNVEIKMRTFGPEHQNKAVFLVVNACSSKD
GmphyB2 685 GKSLVRDLVFKESEETVDKLLSRALKGEEDKNVEIKMRTFGPEHQNKAVFVVVNACSSKD
GmphyB3 636 GKSLVHDLVFKESEETMNKLLSRALKGEEDKNVEIKMRTFGPERQNKAVFLVVNACSSKD
GmphyB4 572 GKSLVRDLVFKESEETVDKLLSRALKGEEDKNVEIKMRTFGPEHQNKAVFVVVNACSSKD
St phyB 665 GKSLVHELVYKESQETAEKLLYNALRGEEDKNVEIKLRTFGAEQLEKAVFVVVNACASKD
Ps phyB 656 GKSLVHDLVYKESRETVDKLLSHALKGEEDKNVEIKMKTFGPGNQNKAVFIVVNACSSKD
Vv phyB 664 GKSLVHDLVYKESEETVDKLLHHALRGEEDKNVEIKLRTFDSQQHKKAVFVVVNACSSRD
At phyB 756 YLNNIVGVCFVGQDVTSQKIVMDKFINIQGDYKAIVHSPNPLIPPIFAADENTCCLEWNM
Zmphy B 755 YTQNIVGVCFVGQDVTGQKVVMDKFVNIQGDYKAIVHNPNPLIPPIFASDENTSCSEWNT
Os phyB 765 YTKNIVGVCFVGQDVTGQKVVMDKFINIQGDYKAIVHNPNPLIPPIFASDENTCCLEWNT
Sb phyB 772 YTQNIVGVCFVGQDVTGQKVVMDKFINIQGDYKAIVHNPNPLIPPIFASDENTSCSEWNT
GmphyB1 733 FTNNVVGVCFVGQDVTGQKIVMDKFINIQGDYKAIVHSPNPLIPPIFASDDNTCCLEWNT
GmphyB2 745 YTNNVVGVCFVGQDVTGQKIVMDKFINIQGDYKAIVHNPNPLIPPIFASDDNTCCLEWNT
GmphyB3 696 FTNNVVGVCFVGQDVTGQKIVMDKFINIQGDYKAIVHSPNPLIPPIFASDDNTCCLEWNT
GmphyB4 632 YTNNVVGVCFVGQDVTGQKIVMDKFINIQGDYKAIVHNPNPLIPPIFASDDNTCCLEWNT
St phyB 725 YTNNIVGVCFVGQDVTGEKVVMDKFINIQGDYKAIVHSPNPLIPPIFASDENTCCSEWNT
Ps phyB 716 YTNNIVGVCFVGQDITGQKVVMDKFINIQGDYKAIVHSPNPLIPPIFASDDNTCCLEWNN
Vv phyB 724 YTNNIVGVCFVGQDVTGQKVVMDKFIHIQGDYKAIVHSPNPLIPPIFASDENTVCSEWNT
At phyB 816 AMEKLTGWSRSEVIGKMIVGEVFGSCCMLKGPDALTKFMIVLHNAIGGQDTDKFPFPFFD
Zmphy B 815 AMEKLTGWSRGEVVGKFLIGEVFGNCCRLKGPDALTKFMVLIHNAIGGQDYEKFPFSFFD
Os phyB 825 AMEKLTGWSRGEVVGKLLVGEVFGNCCRLKGPDALTKFMTVLHNAIGGQDCEKFPFSFFD
Sb phyB 832 AMEKLTGWSRGEVVGKFLIGEVFGSFCRLKGPDALTKFMVVIHNAIGGQDYEKFPFSFFD
GmphyB1 793 AMEKLTGWGRVDVTGKMLVGEVFGSCCQLKGSDSITKFMIVLHNALGGQDTDKFPFSFLD
GmphyB2 805 AMEKLTGWSRADVIGKMLVGEVFGSCCQLKGSDSITKFMIVLHNALGGHDTDRFPFSFLD
GmphyB3 756 AMEKLTGWGRVDVIGKMLVGEVFGSCCQLKGSDSITKFMIVLHNALGGQDTDKFPFSFLD
GmphyB4 692 AMEKLTGWSRADVIGKMLVGEVFGSCCQLKGSDSITKFMIVLHNALGGHDTDRFPFSFLD
St phyB 785 AMEKLTGWSRGEIVGKMLVGEIFGSCGRLKGPDAMTKFMIVLHNAIGGQDTDKFPFSFFD
Ps phyB 776 AMEKLSGWSRADVIGKLLVGEVFGSFCQLKGSDAMTKFMIVLHNALGGHDTDKFPLSFLD
Vv phyB 784 AMEKLTGWSRGDIIGKILVGEIFGSSGRLKGPDALTKFMIVLHNAIGGQDTDKFPFSFFD

FIG. 12C



At phyB = SEQ ID NO.1
Zm phyB = SEQ ID NO.2
Os phyB = SEQ ID NO.3
Sb phyB = SEQ ID NO.4
GmphyB1 = SEQ ID NO.5
GmphyB2 = SEQ ID NO.6
GmphyB3 = SEQ ID NO.7
GmphyB4 = SEQ ID NO.8
St phyB = SEQ ID NO.9
Ps phyB = SEQ ID NO.10
Vv phyB = SEQ ID NO.11

FIG. 12D

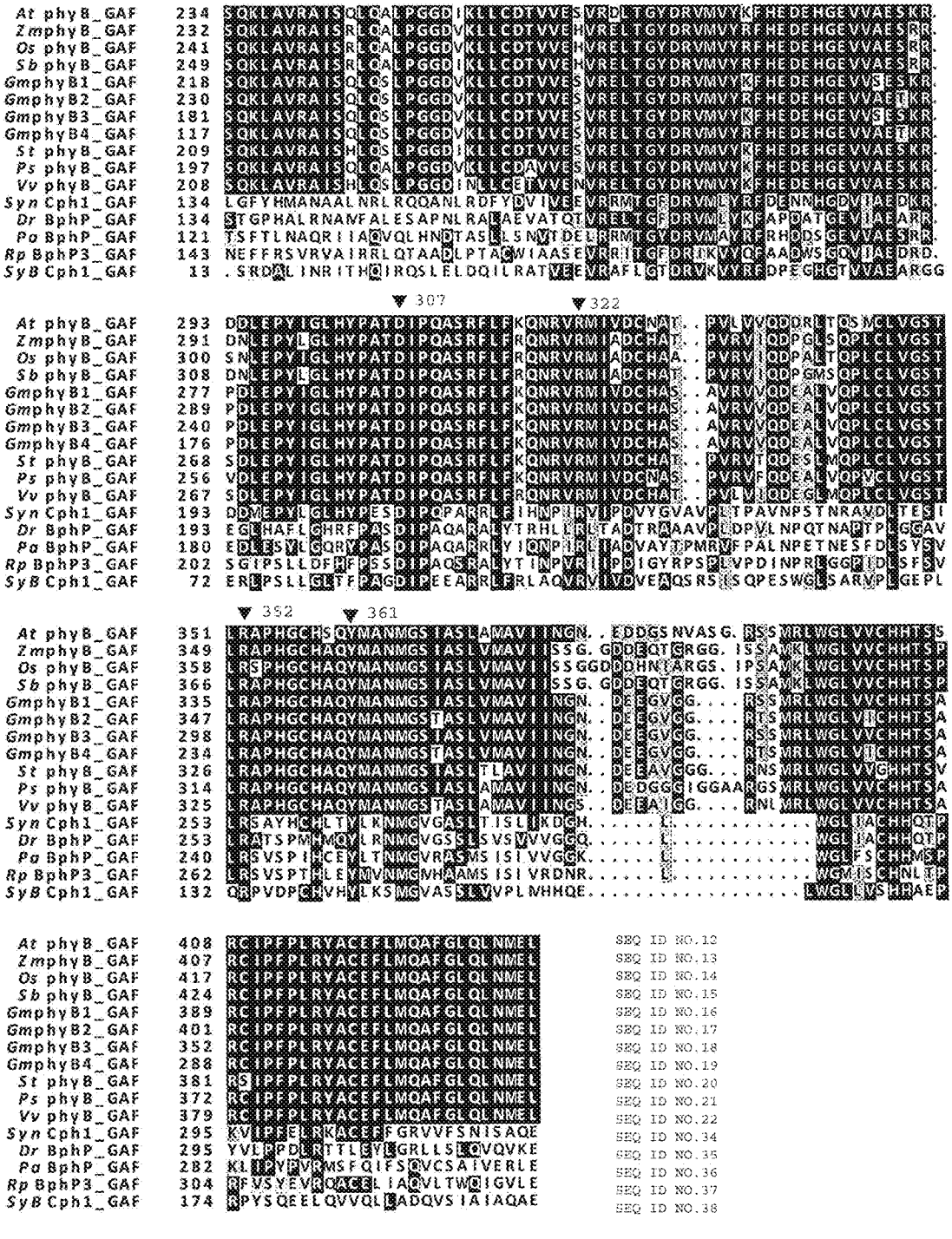

At phyB_GAF
ZmphyB_GAF
Os phyB_GAF
Sb phyB_GAF
GmphyB1_GAF
GmphyB2_GAF
GmphyB3_GAF
GmphyB4_GAF
St phyB_GAF
Ps phyB_GAF
Vv phyB_GAF
Syn Cph1_GAF
Dr BphP_GAF
Pa BphP_GAF
Rp BphP3_GAF
SyB Cph1_GAF
307
322
392
361
SEQ ID NO.12
SEQ ID NO.13
SEQ ID NO.14
SEQ ID NO.15
SEQ ID NO.16
SEQ ID NO.17
SEQ ID NO.18
SEQ ID NO.19
SEQ ID NO.20
SEQ ID NO.21
SEQ ID NO.22
SEQ ID NO.34
SEQ ID NO.35
SEQ ID NO.36
SEQ ID NO.37
SEQ ID NO.38

FIGURE 13

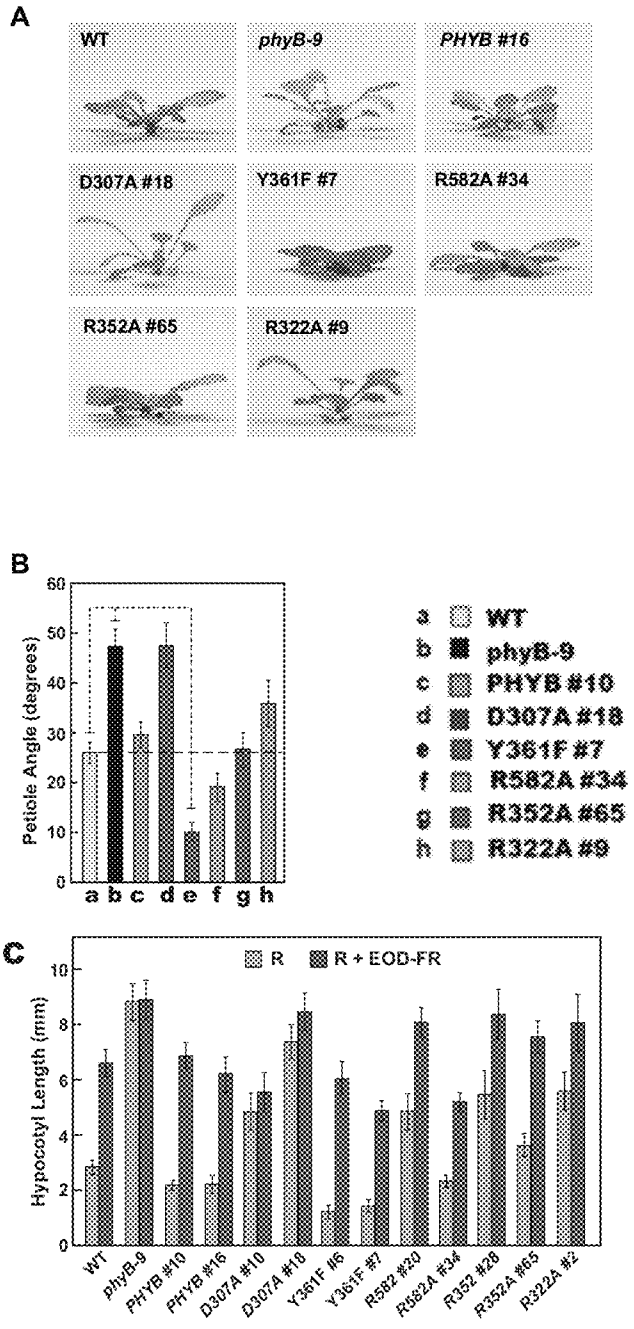

A
WT
phyB-9
PHYB #16
D307A #18
Y361F #7
R582A #34
R352A #65
R322A #9
B
Petiole Angle (degrees)
0
10
20
30
40
50
60
a b c d e f g h
a WT
b phyB-9
c PHYB #10
d D307A #18
e Y361F #7
f R582A #34
g R352A #65
h R322A #9
C
R
R + EOD-FR
Hypocotyl Length (mm)
0
2
4
6
8
10
WT
phyB-9
PHYB #10
PHYB #16
D307A #10
D307A #18
Y361F #6
Y361F #7
R582 #20
R582A #34
R352 #28
R352A #65
R322A #2

FIGURE 14

PLANTS WITH ALTERED PHYTOCHROMES

GOVERNMENT SUPPORT

This invention was made with government support under 07191530 awarded by the National Science Foundation and 13-CRHF-0-6055 awarded by the USDA/NIFA. The government has certain rights in the invention.

INCORPORATION OF SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Oct. 1, 2013, is named ASFILED_Substitute SequenceListing-Text.txt and is 188,936 bytes in size.

BACKGROUND

The rise of the global population and demands for carbon-neutral biofuels have accelerated the need to improve agricultural productivity. An emerging strategy is to control plant reproduction and architecture to better fit specific environments and to increase crop densities. Increasing crop densities may be achieved by producing plants that perform well in more competitive environments. Plant architecture, timing of reproduction, and plant responses to competition may be manipulated to produce plants adapted to growing in crowded conditions.

Phytochromes encompass a diverse collection of biliproteins that enable cellular light perception by photoconverting between a red-light (R)-absorbing ground state—Pr and a far-red light (FR)-absorbing active state—Pfr. In *Arabidopsis thaliana* there are five phytochromes, designated phytochrome A (phyA) to phytochrome E (phyE). Phytochrome B (phyB) is the predominant phytochrome regulating deetiolation responses in R light and shade avoidance. Phytochromes are synthesized in the cytosol as an inactive Pr form, and are converted to the biologically active Pfr form by light irradiation which then is translocated into the nucleus. Phytochromes play fundamental roles in photoperception by a plant and adaptation of its growth to the ambient light environment.

SUMMARY

An isolated polynucleotide comprising a contiguous coding sequence encoding a polypeptide comprising an amino acid sequence having at least 80% identity to at least one sequence selected from SEQ ID NOs: 1-22 and containing an amino acid other than tyrosine at the position corresponding to Y361 of SEQ ID NO. 1, and plants and plant cells containing such polynucleotides are provided. In certain embodiments, a plant comprising the isolated polynucleotide exhibits increased expression of the polypeptide, relative to a control plant, and, relative to the control plant, may exhibit increased light sensitivity, decreased height, decreased diameter, decreased petiole length, decreased internode length, decreased stem diameter, decreased hypocotyl length under an R (red light) fluence rate of less than 1 μmole m^{-2} sec^{-1}, modified hyponasty, or enhanced germination. In certain embodiments, increased light sensitivity results in a smaller plant adapted to provide an increased yield in shaded or competitive conditions.

In another embodiment the invention provides a method of producing a transgenic plant by introducing into a plant cell a polynucleotide encoding a polypeptide comprising an amino acid sequence having at least 80% identity to at least one amino acid sequence selected from SEQ ID NOs: 1-22 and having an amino acid other than tyrosine at the position corresponding to Y361 of SEQ ID NO:1, and regenerating the transformed cell to produce a transgenic plant.

In another embodiment, an isolated polypeptide comprising an amino acid sequence having at least 80% identity to at least one amino acid sequence selected from SEQ ID NOs: 1-22, and having an amino acid other than tyrosine at the position corresponding to Y361 of SEQ ID NO:1 is provided.

In another embodiment, an isolated polynucleotide is provided which comprises a contiguous coding sequence encoding a polypeptide having at least 80% identity to at least one amino acid sequence selected from SEQ ID NOs: 1-22 and which has at least one different amino acid at a select position. The different amino acid may be (i) an amino acid other than aspartate (D) at the position corresponding to 307 of SEQ ID NO:1, (ii) an amino acid other than arginine (R) at the position corresponding to 322 of SEQ ID NO: 1, (iii) an amino acid other than arginine (R) at the position corresponding to 352 of SEQ ID NO: 1, (iv) an amino acid other than arginine (R) at the position corresponding to 582 of SEQ ID NO: 1, or a combination thereof.

Other aspects of the invention will become apparent by consideration of the detailed description and accompanying drawings.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1**. Drawings depicting the scheme of phy action and the three-dimensional relationships of key amino acids within the bilin-binding photosensory module (PSM). (A) Scheme depicting the main steps involved in phy assembly, Pr/Pfr photointerconversion, stability, and action in higher plants. (B) Top (upper) and side (lower) three-dimensional views of the PSM from Syn-Cph1 (PDB code 2VEA [3]) assembled with phycocyanobilin (PCB) highlighting the positions of key conserved amino acids surrounding the bilin and the cysteine involved in bilin attachment (C259). The residue numbers are those for the homolog Syn-Cph1 from the cyanobacterium *Synechocystis* PCC6803. The GAF domain and PHY hairpin are colored in green and orange, respectively. PCB is colored in cyan with the individual pyrrole rings labeled. Sulfur, oxygen and nitrogen atoms are colored yellow, red, and deep blue, respectively. Important contacts are indicated by dashed lines. pw, pyrrole water. (C) Alignment of the GAF domain protein sequences among bacterial phys with available structures with those from the phyB-E family in *Arabidopsis*. Residues pertinent to this study are indicated by red arrowhead; their sequence positions are shown either above for Syn-Cph1 or below the alignment for *A. thaliana* phyA and phyB. At, *Arabidopsis thaliana*; Dr, *Deinococcus radiodurans*; Pa, *Pseudomonas aeruginosa*; Rp, *Rhodopseudomonas palustris*; SyB, *Synechococcus* OS-B'; Syn, *Synechocystis* PCC6803

FIG. **2**. Graphs depicting spectral properties, photochemistry, and thermal reversion rates of wild-type and mutant versions of *Arabidopsis* phyB. The PSM (PAS-GAF-PHY) of each phyB protein was synthesized recombinantly with a C-terminal 6His tag, assembled with PΦB in vivo, and purified. See FIG. **7** for SDS-PAGE analysis. (A) UV-vis absorption spectra of Pr (solid lines) or following its excitation with saturating R (dashed lines). Difference maxima and minima (Pr minus R) are indicated. (B) Rates of Pr→Pfr photoconversion (left), Pfr→Pr photoconversion (middle), and thermal reversion of Pfr back to Pr (right). All rates were

expressed as the percent of Pfr in the sample using the absorption maximum of Pfr near 725 nm for quantification.

FIG. **3**. Photographs showing the phenotypes of an *Arabidopsis* phyB null mutant rescued with transgenes expressing wild-type or mutant versions of full-length phyB. Shown are wild type (WT), the phyB-9 null mutant, and two independent transgenic lines expressing either the wild-type or mutant PHYB cDNAs in the phyB-9 background. (A) Representative 3-week-old plants grown in long days (LDs). (B) Representative 4-d-old seedlings either grown in the dark (D) or under continuous 13 $\mu mol \cdot m^{-2} \cdot s^{-1}$R. (C) Levels of the phyB protein in each of the lines examined in panels A and B as determined by immunoblot analysis of crude extracts from 5-d-old dark grown seedlings with an anti-phyB monoclonal antibody. Near equal protein loading was confirmed with anti-PBA1 antibodies.

FIG. **4**. Graphs depicting R sensitivity of hypocotyl elongation for a phyB null mutant rescued with transgenes expressing wild-type or mutant versions of full-length phyB. Shown are wild type (WT), the phyB-9 null mutant, and two independent transgenic lines expressing either the wild-type or mutant PHYB cDNAs in the phyB-9 background. Hypocotyl length of each line was expressed relative to that measured for dark-grown seedlings. Each data point represents the mean (±SE) from four independent experiments. (A) Sensitivity to a broad range of R fluence rates. (B) Sensitivity of the Y361F variant to very low fluence rates of R.

FIG. **5**. Graphs depicting sensitivity of phyB-9 plants rescued with various phyB mutants to a collection of photomorphogenic processes controlled by phyB. Shown are wild type (WT), the phyB-9 null mutant, and two independent transgenic lines expressing either the wild-type or mutant PHYB cDNAs in the phyB-9 background. (A) Germination efficiency of seeds either treated with 2-hr pulse of WL (white light) alone or followed by a pulse of FR (far-red light). Germination was assessed after a subsequent 5-d incubation in darkness. Each bar represents the average (±SE) of 5 experiments involving at least 40 seeds each. (B) EOD-FR effect on hypocotyl growth. Etiolated seedlings were subject over 4 d to a light regime of continuous R (90 $\mu mole \cdot m^{2} \cdot s^{-1}$) for 8 hr, followed by either darkness or a 10-min pulse of FR (R+EODFR, 100 $\mu mole \cdot m^{-2} \cdot s^{-1}$), and then 16-hr of darkness. Each bar represents the average (±SE) of 4 experiments involving at least 15 seedlings each. The two $phyB^{Y361F}$ lines were significantly more sensitive to R and line #7 was more derepressed by R+EOD-FR than the two $phyB^{WT}$ lines (*, Student's t test: $P<0.05$). (C) Flowering time in short days (SDs) (8-hr light/16-hr dark). Each bar represents the average number of leaves generated before emergence of the inflorescence stem for >20 plants (±SE).

FIG. **6**. Photographs showing the effect of the phyB mutations on the nuclear distribution and R-induced degradation of the photoreceptor. (A) Loss of phyB protein during continuous R irradiation of etiolated seedlings. phyB levels in 4-d-old dark-adapted *Arabidopsis* were measured after various length exposures to 90 $\mu mol \cdot m^{-2} \cdot s^{-1}$ R by immunoblot analysis using an anti-phyB monoclonal antibody. The seedlings were exposed to 100 μM MG132 or an equivalent volume of DMSO 12 hr before irradiation. Near equal protein loading was confirmed with anti-histone H3 antibodies. (B) Subcellular partitioning of wild-type and mutant phyB in continuous R. Wild-type phyB or the various mutants were expressed as fusions to the N-terminus of YFP in the phyB-9 background. Regions surrounding the nucleus were imaged by fluorescence confocal microscopy from hypocotyl cells either kept in the dark or irradiated for 12 hr with continuous 90 $\mu mol \cdot m^{-2} \cdot s^{-1}$ R. Scale bar represents 20 μm. Expression levels of the fusions and their ability to rescue the phyB-9 phenotype with respect to hypocotyl elongation in R can be found in FIG. **8**.

FIG. **7**. Photographs of protein gels showing the purification and assembly of the PSM from wild-type phyB and the various site-directed mutants. The 6His-tagged polypeptides were co-expressed recombinantly with the dual enzyme system that synthesizes the higher plant phy chromophore phytochromobilin (PΦB). The purified chromoproteins were subjected to SDS-PAGE and either stained for protein with Coomassie blue or for the bound bilin by zinc-induced fluorescence (Zn).

FIG. **8**. Photographs (A) and graphs (B) showing the accumulation of YFP fusions of phyB in *Arabidopsis* seedlings. Full-length wild-type phyB or the various mutants (R322A, D307A, Y361F, and R582A) were expressed in the phyB-9 background as fusions to the N-terminus of YFP. Total crude extracts from 5-d-old dark grown seedlings were subjected to immunoblot analysis using a monoclonal antibody against either phyB or GFP (Sigma). Near equal loading was confirmed with anti-PBA1 or anti-histone H3 antibodies. The arrowheads locate phyB and the phyB-YFP fusions.

FIG. **9**. Photographs showing the morphology of phyB null mutant *Arabidopsis* rescued with transgenes expressing wild-type or mutant versions of full length phyB. Shown are wild type (WT), the phyB-9 null mutant, and representative transgenic lines expressing either the wild-type or mutant PHYB cDNAs in the phyB-9 background grown under SD (short day) until bolting.

FIG. **10**. Photographs showing the phenotype of an *Arabidopsis* phyA null mutant rescued with transgenes expressing wild-type or mutant versions of full-length phyA. Shown are wild-type (WT), the phyA-211 null mutant, and two independent transgenic lines expressing either the wild-type or mutant PHYA cDNAs in the phyA-211 background. (A) Representative 3-week-old plants grown under LD. (B) Representative 4-d-old seedlings either grown in the dark (D) or under continuous 5 $\mu mole \cdot m^{-2} \cdot s^{-1}$ FR. (C) Levels of the phyA protein in each of the lines examined in panels A and B as determined by immunoblot analysis of crude extracts from 5-d-old dark grown seedlings with an anti-phyA monoclonal antibody. Near equal protein loading was confirmed with anti-PBA1 antibodies.

FIG. **11**. Graphs depicting FR sensitivity of hypocotyl elongation for a phyA null mutant rescued with transgenes expressing wild-type or mutant versions of full-length phyA. Shown are wild type (WT), the phyA-211 null mutant, and two independent transgenic lines expressing either the wild-type or mutant PHYA cDNAs in the phyA-211 background. Hypocotyl length of each line was expressed relative to that measured for dark-grown seedlings. Each data point represents the mean (±SE) from four independent experiments.

FIG. **12**A, FIG. **12**B, FIG. **12**C, and FIG. **12**D. Chart depicting the alignment of the full-length polypeptide sequences of phyB from *Arabidopsis* and crop species. Residues corresponding to Tyr361 in *Arabidopsis* phyB are indicated by the arrowhead at 361. At, *Arabidopsis thaliana*; Zm, *Zea mays*; Os, *Oryza sativa*; Sb, *Sorghum bicolor*, Gm, *Glycine max*; St, *Solanum tuberosum* L.; Ps, *Pisum sativum*; Vv, *Vitis vinifera*. The protein sequences were obtained from National Center for Biotechnology Information except ZmphyB sequence which was from the Phytozome resource. Alignment was performed using ClustalW (*Nucleic Acids Res.* 22 (22); 4673-80).

FIG. **13**. Chart depicting the alignment of the polypeptide sequences of GAF domains from microbial phys with available structures and phyB among *Arabidopsis* and crop species. Residues corresponding to Asp307, Arg322, Arg352, and Tyr361 in *Arabidopsis* phyB are indicated by the arrowhead. At, *Arabidopsis thaliana*; Zm, *Zea mays*; Os, *Oryza sativa*; Sb, *Sorghum bicolor*; Gm, *Glycine max*; St, *Solanum tuberosum* L.; Ps, *Pisum sativum*; Vv, *Vitis vinifera*; Dr, *Deinococcus radiodurans*; Pa, *Pseudomonas aeruginosa*; Rp, *Rhodopseudomonas palustris*; SyB, *Synechococcus* OS-B'; Syn, *Synechocystis* PCC6803. The protein sequences were obtained from National Center for Biotechnology Information except ZmphyB sequence which was from the Phytozome resource. Alignment was performed using ClustalW (*Nucleic Acids Res.* 22 (22); 4673-80).

FIG. **14**. Photograph and graphs depicting the sensitivity of phyB-9 plants rescued with various phyB mutants to photomorphogenic processes controlled by phyB. Shown are wild type (WT), the phyB-9 null mutant, and one or two independent transgenic lines expressing either the wild-type or mutant PHYB cDNAs in the phyB-9 background. See FIG. **3**D for the description of the mutant lines. (A), Photograph showing the side view of 45-d-old seedlings grown in white light under SD illustrating the influence of phyB on leaf epinasty. (B), Quantification of leaf epinasty for seedlings in panel A. Each bar represents the average angle between the soil surface and the petiole for the 4th and 5th leaves of 10 plants (20 total angles). The 95% confidence interval for each average is shown. The values for WT, phyB-9, and Y361F lines are significantly different from each other by Student's t test ($p<0.05$). (C), Effect of R and EOD-FR on hypocotyl growth. Etiolated seedlings were subjected over 4 d to a 24-hr light regime of continuous R (90 μmole m^{-2} s^{-1}) for 8 hr, followed by either darkness (R) or a 10-min pulse of 100 μmole m^{-2} s^{-1} FR(R+EOD-FR) and then 16-hr of darkness. Each bar represents the average (±SE) of 4 experiments involving at least 15 seedlings each. The Y361F #7 line was significantly different from WT and PHYB for both R and R+EOD-FR by Student's t-test ($p<0.05$).

DETAILED DESCRIPTION

The present disclosure relates to polynucleotides and polypeptides and use of the polynucleotides and polypeptides for modifying the phenotypes of plants or plant cells. Modified plants or plant cells comprising the polynucleotides and/or polypeptides are also provided. In certain embodiments, the modified plants or plant cells exhibit one or more of an altered light sensitivity, an improved or enhanced germination efficiency of seeds, such as in low light, a hypersensitivity to white and red light with respect to hypocotyl and stem growth, improved shade tolerance, and a smaller plant size.

The polypeptides discussed herein are phytochromes and show homology to certain phytochrome sequences from *Arabidopsis thaliana*. The term "phytochrome" is used generically to refer to a phytochrome from any plant species. Plant phytochromes include phyA, phyB, phyC, phyD and phyE.

Phytochrome domains from a variety of organisms may be used as starting points for modifications that will generate the modified phytochromes of the present invention, and isolated polynucleotides encoding the modified phy domains. In certain embodiments the phytochrome is a modified phyB plant phytochrome, or a modified cGMP phosphodiesterase/adenylyl cyclase/FhlA (GAF) domain or modified chromophore binding domain (CBD) of phyB. Modification of phytochromes and/or phytochrome domains can be performed by methods known in the art, e.g., site-directed mutations, additions, deletions, and/or substitutions of one or more amino acid residues of existing phytochromes and/or phytochrome domains. Alternatively, modified phytochromes and/or phytochrome domains can be synthesized de novo, for example by synthesis of novel genes that would encode phytochrome domains with desired modifications.

In certain embodiments, expression in plants of a modified phytochrome having an amino acid sequence with at least 80%, or at least 95% identity to at least one of SEQ ID NOs: 1-22 and having an amino acid other than tyrosine at the position corresponding to Y361 of SEQ ID NO: 1 (for example, by introducing a polynucleotide sequence having at least 95% identity to (i) a sequence selected from SEQ ID NOs 23-33 into the plant, or (ii) a GAF-encoding domain of a sequence selected from SEQ ID NOs: 23-33, and encoding an amino acid other than tyrosine at the position corresponding to Y361 of SEQ ID NO: 1) results in plants that have altered light sensitivity, including, but not limited to, an improved germination efficiency of seeds in low light, a hypersensitivity to white and red light with respect to hypocotyl and stem growth, improved shade tolerance, reduced leaf surface area and combinations thereof, relative to control plants that do not express the modified phytochrome. The shared sequence identity of the nucleotides encoding phyB from a variety of species is shown in Table 1.

TABLE 1

Percent Identities of phyB from a variety of species with *Arabidopsis* phyB

Species phyB	Accession Number	Nucleotide SEQ ID NO:	Percent Identity to SEQ ID NO: 23
Arabidopsis	NM_127435	SEQ ID NO: 23	100%
Zea mays (maize)	GRMZM2G124532	SEQ ID NO: 24	70.2%
Oryza sativa (rice)	JN594210	SEQ ID NO: 25	70.3%
Sorghum bicolor (*sorghum*)	Y466089	SEQ ID NO: 26	69.6%
Glycine max (soybean) phyB1	EU428749	SEQ ID NO: 27	73.1%
G. max phyB2	EU428750	SEQ ID NO: 28	72.6%
G. max phyB3	EU428751	SEQ ID NO: 29	72.5%
G. max phyB4	EU428752	SEQ ID NO: 30	58.6%
Solanum tuberosum L. (potato)	DQ342235	SEQ ID NO: 31	75.1%
Pisum sativum (pea)	AF069305	SEQ ID NO: 32	70.8%
Vitis vinifera (grape):	EU436650	SEQ ID NO: 33	76.1%

The terms "isolated," "purified", or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid of the present invention is separated from open reading frames that flank the desired gene and encode proteins other than the desired protein. The term "purified" denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Par-

ticularly, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure.

Two nucleic acid sequences or polypeptides are said to be "identical" if the sequence of nucleotides or amino acid residues, respectively, in the two sequences are the same when aligned for maximum correspondence as described below. The term "complementary to" is used herein to mean that the sequence is complementary to all or a portion of a reference polynucleotide sequence. In the case of both expression of transgenes and inhibition of endogenous genes (e.g., by antisense or sense suppression) the inserted polynucleotide sequence need not be identical and may be "substantially identical" to a sequence of the gene from which it was derived.

In the case of polynucleotides used to inhibit expression of an endogenous gene, the introduced sequence need not be perfectly identical to a sequence of the target endogenous gene. The introduced polynucleotide sequence will typically be at least substantially identical (as determined below) to the target endogenous sequence.

In the case where the inserted polynucleotide sequence is transcribed and translated to produce a functional polypeptide, because of codon degeneracy, a number of polynucleotide sequences will encode the same polypeptide. These variants are specifically covered by the term "polynucleotide sequence from" a particular gene. In addition, the term specifically includes sequences (e.g., full length sequences) that are substantially identical (determined as described below) with a gene sequence encoding a polypeptide of the present invention and that encode polypeptides or functional polypeptide fragments that retain the function of a polypeptide of the present invention, e.g., a modified bacterial phytochrome with increased fluorescence.

Optimal alignment of sequences for comparison may be conducted by methods commonly known in the art, for example by the search for similarity method described by Pearson and Lipman 1988, Proc. Natl. Acad. Sci. USA 85: 2444-2448, by computerized implementations of algorithms such as GAP, BESTFIT, BLAST®, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), Madison, Wis., or by inspection. In a preferred embodiment, protein and nucleic acid sequence identities are evaluated using the Basic Local Alignment Search Tool ("BLAST®"), which is well known in the art (Karlin and Altschul, 1990, Proc. Natl. Acad. Sci. USA 87: 2267-2268; Altschul et al., 1997, Nucl. Acids Res. 25: 3389-3402), the disclosures of which are incorporated by reference in their entireties. The BLAST® programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. Preferably, the statistical significance of a high-scoring segment pair is evaluated using the statistical significance formula (Karlin and Altschul, 1990). The BLAST® programs can be used with the default parameters or with modified parameters provided by the user.

"Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, where 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.

The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 25% sequence identity compared to a reference sequence as determined using the programs described herein; preferably BLAST® using standard parameters, as described. Alternatively, percent identity can be any integer from 25% to 100%. More preferred embodiments include polynucleotide sequences that have at least about: 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity compared to a reference sequence. These values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Accordingly, polynucleotides of the present invention encoding a protein of the present invention include nucleic acid sequences that have substantial identity to the nucleic acid sequences that encode the polypeptides of the present invention. Polynucleotides encoding a polypeptide comprising an amino acid sequence that has at least about: 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity compared to a reference polypeptide sequence are also preferred.

The term "substantial identity" of amino acid sequences (and of polypeptides having these amino acid sequences) normally means sequence identity of at least 40% compared to a reference sequence as determined using the programs described herein; preferably BLAST® using standard parameters, as described. Preferred percent identity of amino acids can be any integer from 40% to 100%. More preferred embodiments include amino acid sequences that have at least about: 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity compared to a reference sequence. Polypeptides that are "substantially identical" share amino acid sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, aspartic acid-glutamic acid, and asparagine-glutamine. Accordingly, polypeptides or proteins of the present invention include amino acid sequences that have substantial identity to the amino acid sequences of the polypeptides of the present invention, which are modified phytochromes that result in plants having altered sensitivity compared with plants.

In one embodiment, a modified phyB phytochrome is created by substituting the tyrosine at the position corresponding to Tyr361 of SEQ ID NO:1 with a phenylalanine (Phe). It is contemplated that various modifications of this Tyr361 residue (and its functional equivalents in other phytochromes) will result in phytochromes useful for practicing the present invention. Some examples of modified phytochromes useful for the practice of this invention include modifications of the tyrosine domain corresponding to Y361 of SEQ ID NO: 1, for example: Tyr to Phe (i.e., Y to F); Tyr to Trp (i.e., Y to W); Tyr to Ile (i.e., Y to I); Tyr to Leu (i.e., Y to L); Tyr to Val (i.e., Y to V); Tyr to Ala (i.e., Y to A); Tyr to Pro (i.e., Y to P); Tyr to Asn (i.e., Y to N); Tyr to Glu (i.e., Y to E); and Tyr to Thr (i.e., Y to T), Tyr to Gly (i.e., Y to G); Tyr to Ser (i.e., Y to 5); Tyr to Cys (i.e., Y to C); Tyr to Lys (i.e., Y to K); Tyr to Arg (i.e., Y to R); Tyr to His (i.e., Y to H); Tyr to Met (i.e., Y to M); Tyr to Asp (i.e., Y to D); or Tyr to Gln (i.e., Y to Q).

The modified phyB phytochrome may contain amino acid substitutions described herein or known in the art at other locations in the phyB or phyB domain. In certain embodiments, the modified phytochrome may contain an amino acid substitution at the residue corresponding to D307, R322, R352, or R582 of the *Arabidopsis* phytochrome shown in SEQ ID NO: 1. For example, the modified phytochrome may contain at least one of (i) an amino acid other than aspartate (D) at the position corresponding to 307 of SEQ ID NO:1, (ii) an amino acid other than arginine (R) at the position corresponding to 322 of SEQ ID NO: 1, (iii) an amino acid other than arginine (R) at the position corresponding to 352 of SEQ ID NO: 1, and (iv) an amino acid other than arginine (R) at the position corresponding to 582 of SEQ ID NO: 1, or any combination thereof. These substitutions may be present alone, in any combination, including one or more substitutions in addition to a substitution at the position corresponding to Y361 of SEQ ID NO:1. The substitutions may include one or more of the following R352A, R582A, R322A and D307A.

The substitutions at R352 and R582, such as R352A, R582A produce a phytochrome phenotype that is slightly hyperactive with respect to signalling. For example, the substitution at R582 shows slightly stronger repression on hypocotyl growth at intermediate R fluence rates as compared to wild-type. The substitution at R322, such as R322A, produces a photchrome phenotype that is slightly hypoactive with respect to signalling.

As shown in the sequence alignment of FIG. **12**, Tyr361 is conserved in plant phytochromes. Sequence identity of phyB from crop species compared with *Arabidopsis* phyB (SEQ ID NO: 1) is as follows: *Zea mays* (maize; SEQ ID NO: 2): 70.2%; *Oryza sativa* (rice; SEQ ID NO: 3): 70.3%; *Sorghum bicolor* (*sorghum*; SEQ ID NO: 4): 69.6%; *Glycine max* (soybean), phyB1 (SEQ ID NO: 5): 73.1%; phyB2 (SEQ ID NO: 6): 72.6%; phyB3 (SEQ ID NO: 7): 72.5%; phyB4 (SEQ ID NO: 8): 58.6%; *Solanum tuberosum* L. (potato; SEQ ID NO:9): 75.1%; *Pisum sativum* (pea; SEQ ID NO: 10): 70.8%; *Vitis vinifera* (grape; SEQ ID NO: 11): 76.1%.

As shown in FIG. **12**, Tyr361 of SEQ ID NO: 1 (*Arabidopsis* phyB) corresponds to Tyr359 of SEQ ID NO: 2 (maize phyB), Tyr368 of SEQ ID NO: 3 (rice phyB), Tyr376 of SEQ ID NO: 4 (*sorghum* phyB), Tyr345 of SEQ ID NO: 5 (soybean phyB1), Ty357 of SEQ ID NO: 6 (soybean phyB2), Tyr308 of SEQ ID NO: 7 (soybean phyB3), Tyr244 of SEQ ID NO: 8 (soybean phyB4), Tyr336 of SEQ ID NO: 9 (potato phyB), Tyr324 of SEQ ID NO: 10 (pea phyB), and Tyr335 of SEQ ID NO: 11 (grape phyB).

Tyr361 of SEQ ID NO: 1 (*Arabidopsis* phyB) also corresponds to Tyr 263 of the cyanobacteriophytochrome from *Synechocystis* PCC6803, to Tyr 263 of the bacteriophytochrome from *Deinococcus radiodurans*, to Tyr 250 of the bacteriophytochrome from *Pseudomonas aeruginosa*, to Tyr272 of the bacteriophytochrome from *Rhodopseudomonas palustris*, and to Tyr142 of the cyanobacteriophytochrome from *Synechococcus* OS-B'.

As shown in FIG. **13**, the percent identity of the GAF domains to *Arabidopsis* phyB GAF domain (position 234 to 433 of SEQ ID NO: 1; SEQ ID NO. 12) are as follows: *Zea mays* (maize; position 232-432 of SEQ ID NO: 2; SEQ ID NO: 13): 82.1% *Oryza sativa* (rice; position 241 to 442 of SEQ ID NO: 3; SEQ ID NO: 14): 82.7%; *Sorghum bicolor* (*sorghum*; position 249 to 449 of SEQ ID NO: 4; SEQ ID NO: 15): 82.1%; *Glycine max* (soybean), phyB1 (position 218 to 414 of SEQ ID NO: 5; SEQ ID NO: 16): 87.5%; phyB2 (position 230 to 426 of SEQ ID NO: 6; SEQ ID NO: 17): 85.5%; phyB3 (position 181 to 377 of SEQ ID NO: 18): 87.5%; phyB4 (position 117 to 313 of SEQ ID NO: 8; SEQ ID NO: 19): 85.5%; *Solanum tuberosum* L. (potato; position 209 to 406 of SEQ ID NO:9; SEQ ID NO: 20): 87.0%; *Pisum sativum* (pea; position 197 to 397 of SEQ ID NO: 10; SEQ ID NO: 21): 88.1%; *Vitis vinifera* (grape; position 208 to 404 of SEQ ID NO: 11; SEQ ID NO: 22): 85.0%.

As shown in FIG. **13**, Tyr361 of SEQ ID NO: 1 (*Arabidopsis* phyB) corresponds to Tyr128 of SEQ ID NO: 12 (*Arabidopsis* phyB GAF domain); Tyr128 of SEQ ID NO: 13 (maize phyB GAF domain), Tyr128 of SEQ ID NO: 14 (rice phyB GAF domain), Tyr128 of SEQ ID NO: (*sorghum* phyB GAF domain), Tyr128 of SEQ ID NO: 16 (soybean phyB1 GAF domain), Ty128 of SEQ ID NO: 17 (soybean phyB2 GAF domain), Tyr128 of SEQ ID NO: 18 (soybean phyB3 GAF domain), Tyr128 of SEQ ID NO: 19 (soybean phyB4 GAF domain), Tyr128 of SEQ ID NO: 20 (potato phyB GAF domain), Tyr128 of SEQ ID NO: 21 (pea phyB GAF domain), and Tyr128 of SEQ ID NO: 22 (grape phyB GAF domain).

As shown in FIG. **13**, Tyr361 of SEQ ID NO: 1 (At phyB_GAF; *Arabidopsis* phyB) also corresponds to Tyr130 of the cyanobacteriophytochrome GAF domain from *Synechocystis* PCC6803 (Syn Cph_GAF; SEQ ID NO: 34), to Tyr 130 of the bacteriophytochrome GAF domain from *Deinococcus radiodurans* (Dr Bph_GAF; SEQ ID NO: 35), to Tyr 130 of the bacteriophytochrome GAF domain from *Pseudomonas aeruginosa* (Pa BphP_GAF; SEQ ID NO: 36), to Tyr130 of the bacteriophytochrome GAF domain from *Rhodopseudomonas palustris* (Rp BphP3_GAF; SEQ ID NO: 37), and to Tyr130 of the cyanobacteriophytochrome GAF domain from *Synechococcus* OS-B (SyB Cph_GAF; SEQ ID NO: 38).

The invention also relates to nucleic acids that selectively hybridize to the exemplified sequences, including hybridizing to the exact complements of these sequences. The specificity of single-stranded DNA to hybridize complementary fragments is determined by the "stringency" of the reaction conditions (Sambrook et al., 1989). Hybridization stringency increases as the propensity to form DNA duplexes decreases. In nucleic acid hybridization reactions, the stringency can be chosen to favor specific hybridizations (high stringency), which can be used to identify, for example, full-length clones from a library. Less-specific hybridizations (low stringency) can be used to identify related, but not exact (homologous, but not identical), DNA molecules or segments.

DNA duplexes are stabilized by: (1) the number of complementary base pairs; (2) the type of base pairs; (3) salt

concentration (ionic strength) of the reaction mixture; (4) the temperature of the reaction; and (5) the presence of certain organic solvents, such as formamide, which decrease DNA duplex stability. In general, the longer the probe, the higher the temperature required for proper annealing. A common approach is to vary the temperature; higher relative temperatures result in more stringent reaction conditions.

To hybridize under "stringent conditions" describes hybridization protocols in which nucleotide sequences at least 60% homologous to each other remain hybridized. Generally, stringent conditions are selected to be about 5° C. lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at Tm, 50% of the probes are occupied at equilibrium.

"Stringent hybridization conditions" are conditions that enable a probe, primer, or oligonucleotide to hybridize only to its target sequence (e.g., SEQ ID NO:1). Stringent conditions are sequence-dependent and will differ. Stringent conditions comprise: (1) low ionic strength and high temperature washes, for example 15 mM sodium chloride, 1.5 mM sodium citrate, 0.1% sodium dodecyl sulfate, at 50° C.; (2) a denaturing agent during hybridization, e.g. 50% (v/v) formamide, 0.1% bovine serum albumin, 0.1% Ficoll, 0.1% polyvinylpyrrolidone, 50 mM sodium phosphate buffer (750 mM sodium chloride, 75 mM sodium citrate; pH 6.5), at 42° C.; or (3) 50% formamide. Washes typically also comprise 5×SSC (0.75 M NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5×Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS, and 10% dextran sulfate at 42° C., with a wash at 42° C. in 0.2×SSC (sodium chloride/sodium citrate) and 50% formamide at 55° C., followed by a high-stringency wash consisting of 0.1×SSC containing EDTA at 55° C. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. These conditions are presented as examples and are not meant to be limiting.

"Moderately stringent conditions" use washing solutions and hybridization conditions that are less stringent, such that a polynucleotide will hybridize to the entire, fragments, derivatives, or analogs of the target sequence (e.g., SEQ ID NO:1). One example comprises hybridization in 6×SSC, 5×Denhardt's solution, 0.5% SDS and 100 μg/ml denatured salmon sperm DNA at 55° C., followed by one or more washes in 1×SSC, 0.1% SDS at 37° C. The temperature, ionic strength, etc., can be adjusted to accommodate experimental factors such as probe length. Other moderate stringency conditions have been described (Ausubel et al., 1993; Kriegler, 1990).

"Low stringent conditions" use washing solutions and hybridization conditions that are less stringent than those for moderate stringency, such that a polynucleotide will hybridize to the entire, fragments, derivatives, or analogs of the target sequence (e.g., SEQ ID NO:1). A nonlimiting example of low stringency hybridization conditions includes hybridization in 35% formamide, 5×SSC, 50 mM Tris HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 μg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40° C., followed by one or more washes in 2×SSC, 25 mM Tris HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50° C. Other conditions of low stringency, such as those for cross-species hybridizations, are well-described (Ausubel et al., 1993; Kriegler, 1990).

A "functional homolog," "functional equivalent," or "functional fragment" of a polypeptide of the present invention is a polypeptide that is homologous to the specified polypeptide but has one or more amino acid differences from the specified polypeptide. A functional fragment or equivalent of a polypeptide retains at least some, if not all, of the activity of the specified polypeptide.

Transgenic plants and methods of producing transgenic plants are provided. Such transgenic plants are produced, in certain embodiments, by introducing into a plant or plant cell a polynucleotide encoding a polypeptide comprising a sequence having at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% identity to at least one amino acid sequence selected from SEQ ID NOs: 1-22, wherein the tyrosine corresponding to Y361 of SEQ ID NO:1 is replaced with a different amino acid. In certain embodiments, the polynucleotide is provided as a construct in which a promoter is operably linked to the polynucleotide. Such transgenic plants may also be produced, in certain embodiments, by introducing into a plant or plant cell a polynucleotide encoding a polypeptide comprising a sequence having at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% identity to at least one sequence selected from the amino acid sequence selected from SEQ ID NOs: 1-22, wherein the tyrosine corresponding to Y361 of SEQ ID NO:1 is replaced with a different amino acid.

The polynucleotide sequences can be introduced into plants which do not express the corresponding native form of unmodified phyB, such as plants lacking the native gene, or containing a mutated, truncated or downregulated version of the native gene, such that little or no phyB polypeptide is expressed, or a phyB polypeptide is expressed that is partially or substantially inactive. The modified phyB replaces or substitutes for the native gene function. The polynucleotides can also be expressed in wild-type plants containing the corresponding native phyB gene sequence. In this case, the modified phyB over-rides the functions of the wild type endogenous gene in a dominant fashion, since it is hyperactive.

Plants expressing the modified phyB have surprisingly altered light sensitivity and altered photoresponses. Altered photoresponses relative to a control plant include, without limitation, at least one of an improved germination efficiency of seeds, such as in low light or following a pulse of white light, a hypersensitivity to white and red light with respect to hypocotyl and stem growth, improved shade tolerance, a smaller mature plant size, reduced plant height, smaller mature plant diameter, decreased petiole length, reduced internode length, shorter stems, smaller stem diameter, increased leaf chlorophyll concentration, decreased leaf length, increased root length, increased root branching, improved leaf unfolding, flatter leaves (increased hyponasty), reduced leaf surface area and combinations thereof.

Plants expressing modified phyB comprising a substitution at Tyr361 are smaller in size and more tolerant of low light conditions such as would be experienced in crowded field conditions. In one embodiment, plants expressing the modified phyB grow more effectively when planted in higher densities, permitting higher yields over a given planting area.

The Y361F substitution generates a hyperactive photoreceptor that still requires light for activation. As such, plants expressing the modified Y361F phytochrome display accen-

tuated phyB signaling, useful in agricultural settings with fewer side effects. The replacement of wild-type phyB with $phyB^{Y361F}$ in plants increases the sensitivity of hypocotyls to R, generates seeds with a stronger germination response in white light, and further accentuates the end-of-day far-red light (EOD-FR) response of seedlings, substantially without altering flowering time, such as in short days. The phyB-mediated responses to R and EOD-FR are connected to the shade avoidance response. Without wishing to be bound to any theory, it is possible that increased signaling by the $phyB^{Y361F}$ variant attenuates shade avoidance response by enabling the small amounts of Pfr generated by low fluence R, or the residual Pfr remaining after EOD-FR (or presumably in high FR/R light environments) to more effectively promote normal photomorphogenesis.

It is envisaged that a plant produced following the introduction of a polynucleotide disclosed herein exhibits altered or modified characteristics relative to the control plant. The modified characteristics include, but are not limited to, increased hyponasty, decreased height, decreased diameter, decreased petiole length, decreased internode length, decreased stem diameter, decreased hypocotyl length under an R fluence rate of less than 1 μmole m^{-2} sec^{-1} (or less than 0.5 μmole m^{-2} sec^{-1}, less than 0.6 μmole m^{-2} sec^{-1}, less than 0.7 μmole m^{-2} sec^{-1}, or less than 0.8 μmole m^{-2} sec^{-1}), enhanced germination or any combination thereof. The altered characteristic may be decreased or enhanced by at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 100%, at least about 110%, at least about 120%, at least about 130%, at least about 140%, at least about 150%, at least about 175%, at least about 200%, at least about 250%, at least about 300%, or at least about 400% relative to a control plant.

As a nonlimiting example, such modified plants may have a compact size and have a height or diameter that is at least about 20%, at least about 30%, at least about 50%, at least about 75%, or at least about 100% smaller than the height or diameter of a control plant. As another nonlimiting example, such modified plants may provide an increased yield of seed, grain, forage, fruit, root, leaf, or combination thereof that is at least about 5%, at least about 10%, at least about 20%, at least about 25%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 75%, at least about 80%, at least about 90%, or at least about 100% increased over the yield from corresponding control plants. As used herein, "yield" refers to the maximum yield achievable per given planting area, and does not refer to the yield from an individual plant. Maximum or higher yields may be achieved by planting a higher number or density of plants in a given area.

As used herein, a "control plant" is a plant that is substantially equivalent to a test plant or modified plant in all parameters with the exception of the test parameters. For example, when referring to a plant into which a polynucleotide according to the present invention has been introduced, in certain embodiments, a control plant is an equivalent plant into which no such polynucleotide has been introduced. In certain embodiments, a control plant is an equivalent plant into which a control polynucleotide has been introduced. In such instances, the control polynucleotide is one that is expected to result in little or no phenotypic effect on the plant.

The polynucleotides of the present invention may be introduced into a plant cell to produce a transgenic plant. As used herein, "introduced into a plant" with respect to polynucleotides encompasses the delivery of a polynucleotide into a plant, plant tissue, or plant cell using any suitable polynucleotide delivery method. Methods suitable for introducing polynucleotides into a plant useful in the practice of the present invention include, but are not limited to, freeze-thaw method, microparticle bombardment, direct DNA uptake, whisker-mediated transformation, electroporation, sonication, microinjection, plant virus-mediated, and *Agrobacterium*-mediated transfer to the plant. Any suitable *Agrobacterium* strain, vector, or vector system for transforming the plant may be employed according to the present invention. In certain embodiments, the polynucleotide is introduced using at least one of stable transformation methods, transient transformation methods, or virus-mediated methods.

By "stable transformation" is intended that the nucleotide construct introduced into a plant integrates into the genome of the plant and is capable of being inherited by progeny thereof. By "transient transformation" is intended that a nucleotide construct introduced into a plant does not integrate into the genome of the plant.

Transformation protocols as well as protocols for introducing nucleotide 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 nucleotide sequences into plant cells and subsequent insertion into the plant genome 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. Nos. 5,981,840 and 5,563,055), direct gene transfer (Paszkowski et al. (1984) EMBO J. 3:2717-2722), and ballistic particle acceleration (see, for example, U.S. Pat. Nos. 4,945,050; 5,879,918; 5,886,244; 5,932,782; Tomes et al. (1995) in Plant Cell, Tissue, and Organ Culture: Fundamental Methods, ed. Gamborg and Phillips (Springer-Verlag, Berlin); and McCabe et al. (1988) Biotechnology 6:923-926). 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 (London) 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, N.Y.), pp. 197-209 (pollen); Kaeppler et al. (1990) Plant Cell Reports 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 Reports 12:250-255 and Christou and Ford (1995) Annals of Botany 75:407-413 (rice); Osjoda et al. (1996) Nature Biotechnology 14:745-750 (maize via *Agrobacterium tumefaciens*); all of which are herein incorporated by reference in their entireties.

In some embodiments, a plant may be regenerated or grown from the plant, plant tissue or plant cell. Any suitable methods for regenerating or growing a plant from a plant cell

or plant tissue may be used, such as, without limitation, tissue culture or regeneration from protoplasts. Suitably, plants may be regenerated by growing transformed plant cells on callus induction media, shoot induction media and/or root induction media. See, for example, McCormick et al. (1986) Plant Cell Reports 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 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. Thus as used herein, "transformed seeds" refers to seeds that contain the nucleotide construct stably integrated into the plant genome.

In certain embodiments, the polynucleotides to be introduced into the plant are operably linked to a promoter sequence and may be provided as a construct. As used herein, a polynucleotide is "operably linked" when it is placed into a functional relationship with a second polynucleotide sequence. For instance, a promoter is operably linked to a coding sequence if the promoter is connected to the coding sequence such that it may effect transcription of the coding sequence. In various embodiments, the polynucleotides may be operably linked to at least one, at least two, at least three, at least four, at least five, or at least ten promoters.

Promoters useful in the practice of the present invention include, but are not limited to, constitutive, inducible, temporally-regulated, developmentally regulated, chemically regulated, tissue-preferred and tissue-specific promoters. Suitably, the promoter causes sufficient expression in the plant to produce the phenotypes described herein. Suitable promoters include, without limitation, the 35S promoter of the cauliflower mosaic virus, ubiquitin, tCUP cryptic constitutive promoter, the Rsyn7 promoter, pathogen-inducible promoters, the maize In2-2 promoter, the tobacco PR-1a promoter, glucocorticoid-inducible promoters, and tetracycline-inducible and tetracycline-repressible promoters.

It is envisaged that analogous substitutions of tyrosine at positions corresponding to Tyr361 of SEQ ID NO: 1 should elicit similar altered light sensitivity and photo responses when expressed in other plants. Plants that may express a modified phytochrome include, among others, crop plants and ornamental plants.

Suitable plant species include, without limitation, corn (*Zea mays*), soybean (*Glycine max*), *Brassica* sp. (e.g., *Brassica napus, B. rapa*, and *B. juncea*), 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*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense, Gossypium hirsutum*), sweet potato (*Ipomoea batatus*), cassaya (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea 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 sativa*), barley (*Hordeum vulgare*), vegetables, ornamentals, and conifers.

Vegetables include, without limitation, 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*).

Ornamental plants are plants that are grown for decorative purposes in gardens and landscapes, as houseplants, and for cut flowers. Suitable ornamentals include, without limitation, 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* (*Chrysanthemum* spp.).

As used herein, the term "plant" includes reference to whole plants, plant organs (e.g., leaves, stems, roots, etc.), seeds, plant cells, and progeny of same. Parts of transgenic plants comprise, for example, plant cells, protoplasts, tissues, callus, embryos as well as flowers, ovules, stems, fruits, leaves, roots originating in transgenic plants or their progeny previously transformed with a DNA. As used herein, the term "plant cell" includes, without limitation, protoplasts and cells of seeds, suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, and microspores.

Consequently, this invention encompasses transgenic crops and other plants with improved shade tolerance needed for increased planting density and increased yields.

It will be apparent to those of skill in the art that variations may be applied to the compositions and methods described herein and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention.

It is to be understood that the invention is not limited in its application to the details of construction and the arrangement of components set forth in the following description. Also, it is to be understood that the phraseology and terminology used herein is for the purpose of description and should not be regarded as limiting. The use of "including," "comprising," or "having" and variations thereof herein is meant to encompass the items listed thereafter and equivalents thereof as well as additional items.

It also is understood that any numerical range recited herein includes all values from the lower value to the upper value. For example, if a concentration range is stated as 1% to 50%, it is intended that values such as 2% to 40%, 10% to 30%, or 1% to 3%, etc., are expressly enumerated in this specification. These are only examples of what is specifically intended, and all possible combinations of numerical values between and including the lowest value and the highest value enumerated are to be considered to be expressly stated in this application.

The following non-limiting examples are purely illustrative.

Example 1

Materials and Methods

Recombinant phyB Protein Expression, Purification, and Analysis

All the site-directed mutations in PHYB were introduced into the cDNA by the Quikchange method (Stratagene). cDNA fragments encoding the photosensory modules (residues 1-624) were appended in-frame corresponding to the N-terminus of the 6His tag (KLHHHHHH) (SEQ ID NO: 39) by introduction into the pBAD plasmid (Invitrogen), and then co-transformed into *Escherichia coli* BL21 (AI) cells (Invitrogen) with the pPL-PΦB plasmid expressing the *Synechocystis* PCC6803 HO1 heme oxygenase and *A. thaliana* HY2 PΦB synthase enzymes [40, 41] to direct apoprotein expression and chromophore assembly. Following sequential induction of the HO1/HY2 genes and PHYB genes with IPTG and arabinose, the cells were disrupted by sonication in extraction buffer (50 mM HEPES-NaOH (pH 7.8), 300 mM NaCl, 30 mM imidazole, 0.1% Tween-20, 10% glycerol, 1 mM 2-mercaptoethanol, and 1 mM PMSF) with the addition of 1 tablet of protease inhibitor cocktail (Roche) before use. The clarified supernatant was applied to a HisTrap HP column (GE) pre-equilibrated in extraction buffer, and the column was washed with extraction buffer followed by elution with a 30-300 mM imidazole gradient in extraction buffer. The phyB-containing fractions were pooled, dialyzed against 10 mM HEPES-NaOH (pH 7.8), 100 mM NaCl, 5 mM 2-mercaptoethanol, 5 mM Na_2EDTA, 50 mM imidazole, and 0.05% Tween-20 overnight, and subjected to size-exclusion chromatography using a 24-ml Superose 6 (GE) column pre-equilibrated with the same buffer. phyB-containing fractions were pooled and stored in 10 mM HEPES-NaOH (pH 7.8), 50 mM NaCl, 1 mM 2-mercaptoethanol, 0.05% Tween-20, and 10% glycerol.

Pr-Pfr photointerconversion and Pfr→Pr thermal-reversion of each phyB preparation were assayed by UV-vis absorption spectroscopy at 24° C., using white light filtered through 650- and 730-nm interference filters (Orion) to drive Pr→Pfr and Pfr→Pr phototransformation, respectively.

Plant Materials and Growth Conditions

All the plant lines were derived from *A. thaliana* Col-0 ecotype. The phyB-9 and phyA-211 alleles were as described [30, 32]. Seeds were surface-sterilized in chlorine gas, and stratified in water for 3 d at 4° C. before sowing. Unless otherwise noted, seedlings were grown at 22° C. under white light in LD (16-hr light/8-hr dark) on 0.7% (w/v) agar medium containing 1× Gamborg's (GM) salts, 2% (w/v) sucrose, 0.5 g/L MES (pH 5.7). After 10 d, seedlings were transferred to soil and grown at 22° C. under continuous white light in LD or SD (8-hr light/16-hr dark).

Plasmid Constructions for Plant Transformation

The full coding regions of PHYA and PHYB [39] were inserted into the pDONR221 plasmid via BP reactions (Invitrogen), and appended the coding sequence in-frame for the FLAG-epitope (GGGDYKDDDDK) (SEQ ID NO: 40) to their 3' ends. The PHYA/B promoter and 5' UTRs (2634- and 1983-bp upstream beginning at the ATG translation initiation codon), and 3' UTRs (242- and 279-bp downstream of the translation termination codon) were amplified by PCR from the Col-0 genomic DNA, and then sequentially inserted into the pDONR211 plasmids to appropriately flank the coding regions. The completed PHYB and PHYA transgenes were introduced into the pMDC123 plasmid (Invitrogen) via LR reactions. The PHYB-yellow fluorescent protein (YFP) constructions (WT-YFP, R322A-YFP, Y361F-YFP, D307A-YFP, and R582A-YFP) were created by appending the UBQ10 promoter fragment (1986-bp fragment proximal to the ATG codon) and the cDNA encoding YFP, to the 5' and 3' ends of the PHYB cDNA in a pDONR211 plasmid, respectively. The complete transgenes were introduced into the pMDC123 plasmid via LR reactions.

Plant Transformation and Selection of Transgenic Lines

The PHYA and PHYB transgenes were introduced into the homozygous *Arabidopsis* phyA-211 or phyB-9 mutants, respectively, via the *Agrobacterium*-mediated floral dip method using the pMDC123-derived plasmids [42]. Transformed lines were selected by resistance to 10 μg/mL BASTA. T2 transgenic plants with a resistance segregation ratio of ~3:1 were used to obtain isogenic lines in the T4 or T5 generation for all the biochemical, phenotypic, and localization assays.

Protein Extraction and Immunoblot Analysis

Five-d-old, dark-grown *Arabidopsis* seedlings were frozen and pulverized at liquid nitrogen temperatures, and homogenized in 100 mM Tris-HCl (pH 8.5), 10 mM Na_2EDTA, 25% ethylene glycol, 2 mM PMSF, 10 mM N-ethylmaleimide, 5 μg/mL sodium metabisulfite, 2% (w/v) SDS, 10 μg/mL aprotinin, 10 μg/mL leupeptin and 0.5 μg/mL pepstatin [43]. The extracts were heated to 100° C. for 10 min and clarified by centrifugation at 13,000×g for 10 min. The supernatants were subjected to SDS-PAGE and immunoblot analysis with a monoclonal antibody against phyA (073D, [44]), phyB (B1-B7, [45]), or green fluorescent protein (GFP) (Sigma). Anti-PBA1 antiserum or anti-histone H3 antibodies were used to confirm equal protein loading [46].

To measure phyB degradation in response to Rc, seeds were sown in liquid medium containing half-strength Murashige and Skoog (MS) salts, 0.5 g/L MES (pH 5.7), and 10 g/L sucrose, and irradiated with white light (24 hr for seeds carrying the $PHYB^{D307A}$ transgene and 12 hr for all others) to initiate germination before maintaining the seedlings in the dark for 4 d. Seedlings were collected after various exposure times to continuous 20 $\mu mol \cdot m^{-2} \cdot s^{-1}$ R and subjected to immunoblot analysis as above. Seedlings were incubated for 12 hr in the dark with 100 μM MG132 or an equivalent volume of DMSO before R.

Phenotypic Assays

Germination efficiency was measured according to Oh et al. (Plant Cell 19, 1192-1208). The parental plants (5 per genotype) were grown side by side at 22° C. in LDs, and the resulting seeds were harvested as separate seed pools. At least 60 seeds from each pool were sown on 0.7% (w/v) water agar after 20-min FR irradiation (4 $\mu mol\ m^{-2}\ s^{-1}$). The seeds were then exposed to white light for 2 hr, and either kept in dark or irradiated with 4 $\mu mol\ m^{-2}\ s^{-1}$ FR for 5 min. The plates were kept in darkness for an additional 5 d before measurement of germination, which was scored as emergence of the radical from the seed coat. For hypocotyl elongation, seeds were sown on solid half-strength MS salts, 0.5 g/L MES (pH 5.7), and 0.7% (w/v) agar, and irradiated with 12-hr white light. The plates were exposed to either R or FR for 3.5 d using a bank of diodes (E-30LED-controlled environment chamber, Percival), before measurement of hypocotyl length. For measurement of the EOD-FR response, seedlings were irradiated over a 4-d cycle with 90 $\mu mol \cdot m^{-2} \cdot s^{-1}$ R for 8 hr followed by either darkness or by a 10-min pulse of 100 $\mu mol \cdot m^{-2} \cdot s^{-1}$ FR and then darkness for 16 hr. Effect on flowering time was measured for plants grown under white light in SD.

Confocal Microscopic Analysis

Transgenic seeds expressing wild-type and mutant versions of phyB-YFP were sown on solid medium containing half-strength MS salts, 0.5 g/L MES (pH 5.7), 2% (w/v) sucrose, and 0.7% (w/v) agar and irradiated for 12 hr at 22° C. with white light before incubation in the dark for 5 d. Fluorescence of hypocotyl cells, either kept in the dark or irradiated with 90 $\mu mol \cdot m^{-2} \cdot s^{-1}$ R for 12 hr, was imaged using a Zeiss 510-Meta laser scanning confocal microscope. YFP fluorescence was visualized in the single-track mode by excitation with 488-nm light using the BP 500-530 IR filter. Images were processed with the LSM510 image browser.

Example 2

Rational Design of phyB Variants to Alter Light Signaling

Site-directed substitutions of certain amino acids based on the microbial scaffolds were introduced into the *Arabidopsis* phyB isoform. The photochemistry of the mutant photosensory modules was examined after recombinant assembly with the native chromophore phytochromobilin (FOB), and the full-length versions were assessed for their phenotypic rescue of the phyB-9 null mutant using the native PHYB promoter to drive expression. The results collectively demonstrate that various aspects of phy dynamics and signaling can be adjusted (FIG. **1**A), which in some cases generates plants with unique photobehavioral properties.

We examined five mutations predicted to compromise Pr to Pfr photoconversion, interaction of the bilin with its binding pocket, and/or possible signal transmission from the cGMP phosphodiesterase/adenylyl cyclase/FhlA (GAF) domain to the downstream phytochrome (PHY) domain in the photosensory module. As shown in FIGS. **1**B and **1**C, the D307A substitution removes a key aspartate (D207 in *Synechocystis* PCC6803 (Syn)-Cph1) that participates through its main chain carbonyl in a unique hydrogen-bonding lattice involving the A-C pyrrole rings of PΦB and the centrally positioned pyrrole water. This invariant aspartate is essential for the Pr to Pfr photoconversion of bacterial phys as most, if not all, substitutions are stalled in the deprotonation/protonation cycle following R irradiation and become highly fluorescent [18-20]. Two substitutions alter the hydrogen-bond contacts with D307. The relatively mild Y361F substitution (Y263 in SynCph1) maintains the aromatic character but is expected to eliminate the hydrogen bond that helps hold the side chain carboxyl group of D307 in place [18, 22], whereas the R582A substitution (R472 in SynCph1) removes a potential salt bridge between D307 and a novel hairpin, likely universal among canonical phys, that extends from the PHY domain to contact the GAF domain near the bilin. This hairpin may help transmit chromophore movements within the photosensory module to the C-terminal output region during photoconversion [3, 7, 10] (FIG. **1**B,C). The last two mutations (R352A and R322A) eliminate salt bridges between the propionate side chains in PΦB and the bilin-binding pocket, which presumably help restrain the bilin within the photoreceptor (FIG. **1**B,C). Prior studies with bacterial phys (R222 and R254 in *Synechococcus* OS-B' (SyB)-Cph1) showed that these arginines stabilize and destabilize the Pfr conformer, respectively, with their guanidinium side chains undergoing dramatic conformational changes during Pr→Pfr photoconversion.

Based on the phy scheme presented in FIG. **1**A, we tested how well the *Arabidopsis* phyB mutants would: (i) assemble with PΦB, (ii) photointerconvert between Pr and Pfr, (iii) revert thermally from Pfr back to Pr, (iv) accumulate and concentrate after R irradiation into nuclear bodies or "speckles" thought to be important for signaling and/or turnover [23], (v) degrade upon R irradiation, and (vi) stimulate several photomorphogenic processes under full or partial control by phyB, including R-stimulated seed germination, hypocotyl growth inhibition under R, effect of end-of-day (EOD) FR on the hypocotyl R response, and flowering time under a short-day photoperiod (SD) [2, 13, 14]. Pfr turnover is likely driven by the ubiquitin/26S proteasome system (UPS) based on mutant analyses and its sensitivity to the proteasome inhibitor MG132 ([24, 25] see FIG. **6**A). Methods used to synthesize photoactive photosensory module fragments recombinantly from phyB assembled with PΦB and to generate the transgenic plants expressing full-length versions are provided in Example 1.

The photosensory module of all the mutants could be expressed and readily assembled with PΦB in *Escherichia coli*, and generated reasonably normal Pr absorption spectra with maxima at ~663 nm, indicating that none of the substitutions compromised protein folding or bilin conjugation (FIG. **2**A; FIG. **7**). Given that *Arabidopsis* and other plants are highly sensitive to phy levels [26-29], we chose two isogenic phyB-9 lines in the T3 generation that expressed either unaltered phyB or the mutants to levels which matched most closely that in the wild-type Col-0 plants as judged by immunoblot analysis (FIG. **3**D). Importantly, all of the complemented phyB-9 mutant lines had normal etiolated seedling development, indicating that none of the phyB variants signaled in the absence of photoactivation (FIG. **3**B).

To examine the ability of the mutants to concentrate in nuclear bodies/speckles as Pfr, we also created a parallel set of transgenic lines expressing the phyB mutants as N-terminal fusions to yellow fluorescent protein (YFP). These bodies were easily seen by confocal fluorescence microscopy as numerous intense puncta that accumulate in the nucleus upon prolonged R irradiation (see FIG. **6**B). The phyB-YFP mutant proteins also assembled well with PΦB in planta, and phenotypically resembled their non-tagged counterparts based on their ability (or inability) to suppress hypocotyl elongation in R when introduced into the phyB-9 background (FIG. **8**).

Example 3

$phyB^{Y361F}$ is Hypersensitive to R

Given its predicted proximity to D307 within the bilin-binding pocket, Y361 likely helps enclose the GAF domain around the bilin and fix the position of D307 (FIG. **1**B). Surprisingly, the Y361F substitution in *Arabidopsis* phyB permitted proper photochemistry but made the photoreceptor hyperactive with respect to signaling. Recombinant $phyB^{Y361F}$ had relatively normal Pr and Pfr absorption spectra, but displayed slightly reduced Pr→Pfr and Pfr→Pr photoconversion rates and a slower rate of thermal Pfr→Pr reversion (FIG. **2**A,B).

Despite the expectations that some of these photochemical alterations might compromise signaling, $phyB^{Y361F}$ more effectively directed phyB-mediated responses compared to $phyB^{WT}$. Soon after germination, the $PHYB^{Y361F}$ phyB-9 seedlings were more sensitive to continuous R with respect to hypocotyl elongation, and as the seedling developed under a long-day (LD) photoperiod, homozygous $PHYB^{Y361F}$ phyB-9 plants had more compact rosettes with shorter petioles than wild type and $PHYB^{WT}$ phyB-9 plants,

indicative of light hypersensitivity (FIGS. **3**A,C and **4**A). Analyses of hypocotyl elongation at very low R fluence rates (<1 $\mu mol \cdot m^{-2} \cdot s^{-1}$) estimated that the $phyB^{Y361F}$ biliprotein was at least 50 times more active at signaling at least with respect to this response (FIG. **4**B). A modest but statistically significant hypersensitivity to R was also observed for seed germination and the effect of EOD-FR on R-suppressed hypocotyl growth (FIG. **5**A,B). Light hypersensitivity continued for the rosettes of mature plants and dampened the SAR (shade avoidance response) as judged by increased hyponasty (i.e., more prostrate petiole angles) and the smaller leaves and shorter petioles seen for $PHYB^{Y361F}$ plants as compare to $PHYB^{WT}$ plants when grown in SD (FIGS. **14** A,B and **9**). Flowering time in SD was not significantly altered (FIG. **5**C), consistent with the minor role of phyB in detecting photoperiod as compared to phyA [30]. Because the hyperactivity of $phyB^{Y361F}$ in R could be canceled by EOD-FR, we concluded that $phyB^{Y361F}$ photoreceptor still functions in a R-FR reversible manner in planta. Light hypersensitivity was also evident in the rosettes of mature plants as judged by the smaller leaves and shorter petioles seen for $PHYB^{Y361F}$ phyB-9 plants as compared to $PHYB^{WT}$ phyB-9 plants when grown in SD (FIG. **9**). Despite changes in photochemistry and signaling, the turnover of $phyB^{Y361F}$ as Pfr and its sequestering into nuclear bodies appeared normal (FIG. **6**A,B).

Example 4

D307 in phyB is Required for Photoconversion, Robust Signaling and Nuclear Body Formation but not Turnover

In line with the predicted importance of D307 in phyB photochemistry [18-20], we found that the assembled $phyB^{D307A}$ biliprotein failed to photoconvert from Pr to Pfr in R and instead generated a bleached R-absorbing intermediate that would regenerate Pr upon irradiation with FR or more slowly upon prolonged dark incubation (FIG. **2**A). Unlike $phyB^{WT}$ which restored R-suppressed hypocotyl elongation and enhanced seed germination in R when introduced into the phyB-9 background, the $phyB^{D307A}$ mutant appeared phenotypically inactive or was greatly reduced in phenotypic activity (FIGS. **3** and **4** and **14**C). Such compromised activity was also apparent in mature plants as judged by the elongated leaf blades and petioles and strong leaf epinasty (as measured by the large upward angles of petioles) of $PHYB^{D307A}$ phyB-9 plants grown in SD, which better resembled phyB-9 plants as compared to their $PHYB^{WT}$ phyB-9 counterparts (FIGS. **14** A,B and **9**). However, detailed fluence response analysis of hypocotyl growth under very high R fluences and the flowering time in SD revealed that $phyB^{D307A}$ retained some signaling activity despite its inability to photoconvert normally to Pfr (FIGS. **4** and **5**). Consistent with diminished photochemistry, the accumulation of $phyB^{D307A}$-YFP in nuclear bodies upon R irradiation was undetectable even after prolonged irradiation with a high fluence rate of R, a condition where the bodies were clearly evident for the wild-type version. But surprisingly its MG132-sensitive turnover in R was only a little slower (FIG. **6**A,B), thus providing the first indication that nuclear aggregation of phyB and its degradation after R irradiation are not coupled.

Example 5

The R322A, R352A, and R582A Mutations Poorly Compromise phyB Signaling

R472 in the PHY domain hairpin of Syn-Cph1 forms an inter-domain salt bridge with D207. We examined the effects of the comparably positioned arginine in *Arabidopsis* phyB (R582) using an alanine substitution. The $phyB^{R582A}$ PSM had normal Pr and Pfr absorption spectra and Pr→Pfr and Pfr→Pr photoconversion rates but was strikingly slower in Pfr→Pr thermal reversion (initial velocity 9.6 times slower than that of $phyB^{WT}$), indicating that R582 is not required for photochemistry but helps destabilize the Pfr conformer once formed (FIG. **2**A,B). The more stable Pfr for $phyB^{R582A}$ in turn likely generates a slightly higher Pfr/Pr ratio in saturating R as evidenced by the reduced peak height at 655 nm versus that at 724 nm (FIG. **2**A). However, $phyB^{R582A}$ appeared to signal normally based on the fluence response of hypocotyl growth to continuous R and its ability to delay flowering in SD (FIGS. **3**C, **4**A, and **5**C). In fact, the $phyB^{R582A}$ chromoprotein appeared to be marginally hyperactive as judged by the slightly stronger repression on hypocotyl growth in R for the $PHYB^{R582A}$ phyB-9 #34 line at intermediate R fluence rates as compared to wild type and $PHYB^{WT}$ phyB-9 seedlings despite accumulating similar levels of photoreceptor (FIG. **4**A). Moreover, petiole angles were more prostrate and the rosettes appeared more compact than wild-type and $PHYB^{WT}$ plants in SD (FIGS. **14**A,B and **9**). We speculate that at least some of this increased activity of the $phyB^{R582A}$ chromoprotein may be related to its higher Pfr/Pr photoequilibrium in continuous R. Regardless of the effects on photochemistry, the nuclear aggregation of $phyB^{R582A}$-YFP, and the turnover of $phyB^{R582A}$ in R appeared normal (FIG. **6**A,B).

R352 is predicted to form an essential salt bridge with the propionate group of pyrrole ring B in PΦB, and, based on the mutational analyses of several prokaryotic phys, it appears to be important for bilin binding and proper photochemistry [9, 18, 20]. In fact, replacement of this residue with a glutamine in Dr-BphP (R254Q) is one of the few mutations that block covalent attachment of the bilin, whereas the more subtle arginine to alanine mutations in Dr-BphP and SyB-Cph1 effectively inhibit thermal reversion of Pfr back to Pr.

We found that the R352A substitution in *Arabidopsis* phyB has little impact on Pr and Pfr absorption and photochemistry, but like its bacterial relatives [4, 18], the mutation stabilizes Pfr against thermal reversion (FIG. **2**A,B). When introduced into phyB-9 seedlings, $phyB^{R352A}$ behaved similarly to wild-type phyB with respect to its ability to suppress hypocotyl growth in R, restore normal rosette morphology to mature plants, delay flowering in SD, and rapidly degrade after photoconversion to Pfr (FIGS. **3**A,C, **4**A, **5**C, and **6**, FIG. **9**). At most, $phyB^{R352A}$ was marginally hypoactive phenotypically as judged by the reduced response of the $PHYB^{R352A}$ phyB-9 hypocotyls to almost all fluences of R despite accumulating levels of photoreceptor comparable to that in wild type (FIG. **4**A). Such subtle phenotypic effects for both $phyB^{R352A}$ and $phyB^{R582A}$ strongly suggest that the thermal reversion of phyB, which would be expected to diminish the active Pfr conformer over time, does not play a major role in phyB signaling under strong light conditions.

Analogous to R352, R322 in the GAF domain is predicted to contact PΦB, with the solution NMR structure of SyB-Cph1 showing that flexibility of its guanidinium side chain allows for transient interactions with the ring C propionate. $phyB^{R322A}$ PSM assembled with PΦB retained normal absorption spectra and Pr→Pfr and Pfr→Pr photoconversion rates, but unlike the R352A substitution, $phyB^{R322A}$ had a substantially faster rate of Pfr→Pr thermal reversion than $phyB^{WT}$ (1.7 times faster; FIG. **2**A, B). Thus, whereas R322 is not required for photochemistry, it helps stabilize the Pfr conformer of phyB once formed. Phenotypically, $phyB^{R322A}$

behaved similar to phyB^{WT} as judged by its ability to suppress hypocotyl elongation under R in phyB-9 seedlings, rescue the rosette morphology of mature plants, and delay flowering in SD (FIGS. **3**A,C, **4**A, and **5**C, FIG. **8**). Similar to the PhyB^{R582}A, phyB^{R322}A relocalized into nuclear bodies and rapidly degraded like endogenous phyB in response to R (FIG. **6**).

Example 6

Analysis of Comparable Mutations in *Arabidopsis* phyA

Comparable mutations (D273A, Y327F, R551A, R318A and R288A (FIG. **1**C)) were examined to determine if similar effects were observed on phyA signaling. Phenotypically, phyA is the dominant isoform in etiolated seedlings and in plants exposed to FR-rich environments. As shown in FIGS. **10** and **11**, phyA signaling can be easily measured by its ability to restore FR suppression of hypocotyl elongation in phyA null mutants such as phyA-211. Using this assay, we found that the D273A mutation also strongly compromises signaling by phyA with a marginal activity seen only at high FR fluence rates (100 μmole·m^{-2}·s^{-1}). For the Y327F mutation in phyA, the response of the PHYA^{Y327F} phyA-211 seedlings matched that of PHYA^{WT} phyA-211 seedlings at all fluence rates tested. Whereas the R551A and R318A substitutions had no apparent effect on phyA signaling, a slight hypoactivity for phyA harboring the R288A substitution was observed, suggesting that like its phyB counterpart, phyA missing this C ring propionate contact has slightly compromised Pfr activity. When more mature plants grown under white light in LD were examined, all of the phyA mutants developed similar to WT, phyA-211, and PHYA^{WT} phyA-211 plants, suggesting that none of the mutants interfered with phyB signaling or stimulated atypical photomorphogenesis.

Prophetic Example 7

Transgenic Maize

The promoter and coding regions of *Zea maize* (Zm) PHYB1 are cloned from maize genomic DNA and total mRNA, respectively, according to the publically available *Zea mays* genome sequence data (see Nucleic Acids Res. 40 (Database issue):D1178-86), and are built into a construction containing a Bar gene for Basta resistance and the nopaline synthase transcription terminator directly after the PHYB1 coding region. The corresponding Y361F mutation (Y359F in ZmPHYB1, ZmPHYB1^{Y359F}) is further introduced into the coding region of ZmPHYB1 in the construction via Quikchange method (Stratagene). Transgenic maize is made by *Agrobacterium tumefaciens*-mediated transformation (*Nat. Protoc.* 2: 1614-1621), and selected for Basta resistance. A total of eight transgenic lines at T1 generation are chosen for further screening based on transgene number, phyB protein level and genetic stability from a large pool of transgenic plants (>100 plants), and are grown, self-pollinated to T4 generation to produce isogenic lines for phenotypic assays.

The selected homogeneous transgenic maize containing ZmPHYB1^{Y359F} are grown in green house for phenotypic characterization. After 30 days, the plant height, size of both the transgenic and wild-type maize will be measured, and the flowering time and seed yield will also be recorded in mature plants. These phenotypic data will also be statistically analyzed, and compared to wild-type plant. The transgenic lines are expected to have much reduced height and size with unaltered flowering time and seed yield. These dwarf maize are expected to require much less growth space and therefore increase the maize yield per acre.

Prophetic Example 8

Transgenic Rice

The promoter and coding regions of *Oryza sativa* L. (Os) PHYB are cloned from rice genomic DNA and total mRNA, respectively, according to the OsPHYB coding sequence data from National Center for Biotechnology Information, and are built into a construction containing a Neomycin Phosphotransferase II (NPTII) gene for kanamycin resistance and the nopaline synthase transcription terminator directly after the PHYB coding region. The corresponding Y361F mutation (Y368F in OsPHYB) is further introduced into the coding region of OsPHYB in the construction (OsPHYB^{Y368F}) via Quikchange method (Stratagene). Transgenic rice is made by *Agrobacterium tumefaciens*-mediated transformation (*Plant J.* 1994 (2):271-82), and selected for kanamycin resistance. A total of eight transgenic lines at T1 generation are chosen for further screening based on transgene number, phyB protein level and genetic stability from a pool of over 20 transgenic plants, and are grown and self-pollinated to T4 generation to produce isogenic lines for phenotypic assays.

The selected homogeneous transgenic rice containing OsPHYB1^{Y368F} are grown in green house for phenotypic characterization. After 30 days, the plant height and size of both the transgenic and wild-type rice will be measured, and the flowering time and seed yield will also be recorded in mature plants. These phenotypic data will also be statistically analyzed. Compared to the wild-type plant, the transgenic lines are expected to have much reduced height and size with unaltered flowering time and seed yield. These dwarf rice are expected to require much less growth space and therefore increase the rice yield per acre.

Prophetic Example 9

Transgenic Soybean

The promoter and coding regions of *Glycine max* (Gm) PHYB1 are cloned from soybean genomic DNA and total mRNA, respectively, according to the GmPHYB1 coding sequence data from National Center for Biotechnology Information, and are built into a construction containing a Bar gene for Basta resistance and the nopaline synthase transcription terminator directly after the GmPHYB1 coding region. The corresponding Y361F mutation (Y345F in GmPHYB1) is further introduced into the coding region of GmPHYB1 in the construction (GmPHYB1^{Y345F}) via Quikchange method (Stratagene). Transgenic soybean is made by *Agrobacterium tumefaciens*-mediated transformation (*Plant Biotechnol.* 2007, (24): 533-536), and selected for Basta resistance. A total of eight transgenic lines at T1 generation are chosen for further screening based on transgene number, phyB protein level and genetic stability from a large pool of over 100 transgenic plants, and are grown and self-pollinated to T4 generation to produce isogenic lines for phenotypic assays.

The selected homogeneous transgenic soybean containing GmPHYB1^{Y345F} are grown in the green house for phenotypic characterization. After 30 days, the plant height, size of

both the transgenic and wild-type soybean will be measured, and the flowering time and seed yield will also be recorded in mature plants. These phenotypic data will also be statistically analyzed. Compared to the wild-type plant, the transgenic lines are expected to have much reduced height and size with unaltered flowering time and seed yield. These resulting dwarf soybean should require much less growth space and therefore increase the soybean yield per acre.

Prophetic Example 10

Spectroscopy Analyses of Maize phyB Mutants

A library of structure-guided variants has the potential to alter phy signaling in a number of ways, which in turn offers a host of opportunities to manipulate light perception in maize. To test this notion, we will examine how the mutations corresponding to D307A, Y361F, R582A, R352A and R322A of the *Arabidopsis* sequence affect maize phyB photochemistry and/or phyB-directed photomorphogenesis. The residues corresponding to D307A and Y361F alleles are of special interest given their ability to confer hypo- and hypersensitivity to phyB signaling. (For simplicity, the maize alleles are designated in this example using the *Arabidopsis* counterpart residue numbers; D307A is D305A in maize and Y361F is Y359F in maize.)

Using the protocols described herein and illustrated in FIG. **2**, we will first examine the photochemical effects of these amino acid substitutions on the recombinant 6His-tagged PSM of maize phyB1 (amino acids 1-623), the dominance of the two maize phyB paralogs with respect to phenotypes. These mutations will be introduced by the Quikchange method (Stratagene) into the full-length ZmPHYB1 cDNA modified to also contain a C-terminal 6His sequence. They will be expressed in *E. coli* by our well defined, two-plasmid pBAD (Invitrogen) system; one LacZ-controlled plasmid encodes the HO (heme oxygenase) from *Synechocystis* PCC6803 and the PΦB synthase from *Arabidopsis* (HY2 locus) needed to synthesize the PΦB chromophore from heme, and the second arabinose-controlled plasmid encodes the ZmphyB1 polypeptide. By sequential induction with IPTG and arabinose, high level accumulation of fully assembled and photochemically active ZmphyB1 PSMs will be possible. The recombinant biliproteins will then be purified by nickel-nitrilotriacetic acid (NiNTA) affinity (Qiagen) chromatography based on the 6His tag, followed by Phenyl Sepharose chromatography. Bilin occupancy of the purified photoreceptors will be assessed by zinc-induced fluorescence of the bound chromophore following SDS-PAGE of the preparation. These samples will be examined for atypical absorption spectra, photoconversion rates, and Pfr stability by spectrometric techniques using techniques disclosed herein for FIG. **2**.

The maize mutants are expected to show phenotypes similar to those described herein for *Arabidopsis*.

Prophetic Example 11

Assessment of Signaling Strength for the ZmphyB1 Mutants in Maize

The ZmphyB1 mutations generated in prophetic example 10 will be introduced into maize plants and tested for their ability to direct various processes under ZmphyB control. The amino acid substitutions will be introduced into the full-length ZmPHYB1 cDNA, also appended to a DNA sequence encoding a short C-terminal FLAG epitope tag (GGDYKDDDDK) (SEQ ID NO: 41), and expressed under the control of the native ZmPHYB1 promoter (2-kbp region upstream of the initiation codon). Use of the native promoter will help avoid artifactual responses generated by ectopic expression of the mutant chromoproteins. These transgenes along with a transgene encoding wild-type ZmphyB-FLAG will be stably introduced into maize using a Maize Transformation protocol which exploits the Hi Type-II background for most transformations, generated from a cross between the B73 and A188 hybrids followed by selection for efficient regeneration of plantlets from cultured embryos. The transgenic plants expressing a range of ZmphyB1 polypeptide levels will be identified by immunoblot analysis with available FLAG and phyB-specific monoclonal antibodies. Independent transformants that express the mutant phyB proteins near to that in wild-type plants will be identified since artificially increased or decreased levels of ZmphyB might significantly influence photomorphogenesis by themselves. Those lines deemed useful will then be backcrossed at least three times to the B73 inbred to generate lines suitable to phenotypic testing. A library of suitable independent lines for each mutation will be generated to avoid potential artifacts generated by insertion position of the transgene and/or differing accumulation of the ZmphyB1 biliprotein.

Some mutants (e.g., $phyB^{Y361F}$) are expected to work dominantly even in the presence of wild-type ZmphyB1/2. However, others will likely confer more subtle phenotypes that will require eliminating the wild-type photoreceptor for observation. This situation will be accomplished through crosses with the ZmphyB1 and ZmphyB2 mutants developed by Sheenan et al. (2007) using Mu insertional mutagenesis, followed by selfing to identify triple homozygous progeny. Single and double mutant combinations will be generated for the strongest ZmphyB1-Mu563 and ZmphyB2-Mu12053 alleles, which have been backcrossed 4 times into both the B73 and W22 backgrounds.

Plants containing unmodified ZmphyB1-FLAG or the mutant ($phyB^{D307A}$, $phyB^{Y361F}$, $phyB^{R582A}$, $phyB^{R352A}$, and $phyB^{R322A}$) in either the wild-type B73 or the ZmphyB1-Mu563 and ZmphyB2-Mu12053 B73-introgressed backgrounds will be examined by various phenotypic assays that specifically measure phyB activity. The germplasm will be tested along side several controls including, near isogenic wild-type B73, B73 expressing unmodified ZmphyB1, and the ZmphyB1-Mu563 and ZmphyB2-Mu12053 B73-introgressed lines either singly or as double mutants. To reduce environmental variability, the plants will be grown in controlled environment cabinets equipped with monochromatic R and FR LED light sources and growth chambers illuminated with white light within the lab and greenhouses supplemented with artificial lighting if needed. Randomized block design will be used to avoid biases based on positions of the plants within the group. Testing of plants in outdoor agricultural plots under natural lighting conditions will be carried out to assess their impact on maize seed yield and plant stature in more representative field settings.

The phenotypes to be tested have been well established in maize and include:

(1) Architecture of seedling grown in the dark (etiolated), which is expected to be unaffected by the mutations.

(2) Effect of R, FR. R-FR. and white light pulses on coleoptile, mesocotyl, and leaf sheath and blade elongation for young seedlings.

(3) Effect of EOD-FR on mesocotyl, and leaf blade elongation for young seedlings grown in light/dark cycles.

(4) Chlorophyll and anthocyanin accumulation in seedlings grown in light/dark cycles.

(5) Effect on internode length, stem diameter, and overall plant height on plants grown in long-day photoperiods.

(6) Effect on flowering time for plants grown in long- and short-day photoperiods.

(7) Number of tillers, cobs, and kernels produced in long-days.

Examining a range of R and FR fluence rates on the photomorphogenic responses of young seedlings will facilitate the quantification of the degree of hypo- or hyperactivity for each mutant, particularly the D307A and Y361F mutations that are expected to greatly impact phyB signaling. It is expected that at least some of the ZmphyB mutants will confer useful new traits such as altered flowering time or reduced SAR (shade avoidance response) to maize grown in field situations.

Sequences listed in this application include:

SEQ ID NO: 1 is the *Arabidopsis thaliana* phytochrome B (phyB) polypeptide (translation of SEQ ID NO: 23)

SEQ ID NO: 2 is the *Zea mays* phytochrome B polypeptide (translation of SEQ ID NO: 24)

SEQ ID NO: 3 is the *Oryza sativa* Japonica Group isolate SJ-CDI2 phytochrome B (phyB) polypeptide (translation of SEQ ID NO: 25)

SEQ ID NO: 4 is the *Sorghum bicolor* isolate PHYB-Rtx430 phytochrome B (phyB) polypeptide (translation of SEQ ID NO: 26)

SEQ ID NO: 5 is the *Glycine max* phytochrome B-1 (phyB) polypeptide (translation of SEQ ID NO: 27)

SEQ ID NO: 6 is the *Glycine max* phytochrome B-2 (phyB) polypeptide (translation of SEQ ID NO: 28)

SEQ ID NO: 7 is the *Glycine max* phytochrome B-3 (phyB) polypeptide (translation of SEQ ID NO: 29)

SEQ ID NO: 8 is the *Glycine max* phytochrome B-4 (phyB) polypeptide (translation of SEQ ID NO: 30)

SEQ ID NO: 9 is the *Solanum tuberosum* phytochrome B polypeptide (translation of SEQ ID NO: 31)

SEQ ID NO: 10 is the *Pisum sativum* phytochrome B (phyB) polypeptide (translation of SEQ ID NO: 32)

SEQ ID NO: 11 is the *Vitis vinifera* genotype PN40024 phytochrome B (phyB) polypeptide (translation of SEQ ID NO: 33)

SEQ ID NO: 12 is the *Arabidopsis* phyB GAF domain

SEQ ID NO: 13 is the maize phyB GAF domain

SEQ ID NO: 14 is the rice phyB GAF domain

SEQ ID NO: 15 is the *sorghum* phyB GAF domain

SEQ ID NO: 16 is the soybean phyB1 GAF domain

SEQ ID NO: 17 is the soybean phyB2 GAF domain

SEQ ID NO: 18 is the soybean phyB3 GAF domain

SEQ ID NO: 19 is the soybean phyB4 GAF domain

SEQ ID NO: 20 is the potato phyB GAF domain

SEQ ID NO: 21 is the pea phyB GAF domain

SEQ ID NO: 22 is the grape phyB GAF domain

SEQ ID NO: 23 is the *Arabidopsis thaliana* phytochrome B (PHYB) nucleotide (Gen Bank Accession No NM_127435)

SEQ ID NO: 24 is the *Zea mays* phytochrome B nucleotide (Phytozome Accession No. GRMZM2G124532)

SEQ ID NO: 25 is the *Oryza sativa* Japonica Group isolate SJ-CDI2 phytochrome B (PHYB) nucleotide (GenBank Accession No: JN594210)

SEQ ID NO: 26 is the *Sorghum bicolor* isolate PHYB-Rtx430 phytochrome B (PHYB) nucleotide (GenBank Accession No: AY466089)

SEQ ID NO: 27 is the *Glycine max* phytochrome B-1 (PHYB) nucleotide (GenBank: Accession No: EU428749)

SEQ ID NO: 28 is the *Glycine max* phytochrome B-2 (PHYB) nucleotide (GenBank Accession No: EU428750.2)

SEQ ID NO: 29 is the *Glycine max* phytochrome B-3 (PHYB) nucleotide (GenBank Accession No: EU428751.1)

SEQ ID NO: 30 is the *Glycine max* phytochrome B-4 (PHYB) nucleotide (GenBank Accession No: EU428752.1)

SEQ ID NO: 31 is the *Solanum tuberosum* phytochrome B nucleotide (GenBank Accession No: DQ342235.1

SEQ ID NO: 32 is the *Pisum sativum* phytochrome B (PHYB) nucleotide (GenBank Accession No: AF069305.1)

SEQ ID NO: 33 is the *Vitis vinifera* genotype PN40024 phytochrome B (PHYB) nucleotide (GenBank Accession No: EU436650.1)

SEQ ID NO: 34 is the cyanobacteriophytochrome GAF domain from *Synechocystis* PCC6803 (Syn Cph_GAF)

SEQ ID NO: 35 is the bacteriophytochrome GAF domain from *Deinococcus radiodurans* (Dr Bph_GAF)

SEQ ID NO: 36 is the bacteriophytochrome GAF domain from *Pseudomonas aeruginosa* (Pa BphP_GAF)

SEQ ID NO: 37 is the bacteriophytochrome GAF domain from *Rhodopseudomonas palustris* (Rp BphP3_GAF)

SEQ ID NO: 38 is the cyanobacteriophytochrome GAF domain from *Synechococcus* OS-B (SyB Cph_GAF)

(SEQ ID NO: 1)

MVSGVGGSGGGRGGGRGGEEEPSSSHTPNNRRGGEQAQSSGTKS

LRPRSNTESMSKAIQQYTVDARLHAVFEQSGESGKSFDYSQSLKTTTYGSSVPEQQIT

AYLSRIQRGGYIQPFGCMIAVDESSFRIIGYSENAREMLGIMPQSVPTLEKPEILAMG

TDVRSLFTSSSSILLERAFVAREITLLNPVWIHSKNTGKPFYAILHRIDVGVVIDLEP

ARTEDPALSIAGAVQSQKLAVRAISQLQALPGGDIKLLCDTVVESVRDLTGYDRVMVY

KFHEDEHGEVVAESKRDDLEPYIGLHYPATDIPQASRFLFKQNRVRMIVDCNATPVLV

VQDDRLTQSMCLVGSTLRAPHGCHSQYMANMGSIASLAMAVIINGNEDDGSNVASGRS

SMRLWGLVVCHHTSSRCIPFPLRYACEFLMQAFGLQLNMELQLALQMSEKRVLRTQTL

LCDMLLRDSPAGIVTQSPSIMDLVKCDGAAFLYHGKYYPLGVAPSEVQIKDVVEWLLA

NHADSTGLSTDSLGDAGYPGAAALGDAVCGMAVAYITKRDFLFWFRSHTAKEIKWGGA

KHHPEDKDDGQRMHPRSSFQAFLEVVKSRSQPWETAEMDAIHSLQLILRDSFKESEAA

MNSKVVDGVVQPCRDMAGEQGIDELGAVAREMVRLIETATVPIFAVDAGGCINGWNAK

-continued

IAELTGLSVEEAMGKSLVSDLIYKENEATVNKLLSRALRGDEEKNVEVKLKTFSPELQ

GKAVFVVVNACSSKDYLNNIVGVCFVGQDVTSQKIVMDKFINIQGDYKAIVHSPNPLI

PPIFAADENTCCLEWNMAMEKLTGWSRSEVIGKMIVGEVFGSCCMLKGPDALTKFMIV

LHNAIGGQDTDKFPFPFFDRNGKFVQALLTANKRVSLEGKVIGAFCFLQIPSPELQQA

LAVQRRQDTECFTKAKELAYICQVIKNPLSGMRFANSLLEATDLNEDQKQLLETSVSC

EKQISRIVGDMDLESIEDGSFVLKREEFFLGSVINAIVSQAMFLLRDRGLQLIRDIPE

EIKSIEVFGDQIRIQQLLAEFLLSIIRYAPSQEWVEIHLSQLSKQMADGFAAIRTEFR

MACPGEGLPPELVRDMFHSSRWTSPEGLGLSVCRKILKLMNGEVQYIRESERSYFLII

LELPVPRKRPLSTASGSGDMMLMMPY

(SEQ ID NO: 2)

MASGSRATPTRSPSSARPEAPRHAHHHHHSQSSGGSTSRAGGGAAATESVSKAVAQYT

LDARLHAVFEQSGASGRSFDYSQSLRAPPTPSSEQQIAAYLS

RIQRGGHIQPFGCTLAVADDSSFRLLAFSENSPDLLDLSPHHSVPSLDSSAPPHVSLG

ADARLLFSPSSAVLLERAFAAREISLLNPIWIHSRVSSKPFY

AILHRIDVGVVIDLEPARTEDPALSIAGAVQSQKLAVRAISRLQALPGGDVKLLCDTV

VEHVRELTGYDRVMVYRFHEDEHGEVVAESRRDNLEPYLGLH

YPATDIPQASRFLFRQNRVRMIADCHATPVRVIQDPGLSQPLCLVGSTLRAPHGCHAQ

YMANMGSIASLVMAVIISSGGDDEQTGRGGISSAMKLWGLVV

CHHTSPRCIPFPLRYACEFLMQAFGLQLNMELQLAHQLSEKHILRTQTLLCDMLLRDS

PTGIVTQSPSIMDLVKCDGAALYYHGKYYPLGVTPTESQIKD

IIEWLTVFHGDSTGLSTDSLADAGYLGAAALGEAVCGMAVAYITPSDYLFWFRSHTAK

EIKWGGAKHHPEDKDDGQRMHPRSSFKAFLEVVKSRSLPWEN

AEMDAIHSLQLILRDSFRDAAEGTNNSKAIVNGQVQLRELELRGINELSSVAREMVRL

IETATVPIFAVDTDGCINGWNAKIAELTGLSVEEAMGKSLVN

DLIFKESEATVEKLLSRALRGEEDKNVEIKLKTFGSEQYKGPIFVVVNACSSRDYTQN

IVGVCFVGQDVTGQKVVMDKFVNIQGDYKAIVHNPNPLIPPI

FASDENTSCSEWNTAMEKLTGWSRGEVVGKFLIGEVFGNCCRLKGPDALTKFMVIIHN

AIGGQDYEKFPFSFFDKNGKYVQALLTANTRSKMDGKSIGAF

CFLQIASTEIQQAFEIQRQQEKKCYARMKELAYICQEIKNPLSGIRFTNSLLQMTDLN

DDQRQFLETSSACEKQMSKIVKDASLQSIEDGSLVLEQSEFS

LGDVMNAVVSQAMLLLRERDLQLIRDIPDETKDASAYGDQCRIQQVLADFLLSMVRSA

PSENGWVEIQVRPNVKQNSDGTNTELFIFRFACPGEGLPADV

VQDMFSNSQWSTQEGVGLSTCRKILKLMGGEVQYIRESERSFFLIVLEQPQPRPAAGR

EIV

(SEQ ID NO: 3)

MGSGSRATPTRSPSSARPAAPRHQHHHSQSSGGSTSRAGGGGGG

GGGGGGGAAAAESVSKAVAQYTLDARLHAVFEQSGASGRSFDYTQSLRASPTPSSEQQ

IAAYLSRIQRGGHIQPFGCTLAVADDSSFRLLAYSENTADLLDLSPHHSVPSLDSSAV

PPPVSLGADARLLFAPSSAVLLERAFAAREISLLNPLWIHSRVSSKPFYAILHRIDVG

VVIDLEPARTEDPALSIAGAVQSQKLAVRAISRLQALPGGDVKLLCDTVVEHVRELTG

YDRVMVYRFHEDEHGEVVAESRRSNLEPYIGLHYPATDIPQASRFLFRQNRVRMIADC

-continued

HAAPVRVIQDPALTQPLCLVGSTLRSPHGCHAQYMANMGSIASLVMAVIISSGGDDDH

NIARGSIPSAMKLWGLVVCHHTSPRCIPFPLRYACEFLMQAFGLQLNMELQLAHQLSE

KHILRTQTLLCDMLLRDSPTGIVTQSPSIMDLVKCDGAALYYHGKYYPLGVTPTEVQI

KDIIEWLTMCHGDSTGLSTDSLADAGYSGAAALGDAVSGMAVAYITPSDYLFWFRSHT

AKEIKWGGAKHHPEDKDDGQRMHPRSSFKAFLEVVKSRSLPWENAEMDAIHSLQLILR

DSFRDSAEGTSNSKAIVNGQVQLGELELRGIDELSSVAREMVRLIETATVPIFAVDTD

GCINGWNAKVAELTGLSVEEAMGKSLVNDLIFKESEETVNKLLSRALRGDEDKNVEIK

LKTFGPEQSKGPIFVIVNACSSRDYTKNIVGVCFVGQDVTGQKVVMDKFINIQGDYKA

IVHNPNPLIPPIFASDENTCCLEWNTAMEKLTGWSRGEVVGKLLVGEVFGNCCRLKGP

DALTKFMIVLHNAIGGQDCEKFPFSFFDKNGKYVQALLTANTRSRMDGEAIGAFCFLQ

IASPELQQAFEIQRHHEKKCYARMKELAYIYQEIKNPLNGIRFTNSLLEMTDLKDDQR

QFLETSTACEKQMSKIVKDASLQSIEDGSLVLEKGEFSLGSVMNAVVSQVMIQLRERD

LQLIRDIPDEIKEASAYGDQYRIQQVLCDFLLSMVRFAPAENGWVEIQVRPNIKQNSD

GTDTMLFLFRFACPGEGLPPEIVQDMFSNSRWTTQEGIGLSICRKILKLMGGEVQYIR

ESERSFFHIVLELPQPQQAASRGTS

(SEQ ID NO: 4)

MASGSRATPTRSPSSARPEAPRHAHHHHHHHSQSSGGSTSRAGG

GGGGGGGGGGTAATATATATESVSKAVAQYTLDARLHAVFEQSGASGRSFDYSQSLRA

PPTPSSEQQIAAYLSRIQRGGHIQPFGCTLAVADDSSFRLLAFSENAADLLDLSPHHS

VPSLDSAAPPPVSLGADARLLFSPSSAVLLERAFAAREISLLNPLWIHSRVSSKPFYA

ILHRIDVGVVIDLEPARTEDPALSIAGAVQSQKLAVRAISRLQALPGGDIKLLCDTVV

EHVRELTGYDRVMVYRFHEDEHGEVVAESRRDNLEPYLGLHYPATDIPQASRFLFRQN

RVRMIADCHATPVRVIQDPGMSQPLCLVGSTLRAPHGCHAQYMANMGSIASLVMAVII

SSGGDDEQTGRGGISSAMKLWGLVVCHHTSPRCIPFPLRYACEFLMQAFGLQLNMELQ

LAHQLSEKHILRTQTLLCDMLLRDSPTGIVTQSPSIMDLVKCDGAALYYHGKYYPLGV

TPTESQIKDIIEWLTVCHGDSTGLSTDSLADAGYLGAAALGDAVCGMAVAYITPSDYL

FWFRSHTAKEIKWGGAKHHPEDKDDGQRMHPRSSFKAFLEVVKSRSLPWENAEMDAIH

SLQLILRDSFRDAAEGTSNSKAIVNGQAQLGELELRGINELSSVPREMVRLIETATVP

IFAVDTDGCINGWNAKIAELTGLSVEEAMGKSLVNDLIFKESEEIVEKLLSRALRGEE

DKNVEIKLKTFGSEQSNGAIFVIVNACSSRDYTQNIVGVCFVGQDVTGQKVVMDKFIN

IQGDYKAIVHNPNPLIPPIFASDENTSCSEWNTAMEKLTGWSRGEVVGKFLIGEVFGS

FCRLKGPDALTKFMVVIHNAIGGQDYEKFPFSFFDKNGKYVQALLTANTRSKMDGKSI

GAFCFLQIASAEIQQAFEIQRQQEKKCYARMKELAYICQEIKNPLSGIRFTNSLLQMT

DLNDDQRQFLETCSACEKQMSKIVKDATLQSIEDGSLVLEKSEFSFGDVMNAVVSQAM

LLLRERDLQLIRDIPDEIKDASAYGDQFRIQQVLADFLLSMVRSAPSENGWVEIQVRP

NVKQNSDGTDTELFIFRFACPGEGLPADIVQDMFSNSQWSTQEGVGLSTCRKILKLMG

GEVQYIRESERSFFLIVLELPQPRPAADREIS

(SEQ ID NO: 5)

MASASGAANSSVPPPQIHTSRTKLSHHSSNNNNNIDSMSKAIAQ

YTEDARLHAVFEQSGESGRSFNYSESIRIASESVPEQQITAYLVKIQRGGFIQPFGSM

IAVDEPSFRILGYSDNARDMLGITPQSVPSLDDKNDAAFALGTDVRALFTHSSALLLE

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KAFSAREISLMNPIWIHSRTSGKPFYGILHRIDVGIVIDLEPARTEDPALSIAGAVQS

QKLAVRAISQLQSLPGGDVKLLCDTVVESVRELTGYDRVMVYKFHEDEHGEVVSESKR

PDLEPYIGLHYPATDIPQASRFLFKQNRVRMIVDCHASAVRVVQDEALVQPLCLVGST

LRAPHGCHAQYMANMGSIASLVMAVIINGNDEEGVGGRSSMRLWGLVVCHHTSARCIP

FPLRYACEFLMQAFGLQLNMELQLAAQSLEKRVLRTQTLLCDMLLRDSPTGIVTQSPS

IMDLVKCDGAALYFQGNYYPLGVTPTEAQIRDIIEWLLAFHGDSTGLSTDSLGDAGYP

GAASLGDAVCGMAVAYITEKDFLFWFRSHTAKEIKWGGAKHHPEDKDDGQRMHPRSSF

KAFLEVVKSRSLPWENAEMDAIHSLQLILRDSFKDAEHRNSKAVVDPHVSEQELQGVD

ELSSVAREMVRLIETATAPIFAVDVDGHVNGWNAKVSELTGLPVEEAMGKSLVHDLVF

KESEETMNKLLSRALKGEEDKNVEIKMRTFGPEHQNKAVFLVVNACSSKDFTNNVVGV

CFVGQDVTGQKIVMDKFINIQGDYKAIVHSPNPLIPPIFASDDNTCCLEWNTAMEKLT

GWGRVDVIGKMLVGEVFGSCCQLKGSDSITKFMIVLHNALGGQDTDKFPFSFLDRHGK

YVQTFLTANKRVNMEGQIIGAFCFLQIMSPELQQALKAQRQQEKNSFGRMKELAYICQ

GVKNPLSGIRFTNSLLEATSLTNEQKQFLETSVACEKQMLKIIRDVDLESIEDGSLEL

EKGEFLLGNVINAVVSQVMLLLRERNLQLIRDIPEEIKTLAVYGDQLRIQQVLSDFLL

NIVRYAPSPDGWVEIHVRPRIKQISDGLTLLHAEFRMVCPGEGLPPELIQDMFNNSRW

GTQEGLGLSMSRKILKLMNGEVQYIREAERCYFYVLLELPVTRRSSKKC

(SEQ ID NO: 6)

MASASGAENSSVPPSPLPPPPPPQIHTSRTKLSHHHHNNNNNNN

NNIDSTSKAIAQYTEDARLHAVFEQSGESGRSFDYSQSIRVTSESVPEQQITAYLLKI

QRGGFIQPFGSMIAVDEPSFRILAYSDNARDMLGITPQSVPSLDDKNDAAFALGTDIR

TLFTHSSAVLLEKAFSAREISLMNPIWIHSRTSGKPFYGILHRIDVGIVIDLEPARTE

DPALSIAGAVQSQKLAVRAISQLQSLPGGDVKLLCDTVVESVRELTGYDRVMVYRFHE

DEHGEVVAETKRPDLEPYIGLHYPATDIPQASRFLFKQNRVRMIVDCHASAVRVVQDE

ALVQPLCLVGSTLRAPHGCHAQYMANMGSTASLVMAVIINGNDEEGVGGRTSMRLWGL

VICHHTSARCIPFPLRYACEFLMQAFGLQLNMELQLAAQSLEKRVLRTQTLLCDMLLR

DSPTGIVTQSPSIMDLVKCDGAALYYQGNYYPLGVTPTEAQIRDIIEWLLAFHRDSTG

LSTDSLADAGYPGAASLGDAVCGMAVAYITEKDFLFWFRSHTAKEIKWGGAKHHPEDK

DDGQRMHPRSSFKAFLEVVKSRSLPWENAEMDAIHSLQLILRDSFKDAEHSNSKAVLD

PRMSELELQGVDELSSVAREMVRLIETATAPIFAVDVDGRINGWNAKVSELTGLPVEE

AMGKSLVRDLVFKESEETVDKLLSRALKGEEDKNVEIKMRTFGPEHQNKAVFVVVNAC

SSKDYTNNVVGVCFVGQDVTGQKIVMDKFINIQGDYKAIVHNPNPLIPPIFASDDNTC

CLEWNTAMEKLTGWSRADVIGKMLVGEVFGSCCQLKGSDSITKFMIVLHNALGGHDTD

RFPFSFLDRYGKHVQAFLTANKRVNMDGQIIGAFCFLQIVSPELQQALKAQRQQEKNS

FARMKELAYICQGVKNPLSGIRFTNSLLEATCLSNEQKQFLETSAACEKQMLKIIHDV

DIESIEDGSLELEKGEFLLGNVINAVVSQVMLLLRERNLQLIRDIPEEIKTLAVYGDQ

LRIQQVLSDFLLNIVRYAPSPDGWVEIHVHPRIKQISDGLTLLHAEFRMVCPGEGLPP

ELIQNMFNNSGWGTQEGLGLSMSRKILKLMNGEVQYIREAQRCYFYVLLELPVTRRSS

KKC

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(SEQ ID NO: 7)

MSKAIAQYTEDARLHAVFEQSGESGRSFNYSESIRIASESVPEQ

QITAYLVKIQRGGFIQPFGSMIAVDEPSFRILGYSDNARDMLGITPQSVPSLDDKNDA

AFALGTDVRALFTHSSALLLEKAFSAREISLMNPIWIHSRTSGKPFYGILHRIDVGIV

IDLEPARTEDPALSIAGAVQSQKLAVRAISQLQSLPGGDVKLLCDTVVESVRELTGYD

RVMVYKFHEDEHGEVVSESKRPDLEPYIGLHYPATDIPQASRFLFKQNRVRMIVDCHA

SAVRVVQDEALVQPLCLVGSTLRAPHGCHAQYMANMGSIASLVMAVIINGNDEEGVGG

RSSMRLWGLVVCHHTSARCIPFPLRYACEFLMQAFGLQLNMELQLAAQSLEKRVLRTQ

TLLCDMLLRDSPTGIVTQSPSIMDLVKCDGAALYFQGNYYPLGVTPTEAQIRDIIEWL

LAFHGDSTGLSTDSLGDAGYPGAASLGDAVCGMAVAYITEKDFLFWFRSHTAKEIKWG

GAKHHPEDKDDGQRMHPRSSFKAFLEVVKSRSLPWENAEMDAIHSLQLILRDSFKDAE

HRNSKAVADPRVSEQELQGVDELSSVAREMVRLIETATAPIFAVDVDGHVNGWNAKVS

ELTGLPVEEAMGKSLVHDLVFKESEETMNKLLSRALKGEEDKNVEIKMRTFGPERQNK

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IFASDDNTCCLEWNTAMEKLTGWGRVDVIGKMLVGEVFGSCCQLKGSDSITKFMIVLH

NALGGQDTDKFPFSFLDRHGKYVQTFLTANKRVNMEGQIIGAFCFLQIMSPELQQALK

AQRQQEKNSFGRMKELAYICQGVKNPLSGIRFTNSLLEATSLTNEQKQFLETSVACEK

QMLKIIRDVDLESIEDGSLELEKGEFLLGNVINAVVSQVMLLLRERNLQLIRDIPEEI

KTLAVYGDQLRIQQVLSDFLLNIVRYAPSPDGWVEIHVRPRIKQISDGLTLLHAEFRM

VCPGEGLPPELIQDMFNNSRWGTQEGLGLSMSRKILKLMNGEVQYIREAERCYFYVLL

ELPVTRRSSKKC

(SEQ ID NO: 8)

MIAVDEPSFRILAYSDNARDMLGITPQSVPSLDDKNDAAFALGT

DIRTLFTHSSAVLLEKAFSAREISLMNPIWIHSRTSGKPFYGILHRIDVGIVIDLEPA

RTEDPALSIAGAVQSQKLAVRAISQLQSLPGGDVKLLCDTVVESVRELTGYDRVMVYR

FHEDEHGEVVAETKRPDLEPYIGLHYPATDIPQASRFLFKQNRVRMIVDCHASAVRVV

QDEALVQPLCLVGSTLRAPHGCHAQYMANMGSTASLVMAVIINGNDEEGVGGRTSMRL

WGLVICHHTSARCIPFPLRYACEFLMQAFGLQLNMELQLAAQSLEKRVLRTQTLLCDM

LLRDSPTGIVTQSPSIMDLVKCDGAALYYQGNYYPLGVTPTEAQIRDIIEWLLAFHRD

STGLSTDSLADAGYPGAASLGDAVCGMAVAYITEKDFLFWFRSHTAKEIKWGGAKHHP

EDKDDGQRMHPRSSFKAFLEVVKSRSLPWESAEMDAIHSLQLILRDSFKDAEHSNSKA

VLDPRMSELELQGVDELSSVAREMVRLIETATAPIFAVDVDGRINGWNAKVSELTGLP

VEEAMGKSLVRDLVFKESEETVDKLLSRALKGEEDKNVEIKMRTFGPEHQNKAVFVVV

NACSSKDYTNNVVGVCFVGQDVTGQKIVMDKFINIQGDYKAIVHNPNPLIPPIFASDD

NTCCLEWNTAMEKLTGWSRADVIGKMLVGEVFGSCCQLKGSDSITKFMIVLHNALGGH

DTDRFPFSFLDRYGKHVQAFLTANKRVNMDGQIIGAFCFLQIVSPELQQALKAQRQQE

KNSFARMKELAYICQGVKNPLSGIRFTNSLLEATCLSNEQKQFLETSAACEKQMLKII

HDVDIESIEDG

(SEQ ID NO: 9)

MASGSRTKHSHHNSSQAQSSGTSNVNYKDSISKAIAQYTADARL

HAVFEQSGESGKFFDYSESVKTTTQSVPERQITAYLTKIQRGGHIQPFGCMIAVDEAS

FRVIAYSENAFEMLSLTPQSVPSLEKCEILTIGTDVRTLFTPSSSVLLERAFGAREIT

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HYPATDIPQASRFLFKQNRVRMIVDCHATPVRVTQDESLMQPLCLVGSTLRAPHGCHA

QYMANMGSIASLTLAVIINGNDEEAVGGGRNSMRLWGLVVGHHTSVRSIPFPLRYACE

FLMQAFGLQLNMELQLASQLSEKHVLRTQTLLCDMLLRDSPPGIVTQSPSIMDLVKCD

GAALYYQGKYYPLGVTPTEAQIKDIVEWLLAYHGDSTGLSTDSLADAGYPGAASLGDA

VCGMAVAYISSKDFLFWFRSHTAKEIKWGGAKHHPEDKDDGLRMHPRSSFKAFLEVVK

SRSSPWENAEMDAIHSLQLILRDSFKDAEASNSKAIVHAHLGEMELQGIDELSSVARE

MVRLIETATAPIFAVDVEGRINGWNAKVAELTGLSVEEAMGKSLVHELVYKESQETAE

KLLYNALRGEEDKNVEIKLRTFGAEQLEKAVFVVVNACASKDYTNNIVGVCFVGQDVT

GEKVVMDKFINIQGDYKAIVHSPNPLIPPIFASDENTCCSEWNTAMEKLTGWSRGEIV

GKMLVGEIFGSCCRLKGPDAMTKFMIVLHNAIGGQDTDKFPFSFFDRNGKYVQALLTA

NKRVNMEGNTIGAFCFIQIASPELQQALRVQRQQEKKCYSQMKELAYICQEIKSPLNG

IRFTNSLLEATNLTENQKQYLETSAACERQMSKIIRDVDLENIEDGSLTLEKEDFFLG

SVIDAVVSQVMLLLREKGVQLIRDIPEEIKTLTVHGDQVRIQQVLADFLLNMVRYAPS

PDGWVEIQLRPSMMPISDGVTGVHIELRIICPGEGLPPELVQDMFHSSRWVTQEGLGL

STCRKMLKLMNGEIQYIRESERCYFLIVLDLPMTRKGPKSVG

(SEQ ID NO: 10)

SNNNNNRNIKRESLSMRKAIAQYTEDAXLHAVFEKSGDSFDYAQ

SIRVTAATESVPEQQITAYLAKIQRGGFIQPFGSMIAVDETSFRVLAYSENARDMLGI

APQSVPSMEDDSSSSSFFSLGVDVRSLFSASSSVLLEKAFSAREISLMNPIWIHSRST

GKPFYGILHRIDIGVVIDLEPARSEDPALSIAGAVQSQKLAVRAISQLQALPGGDVKL

LCDAVVESVRELTGYDRVMVYKFHEDEHGEVVAESKRVDLEPYIGLHYPATDIPQASR

FLFKQNRVRMIVDCNASPVRVFQDEALVQPVCLVGSTLRAPHGCHAQYMANMGSIASL

AMAVIINGNDEDGGGIGGAARGSMRLWGLVVCHHTSARCIPFPLRYACEFLMQAFGLQ

LNMELQLAVQSLEKRVLKTQTLLCDMLLRDSHTGIVTQSPSIMDLVKCDGAALYYQGN

YHPLGVTPTESQIRDIIDWLLAFHSDSTGLSTDSLADAGYPGAASLGDAVCGMAVAYI

TEKDFLFWFRSHTAKEIKWGGAKHHPEDKDDGQKMHPRSSFKAFLEVVKIRSMQWDNA

EMDAIHSLQLILRDSFKEAENNDSKAVVHTHMAELELQGVDELSSVAREMVRLIETAT

APIFAVDVDGRINGWNAKVSELTGLLVEEAMGKSLVHDLVYKESRETVDKLLSHALKG

EEDKNVEIKMKTFGPGNQNKAVFIVVNACSSKDYTNNIVGVCFVGQDITGQKVVMDKF

INIQGDYKAIVHSPNPLIPPIFASDDNTCCLEWNNAMEKLSGWSRADVIGKLLVGEVF

GSFCQLKGSDAMTKFMIVLHNALGGHDTDKFPLSFLDRHGKYVHTFLTANKRVNMDGQ

IIGAFCFLQIVNPELQQALTVQRQQDSSSLARMKELAYICQEVKNPLSGIRFTNSLLE

STCLTDEQKQLLETSVACEKQMLKIVRDIALESIEDGSLELEKQEFLLENVINAVVSQ

VMLLLRDRKLQLIRDIPEEIKALAVYGDQLRIQQVLADFLMNVVRYAPSPDGWVEIHV

FPRIKQISEGLTLLHAEFRMVCPGEGLPPELIQDMFHNSRWVTQEGLGLSMSRKIIKL

MNGEVQYVREAERCYFLVLLELPVTRRSSKAIN

(SEQ ID NO: 11)

MSSGNRGTQSHHQAQSSGTSNLRVYHTDSMSKAIAQYTMDARLH

AVYEQSGESGKSFDYSQSVRTTTQSVPEQQITAYLSKIQRGGHIQPFGCMLAVDEATF

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RVIAFSENAREMLGLTPQSVPSLEKPEILLVGTDVRTLFTPSSAVLLEKAFRAREITL

LNPVWIHSKNSGKPFYAILHRIDVGIVIDLEPARTEDPALSIAGAVQSQKLAVRAISH

LQSLPGGDINLLCETVVENVRELTGYDRVMVYKFHEDEHGEVVAESKRSDLEPYIGLH

YPATDIPQASRFLFRQNRVRMIVDCHATPVLVIQDEGLMQPLCLVGSTLRAPHGCHAQ

YMANMGSTASLAMAVIINGSDEEAIGGRNLMRLWGLVVCHHTSARCIPFPLRYACEFL

MQAFGLQLNMELQLASQLSEKHVLRTQTLLCDMLLRDSPTGIVTQSPSIMDLVKCDGA

ALYYQGKYYPTGVTPTEAQIKDIAEWLLANHADSTGLSTDSLADAGYPGAASLGDAVC

GMAVAYITSRDFLFWFRSHTAKEIKWGGAKHHPEDKDDGQRMHPRSSFKAFLEVVKSR

SLPWENAEMDAIHSLQLILRDSFKDATDGSNSKAVMHAQLGELELQGMDELSSVAREM

VRLIETATAPIFAVDVDGCINGWNAKVAELTGLSVEEAMGKSLVHDLVYKESEETVDK

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QKVVMDKFIHIQGDYKAIVHSPNPLIPPIFASDENTVCSEWNTAMEKLTGWSRGDIIG

KILVGEIFGSSCRLKGPDALTKFMIVLHNAIGGQDTDKFPFSFFDQNGKYVQALLTAN

KRVNIEGQIIGAFCFLQIASPELQQALKVQRQQEKKCFARMKELAYICQEIKNPLSGI

RFTNSLLEATDLTEDQKQFLETSAACEKQMSKIIRDVDLDSIEDGSLELERAEFLLGS

VINAVVSQVMILLRERDLQLIRDIPEEVKTLAVYGDQVRIQQVLADFLLNMVRYAPSP

DGWIEIQVCPRLKQISEEVKLMHIEFRMVCPGEGLPPNLIQDMFHSSRWMTQEGLGLS

MCRKILKLINGEVQYIRESERCYFLISIELPIPHRGSKSVD"

SEQ ID NO: 12
(See FIG. 13)

SEQ ID NO: 13
(See FIG. 13)

SEQ ID NO: 14
(See FIG. 13)

SEQ ID NO: 15
(See FIG. 13)

SEQ ID NO: 16
(See FIG. 13)

SEQ ID NO: 17
(See FIG. 13)

SEQ ID NO: 18
(See FIG. 13)

SEQ ID NO: 19
(See FIG. 13)

SEQ ID NO: 20
(See FIG. 13)

SEQ ID NO: 21
(See FIG. 13)

SEQ ID NO: 22
(See FIG. 13)

Arabidopsis thaliana phytochrome B (PHYB) nucleotide (GenBank Accession No NM_127435)

(SEQ ID NO: 23)

at ggtttccgga gtcgggggta gtggcggtgg ccgtggcggt

ggccgtggcg gagaagaaga accgtcgtca agtcacactc ctaataaccg aagaggagga

gaacaagctc aatcgtcggg aacgaaatct ctcagaccaa gaagcaacac tgaatcaatg

agcaaagcaa ttcaacagta caccgtcgac gcaagactcc acgccgtttt cgaacaatcc

ggcgaatcag ggaaatcatt cgactactca caatcactca aaacgacgac gtacggttcc

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aaccctctaa tcccgccaat ttttgctgct gacgagaaca cgtgctgcct ggaatggaac

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gaccgcaatg ggaagtttgt tcaggctcta ttgactgcaa acaagcgggt tagcctcgag

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gccacagact tgaacgagga ccagaagcag ttacttgaaa caagtgtttc ttgcgagaaa

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cgaccattgt caactgctag tggaagtggt gacatgatgc tgatgatgcc atat

Zea mays phytochrome B nucleotide (Phytozome Accession No. GRMZM2G124532)

(SEQ ID NO: 24)

ATGGCGTCGGGCAGCCGCGCCACGCCCACGCGCTCCCCCTCCTCCGCGCGGCCCGAGGCGCCGCGTCACGCGCACCA

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AGGCCGTCGCCCAGTACACCCTAGACGCGCGCCTACACGCGGTGTTCGAGCAATCGGGCGCGTCGGGCCGCAGCTTC

GACTACTCCCAATCGCTGCGCGCGCCGCCCACGCCGTCCTCCGAGCAGCAGATCGCCGCCTACCTCTCCCGCATCCA

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CCGAGAACTCCCCCGACCTGCTCGACCTGTCGCCTCACCACTCCGTTCCCTCGCTGGACTCCTCTGCGCCGCCCCAC

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Oryza sativa Japonica Group isolate SJ-CDI2 phytochrome b (phyB) nucleotide (GenBank Accession No: JN594210)

(SEQ ID NO: 25)

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Sorghum bicolor isolate PHYB-Rtx430 phytochrome B (PHYB) nucleotide (GenBank Accession No: AY466089)

(SEQ ID NO: 26)

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Glycine max phytochrome B-1 (phyB) nucletoide (GenBank: EU428749)

(SEQ ID NO: 27)

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(SEQ ID NO: 28)

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Glycine max phytochrome B-3 (phyB) nucleotide (GenBank Accession No: EU428751.1)

(SEQ ID NO: 29)

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Glycine max phytochrome B-4 (phyB) nucletoide
GenBank: EU428752.1

(SEQ ID NO: 30)

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Solanum tuberosum phytochrome B nucleotide
GenBank: DQ342235.1

(SEQ ID NO: 31)

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Pisum sativum phytochrome B (PHYB) nucleotide
GenBank: AF069305.1

(SEQ ID NO: 32)

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2221 attaacatac aaggtgacta caaggctatt gtacatagtc caaatccatt gatccctccc

2281 atttttgcat cggatgacaa cacatgttgc ttagagtgga acaatgctat ggaaaagctc

2341 agcggctgga gccgtgcaga tgtcattggc aaattgttag tgggagaggt ttttggtagt

2401 ttctgtcagt tgaagggttc ggatgctatg acaaaattca tgattgtttt gcacaatgca

2461 cttggtggac acgacacaga caaattccca ttgtcatttc ttgacagaca tggaaagtat

2521 gtgcatactt tcttgaccgc aaataagagg gttaacatgg atggtcagat cattggcgca

2581 ttttgctttt tacaaattgt gaaccctgaa cttcaacagg ctttgacagt ccagagacaa

2641 caggatagta gttccttagc tagaatgaag gagttagctt atatttgtca agaagtaaag

2701 aatcccttga gtggcatacg ctttacaaac tctcttttgg agtctacatg cctgactgat

2761 gagcaaaagc agcttcttga gactagtgtt gcttgtgaga agcaaatgct gaagatagta

2821 cgggacattg ctctagaaag catcgaggat gggtccctgg agcttgaaaa gcaggaattc

2881 ttgctcgaga atgtcataaa tgcagttgtt agccaagtaa tgctattgct aagagataga

2941 aagttacagt taattcgtga tattcctgaa gaaatcaagg cattggctgt ttatggtgat

3001 cagttgagga ttcaacaagt cttggctgat ttcttaatga atgtggtgcg ctatgcacca

3061 tctccagatg gttgggtaga gattcatgta tttccaagaa taaaacaaat ttcagagggg

3121 ctcactcttc tgcatgctga atttaggatg gtgtgtcctg gtgaaggtct tccacctgaa

3181 ttgattcaag acatgttcca taacagtcgg tgggtgactc aagaaggctt agggctgagc

3241 atgagcagga agattataaa gttaatgaac ggcgaagtcc agtatgtaag ggaggcagaa

3301 cggtgctact tcttagttct tcttgaacta cccgtgacac ggagaagctc taaagctatt

3361 aat

Vitis vinifera genotype PN40024 phytochrome B (PHYB) nucleotide
GenBank: EU436650.1

(SEQ ID NO: 33)

atgagttcagga aacagaggaa cgcagtcgca ccaccaagct cagtcgtcgg ggacaagcaa

361 tttgagagtt taccacactg attcaatgag caaagccatt gcgcaatata caatggatgc

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421 tcgcctccac gccgtatacg aacagtccgg cgagtccggt aagtcattcg actactcgca

481 gtcggttaga accacaacgc aatcggtccc tgagcaacaa atcactgcgt atttatcgaa

541 aattcaacgg ggtggccata tacagccctt tgggtgtatg cttgcggtcg atgaggccac

601 ttttcgggtc attgctttca gcgaaaatgc ccgagaaatg ctcggtctca ctccgcaatc

661 ggttccgagc cttgagaagc ccgagatcct cctagtaggt actgatgttc gcacgctttt

721 cactccctcg agcgcagttc tcctcgaaaa ggcgtttcgg gctcgggaaa ttacgttgtt

781 aaatcccgtg tggattcatt ccaagaattc tggaaaaccc ttttacgcaa ttttgcatag

841 aattgatgtg ggaattgtaa ttgatttgga gcctgcaagg actgaggacc ctgctctgtc

901 cattgctggg gcggtgcagt cgcagaagtt ggccgttcga gcaatttccc atcttcaatc

961 tcttcccggt ggtgatatta acctttttgtg tgaaactgtg gttgagaatg tgagggagct

1021 tactgggtat gatcgggtca tggtttacaa atttcacgag gatgaacatg gtgaggtcgt

1081 ggctgagagc aagaggtctg atttggagcc ttatattggg ttacactatc ctgccacgga

1141 cattccacag gcttcaaggt ttttgtttag gcagaatcgg gttaggatga tcgttgattg

1201 ccatgccacg cctgttctgg tgattcaaga tgaagggctt atgcagcctc tatgcttagt

1261 tggttcaacc cttcgggctc ctcatggctg ccatgcacag tatatggcca acatgggttc

1321 aactgcctca ttagcgatgg ctgtcatcat caatggaagt gatgaggaag ctattggtgg

1381 gcgaaacttg atgaggctat ggggcctggt tgtttgtcat cacacatctg ctaggtgcat

1441 tccatttcct cttcgatatg cctgtgagtt cctaatgcag gcatttggac tccaattgaa

1501 catggaactg cagttagcat cgcaattgtc tgagaaacat gttttaagga cacagactct

1561 cttgtgtgac atgctccttc gtgattcccc tactggaatt gttacccaaa gtcctagtat

1621 tatggatctt gtgaagtgtg atggagcagc actttattac caggggaagt attatccaac

1681 tggggtgacc ccgactgaag cccagataaa ggatattgca gagtggttgt tggcaaacca

1741 tgcggattca acaggtttaa gcactgacag tttggctgat gctggctacc ctggggcagc

1801 ctcacttggt gatgcagttt gtggaatggc tgttgcttat atcacttcaa gagattttct

1861 attctggttt cggtcccaca cagcaaaaga gatcaaatgg ggtggtgcaa agcatcatcc

1921 agaggacaag gacgatgggc agaggatgca tcctcgttct tcattcaagg catttttaga

1981 agtggtcaag agtcggagtt tgccatggga gaatgcggaa atggatgcaa ttcattctct

2041 gcagcttatt ctgcgtgact cttttaagga tgctactgat ggaagcaatt ctaaggctgt

2101 aatgcatgct cagctcgggg agctagagtt gcaagggatg gatgagttga gctctgttgc

2161 aagagaaatg gttaggttga ttgaaactgc aacagctccc atatttgcgg tcgatgttga

2221 tggctgcata aatggttgga atgcaaaggt tgcggagttg acggggcttt ctgttgagga

2281 agctatgggg aagtccttgg ttcatgatct tgtttacaag gaatctgaag aaactgttga

2341 caagcttctt catcatgctc tacgag gt gaagaagata

3361 agaatgtaga gataaaattg aggacatttg actcacaaca gcataagaag gctgtttttg

3421 tggtcgttaa tgcttgctcc agtagggatt acacaaataa tatagttgga gtttgctttg

3481 ttggtcagga tgttactggt cagaaagtgg taatggacaa atttatccat atacaaggtg

3541 attacaaagc tattgtacat agtcccaacc ctttgattcc tcctatattt gcttcagatg

3601 agaacacagt ttgctctgag tggaacactg ccatggaaaa gctcactggg tggagcaggg

3661 gggacatcat tgggaagatc ttggttgggg agatttttgg cagtagctgt cggctgaagg

3721 gtccggatgc tctgacaaaa ttcatgattg tgttgcacaa tgcaattgga gggcaagaca

3781 cagacaagtt tccattttcc ttctttgacc agaatggaaa atatgtgcaa gctcttttga

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3841 cagcaaataa gagagttaat attgagggcc agattattgg tgccttctgc tttttgcaga

3901 ttgcaagtcc tgaattgcag caagctctca aagtccaaag gcaacaggag aaaaaatgtt

3961 ttgcaaggat gaaagagttg gcttacattt gtcaggaaat aaagaaccct ttaagtggca

4021 tacgtttcac taactctctt ttggaggcca ctgacttaac tgaagatcaa aagcagtttc

4081 ttgagactag tgctgcttgt gagaagcaga tgtcaaagat cataagggat gttgatctgg

4141 acagcattga ggatgg ttcactg gagcttgaga

5041 gggctgaatt tttacttgga agtgtcataa atgctgttgt tagccaagta atgatattgt

5101 tgagggaaag agatttacaa ttgatccggg acattcctga ggaagtcaaa acactggctg

5161 tttatggcga tcaagtaaga attcaacagg ttttggctga tttcttactg aatatggtgc

5221 gttatgcacc atccccagac ggttggatag agattcaagt ttgtccaaga ttgaagcaaa

5281 tttctgaaga agtaaaactt atgcatattg aattcag gat ggtatgccct

ggtgaaggtc ttcctcctaa

7621 tctgattcaa gacatgttcc atagcagtcg ttggatgact caggaaggtc tagggctgag

7681 catgtgcagg aagatcttaa agctcattaa tggcgaagtc caatatatca gagaatcaga

7741 aagatgttat tttctaatca gcatagaact tcctatacct cacagaggct caaagagcgt

7801 tgac

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 77

<210> SEQ ID NO 1
<211> LENGTH: 1172
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 1

Met Val Ser Gly Val Gly Gly Ser Gly Gly Gly Arg Gly Gly Gly Arg
1 5 10 15

Gly Gly Glu Glu Glu Pro Ser Ser Ser His Thr Pro Asn Asn Arg Arg
20 25 30

Gly Gly Glu Gln Ala Gln Ser Ser Gly Thr Lys Ser Leu Arg Pro Arg
35 40 45

Ser Asn Thr Glu Ser Met Ser Lys Ala Ile Gln Gln Tyr Thr Val Asp
50 55 60

Ala Arg Leu His Ala Val Phe Glu Gln Ser Gly Glu Ser Gly Lys Ser
65 70 75 80

Phe Asp Tyr Ser Gln Ser Leu Lys Thr Thr Thr Tyr Gly Ser Ser Val
85 90 95

Pro Glu Gln Gln Ile Thr Ala Tyr Leu Ser Arg Ile Gln Arg Gly Gly
100 105 110

Tyr Ile Gln Pro Phe Gly Cys Met Ile Ala Val Asp Glu Ser Ser Phe
115 120 125

Arg Ile Ile Gly Tyr Ser Glu Asn Ala Arg Glu Met Leu Gly Ile Met
130 135 140

Pro Gln Ser Val Pro Thr Leu Glu Lys Pro Glu Ile Leu Ala Met Gly
145 150 155 160

Thr Asp Val Arg Ser Leu Phe Thr Ser Ser Ser Ser Ile Leu Leu Glu
165 170 175

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Arg Ala Phe Val Ala Arg Glu Ile Thr Leu Leu Asn Pro Val Trp Ile
            180                 185                 190

His Ser Lys Asn Thr Gly Lys Pro Phe Tyr Ala Ile Leu His Arg Ile
        195                 200                 205

Asp Val Gly Val Val Ile Asp Leu Glu Pro Ala Arg Thr Glu Asp Pro
    210                 215                 220

Ala Leu Ser Ile Ala Gly Ala Val Gln Ser Gln Lys Leu Ala Val Arg
225                 230                 235                 240

Ala Ile Ser Gln Leu Gln Ala Leu Pro Gly Gly Asp Ile Lys Leu Leu
                245                 250                 255

Cys Asp Thr Val Val Glu Ser Val Arg Asp Leu Thr Gly Tyr Asp Arg
            260                 265                 270

Val Met Val Tyr Lys Phe His Glu Asp Glu His Gly Glu Val Val Ala
        275                 280                 285

Glu Ser Lys Arg Asp Asp Leu Glu Pro Tyr Ile Gly Leu His Tyr Pro
    290                 295                 300

Ala Thr Asp Ile Pro Gln Ala Ser Arg Phe Leu Phe Lys Gln Asn Arg
305                 310                 315                 320

Val Arg Met Ile Val Asp Cys Asn Ala Thr Pro Val Leu Val Val Gln
                325                 330                 335

Asp Asp Arg Leu Thr Gln Ser Met Cys Leu Val Gly Ser Thr Leu Arg
            340                 345                 350

Ala Pro His Gly Cys His Ser Gln Tyr Met Ala Asn Met Gly Ser Ile
        355                 360                 365

Ala Ser Leu Ala Met Ala Val Ile Ile Asn Gly Asn Glu Asp Asp Gly
    370                 375                 380

Ser Asn Val Ala Ser Gly Arg Ser Ser Met Arg Leu Trp Gly Leu Val
385                 390                 395                 400

Val Cys His His Thr Ser Ser Arg Cys Ile Pro Phe Pro Leu Arg Tyr
                405                 410                 415

Ala Cys Glu Phe Leu Met Gln Ala Phe Gly Leu Gln Leu Asn Met Glu
            420                 425                 430

Leu Gln Leu Ala Leu Gln Met Ser Glu Lys Arg Val Leu Arg Thr Gln
        435                 440                 445

Thr Leu Leu Cys Asp Met Leu Leu Arg Asp Ser Pro Ala Gly Ile Val
    450                 455                 460

Thr Gln Ser Pro Ser Ile Met Asp Leu Val Lys Cys Asp Gly Ala Ala
465                 470                 475                 480

Phe Leu Tyr His Gly Lys Tyr Tyr Pro Leu Gly Val Ala Pro Ser Glu
                485                 490                 495

Val Gln Ile Lys Asp Val Val Glu Trp Leu Leu Ala Asn His Ala Asp
            500                 505                 510

Ser Thr Gly Leu Ser Thr Asp Ser Leu Gly Asp Ala Gly Tyr Pro Gly
        515                 520                 525

Ala Ala Ala Leu Gly Asp Ala Val Cys Gly Met Ala Val Ala Tyr Ile
    530                 535                 540

Thr Lys Arg Asp Phe Leu Phe Trp Phe Arg Ser His Thr Ala Lys Glu
545                 550                 555                 560

Ile Lys Trp Gly Gly Ala Lys His His Pro Glu Asp Lys Asp Asp Gly
                565                 570                 575

Gln Arg Met His Pro Arg Ser Ser Phe Gln Ala Phe Leu Glu Val Val
            580                 585                 590

Lys Ser Arg Ser Gln Pro Trp Glu Thr Ala Glu Met Asp Ala Ile His
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        595                 600                 605

Ser Leu Gln Leu Ile Leu Arg Asp Ser Phe Lys Glu Ser Glu Ala Ala
    610                 615                 620

Met Asn Ser Lys Val Val Asp Gly Val Val Gln Pro Cys Arg Asp Met
625                 630                 635                 640

Ala Gly Glu Gln Gly Ile Asp Glu Leu Gly Ala Val Ala Arg Glu Met
                645                 650                 655

Val Arg Leu Ile Glu Thr Ala Thr Val Pro Ile Phe Ala Val Asp Ala
            660                 665                 670

Gly Gly Cys Ile Asn Gly Trp Asn Ala Lys Ile Ala Glu Leu Thr Gly
        675                 680                 685

Leu Ser Val Glu Glu Ala Met Gly Lys Ser Leu Val Ser Asp Leu Ile
    690                 695                 700

Tyr Lys Glu Asn Glu Ala Thr Val Asn Lys Leu Leu Ser Arg Ala Leu
705                 710                 715                 720

Arg Gly Asp Glu Glu Lys Asn Val Glu Val Lys Leu Lys Thr Phe Ser
                725                 730                 735

Pro Glu Leu Gln Gly Lys Ala Val Phe Val Val Val Asn Ala Cys Ser
            740                 745                 750

Ser Lys Asp Tyr Leu Asn Asn Ile Val Gly Val Cys Phe Val Gly Gln
        755                 760                 765

Asp Val Thr Ser Gln Lys Ile Val Met Asp Lys Phe Ile Asn Ile Gln
    770                 775                 780

Gly Asp Tyr Lys Ala Ile Val His Ser Pro Asn Pro Leu Ile Pro Pro
785                 790                 795                 800

Ile Phe Ala Ala Asp Glu Asn Thr Cys Cys Leu Glu Trp Asn Met Ala
                805                 810                 815

Met Glu Lys Leu Thr Gly Trp Ser Arg Ser Glu Val Ile Gly Lys Met
            820                 825                 830

Ile Val Gly Glu Val Phe Gly Ser Cys Cys Met Leu Lys Gly Pro Asp
        835                 840                 845

Ala Leu Thr Lys Phe Met Ile Val Leu His Asn Ala Ile Gly Gly Gln
    850                 855                 860

Asp Thr Asp Lys Phe Pro Phe Pro Phe Phe Asp Arg Asn Gly Lys Phe
865                 870                 875                 880

Val Gln Ala Leu Leu Thr Ala Asn Lys Arg Val Ser Leu Glu Gly Lys
                885                 890                 895

Val Ile Gly Ala Phe Cys Phe Leu Gln Ile Pro Ser Pro Glu Leu Gln
            900                 905                 910

Gln Ala Leu Ala Val Gln Arg Arg Gln Asp Thr Glu Cys Phe Thr Lys
        915                 920                 925

Ala Lys Glu Leu Ala Tyr Ile Cys Gln Val Ile Lys Asn Pro Leu Ser
    930                 935                 940

Gly Met Arg Phe Ala Asn Ser Leu Leu Glu Ala Thr Asp Leu Asn Glu
945                 950                 955                 960

Asp Gln Lys Gln Leu Leu Glu Thr Ser Val Ser Cys Glu Lys Gln Ile
                965                 970                 975

Ser Arg Ile Val Gly Asp Met Asp Leu Glu Ser Ile Glu Asp Gly Ser
            980                 985                 990

Phe Val Leu Lys Arg Glu Glu Phe  Phe Leu Gly Ser Val  Ile Asn Ala
        995                 1000                1005

Ile Val  Ser Gln Ala Met Phe  Leu Leu Arg Asp Arg  Gly Leu Gln
    1010                1015                1020
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Leu Ile  Arg Asp Ile Pro Glu  Glu Ile Lys Ser Ile  Glu Val Phe
    1025                1030                1035

Gly Asp  Gln Ile Arg Ile Gln  Gln Leu Leu Ala Glu  Phe Leu Leu
    1040                1045                1050

Ser Ile  Ile Arg Tyr Ala Pro  Ser Gln Glu Trp Val  Glu Ile His
    1055                1060                1065

Leu Ser  Gln Leu Ser Lys Gln  Met Ala Asp Gly Phe  Ala Ala Ile
    1070                1075                1080

Arg Thr  Glu Phe Arg Met Ala  Cys Pro Gly Glu Gly  Leu Pro Pro
    1085                1090                1095

Glu Leu  Val Arg Asp Met Phe  His Ser Ser Arg Trp  Thr Ser Pro
    1100                1105                1110

Glu Gly  Leu Gly Leu Ser Val  Cys Arg Lys Ile Leu  Lys Leu Met
    1115                1120                1125

Asn Gly  Glu Val Gln Tyr Ile  Arg Glu Ser Glu Arg  Ser Tyr Phe
    1130                1135                1140

Leu Ile  Ile Leu Glu Leu Pro  Val Pro Arg Lys Arg  Pro Leu Ser
    1145                1150                1155

Thr Ala  Ser Gly Ser Gly Asp  Met Met Leu Met Met  Pro Tyr
    1160                1165                1170


<210> SEQ ID NO 2
<211> LENGTH: 1161
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 2

Met Ala Ser Gly Ser Arg Ala Thr Pro Thr Arg Ser Pro Ser Ser Ala
1               5                   10                  15

Arg Pro Glu Ala Pro Arg His Ala His His His His His Ser Gln Ser
            20                  25                  30

Ser Gly Gly Ser Thr Ser Arg Ala Gly Gly Gly Ala Ala Ala Thr Glu
        35                  40                  45

Ser Val Ser Lys Ala Val Ala Gln Tyr Thr Leu Asp Ala Arg Leu His
    50                  55                  60

Ala Val Phe Glu Gln Ser Gly Ala Ser Gly Arg Ser Phe Asp Tyr Ser
65                  70                  75                  80

Gln Ser Leu Arg Ala Pro Pro Thr Pro Ser Ser Glu Gln Gln Ile Ala
                85                  90                  95

Ala Tyr Leu Ser Arg Ile Gln Arg Gly Gly His Ile Gln Pro Phe Gly
            100                 105                 110

Cys Thr Leu Ala Val Ala Asp Asp Ser Ser Phe Arg Leu Leu Ala Phe
        115                 120                 125

Ser Glu Asn Ser Pro Asp Leu Leu Asp Leu Ser Pro His His Ser Val
    130                 135                 140

Pro Ser Leu Asp Ser Ser Ala Pro Pro His Val Ser Leu Gly Ala Asp
145                 150                 155                 160

Ala Arg Leu Leu Phe Ser Pro Ser Ser Ala Val Leu Leu Glu Arg Ala
                165                 170                 175

Phe Ala Ala Arg Glu Ile Ser Leu Leu Asn Pro Ile Trp Ile His Ser
            180                 185                 190

Arg Val Ser Ser Lys Pro Phe Tyr Ala Ile Leu His Arg Ile Asp Val
        195                 200                 205

Gly Val Val Ile Asp Leu Glu Pro Ala Arg Thr Glu Asp Pro Ala Leu
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    210                 215                 220

Ser Ile Ala Gly Ala Val Gln Ser Gln Lys Leu Ala Val Arg Ala Ile
225                 230                 235                 240

Ser Arg Leu Gln Ala Leu Pro Gly Gly Asp Val Lys Leu Leu Cys Asp
                245                 250                 255

Thr Val Val Glu His Val Arg Glu Leu Thr Gly Tyr Asp Arg Val Met
            260                 265                 270

Val Tyr Arg Phe His Glu Asp Glu His Gly Glu Val Val Ala Glu Ser
        275                 280                 285

Arg Arg Asp Asn Leu Glu Pro Tyr Leu Gly Leu His Tyr Pro Ala Thr
    290                 295                 300

Asp Ile Pro Gln Ala Ser Arg Phe Leu Phe Arg Gln Asn Arg Val Arg
305                 310                 315                 320

Met Ile Ala Asp Cys His Ala Thr Pro Val Arg Val Ile Gln Asp Pro
                325                 330                 335

Gly Leu Ser Gln Pro Leu Cys Leu Val Gly Ser Thr Leu Arg Ala Pro
            340                 345                 350

His Gly Cys His Ala Gln Tyr Met Ala Asn Met Gly Ser Ile Ala Ser
        355                 360                 365

Leu Val Met Ala Val Ile Ile Ser Ser Gly Gly Asp Asp Glu Gln Thr
    370                 375                 380

Gly Arg Gly Gly Ile Ser Ser Ala Met Lys Leu Trp Gly Leu Val Val
385                 390                 395                 400

Cys His His Thr Ser Pro Arg Cys Ile Pro Phe Pro Leu Arg Tyr Ala
                405                 410                 415

Cys Glu Phe Leu Met Gln Ala Phe Gly Leu Gln Leu Asn Met Glu Leu
            420                 425                 430

Gln Leu Ala His Gln Leu Ser Glu Lys His Ile Leu Arg Thr Gln Thr
        435                 440                 445

Leu Leu Cys Asp Met Leu Leu Arg Asp Ser Pro Thr Gly Ile Val Thr
    450                 455                 460

Gln Ser Pro Ser Ile Met Asp Leu Val Lys Cys Asp Gly Ala Ala Leu
465                 470                 475                 480

Tyr Tyr His Gly Lys Tyr Tyr Pro Leu Gly Val Thr Pro Thr Glu Ser
                485                 490                 495

Gln Ile Lys Asp Ile Ile Glu Trp Leu Thr Val Phe His Gly Asp Ser
            500                 505                 510

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

Ala Ala Leu Gly Glu Ala Val Cys Gly Met Ala Val Ala Tyr Ile Thr
    530                 535                 540

Pro Ser Asp Tyr Leu Phe Trp Phe Arg Ser His Thr Ala Lys Glu Ile
545                 550                 555                 560

Lys Trp Gly Gly Ala Lys His His Pro Glu Asp Lys Asp Asp Gly Gln
                565                 570                 575

Arg Met His Pro Arg Ser Ser Phe Lys Ala Phe Leu Glu Val Val Lys
            580                 585                 590

Ser Arg Ser Leu Pro Trp Glu Asn Ala Glu Met Asp Ala Ile His Ser
        595                 600                 605

Leu Gln Leu Ile Leu Arg Asp Ser Phe Arg Asp Ala Ala Glu Gly Thr
    610                 615                 620

Asn Asn Ser Lys Ala Ile Val Asn Gly Gln Val Gln Leu Arg Glu Leu
625                 630                 635                 640
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Glu Leu Arg Gly Ile Asn Glu Leu Ser Ser Val Ala Arg Glu Met Val
                645                 650                 655

Arg Leu Ile Glu Thr Ala Thr Val Pro Ile Phe Ala Val Asp Thr Asp
            660                 665                 670

Gly Cys Ile Asn Gly Trp Asn Ala Lys Ile Ala Glu Leu Thr Gly Leu
        675                 680                 685

Ser Val Glu Glu Ala Met Gly Lys Ser Leu Val Asn Asp Leu Ile Phe
    690                 695                 700

Lys Glu Ser Glu Ala Thr Val Glu Lys Leu Leu Ser Arg Ala Leu Arg
705                 710                 715                 720

Gly Glu Glu Asp Lys Asn Val Glu Ile Lys Leu Lys Thr Phe Gly Ser
                725                 730                 735

Glu Gln Tyr Lys Gly Pro Ile Phe Val Val Val Asn Ala Cys Ser Ser
            740                 745                 750

Arg Asp Tyr Thr Gln Asn Ile Val Gly Val Cys Phe Val Gly Gln Asp
        755                 760                 765

Val Thr Gly Gln Lys Val Val Met Asp Lys Phe Val Asn Ile Gln Gly
    770                 775                 780

Asp Tyr Lys Ala Ile Val His Asn Pro Asn Pro Leu Ile Pro Pro Ile
785                 790                 795                 800

Phe Ala Ser Asp Glu Asn Thr Ser Cys Ser Glu Trp Asn Thr Ala Met
                805                 810                 815

Glu Lys Leu Thr Gly Trp Ser Arg Gly Glu Val Val Gly Lys Phe Leu
            820                 825                 830

Ile Gly Glu Val Phe Gly Asn Cys Cys Arg Leu Lys Gly Pro Asp Ala
        835                 840                 845

Leu Thr Lys Phe Met Val Ile Ile His Asn Ala Ile Gly Gly Gln Asp
    850                 855                 860

Tyr Glu Lys Phe Pro Phe Ser Phe Phe Asp Lys Asn Gly Lys Tyr Val
865                 870                 875                 880

Gln Ala Leu Leu Thr Ala Asn Thr Arg Ser Lys Met Asp Gly Lys Ser
                885                 890                 895

Ile Gly Ala Phe Cys Phe Leu Gln Ile Ala Ser Thr Glu Ile Gln Gln
            900                 905                 910

Ala Phe Glu Ile Gln Arg Gln Gln Glu Lys Lys Cys Tyr Ala Arg Met
        915                 920                 925

Lys Glu Leu Ala Tyr Ile Cys Gln Glu Ile Lys Asn Pro Leu Ser Gly
    930                 935                 940

Ile Arg Phe Thr Asn Ser Leu Leu Gln Met Thr Asp Leu Asn Asp Asp
945                 950                 955                 960

Gln Arg Gln Phe Leu Glu Thr Ser Ser Ala Cys Glu Lys Gln Met Ser
                965                 970                 975

Lys Ile Val Lys Asp Ala Ser Leu Gln Ser Ile Glu Asp Gly Ser Leu
            980                 985                 990

Val Leu Glu Gln Ser Glu Phe Ser  Leu Gly Asp Val Met  Asn Ala Val
        995                 1000                1005

Val Ser  Gln Ala Met Leu Leu  Leu Arg Glu Arg Asp  Leu Gln Leu
    1010                1015                1020

Ile Arg  Asp Ile Pro Asp Glu  Ile Lys Asp Ala Ser  Ala Tyr Gly
    1025                1030                1035

Asp Gln  Cys Arg Ile Gln Gln  Val Leu Ala Asp Phe  Leu Leu Ser
    1040                1045                1050
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Met Val  Arg Ser Ala Pro Ser  Glu Asn Gly Trp Val  Glu Ile Gln
    1055                1060                1065

Val Arg  Pro Asn Val Lys Gln  Asn Ser Asp Gly Thr  Asn Thr Glu
    1070                1075                1080

Leu Phe  Ile Phe Arg Phe Ala  Cys Pro Gly Glu Gly  Leu Pro Ala
    1085                1090                1095

Asp Val  Val Gln Asp Met Phe  Ser Asn Ser Gln Trp  Ser Thr Gln
    1100                1105                1110

Glu Gly  Val Gly Leu Ser Thr  Cys Arg Lys Ile Leu  Lys Leu Met
    1115                1120                1125

Gly Gly  Glu Val Gln Tyr Ile  Arg Glu Ser Glu Arg  Ser Phe Phe
    1130                1135                1140

Leu Ile  Val Leu Glu Gln Pro  Gln Pro Arg Pro Ala  Ala Gly Arg
    1145                1150                1155

Glu Ile  Val
    1160


<210> SEQ ID NO 3
<211> LENGTH: 1171
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 3

Met Gly Ser Gly Ser Arg Ala Thr Pro Thr Arg Ser Pro Ser Ser Ala
1               5                  10                  15

Arg Pro Ala Ala Pro Arg His Gln His His His Ser Gln Ser Ser Gly
            20                  25                  30

Gly Ser Thr Ser Arg Ala Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
        35                  40                  45

Gly Gly Gly Ala Ala Ala Ala Glu Ser Val Ser Lys Ala Val Ala Gln
    50                  55                  60

Tyr Thr Leu Asp Ala Arg Leu His Ala Val Phe Glu Gln Ser Gly Ala
65                  70                  75                  80

Ser Gly Arg Ser Phe Asp Tyr Thr Gln Ser Leu Arg Ala Ser Pro Thr
                85                  90                  95

Pro Ser Ser Glu Gln Gln Ile Ala Ala Tyr Leu Ser Arg Ile Gln Arg
            100                 105                 110

Gly Gly His Ile Gln Pro Phe Gly Cys Thr Leu Ala Val Ala Asp Asp
        115                 120                 125

Ser Ser Phe Arg Leu Leu Ala Tyr Ser Glu Asn Thr Ala Asp Leu Leu
    130                 135                 140

Asp Leu Ser Pro His His Ser Val Pro Ser Leu Asp Ser Ser Ala Val
145                 150                 155                 160

Pro Pro Pro Val Ser Leu Gly Ala Asp Ala Arg Leu Leu Phe Ala Pro
                165                 170                 175

Ser Ser Ala Val Leu Leu Glu Arg Ala Phe Ala Ala Arg Glu Ile Ser
            180                 185                 190

Leu Leu Asn Pro Leu Trp Ile His Ser Arg Val Ser Ser Lys Pro Phe
        195                 200                 205

Tyr Ala Ile Leu His Arg Ile Asp Val Gly Val Val Ile Asp Leu Glu
    210                 215                 220

Pro Ala Arg Thr Glu Asp Pro Ala Leu Ser Ile Ala Gly Ala Val Gln
225                 230                 235                 240

Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Arg Leu Gln Ala Leu Pro
                245                 250                 255
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Gly Gly Asp Val Lys Leu Leu Cys Asp Thr Val Val Glu His Val Arg
            260                 265                 270

Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Arg Phe His Glu Asp
        275                 280                 285

Glu His Gly Glu Val Val Ala Glu Ser Arg Arg Ser Asn Leu Glu Pro
    290                 295                 300

Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg
305                 310                 315                 320

Phe Leu Phe Arg Gln Asn Arg Val Arg Met Ile Ala Asp Cys His Ala
                325                 330                 335

Ala Pro Val Arg Val Ile Gln Asp Pro Ala Leu Thr Gln Pro Leu Cys
            340                 345                 350

Leu Val Gly Ser Thr Leu Arg Ser Pro His Gly Cys His Ala Gln Tyr
        355                 360                 365

Met Ala Asn Met Gly Ser Ile Ala Ser Leu Val Met Ala Val Ile Ile
    370                 375                 380

Ser Ser Gly Gly Asp Asp Asp His Asn Ile Ala Arg Gly Ser Ile Pro
385                 390                 395                 400

Ser Ala Met Lys Leu Trp Gly Leu Val Val Cys His His Thr Ser Pro
                405                 410                 415

Arg Cys Ile Pro Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln
            420                 425                 430

Ala Phe Gly Leu Gln Leu Asn Met Glu Leu Gln Leu Ala His Gln Leu
        435                 440                 445

Ser Glu Lys His Ile Leu Arg Thr Gln Thr Leu Leu Cys Asp Met Leu
    450                 455                 460

Leu Arg Asp Ser Pro Thr Gly Ile Val Thr Gln Ser Pro Ser Ile Met
465                 470                 475                 480

Asp Leu Val Lys Cys Asp Gly Ala Ala Leu Tyr Tyr His Gly Lys Tyr
                485                 490                 495

Tyr Pro Leu Gly Val Thr Pro Thr Glu Val Gln Ile Lys Asp Ile Ile
            500                 505                 510

Glu Trp Leu Thr Met Cys His Gly Asp Ser Thr Gly Leu Ser Thr Asp
        515                 520                 525

Ser Leu Ala Asp Ala Gly Tyr Ser Gly Ala Ala Ala Leu Gly Asp Ala
    530                 535                 540

Val Ser Gly Met Ala Val Ala Tyr Ile Thr Pro Ser Asp Tyr Leu Phe
545                 550                 555                 560

Trp Phe Arg Ser His Thr Ala Lys Glu Ile Lys Trp Gly Gly Ala Lys
                565                 570                 575

His His Pro Glu Asp Lys Asp Asp Gly Gln Arg Met His Pro Arg Ser
            580                 585                 590

Ser Phe Lys Ala Phe Leu Glu Val Val Lys Ser Arg Ser Leu Pro Trp
        595                 600                 605

Glu Asn Ala Glu Met Asp Ala Ile His Ser Leu Gln Leu Ile Leu Arg
    610                 615                 620

Asp Ser Phe Arg Asp Ser Ala Glu Gly Thr Ser Asn Ser Lys Ala Ile
625                 630                 635                 640

Val Asn Gly Gln Val Gln Leu Gly Glu Leu Glu Leu Arg Gly Ile Asp
                645                 650                 655

Glu Leu Ser Ser Val Ala Arg Glu Met Val Arg Leu Ile Glu Thr Ala
            660                 665                 670
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Thr Val Pro Ile Phe Ala Val Asp Thr Asp Gly Cys Ile Asn Gly Trp
        675                 680                 685

Asn Ala Lys Val Ala Glu Leu Thr Gly Leu Ser Val Glu Glu Ala Met
    690                 695                 700

Gly Lys Ser Leu Val Asn Asp Leu Ile Phe Lys Glu Ser Glu Glu Thr
705                 710                 715                 720

Val Asn Lys Leu Leu Ser Arg Ala Leu Arg Gly Asp Glu Asp Lys Asn
                725                 730                 735

Val Glu Ile Lys Leu Lys Thr Phe Gly Pro Glu Gln Ser Lys Gly Pro
            740                 745                 750

Ile Phe Val Ile Val Asn Ala Cys Ser Ser Arg Asp Tyr Thr Lys Asn
        755                 760                 765

Ile Val Gly Val Cys Phe Val Gly Gln Asp Val Thr Gly Gln Lys Val
    770                 775                 780

Val Met Asp Lys Phe Ile Asn Ile Gln Gly Asp Tyr Lys Ala Ile Val
785                 790                 795                 800

His Asn Pro Asn Pro Leu Ile Pro Pro Ile Phe Ala Ser Asp Glu Asn
                805                 810                 815

Thr Cys Cys Leu Glu Trp Asn Thr Ala Met Glu Lys Leu Thr Gly Trp
            820                 825                 830

Ser Arg Gly Glu Val Val Gly Lys Leu Leu Val Gly Glu Val Phe Gly
        835                 840                 845

Asn Cys Cys Arg Leu Lys Gly Pro Asp Ala Leu Thr Lys Phe Met Ile
    850                 855                 860

Val Leu His Asn Ala Ile Gly Gly Gln Asp Cys Glu Lys Phe Pro Phe
865                 870                 875                 880

Ser Phe Phe Asp Lys Asn Gly Lys Tyr Val Gln Ala Leu Leu Thr Ala
                885                 890                 895

Asn Thr Arg Ser Arg Met Asp Gly Glu Ala Ile Gly Ala Phe Cys Phe
            900                 905                 910

Leu Gln Ile Ala Ser Pro Glu Leu Gln Gln Ala Phe Glu Ile Gln Arg
        915                 920                 925

His His Glu Lys Lys Cys Tyr Ala Arg Met Lys Glu Leu Ala Tyr Ile
    930                 935                 940

Tyr Gln Glu Ile Lys Asn Pro Leu Asn Gly Ile Arg Phe Thr Asn Ser
945                 950                 955                 960

Leu Leu Glu Met Thr Asp Leu Lys Asp Asp Gln Arg Gln Phe Leu Glu
                965                 970                 975

Thr Ser Thr Ala Cys Glu Lys Gln Met Ser Lys Ile Val Lys Asp Ala
            980                 985                 990

Ser Leu Gln Ser Ile Glu Asp Gly  Ser Leu Val Leu Glu  Lys Gly Glu
        995                 1000                1005

Phe Ser  Leu Gly Ser Val Met  Asn Ala Val Val Ser  Gln Val Met
    1010                1015                1020

Ile Gln  Leu Arg Glu Arg Asp  Leu Gln Leu Ile Arg  Asp Ile Pro
    1025                1030                1035

Asp Glu  Ile Lys Glu Ala Ser  Ala Tyr Gly Asp Gln  Tyr Arg Ile
    1040                1045                1050

Gln Gln  Val Leu Cys Asp Phe  Leu Leu Ser Met Val  Arg Phe Ala
    1055                1060                1065

Pro Ala  Glu Asn Gly Trp Val  Glu Ile Gln Val Arg  Pro Asn Ile
    1070                1075                1080

Lys Gln  Asn Ser Asp Gly Thr  Asp Thr Met Leu Phe  Leu Phe Arg
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    1085                1090                1095

Phe Ala  Cys Pro Gly Glu Gly  Leu Pro Pro Glu Ile  Val Gln Asp
    1100                1105                1110

Met Phe  Ser Asn Ser Arg Trp  Thr Thr Gln Glu Gly  Ile Gly Leu
    1115                1120                1125

Ser Ile  Cys Arg Lys Ile Leu  Lys Leu Met Gly Gly  Glu Val Gln
    1130                1135                1140

Tyr Ile  Arg Glu Ser Glu Arg  Ser Phe Phe His Ile  Val Leu Glu
    1145                1150                1155

Leu Pro  Gln Pro Gln Gln Ala  Ala Ser Arg Gly Thr  Ser
    1160                1165                1170


<210> SEQ ID NO 4
<211> LENGTH: 1178
<212> TYPE: PRT
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 4

Met Ala Ser Gly Ser Arg Ala Thr Pro Thr Arg Ser Pro Ser Ser Ala
1               5                   10                  15

Arg Pro Glu Ala Pro Arg His Ala His His His His His His His Ser
            20                  25                  30

Gln Ser Ser Gly Gly Ser Thr Ser Arg Ala Gly Gly Gly Gly Gly Gly
        35                  40                  45

Gly Gly Gly Gly Gly Gly Thr Ala Ala Thr Ala Thr Ala Thr Ala Thr
    50                  55                  60

Glu Ser Val Ser Lys Ala Val Ala Gln Tyr Thr Leu Asp Ala Arg Leu
65                  70                  75                  80

His Ala Val Phe Glu Gln Ser Gly Ala Ser Gly Arg Ser Phe Asp Tyr
                85                  90                  95

Ser Gln Ser Leu Arg Ala Pro Pro Thr Pro Ser Ser Glu Gln Gln Ile
            100                 105                 110

Ala Ala Tyr Leu Ser Arg Ile Gln Arg Gly Gly His Ile Gln Pro Phe
        115                 120                 125

Gly Cys Thr Leu Ala Val Ala Asp Asp Ser Ser Phe Arg Leu Leu Ala
    130                 135                 140

Phe Ser Glu Asn Ala Ala Asp Leu Leu Asp Leu Ser Pro His His Ser
145                 150                 155                 160

Val Pro Ser Leu Asp Ser Ala Ala Pro Pro Pro Val Ser Leu Gly Ala
                165                 170                 175

Asp Ala Arg Leu Leu Phe Ser Pro Ser Ser Ala Val Leu Leu Glu Arg
            180                 185                 190

Ala Phe Ala Ala Arg Glu Ile Ser Leu Leu Asn Pro Leu Trp Ile His
        195                 200                 205

Ser Arg Val Ser Ser Lys Pro Phe Tyr Ala Ile Leu His Arg Ile Asp
    210                 215                 220

Val Gly Val Val Ile Asp Leu Glu Pro Ala Arg Thr Glu Asp Pro Ala
225                 230                 235                 240

Leu Ser Ile Ala Gly Ala Val Gln Ser Gln Lys Leu Ala Val Arg Ala
                245                 250                 255

Ile Ser Arg Leu Gln Ala Leu Pro Gly Gly Asp Ile Lys Leu Leu Cys
            260                 265                 270

Asp Thr Val Val Glu His Val Arg Glu Leu Thr Gly Tyr Asp Arg Val
        275                 280                 285
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Met Val Tyr Arg Phe His Glu Asp Glu His Gly Glu Val Val Ala Glu
    290                 295                 300

Ser Arg Arg Asp Asn Leu Glu Pro Tyr Leu Gly Leu His Tyr Pro Ala
305                 310                 315                 320

Thr Asp Ile Pro Gln Ala Ser Arg Phe Leu Phe Arg Gln Asn Arg Val
                325                 330                 335

Arg Met Ile Ala Asp Cys His Ala Thr Pro Val Arg Val Ile Gln Asp
            340                 345                 350

Pro Gly Met Ser Gln Pro Leu Cys Leu Val Gly Ser Thr Leu Arg Ala
        355                 360                 365

Pro His Gly Cys His Ala Gln Tyr Met Ala Asn Met Gly Ser Ile Ala
    370                 375                 380

Ser Leu Val Met Ala Val Ile Ile Ser Ser Gly Gly Asp Asp Glu Gln
385                 390                 395                 400

Thr Gly Arg Gly Gly Ile Ser Ser Ala Met Lys Leu Trp Gly Leu Val
                405                 410                 415

Val Cys His His Thr Ser Pro Arg Cys Ile Pro Phe Pro Leu Arg Tyr
            420                 425                 430

Ala Cys Glu Phe Leu Met Gln Ala Phe Gly Leu Gln Leu Asn Met Glu
        435                 440                 445

Leu Gln Leu Ala His Gln Leu Ser Glu Lys His Ile Leu Arg Thr Gln
    450                 455                 460

Thr Leu Leu Cys Asp Met Leu Leu Arg Asp Ser Pro Thr Gly Ile Val
465                 470                 475                 480

Thr Gln Ser Pro Ser Ile Met Asp Leu Val Lys Cys Asp Gly Ala Ala
                485                 490                 495

Leu Tyr Tyr His Gly Lys Tyr Tyr Pro Leu Gly Val Thr Pro Thr Glu
            500                 505                 510

Ser Gln Ile Lys Asp Ile Ile Glu Trp Leu Thr Val Cys His Gly Asp
        515                 520                 525

Ser Thr Gly Leu Ser Thr Asp Ser Leu Ala Asp Ala Gly Tyr Leu Gly
    530                 535                 540

Ala Ala Ala Leu Gly Asp Ala Val Cys Gly Met Ala Val Ala Tyr Ile
545                 550                 555                 560

Thr Pro Ser Asp Tyr Leu Phe Trp Phe Arg Ser His Thr Ala Lys Glu
                565                 570                 575

Ile Lys Trp Gly Gly Ala Lys His His Pro Glu Asp Lys Asp Asp Gly
            580                 585                 590

Gln Arg Met His Pro Arg Ser Ser Phe Lys Ala Phe Leu Glu Val Val
        595                 600                 605

Lys Ser Arg Ser Leu Pro Trp Glu Asn Ala Glu Met Asp Ala Ile His
    610                 615                 620

Ser Leu Gln Leu Ile Leu Arg Asp Ser Phe Arg Asp Ala Ala Glu Gly
625                 630                 635                 640

Thr Ser Asn Ser Lys Ala Ile Val Asn Gly Gln Ala Gln Leu Gly Glu
                645                 650                 655

Leu Glu Leu Arg Gly Ile Asn Glu Leu Ser Ser Val Pro Arg Glu Met
            660                 665                 670

Val Arg Leu Ile Glu Thr Ala Thr Val Pro Ile Phe Ala Val Asp Thr
        675                 680                 685

Asp Gly Cys Ile Asn Gly Trp Asn Ala Lys Ile Ala Glu Leu Thr Gly
    690                 695                 700

Leu Ser Val Glu Glu Ala Met Gly Lys Ser Leu Val Asn Asp Leu Ile
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705                 710                 715                 720

Phe Lys Glu Ser Glu Glu Ile Val Glu Lys Leu Leu Ser Arg Ala Leu
                725                 730                 735

Arg Gly Glu Glu Asp Lys Asn Val Glu Ile Lys Leu Lys Thr Phe Gly
            740                 745                 750

Ser Glu Gln Ser Asn Gly Ala Ile Phe Val Ile Val Asn Ala Cys Ser
        755                 760                 765

Ser Arg Asp Tyr Thr Gln Asn Ile Val Gly Val Cys Phe Val Gly Gln
    770                 775                 780

Asp Val Thr Gly Gln Lys Val Val Met Asp Lys Phe Ile Asn Ile Gln
785                 790                 795                 800

Gly Asp Tyr Lys Ala Ile Val His Asn Pro Asn Pro Leu Ile Pro Pro
                805                 810                 815

Ile Phe Ala Ser Asp Glu Asn Thr Ser Cys Ser Glu Trp Asn Thr Ala
            820                 825                 830

Met Glu Lys Leu Thr Gly Trp Ser Arg Gly Glu Val Val Gly Lys Phe
        835                 840                 845

Leu Ile Gly Glu Val Phe Gly Ser Phe Cys Arg Leu Lys Gly Pro Asp
    850                 855                 860

Ala Leu Thr Lys Phe Met Val Val Ile His Asn Ala Ile Gly Gly Gln
865                 870                 875                 880

Asp Tyr Glu Lys Phe Pro Phe Ser Phe Phe Asp Lys Asn Gly Lys Tyr
                885                 890                 895

Val Gln Ala Leu Leu Thr Ala Asn Thr Arg Ser Lys Met Asp Gly Lys
            900                 905                 910

Ser Ile Gly Ala Phe Cys Phe Leu Gln Ile Ala Ser Ala Glu Ile Gln
        915                 920                 925

Gln Ala Phe Glu Ile Gln Arg Gln Gln Glu Lys Lys Cys Tyr Ala Arg
    930                 935                 940

Met Lys Glu Leu Ala Tyr Ile Cys Gln Glu Ile Lys Asn Pro Leu Ser
945                 950                 955                 960

Gly Ile Arg Phe Thr Asn Ser Leu Leu Gln Met Thr Asp Leu Asn Asp
                965                 970                 975

Asp Gln Arg Gln Phe Leu Glu Thr Cys Ser Ala Cys Glu Lys Gln Met
            980                 985                 990

Ser Lys Ile Val Lys Asp Ala Thr  Leu Gln Ser Ile Glu  Asp Gly Ser
        995                 1000                1005

Leu Val  Leu Glu Lys Ser Glu  Phe Ser Phe Gly Asp  Val Met Asn
    1010                1015                1020

Ala Val  Val Ser Gln Ala Met  Leu Leu Leu Arg Glu  Arg Asp Leu
    1025                1030                1035

Gln Leu  Ile Arg Asp Ile Pro  Asp Glu Ile Lys Asp  Ala Ser Ala
    1040                1045                1050

Tyr Gly  Asp Gln Phe Arg Ile  Gln Gln Val Leu Ala  Asp Phe Leu
    1055                1060                1065

Leu Ser  Met Val Arg Ser Ala  Pro Ser Glu Asn Gly  Trp Val Glu
    1070                1075                1080

Ile Gln  Val Arg Pro Asn Val  Lys Gln Asn Ser Asp  Gly Thr Asp
    1085                1090                1095

Thr Glu  Leu Phe Ile Phe Arg  Phe Ala Cys Pro Gly  Glu Gly Leu
    1100                1105                1110

Pro Ala  Asp Ile Val Gln Asp  Met Phe Ser Asn Ser  Gln Trp Ser
    1115                1120                1125
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Thr Gln  Glu Gly Val Gly Leu  Ser Thr Cys Arg Lys  Ile Leu Lys
    1130                1135                1140

Leu Met  Gly Gly Glu Val Gln  Tyr Ile Arg Glu Ser  Glu Arg Ser
    1145                1150                1155

Phe Phe  Leu Ile Val Leu Glu  Leu Pro Gln Pro Arg  Pro Ala Ala
    1160                1165                1170

Asp Arg  Glu Ile Ser
    1175


<210> SEQ ID NO 5
<211> LENGTH: 1137
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 5

Met Ala Ser Ala Ser Gly Ala Ala Asn Ser Ser Val Pro Pro Pro Gln
1               5                   10                  15

Ile His Thr Ser Arg Thr Lys Leu Ser His His Ser Ser Asn Asn Asn
            20                  25                  30

Asn Asn Ile Asp Ser Met Ser Lys Ala Ile Ala Gln Tyr Thr Glu Asp
        35                  40                  45

Ala Arg Leu His Ala Val Phe Glu Gln Ser Gly Glu Ser Gly Arg Ser
    50                  55                  60

Phe Asn Tyr Ser Glu Ser Ile Arg Ile Ala Ser Glu Ser Val Pro Glu
65                  70                  75                  80

Gln Gln Ile Thr Ala Tyr Leu Val Lys Ile Gln Arg Gly Gly Phe Ile
                85                  90                  95

Gln Pro Phe Gly Ser Met Ile Ala Val Asp Glu Pro Ser Phe Arg Ile
            100                 105                 110

Leu Gly Tyr Ser Asp Asn Ala Arg Asp Met Leu Gly Ile Thr Pro Gln
        115                 120                 125

Ser Val Pro Ser Leu Asp Asp Lys Asn Asp Ala Ala Phe Ala Leu Gly
    130                 135                 140

Thr Asp Val Arg Ala Leu Phe Thr His Ser Ser Ala Leu Leu Leu Glu
145                 150                 155                 160

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

His Ser Arg Thr Ser Gly Lys Pro Phe Tyr Gly Ile Leu His Arg Ile
            180                 185                 190

Asp Val Gly Ile Val Ile Asp Leu Glu Pro Ala Arg Thr Glu Asp Pro
        195                 200                 205

Ala Leu Ser Ile Ala Gly Ala Val Gln Ser Gln Lys Leu Ala Val Arg
    210                 215                 220

Ala Ile Ser Gln Leu Gln Ser Leu Pro Gly Gly Asp Val Lys Leu Leu
225                 230                 235                 240

Cys Asp Thr Val Val Glu Ser Val Arg Glu Leu Thr Gly Tyr Asp Arg
                245                 250                 255

Val Met Val Tyr Lys Phe His Glu Asp Glu His Gly Glu Val Val Ser
            260                 265                 270

Glu Ser Lys Arg Pro Asp Leu Glu Pro Tyr Ile Gly Leu His Tyr Pro
        275                 280                 285

Ala Thr Asp Ile Pro Gln Ala Ser Arg Phe Leu Phe Lys Gln Asn Arg
    290                 295                 300

Val Arg Met Ile Val Asp Cys His Ala Ser Ala Val Arg Val Val Gln
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305                 310                 315                 320

Asp Glu Ala Leu Val Gln Pro Leu Cys Leu Val Gly Ser Thr Leu Arg
                325                 330                 335

Ala Pro His Gly Cys His Ala Gln Tyr Met Ala Asn Met Gly Ser Ile
            340                 345                 350

Ala Ser Leu Val Met Ala Val Ile Ile Asn Gly Asn Asp Glu Glu Gly
        355                 360                 365

Val Gly Gly Arg Ser Ser Met Arg Leu Trp Gly Leu Val Val Cys His
    370                 375                 380

His Thr Ser Ala Arg Cys Ile Pro Phe Pro Leu Arg Tyr Ala Cys Glu
385                 390                 395                 400

Phe Leu Met Gln Ala Phe Gly Leu Gln Leu Asn Met Glu Leu Gln Leu
                405                 410                 415

Ala Ala Gln Ser Leu Glu Lys Arg Val Leu Arg Thr Gln Thr Leu Leu
            420                 425                 430

Cys Asp Met Leu Leu Arg Asp Ser Pro Thr Gly Ile Val Thr Gln Ser
        435                 440                 445

Pro Ser Ile Met Asp Leu Val Lys Cys Asp Gly Ala Ala Leu Tyr Phe
    450                 455                 460

Gln Gly Asn Tyr Tyr Pro Leu Gly Val Thr Pro Thr Glu Ala Gln Ile
465                 470                 475                 480

Arg Asp Ile Ile Glu Trp Leu Leu Ala Phe His Gly Asp Ser Thr Gly
                485                 490                 495

Leu Ser Thr Asp Ser Leu Gly Asp Ala Gly Tyr Pro Gly Ala Ala Ser
            500                 505                 510

Leu Gly Asp Ala Val Cys Gly Met Ala Val Ala Tyr Ile Thr Glu Lys
        515                 520                 525

Asp Phe Leu Phe Trp Phe Arg Ser His Thr Ala Lys Glu Ile Lys Trp
    530                 535                 540

Gly Gly Ala Lys His His Pro Glu Asp Lys Asp Asp Gly Gln Arg Met
545                 550                 555                 560

His Pro Arg Ser Ser Phe Lys Ala Phe Leu Glu Val Val Lys Ser Arg
                565                 570                 575

Ser Leu Pro Trp Glu Asn Ala Glu Met Asp Ala Ile His Ser Leu Gln
            580                 585                 590

Leu Ile Leu Arg Asp Ser Phe Lys Asp Ala Glu His Arg Asn Ser Lys
        595                 600                 605

Ala Val Val Asp Pro His Val Ser Glu Gln Glu Leu Gln Gly Val Asp
    610                 615                 620

Glu Leu Ser Ser Val Ala Arg Glu Met Val Arg Leu Ile Glu Thr Ala
625                 630                 635                 640

Thr Ala Pro Ile Phe Ala Val Asp Val Asp Gly His Val Asn Gly Trp
                645                 650                 655

Asn Ala Lys Val Ser Glu Leu Thr Gly Leu Pro Val Glu Glu Ala Met
            660                 665                 670

Gly Lys Ser Leu Val His Asp Leu Val Phe Lys Glu Ser Glu Glu Thr
        675                 680                 685

Met Asn Lys Leu Leu Ser Arg Ala Leu Lys Gly Glu Glu Asp Lys Asn
    690                 695                 700

Val Glu Ile Lys Met Arg Thr Phe Gly Pro Glu His Gln Asn Lys Ala
705                 710                 715                 720

Val Phe Leu Val Val Asn Ala Cys Ser Ser Lys Asp Phe Thr Asn Asn
                725                 730                 735
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Val Val Gly Val Cys Phe Val Gly Gln Asp Val Thr Gly Gln Lys Ile
            740                 745                 750

Val Met Asp Lys Phe Ile Asn Ile Gln Gly Asp Tyr Lys Ala Ile Val
        755                 760                 765

His Ser Pro Asn Pro Leu Ile Pro Pro Ile Phe Ala Ser Asp Asp Asn
    770                 775                 780

Thr Cys Cys Leu Glu Trp Asn Thr Ala Met Glu Lys Leu Thr Gly Trp
785                 790                 795                 800

Gly Arg Val Asp Val Ile Gly Lys Met Leu Val Gly Glu Val Phe Gly
                805                 810                 815

Ser Cys Cys Gln Leu Lys Gly Ser Asp Ser Ile Thr Lys Phe Met Ile
            820                 825                 830

Val Leu His Asn Ala Leu Gly Gly Gln Asp Thr Asp Lys Phe Pro Phe
        835                 840                 845

Ser Phe Leu Asp Arg His Gly Lys Tyr Val Gln Thr Phe Leu Thr Ala
    850                 855                 860

Asn Lys Arg Val Asn Met Glu Gly Gln Ile Ile Gly Ala Phe Cys Phe
865                 870                 875                 880

Leu Gln Ile Met Ser Pro Glu Leu Gln Gln Ala Leu Lys Ala Gln Arg
                885                 890                 895

Gln Gln Glu Lys Asn Ser Phe Gly Arg Met Lys Glu Leu Ala Tyr Ile
            900                 905                 910

Cys Gln Gly Val Lys Asn Pro Leu Ser Gly Ile Arg Phe Thr Asn Ser
        915                 920                 925

Leu Leu Glu Ala Thr Ser Leu Thr Asn Glu Gln Lys Gln Phe Leu Glu
    930                 935                 940

Thr Ser Val Ala Cys Glu Lys Gln Met Leu Lys Ile Ile Arg Asp Val
945                 950                 955                 960

Asp Leu Glu Ser Ile Glu Asp Gly Ser Leu Glu Leu Glu Lys Gly Glu
                965                 970                 975

Phe Leu Leu Gly Asn Val Ile Asn Ala Val Val Ser Gln Val Met Leu
            980                 985                 990

Leu Leu Arg Glu Arg Asn Leu Gln  Leu Ile Arg Asp Ile  Pro Glu Glu
        995                 1000                1005

Ile Lys  Thr Leu Ala Val Tyr  Gly Asp Gln Leu Arg  Ile Gln Gln
    1010                1015                1020

Val Leu  Ser Asp Phe Leu Leu  Asn Ile Val Arg Tyr  Ala Pro Ser
    1025                1030                1035

Pro Asp  Gly Trp Val Glu Ile  His Val Arg Pro Arg  Ile Lys Gln
    1040                1045                1050

Ile Ser  Asp Gly Leu Thr Leu  Leu His Ala Glu Phe  Arg Met Val
    1055                1060                1065

Cys Pro  Gly Glu Gly Leu Pro  Pro Glu Leu Ile Gln  Asp Met Phe
    1070                1075                1080

Asn Asn  Ser Arg Trp Gly Thr  Gln Glu Gly Leu Gly  Leu Ser Met
    1085                1090                1095

Ser Arg  Lys Ile Leu Lys Leu  Met Asn Gly Glu Val  Gln Tyr Ile
    1100                1105                1110

Arg Glu  Ala Glu Arg Cys Tyr  Phe Tyr Val Leu Leu  Glu Leu Pro
    1115                1120                1125

Val Thr  Arg Arg Ser Ser Lys  Lys Cys
    1130                1135
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<210> SEQ ID NO 6
<211> LENGTH: 1149
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 6

Met Ala Ser Ala Ser Gly Ala Glu Asn Ser Ser Val Pro Pro Ser Pro
1 5 10 15

Leu Pro Pro Pro Pro Pro Pro Gln Ile His Thr Ser Arg Thr Lys Leu
20 25 30

Ser His His His His Asn Asn Asn Asn Asn Asn Asn Asn Asn Ile Asp
35 40 45

Ser Thr Ser Lys Ala Ile Ala Gln Tyr Thr Glu Asp Ala Arg Leu His
50 55 60

Ala Val Phe Glu Gln Ser Gly Glu Ser Gly Arg Ser Phe Asp Tyr Ser
65 70 75 80

Gln Ser Ile Arg Val Thr Ser Glu Ser Val Pro Glu Gln Gln Ile Thr
85 90 95

Ala Tyr Leu Leu Lys Ile Gln Arg Gly Gly Phe Ile Gln Pro Phe Gly
100 105 110

Ser Met Ile Ala Val Asp Glu Pro Ser Phe Arg Ile Leu Ala Tyr Ser
115 120 125

Asp Asn Ala Arg Asp Met Leu Gly Ile Thr Pro Gln Ser Val Pro Ser
130 135 140

Leu Asp Asp Lys Asn Asp Ala Ala Phe Ala Leu Gly Thr Asp Ile Arg
145 150 155 160

Thr Leu Phe Thr His Ser Ser Ala Val Leu Leu Glu Lys Ala Phe Ser
165 170 175

Ala Arg Glu Ile Ser Leu Met Asn Pro Ile Trp Ile His Ser Arg Thr
180 185 190

Ser Gly Lys Pro Phe Tyr Gly Ile Leu His Arg Ile Asp Val Gly Ile
195 200 205

Val Ile Asp Leu Glu Pro Ala Arg Thr Glu Asp Pro Ala Leu Ser Ile
210 215 220

Ala Gly Ala Val Gln Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Gln
225 230 235 240

Leu Gln Ser Leu Pro Gly Gly Asp Val Lys Leu Leu Cys Asp Thr Val
245 250 255

Val Glu Ser Val Arg Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr
260 265 270

Arg Phe His Glu Asp Glu His Gly Glu Val Val Ala Glu Thr Lys Arg
275 280 285

Pro Asp Leu Glu Pro Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile
290 295 300

Pro Gln Ala Ser Arg Phe Leu Phe Lys Gln Asn Arg Val Arg Met Ile
305 310 315 320

Val Asp Cys His Ala Ser Ala Val Arg Val Val Gln Asp Glu Ala Leu
325 330 335

Val Gln Pro Leu Cys Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly
340 345 350

Cys His Ala Gln Tyr Met Ala Asn Met Gly Ser Thr Ala Ser Leu Val
355 360 365

Met Ala Val Ile Ile Asn Gly Asn Asp Glu Glu Gly Val Gly Gly Arg
370 375 380

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```
Thr Ser Met Arg Leu Trp Gly Leu Val Ile Cys His His Thr Ser Ala
385                 390                 395                 400

Arg Cys Ile Pro Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln
                405                 410                 415

Ala Phe Gly Leu Gln Leu Asn Met Glu Leu Gln Leu Ala Ala Gln Ser
            420                 425                 430

Leu Glu Lys Arg Val Leu Arg Thr Gln Thr Leu Leu Cys Asp Met Leu
        435                 440                 445

Leu Arg Asp Ser Pro Thr Gly Ile Val Thr Gln Ser Pro Ser Ile Met
    450                 455                 460

Asp Leu Val Lys Cys Asp Gly Ala Ala Leu Tyr Tyr Gln Gly Asn Tyr
465                 470                 475                 480

Tyr Pro Leu Gly Val Thr Pro Thr Glu Ala Gln Ile Arg Asp Ile Ile
                485                 490                 495

Glu Trp Leu Leu Ala Phe His Arg Asp Ser Thr Gly Leu Ser Thr Asp
            500                 505                 510

Ser Leu Ala Asp Ala Gly Tyr Pro Gly Ala Ala Ser Leu Gly Asp Ala
        515                 520                 525

Val Cys Gly Met Ala Val Ala Tyr Ile Thr Glu Lys Asp Phe Leu Phe
    530                 535                 540

Trp Phe Arg Ser His Thr Ala Lys Glu Ile Lys Trp Gly Gly Ala Lys
545                 550                 555                 560

His His Pro Glu Asp Lys Asp Asp Gly Gln Arg Met His Pro Arg Ser
                565                 570                 575

Ser Phe Lys Ala Phe Leu Glu Val Val Lys Ser Arg Ser Leu Pro Trp
            580                 585                 590

Glu Asn Ala Glu Met Asp Ala Ile His Ser Leu Gln Leu Ile Leu Arg
        595                 600                 605

Asp Ser Phe Lys Asp Ala Glu His Ser Asn Ser Lys Ala Val Leu Asp
    610                 615                 620

Pro Arg Met Ser Glu Leu Glu Leu Gln Gly Val Asp Glu Leu Ser Ser
625                 630                 635                 640

Val Ala Arg Glu Met Val Arg Leu Ile Glu Thr Ala Thr Ala Pro Ile
                645                 650                 655

Phe Ala Val Asp Val Asp Gly Arg Ile Asn Gly Trp Asn Ala Lys Val
            660                 665                 670

Ser Glu Leu Thr Gly Leu Pro Val Glu Glu Ala Met Gly Lys Ser Leu
        675                 680                 685

Val Arg Asp Leu Val Phe Lys Glu Ser Glu Glu Thr Val Asp Lys Leu
    690                 695                 700

Leu Ser Arg Ala Leu Lys Gly Glu Glu Asp Lys Asn Val Glu Ile Lys
705                 710                 715                 720

Met Arg Thr Phe Gly Pro Glu His Gln Asn Lys Ala Val Phe Val Val
                725                 730                 735

Val Asn Ala Cys Ser Ser Lys Asp Tyr Thr Asn Asn Val Val Gly Val
            740                 745                 750

Cys Phe Val Gly Gln Asp Val Thr Gly Gln Lys Ile Val Met Asp Lys
        755                 760                 765

Phe Ile Asn Ile Gln Gly Asp Tyr Lys Ala Ile Val His Asn Pro Asn
    770                 775                 780

Pro Leu Ile Pro Pro Ile Phe Ala Ser Asp Asp Asn Thr Cys Cys Leu
785                 790                 795                 800
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Glu Trp Asn Thr Ala Met Glu Lys Leu Thr Gly Trp Ser Arg Ala Asp
                805                 810                 815

Val Ile Gly Lys Met Leu Val Gly Glu Val Phe Gly Ser Cys Cys Gln
            820                 825                 830

Leu Lys Gly Ser Asp Ser Ile Thr Lys Phe Met Ile Val Leu His Asn
        835                 840                 845

Ala Leu Gly Gly His Asp Thr Asp Arg Phe Pro Phe Ser Phe Leu Asp
    850                 855                 860

Arg Tyr Gly Lys His Val Gln Ala Phe Leu Thr Ala Asn Lys Arg Val
865                 870                 875                 880

Asn Met Asp Gly Gln Ile Ile Gly Ala Phe Cys Phe Leu Gln Ile Val
                885                 890                 895

Ser Pro Glu Leu Gln Gln Ala Leu Lys Ala Gln Arg Gln Gln Glu Lys
            900                 905                 910

Asn Ser Phe Ala Arg Met Lys Glu Leu Ala Tyr Ile Cys Gln Gly Val
        915                 920                 925

Lys Asn Pro Leu Ser Gly Ile Arg Phe Thr Asn Ser Leu Leu Glu Ala
    930                 935                 940

Thr Cys Leu Ser Asn Glu Gln Lys Gln Phe Leu Glu Thr Ser Ala Ala
945                 950                 955                 960

Cys Glu Lys Gln Met Leu Lys Ile Ile His Asp Val Asp Ile Glu Ser
                965                 970                 975

Ile Glu Asp Gly Ser Leu Glu Leu Glu Lys Gly Glu Phe Leu Leu Gly
            980                 985                 990

Asn Val Ile Asn Ala Val Val Ser  Gln Val Met Leu Leu  Leu Arg Glu
        995                 1000                1005

Arg Asn  Leu Gln Leu Ile Arg  Asp Ile Pro Glu Glu  Ile Lys Thr
    1010                1015                1020

Leu Ala  Val Tyr Gly Asp Gln  Leu Arg Ile Gln Gln  Val Leu Ser
    1025                1030                1035

Asp Phe  Leu Leu Asn Ile Val  Arg Tyr Ala Pro Ser  Pro Asp Gly
    1040                1045                1050

Trp Val  Glu Ile His Val His  Pro Arg Ile Lys Gln  Ile Ser Asp
    1055                1060                1065

Gly Leu  Thr Leu Leu His Ala  Glu Phe Arg Met Val  Cys Pro Gly
    1070                1075                1080

Glu Gly  Leu Pro Pro Glu Leu  Ile Gln Asn Met Phe  Asn Asn Ser
    1085                1090                1095

Gly Trp  Gly Thr Gln Glu Gly  Leu Gly Leu Ser Met  Ser Arg Lys
    1100                1105                1110

Ile Leu  Lys Leu Met Asn Gly  Glu Val Gln Tyr Ile  Arg Glu Ala
    1115                1120                1125

Gln Arg  Cys Tyr Phe Tyr Val  Leu Leu Glu Leu Pro  Val Thr Arg
    1130                1135                1140

Arg Ser  Ser Lys Lys Cys
    1145


<210> SEQ ID NO 7
<211> LENGTH: 1100
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 7

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

Ser Ile Arg Ile Ala Ser Glu Ser Val Pro Glu Gln Gln Ile Thr Ala
        35                  40                  45

Tyr Leu Val Lys Ile Gln Arg Gly Gly Phe Ile Gln Pro Phe Gly Ser
    50                  55                  60

Met Ile Ala Val Asp Glu Pro Ser Phe Arg Ile Leu Gly Tyr Ser Asp
65                  70                  75                  80

Asn Ala Arg Asp Met Leu Gly Ile Thr Pro Gln Ser Val Pro Ser Leu
                85                  90                  95

Asp Asp Lys Asn Asp Ala Ala Phe Ala Leu Gly Thr Asp Val Arg Ala
            100                 105                 110

Leu Phe Thr His Ser Ser Ala Leu Leu Leu Glu Lys Ala Phe Ser Ala
        115                 120                 125

Arg Glu Ile Ser Leu Met Asn Pro Ile Trp Ile His Ser Arg Thr Ser
    130                 135                 140

Gly Lys Pro Phe Tyr Gly Ile Leu His Arg Ile Asp Val Gly Ile Val
145                 150                 155                 160

Ile Asp Leu Glu Pro Ala Arg Thr Glu Asp Pro Ala Leu Ser Ile Ala
                165                 170                 175

Gly Ala Val Gln Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Gln Leu
            180                 185                 190

Gln Ser Leu Pro Gly Gly Asp Val Lys Leu Leu Cys Asp Thr Val Val
        195                 200                 205

Glu Ser Val Arg Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Lys
    210                 215                 220

Phe His Glu Asp Glu His Gly Glu Val Val Ser Glu Ser Lys Arg Pro
225                 230                 235                 240

Asp Leu Glu Pro Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro
                245                 250                 255

Gln Ala Ser Arg Phe Leu Phe Lys Gln Asn Arg Val Arg Met Ile Val
            260                 265                 270

Asp Cys His Ala Ser Ala Val Arg Val Val Gln Asp Glu Ala Leu Val
        275                 280                 285

Gln Pro Leu Cys Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys
    290                 295                 300

His Ala Gln Tyr Met Ala Asn Met Gly Ser Ile Ala Ser Leu Val Met
305                 310                 315                 320

Ala Val Ile Ile Asn Gly Asn Asp Glu Glu Gly Val Gly Gly Arg Ser
                325                 330                 335

Ser Met Arg Leu Trp Gly Leu Val Val Cys His His Thr Ser Ala Arg
            340                 345                 350

Cys Ile Pro Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala
        355                 360                 365

Phe Gly Leu Gln Leu Asn Met Glu Leu Gln Leu Ala Ala Gln Ser Leu
    370                 375                 380

Glu Lys Arg Val Leu Arg Thr Gln Thr Leu Leu Cys Asp Met Leu Leu
385                 390                 395                 400

Arg Asp Ser Pro Thr Gly Ile Val Thr Gln Ser Pro Ser Ile Met Asp
                405                 410                 415

Leu Val Lys Cys Asp Gly Ala Ala Leu Tyr Phe Gln Gly Asn Tyr Tyr
            420                 425                 430
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Pro Leu Gly Val Thr Pro Thr Glu Ala Gln Ile Arg Asp Ile Ile Glu
        435                 440                 445

Trp Leu Leu Ala Phe His Gly Asp Ser Thr Gly Leu Ser Thr Asp Ser
    450                 455                 460

Leu Gly Asp Ala Gly Tyr Pro Gly Ala Ala Ser Leu Gly Asp Ala Val
465                 470                 475                 480

Cys Gly Met Ala Val Ala Tyr Ile Thr Glu Lys Asp Phe Leu Phe Trp
                485                 490                 495

Phe Arg Ser His Thr Ala Lys Glu Ile Lys Trp Gly Gly Ala Lys His
            500                 505                 510

His Pro Glu Asp Lys Asp Asp Gly Gln Arg Met His Pro Arg Ser Ser
        515                 520                 525

Phe Lys Ala Phe Leu Glu Val Val Lys Ser Arg Ser Leu Pro Trp Glu
    530                 535                 540

Asn Ala Glu Met Asp Ala Ile His Ser Leu Gln Leu Ile Leu Arg Asp
545                 550                 555                 560

Ser Phe Lys Asp Ala Glu His Arg Asn Ser Lys Ala Val Ala Asp Pro
                565                 570                 575

Arg Val Ser Glu Gln Glu Leu Gln Gly Val Asp Glu Leu Ser Ser Val
            580                 585                 590

Ala Arg Glu Met Val Arg Leu Ile Glu Thr Ala Thr Ala Pro Ile Phe
        595                 600                 605

Ala Val Asp Val Asp Gly His Val Asn Gly Trp Asn Ala Lys Val Ser
    610                 615                 620

Glu Leu Thr Gly Leu Pro Val Glu Glu Ala Met Gly Lys Ser Leu Val
625                 630                 635                 640

His Asp Leu Val Phe Lys Glu Ser Glu Glu Thr Met Asn Lys Leu Leu
                645                 650                 655

Ser Arg Ala Leu Lys Gly Glu Glu Asp Lys Asn Val Glu Ile Lys Met
            660                 665                 670

Arg Thr Phe Gly Pro Glu Arg Gln Asn Lys Ala Val Phe Leu Val Val
        675                 680                 685

Asn Ala Cys Ser Ser Lys Asp Phe Thr Asn Asn Val Val Gly Val Cys
    690                 695                 700

Phe Val Gly Gln Asp Val Thr Gly Gln Lys Ile Val Met Asp Lys Phe
705                 710                 715                 720

Ile Asn Ile Gln Gly Asp Tyr Lys Ala Ile Val His Ser Pro Asn Pro
                725                 730                 735

Leu Ile Pro Pro Ile Phe Ala Ser Asp Asp Asn Thr Cys Cys Leu Glu
            740                 745                 750

Trp Asn Thr Ala Met Glu Lys Leu Thr Gly Trp Gly Arg Val Asp Val
        755                 760                 765

Ile Gly Lys Met Leu Val Gly Glu Val Phe Gly Ser Cys Cys Gln Leu
    770                 775                 780

Lys Gly Ser Asp Ser Ile Thr Lys Phe Met Ile Val Leu His Asn Ala
785                 790                 795                 800

Leu Gly Gly Gln Asp Thr Asp Lys Phe Pro Phe Ser Phe Leu Asp Arg
                805                 810                 815

His Gly Lys Tyr Val Gln Thr Phe Leu Thr Ala Asn Lys Arg Val Asn
            820                 825                 830

Met Glu Gly Gln Ile Ile Gly Ala Phe Cys Phe Leu Gln Ile Met Ser
        835                 840                 845

Pro Glu Leu Gln Gln Ala Leu Lys Ala Gln Arg Gln Gln Glu Lys Asn
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    850                 855                 860

Ser Phe Gly Arg Met Lys Glu Leu Ala Tyr Ile Cys Gln Gly Val Lys
865                 870                 875                 880

Asn Pro Leu Ser Gly Ile Arg Phe Thr Asn Ser Leu Leu Glu Ala Thr
                885                 890                 895

Ser Leu Thr Asn Glu Gln Lys Gln Phe Leu Glu Thr Ser Val Ala Cys
            900                 905                 910

Glu Lys Gln Met Leu Lys Ile Ile Arg Asp Val Asp Leu Glu Ser Ile
        915                 920                 925

Glu Asp Gly Ser Leu Glu Leu Glu Lys Gly Glu Phe Leu Leu Gly Asn
    930                 935                 940

Val Ile Asn Ala Val Val Ser Gln Val Met Leu Leu Leu Arg Glu Arg
945                 950                 955                 960

Asn Leu Gln Leu Ile Arg Asp Ile Pro Glu Glu Ile Lys Thr Leu Ala
                965                 970                 975

Val Tyr Gly Asp Gln Leu Arg Ile Gln Gln Val Leu Ser Asp Phe Leu
            980                 985                 990

Leu Asn Ile Val Arg Tyr Ala Pro  Ser Pro Asp Gly Trp  Val Glu Ile
        995                 1000                1005

His Val  Arg Pro Arg Ile Lys  Gln Ile Ser Asp Gly  Leu Thr Leu
    1010                1015                1020

Leu His  Ala Glu Phe Arg Met  Val Cys Pro Gly Glu  Gly Leu Pro
    1025                1030                1035

Pro Glu  Leu Ile Gln Asp Met  Phe Asn Asn Ser Arg  Trp Gly Thr
    1040                1045                1050

Gln Glu  Gly Leu Gly Leu Ser  Met Ser Arg Lys Ile  Leu Lys Leu
    1055                1060                1065

Met Asn  Gly Glu Val Gln Tyr  Ile Arg Glu Ala Glu  Arg Cys Tyr
    1070                1075                1080

Phe Tyr  Val Leu Leu Glu Leu  Pro Val Thr Arg Arg  Ser Ser Lys
    1085                1090                1095

Lys Cys
    1100


<210> SEQ ID NO 8
<211> LENGTH: 867
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 8

Met Ile Ala Val Asp Glu Pro Ser Phe Arg Ile Leu Ala Tyr Ser Asp
1               5                   10                  15

Asn Ala Arg Asp Met Leu Gly Ile Thr Pro Gln Ser Val Pro Ser Leu
            20                  25                  30

Asp Asp Lys Asn Asp Ala Ala Phe Ala Leu Gly Thr Asp Ile Arg Thr
        35                  40                  45

Leu Phe Thr His Ser Ser Ala Val Leu Leu Glu Lys Ala Phe Ser Ala
    50                  55                  60

Arg Glu Ile Ser Leu Met Asn Pro Ile Trp Ile His Ser Arg Thr Ser
65                  70                  75                  80

Gly Lys Pro Phe Tyr Gly Ile Leu His Arg Ile Asp Val Gly Ile Val
                85                  90                  95

Ile Asp Leu Glu Pro Ala Arg Thr Glu Asp Pro Ala Leu Ser Ile Ala
            100                 105                 110
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Gly Ala Val Gln Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Gln Leu
        115                 120                 125

Gln Ser Leu Pro Gly Gly Asp Val Lys Leu Leu Cys Asp Thr Val Val
    130                 135                 140

Glu Ser Val Arg Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Arg
145                 150                 155                 160

Phe His Glu Asp Glu His Gly Glu Val Val Ala Glu Thr Lys Arg Pro
                165                 170                 175

Asp Leu Glu Pro Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro
            180                 185                 190

Gln Ala Ser Arg Phe Leu Phe Lys Gln Asn Arg Val Arg Met Ile Val
        195                 200                 205

Asp Cys His Ala Ser Ala Val Arg Val Val Gln Asp Glu Ala Leu Val
    210                 215                 220

Gln Pro Leu Cys Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys
225                 230                 235                 240

His Ala Gln Tyr Met Ala Asn Met Gly Ser Thr Ala Ser Leu Val Met
                245                 250                 255

Ala Val Ile Ile Asn Gly Asn Asp Glu Glu Gly Val Gly Gly Arg Thr
            260                 265                 270

Ser Met Arg Leu Trp Gly Leu Val Ile Cys His His Thr Ser Ala Arg
        275                 280                 285

Cys Ile Pro Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala
    290                 295                 300

Phe Gly Leu Gln Leu Asn Met Glu Leu Gln Leu Ala Ala Gln Ser Leu
305                 310                 315                 320

Glu Lys Arg Val Leu Arg Thr Gln Thr Leu Leu Cys Asp Met Leu Leu
                325                 330                 335

Arg Asp Ser Pro Thr Gly Ile Val Thr Gln Ser Pro Ser Ile Met Asp
            340                 345                 350

Leu Val Lys Cys Asp Gly Ala Ala Leu Tyr Tyr Gln Gly Asn Tyr Tyr
        355                 360                 365

Pro Leu Gly Val Thr Pro Thr Glu Ala Gln Ile Arg Asp Ile Ile Glu
    370                 375                 380

Trp Leu Leu Ala Phe His Arg Asp Ser Thr Gly Leu Ser Thr Asp Ser
385                 390                 395                 400

Leu Ala Asp Ala Gly Tyr Pro Gly Ala Ala Ser Leu Gly Asp Ala Val
                405                 410                 415

Cys Gly Met Ala Val Ala Tyr Ile Thr Glu Lys Asp Phe Leu Phe Trp
            420                 425                 430

Phe Arg Ser His Thr Ala Lys Glu Ile Lys Trp Gly Gly Ala Lys His
        435                 440                 445

His Pro Glu Asp Lys Asp Asp Gly Gln Arg Met His Pro Arg Ser Ser
    450                 455                 460

Phe Lys Ala Phe Leu Glu Val Val Lys Ser Arg Ser Leu Pro Trp Glu
465                 470                 475                 480

Ser Ala Glu Met Asp Ala Ile His Ser Leu Gln Leu Ile Leu Arg Asp
                485                 490                 495

Ser Phe Lys Asp Ala Glu His Ser Asn Ser Lys Ala Val Leu Asp Pro
            500                 505                 510

Arg Met Ser Glu Leu Glu Leu Gln Gly Val Asp Glu Leu Ser Ser Val
        515                 520                 525

Ala Arg Glu Met Val Arg Leu Ile Glu Thr Ala Thr Ala Pro Ile Phe
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    530                 535                 540

Ala Val Asp Val Asp Gly Arg Ile Asn Gly Trp Asn Ala Lys Val Ser
545                 550                 555                 560

Glu Leu Thr Gly Leu Pro Val Glu Glu Ala Met Gly Lys Ser Leu Val
                565                 570                 575

Arg Asp Leu Val Phe Lys Glu Ser Glu Glu Thr Val Asp Lys Leu Leu
            580                 585                 590

Ser Arg Ala Leu Lys Gly Glu Glu Asp Lys Asn Val Glu Ile Lys Met
        595                 600                 605

Arg Thr Phe Gly Pro Glu His Gln Asn Lys Ala Val Phe Val Val Val
    610                 615                 620

Asn Ala Cys Ser Ser Lys Asp Tyr Thr Asn Asn Val Val Gly Val Cys
625                 630                 635                 640

Phe Val Gly Gln Asp Val Thr Gly Gln Lys Ile Val Met Asp Lys Phe
                645                 650                 655

Ile Asn Ile Gln Gly Asp Tyr Lys Ala Ile Val His Asn Pro Asn Pro
            660                 665                 670

Leu Ile Pro Pro Ile Phe Ala Ser Asp Asp Asn Thr Cys Cys Leu Glu
        675                 680                 685

Trp Asn Thr Ala Met Glu Lys Leu Thr Gly Trp Ser Arg Ala Asp Val
    690                 695                 700

Ile Gly Lys Met Leu Val Gly Glu Val Phe Gly Ser Cys Cys Gln Leu
705                 710                 715                 720

Lys Gly Ser Asp Ser Ile Thr Lys Phe Met Ile Val Leu His Asn Ala
                725                 730                 735

Leu Gly Gly His Asp Thr Asp Arg Phe Pro Phe Ser Phe Leu Asp Arg
            740                 745                 750

Tyr Gly Lys His Val Gln Ala Phe Leu Thr Ala Asn Lys Arg Val Asn
        755                 760                 765

Met Asp Gly Gln Ile Ile Gly Ala Phe Cys Phe Leu Gln Ile Val Ser
    770                 775                 780

Pro Glu Leu Gln Gln Ala Leu Lys Ala Gln Arg Gln Gln Glu Lys Asn
785                 790                 795                 800

Ser Phe Ala Arg Met Lys Glu Leu Ala Tyr Ile Cys Gln Gly Val Lys
                805                 810                 815

Asn Pro Leu Ser Gly Ile Arg Phe Thr Asn Ser Leu Leu Glu Ala Thr
            820                 825                 830

Cys Leu Ser Asn Glu Gln Lys Gln Phe Leu Glu Thr Ser Ala Ala Cys
        835                 840                 845

Glu Lys Gln Met Leu Lys Ile Ile His Asp Val Asp Ile Glu Ser Ile
    850                 855                 860

Glu Asp Gly
865


<210> SEQ ID NO 9
<211> LENGTH: 1130
<212> TYPE: PRT
<213> ORGANISM: Solanum tuberosum

<400> SEQUENCE: 9

Met Ala Ser Gly Ser Arg Thr Lys His Ser His His Asn Ser Ser Gln
1               5                   10                  15

Ala Gln Ser Ser Gly Thr Ser Asn Val Asn Tyr Lys Asp Ser Ile Ser
            20                  25                  30
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```
Lys Ala Ile Ala Gln Tyr Thr Ala Asp Ala Arg Leu His Ala Val Phe
        35                  40                  45

Glu Gln Ser Gly Glu Ser Gly Lys Phe Phe Asp Tyr Ser Glu Ser Val
    50                  55                  60

Lys Thr Thr Thr Gln Ser Val Pro Glu Arg Gln Ile Thr Ala Tyr Leu
65                  70                  75                  80

Thr Lys Ile Gln Arg Gly Gly His Ile Gln Pro Phe Gly Cys Met Ile
                85                  90                  95

Ala Val Asp Glu Ala Ser Phe Arg Val Ile Ala Tyr Ser Glu Asn Ala
            100                 105                 110

Phe Glu Met Leu Ser Leu Thr Pro Gln Ser Val Pro Ser Leu Glu Lys
        115                 120                 125

Cys Glu Ile Leu Thr Ile Gly Thr Asp Val Arg Thr Leu Phe Thr Pro
    130                 135                 140

Ser Ser Ser Val Leu Leu Glu Arg Ala Phe Gly Ala Arg Glu Ile Thr
145                 150                 155                 160

Leu Leu Asn Pro Ile Trp Ile His Ser Lys Asn Ser Gly Lys Pro Phe
                165                 170                 175

Tyr Ala Ile Leu His Arg Val Asp Val Gly Ile Ala Ile Asp Leu Glu
            180                 185                 190

Pro Ala Arg Thr Glu Asp Pro Ala Leu Ser Ile Ala Gly Ala Val Gln
        195                 200                 205

Ser Gln Lys Leu Ala Val Arg Ala Ile Ser His Leu Gln Ser Leu Pro
    210                 215                 220

Gly Gly Asp Ile Lys Leu Leu Cys Asp Thr Val Val Glu Ser Val Arg
225                 230                 235                 240

Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Lys Phe His Glu Asp
                245                 250                 255

Glu His Gly Glu Val Val Ala Glu Ser Lys Arg Ser Asp Leu Glu Pro
            260                 265                 270

Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg
        275                 280                 285

Phe Leu Phe Lys Gln Asn Arg Val Arg Met Ile Val Asp Cys His Ala
    290                 295                 300

Thr Pro Val Arg Val Thr Gln Asp Glu Ser Leu Met Gln Pro Leu Cys
305                 310                 315                 320

Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ala Gln Tyr
                325                 330                 335

Met Ala Asn Met Gly Ser Ile Ala Ser Leu Thr Leu Ala Val Ile Ile
            340                 345                 350

Asn Gly Asn Asp Glu Glu Ala Val Gly Gly Gly Arg Asn Ser Met Arg
        355                 360                 365

Leu Trp Gly Leu Val Val Gly His His Thr Ser Val Arg Ser Ile Pro
    370                 375                 380

Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala Phe Gly Leu
385                 390                 395                 400

Gln Leu Asn Met Glu Leu Gln Leu Ala Ser Gln Leu Ser Glu Lys His
                405                 410                 415

Val Leu Arg Thr Gln Thr Leu Leu Cys Asp Met Leu Leu Arg Asp Ser
            420                 425                 430

Pro Pro Gly Ile Val Thr Gln Ser Pro Ser Ile Met Asp Leu Val Lys
        435                 440                 445

Cys Asp Gly Ala Ala Leu Tyr Tyr Gln Gly Lys Tyr Tyr Pro Leu Gly
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```
    450                 455                 460

Val Thr Pro Thr Glu Ala Gln Ile Lys Asp Ile Val Glu Trp Leu Leu
465                 470                 475                 480

Ala Tyr His Gly Asp Ser Thr Gly Leu Ser Thr Asp Ser Leu Ala Asp
                485                 490                 495

Ala Gly Tyr Pro Gly Ala Ala Ser Leu Gly Asp Ala Val Cys Gly Met
            500                 505                 510

Ala Val Ala Tyr Ile Ser Ser Lys Asp Phe Leu Phe Trp Phe Arg Ser
        515                 520                 525

His Thr Ala Lys Glu Ile Lys Trp Gly Gly Ala Lys His His Pro Glu
    530                 535                 540

Asp Lys Asp Asp Gly Leu Arg Met His Pro Arg Ser Ser Phe Lys Ala
545                 550                 555                 560

Phe Leu Glu Val Val Lys Ser Arg Ser Ser Pro Trp Glu Asn Ala Glu
                565                 570                 575

Met Asp Ala Ile His Ser Leu Gln Leu Ile Leu Arg Asp Ser Phe Lys
            580                 585                 590

Asp Ala Glu Ala Ser Asn Ser Lys Ala Ile Val His Ala His Leu Gly
        595                 600                 605

Glu Met Glu Leu Gln Gly Ile Asp Glu Leu Ser Ser Val Ala Arg Glu
    610                 615                 620

Met Val Arg Leu Ile Glu Thr Ala Thr Ala Pro Ile Phe Ala Val Asp
625                 630                 635                 640

Val Glu Gly Arg Ile Asn Gly Trp Asn Ala Lys Val Ala Glu Leu Thr
                645                 650                 655

Gly Leu Ser Val Glu Glu Ala Met Gly Lys Ser Leu Val His Glu Leu
            660                 665                 670

Val Tyr Lys Glu Ser Gln Glu Thr Ala Glu Lys Leu Leu Tyr Asn Ala
        675                 680                 685

Leu Arg Gly Glu Glu Asp Lys Asn Val Glu Ile Lys Leu Arg Thr Phe
    690                 695                 700

Gly Ala Glu Gln Leu Glu Lys Ala Val Phe Val Val Val Asn Ala Cys
705                 710                 715                 720

Ala Ser Lys Asp Tyr Thr Asn Asn Ile Val Gly Val Cys Phe Val Gly
                725                 730                 735

Gln Asp Val Thr Gly Glu Lys Val Val Met Asp Lys Phe Ile Asn Ile
            740                 745                 750

Gln Gly Asp Tyr Lys Ala Ile Val His Ser Pro Asn Pro Leu Ile Pro
        755                 760                 765

Pro Ile Phe Ala Ser Asp Glu Asn Thr Cys Cys Ser Glu Trp Asn Thr
    770                 775                 780

Ala Met Glu Lys Leu Thr Gly Trp Ser Arg Gly Glu Ile Val Gly Lys
785                 790                 795                 800

Met Leu Val Gly Glu Ile Phe Gly Ser Cys Cys Arg Leu Lys Gly Pro
                805                 810                 815

Asp Ala Met Thr Lys Phe Met Ile Val Leu His Asn Ala Ile Gly Gly
            820                 825                 830

Gln Asp Thr Asp Lys Phe Pro Phe Ser Phe Phe Asp Arg Asn Gly Lys
        835                 840                 845

Tyr Val Gln Ala Leu Leu Thr Ala Asn Lys Arg Val Asn Met Glu Gly
    850                 855                 860

Asn Thr Ile Gly Ala Phe Cys Phe Ile Gln Ile Ala Ser Pro Glu Leu
865                 870                 875                 880
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-continued

```
Gln Gln Ala Leu Arg Val Gln Arg Gln Gln Glu Lys Lys Cys Tyr Ser
                885                 890                 895

Gln Met Lys Glu Leu Ala Tyr Ile Cys Gln Glu Ile Lys Ser Pro Leu
            900                 905                 910

Asn Gly Ile Arg Phe Thr Asn Ser Leu Leu Glu Ala Thr Asn Leu Thr
        915                 920                 925

Glu Asn Gln Lys Gln Tyr Leu Glu Thr Ser Ala Ala Cys Glu Arg Gln
    930                 935                 940

Met Ser Lys Ile Ile Arg Asp Val Asp Leu Glu Asn Ile Glu Asp Gly
945                 950                 955                 960

Ser Leu Thr Leu Glu Lys Glu Asp Phe Phe Leu Gly Ser Val Ile Asp
                965                 970                 975

Ala Val Val Ser Gln Val Met Leu Leu Leu Arg Glu Lys Gly Val Gln
            980                 985                 990

Leu Ile Arg Asp Ile Pro Glu Glu  Ile Lys Thr Leu Thr  Val His Gly
        995                 1000                1005

Asp Gln  Val Arg Ile Gln Gln  Val Leu Ala Asp Phe  Leu Leu Asn
    1010                1015                1020

Met Val  Arg Tyr Ala Pro Ser  Pro Asp Gly Trp Val  Glu Ile Gln
    1025                1030                1035

Leu Arg  Pro Ser Met Met Pro  Ile Ser Asp Gly Val  Thr Gly Val
    1040                1045                1050

His Ile  Glu Leu Arg Ile Ile  Cys Pro Gly Glu Gly  Leu Pro Pro
    1055                1060                1065

Glu Leu  Val Gln Asp Met Phe  His Ser Ser Arg Trp  Val Thr Gln
    1070                1075                1080

Glu Gly  Leu Gly Leu Ser Thr  Cys Arg Lys Met Leu  Lys Leu Met
    1085                1090                1095

Asn Gly  Glu Ile Gln Tyr Ile  Arg Glu Ser Glu Arg  Cys Tyr Phe
    1100                1105                1110

Leu Ile  Val Leu Asp Leu Pro  Met Thr Arg Lys Gly  Pro Lys Ser
    1115                1120                1125

Val Gly
    1130


<210> SEQ ID NO 10
<211> LENGTH: 1121
<212> TYPE: PRT
<213> ORGANISM: Pisum sativum
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (28)..(28)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
      (Ser or Arg)

<400> SEQUENCE: 10

Ser Asn Asn Asn Asn Asn Arg Asn Ile Lys Arg Glu Ser Leu Ser Met
1               5                   10                  15

Arg Lys Ala Ile Ala Gln Tyr Thr Glu Asp Ala Xaa Leu His Ala Val
            20                  25                  30

Phe Glu Lys Ser Gly Asp Ser Phe Asp Tyr Ala Gln Ser Ile Arg Val
        35                  40                  45

Thr Ala Ala Thr Glu Ser Val Pro Glu Gln Gln Ile Thr Ala Tyr Leu
    50                  55                  60

Ala Lys Ile Gln Arg Gly Gly Phe Ile Gln Pro Phe Gly Ser Met Ile
65                  70                  75                  80
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-continued

```
Ala Val Asp Glu Thr Ser Phe Arg Val Leu Ala Tyr Ser Glu Asn Ala
                85                  90                  95

Arg Asp Met Leu Gly Ile Ala Pro Gln Ser Val Pro Ser Met Glu Asp
            100                 105                 110

Asp Ser Ser Ser Ser Ser Phe Phe Ser Leu Gly Val Asp Val Arg Ser
        115                 120                 125

Leu Phe Ser Ala Ser Ser Ser Val Leu Leu Glu Lys Ala Phe Ser Ala
    130                 135                 140

Arg Glu Ile Ser Leu Met Asn Pro Ile Trp Ile His Ser Arg Ser Thr
145                 150                 155                 160

Gly Lys Pro Phe Tyr Gly Ile Leu His Arg Ile Asp Ile Gly Val Val
                165                 170                 175

Ile Asp Leu Glu Pro Ala Arg Ser Glu Asp Pro Ala Leu Ser Ile Ala
            180                 185                 190

Gly Ala Val Gln Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Gln Leu
        195                 200                 205

Gln Ala Leu Pro Gly Gly Asp Val Lys Leu Leu Cys Asp Ala Val Val
    210                 215                 220

Glu Ser Val Arg Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Lys
225                 230                 235                 240

Phe His Glu Asp Glu His Gly Glu Val Val Ala Glu Ser Lys Arg Val
                245                 250                 255

Asp Leu Glu Pro Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro
            260                 265                 270

Gln Ala Ser Arg Phe Leu Phe Lys Gln Asn Arg Val Arg Met Ile Val
        275                 280                 285

Asp Cys Asn Ala Ser Pro Val Arg Val Phe Gln Asp Glu Ala Leu Val
    290                 295                 300

Gln Pro Val Cys Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys
305                 310                 315                 320

His Ala Gln Tyr Met Ala Asn Met Gly Ser Ile Ala Ser Leu Ala Met
                325                 330                 335

Ala Val Ile Ile Asn Gly Asn Asp Glu Asp Gly Gly Gly Ile Gly Gly
            340                 345                 350

Ala Ala Arg Gly Ser Met Arg Leu Trp Gly Leu Val Val Cys His His
        355                 360                 365

Thr Ser Ala Arg Cys Ile Pro Phe Pro Leu Arg Tyr Ala Cys Glu Phe
    370                 375                 380

Leu Met Gln Ala Phe Gly Leu Gln Leu Asn Met Glu Leu Gln Leu Ala
385                 390                 395                 400

Val Gln Ser Leu Glu Lys Arg Val Leu Lys Thr Gln Thr Leu Leu Cys
                405                 410                 415

Asp Met Leu Leu Arg Asp Ser His Thr Gly Ile Val Thr Gln Ser Pro
            420                 425                 430

Ser Ile Met Asp Leu Val Lys Cys Asp Gly Ala Ala Leu Tyr Tyr Gln
        435                 440                 445

Gly Asn Tyr His Pro Leu Gly Val Thr Pro Thr Glu Ser Gln Ile Arg
    450                 455                 460

Asp Ile Ile Asp Trp Leu Leu Ala Phe His Ser Asp Ser Thr Gly Leu
465                 470                 475                 480

Ser Thr Asp Ser Leu Ala Asp Ala Gly Tyr Pro Gly Ala Ala Ser Leu
                485                 490                 495
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Gly Asp Ala Val Cys Gly Met Ala Val Ala Tyr Ile Thr Glu Lys Asp
            500                 505                 510

Phe Leu Phe Trp Phe Arg Ser His Thr Ala Lys Glu Ile Lys Trp Gly
        515                 520                 525

Gly Ala Lys His His Pro Glu Asp Lys Asp Asp Gly Gln Lys Met His
    530                 535                 540

Pro Arg Ser Ser Phe Lys Ala Phe Leu Glu Val Val Lys Ile Arg Ser
545                 550                 555                 560

Met Gln Trp Asp Asn Ala Glu Met Asp Ala Ile His Ser Leu Gln Leu
                565                 570                 575

Ile Leu Arg Asp Ser Phe Lys Glu Ala Glu Asn Asn Asp Ser Lys Ala
            580                 585                 590

Val Val His Thr His Met Ala Glu Leu Glu Leu Gln Gly Val Asp Glu
        595                 600                 605

Leu Ser Ser Val Ala Arg Glu Met Val Arg Leu Ile Glu Thr Ala Thr
    610                 615                 620

Ala Pro Ile Phe Ala Val Asp Val Asp Gly Arg Ile Asn Gly Trp Asn
625                 630                 635                 640

Ala Lys Val Ser Glu Leu Thr Gly Leu Leu Val Glu Glu Ala Met Gly
                645                 650                 655

Lys Ser Leu Val His Asp Leu Val Tyr Lys Glu Ser Arg Glu Thr Val
            660                 665                 670

Asp Lys Leu Leu Ser His Ala Leu Lys Gly Glu Glu Asp Lys Asn Val
        675                 680                 685

Glu Ile Lys Met Lys Thr Phe Gly Pro Gly Asn Gln Asn Lys Ala Val
    690                 695                 700

Phe Ile Val Val Asn Ala Cys Ser Ser Lys Asp Tyr Thr Asn Asn Ile
705                 710                 715                 720

Val Gly Val Cys Phe Val Gly Gln Asp Ile Thr Gly Gln Lys Val Val
                725                 730                 735

Met Asp Lys Phe Ile Asn Ile Gln Gly Asp Tyr Lys Ala Ile Val His
            740                 745                 750

Ser Pro Asn Pro Leu Ile Pro Pro Ile Phe Ala Ser Asp Asp Asn Thr
        755                 760                 765

Cys Cys Leu Glu Trp Asn Asn Ala Met Glu Lys Leu Ser Gly Trp Ser
    770                 775                 780

Arg Ala Asp Val Ile Gly Lys Leu Leu Val Gly Glu Val Phe Gly Ser
785                 790                 795                 800

Phe Cys Gln Leu Lys Gly Ser Asp Ala Met Thr Lys Phe Met Ile Val
                805                 810                 815

Leu His Asn Ala Leu Gly Gly His Asp Thr Asp Lys Phe Pro Leu Ser
            820                 825                 830

Phe Leu Asp Arg His Gly Lys Tyr Val His Thr Phe Leu Thr Ala Asn
        835                 840                 845

Lys Arg Val Asn Met Asp Gly Gln Ile Ile Gly Ala Phe Cys Phe Leu
    850                 855                 860

Gln Ile Val Asn Pro Glu Leu Gln Gln Ala Leu Thr Val Gln Arg Gln
865                 870                 875                 880

Gln Asp Ser Ser Ser Leu Ala Arg Met Lys Glu Leu Ala Tyr Ile Cys
                885                 890                 895

Gln Glu Val Lys Asn Pro Leu Ser Gly Ile Arg Phe Thr Asn Ser Leu
            900                 905                 910

Leu Glu Ser Thr Cys Leu Thr Asp Glu Gln Lys Gln Leu Leu Glu Thr
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        915                 920                 925

Ser Val Ala Cys Glu Lys Gln Met Leu Lys Ile Val Arg Asp Ile Ala
    930                 935                 940

Leu Glu Ser Ile Glu Asp Gly Ser Leu Glu Leu Glu Lys Gln Glu Phe
945                 950                 955                 960

Leu Leu Glu Asn Val Ile Asn Ala Val Val Ser Gln Val Met Leu Leu
                965                 970                 975

Leu Arg Asp Arg Lys Leu Gln Leu Ile Arg Asp Ile Pro Glu Glu Ile
            980                 985                 990

Lys Ala Leu Ala Val Tyr Gly Asp  Gln Leu Arg Ile Gln  Gln Val Leu
        995                 1000                1005

Ala Asp  Phe Leu Met Asn Val  Val Arg Tyr Ala Pro  Ser Pro Asp
    1010                1015                1020

Gly Trp  Val Glu Ile His Val  Phe Pro Arg Ile Lys  Gln Ile Ser
    1025                1030                1035

Glu Gly  Leu Thr Leu Leu His  Ala Glu Phe Arg Met  Val Cys Pro
    1040                1045                1050

Gly Glu  Gly Leu Pro Pro Glu  Leu Ile Gln Asp Met  Phe His Asn
    1055                1060                1065

Ser Arg  Trp Val Thr Gln Glu  Gly Leu Gly Leu Ser  Met Ser Arg
    1070                1075                1080

Lys Ile  Ile Lys Leu Met Asn  Gly Glu Val Gln Tyr  Val Arg Glu
    1085                1090                1095

Ala Glu  Arg Cys Tyr Phe Leu  Val Leu Leu Glu Leu  Pro Val Thr
    1100                1105                1110

Arg Arg  Ser Ser Lys Ala Ile  Asn
    1115                1120


<210> SEQ ID NO 11
<211> LENGTH: 1129
<212> TYPE: PRT
<213> ORGANISM: Vitis vinifera

<400> SEQUENCE: 11

Met Ser Ser Gly Asn Arg Gly Thr Gln Ser His His Gln Ala Gln Ser
1               5                   10                  15

Ser Gly Thr Ser Asn Leu Arg Val Tyr His Thr Asp Ser Met Ser Lys
            20                  25                  30

Ala Ile Ala Gln Tyr Thr Met Asp Ala Arg Leu His Ala Val Tyr Glu
        35                  40                  45

Gln Ser Gly Glu Ser Gly Lys Ser Phe Asp Tyr Ser Gln Ser Val Arg
    50                  55                  60

Thr Thr Thr Gln Ser Val Pro Glu Gln Gln Ile Thr Ala Tyr Leu Ser
65                  70                  75                  80

Lys Ile Gln Arg Gly Gly His Ile Gln Pro Phe Gly Cys Met Leu Ala
                85                  90                  95

Val Asp Glu Ala Thr Phe Arg Val Ile Ala Phe Ser Glu Asn Ala Arg
            100                 105                 110

Glu Met Leu Gly Leu Thr Pro Gln Ser Val Pro Ser Leu Glu Lys Pro
        115                 120                 125

Glu Ile Leu Leu Val Gly Thr Asp Val Arg Thr Leu Phe Thr Pro Ser
    130                 135                 140

Ser Ala Val Leu Leu Glu Lys Ala Phe Arg Ala Arg Glu Ile Thr Leu
145                 150                 155                 160
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Leu Asn Pro Val Trp Ile His Ser Lys Asn Ser Gly Lys Pro Phe Tyr
                165                 170                 175

Ala Ile Leu His Arg Ile Asp Val Gly Ile Val Ile Asp Leu Glu Pro
            180                 185                 190

Ala Arg Thr Glu Asp Pro Ala Leu Ser Ile Ala Gly Ala Val Gln Ser
        195                 200                 205

Gln Lys Leu Ala Val Arg Ala Ile Ser His Leu Gln Ser Leu Pro Gly
    210                 215                 220

Gly Asp Ile Asn Leu Leu Cys Glu Thr Val Val Glu Asn Val Arg Glu
225                 230                 235                 240

Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Lys Phe His Glu Asp Glu
                245                 250                 255

His Gly Glu Val Val Ala Glu Ser Lys Arg Ser Asp Leu Glu Pro Tyr
            260                 265                 270

Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg Phe
        275                 280                 285

Leu Phe Arg Gln Asn Arg Val Arg Met Ile Val Asp Cys His Ala Thr
    290                 295                 300

Pro Val Leu Val Ile Gln Asp Glu Gly Leu Met Gln Pro Leu Cys Leu
305                 310                 315                 320

Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ala Gln Tyr Met
                325                 330                 335

Ala Asn Met Gly Ser Thr Ala Ser Leu Ala Met Ala Val Ile Ile Asn
            340                 345                 350

Gly Ser Asp Glu Glu Ala Ile Gly Gly Arg Asn Leu Met Arg Leu Trp
        355                 360                 365

Gly Leu Val Val Cys His His Thr Ser Ala Arg Cys Ile Pro Phe Pro
    370                 375                 380

Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala Phe Gly Leu Gln Leu
385                 390                 395                 400

Asn Met Glu Leu Gln Leu Ala Ser Gln Leu Ser Glu Lys His Val Leu
                405                 410                 415

Arg Thr Gln Thr Leu Leu Cys Asp Met Leu Leu Arg Asp Ser Pro Thr
            420                 425                 430

Gly Ile Val Thr Gln Ser Pro Ser Ile Met Asp Leu Val Lys Cys Asp
        435                 440                 445

Gly Ala Ala Leu Tyr Tyr Gln Gly Lys Tyr Tyr Pro Thr Gly Val Thr
    450                 455                 460

Pro Thr Glu Ala Gln Ile Lys Asp Ile Ala Glu Trp Leu Leu Ala Asn
465                 470                 475                 480

His Ala Asp Ser Thr Gly Leu Ser Thr Asp Ser Leu Ala Asp Ala Gly
                485                 490                 495

Tyr Pro Gly Ala Ala Ser Leu Gly Asp Ala Val Cys Gly Met Ala Val
            500                 505                 510

Ala Tyr Ile Thr Ser Arg Asp Phe Leu Phe Trp Phe Arg Ser His Thr
        515                 520                 525

Ala Lys Glu Ile Lys Trp Gly Gly Ala Lys His His Pro Glu Asp Lys
    530                 535                 540

Asp Asp Gly Gln Arg Met His Pro Arg Ser Ser Phe Lys Ala Phe Leu
545                 550                 555                 560

Glu Val Val Lys Ser Arg Ser Leu Pro Trp Glu Asn Ala Glu Met Asp
                565                 570                 575

Ala Ile His Ser Leu Gln Leu Ile Leu Arg Asp Ser Phe Lys Asp Ala
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           580                 585                 590

Thr Asp Gly Ser Asn Ser Lys Ala Val Met His Ala Gln Leu Gly Glu
        595                 600                 605

Leu Glu Leu Gln Gly Met Asp Glu Leu Ser Ser Val Ala Arg Glu Met
    610                 615                 620

Val Arg Leu Ile Glu Thr Ala Thr Ala Pro Ile Phe Ala Val Asp Val
625                 630                 635                 640

Asp Gly Cys Ile Asn Gly Trp Asn Ala Lys Val Ala Glu Leu Thr Gly
                645                 650                 655

Leu Ser Val Glu Glu Ala Met Gly Lys Ser Leu Val His Asp Leu Val
            660                 665                 670

Tyr Lys Glu Ser Glu Glu Thr Val Asp Lys Leu Leu His His Ala Leu
        675                 680                 685

Arg Gly Glu Glu Asp Lys Asn Val Glu Ile Lys Leu Arg Thr Phe Asp
    690                 695                 700

Ser Gln Gln His Lys Lys Ala Val Phe Val Val Val Asn Ala Cys Ser
705                 710                 715                 720

Ser Arg Asp Tyr Thr Asn Asn Ile Val Gly Val Cys Phe Val Gly Gln
                725                 730                 735

Asp Val Thr Gly Gln Lys Val Val Met Asp Lys Phe Ile His Ile Gln
            740                 745                 750

Gly Asp Tyr Lys Ala Ile Val His Ser Pro Asn Pro Leu Ile Pro Pro
        755                 760                 765

Ile Phe Ala Ser Asp Glu Asn Thr Val Cys Ser Glu Trp Asn Thr Ala
    770                 775                 780

Met Glu Lys Leu Thr Gly Trp Ser Arg Gly Asp Ile Ile Gly Lys Ile
785                 790                 795                 800

Leu Val Gly Glu Ile Phe Gly Ser Ser Cys Arg Leu Lys Gly Pro Asp
                805                 810                 815

Ala Leu Thr Lys Phe Met Ile Val Leu His Asn Ala Ile Gly Gly Gln
            820                 825                 830

Asp Thr Asp Lys Phe Pro Phe Ser Phe Phe Asp Gln Asn Gly Lys Tyr
        835                 840                 845

Val Gln Ala Leu Leu Thr Ala Asn Lys Arg Val Asn Ile Glu Gly Gln
    850                 855                 860

Ile Ile Gly Ala Phe Cys Phe Leu Gln Ile Ala Ser Pro Glu Leu Gln
865                 870                 875                 880

Gln Ala Leu Lys Val Gln Arg Gln Gln Glu Lys Lys Cys Phe Ala Arg
                885                 890                 895

Met Lys Glu Leu Ala Tyr Ile Cys Gln Glu Ile Lys Asn Pro Leu Ser
            900                 905                 910

Gly Ile Arg Phe Thr Asn Ser Leu Leu Glu Ala Thr Asp Leu Thr Glu
        915                 920                 925

Asp Gln Lys Gln Phe Leu Glu Thr Ser Ala Ala Cys Glu Lys Gln Met
    930                 935                 940

Ser Lys Ile Ile Arg Asp Val Asp Leu Asp Ser Ile Glu Asp Gly Ser
945                 950                 955                 960

Leu Glu Leu Glu Arg Ala Glu Phe Leu Leu Gly Ser Val Ile Asn Ala
                965                 970                 975

Val Val Ser Gln Val Met Ile Leu Leu Arg Glu Arg Asp Leu Gln Leu
            980                 985                 990

Ile Arg Asp Ile Pro Glu Glu Val  Lys Thr Leu Ala Val  Tyr Gly Asp
        995                 1000                1005
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Gln Val  Arg Ile Gln Gln Val  Leu Ala Asp Phe Leu  Leu Asn Met
    1010                1015                1020

Val Arg  Tyr Ala Pro Ser Pro  Asp Gly Trp Ile Glu  Ile Gln Val
    1025                1030                1035

Cys Pro  Arg Leu Lys Gln Ile  Ser Glu Glu Val Lys  Leu Met His
    1040                1045                1050

Ile Glu  Phe Arg Met Val Cys  Pro Gly Glu Gly Leu  Pro Pro Asn
    1055                1060                1065

Leu Ile  Gln Asp Met Phe His  Ser Ser Arg Trp Met  Thr Gln Glu
    1070                1075                1080

Gly Leu  Gly Leu Ser Met Cys  Arg Lys Ile Leu Lys  Leu Ile Asn
    1085                1090                1095

Gly Glu  Val Gln Tyr Ile Arg  Glu Ser Glu Arg Cys  Tyr Phe Leu
    1100                1105                1110

Ile Ser  Ile Glu Leu Pro Ile  Pro His Arg Gly Ser  Lys Ser Val
    1115                1120                1125

Asp
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<210> SEQ ID NO 12
<211> LENGTH: 200
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 12

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Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Gln Leu Gln Ala Leu Pro
1               5                   10                  15

Gly Gly Asp Ile Lys Leu Leu Cys Asp Thr Val Val Glu Ser Val Arg
            20                  25                  30

Asp Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Lys Phe His Glu Asp
        35                  40                  45

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

Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg
65                  70                  75                  80

Phe Leu Phe Lys Gln Asn Arg Val Arg Met Ile Val Asp Cys Asn Ala
                85                  90                  95

Thr Pro Val Leu Val Val Gln Asp Asp Arg Leu Thr Gln Ser Met Cys
            100                 105                 110

Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ser Gln Tyr
        115                 120                 125

Met Ala Asn Met Gly Ser Ile Ala Ser Leu Ala Met Ala Val Ile Ile
    130                 135                 140

Asn Gly Asn Glu Asp Asp Gly Ser Asn Val Ala Ser Gly Arg Ser Ser
145                 150                 155                 160

Met Arg Leu Trp Gly Leu Val Val Cys His His Thr Ser Ser Arg Cys
                165                 170                 175

Ile Pro Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala Phe
            180                 185                 190

Gly Leu Gln Leu Asn Met Glu Leu
        195                 200
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<210> SEQ ID NO 13
<211> LENGTH: 201
<212> TYPE: PRT
<213> ORGANISM: Zea mays

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<400> SEQUENCE: 13

Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Arg Leu Gln Ala Leu Pro
1 5 10 15

Gly Gly Asp Val Lys Leu Leu Cys Asp Thr Val Val Glu His Val Arg
20 25 30

Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Arg Phe His Glu Asp
35 40 45

Glu His Gly Glu Val Val Ala Glu Ser Arg Arg Asp Asn Leu Glu Pro
50 55 60

Tyr Leu Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg
65 70 75 80

Phe Leu Phe Arg Gln Asn Arg Val Arg Met Ile Ala Asp Cys His Ala
85 90 95

Thr Pro Val Arg Val Ile Gln Asp Pro Gly Leu Ser Gln Pro Leu Cys
100 105 110

Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ala Gln Tyr
115 120 125

Met Ala Asn Met Gly Ser Ile Ala Ser Leu Val Met Ala Val Ile Ile
130 135 140

Ser Ser Gly Gly Asp Asp Glu Gln Thr Gly Arg Gly Gly Ile Ser Ser
145 150 155 160

Ala Met Lys Leu Trp Gly Leu Val Val Cys His His Thr Ser Pro Arg
165 170 175

Cys Ile Pro Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala
180 185 190

Phe Gly Leu Gln Leu Asn Met Glu Leu
195 200

<210> SEQ ID NO 14
<211> LENGTH: 202
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 14

Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Arg Leu Gln Ala Leu Pro
1 5 10 15

Gly Gly Asp Val Lys Leu Leu Cys Asp Thr Val Val Glu His Val Arg
20 25 30

Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Arg Phe His Glu Asp
35 40 45

Glu His Gly Glu Val Val Ala Glu Ser Arg Arg Ser Asn Leu Glu Pro
50 55 60

Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg
65 70 75 80

Phe Leu Phe Arg Gln Asn Arg Val Arg Met Ile Ala Asp Cys His Ala
85 90 95

Ala Pro Val Arg Val Ile Gln Asp Pro Ala Leu Thr Gln Pro Leu Cys
100 105 110

Leu Val Gly Ser Thr Leu Arg Ser Pro His Gly Cys His Ala Gln Tyr
115 120 125

Met Ala Asn Met Gly Ser Ile Ala Ser Leu Val Met Ala Val Ile Ile
130 135 140

Ser Ser Gly Gly Asp Asp Asp His Asn Ile Ala Arg Gly Ser Ile Pro
145 150 155 160

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Ser Ala Met Lys Leu Trp Gly Leu Val Val Cys His His Thr Ser Pro
                165                 170                 175

Arg Cys Ile Pro Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln
            180                 185                 190

Ala Phe Gly Leu Gln Leu Asn Met Glu Leu
        195                 200


<210> SEQ ID NO 15
<211> LENGTH: 201
<212> TYPE: PRT
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 15

Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Arg Leu Gln Ala Leu Pro
1               5                   10                  15

Gly Gly Asp Ile Lys Leu Leu Cys Asp Thr Val Val Glu His Val Arg
            20                  25                  30

Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Arg Phe His Glu Asp
        35                  40                  45

Glu His Gly Glu Val Val Ala Glu Ser Arg Arg Asp Asn Leu Glu Pro
    50                  55                  60

Tyr Leu Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg
65                  70                  75                  80

Phe Leu Phe Arg Gln Asn Arg Val Arg Met Ile Ala Asp Cys His Ala
                85                  90                  95

Thr Pro Val Arg Val Ile Gln Asp Pro Gly Met Ser Gln Pro Leu Cys
            100                 105                 110

Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ala Gln Tyr
        115                 120                 125

Met Ala Asn Met Gly Ser Ile Ala Ser Leu Val Met Ala Val Ile Ile
    130                 135                 140

Ser Ser Gly Gly Asp Asp Glu Gln Thr Gly Arg Gly Gly Ile Ser Ser
145                 150                 155                 160

Ala Met Lys Leu Trp Gly Leu Val Val Cys His His Thr Ser Pro Arg
                165                 170                 175

Cys Ile Pro Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala
            180                 185                 190

Phe Gly Leu Gln Leu Asn Met Glu Leu
        195                 200


<210> SEQ ID NO 16
<211> LENGTH: 197
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 16

Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Gln Leu Gln Ser Leu Pro
1               5                   10                  15

Gly Gly Asp Val Lys Leu Leu Cys Asp Thr Val Val Glu Ser Val Arg
            20                  25                  30

Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Lys Phe His Glu Asp
        35                  40                  45

Glu His Gly Glu Val Val Ser Glu Ser Lys Arg Pro Asp Leu Glu Pro
    50                  55                  60

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

Ser Ala Val Arg Val Val Gln Asp Glu Ala Leu Val Gln Pro Leu Cys
            100                 105                 110

Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ala Gln Tyr
        115                 120                 125

Met Ala Asn Met Gly Ser Ile Ala Ser Leu Val Met Ala Val Ile Ile
    130                 135                 140

Asn Gly Asn Asp Glu Glu Gly Val Gly Gly Arg Ser Ser Met Arg Leu
145                 150                 155                 160

Trp Gly Leu Val Val Cys His His Thr Ser Ala Arg Cys Ile Pro Phe
                165                 170                 175

Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala Phe Gly Leu Gln
            180                 185                 190

Leu Asn Met Glu Leu
        195


<210> SEQ ID NO 17
<211> LENGTH: 197
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 17

Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Gln Leu Gln Ser Leu Pro
1               5                   10                  15

Gly Gly Asp Val Lys Leu Leu Cys Asp Thr Val Val Glu Ser Val Arg
            20                  25                  30

Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Arg Phe His Glu Asp
        35                  40                  45

Glu His Gly Glu Val Val Ala Glu Thr Lys Arg Pro Asp Leu Glu Pro
    50                  55                  60

Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg
65                  70                  75                  80

Phe Leu Phe Lys Gln Asn Arg Val Arg Met Ile Val Asp Cys His Ala
                85                  90                  95

Ser Ala Val Arg Val Val Gln Asp Glu Ala Leu Val Gln Pro Leu Cys
            100                 105                 110

Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ala Gln Tyr
        115                 120                 125

Met Ala Asn Met Gly Ser Thr Ala Ser Leu Val Met Ala Val Ile Ile
    130                 135                 140

Asn Gly Asn Asp Glu Glu Gly Val Gly Gly Arg Thr Ser Met Arg Leu
145                 150                 155                 160

Trp Gly Leu Val Ile Cys His His Thr Ser Ala Arg Cys Ile Pro Phe
                165                 170                 175

Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala Phe Gly Leu Gln
            180                 185                 190

Leu Asn Met Glu Leu
        195


<210> SEQ ID NO 18
<211> LENGTH: 197
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 18
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```
Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Gln Leu Gln Ser Leu Pro
1               5                   10                  15

Gly Gly Asp Val Lys Leu Leu Cys Asp Thr Val Val Glu Ser Val Arg
            20                  25                  30

Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Lys Phe His Glu Asp
        35                  40                  45

Glu His Gly Glu Val Val Ser Glu Ser Lys Arg Pro Asp Leu Glu Pro
    50                  55                  60

Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg
65                  70                  75                  80

Phe Leu Phe Lys Gln Asn Arg Val Arg Met Ile Val Asp Cys His Ala
                85                  90                  95

Ser Ala Val Arg Val Val Gln Asp Glu Ala Leu Val Gln Pro Leu Cys
            100                 105                 110

Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ala Gln Tyr
        115                 120                 125

Met Ala Asn Met Gly Ser Ile Ala Ser Leu Val Met Ala Val Ile Ile
    130                 135                 140

Asn Gly Asn Asp Glu Glu Gly Val Gly Gly Arg Ser Ser Met Arg Leu
145                 150                 155                 160

Trp Gly Leu Val Val Cys His His Thr Ser Ala Arg Cys Ile Pro Phe
                165                 170                 175

Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala Phe Gly Leu Gln
            180                 185                 190

Leu Asn Met Glu Leu
        195


<210> SEQ ID NO 19
<211> LENGTH: 197
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 19

Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Gln Leu Gln Ser Leu Pro
1               5                   10                  15

Gly Gly Asp Val Lys Leu Leu Cys Asp Thr Val Val Glu Ser Val Arg
            20                  25                  30

Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Arg Phe His Glu Asp
        35                  40                  45

Glu His Gly Glu Val Val Ala Glu Thr Lys Arg Pro Asp Leu Glu Pro
    50                  55                  60

Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg
65                  70                  75                  80

Phe Leu Phe Lys Gln Asn Arg Val Arg Met Ile Val Asp Cys His Ala
                85                  90                  95

Ser Ala Val Arg Val Val Gln Asp Glu Ala Leu Val Gln Pro Leu Cys
            100                 105                 110

Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ala Gln Tyr
        115                 120                 125

Met Ala Asn Met Gly Ser Thr Ala Ser Leu Val Met Ala Val Ile Ile
    130                 135                 140

Asn Gly Asn Asp Glu Glu Gly Val Gly Gly Arg Thr Ser Met Arg Leu
145                 150                 155                 160

Trp Gly Leu Val Ile Cys His His Thr Ser Ala Arg Cys Ile Pro Phe
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                165                 170                 175

Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala Phe Gly Leu Gln
            180                 185                 190

Leu Asn Met Glu Leu
        195


<210> SEQ ID NO 20
<211> LENGTH: 198
<212> TYPE: PRT
<213> ORGANISM: Solanum tuberosum

<400> SEQUENCE: 20

Ser Gln Lys Leu Ala Val Arg Ala Ile Ser His Leu Gln Ser Leu Pro
1               5                   10                  15

Gly Gly Asp Ile Lys Leu Leu Cys Asp Thr Val Val Glu Ser Val Arg
            20                  25                  30

Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Lys Phe His Glu Asp
        35                  40                  45

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

Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg
65                  70                  75                  80

Phe Leu Phe Lys Gln Asn Arg Val Arg Met Ile Val Asp Cys His Ala
                85                  90                  95

Thr Pro Val Arg Val Thr Gln Asp Glu Ser Leu Met Gln Pro Leu Cys
            100                 105                 110

Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ala Gln Tyr
        115                 120                 125

Met Ala Asn Met Gly Ser Ile Ala Ser Leu Thr Leu Ala Val Ile Ile
    130                 135                 140

Asn Gly Asn Asp Glu Glu Ala Val Gly Gly Gly Arg Asn Ser Met Arg
145                 150                 155                 160

Leu Trp Gly Leu Val Val Gly His His Thr Ser Val Arg Ser Ile Pro
                165                 170                 175

Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala Phe Gly Leu
            180                 185                 190

Gln Leu Asn Met Glu Leu
        195


<210> SEQ ID NO 21
<211> LENGTH: 201
<212> TYPE: PRT
<213> ORGANISM: Pisum sativum

<400> SEQUENCE: 21

Ser Gln Lys Leu Ala Val Arg Ala Ile Ser Gln Leu Gln Ala Leu Pro
1               5                   10                  15

Gly Gly Asp Val Lys Leu Leu Cys Asp Ala Val Val Glu Ser Val Arg
            20                  25                  30

Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Lys Phe His Glu Asp
        35                  40                  45

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

Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg
65                  70                  75                  80

Phe Leu Phe Lys Gln Asn Arg Val Arg Met Ile Val Asp Cys Asn Ala
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                85                  90                  95

Ser Pro Val Arg Val Phe Gln Asp Glu Ala Leu Val Gln Pro Val Cys
            100                 105                 110

Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ala Gln Tyr
        115                 120                 125

Met Ala Asn Met Gly Ser Ile Ala Ser Leu Ala Met Ala Val Ile Ile
    130                 135                 140

Asn Gly Asn Asp Glu Asp Gly Gly Gly Ile Gly Gly Ala Ala Arg Gly
145                 150                 155                 160

Ser Met Arg Leu Trp Gly Leu Val Val Cys His His Thr Ser Ala Arg
                165                 170                 175

Cys Ile Pro Phe Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala
            180                 185                 190

Phe Gly Leu Gln Leu Asn Met Glu Leu
        195                 200


<210> SEQ ID NO 22
<211> LENGTH: 197
<212> TYPE: PRT
<213> ORGANISM: Vitis vinifera

<400> SEQUENCE: 22

Ser Gln Lys Leu Ala Val Arg Ala Ile Ser His Leu Gln Ser Leu Pro
1               5                   10                  15

Gly Gly Asp Ile Asn Leu Leu Cys Glu Thr Val Val Glu Asn Val Arg
            20                  25                  30

Glu Leu Thr Gly Tyr Asp Arg Val Met Val Tyr Lys Phe His Glu Asp
        35                  40                  45

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

Tyr Ile Gly Leu His Tyr Pro Ala Thr Asp Ile Pro Gln Ala Ser Arg
65                  70                  75                  80

Phe Leu Phe Arg Gln Asn Arg Val Arg Met Ile Val Asp Cys His Ala
                85                  90                  95

Thr Pro Val Leu Val Ile Gln Asp Glu Gly Leu Met Gln Pro Leu Cys
            100                 105                 110

Leu Val Gly Ser Thr Leu Arg Ala Pro His Gly Cys His Ala Gln Tyr
        115                 120                 125

Met Ala Asn Met Gly Ser Thr Ala Ser Leu Ala Met Ala Val Ile Ile
    130                 135                 140

Asn Gly Ser Asp Glu Glu Ala Ile Gly Gly Arg Asn Leu Met Arg Leu
145                 150                 155                 160

Trp Gly Leu Val Val Cys His His Thr Ser Ala Arg Cys Ile Pro Phe
                165                 170                 175

Pro Leu Arg Tyr Ala Cys Glu Phe Leu Met Gln Ala Phe Gly Leu Gln
            180                 185                 190

Leu Asn Met Glu Leu
        195


<210> SEQ ID NO 23
<211> LENGTH: 3516
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 23

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ggaacgaaat ctctcagacc aagaagcaac actgaatcaa tgagcaaagc aattcaacag 180

tacaccgtcg acgcaagact ccacgccgtt ttcgaacaat ccggcgaatc agggaaatca 240

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atcacagctt atctctctcg aatccagcga ggtggttaca ttcagccttt cggatgtatg 360

atcgccgtcg atgaatccag tttccggatc atcggttaca gtgaaaacgc cagagaaatg 420

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agaggggacg aggaaaagaa tgtggaggtt aagctgaaaa ctttcagccc cgaactacaa 2220

gggaaagcag tttttgtggt tgtgaatgct tgttccagca aggactactt gaacaacatt 2280

gtcggcgttt gttttgttgg acaagacgtt actagtcaga aaatcgtaat ggataagttc 2340

atcaacatac aaggagatta caaggctatt gtacatagcc caaaccctct aatcccgcca 2400

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acgggttggt ctcgcagtga agtgattggg aaaatgattg tcggggaagt gtttgggagc   2520

tgttgcatgc taaagggtcc tgatgcttta accaagttca tgattgtatt gcataatgcg   2580

attggtggcc aagatacgga taagttccct ttcccattct ttgaccgcaa tgggaagttt   2640

gttcaggctc tattgactgc aaacaagcgg gttagcctcg agggaaaggt tattggggct   2700

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caggacacag agtgtttcac gaaggcaaaa gagttggctt atatttgtca ggtgataaag   2820

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cagataagga ttcaacagct cctggctgag tttctgctga gtataatccg gtatgcacca   3180

tctcaagagt gggtggagat ccatttaagc caactttcaa agcaaatggc tgatggattc   3240

gccgccatcc gcacagaatt cagaatggcg tgtccaggtg aaggtctgcc tccagagcta   3300

gtccgagaca tgttccatag cagcaggtgg acaagccctg aaggtttagg tctaagcgta   3360

tgtcgaaaga ttttaaagct aatgaacggt gaggttcaat acatccgaga atcagaacgg   3420

tcctatttcc tcatcattct ggaactccct gtacctcgaa agcgaccatt gtcaactgct   3480

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<210> SEQ ID NO 24
<211> LENGTH: 3483
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 24

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gcgcgcctac acgcggtgtt cgagcaatcg ggcgcgtcgg gccgcagctt cgactactcc    240

caatcgctgc gcgcgccgcc cacgccgtcc tccgagcagc agatcgccgc ctacctctcc    300

cgcatccagc gcggcggcca catccagccc ttcggctgca cgctcgccgt cgccgacgac    360

tcctccttcc gcctcctcgc cttctccgag aactcccccg acctgctcga cctgtcgcct    420

caccactccg ttccctcgct ggactcctct gcgccgcccc acgtttccct gggtgccgac    480

gcgcgcctcc tcttctcccc ctcgtccgcg gtcctcctag agcgcgcctt cgccgcgcgc    540

gagatctcgc tgctcaaccc gatatggatc cactccaggg tctcctccaa gccgttctac    600

gccatcctcc accgcatcga cgtcggcgtc gtcatcgacc tcgagcccgc ccgcaccgag    660

gaccccgctc tctccatcgc cggtgcagtc cagtcccaga aactggcggt ccgcgccatc    720

tcccgcctcc aggcgctacc cggcggggac gtcaagcttc tctgcgacac agtcgtggag    780

catgttcgcg agctcacggg ttatgaccgt gtcatggtgt acaggttcca tgaagacgag    840

cacggggaag ttgtcgccga gagccggcgc gacaaccttg agccttacct cggattgcat    900

tatcccgcca cagatatccc ccaggcgtcg cgcttcctgt tccggcagaa ccgcgtgcga    960

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gtc 3483

<210> SEQ ID NO 25
<211> LENGTH: 3513
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 25

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cagcagatcg ccgcctacct ctcccgcatc cagcgcggcg ggcacataca gcccttcggc 360

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caagtgatga tacagttgag agaaagagat ttacaactta ttcgagatat ccctgatgaa 3120

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acaacccaag agggtattgg cctaagcata tgcaggaaga tcctaaaatt gatgggtggc 3420

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<210> SEQ ID NO 26
<211> LENGTH: 3534
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 26

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<210> SEQ ID NO 27
<211> LENGTH: 3411
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 27

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<210> SEQ ID NO 28
<211> LENGTH: 3447
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 28

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aacaacaaca acaacaacat cgactccacg agcaaggcca tcgcgcagta cacggaggac 180

gcgcggctcc acgccgtctt tgagcagtcc ggcgagtccg ggaggtcctt tgactactcc 240

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gaagtgcagt atatcaggga ggcccaacgg tgctacttct atgttcttct tgaactacct 3420

gtgacacgga gaagctctaa aaagtgt 3447

<210> SEQ ID NO 29
<211> LENGTH: 3300
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 29

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gtccccgagc agcagataac ggcttacctt gtcaaaatcc agcgcggcgg cttcatccag 180

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<210> SEQ ID NO 30
<211> LENGTH: 2601
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 30

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gatacagata gattcccttt ttcatttctt gatcggtatg gcaagcatgt gcaagctttc 2280

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attgaaagca ttgaggatgg a 2601

<210> SEQ ID NO 31
<211> LENGTH: 3390
<212> TYPE: DNA
<213> ORGANISM: Solanum tuberosum

<400> SEQUENCE: 31

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tcagagtctg ttaaaactac tacacaatct gtgcctgaaa ggcaaatcac tgcttatttg 240

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gctagttttc gtgtaatagc ttatagtgaa aatgcctttg aaatgcttag tttaactcca 360

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ctttttaccc cttctagctc tgttttgcta gaaagagcat ttggggcacg tgagatcact 480

ttactcaacc caatttggat tcattccaag aattctggaa agccctttta tgcaattttg 540

cacagggttg atgttggtat tgccattgat ttggagcctg ctagaactga ggaccctgct 600

ttatctattg ctggagcagt gcagtcacag aaacttgcag tgagggctat ttctcatttg 660

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cacagcccca atcctctgat ccctccaata tttgcatcag atgagaacac ttgttgctcc 2340

gagtggaaca ctgccatgga aaaactcact ggttggtcta gaggggagat tgttggaaaa 2400

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tgccctggcg aagggcttcc tcctgaattg gttcaagata tgttccacag cagtcggtgg 3240

gtaactcagg aaggcctagg actgagcacg tgcagaaaaa tgttaaagct tatgaatgga 3300

gaaatccagt atatcagaga atcagaaaga tgctatttcc tgattgtcct tgacctgcca 3360

atgacccgca aaggtccaaa gagtgttggc 3390

<210> SEQ ID NO 32
<211> LENGTH: 3363
<212> TYPE: DNA
<213> ORGANISM: Pisum sativum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (84)..(84)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 32

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gctcagtaca cagaagacgc aagnctccat gctgtttttg aaaaatccgg tgactctttc 120

gattatgccc aatccattcg cgtcacggcg gctactgaat cagttcctga acagcaaatc 180

actgcttact tagccaaaat ccaacgcggt ggtttcattc aacctttcgg ttcaatgatc 240

gccgtcgacg aaacttcttt tcgcgttctt gcttactctg aaaacgcacg tgacatgctt 300

ggtatcgcgc ctcaatcggt tccttctatg gaagatgatt cttcttcttc ttcgtttttc 360

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gctttttcag ctcgggagat tagtttaatg aatcctattt ggatccactc tcgttctact 480

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aat 3363

<210> SEQ ID NO 33
<211> LENGTH: 3387
<212> TYPE: DNA
<213> ORGANISM: Vitis vinifera

<400> SEQUENCE: 33

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gctcgcctcc acgccgtata cgaacagtcc ggcgagtccg gtaagtcatt cgactactcg 180

cagtcggtta gaaccacaac gcaatcggtc cctgagcaac aaatcactgc gtatttatcg 240

aaaattcaac ggggtggcca tatacagccc tttgggtgta tgcttgcggt cgatgaggcc 300

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gcctcacttg gtgatgcagt ttgtggaatg gctgttgctt atatcacttc aagagatttt 1560

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gtccaatata tcagagaatc agaaagatgt tattttctaa tcagcataga acttcctata 3360

cctcacagag gctcaaagag cgttgac 3387

<210> SEQ ID NO 34
<211> LENGTH: 187
<212> TYPE: PRT
<213> ORGANISM: Synechocystis PCC6803

<400> SEQUENCE: 34

Leu Gly Phe Tyr His Met Ala Asn Ala Ala Leu Asn Arg Leu Arg Gln
1 5 10 15

Gln Ala Asn Leu Arg Asp Phe Tyr Asp Val Ile Val Glu Glu Val Arg
20 25 30

Arg Met Thr Gly Phe Asp Arg Val Met Leu Tyr Arg Phe Asp Glu Asn
35 40 45

Asn His Gly Asp Val Ile Ala Glu Asp Lys Arg Asp Asp Met Glu Pro

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    50                  55                  60

Tyr Leu Gly Leu His Tyr Pro Glu Ser Asp Ile Pro Gln Pro Ala Arg
65                  70                  75                  80

Arg Leu Phe Ile His Asn Pro Ile Arg Val Ile Pro Asp Val Tyr Gly
                85                  90                  95

Val Ala Val Pro Leu Thr Pro Ala Val Asn Pro Ser Thr Asn Arg Ala
            100                 105                 110

Val Asp Leu Thr Glu Ser Ile Leu Arg Ser Ala Tyr His Cys His Leu
        115                 120                 125

Thr Tyr Leu Lys Asn Met Gly Val Gly Ala Ser Leu Thr Ile Ser Leu
    130                 135                 140

Ile Lys Asp Gly His Leu Trp Gly Leu Ile Ala Cys His His Gln Thr
145                 150                 155                 160

Pro Lys Val Ile Pro Phe Glu Leu Arg Lys Ala Cys Glu Phe Phe Gly
                165                 170                 175

Arg Val Val Phe Ser Asn Ile Ser Ala Gln Glu
            180                 185


<210> SEQ ID NO 35
<211> LENGTH: 187
<212> TYPE: PRT
<213> ORGANISM: Deinococcus radiodurans

<400> SEQUENCE: 35

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

Ala Pro Asn Leu Arg Ala Leu Ala Glu Val Ala Thr Gln Thr Val Arg
            20                  25                  30

Glu Leu Thr Gly Phe Asp Arg Val Met Leu Tyr Lys Phe Ala Pro Asp
        35                  40                  45

Ala Thr Gly Glu Val Ile Ala Glu Ala Arg Arg Glu Gly Leu His Ala
    50                  55                  60

Phe Leu Gly His Arg Phe Pro Ala Ser Asp Ile Pro Ala Gln Ala Arg
65                  70                  75                  80

Ala Leu Tyr Thr Arg His Leu Leu Arg Leu Thr Ala Asp Thr Arg Ala
                85                  90                  95

Ala Ala Val Pro Leu Asp Pro Val Leu Asn Pro Gln Thr Asn Ala Pro
            100                 105                 110

Thr Pro Leu Gly Gly Ala Val Leu Arg Ala Thr Ser Pro Met His Met
        115                 120                 125

Gln Tyr Leu Arg Asn Met Gly Val Gly Ser Ser Leu Ser Val Ser Val
    130                 135                 140

Val Val Gly Gly Gln Leu Trp Gly Leu Ile Ala Cys His His Gln Thr
145                 150                 155                 160

Pro Tyr Val Leu Pro Pro Asp Leu Arg Thr Thr Leu Glu Tyr Leu Gly
                165                 170                 175

Arg Leu Leu Ser Leu Gln Val Gln Val Lys Glu
            180                 185


<210> SEQ ID NO 36
<211> LENGTH: 187
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 36

Thr Ser Phe Thr Leu Asn Ala Gln Arg Ile Ile Ala Gln Val Gln Leu
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1               5                   10                  15

His Asn Asp Thr Ala Ser Leu Leu Ser Asn Val Thr Asp Glu Leu Arg
            20                  25                  30

Arg Met Thr Gly Tyr Asp Arg Val Met Ala Tyr Arg Phe Arg His Asp
        35                  40                  45

Asp Ser Gly Glu Val Val Ala Glu Ser Arg Arg Glu Asp Leu Glu Ser
    50                  55                  60

Tyr Leu Gly Gln Arg Tyr Pro Ala Ser Asp Ile Pro Ala Gln Ala Arg
65                  70                  75                  80

Arg Leu Tyr Ile Gln Asn Pro Ile Arg Leu Ile Ala Asp Val Ala Tyr
                85                  90                  95

Thr Pro Met Arg Val Phe Pro Ala Leu Asn Pro Glu Thr Asn Glu Ser
            100                 105                 110

Phe Asp Leu Ser Tyr Ser Val Leu Arg Ser Val Ser Pro Ile His Cys
        115                 120                 125

Glu Tyr Leu Thr Asn Met Gly Val Arg Ala Ser Met Ser Ile Ser Ile
    130                 135                 140

Val Val Gly Gly Lys Leu Trp Gly Leu Phe Ser Cys His His Met Ser
145                 150                 155                 160

Pro Lys Leu Ile Pro Tyr Pro Val Arg Met Ser Phe Gln Ile Phe Ser
                165                 170                 175

Gln Val Cys Ser Ala Ile Val Glu Arg Leu Glu
            180                 185


<210> SEQ ID NO 37
<211> LENGTH: 187
<212> TYPE: PRT
<213> ORGANISM: Rhodopseudomonas palustris

<400> SEQUENCE: 37

Asn Glu Phe Phe Arg Ser Val Arg Val Ala Ile Arg Arg Leu Gln Thr
1               5                   10                  15

Ala Ala Asp Leu Pro Thr Ala Cys Trp Ile Ala Ala Ser Glu Val Arg
            20                  25                  30

Arg Ile Thr Gly Phe Asp Arg Ile Lys Val Tyr Gln Phe Ala Ala Asp
        35                  40                  45

Trp Ser Gly Gln Val Ile Ala Glu Asp Arg Asp Ser Gly Ile Pro Ser
    50                  55                  60

Leu Leu Asp Phe His Phe Pro Ser Ser Asp Ile Pro Ala Gln Ser Arg
65                  70                  75                  80

Ala Leu Tyr Thr Ile Asn Pro Val Arg Ile Ile Pro Asp Ile Gly Tyr
                85                  90                  95

Arg Pro Ser Pro Leu Val Pro Asp Ile Asn Pro Arg Leu Gly Gly Pro
            100                 105                 110

Ile Asp Leu Ser Phe Ser Val Leu Arg Ser Val Ser Pro Thr His Leu
        115                 120                 125

Glu Tyr Met Val Asn Met Gly Met His Ala Ala Met Ser Ile Ser Ile
    130                 135                 140

Val Arg Asp Asn Arg Leu Trp Gly Met Ile Ser Cys His Asn Leu Thr
145                 150                 155                 160

Pro Arg Phe Val Ser Tyr Glu Val Arg Gln Ala Cys Glu Leu Ile Ala
                165                 170                 175

Gln Val Leu Thr Trp Gln Ile Gly Val Leu Glu
            180                 185
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<210> SEQ ID NO 38
<211> LENGTH: 187
<212> TYPE: PRT
<213> ORGANISM: Synechococcus

<400> SEQUENCE: 38

Ser Arg Asp Ala Leu Ile Asn Arg Ile Thr His Gln Ile Arg Gln Ser
1 5 10 15

Leu Glu Leu Asp Gln Ile Leu Arg Ala Thr Val Glu Glu Val Arg Ala
20 25 30

Phe Leu Gly Thr Asp Arg Val Lys Val Tyr Arg Phe Asp Pro Glu Gly
35 40 45

His Gly Thr Val Val Ala Glu Ala Arg Gly Gly Glu Arg Leu Pro Ser
50 55 60

Leu Leu Gly Leu Thr Phe Pro Ala Gly Asp Ile Pro Glu Glu Ala Arg
65 70 75 80

Arg Leu Phe Arg Leu Ala Gln Val Arg Val Ile Val Asp Val Glu Ala
85 90 95

Gln Ser Arg Ser Ile Ser Gln Pro Glu Ser Trp Gly Leu Ser Ala Arg
100 105 110

Val Pro Leu Gly Glu Pro Leu Gln Arg Pro Val Asp Pro Cys His Val
115 120 125

His Tyr Leu Lys Ser Met Gly Val Ala Ser Ser Leu Val Val Pro Leu
130 135 140

Met His His Gln Glu Leu Trp Gly Leu Leu Val Ser His His Ala Glu
145 150 155 160

Pro Arg Pro Tyr Ser Gln Glu Glu Leu Gln Val Val Gln Leu Leu Ala
165 170 175

Asp Gln Val Ser Ile Ala Ile Ala Gln Ala Glu
180 185

<210> SEQ ID NO 39
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Peptide

<400> SEQUENCE: 39

Lys Leu His His His His His His
1 5

<210> SEQ ID NO 40
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Peptide

<400> SEQUENCE: 40

Gly Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys
1 5 10

<210> SEQ ID NO 41
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Peptide

<400> SEQUENCE: 41

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Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys
1 5 10

<210> SEQ ID NO 42
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Synechocystis PCC6803

<400> SEQUENCE: 42

Glu Ser Asp Ile Pro Gln
1 5

<210> SEQ ID NO 43
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Synechocystis PCC6803

<400> SEQUENCE: 43

Pro Ile Arg Val Ile
1 5

<210> SEQ ID NO 44
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Synechocystis PCC6803

<400> SEQUENCE: 44

Ile Leu Arg Ser Ala
1 5

<210> SEQ ID NO 45
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Synechocystis PCC6803

<400> SEQUENCE: 45

Leu Thr Tyr Leu Lys
1 5

<210> SEQ ID NO 46
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Synechocystis PCC6803

<400> SEQUENCE: 46

His Pro Arg Gln Ser Phe
1 5

<210> SEQ ID NO 47
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Deinococcus radiodurans

<400> SEQUENCE: 47

Ala Ser Asp Ile Pro Ala
1 5

<210> SEQ ID NO 48
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Deinococcus radiodurans

<400> SEQUENCE: 48

Leu Leu Arg Leu Thr

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1 5

<210> SEQ ID NO 49
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Deinococcus radiodurans

<400> SEQUENCE: 49

Val Leu Arg Ala Thr
1 5

<210> SEQ ID NO 50
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Deinococcus radiodurans

<400> SEQUENCE: 50

Met Gln Tyr Leu Arg
1 5

<210> SEQ ID NO 51
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Deinococcus radiodurans

<400> SEQUENCE: 51

Gly Pro Arg His Ser Phe
1 5

<210> SEQ ID NO 52
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 52

Ala Ser Asp Ile Pro Ala
1 5

<210> SEQ ID NO 53
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 53

Pro Ile Arg Leu Ile
1 5

<210> SEQ ID NO 54
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 54

Val Leu Arg Ser Val
1 5

<210> SEQ ID NO 55
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 55

Cys Glu Tyr Leu Thr
1 5

<210> SEQ ID NO 56
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 56

Thr Pro Arg Gly Ser Phe
1 5

<210> SEQ ID NO 57
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Rhodopseudomonas palustris

<400> SEQUENCE: 57

Ser Ser Asp Ile Pro Ala
1 5

<210> SEQ ID NO 58
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Rhodopseudomonas palustris

<400> SEQUENCE: 58

Pro Val Arg Ile Ile
1 5

<210> SEQ ID NO 59
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Rhodopseudomonas palustris

<400> SEQUENCE: 59

Val Leu Arg Ser Val
1 5

<210> SEQ ID NO 60
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Rhodopseudomonas palustris

<400> SEQUENCE: 60

Leu Glu Tyr Met Val
1 5

<210> SEQ ID NO 61
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Rhodopseudomonas palustris

<400> SEQUENCE: 61

Gln Thr Arg Ala Ser Phe
1 5

<210> SEQ ID NO 62
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Synechococcus OS-B

<400> SEQUENCE: 62

Ala Gly Asp Ile Pro Glu
1 5

<210> SEQ ID NO 63

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<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Synechococcus OS-B

<400> SEQUENCE: 63

Gln Val Arg Val Ile
1 5

<210> SEQ ID NO 64
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Synechococcus OS-B

<400> SEQUENCE: 64

Leu Gln Arg Pro Val
1 5

<210> SEQ ID NO 65
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Synechococcus OS-B

<400> SEQUENCE: 65

Val His Tyr Leu Lys
1 5

<210> SEQ ID NO 66
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Synechococcus OS-B

<400> SEQUENCE: 66

Leu Pro Leu Ile Ser Phe
1 5

<210> SEQ ID NO 67
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 67

Ala Thr Asp Ile Pro Gln
1 5

<210> SEQ ID NO 68
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 68

Lys Val Arg Met Ile
1 5

<210> SEQ ID NO 69
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 69

Arg Val Arg Met Ile
1 5

<210> SEQ ID NO 70
<211> LENGTH: 5
<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 70

Thr Leu Arg Ala Pro
1 5

<210> SEQ ID NO 71
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 71

Leu Gln Tyr Met Ala
1 5

<210> SEQ ID NO 72
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 72

Ser Gln Tyr Met Ala
1 5

<210> SEQ ID NO 73
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 73

Ala Gln Tyr Met Ser
1 5

<210> SEQ ID NO 74
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 74

Ala Gln Tyr Met Thr
1 5

<210> SEQ ID NO 75
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 75

Thr Gln Tyr Met Ala
1 5

<210> SEQ ID NO 76
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 76

His Pro Arg Ser Ser Phe
1 5

<210> SEQ ID NO 77
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

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<400> SEQUENCE: 77

Asn Pro Arg Ser Ser Phe
1 5

What is claimed is:

1. An isolated polynucleotide comprising a contiguous coding sequence encoding a polypeptide having at least 95% identity to at least one amino acid sequence selected from SEQ ID NOs: 1-22, and having an amino acid other than tyrosine at the position corresponding to Y361 of SEQ ID NO:1, wherein the polypeptide confers increased light sensitivity in a plant expressing the polypeptide relative to a control plant lacking the polypeptide.

2. A vector comprising the polynucleotide of claim 1.

3. A polynucleotide construct comprising a promoter not natively associated with the polynucleotide of claim 1 operably linked to the polynucleotide of claim 1.

4. A plant cell comprising the polynucleotide of claim 1 operably linked to a promoter not natively associated with the polynucleotide of claim 1.

5. A plant comprising the plant cell of claim 4.

6. The plant of claim 5, wherein the plant exhibits increased light sensitivity relative to a control plant lacking the polynucleotide.

7. The plant of claim 5, wherein the plant exhibits a decreased height, decreased diameter or a combination thereof relative to a control plant lacking the polynucleotide.

8. The plant of claim 5, wherein the plant exhibits at least one characteristic selected from, increased hyponasty, decreased petiole length, decreased internode length, and decreased hypocotyl length under an R fluence rate of less than 1 μmole m^{-2} sec^{-1}, relative to a control plant lacking the polynucleotide.

9. The plant of claim 5, wherein the plant exhibits enhanced germination relative to the control plant.

10. The plant of claim 9, wherein the plant is corn, soybean or rice.

11. The plant of claim 9, wherein the plant is an ornamental plant.

12. A method of producing a transgenic plant comprising:

(a) introducing into a plant cell a polynucleotide encoding a polypeptide comprising an amino acid sequence having at least 95% identity to at least one amino acid sequence selected from SEQ ID NOs: 1-22 and having an amino acid other than tyrosine at the position corresponding to Y361 of SEQ ID NO:1, wherein the polypeptide confers increased light sensitivity in a plant expressing the polypeptide relative to a control plant lacking the polypeptide; and

(b) regenerating the transformed cell to produce a transgenic plant.

13. The method of claim 12, wherein the transgenic plant exhibits increased light sensitivity relative to a control plant lacking the polynucleotide.

14. The method of claim 13, wherein the transgenic plant exhibits decreased height, decreased diameter, or a combination thereof relative to a control plant lacking the polynucleotide.

15. The method of claim 13, wherein the transgenic plant exhibits at least one characteristic selected from decreased petiole length, decreased internode number, increased hyponasty, and decreased hypocotyl length under an R fluence rate of less than 1 μmole m^{-2} sec^{-1}, relative to a control plant lacking the polynucleotide.

16. The method of claim 12, wherein the transgenic plant exhibits enhanced germination relative to the control plant.

17. The method of claim 16, wherein the transgenic plant is a corn, soybean or rice plant.

18. The method of claim 16, wherein the transgenic plant is an ornamental plant.

19. A transgenic plant produced by the method of claim 12.

20. An isolated polypeptide comprising an amino acid sequence having at least 95% identity to at least one amino acid sequence selected from SEQ ID NOs: 1-22, and having an amino acid other than tyrosine at the position corresponding to Y361 of SEQ ID NO:1, wherein the polypeptide confers increased light sensitivity in a plant expressing the polypeptide relative to a control plant lacking the polypeptide.

21. The isolated polynucleotide of claim 1, further comprising at least one of (i) an amino acid other than aspartate (D) at the position corresponding to 307 of SEQ ID NO:1, (ii) an amino acid other than arginine (R) at the position corresponding to 322 of SEQ ID NO: 1, (iii) an amino acid other than arginine (R) at the position corresponding to 352 of SEQ ID NO: 1, and (iv) an amino acid other than arginine (R) at the position corresponding to 582 of SEQ ID NO: 1.

* * * * *