US 20200354735A1

(19) **United States**

(12) **Patent Application Publication**

LI

(10) **Pub. No.: US 2020/0354735 A1**

(43) **Pub. Date: Nov. 12, 2020**

(54) PLANTS WITH INCREASED SEED SIZE

(71) Applicant: **INSTITUTE OF GENETICS AND DEVELOPMENTAL BIOLOGY CHINESE ACADEMY OF SCIENCES**, Beijing (CN)

(72) Inventor: **YUNHAI LI**, BEIJING (CN)

(21) Appl. No.: **16/946,783**

(22) Filed: **Jul. 6, 2020**

Related U.S. Application Data

(63) Continuation of application No. 15/548,398, filed on Aug. 2, 2017, filed as application No. PCT/GB2016/050245 on Feb. 3, 2016.

(30) **Foreign Application Priority Data**

Feb. 3, 2015 (CN) PCT/CN2015/072143

Publication Classification

(51) **Int. Cl.**

C12N 15/82 (2006.01)

C07K 14/415 (2006.01)

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

CPC ***C12N 15/8218*** (2013.01); ***C12N 15/8261*** (2013.01); ***C07K 14/415*** (2013.01)

(57) ABSTRACT

The invention relates to genetically modified plants with an altered seed phenotype, in particular increased seed size. The invention relates to a plant that does not produce a functional NGAL2 polypeptide or functional NGAL2 and NGAL3 polypeptides. NGAL2 and NGAL3 are members of the RAV family and comprise a B3 DNA-binding domain and a transcriptional repression motif.

Specification includes a Sequence Listing.

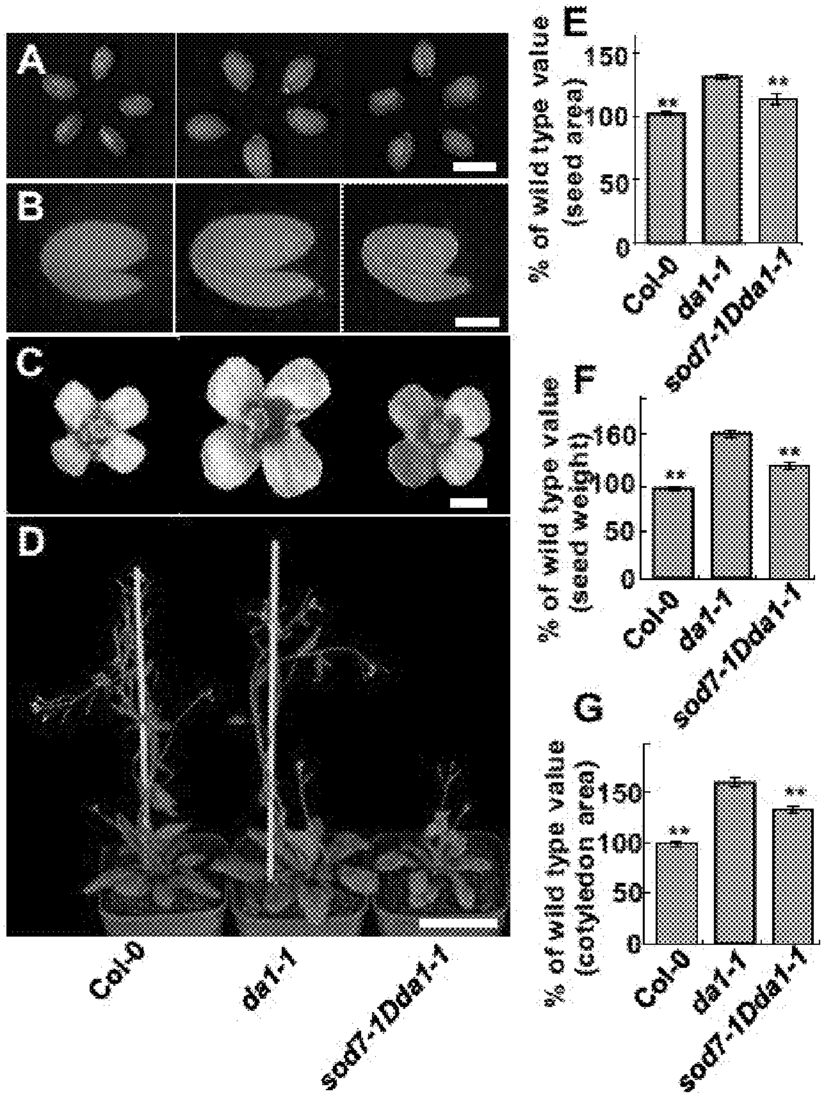


Figure 1

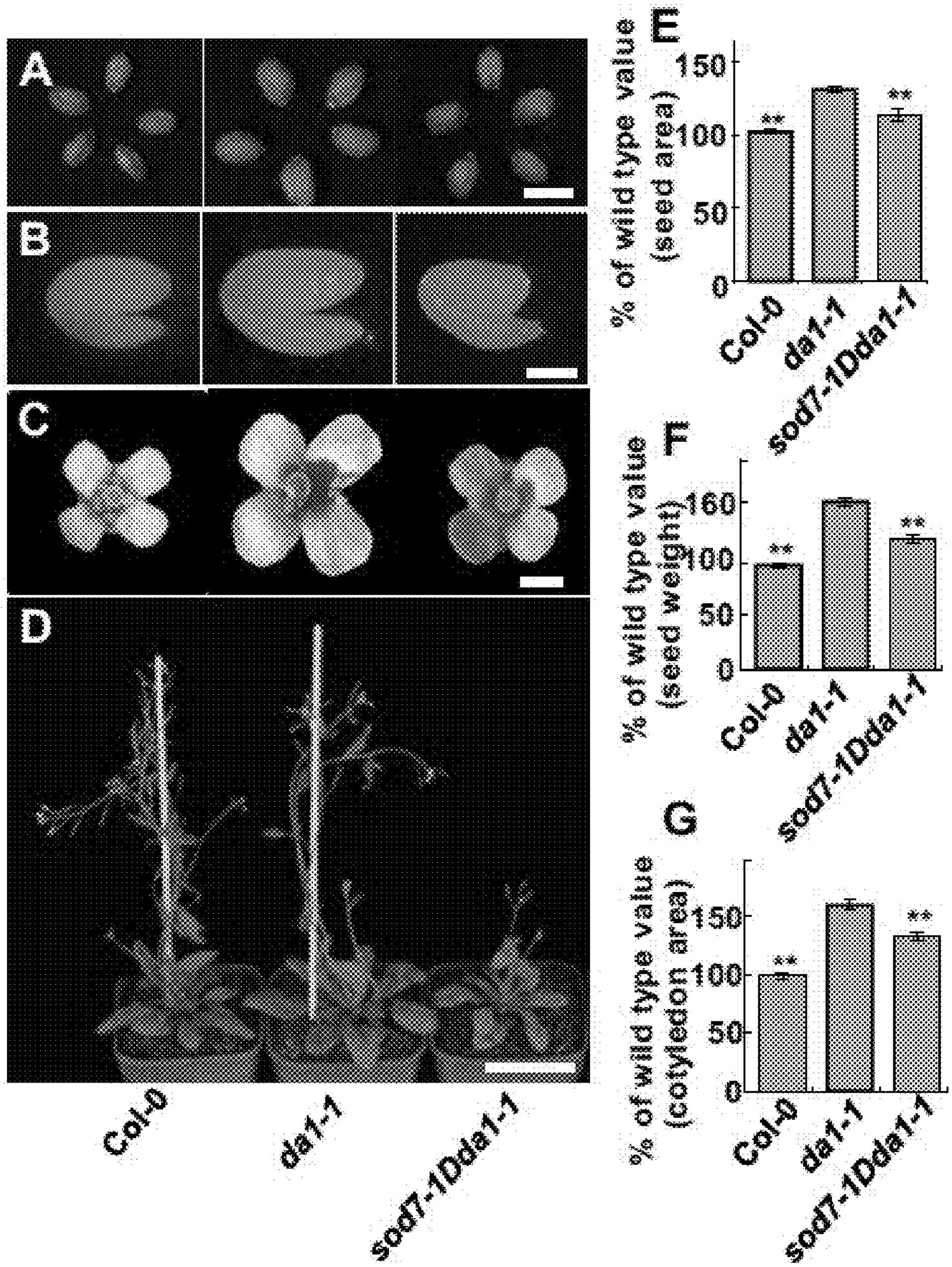

A
B
C
D
Col-0
da1-1
sod7-1Dda1-1
E
% of wild type value (seed area)
0
50
100
150
**
**
Col-0
da1-1
sod7-1Dda1-1
F
% of wild type value (seed weight)
0
50
100
150
**
**
Col-0
da1-1
sod7-1Dda1-1
G
% of wild type value (cotyledon area)
0
50
100
150
**
**
Col-0
da1-1
sod7-1Dda1-1

Figure 2

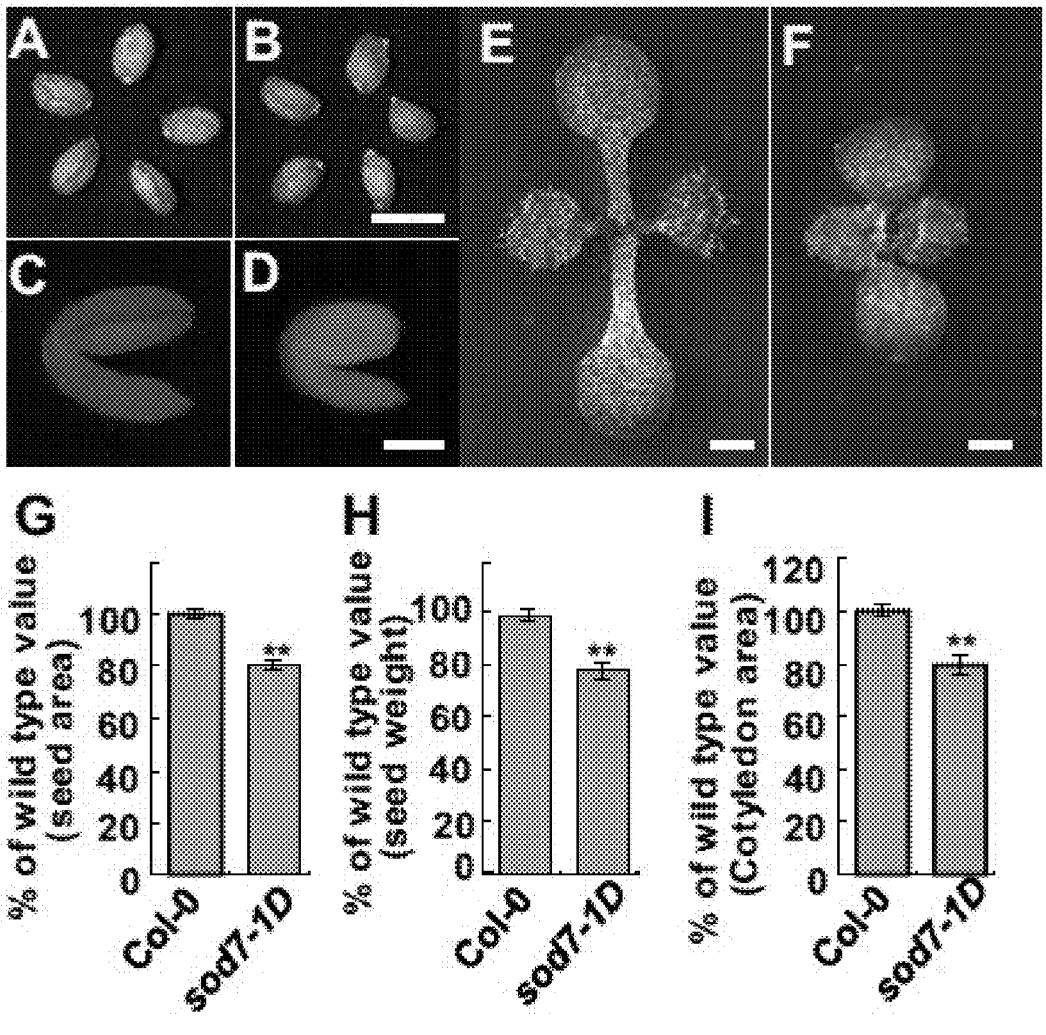

A
B
C
D
E
F
G
% of wild type value (seed area)
0
20
40
60
80
100
Col-0
sod7-1D
**
H
% of wild type value (seed weight)
0
20
40
60
80
100
Col-0
sod7-1D
**
I
% of wild type value (Cotyledon area)
0
20
40
60
80
100
120
Col-0
sod7-1D
**

Figure 3

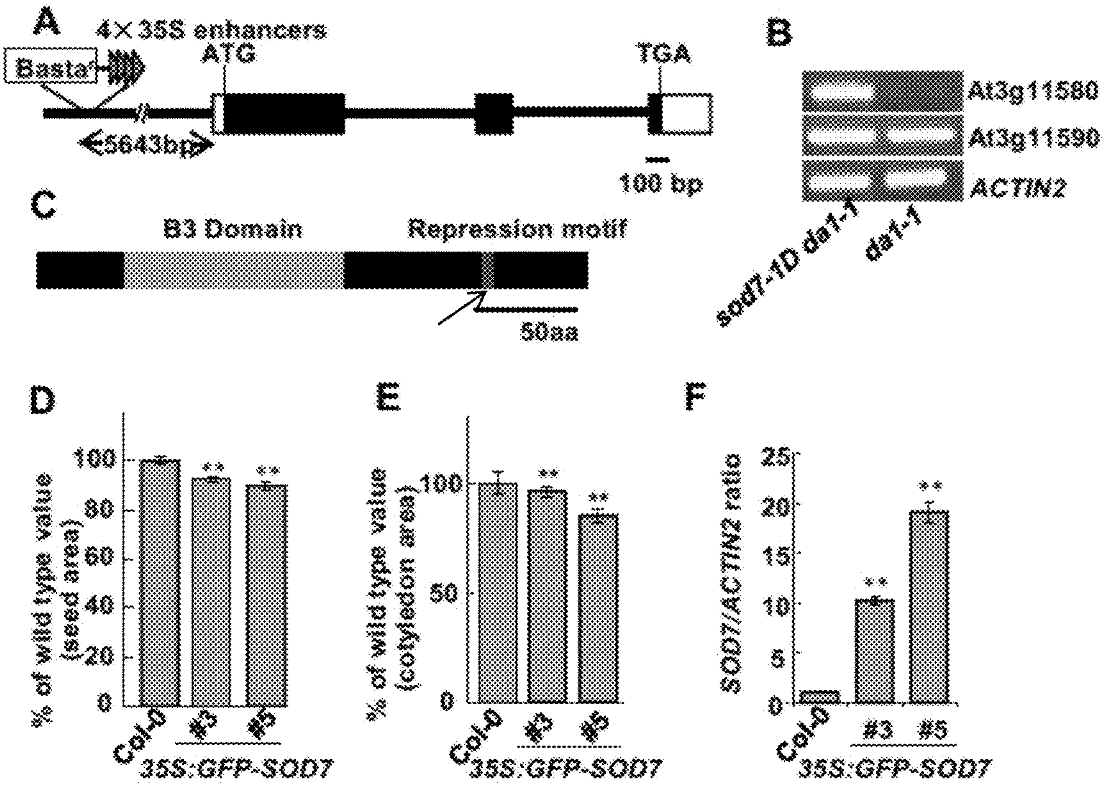

A
4×35S enhancers
Basta
ATG
TGA
5643bp
100 bp
B
At3g11580
At3g11590
ACTIN2
sod7-1D da1-1
da1-1
C
B3 Domain
Repression motif
50aa
D
% of wild type value (seed area)
100
80
60
40
20
0
Col-0
#3
#5
35S:GFP-SOD7
**
E
% of wild type value (cotyledon area)
100
50
0
Col-0
#3
#5
35S:GFP-SOD7
F
SOD7/ACTIN2 ratio
25
20
15
10
5
0
Col-0
#3
#5
35S:GFP-SOD7

Figure 4

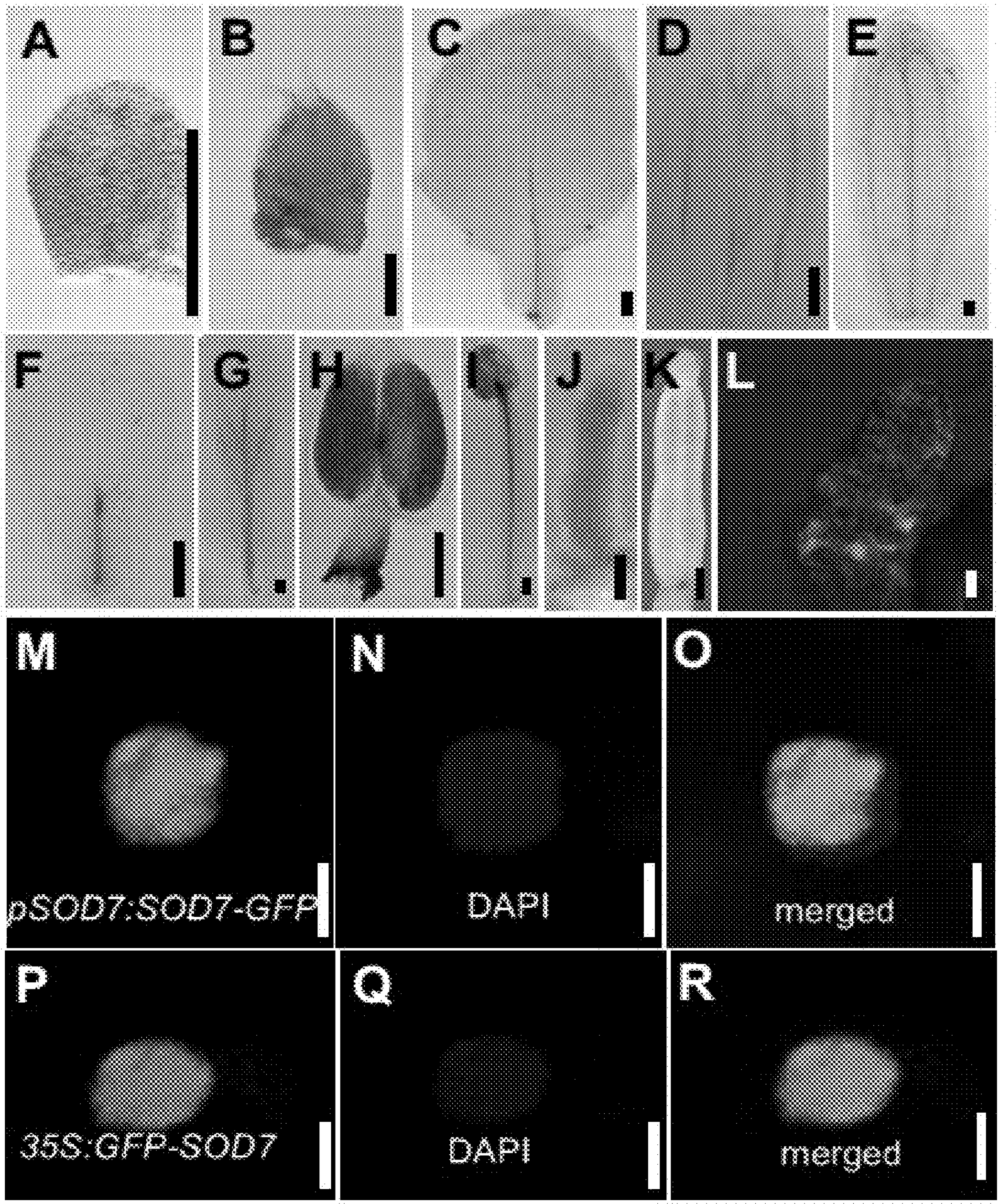

A
B
C
D
E
F
G
H
I
J
K
L
M
pSOD7:SOD7-GFP
N
DAPI
O
merged
P
35S:GFP-SOD7
Q
DAPI
R
merged

Figure 5

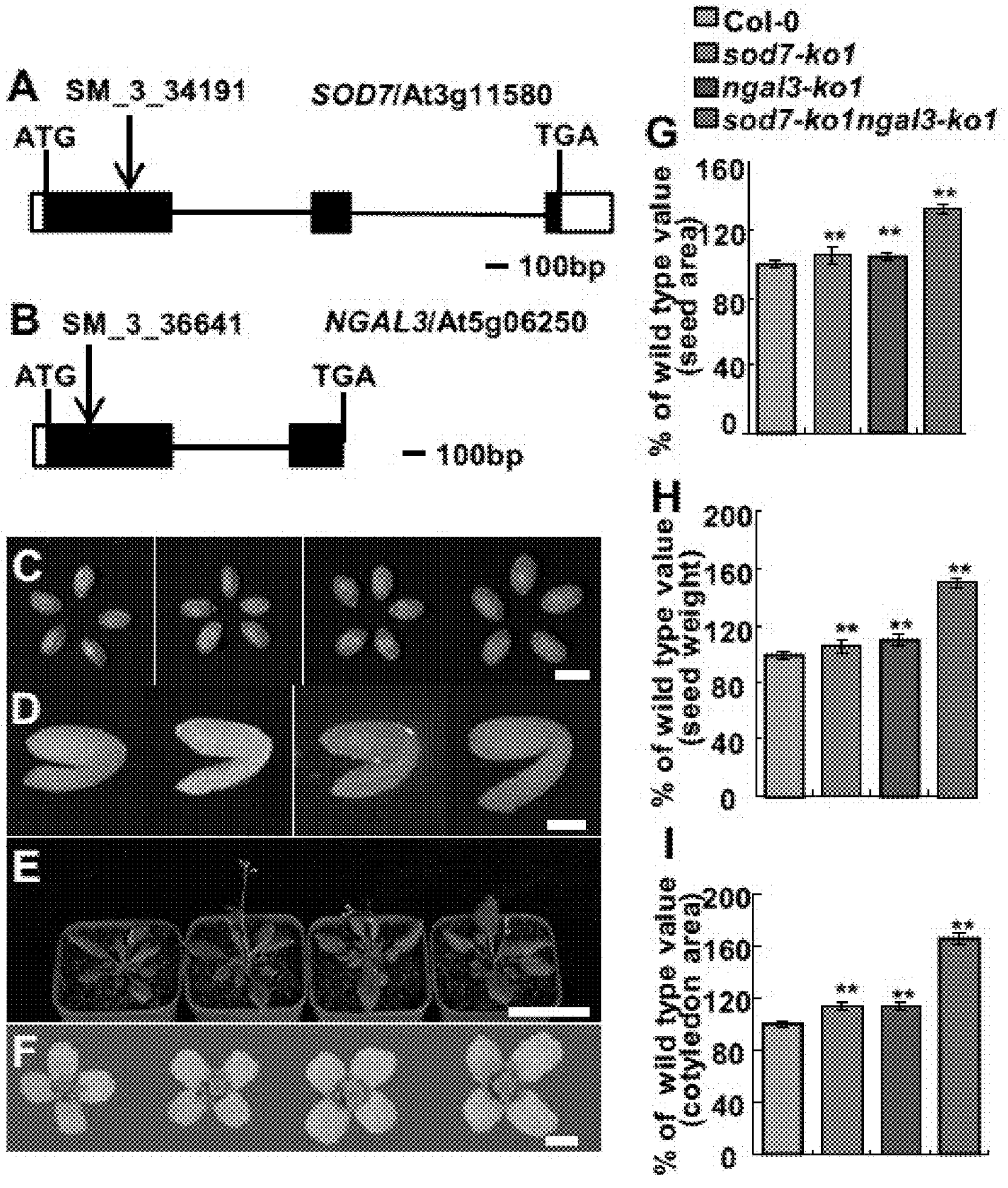

A
SM_3_34191
SOD7/At3g11580
ATG
TGA
100bp
B
SM_3_36641
NGAL3/At5g06250
ATG
TGA
100bp
C
D
E
F
▨Col-0
▨*sod7-ko1*
▨*ngal3-ko1*
▨*sod7-ko1ngal3-ko1*
G
% of wild type value (seed area)
0
40
80
120
160
**
H
% of wild type value (seed weight)
0
40
80
120
160
200
I
% of wild type value (cotyledon area)
0
40
80
120
160
200

Figure 6

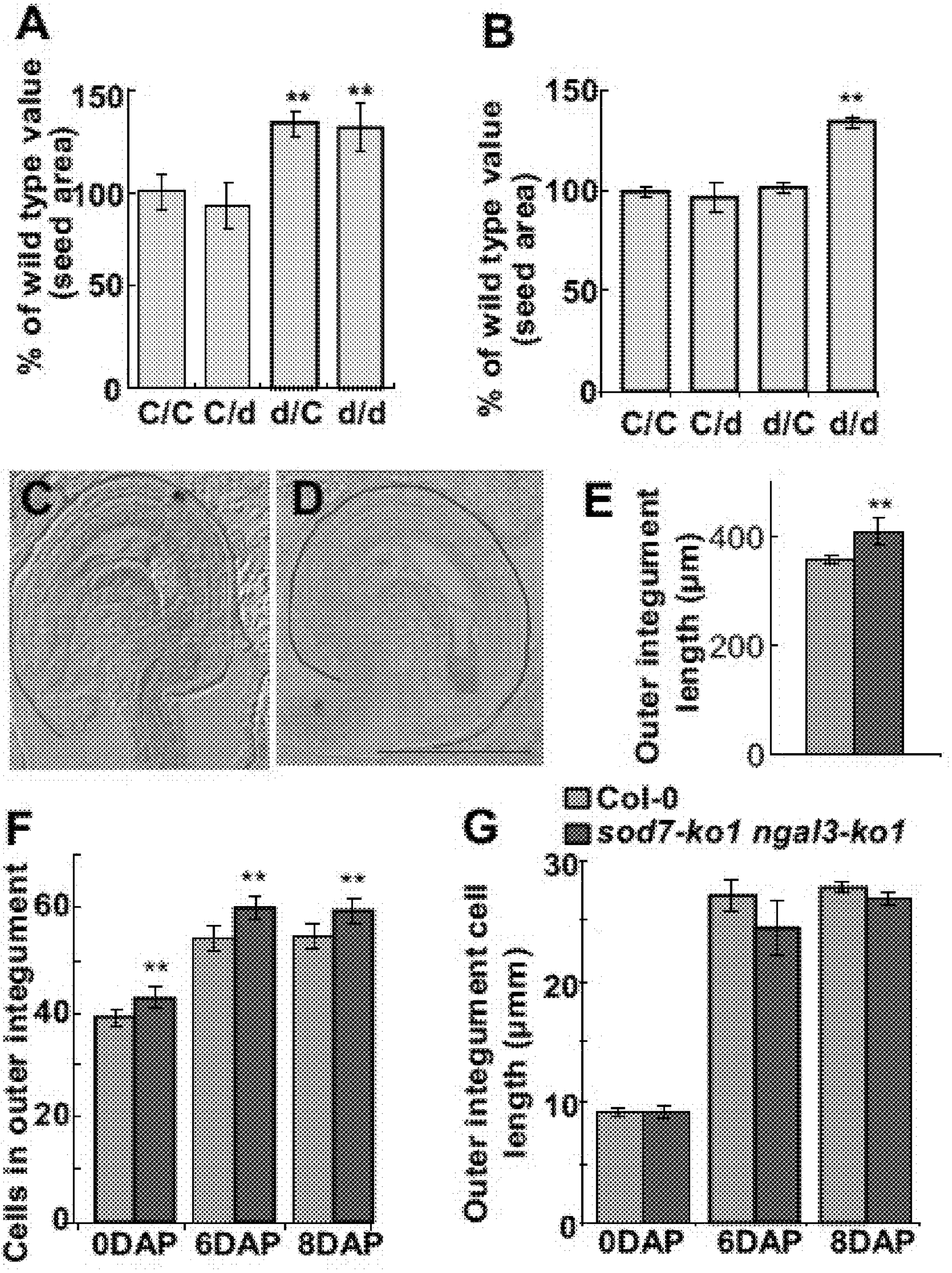

A
% of wild type value (seed area)
150
100
50
0
**
**
C/C C/d d/C d/d
B
% of wild type value (seed area)
150
100
50
0
**
C/C C/d d/C d/d
C
D
E
Outer integument length (μm)
400
200
0
**
F
Cells in outer integument
60
40
20
0
**
**
**
0DAP 6DAP 8DAP
G
▨ Col-0
■ sod7-ko1 ngal3-ko1
Outer integument cell length (μmm)
30
20
10
0
0DAP 6DAP 8DAP

Figure 7

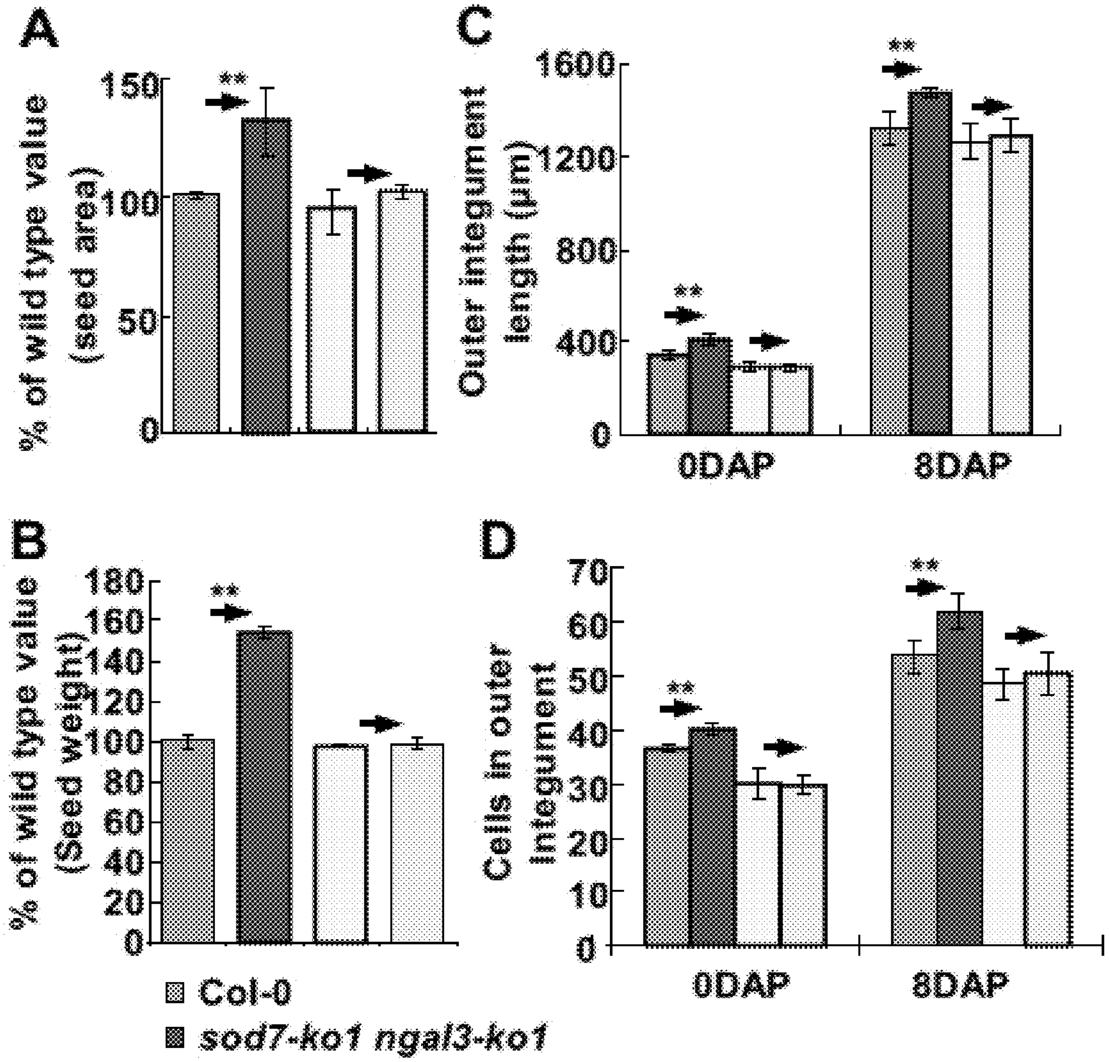

A
% of wild type value (seed area)
150
100
50
0
**
B
% of wild type value (Seed weight)
180
160
140
120
100
80
60
40
20
0
**
C
Outer integument length (μm)
1600
1200
800
400
0
**
**
0DAP
8DAP
D
Cells in outer integument
70
60
50
40
30
20
10
0
**
**
0DAP
8DAP
▨ Col-0
▨ *sod7-ko1 ngal3-ko1*
☐ *klu-4*
☐ *klu-4 sod7-ko1 ngal3-ko1*

Figure 8

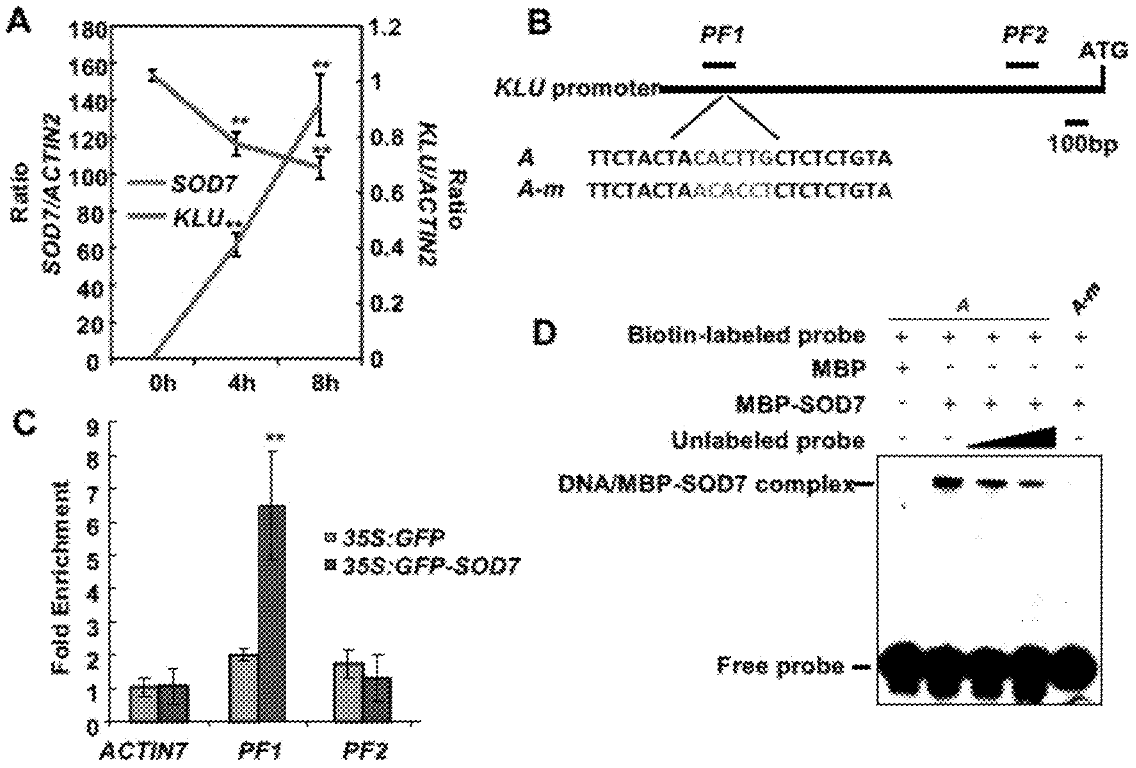

A
Ratio SOD7/ACTIN2
180
160
140
120
100
80
60
40
20
0
Ratio KLU/ACTIN2
1.2
1
0.8
0.6
0.4
0.2
0
SOD7
KLU
**
0h
4h
8h
B
PF1
PF2
ATG
KLU promoter
100bp
A TTCTACTACACTTGCTCTCTGTA
A-m TTCTACTAACACCTCTCTCTGTA
C
Fold Enrichment
9
8
7
6
5
4
3
2
1
0
35S:GFP
35S:GFP-SOD7
**
ACTIN7
PF1
PF2
D
A
A-m
Biotin-labeled probe + + + + +
MBP + - - - -
MBP-SOD7 - + + + +
Unlabeled probe - -
DNA/MBP-SOD7 complex
Free probe

Figure 9

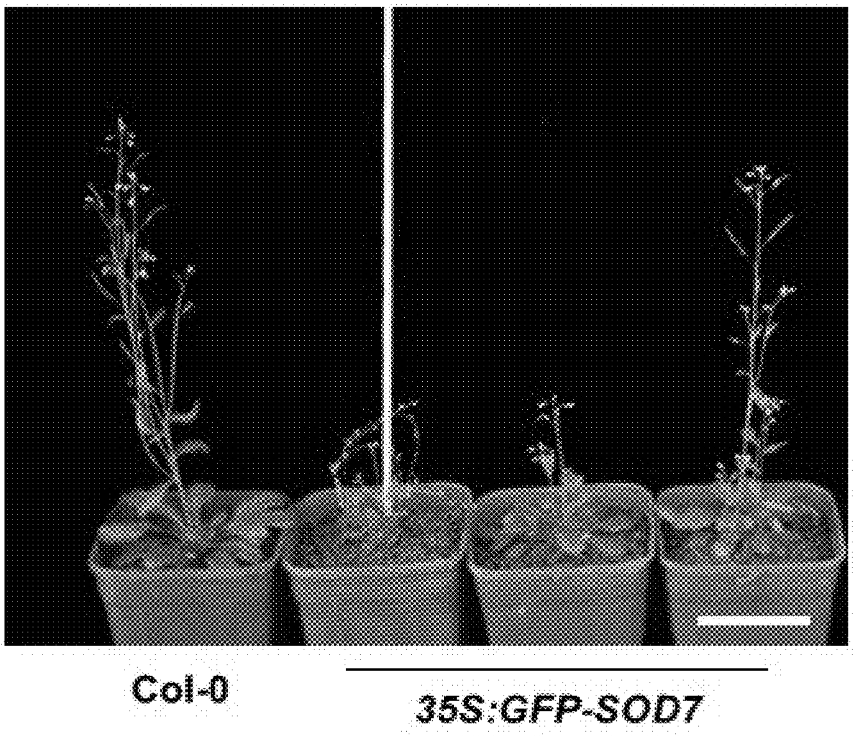


Figure 10

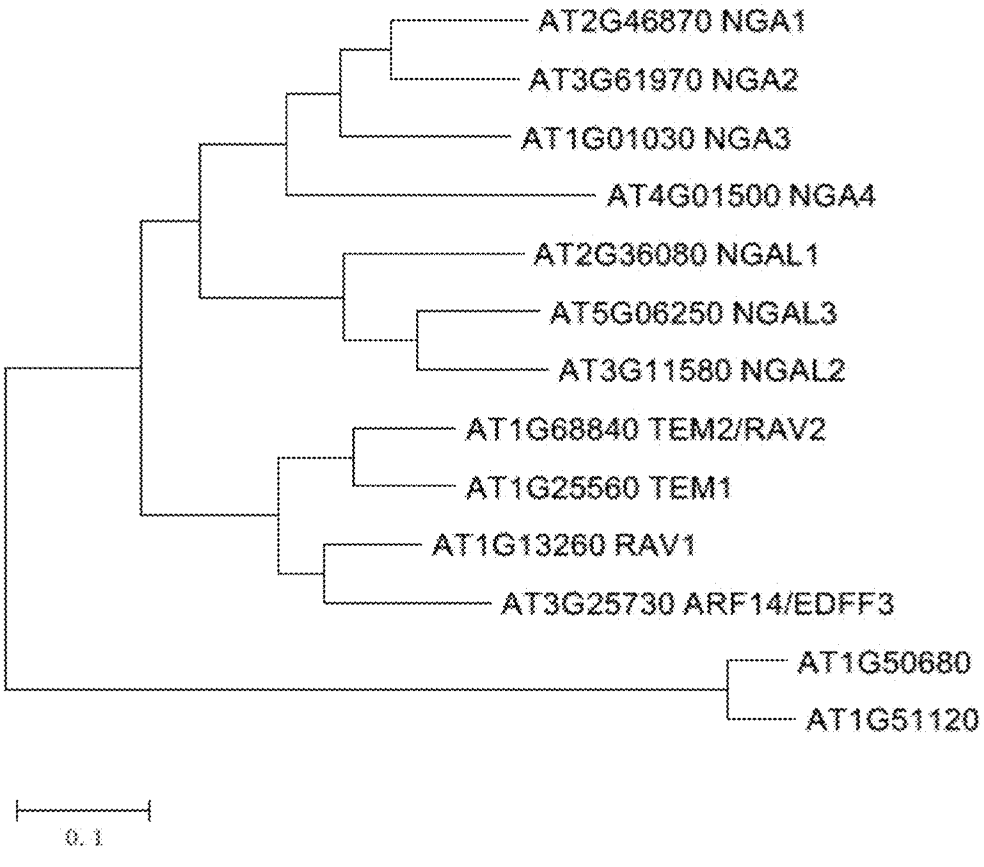

AT2G46870 NGA1
AT3G61970 NGA2
AT1G01030 NGA3
AT4G01500 NGA4
AT2G36080 NGAL1
AT5G06250 NGAL3
AT3G11580 NGAL2
AT1G68840 TEM2/RAV2
AT1G25560 TEM1
AT1G13260 RAV1
AT3G25730 ARF14/EDFF3
AT1G50680
AT1G51120
0.1

Figure 11

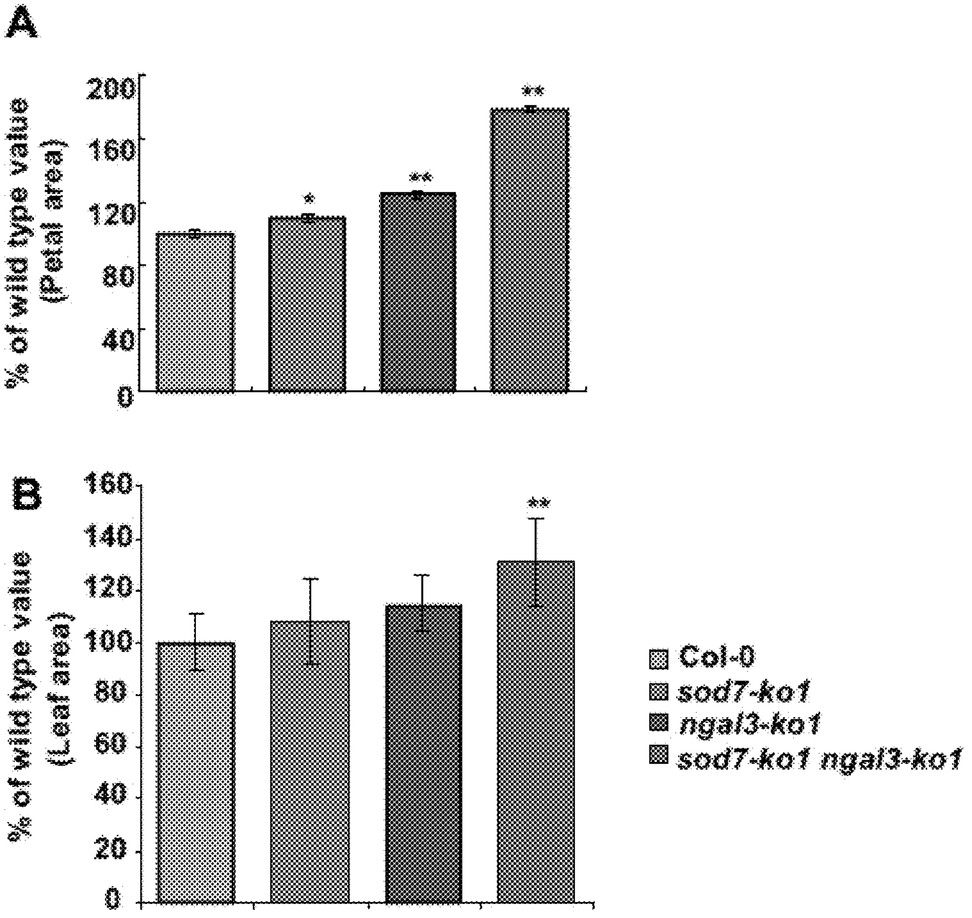
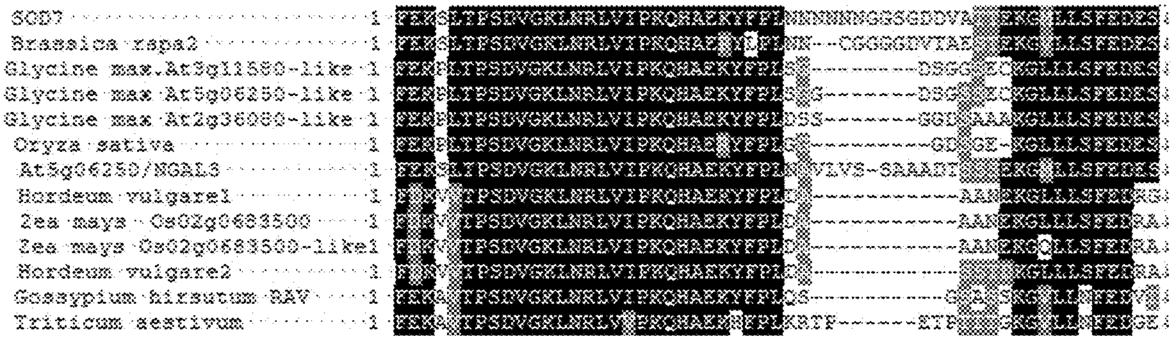


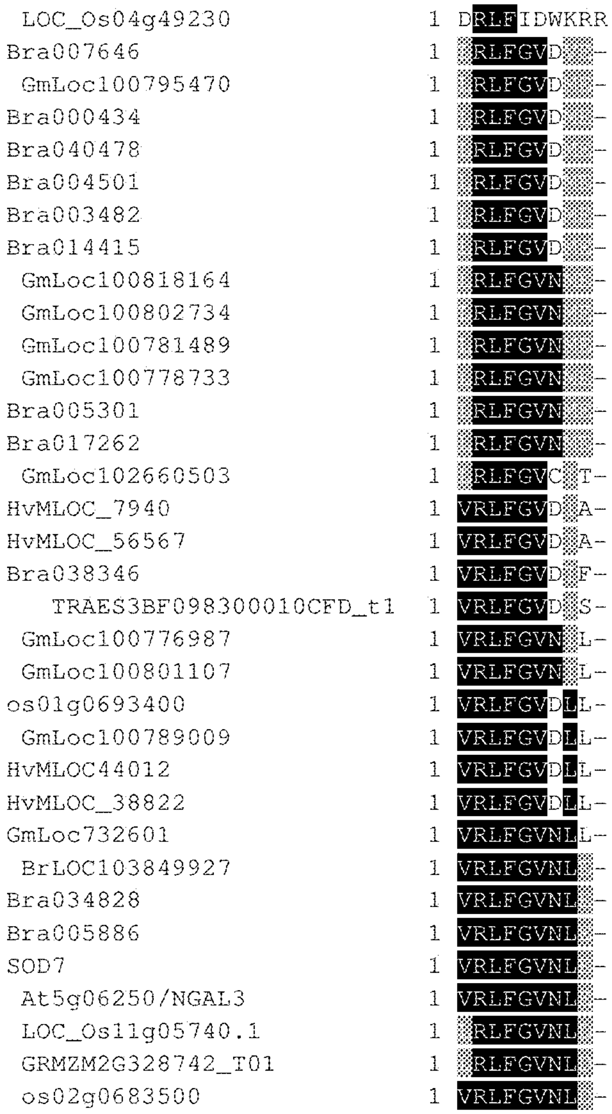
Figure 12

A




58 GKCW FRYSYWNSSQSYVLTKGWSR VK KHLDAGDVVFFQRHR--FDLHRLFIGW-RRRGE 116
56 GKSW FRYSYWNSSQSYVLTKGWSR VK KHLNAGDVVLFQRHR--FDIHRLFIGWRRRGE 114
50 GKCWRFRYSYWNSSQSYVLTKGWSR VK KRLDAGDVVLFERHR--VDAQRLFIGWRRR-- 106
51 GKCWRFRYSYWNSSQSYVLTKGWSR VK KRLDAGDVVLFQRHR-- DAQRLFIGWRRR-- 107
51 GKCWRFRYSYWNSSQSYVLTKGWSR VK KRLHAGDVVLFHRHR-- HPQRFFISCTRH-- 107
48 GKPWRFRYSYWTSSQSYVLTKGWSR VK KRLDAGDVVHFERVRGL AADRLFIGCRRRGE 108
57 GKSWRFRYSYWNSSQSYVLTKGWSR VK KQLDPGDVVFFQRHR--SDSRRLFIGWRRRGQ 115
47 GKLWRFRYSYWNSSQSYV TKGWSR VK KRLDAGDIVSFCRGAAD TRDRLFIDW RRVE 107
47 GKLWRFRYSYWNSSQSYV TKGWSR VK KRLDAGDIVSFCRGAAD ARDRLFIDWR R-- 105
47 GKLWRFRYSYWNSSQSYV TKGWSR VK KRLDAGDIVSFCRGAGDTARDRLFIDW RRAD 107
47 GKPWRFRYSYWNSSQSYV TKGWSR VK KRLDAGDIVSFGRGVGE ARGRLFIDWRRRPD 107
48 GKVWRFRYSYWNSSQSYVLIKGWSR VK KNLNAGD VSFIKST-- TEKQL IDW AR-- 104
52 GKVWRFRYSYWNSSQSYVLTKGWSR V KGLGAGDS LFSCSL--YEQE QF-------- 102

B


LOC_Os04g49230 1 DRLFIDWKRR
Bra007646 1 RLFGVD -
GmLoc100795470 1 RLFGVD -
Bra000434 1 RLFGVD -
Bra040478 1 RLFGVD -
Bra004501 1 RLFGVD -
Bra003482 1 RLFGVD -
Bra014415 1 RLFGVD -
GmLoc100818164 1 RLFGVN -
GmLoc100802734 1 RLFGVN -
GmLoc100781489 1 RLFGVN -
GmLoc100778733 1 RLFGVN -
Bra005301 1 RLFGVN -
Bra017262 1 RLFGVN -
GmLoc102660503 1 RLFGVC T-
HvMLOC_7940 1 VRLFGVD A-
HvMLOC_56567 1 VRLFGVD A-
Bra038346 1 VRLFGVD F-
TRAES3BF098300010CFD_t1 1 VRLFGVD S-
GmLoc100776987 1 VRLFGVN L-
GmLoc100801107 1 VRLFGVN L-
os01g0693400 1 VRLFGVDLL-
GmLoc100789009 1 VRLFGVDLL-
HvMLOC44012 1 VRLFGVDLL-
HvMLOC_38822 1 VRLFGVDLL-
GmLoc732601 1 VRLFGVNLL-
BrLOC103849927 1 VRLFGVNL -
Bra034828 1 VRLFGVNL -
Bra005886 1 VRLFGVNL -
SOD7 1 VRLFGVNL -
At5g06250/NGAL3 1 VRLFGVNL -
LOC_Os11g05740.1 1 RLFGVNL -
GRMZM2G328742_T01 1 RLFGVNL -
os02g0683500 1 VRLFGVNL -

```
LOC_Os03g02900            1 VRLFGVNL░-
Os10g0537100              1 VRLFGVNL░-
HvMLOC_66387              1 VRLFGVNL░-
GRMZM2G102059_T01         1 VRLFGVNL░-
GRMZM2G082227_T01         1 VRLFGVNL░-
GRMZM2G024948_T01         1 VRLFGVNL░-
GRMZM2G142999_T01         1 VRLFGVNL░-
GRMZM2G125095_T01         1 VRLFGVNL░-
```

Figure 13

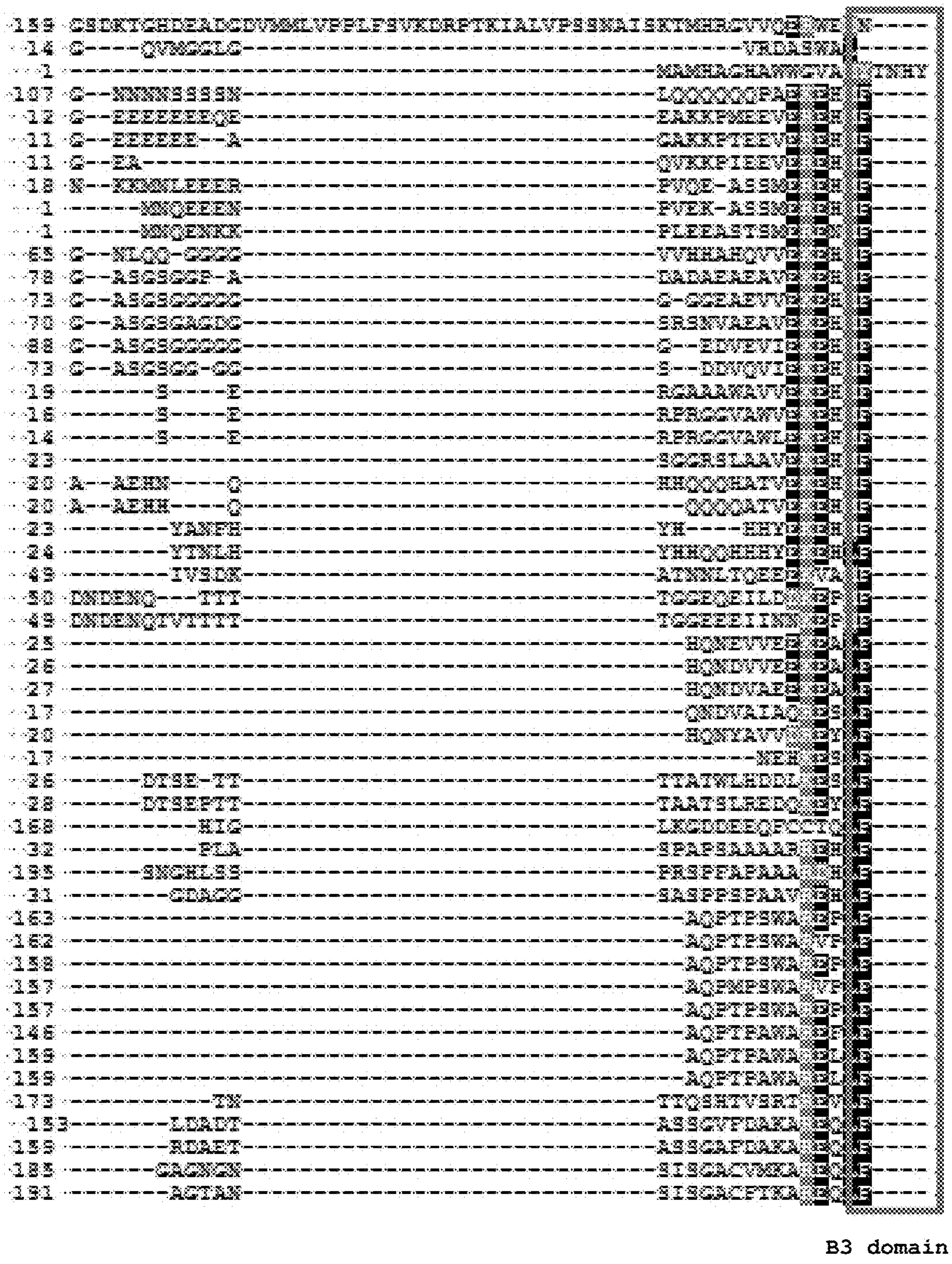
```
1 ----------------------------MAAS----------------PSSPLTAPPEPV
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 ------------------------------------------------------------
1 -------MIGVEKVTICMRIEVNT------------------------EKGRR------A
1 ------------------------------------------------------------
1 ----------MDSS-SCLVDDTNSGCSS---------TDKL---------RALAAAAAET
1 ------------------------------------------------------------
1 --------MGVEIL-SSTGEHSS------QYSSGAASTATT-------ESGVGGRPPTAP
1 --------MGMEIL-SSTVEHCS------QYSSSA-STATT-------ESGAAGRSTTAL
1 --------MGVEIL-SSMVEDSS------QYSSGA-STATT-------ESGTTGRALTAL
1 --------MGVEIL-SSMVEHSF------QYSSGA-SSATA-------ESGAVGTPPRHL
1 --------MGVEIL-SSMVEHSF------QYSSGV-STATT-------ESGTAGTPPRPL
1 MASSKPTNP--EVD-MD-----M------ECSS-------P-------ESGAEDAV-ESS
1 MASGKPTNHGMEDD-MD-----M------EYSS-------A-------ESGAEDAA-EPS
1 MASGKPTNHGMEDD-MD-----M------EYSS-------A-------ESGAEDAA-EPS
1 -----------MVF-SCIDESSST---SESFSPAT-ATAT-------ATATKPSAPPLPP
1 ----------MDGG-CVIDETT-TSSDS--------------------LSV------PP-
1 ----------MDGG-SVIDETT-TTSNS--------------------LSVPANLSPPP-
1 ----------MDAI-SCLDESTTTESLSIS---------QAKPSSTIMSSEKASPSPPPP
1 ----------MDAI-SCNDESTTTESLSISLSPTS-SSEKAKPSSMITSSEKVSLSPPPS
```

```
17 TPPSPWTITDGAISGTLPAAEAFAVHYPGYPSSP---ARAARTLGGLPGLAKVRSSDPGA ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
-1 ------------------------------------------------------------ ↵
24 LMDC-WQIS-G-------------VHESSDC-SEIK-----FAFDAVVKRAR---HEENN ↵
-1 ------------------------------------------------------------ ↵
32 APLE-RMGS-GA----------SAVVDAAEPGAEADSGSGGRVGGGGGGGAG---GAGGK ↵
-1 ------------------------------------------------------------ ↵
39 SLP---------------------VSIAD---ES--------------ATSR---SASAQ ↵
38 SLP---------------------VAITD---ES--------------VTSR---SASAQ ↵
38 SLP---------------------VAIAD---ES--------------VTS-------AQ ↵
38 SLP---------------------VAIAD---ES--------------LTS--------R ↵
38 SLP---------------------VAIAD---ES--------------VTS--------R ↵
32 --------------------------------------------------------SPVA ↵
34 SSP-----------------------------------------------VL---APPRA ↵
34 SSP-----------------------------------------------VL---APPRA ↵
38 LRLN-RMRS-GS----------SNVVLDSKNG------------------VD---IDSRK ↵
22 --PS-RVGS-VA----------SAVVDPDGCCVS----------------GE---AESRK ↵
28 --LS-LVGS-GA----------TAVVYPDGCCVS----------------GE---AESRK ↵
41 MRLC-RVGS-GA----------SAVVDSDGGGGG--------------GSTE---VESRK ↵
49 MRLC-RVGS-GA----------SAVVDPDGGGSG----------------AE---VESRK ↵
```

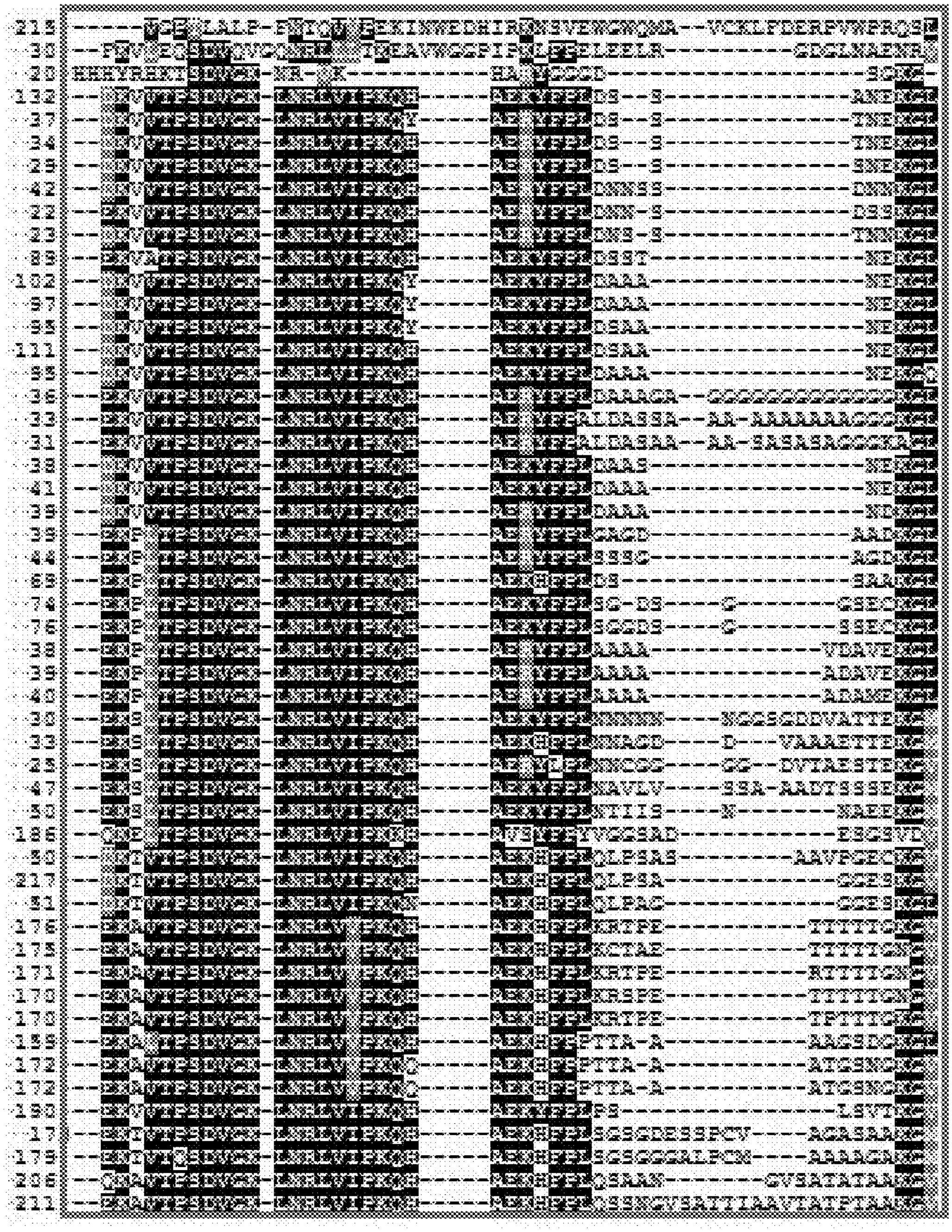
```
74 RLELRFRPEDPYCHPAFGQSRAST---GLLLRLSKRKGAAAPCAHVVA------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ---------------------MELMQ-EVKG-YSDGREEEEEEEEAAEEII---------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ---------------------MELMQ-QVKGNYSDSREEEE-------------------
 1 ---------------------MDQFA--ASGRFSREEEADE-------------------
 1 ---------------------MEFTT---SSRFSKE--EED-------------------
 1 ---------------------MEFTA--TSSRFSKGEEEVE-------------------
 1 ---------------------MEFAT--TSSRFSKEEEEEEEGEQEMEQEQ---------
 1 ---------------------MEFAS--SSSRFSREEDEEEE--------Q---------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
 1 ------------------------------------------------------------
60 AAAQKFKGVVSQQNGNWGAQIYAHQQRIWLGTFKSEREAAMAYDSASIKLRSGECHRNFP
 1 ------------------------------------------------------------
77 LPSSKFKGVVPQPNGRWGAQIYERHQRVWLGTFAGEDDAARAYDVAAQRFRGRDAVTNFR
 1 ------------------------------------------------------------
58 STSSRFKGVVPQPNGRWGAQIYERHARVWLGTFPDEDSAARAYDVAALRYRGREAATNFP
57 PASSRFKGVVPQPNGRWGSQIYERHARVWLGTFPDQDSAARAYDVASLRYRGRDAATNFP
53 SAPSRFKGVVPQPNGRWGSQIYERHARVWLGTFPDQDLAARAYDVAALRYRGRDAATNFP
52 SASSRFKGVVPQPNGRWGAQIYERHARVWLGTFPDQDSAARAYDVASLRYRGGDAAFNFP
52 SASSRFKGVVPQPNGRWGAQIYERHARVWLGTFPDQDSAARAYDVASLRYRGRDVAFNFP
36 APSSRFKGVVPQPNGRWGAQIYEKHSRVWLGTFGDEEAAACAYDVAALRFRGRDAVTNHQ
44 APSSRFKGVVPQPNGRWGAQIYEKHSRVWLGTFPDEDAAVRAYDVAALRFRGPDAVINHQ
44 APSSRFKGVVPQPNGRWGAQIYEKHSRVWLGTFPDEDAAARAYDVAALRFRGPDAVINHQ
65 LSSSKYKGVVPQPNGRWGAQIYVKHQRVWLGTFCDEEEAAHSYDIAARKFRGRDAVVNFK
49 LPSSKYKGVVPQPNGRWGAQIYEKHQRVWLGTFNEEDEAARAYDIAALRFRGPDAVTNFK
55 LPSSKYKGVVPQPNGRWGAQIYEKHQRVWLGTFNEEDEAARAYDIAAHRFRGRDAVTNFK
72 LPSSKYKGVVPQPNGRWGSQIYEKHQRVWLGTFNEEDEAARAYDVAVQRFRGKDAVTNFK
78 LPSSKYKGVVPQPNGRWGAQIYEKHQRVWLGTFNEEDEAARAYDIAAQRFRGKDAVTNFK
```

```
119 -----------------------------------RSRTAYYFEGMADFQ---HVVFVHA
  1 ------------------------------------------------------------
  1 ------------------------------------------------------------
 25 ---------------TREESSRLLHQHQEAAGSNFISNNHHHHQHHHH------------
  1 ------------------------------------------------------------
  1 ------------------------------------------------------------
  1 ------------------------------------------------------------
  1 ------------------------------------------------------------
  1 ------------------------------------------------------------
  1 ------------------------------------------------------------
 20 ------------------EE-------------------------EAA------------
 19 -----------------EQE-------------------------DAS------------
 16 ------------------EE-------------------------QDE------------
 19 ------------------EE-------------------------QEE------------
 29 ---------------DEEEE-------------------------EAE------------
 21 ---------------EEEEE-------------------------EEE------------
  1 ------------------------------------------------------------
  1 ------------------------------------------------------------
  1 ------------------------------------------------------------
  1 ------------------------------------------------------------
  1 ------------------------------------------------------------
  1 ------------------------------------------------------------
  1 ------------------------------------MAMNHFL-FSQEQP---QSNPWGV
  1 ------------------------------------MATNHLSQGQHQHP---QANPWGV
  1 -----------------------------------MSSINHY---SPETT---LYWTNDQ
  1 ------------------------------------MSINHYSMDLPEPT---LWWPHPH
  1 ------------------------------------MSTNHYTMDLPEPT---LWWPHPH
  1 ------------------------------------MSINQYSSEFYYH---SLNWQQQQ
  1 ------------------------------------MSINQYSSDFHYH---SLNWQQQQ
  1 ------------------------------------MSINQYSSDFNYH---SLNWQQQQ
  1 ------------------------------------MSVNHYHN----TLS-----LH--
  1 ------------------------------------MSCNHYSRDIHHNTPS----V---
  1 ------------------------------------MSVNHYSNTL----S-----SH--
  1 ------------------------------------MSVNHYSTDHHHTL----LWQQQQ
  1 ------------------------------------MSVNHYSTDHHQVHHHHTLFLQ--
120 WNDQ------------TVQEPQFQSHYSAETVLN-MSRDGTYPSKFAT------------
  1 -----------------------------------MSRKHIYFDELAQ------------
137 PLAEADP--------DAAAELRFLATRSKAEVVD-MSRKHIYFDELAQ------------
  1 -----------------------------------MSRKHTYFDELAQ------------
118 CAA-------------AEAELAFLAAHSKAEIVD-MSRKHTYTDELRQ------------
117 CAA-------------AEAELAFLTAHSKAEIVD-MSRKHTYADELRQ------------
113 CAA-------------AEAELAFLGAHSKAEIVD-MSRKHTYADELRQ------------
112 CVV-------------VEAELAFLAAHSKAEIVD-MSRKQTYADELRQ------------
112 CAA-------------VEGELAFLAAHSKAEIVD-MSRKQTYADELRQ------------
 96 RLPAAEGAGWSS-----TSELAFLADHSKAEIVD-MSRKHTYDDELRQ------------
104 RPTAAEEAGSSSSRSELDPELGFLADHSKAEIVD-MSRKHTYDDELRQ------------
104 RPTAAEEAGSSSSRSELDPELGFLADHSKAEIVD-MSRKHTYDDELRQ------------
125 TFLASED---------DNGELCFLEAHSKAEIVD-MSRKHTYADELAQ------------
 108SPPAASD-----------DAESEFLNSHSKPEIVD-MSRKHTYDDELQQ------------
115 PLAGAD-----------DAEAEFLSTHSKSEIVD-MSRKHTYDNELQQ------------
132 PLSGTDD---------DDGESEFLNSHSKSEIVD-MSRKHTYNDELEQ------------
138 PLAGADD---------DDGESEFLNSHSKPEIVD-MSRKHTYNDELEQ------------
```

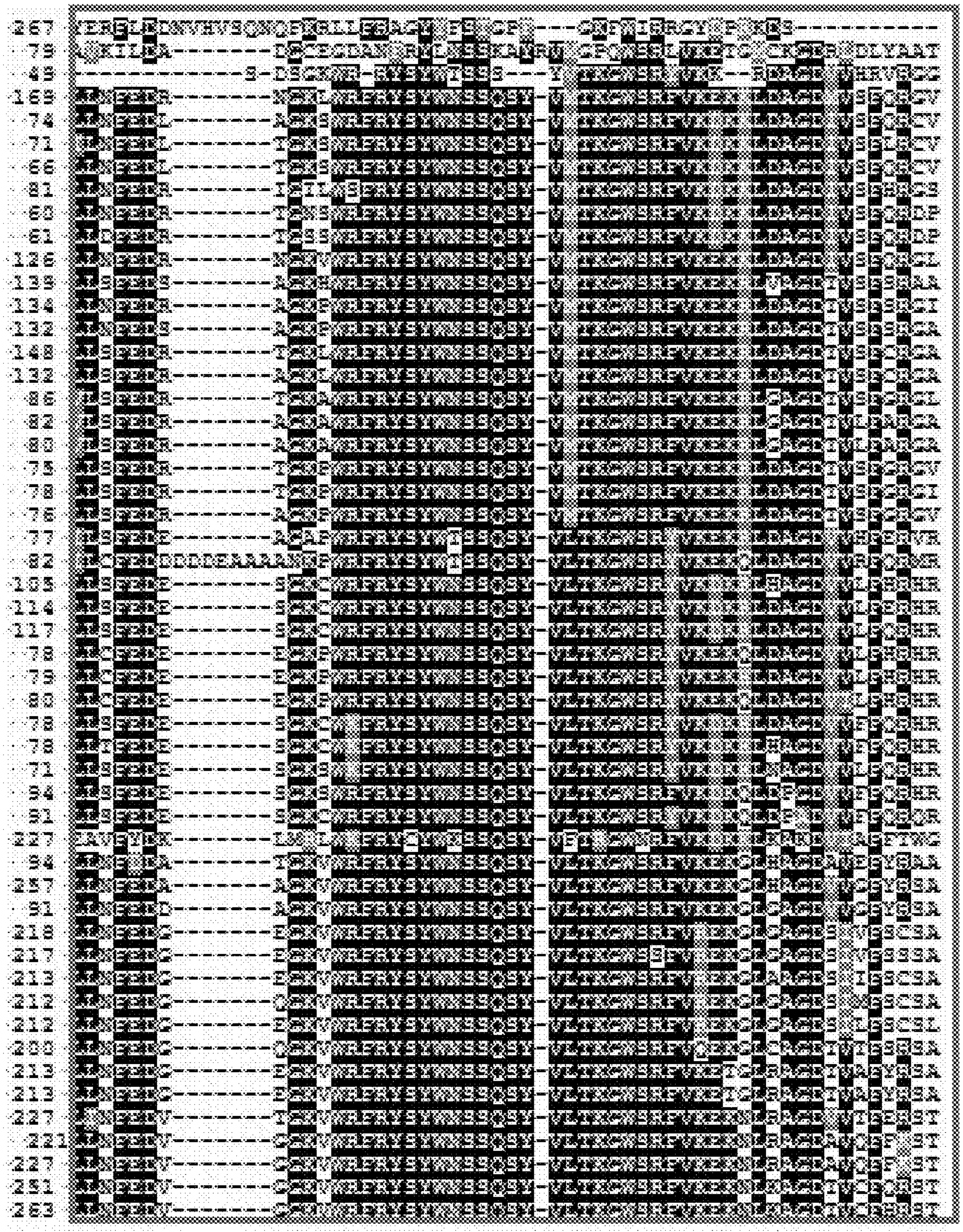
```
141 AQT▨KR------------------------------------------KHSDSQNDMENF
  1 ----------------------------------MYC-SR------GRIDPAE------E
  1 ------------------------------------------------------------
 63 HTT▨QLDFMDLSLGSSKDEGNLQ------GSSSSVYAHH-----HHAASA--SS---SAN
  1 -----MMMTNLS-----------------------------------------L---SRE
  1 ------MMTNLS-----------------------------------------L---ARE
  1 ------MMTNLS-----------------------------------------L---ARE
  1 -----MERKSNDL---------------------------------ERSE--NI---DSQ
  1 ------------------------------------------------------------
  1 ------------------------------------------------------------
 25 AIT▨ESESSRLHQQ----------------DTASNFGKKLDLMDLSLGS-SKEE---EEE
 25 NSM▨EISFMPPAAASSSSAAASASA----SASTSASACASGSSSAPFRSASASG---DAA
 21 AGR▨EIPFMTATAEAAPAPTSSSSSPAHHAASASASASAS-GSSTPFRSD-------DGA
 24 ASM▨EIPFMTPAAATCAA------APPSASASASTPASAS-GSSPPFRSG-------DDA
 37 ASF▨EIPFMTSAAAAATASSSSPTSV-SPSATASAAA-STSASCSPFRSS-------DGA
 29 ASP▨EIPFMTAAATADTGAAASSSS---PSA-----A-ASSCPAAAPRSS-------DGA
  1 -----MEFTPIS-------------------------------PP-TRVAGGEE---D--
  1 -----MEFTPAH-------------------------------AH-ARVVE------D--
  1 -----MEFRPA---------------------------------H-ARVFE------D--
  1 -----MEFITPIVR-----------------------------PASAAAGGGEV---QE-
  1 -----MEFTTPP--------------------------------PATRSGGGEE---RA-
  1 -----MEFTAPP--------------------------------PATRSGGGEE---RA-
 21 AM----------------------------------------------------------
 22 AM----------------------------------------------------------
 20 QQQAAMWLSNSH-------------------------------TPRFNLNDEEEEEEDDV
 22 HQQQQLTLMDPD-------------------------------PLRLNLNSDDG-NGNDN
 22 Q--QQLTLIDPD-------------------------------PLPLNLNNDDNDNGDDN
 22 Q--▨H-------------------------------------------------------
 22 QQ-QQ-------------------------------------------------------
 22 HRH▨H-------------------------------------------------------
 14 HHH---------------------------------------------------------
 18 -HH---------------------------------------------------------
 14 NHH---------------------------------------------------------
 21 HRHTT-------------------------------------------------------
 23 NLHTT-------------------------------------------------------
155 -FL▨TRQTQKGV---------------------------------AK-------------
 14 -HK▨AFFPAAAS-------------------------------SPTSSS---S-------
176 -SK▨TFAASTPS-------------------------------AATTTA---SL------
 14 -SK▨AFAASAAL-------------------------------SAPTTS-----------
152 -GL▨RGRGMGAR------------------------------------------------
151 -GL▨RGRGMGAR------------------------------------------------
147 -GL▨RGRGMGAR------------------------------------------------
146 -GL▨RGRGMGVR------------------------------------------------
146 -GL▨RGRGMGAR------------------------------------------------
138 -GL▨RGHG---R------------------------------------------------
151 -GL▨RGRG---R------------------------------------------------
151 -GL▨RGRG---R------------------------------------------------
163 -SN▨RSGANTN-------------------------------------------------
 145-ST▨GGR--RR-------------------------------------------------
151 -ST▨GGR--RR-------------------------------------------------
170 -SK▨SRGFVRRR-------------------------------GSAA-------------
176 -SK▨SRGVVRRR-------------------------------GSAA-------------
```



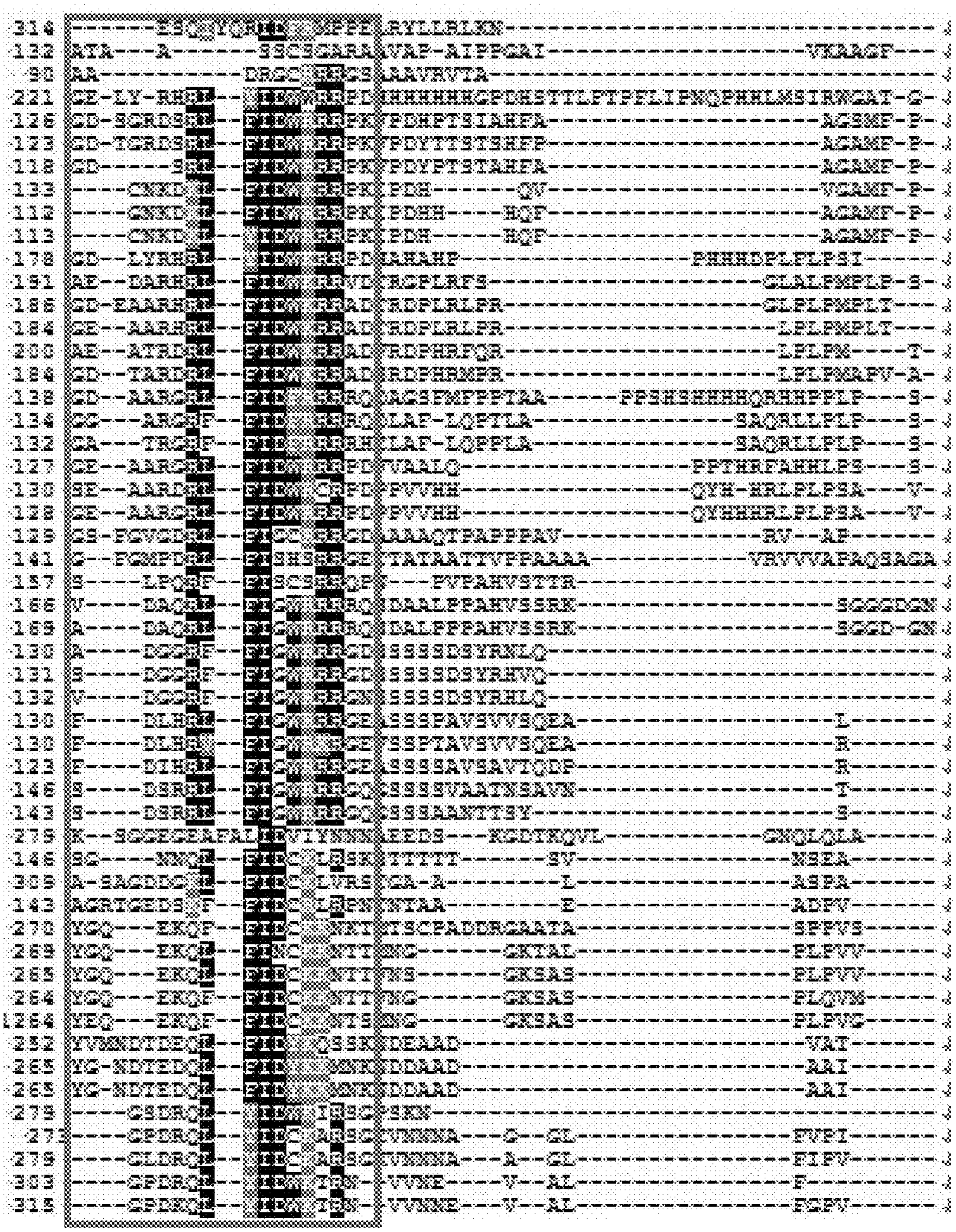
B3 domain



B3 domain



B3 domain

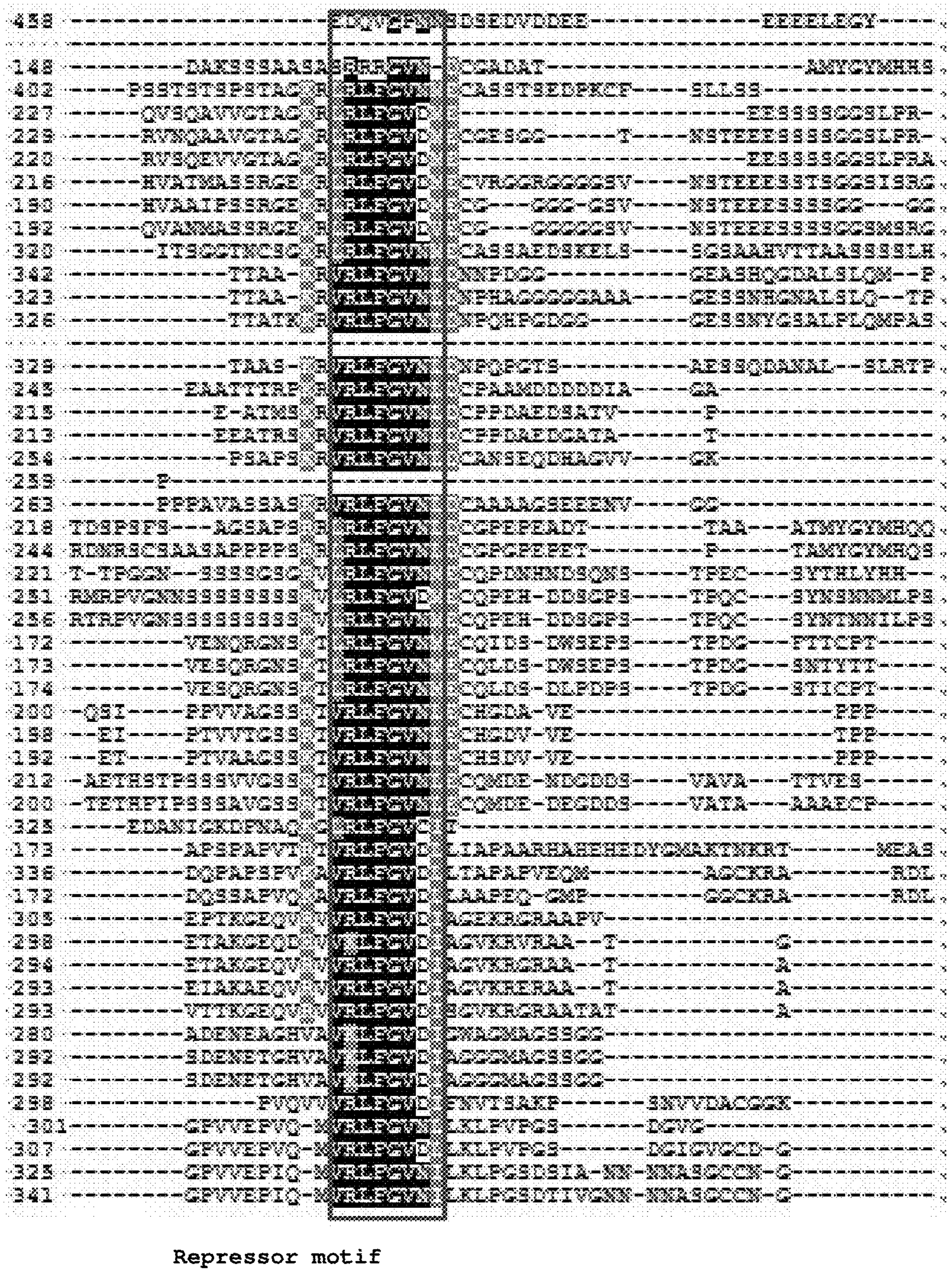


B3 domain

```
338 ------SESRKWADMCKLETMPSQSFIYLQLYELKDDFIQAEIRKPSYQSVCSRSTGWFS
    ------------------------------------------------------------
109 --------NQGWSMCYSTSG---SSYDT--S-----------------------------
275 RLYSLPSPTPPRHHEH---------LNYNNNA------------MYH-------------
162 RFYSPPTAT---SYNL---------YNYQQP-----------------------------
159 RFYSPQTATTSTSYNP---------YNHQQP-----------------------------
150 RFYSPPTATTSTCYDL---------YNHQPP-----------------------------
160 RFYSYPYPQIQASYER--------------------------------------------
141 RFYSPSHPQN--------------------------------------------------
141 RFYSPPHPQMPTSPES--------------------------------------------
213 RLYSLPPTMPPRYHHDHHFH---HHLNYNNLF------------T---------------
226 SHYGSPHHYSPWGPGGGGG----------------------------------GGGGFFM
222 ------SHYAPWGIGGG--------------------------------------GGFFV
218 ------SHYSPWGLGAG-------------------------------------ARGFFM
232 ------SPYGPWGGGA-GA----------------------------------SSCRPRR
219 ------SPYGPWGGGG-GG----------------------------------GAGGFFM
185 ------VPLCPWRDYTTAYG---GSYGY--------------------------------
170 ------VPICPWQDYG--------------------------------------------
168 ------VPICPWQGYG--------------------------------------------
163 ------IPPAPWAHHH---G---H-------G------------AAAAA-AAAAGARFLL
165 ------VPYAPWAA--HAHH---HHYPADGHT------------EPVTPCLCATLVATEM
164 ------VPYAPWAAAAHAHH---HHYPAAGVG------------AARTTTTTTTTVLHHL
164 -AAQNAGEQQPWSPMCYSTS---GGGSY--------------------------------
186 -DHQQQQQPSPWSPMCYSTS---GSYSY--------------------------------
183 -----------SSASFYSAH---PP--Y--------------------------------
202 SNK-----NEGWTRGFYSAH---HP--Y--------------------------------
204 SSKNEGDVGVGWTRGFYPAH---HP--Y--------------------------------
157 ------------------------------------------------------------
158 ------------------------------------------------------------
159 ------------------------------------------------------------
160 -----VNTTAYWSGLT-------TP--Y--------------------------------
160 -----VNTTAYWSGLT-------TP--Y--------------------------------
153 -----ANTTAYWNGLT-------TP--Y--------------------------------
176 -----SS------MGA-------LS--Y--------------------------------
170 -----SS------MT---------------------------------------------
318 ------------------------------------------------------------
173 ------------------------------------------------------------
336 ------------------------------------------------------------
172 ------------------------------------------------------------
305 ------------------------------------------------------------
298 ------------------------------------------------------------
294 ------------------------------------------------------------
293 ------------------------------------------------------------
293 ------------------------------------------------------------
280 ------------------------------------------------------------
292 ------------------------------------------------------------
292 ------------------------------------------------------------
298 ------------------------------------------------------------
 301------------------------------------------------------------
307 ------------------------------------------------------------
325 ------------------------------------------------------------
341 ------------------------------------------------------------
```

```
392 KPMIKTL-RLQVSIR---------------------------LLSLLHNE---------- ↓
    ------------------------------------------------------------ ↓
127 -----------------------------------------ANSYAYHRSV--------- ↓
301 ------P-FHHHGAGSGINATTHHYNNYHEMSSTTT--SGSAGSVFYHRS-TPPISMPLA ↓
181 --------RHHHHSG----------YNYPQIPRE-------PGYGYLV------------ ↓
181 --------RH-HHSG----------YCYPQIPRE-------PGYGYVVRS-V-------- ↓
172 --------RH-HHIG----------YGYPQIPRE-------PGYGYFVRS-V-------- ↓
176 ------------H------------NLYHRYQRD-------IGIGYYVRS-M-------- ↓
151 --------------------------LYHRYQQD-------LGIGYYVSS-M-------- ↓
157 ------------SHN----------LYHHRFQRD-------LGIGYY------------- ↓
243 --------FQQHQYQQLGAATTTHHNNYGY-------QNSGSGSLYYLRSSMSMSG---- ↓
252 PPSPPATLYEH-RLR---Q-----GLDFRSMTTTYPAPTVGRQLLFFGSARMPPHHAPPP ↓
238 QPSPPATLYEH-RLR---Q-----GLDFRAFNPA-A--AMGRQVLLFGSAR-IPPQAP-- ↓
235 PPSPPATLYEH-RLR---Q-----GFDFRGMNPSYP--TMGRQVILFGSAARMPPHGPAP ↓
251 PPRSTSI----TAFA---R-----AST----SATS------TPLCRRSSSS----SSAPQ ↓
238 PPAPPATLYEHHRFR---Q-----ALDFRNINAAA---APARQLLFFGSAGMPPRASMPQ ↓
204 --------------------------GYG----GGSTPASSRHVLFL------------- ↓
180 ----------------------------------ASAPAPNRHVLFL------------- ↓
178 ----------------------------------ASAPAPSRHVLFL------------- ↓
191 PPSST-PIYDHHRRH-------AHAVGYDAYA-----AATSRQVLFY------------- ↓
202 RASSS-QLSLTRSNLS--RPPQPRIARVDGAQPRPSSSPRQPQSLWC------------- ↓
203 PPSPS-PLYLDTRRR---------HVGYDAY------GAGTRQLLFY------------- ↓
188 ---------PT-----------SPANSY-----------------AY------------- ↓
210 ---------PT-----------SSPANSQH---------------AYH------------ ↓
195 ---------PA-----------HH---------------------F-------------- ↓
220 ---------PT-----------HH---------------------LHH------------ ↓
227 ---------PT-----------HH------------------------------------ ↓
157 ------------------------------------------------------------ ↓
158 ------------------------------------------------------------ ↓
159 ------------------------------------------------------------ ↓
174 ---------RQ-----------VH---------------------AST------------ ↓
174 ---------RQ-----------VH---------------------AST------------ ↓
167 ---------RQ-----------VH---------------------AST------------ ↓
184 ---------HQ-----------IH---------------------ATS------------ ↓
174 ----------------------AP---------------------PYS------------ ↓
318 ------------------------------------------------------------ ↓
173 ------------------------------------------------------------ ↓
336 ------------------------------------------------------------ ↓
172 ------------------------------------------------------------ ↓
305 ------------------------------------------------------------ ↓
298 ------------------------------------------------------------ ↓
294 ------------------------------------------------------------ ↓
293 ------------------------------------------------------------ ↓
293 ------------------------------------------------------------ ↓
280 ------------------------------------------------------------ ↓
292 ------------------------------------------------------------ ↓
292 ------------------------------------------------------------ ↓
298 ------------------------------------------------------------ ↓
 301------------------------------------------------------------ ↓
307 ------------------------------------------------------------ ↓
325 ------------------------------------------------------------ ↓
341 ------------------------------------------------------------ ↓
```

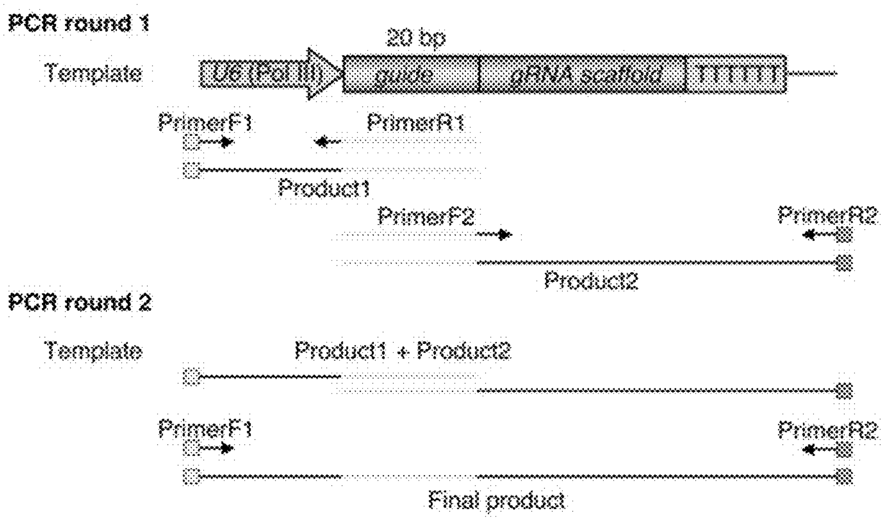
```
414 -----EARNLLRNAHELIER--SKKQEALSRSELSIEYNDA--DQVSAAHTGT-------
    ------------------------------------------------------------
137 --------------------------------------------DDHSDHAGSRA-----
381 DHQTLNTRQ------QQQQQQQQEGAGNVSLSPMIIDSVPVAHHLHHQQHHGGKSSG---
204 ------------------------DQRAVVADPLVIESVPVMMHGG-A------------
206 ------------------------DQRAVVADPLVIESVPVMMHGG-A------------
197 ------------------------DQRAVVADPLVIESVPVMMRGG-A------------
196 ------------------------ERYD---PTAVIESVPVIMQRR-A------------
169 ------------------------ERND---PTAVIESVPLIMQRRAA------------
175 -------------------------------PTAVIESVPVIMQRREA------------
284 -------------------GDQNLQGRGSNIVPMIIDSVPVNVAHHNNNRHGNGG-----
303 QP-----RPFSLPLHHYTVQP-SAAGVTAASRPVLLDSVPVIESP---------------
283 -L---LARAPSPLHHHYTLQP-SGDGVRAAGSPVVLDSVPVIESP---------------
284 LL---VPRPPPPLHPTVQQQGSDAGGSVTAGSPVVLDSVPVIESP---------------
285 GRGFISTRPCHRRRRHLRLLT-NSTLRCTTRAP---------------------------
287 QQ--QPPPPPHPPLHSIMLVQ-PSPAPPTASVPMLLDSVPLVNSP---------------
221 -------RPQV-------------------PAAVVLKSVPVHVAATSAVQ----------
193 -------RPQV-------------------PAAVVLKSVPVHVAASAV------------
191 -------RPQV-------------------PAAVVLTSVPVRVAASAV------------
225 -------RPLPPQQ--------------QHHPAVVLESVPVRMTAGH---A--EP-----
246 -------RSC---------------------------------QPQPRRTA--DV-----
234 -------RPH---Q--------------QPSTTVMLDSVPVRLPPTPGQHA--EP-----
198 -------RRAADHDH------------------------------GDMHHADES---PRD
223 -------RHSADHDH-----------------------------SNNMQHAGES---QSD
200 ---------PFPYQ------------------------------PHSLHAPGGGSQGQNE
227 -------HQPSPYQ-----------------------------QQHDCLHAGRGSQGQNQ
231 -------HHPSPYHH----------------------------QQDDSLHAVRGSQGQNQ
157 ----------SNSSL----------------------------QY--YPHAG--AQA---
158 ----------SNASL----------------------------QY--YPHAG--AQA---
159 ----------SNASL----------------------------QY--YPHAG--VQA---
181 --------TYPN-IH----------------------------QE--YSHYG--AVVDHA
181 -------SSYPN-IH----------------------------QE--YSHYG--AVA---
174 -------SSYPNNIH----------------------------QE--YSHYG--PVA---
191 -------NYSNPPSH----------------------------SE--YSHYG--AAVATA
179 -------NYSNRPAH----------------------------SE--YSHYG--AAVATA
318 ------------------------------------------GSEE-----GED------
173 ------------------------------------------------------------
336 ------------------------------------------------------------
172 ------------------------------------------------------------
305 ------------------------------------------------------------
298 ------------------------------------------------------------
294 ------------------------------------------------------------
293 ------------------------------------------------------------
293 ------------------------------------------------------------
280 ------------------------------------------------------------
292 ------------------------------------------------------------
292 ------------------------------------------------------------
298 ------------------------------------------------------------
 301------------------------------------------------------------
307 ------------------------------------------------------------
325 ------------------------------------------------------------
341 ------------------------------------------------------------
```


Repressor motif

```
484 -------------DSP-----------------PKADDIHEFTLG---DSYAFSEGPSNG,
    ------------------------------------------------------------,
181 YAA---VSTVNY▒SV---------------------------------------------,
442 --S-SMANSNSQPPLQLLREDTLSSSS-----ARPGD-----QRGVGEPSMLFD▒DPSLQ,
261 --G-DASPSSS▒▒QLRLGSSSEDDH-----------------PSKKGKSSLPFD▒DQ---,
274 --G-GASPSSS▒▒QLRLGNSSEDDH-----------------LFKKGKSSLPFN▒DQ---,
255 GGG-GASSSSS▒▒QLRLGSSCEDDH-----------------PSKKGKSSLPFD▒DQ---,
267 GV--SMAGVGSPLQLRLVSSDGDDQSLVARGAARVDEDHHLPT-KKGKSSLSFD▒DK---,
234 GV--SMASVGS▒LQLRLVSSD--DESLVAMEAASVDEDHHLPT-KKGKSSLSFD▒DRK--,
240 GV--SMAGVGS▒LQLRLVSSD--DESLVAMEGATVDEDHHLPTTKKGKSSLSFD▒DI---,
370 HQR-LRV------PVPVPLEDPLSSSA--AAAARPG----DHKGASTGTSLLFD▒DPSLQ,
378 GWQ-QRTPTLR▒LELPRHG---GESSA--ASSPSSS----SSSKREARSALDLD▒-----,
365 AWM-RRDPTLR▒LELPPHHHHGAESSA--ASSPSSS----SSSKRDAHSALDLD▒-----,
368 AWR-PRDHTLR▒LEFPSHGA------E--ASSPSSS----SSSKREAHSGLDLD▒-----,
    ------------------------------------------------------------,
366 GWQ-RPGP-LRP▒ESPQR---GAESSA--ASSPSSS----SSSKREAHSSLDLD▒-----,
278 -AS-RTAA-SS▒LQLPSP-------------SSSTS----SSTAGKKDCSLDLG▒-----,
243 -RG-RAAS-TT▒LQLPSP-------------SSSTS----SSTAGKDVCCLDLG▒-----,
242 -R----TP-ST▒LQLPSP-------------SSSTS----SSTGGKDVRSLDLG▒-----,
284 ----TAPP-----PLPSP-------------P-SSS----SSSSGKARCSLNLD▒-----,
    ------------------------------------------------------------,
298 -WR-TSAP-----PTQQA-------------S-SSS----SYSSGKARCSLNLD▒-----,
264 SSYAAMS---A------V-------------PSYWGN------------S----------,
291 PYA----------------------------YNNWGS------------PYQHDEEI---,
269 --------------QTSS-------------YSSSSN------------PHHHM▒PQQP-,
303 TQSTDH-SHHNF▒QQ-QP-------------SNSNPS------------PHHMM▒HHQPY,
308 TQSTDIHSHLNF▒QQQQT-------------SNSKPP------------PHHMM▒RHQPY,
212 --NHD---QPP▒▒P--EH----------------PPP------------PYYMD▒SPTGD,
213 --NHD---QPHP▒PQQQH----------------YPP------------PYYMD▒SPTGD,
214 --SHD---QPH▒▒PQ-QH----------------YPP------------PYYMD▒SPTGD,
232 --RPDVYNDQH▒▒----Y----------------YST------------PHPMN▒SPAGE,
229 --CPDGYNGQHP▒----Y----------------YST------------PDPMN▒SPAGE,
223 --CPDAYNGQH▒▒----Y----------------YST------------PHPMN▒SPAGE,
258 ---PDGYYGQN▒▒----Y----------------YYS------------HPHNM▒ILTLL,
247 --RQDSYYDQN▒▒----N----------------YYT------------PHSSAS-----,
    ------------------------------------------------------------,
219 V-A-APTPAHA▒▒KKRCV-----------------------------DPALTYR▒ATTPQ,
373 A-A-TTPPQAAA▒KKQCI-----------------------------ELALV--------,
208 V-K-PP-PPKVA▒KKQCI-----------------------------ELALA--------,
334 --------EQE▒▒KRQCV-----------------------------AHS--QH---SPA,
327 -----ELGPPE▒▒KRQSV-----------------------------AHGCCRM---NYI,
323 -----EQGPPE▒LKRQCV-----------------------------PLPHGQR---SPA,
322 -----EQGPQGW▒KRQCM-------------------------------AHGQH---SPA,
324 -----EQGLQE▒▒KRQCV-------------------------------APGQH---SPA,
    ------------------------------------------------------------,
1   ------------------------------------------------------------,
1   ------------------------------------------------------------,
329 -----RSRDVD▒▒ALRCS-----------------------------KKH----------,
 330-----KRKEME▒▒AFECC-----------------------------KKL----------,
341 -----KRKEME▒▒AFECS-----------------------------KKL----------,
363 -----KRREME▒▒SLECS-----------------------------KKP----------,
380 -----KRREME▒▒SLECS-----------------------------KKP----------,
```

```
511 YLEEVLRSLPLQEDGQKKL-CDAPINADASD
    -------------------------------
    -------------------------------
489 YRQ----------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
417 YHRH---------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
    -------------------------------
336 YY-----------------------------
343 YY-----------------------------
237 VHQTSS-Q-----QC----------------
240 MNRTS--------------------------
240 VHQTRS-P-----QC----------------
258 ALEQVGDG-----RG----------------
255 AMEQVGDG-----RR----------------
249 AMEQVGDG-----RG----------------
283 -------------------------------
    -------------------------------
    -------------------------------
248 CPRSRDQL-----EGVQAAGSTFAL------
    -------------------------------
    -------------------------------
352 ------------------L-GAFVL------
350 CYSIG------------TI-GPLMLN-----
346 ------------------L-GAFVL------
343 ------------------L-GDFAL------
345 ------------------L-GAFAL------
    -------------------------------
    -------------------------------
    -------------------------------
345 -----A-----------II-NAL--------
346 -----K-----------VI-GAL--------
357 -----K-----------VI-GAL--------
379 -----K-----------II-GAL--------
396 -----K-----------II-GAL--------
```

Figure 14



gRNA sequence

gacggccagtgccaagcttCTCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTGCCCTTGGATCATGAACCAACGGCCTGGCTGTATTTGGTGGTTGTGTAGGGAGATGGGGAGAAGAAAAGCCCGATTCTCTTCGCTGTGATGGGCTGGATGCATGCGGGGGAGCGGGAGGCCCAAGTACGTGCACGGTGAGCGGCCCACAGGGCGAGTGTGAGCGCGAGAGGCGGGAGGAACAGTTTAGTACCACATTGCCCAGCTAACTCGAACGCGACCAACTTATAAACCCGCGCGCTGTCGCTTGTGT**GGGAAGGAAGAGACAGATTG**GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTTGTCCCTTCGAAGGGCAATTCTGCAGATATCCATCAC*ACTGGCGGCCGCTCGAGGTCGaagcttgcatgcctgcagg*

os11g01560000

A-R1

GGACTGGGGTTGCTCCTGGG**ACACAAGCGACAGCGCGCGGG**

A-F2

CCCAGGAGCAACCCCAGTCC**GTTTTAGAGCTAGAAATAGCA**

B-R1

TGCTATTTCTAGCTCTAAAAC**ACACAAGCGACAGCGCGCGGG**

B-F2

GCCCCTGACGCCCAGTGACG**GTTTTAGAGCTAGAAATAGCA**

Os12g0157000

C-R1

GGGGGTGCCCCTGGGCGAGA**ACACAAGCGACAGCGCGCGGG**

C-F2

TCTCGCCCAGGGGCACCCCC**GTTTTAGAGCTAGAAATAGCA**

D-R1

CTCGTAGTGGTGGTGGTAGT**ACACAAGCGACAGCGCGCGGG**

D-F2

ACTACCACCACCACTACGAG**GTTTTAGAGCTAGAAATAGCA**

PLANTS WITH INCREASED SEED SIZE

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This is a continuation application of U.S. Ser. No. 15/548,398 filed Aug. 2, 2017, which is a National Phase application claiming priority to PCT/GB2016/050245, filed Feb. 3, 2016, which claims priority to PCT/CN2015/072143, filed Feb. 3, 2015, all of which are herein incorporated by reference in their entirety.

FIELD OF THE INVENTION

[0002] The invention relates to transgenic plants with improved growth and yield-related traits, in particular increased seed size. Also within the scope of the invention are related methods, uses, isolated nucleic acids and vector constructs.

INTRODUCTION

[0003] The ever-increasing world population and the dwindling supply of arable land available for agriculture fuels research towards increasing the efficiency of agriculture and providing food security. Conventional means for crop and horticultural improvements utilise selective breeding techniques to identify plants having desirable characteristics. However, such selective breeding techniques have several drawbacks, namely that these techniques are typically labour intensive and result in plants that often contain heterogeneous genetic components that may not always result in the desirable trait being passed on from parent plants. Advances in molecular biology have allowed mankind to modify the germplasm of animals and plants. Genetic engineering of plants entails the isolation and manipulation of genetic material (typically in the form of DNA or RNA) and the subsequent introduction of that genetic material into a plant. Such technology has the capacity to deliver crops or plants having various improved economic, agronomic or horticultural traits, including increased yield. There are a number of methods that can be used, for example genome editing (using CRISPR or TALEN) or mutagenesis.

[0004] A trait of particular economic interest is increased seed size. Seed size is an important agronomic trait which increased crop yield, and is also a key ecological trait that influences many aspects of a species' regeneration strategy, such as seedling survival rates and seed dispersal syndrome (Harper et al., 1970; Westoby et al., 2002; Moles et al., 2005; Fan et al., 2006; Orsi and Tanksley, 2009; Gegas et al., 2010). Although the size of seeds is one of the most important agronomic traits in plants, the genetic and molecular mechanisms that set the final size of seeds are almost unknown. In higher plants, seed development starts with a double fertilization process, in which one of the two haploid pollen nuclei fuses with the haploid egg cell to produce the diploid embryo, while the other sperm nucleus fuses with the diploid central cell to form the triploid endosperm (Lopes and Larkins, 1993). The integuments surrounding the ovule are maternal tissues and form the seed coat after fertilization. Therefore, the size of the seed is the result of the growth of the embryo, the endosperm and the maternal tissues. However, the genetic and molecular mechanisms setting the limits of seed growth are almost unknown in plants.

[0005] Several factors that function maternally to regulate seed size have been identified in *Arabidopsis*. For example, TRANSPARENT TESTA GLABRA 2 (TTG2) influences seed growth by increasing cell elongation in the maternal integuments (Garcia et al., 2005; Ohto et al., 2009), while APETALA2 (AP2) may control seed growth by limiting cell elongation in the maternal integuments (Jofuku et al., 2005; Ohto et al., 2005; Ohto et al., 2009). By contrast, AUXIN RESPONSE FACTOR 2 (ARF2) acts maternally to control seed growth by restricting cell proliferation (Schruff et al., 2006). Similarly, the ubiquitin receptor DA1 acts synergistically with the E3 ubiquitin ligases DA2 and EOD1/BB to control seed size by limiting cell proliferation in the maternal integuments (Li et al., 2008; Xia et al., 2013). Mutations in the suppressor of da1-1 (SOD2), which encodes the ubiquitin-specific protease (UBP15), suppress the large seed phenotype of da1-1 (Du et al., 2014). DA1 physically associates with UBP15/SOD2 and modulates the stability of UBP15. These studies show that the ubiquitin pathway plays an important part in the maternal control of seed size. KLU/CYTOCHROME P450 78A5 (CYP78A5) regulates seed size by increasing cell proliferation in the maternal integuments of ovules (Adamski et al., 2009). KLU has also been suggested to generate mobile plant-growth substances that promote cell proliferation (Anastasiou et al., 2007; Adamski et al., 2009). By contrast, overexpression of CYP78A6/EOD3 increases both cell proliferation and cell elongation in the integuments, resulting in large seeds (Fang et al., 2012). Seed size is also determined by zygotic tissues. Several factors have been described to influence seed size via the zygotic tissues in *Arabidopsis*, including HAIKU1 (IKU1), IKU2, MINISEED3 (MINI3) and SHORT HYPOCOTYL UNDER BLUE1 (SHB1) (Garcia et al., 2003; Luo et al., 2005; Zhou et al., 2009; Wang et al., 2010; Kang et al., 2013). iku and mini3 mutants form small seeds due to precocious cellularization of the endosperm (Garcia et al., 2003; Luo et al., 2005; Wang et al., 2010). SHB1 associates with MINI3 and IKU2 promoters and regulates expression of MINI3 and IKU2 (Zhou et al., 2009; Kang et al., 2013). ABA INSENSITIVE5 (AB15) has been recently described to repress the expression of SHB1 (Cheng et al., 2014), and MINI3 has been reported to activate expression of the cytokinin oxidase (CKX2) (Li et al., 2013), suggesting the roles of phytohormones in regulating endosperm growth. In addition, the endosperm growth is influenced by parent of-origin effects (Scott et al., 1998; Xiao et al., 2006).

[0006] The invention is aimed at providing plants with improved yield traits that are beneficial to agriculture.

SUMMARY OF THE INVENTION

[0007] In a first aspect, the invention relates to a plant generated that does not produce a functional NGAL2 polypeptide or does not produce functional NGAL2 and NGAL3 polypeptides.

[0008] In another aspect, the invention relates to a method for altering a plant phenotype comprising reducing or abolishing the expression of a nucleic acid sequence encoding a NGAL2 polypeptide or reducing or abolishing the activity of a NGAL2 or reducing or abolishing the expression of a nucleic acid sequences encoding NGAL2 and NGAL3 polypeptides or reducing or abolishing the activity of a NGAL2 and NGAL3 polypeptide relative to a control plant.

[0009] In another aspect, the invention relates to a method for making a plant with an altered phenotype comprising reducing or abolishing the expression of a nucleic acid sequence encoding a NGAL2 polypeptide or reducing or abolishing the activity of a NGAL2 or reducing or abolishing the expression of a nucleic acid sequences encoding NGAL2 and NGAL3 polypeptides or reducing or abolishing the activity of a NGAL2 and NGAL3 polypeptide relative to a control plant.

[0010] In another aspect, the invention relates to a plant obtained or obtainable any method described above.

[0011] In another aspect, the invention relates to an isolated nucleic acid comprising a sequence comprising or consisting of SEQ ID NO: 1 or 2 or a functional variant or homologue thereof.

[0012] In another aspect, the invention relates to a vector comprising an isolated nucleic acid described above.

[0013] In another aspect, the invention relates to a silencing nucleic acid construct targeting sequence comprising or consisting of

[0014] 1, 2 or 3 or a functional variant, part or homologue thereof.

FIGURES

[0015] The invention is further described in the following non-limiting figures.

[0016] FIG. **1**. Isolation of a suppressor of da1-1 (sod7-1).

[0017] (A) Seeds from wild-type, da1-1 and sod7-1D da1-1 plants (from left to right). (B) Mature embryos of the wild type, da1-1 and sod7-1D da1-1 (from left to right). (C) Flowers from wild-type, da1-1 and sod7-1D da1-1 plants (from left to right). (D) 30-day-old plants of the wild type, da1-1 and sod7-1D da1-1 (from left to right). (E) Projective area of wild-type, da1-1 and sod7-1D da1-1 seeds. (F) Weight of wild-type, da1-1 and sod7-1D da1-1 seeds. (G) Cotyledon area of 10-d-old wild-type, da1-1 and sod7-1D da1-1 seedlings. Values (E-G) are given as mean±SD relative to the respective wild-type values, set at 100%. **, $P<0.01$ compared with da1-1 (Student's t-test). Bars=0.5 mm in (A), 0.2 mm in (B), 1 mm in (C) and 5 cm in (D).

[0018] FIG. **2**. Seed and organ size in the sod7-1D mutant.

[0019] (A and B) Seeds of Col-0 (A) and sod7-1D (B). (C and D) Mature embryos of Col-0 (C) and sod7-1D (D). (E and F) 10-day-old seedlings of Col-0 (E) and sod7-1D (F). (G) Projective area of Col-0 and sod7-1D seeds. (H) Weight of Col-0 and sod7-1D seeds. (I) Cotyledon area of 10-day-old Col-0 and sod7-1D seedlings. Values (G-I) are given as mean±SD relative to the respective wild-type values, set at 100%. **, $P<0.01$ compared with the wild type (Student's t-test). Bars=0.5 mm in (A) and (B), 0.2 mm in (C) and (D), and 1 mm in (E) and (F).

[0020] FIG. **3**. Cloning of the SOD7 gene.

[0021] (A) Structure of the T-DNA insertion in the sod7-1D mutant. (B) Expression levels of At3g11580 (SOD7) and At3g11590 in da1-1 and sod7-1D da1 seedlings.

[0022] (C) The SOD7 protein contains a B3 DNA binding domain (second domain in lighter shading) and a transcriptional repression motif (small light box in darker shading, marked with an arrow). (D) Projective area of Col-0, 35S:GFP-SOD7#3 and 35S:GFP-SOD7#5 seeds. (E) Cotyledon area of 10-day-old Col-0, 35S:GFP-SOD7#3 and 35S:GFP-SOD7#5 seedlings. (F) Expression levels of SOD7 in Col-0, 35S:GFP-SOD7#3 and 35S:GFP-SOD7#5 seedlings. Values (D-F) are given as mean±SD relative to the respective wild-type values, set at 100%. **, $P<0.01$ compared with the wild type (Student's t-test).

[0023] FIG. **4**. Expression pattern and subcellular localization of SOD7.

[0024] (A-K) SOD7 expression activity was monitored by pSOD7:GUS transgene expression. Histochemical analysis of GUS activity in the developing leaves (A, B and C), the developing sepals (D, E), the developing petals (F, G), the developing stamens (H, I), and the developing carpels (J, K). (L) GFP florescence of SOD7-GFP in a young ovule of pSOD7:SOD7-GFP transgenic plants. (M-O) GFP fluorescence of SOD7-GFP (M), DAPI staining (N), and merged (0) images are shown. Epidermal cells in pSOD7:SOD7-GFP leaves were used to observe GFP signal. (P-R) GFP fluorescence of GFP-SOD7 (P), DAPI staining (Q), and merged (R) images are shown. Epidermal cells in 35S:GFP-SOD7 leaves were used to observe GFP signal. Bars=100 μm in (A-K), 10 μm in (L), and 2 μm in (M-R).

[0025] FIG. **5**. SOD7 acts redundantly with NGAL3 to control seed size.

[0026] (A) The SOD7 gene structure. The start codon (ATG) and the stop codon (TGA) are shown. Closed boxes indicate the coding sequence, and the line between boxes indicates intron. The T-DNA insertion site (sod7-ko1) in the SOD7 gene was indicated.

[0027] (B) The NGAL3 gene structure. The start codon (ATG) and the stop codon (TGA) are shown. Closed boxes indicate the coding sequence, and the line between boxes indicates intron. The T-DNA insertion site (ngal3-ko1) in the NGAL3 gene was indicated. (C) Seeds from Col-0, sod7-ko1, ngal3-ko1 and sod7-ko1 ngal3-ko1 plants (from left to right). (D) Mature embryos of Col-0, sod7-ko1, ngal3-ko1 and sod7-ko1 ngal3-ko1 (from left to right). (E) 25-day-old plants of Col-0, sod7-ko1, ngal3-ko1 and sod7-ko1 ngal3-ko1 (from left to right). (F) Flowers of Col-0, sod7-ko1, ngal3-ko1 and sod7-ko1 ngal3-ko1 (from left to right). (G) Projective area of Col-0, sod7-ko1, ngal3-ko1 and sod7-ko1 ngal3-ko1 seeds. (H) Weight of Col-0, sod7-ko1, ngal3-ko1 and sod7-ko1 ngal3-ko1 seeds. (I) Cotyledon area of Col-0, sod7-ko1, ngal3-ko1 and sod7-ko1 ngal3-ko1 seedlings. Values (G-I) are given as mean±SD relative to the respective wild-type values, set at 100%. **, $P<0.01$ compared with the wild type (Col-0) (Student's t-test). Bars=0.5 mm in (C), 0.2 mm in (D), 5 cm in (E), and 1 mm in (F).

[0028] FIG. **6**. SOD7 acts maternally to determine seed size.

[0029] (A) Projective area of Col-0×Col-0 (C/C) F1, Col-0×sod7-ko1 ngal3-ko1 (C/d) F1, sod7-ko1 ngal3-ko1×Col-0 (d/C) F1 and sod7-ko1 ngal3-ko1×sod7-ko1 ngal3-ko1 (d/d) F1 seeds. Values are given as mean±SD relative to the respective wild-type values, set at 100%. (B) Projective area of Col-0×Col-0 (C/C) F2, Col-0×sod7-ko1 ngal3-ko1 (C/d) F2, sod7-ko1 ngal3-ko1×Col-0 (d/C) F2 and sod7-ko1 ngal3-ko1×sod7-ko1 ngal3-ko1 (d/d) F2 seeds. Values are given as mean±SD relative to the respective wild-type values, set at 100%. (C and D) Mature ovules of Col-0 (C) and sod7-ko1 ngal3-ko1 (D). (E) Outer integument length of mature Col-0 (lighter bar to the left) and sod7-ko1 ngal3-ko1 (darker bar to the right) ovules. Values are given as mean±SD. (F) The number of cells in the outer integuments of Col-0 and sod7-ko1 ngal3-ko1 at 0, 6 and 8 DAP. Values are given as mean±SD. (F) The length of cells in the outer integuments of Col-0 and sod7-ko1 ngal3-ko1 at 0, 6 and 8 DAP. Values are given as mean±SD. **, $P<0.01$ compared with the wild type (Col-0) (Student's t-test). Bars=50 μm in (C) and (D).

[0030] FIG. **7**. klu-4 is epistatic to sod7-ko1 ngal3-ko1 with respect to seed size.

[0031] (A) Seed area of Col-0, klu-4, sod7-ko1 ngal3-ko1 and klu-4 sod7-ko1 ngal3-ko1 (from left to right). Values are given as mean±SD relative to the respective wild-type values, set at 100%. (B) Seed weight of Col-0, klu-4, sod7-ko1 ngal3-ko1 and klu-4 sod7-ko1 ngal3-ko1 (from left to right). Values are given as mean±SD relative to the respective wild-type values, set at 100%. (C) The outer integument length of Col-0, klu-4, sod7-ko1 ngal3-ko1 and klu-4 sod7-ko1 ngal3-ko1 (from left to right). ngal3-ko1 at 0 and 8 DAP. Values are given as mean±SD. (D) The number of cells in the outer integuments of Col-0, klu-4, sod7-ko1 ngal3-ko1 and klu-4 sod7-ko1 ngal3-ko1 (from left to right) at 0 and 8 DAP. Values are given as mean±SD. **, $P<0.01$ compared with their respective controls (Student's t-test).

[0032] FIG. **8**. SOD7 directly binds to the promoter of KLU and represses the expression of KLU.

[0033] (A) Expression dynamics of SOD7 and KLU in pER8-SOD7 transgenic plants treated with β-estradiol for 0, 4 and 8 hours. Means were calculated from three biological samples. Values are given as mean±SD. **, $P<0.01$, compared with the expression level of KLU and SOD7 at 0 hour, respectively (Student's t-test). (B) A 2-kb promoter region of KLU upstream of its ATG codon contains a CACTTG sequence. PF1 and PF2 represent PCR fragments used for ChIP-quantitative PCR analysis. A and A-m indicate the wild-type probe and the mutated probe used in the EMSA essay, respectively. (C) ChIP-qPCR analysis shows that SOD7 binds to the promoter fragment PF1 of KLU. Chromatin from 35S:GFP and 35S:GFP-SOD7 transgenic plants was immunoprecipitated by anti-GFP, and the enrichment of the fragments was determined by quantitative real-time PCR. The ACTIN7 promoter was used as a negative control. The fold enrichment was normalized to the ACTIN7 amplicon, set at 1. Means were calculated from three biological samples. Values are given as mean±SD. **, $P<0.01$, compared with 35S:GFP transgenic plants (Student's t-test). (D) Direct interaction between SOD7 and the KLU promoter determined by EMSA. The biotin-labeled probe A and MBP-SOD7 formed the DNA-protein complex, but the mutated probe A-m and MBP-SOD7 did not form the DNA-protein complex. The retarded DNA-protein complex was reduced by competition using the unlabeled probe A.

[0034] FIG. **9**. The organ size phenotype of 35S:GFP-SOD7 transgenic plants.

[0035] Overexpression of SOD7 results in small plants compared with the wild type. Bar=5 cm.

[0036] FIG. **10**. Phylogenetic tree of the RAV family members in *Arabidopsis.*

[0037] FIG. **11**. SOD7 acts redundantly with NGAL3 to influence organ size.

[0038] Petal area of Col-0, sod7-ko1, ngal3-ko1 and sod7-ko1 ngal3-ko1. (B) The seventh leaf area of Col-0, sod7-ko1, ngal3-ko1 and sod7-ko1 ngal3-ko1. Values (A and B) are given as mean±SD relative to the respective wild-type values, set at 100%. **, $P<0.01$ and *, $P<0.05$ compared with the wild type (Col-0).

[0039] FIG. **12**: Conserved domains in NGAL2, NGAL3 and homologs. a) B box motif. b) Repressor motif

[0040] FIG. **13**: Alignment of sequences. The following sequences are shown (from top to bottom): RMZM2G053008, HvMLOC_57250, Os12g0157000, GmLoc100778733, Bra004501, Bra000434, Bra040478, Bra014415, Bra003482, Bra007646, GmLoc100781489, GRMZM2G024948_T01, os02g0683500, HvMLOC_66387, os04g0581400, GRMZM2G102059_T01, os10g0537100, GRMZM2G142999_T01, GRMZM2G125095_T01, os03g0120900, GRMZM2G098443_T01, GRMZM2G082227_T01, Os11g0156000, GRMZM2G328742_T01, GmLoc100802734 GmLoc100795470, GmLoc100818164, Bra017262, At2g36080/NGAL1, Bra005301, At3g11580/SOD7, BraLOC103849927, Bra034828, At5g06250/NGAL3, Bra005886, GmLoc102660503, HvMLOC_38822, os01g0693400, HvMLOC44012, HvMLOC_7940 HvMLOC_75135, TRAECDM81004, HvMLOC_56567, TRAES3BF098300010CFD21 HvMLOC_63261, TRAES3BF062700040CFD21, TRAES3BF062600010CFD21, Bra038346, GmLoc732601, GmLoc100789009, GmLoc100776987, GmLoc100801107. Conserved B3 domain and repressor motif are boxed.

[0041] FIG. **14**: Genome editing experiments to knock out rice genes Os11g01560000 and Os12g0157000 in rice. gRNA stands for guide RNA, target site linked with gRNA scaffold will recruit CAS9 enzyme to target site in the genome and cause gene-editing.

DETAILED DESCRIPTION

[0042] The present invention will now be further described. In the following passages, different aspects of the invention are defined in more detail. Each aspect so defined may be combined with any other aspect or aspects unless clearly indicated to the contrary. In particular, any feature indicated as being preferred or advantageous may be combined with any other feature or features indicated as being preferred or advantageous.

[0043] The practice of the present invention will employ, unless otherwise indicated, conventional techniques of botany, microbiology, tissue culture, molecular biology, chemistry, biochemistry and recombinant DNA technology, bioinformatics which are within the skill of the art. Such techniques are explained fully in the literature.

[0044] As used herein, the words "nucleic acid", "nucleic acid sequence", "nucleotide", "nucleic acid molecule" or "polynucleotide" are intended to include DNA molecules (e.g., cDNA or genomic DNA), RNA molecules (e.g., mRNA), naturally occurring, mutated, synthetic DNA or RNA molecules, and analogues of the DNA or RNA generated using nucleotide analogues. It can be single-stranded or double-stranded. Such nucleic acids or polynucleotides include, but are not limited to, coding sequences of structural genes, anti-sense sequences, and non-coding regulatory sequences that do not encode mRNAs or protein products. These terms also encompass a gene. The term "gene" or "gene sequence" is used broadly to refer to a DNA nucleic acid associated with a biological function. Thus, genes may include introns and exons as in the genomic sequence, or may comprise only a coding sequence as in cDNAs, and/or may include cDNAs in combination with regulatory sequences.

[0045] The terms "peptide", "polypeptide" and "protein" are used interchangeably herein and refer to amino acids in a polymeric form of any length, linked together by peptide bonds.

[0046] For the purposes of the invention, "transgenic", "transgene" or "recombinant" means with regard to, for example, a nucleic acid sequence, an expression cassette, gene construct or a vector comprising the nucleic acid sequence or an organism transformed with the nucleic acid sequences, expression cassettes or vectors according to the invention, all those constructions brought about by recombinant methods in which either

[0047] (a) the nucleic acid sequences encoding proteins useful in the methods of the invention, or

[0048] (b) genetic control sequence(s) which is operably linked with the nucleic acid sequence according to the invention, for example a promoter, or

[0049] (c) both (a) and (b)

[0050] are not located in their natural genetic environment or have been modified by genetic intervention techniques, it being possible for the modification to take the form of, for example, a substitution, addition, deletion, inversion or insertion of one or more nucleotide residues. The natural genetic environment is understood as meaning the natural genomic or chromosomal locus in the original plant or the presence in a genomic library. In the case of a genomic library, the natural genetic environment of the nucleic acid sequence is preferably retained, at least in part. The environment flanks the nucleic acid sequence at least on one side and has a sequence length of at least 50 bp, preferably at least 500 bp, especially preferably at least 1000 bp, most preferably at least 5000 bp. A naturally occurring expression cassette—for example the naturally occurring combination of the natural promoter of the nucleic acid sequences with the corresponding nucleic acid sequence encoding a polypeptide useful in the methods of the present invention, as defined above—becomes a transgenic expression cassette when this expression cassette is modified by non-natural, synthetic ("artificial") methods such as, for example, mutagenic treatment. Suitable methods are described, for example, in U.S. Pat. No. 5,565,350 or WO 00/15815 both incorporated by reference.

[0051] In certain embodiments, a transgenic plant for the purposes of the invention is thus understood as meaning, as above, that the nucleic acids used in the method of the invention are not at their natural locus in the genome of said plant, it being possible for the nucleic acids to be expressed homologously or heterologously. Thus, the plant can express a silencing construct transgene. However, as mentioned, in certain embodiments, transgenic also means that, while the nucleic acids according to the different embodiments of the invention are at their natural position in the genome of a plant, the sequence has been modified with regard to the natural sequence, and/or that the regulatory sequences of the natural sequences have been modified, for example by mutagenesis.

[0052] Transgenic is preferably understood as meaning the expression of the nucleic acids according to the invention at an unnatural locus in the genome, i.e. homologous or, preferably, heterologous expression of the nucleic acids takes place. According to the invention, the transgene is stably integrated into the plant and the plant is preferably homozygous for the transgene.

[0053] The various aspects of the invention use genetic engineering methods. Thus, the plants have been generated using genetic engineering methods, for example transgene expression, mutagenesis, gene targeting, gene silencing or genome editing as detailed below. Thus, the various aspects of the invention can involve recombinant DNA technology. The plants of the invention are thus mutant plants which have been genetically engineered, that is manipulated by human intervention. The plants of the various aspects of the invention do not relate to natural variants which have not been manipulated by genetic engineering methods. The plant may be a transgenic plant in some embodiments, for example a plant which comprises a nucleic acid construct expressing a silencing construct.

[0054] In preferred embodiments exclude embodiments that are solely based on generating plants by traditional breeding methods.

[0055] The inventor has identified a B3 domain transcriptional repressor termed AtNGAL2, encoded by the suppressor of Atda1-1 (AtSOD7), which acts maternally to control seed size by restricting cell proliferation in the integuments of ovules and developing seeds.

[0056] The inventor previously identified the ubiquitin receptor DA1 as a negative regulator of seed size in *Arabidopsis* (Li et al., 2008). The da1-1 mutant formed large seeds due to increased cell proliferation in the maternal integuments (Li et al., 2008; Xia et al., 2013). To identify novel components in the DA1 pathway or other seed size regulators, the inventor initiated a T-DNA activation tagging screen for modifiers of da1-1 (Fang et al., 2012). A dominant suppressor of da1-1 (sod7-1D) was isolated from seeds produced from approximate 16,000 T1 plants (FIG. **1**A). Seeds of the sod7-1D da1-1 double mutant were significantly smaller and lighter than da1-1 seeds (FIGS. **1**A, E and F). The results show that the sod7-1D mutation suppressed the seed and organ size phenotypes of da1-1. The SOD7 gene was isolated and found to encode a NGATHA like protein (NGAL2) containing a B3 DNA-binding domain and a transcriptional repression motif (FIG. **3**C) (Alvarez et al., 2009; Ikeda and Ohme-Takagi, 2009; Trigueros et al., 2009). SOD7 belongs to the RAV gene family that consists of 13 members in *Arabidopsis* (FIG. **10**) (Swaminathan et al., 2008). Several members of the RAV family contain the putative transcriptional repression motifs, including NGA1, NGA2, NGA3, NGA4, NGAL1, NGAL2/SOD7 and NGAL3 (FIG. **10**) (Ikeda and Ohme-Takagi, 2009). The transcriptional repression motifs in NGA1, NGAL1 and NGAL2/SOD7 have been known to possess the repressive activity (Ikeda and Ohme-Takagi, 2009), indicating that they are transcriptional repressors. SOD7 exhibits the highest similarity to *Arabidopsis* NGAL3/DEVELOPMENT-RELATED PcG TARGET IN THE APEX 4 (DPA4) (FIG. **10**), which has known roles in the regulation of leaf serrations (Engelhorn et al., 2012), but no previously identified function in seed size control.

[0057] The inventor has shown that overexpression of AtSOD7 significantly decreases seed size of wild-type plants, while the disruption of AtSOD7 increases seed size. The inventors have shown that disruption of AtNGAL3, a close homolog of AtSOD7 also increases seed size. Moreover, the simultaneous disruption of AtSOD7 and AtNGAL3 further increases seed size in a synergistic manner. Genetic analyses carried out by the inventor indicate that AtSOD7 acts in a common pathway with the seed size regulator AtKLU to control seed growth, but does so independently of AtDA1. Further results show that AtSOD7 directly binds to the promoter of AtKLU in vitro and in vivo and represses expression of AtKLU. Therefore, the inventor's findings show that AtSOD7 (aka AtNGAL2) is a target for seed size improvement in crops. The plants of the invention are characterised by increased organ size, for example increased seed size, and also increased petal size, increased embryo size, for example. Increased seed size leads to an increase in seed yield and the plants of the invention are thus characterised by increased seed yield.

[0058] Thus, the invention relates to a plant wherein said plant does not produce a functional NGAL2 and/or NGAL3 polypeptide. For example, the plant does not produce a full length transcript of a nucleic acid sequence encoding a NGAL2 and/or NGAL3 protein. In another embodiment, the plant produces a full length transcript of a nucleic acid sequence encoding a NGAL2 and/or NGAL3, but the resulting protein is not functional. In a preferred embodiment, said plant does not produce a functional NGAL2 polypeptide and also does not produce a functional NGAL3 polypeptide. Such plants are double knock-out or knock-down mutants (loss of function mutants) and methods according to the invention as described below relate to making such double mutants.

[0059] The plants of the invention are mutant plants which have been genetically modified and are not naturally occurring varieties. Thus, the plants have been generated using genetic engineering methods, for example mutagenesis, gene targeting, gene silencing or genome editing as detailed below. Thus, the various aspects of the invention can involve recombinant DNA technology. The plant may be a transgenic plant in some embodiments, for example a plant which comprises a transgene to silence gene expression of SOD7 and/or NGAL3. In other embodiments, the plant does not carry a transgene, but is a mutant plant wherein the endogenous nucleic acid sequence encoding a NGAL2 and/or NGAL3 polypeptide or the endogenous SOD7 and/or NGAL3 promoter sequence has been manipulated to either reduce or abolish expression of a nucleic acid sequence encoding a NGAL2 and/or NGAL3 polypeptide or reduce or abolish the activity of a NGAL2 and/or NGAL3 polypeptide. The plants of the various aspects of the invention do not relate to natural variants which have not been manipulated by genetic engineering methods.

[0060] In one aspect, the invention relates to a plant generated by genetic engineering methods wherein the expression of a nucleic acid sequence encoding a NGAL2 and/or NGAL3 polypeptide and/or the activity of a NGAL2 and/or NGAL3 polypeptide is reduced or abolished relative to a control plant. In one embodiment, expression of a nucleic acid sequence encoding a NGAL2 polypeptide or the activity of a NGAL2 polypeptide is reduced or abolished. In another embodiment, expression of a nucleic acid sequence encoding a NGAL3 polypeptide or the activity of a NGAL3 polypeptide is reduced or abolished. In a preferred embodiment the presence of function of both proteins is affected, in other words, the plant is characterised in that expression of a nucleic acid sequence encoding a NGAL2 polypeptide or the activity of a NGAL2 polypeptide is reduced or abolished and also expression of a nucleic acid sequence encoding a NGAL3 polypeptide or the activity of a NGAL3 polypeptide is reduced or abolished in said plant.

[0061] For example, said plant can have reduced or abolished expression of a nucleic acid sequence encoding a NGAL2 polypeptide and reduced or abolished expression of a nucleic acid sequence encoding a NGAL3 polypeptide. In another embodiment, said plant can have reduced or abolished activity of a NGAL2 polypeptide and reduced or abolished activity of a NGAL3 polypeptide. In another embodiment, said plant can have reduced or abolished expression of a nucleic acid sequence encoding a NGAL2 polypeptide and reduced or abolished activity of a NGAL3 polypeptide. In another embodiment, said plant can have reduced or abolished expression of a nucleic acid sequence encoding a NGAL3 polypeptide and reduced or abolished activity of a NGAL2 polypeptide.

[0062] A NGAL2 or NGAL3 polypeptide as described in the various aspects of the invention has a characteristic domain structure as explained below.

[0063] A NGAL2 OR NGLA3 polypeptide as described in the various aspects of the invention comprises a B3 DNA binding domain which has the structure shown in FIG. **12**.

[0064] In one embodiment, the domain is: SNNNNNNGGSGDDVACHFQRFDLHRLFIGWRGE (SEQ ID NO:6) or a domain with at least 80%, at least 95% or at least 95% sequence identity thereto.

[0065] A NGAL2 OR NGAL3 polypeptide as described in the various aspects of the invention also comprises a transcriptional repression motif shown in FIG. **12**.

[0066] In one embodiment, the domain is: VRLFGVNLE (SEQ ID NO:7) or a domain with at least 95% sequence identity thereto.

[0067] In one embodiment, the NGAL2 protein is AtNGAL2, a functional variant, part or homologue thereof. AtNGAL2 is encoded by AtSOD7. The term AtSOD7 refers to the wild type AtSOD7 nucleic acid sequence comprising or consisting of SEQ ID NO. 1 (CDNA) or SEQ ID NO 2 (genomic DNA). The protein encoded by AtSOD7 is termed AtNGAL2 SEQ ID NO.3. In one embodiment, said functional homologue is not AtNGAL3.

[0068] In one embodiment, the NGAL3 protein is AtNGAL3, a functional variant, part or homologue thereof. The term AtNGAL3 refers to the wild type AtNGAL3 nucleic acid sequence comprising or consisting of SEQ ID NO. 4. The protein encoded by AtNGAL3 is termed AtNGAL3 SEQ ID NO.5.

[0069] The term "functional" refers to the biological function of the NGAL2 or NGAL3, that is their function in controlling organ size, in particular seed size. The terms "functional variant" or "functional part" as used herein, for example with reference to SEQ ID NOs: 1, 2 or 3, or SEQ ID NOs: 4 or 5 refers to a variant gene or polypeptide sequence or part of the gene or polypeptide sequence which retains the biological function of the full non-variant SOD7/NGAL2 or NGAL2/NGAL3 sequence, that is regulation of seed size. Such sequences complement the Atsod7-1D mutant or Atngal3 mutant respectively.

[0070] Thus, it is understood, as those skilled in the art will appreciate, that the aspects of the invention, encompass not only targeting a AtSOD7 and/or AtNGAL3 nucleic acid, for example a nucleic acid sequence comprising or consisting of SEQ ID NO: 1 or SEQ ID NO: 2, or SEQ ID NO: 4 respectively or a polypeptide comprising or consisting of SEQ ID NO: 3, or SEQ ID NO: 5, or a promoter of a AtSOD7 and/or AtNGAL3 nucleic acid. The aspects of the invention encompass also functional variants of AtNGAL2 or AtNGAL3 that do not affect the biological activity and function of the resulting protein. Alterations in a nucleic acid sequence which result in the production of a different amino acid at a given site that do however not affect the functional properties of the encoded polypeptide, are well known in the art. For example, a codon for the amino acid alanine, a hydrophobic amino acid, may be substituted by a codon encoding another less hydrophobic residue, such as glycine, or a more hydrophobic residue, such as valine, leucine, or isoleucine. Similarly, changes which result in substitution of one negatively charged residue for another, such as aspartic acid for glutamic acid, or one positively charged residue for another, such as lysine for arginine, can also produce a functionally equivalent product. Each of the proposed modifications is well within the routine skill in the art, as is determination of retention of biological activity of the encoded products. Also encompassed is a variant that is substantially identical, i.e. has only some sequence variations, for example in non-conserved residues, to the wild type sequences as shown herein and is biologically active.

[0071] Generally, variants of a particular SOD7/NGAL3 nucleotide sequence or NGAL2/NGAL3 polypeptide as described herein will have at least about 60%, preferably at least about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 92%, 94%, 95%, 96%, 97%, 98% or 99% or more sequence identity to that particular non-variant nucleotide sequence, as determined by sequence alignment programs described elsewhere herein.

[0072] Furthermore, the various the aspects of the invention encompass not only a AtSOD7 and/or AtNGAL3 nucleic acid, for example a nucleic acid sequence comprising or consisting of

[0073] 1 or SEQ ID NO: 2, or SEQ ID NO: 4 respectively or a polypeptide comprising or consisting of SEQ ID NO: 3, or SEQ ID NO: 5, or their functional variants but also homologues of AtSOD7 and/or AtNGAL3 in *Arabidopsis* or other plants. Also within the scope of the invention are functional variants of such homologues as defined above.

[0074] The term homologue as used herein also designates an AtSOD7 and/or AtNGAL3 orthologue from other plant species. A homologue of AtNGAL2 or AtNGAL3 polypeptide respectively has, in increasing order of preference, at least 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or at least 99% overall sequence identity to the amino acid represented by SEQ ID NO: 3 or 5 respectively. Preferably, overall sequence identity is at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%, most preferably 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or at least 99%.

[0075] In another embodiment, the homologue of a AtSOD7 or AtNGAL3 nucleic acid sequence respectively has, in increasing order of preference, at least 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or at least 99% overall sequence identity to the nucleic acid represented by SEQ ID NO: 1 or 2 or 4 respectively.

[0076] Preferably, overall sequence identity is at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%, most preferably 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or at least 99%. The overall sequence identity is determined using a global alignment algorithm known in the art, such as the Needleman Wunsch algorithm in the program GAP (GCG Wisconsin Package, Accelrys).

[0077] In a preferred embodiment, the NGAL2 or NGAL3 homologue is from a plant that is not *Arabidopsis.*

[0078] In one embodiment, an AtNGAL2 or a homologue thereof or AtNGAL3 or a homologue thereof comprises a B3 domain having the sequence as defined above

[0079] In one embodiment, an AtNGAL2 or a homologue thereof or AtNGAL3 or a homologue thereof comprises a transcriptional repression motif having the sequence as defined above

[0080] Examples of homologues are shown in FIG. **13** and in SEQ ID NO: 49-145. In certain embodiments, if a plant has more than one AtNGAL2 and/or AtNGAL3 homologue, then all homologues are knocked out or knocked down. Suitable homologues can be identified by sequence comparisons and identifications of conserved domains. There are predictors in the art that can be used to identify such sequences. The function of the homologue can be identified as described herein and a skilled person would thus be able to confirm the function, for example when overexpressed in a plant or knocked out in a plant or when expressed in a plant or by expressing the homologous nucleic acid sequence in an *Arabidopsis* gain of function mutant.

[0081] Thus, the nucleotide sequences of the invention and described herein can also be used to isolate corresponding sequences from other organisms, particularly other plants, for example crop plants. In this manner, methods such as PCR, hybridization, and the like can be used to identify such sequences based on their sequence homology to the sequences described herein. Topology of the sequences and the characteristic domains structure can also be considered when identifying and isolating homologues. Sequences may be isolated based on their sequence identity to the entire sequence or to fragments thereof. In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen plant. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labelled with a detectable group, or any other detectable marker. Thus, for example, probes for hybridization can be made by labelling synthetic oligonucleotides based on the ABA-associated sequences of the invention. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook, et al., (1989) Molecular Cloning: A Library Manual (2d ed., Cold Spring Harbor Laboratory Press, Plainview, N.Y.).

[0082] Hybridization of such sequences may be carried out under stringent conditions. By “stringent conditions” or “stringent hybridization conditions” is intended conditions under which a probe will hybridize to its target sequence to a detectably greater degree than to other sequences (e.g., at least 2-fold over background). Stringent conditions are sequence dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences that are 100% complementary to the probe can be identified (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000 nucleotides in length, preferably less than 500 nucleotides in length.

[0083] Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C. for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C. for long probes (e.g., greater than 50 nucleotides). Duration of hybridization is generally less than about 24 hours, usually about 4 to 12. Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

[0084] According to the invention, preferred homologues of AtSOD7 and AtNGAL3 peptides are selected from crop plants, for example cereal crops. Preferred homologues of AtNGAL2 and AtNGAL3 and their polypeptide sequences are also shown in FIG. **13**.

[0085] A plant according to the various aspects of the invention, including the transgenic plants, methods and uses described herein may be a monocot or a dicot plant.

[0086] A dicot plant may be selected from the families including, but not limited to Asteraceae, Brassicaceae (e.g. *Brassica napus*), Chenopodiaceae, Cucurbitaceae, Leguminosae (Caesalpiniaceae, Aesalpiniaceae Mimosaceae, Papilionaceae or Fabaceae), Malvaceae, Rosaceae or Solanaceae. For example, the plant may be selected from lettuce, sunflower, *Arabidopsis*, broccoli, spinach, water melon, squash, cabbage, tomato, potato, yam, *capsicum*, tobacco, cotton, okra, apple, rose, strawberry, alfalfa, bean, soybean, field (fava) bean, pea, lentil, peanut, chickpea, apricots, pears, peach, grape vine, bell pepper, chilli or citrus species.

[0087] A monocot plant may, for example, be selected from the families Arecaceae, Amaryllidaceae or Poaceae. For example, the plant may be a cereal crop, such as maize, wheat, rice, barley, oat, sorghum, rye, millet, buckwheat, or a grass crop such as *Lolium* species or *Festuca* species, or a crop such as sugar cane, onion, leek, yam or banana.

[0088] Also included are biofuel and bioenergy crops such as rape/canola, sugar cane, sweet sorghum, *Panicum virgatum* (switchgrass), linseed, lupin and willow, poplar, poplar hybrids, *Miscanthus* or gymnosperms, such as loblolly pine. Also included are crops for silage (maize), grazing or fodder (grasses, clover, sanfoin, alfalfa), fibres (e.g. cotton, flax), building materials (e.g. pine, oak), pulping (e.g. poplar), feeder stocks for the chemical industry (e.g. high erucic acid oil seed rape, linseed) and for amenity purposes (e.g. turf grasses for golf courses), ornamentals for public and private gardens (e.g. snapdragon, *petunia*, roses, geranium, *Nicotiana* sp.) and plants and cut flowers for the home (African violets, Begonias, chrysanthemums, geraniums, *Coleus* spider plants, Dracaena, rubber plant).

[0089] Preferably, the plant is a crop plant. By crop plant is meant any plant which is grown on a commercial scale for human or animal consumption or use. In a preferred embodiment, the plant is a cereal.

[0090] Most preferred plants are maize, rice, wheat, oilseed rape/canola, sorghum, soybean, sunflower, alfalfa, potato, tomato, tobacco, grape, barley, pea, bean, field bean, lettuce, cotton, sugar cane, sugar beet, broccoli or other vegetable brassicas or poplar.

[0091] The term "plant" as used herein encompasses whole plants, ancestors and progeny of the plants and plant parts, including seeds, fruit, shoots, stems, leaves, roots (including tubers), flowers, and tissues and organs, wherein each of the aforementioned comprise the gene/nucleic acid of interest. The term "plant" also encompasses plant cells, suspension cultures, callus tissue, embryos, meristematic regions, gametophytes, sporophytes, pollen and microspores, again wherein each of the aforementioned comprises the gene/nucleic acid of interest.

[0092] According to the various aspects of the invention, including the plants and methods of the invention, abolishing, inactivating, repressing, reducing or down-regulating the activity of a NGAL2 and/or NGAL3 polypeptide can be achieved through different means. Such means that are within the scope of the various aspects of the invention are methods for abolishing or reducing translation or transcription of the SOD7 and/or NGAL3 gene, destabilizing SOD7 and/or NGAL3 transcript stability, destabilizing NGAL2 and/or NGAL3 polypeptide stability or abolishing or reducing the activation or activity of the NGAL2 and/or NGAL3 or polypeptide. Thus, in one embodiment, endogenous SOD7 and/or NGAL3 gene or its promoter carry a functional mutation so that no full length transcript is made. In another embodiment, the SOD7 and/or NGAL3 gene is silenced in said plant using gene silencing techniques. In another embodiment, the SOD7 and/or NGAL3 nucleic acid sequence has been altered to introduce a mutation which results in a NGAL2/NGAL3 protein with reduced or abolished activity. These embodiments and the techniques used are described in more detail below.

[0093] In another aspect, the invention relates to a method for altering a plant phenotype comprising reducing or abolishing the expression of a nucleic acid sequence encoding a NGAL2 and/or NGAL3 polypeptide and/or reducing or abolishing the activity of a NGAL2 and/or NGAL3 polypeptide relative to a control plant.

[0094] In another aspect, the invention relates to a method for making a plant with an altered phenotype comprising reducing or abolishing the expression of a nucleic acid sequence encoding a NGAL2 and/or NGAL3 polypeptide and/or reducing or abolishing the activity of a NGAL2 and/or NGAL3 polypeptide relative to a control plant.

[0095] As previously described, such methods above use genetic engineering methods.

[0096] In this aspect, a wild type plant may be targeted to simultaneously knock out or down both SOD7 and NGAL3 function. Alternatively, the method may comprise the following steps

[0097] a) Knocking out or down SOD7 function in a first plant;

[0098] b) knocking out or down NGAL3 function in a second plant and

[0099] c) crossing plants regenerated from said first plant with plants regenerated from said second plant.

[0100] In one embodiment of these methods, expression of a nucleic acid sequence encoding a NGAL2 polypeptide or the activity of a NGAL2 polypeptide is reduced or abolished. In another embodiment, expression of a nucleic acid sequence encoding a NGAL3 polypeptide or the activity of a NGAL3 polypeptide is reduced or abolished. In a preferred embodiment, the method comprises reducing or abolishing expression of a nucleic acid sequence encoding a NGAL2 polypeptide or the activity of a NGAL2 polypeptide and reducing or abolishing expression of a nucleic acid sequence encoding a NGAL3 polypeptide or the activity of a NGAL3 polypeptide to create a double loss of function mutant.

[0101] For example, the method comprises reducing or abolishing expression of a nucleic acid sequence encoding a NGAL2 polypeptide and reducing or abolishing expression of a nucleic acid sequence encoding a NGAL3 polypeptide. In another embodiment, the method comprises reducing or abolishing activity of a NGAL2 polypeptide and reducing or abolishing activity of a NGAL3 polypeptide. In another embodiment, the method comprises reducing or abolishing expression of a nucleic acid sequence encoding a NGAL2 polypeptide and reducing or abolishing activity of a NGAL3 polypeptide. In another embodiment the method comprises reducing or abolishing expression of a nucleic acid sequence encoding a NGAL3 polypeptide or reducing or abolishing activity of a NGAL2 polypeptide.

[0102] According to these methods, the phenotype is preferably selected from increased organ size, for example increased seed size or increased seed weight. Increased seed size leads to an increase in yield and the methods of the invention also increased yield.

[0103] The term “yield” in general means a measurable produce of economic value, typically related to a specified crop, to an area, and to a period of time. Individual plant parts directly contribute to yield based on their number, size and/or weight, or the actual yield is the yield per square meter for a crop and year, which is determined by dividing total production (includes both harvested and appraised production) by planted square meters. The term “yield” as described herein relates to yield-related traits and may relate to vegetative biomass (root and/or shoot biomass), to reproductive organs, and/or to propagules (such as seeds) of that plant. Thus, according to the invention, the term yield refers to organ size, in particular seed size and can be measured by assessing seed size or seed weight or cotyledon size.

[0104] The terms “increase”, “improve” or “enhance” are interchangeable. Yield or seed size for example is increased by at least a 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or 10%, preferably at least 15% or 20%, more preferably 25%, 30%, 35%, 40% or 50% or more in comparison to a control plant.

[0105] A control plant as used herein according to all of the aspects of the invention is a plant which has not been modified according to the methods of the invention. Accordingly, the control plant has not been genetically modified to alter either expression of a nucleic acid encoding a NGAL2 or NGAL3 polypeptide or to alter the activity of a NGAL2 or NGAL3 polypeptide as described herein. In one embodiment, the control plant is a wild type plant that has not been genetically altered. In another embodiment, the control plant is a transgenic plant that does not have altered expression of a nucleic acid encoding a NGAL2 or NGAL3 polypeptide or altered activity of a NGAL2 or NGAL3 polypeptide, but has been genetically altered in other ways, for example by expressing a desirable transgene to confer certain traits.

[0106] The reduction, decrease, down-regulation or repression of the activity of the NGAL2 and/or NGAL3 polypeptide or corresponding SOD7 and/or NGAL3 nucleic acid sequences according to the aspects of the invention is at least 10%, 20%, 30%, 40% or 50% in comparison to the control plant.

[0107] For example, the plant is a reduction (knock down) or loss of function (knock out) mutant wherein the function of the SOD7 and/or NGAL3 nucleic acid sequence is reduced or lost compared to a wild type control plant. To this end, a mutation is introduced into the SOD7 and/or NGAL3 nucleic acid sequence or the corresponding promoter sequence which disrupts the transcription of the gene leading to a gene product which is not functional or has a reduced function. The mutation may be a deletion, insertion or substitution. The expression of active protein may thus be abolished by mutating the nucleic acid sequences in the plant cell which encode the NGAL2 or NGAL3 polypeptide and regenerating a plant from the mutated cell. The nucleic acids may be mutated by insertion or deletion of one or more nucleotides. Techniques for the inactivation or knockout of target genes are well-known in the art. These techniques include gene target using vectors that target the gene of interest and which allow integration allows for integration of transgene at a specific site. The targeting construct is engineered to recombine with the target gene, which is accomplished by incorporating sequences from the gene itself into the construct. Recombination then occurs in the region of that sequence within the gene, resulting in the insertion of a foreign sequence to disrupt the gene. With its sequence interrupted, the altered gene will be translated into a nonfunctional protein, if it is translated at all. Other techniques include genome editing (targeted genome engineering) as described below. Using either of these techniques, in preferred embodiment, conserved domains which confer function of NGAL2 or NGAL3 respectively are modified.

[0108] A skilled person will know further approaches can be used to generate such mutants. In one embodiment, insertional mutagenesis is used, for example using T-DNA mutagenesis (which inserts pieces of the T-DNA from the *Agrobacterium tumefaciens* T-Plasmid into DNA causing either loss of gene function or gain of gene function mutations), site-directed nucleases (SDNs) or transposons as mutagens. Insertional mutagenesis is an alternative means of disrupting gene function and is based on the insertion of foreign DNA into the gene of interest (see Krysan et al, The Plant Cell, Vol. 11, 2283-2290, December 1999).

[0109] In one embodiment, as discussed in the examples, T-DNA may be used as an insertional mutagen which disrupts SOD7 and/or NGAL3 gene expression. T-DNA not only disrupts the expression of the gene into which it is inserted, but also acts as a marker for subsequent identification of the mutation. Since the sequence of the inserted element is known, the gene in which the insertion has occurred can be recovered, using various cloning or PCR-based strategies. The insertion of a piece of T-DNA on the order of 5 to 25 kb in length generally produces a disruption of gene function. If a large enough population of T-DNA transformed lines is generated, there are reasonably good chances of finding a transgenic plant carrying a T-DNA insert within any gene of interest. Transformation of spores with T-DNA is achieved by an *Agrobacterium*-mediated method which involves exposing plant cells and tissues to a suspension of *Agrobacterium* cells.

[0110] The details of this method are well known to a skilled person. In short, plant transformation by *Agrobacterium* results in the integration into the nuclear genome of a sequence called T-DNA, which is carried on a bacterial plasmid. The use of T-DNA transformation leads to stable single insertions. Further mutant analysis of the resultant transformed lines is straightforward and each individual insertion line can be rapidly characterized by direct sequencing and analysis of DNA flanking the insertion. Gene expression in the mutant is compared to expression of the SOD7 and/or NGAL3 nucleic acid sequence in a wild type plant and phenotypic analysis is also carried out. Other techniques for insertional mutagenesis include the use of transposons.

[0111] In another embodiment, mutagenesis is physical mutagenesis, such as application of ultraviolet radiation, X-rays, gamma rays, fast or thermal neutrons or protons. The targeted population can then be screened to identify a SOD7 or NGAL3 loss of function mutant.

[0112] In another embodiment of the various aspects of the invention, the plant is a mutant plant derived from a plant population mutagenised with a mutagen. The mutagen may be fast neutron irradiation or a chemical mutagen, for example selected from the following non-limiting list: ethyl methanesulfonate (EMS), methylmethane sulfonate (MMS), N-ethyl-N-nitrosurea (ENU), triethylmelamine (1'EM), N-methyl-N-nitrosourea (MNU), procarbazine, chlorambucil, cyclophosphamide, diethyl sulfate, acrylamide monomer, melphalan, nitrogen mustard, vincristine, dimethylnitosamine, N-methyl-N'-nitro-Nitrosoguanidine (MNNG), nitrosoguanidine, 2-aminopurine, 7,12 dimethyl-benz(a)anthracene (DMBA), ethylene oxide, hexamethylphosphoramide, bisulfan, diepoxyalkanes (diepoxyoctane (DEO), diepoxybutane (BEB), and the like), 2-methoxy-6-chloro-9 [3-(ethyl-2-chloroethyl)aminopropylamino]acridine dihydrochloride (ICR-170) or formaldehyde.

[0113] In one embodiment, the method used to create and analyse mutations is targeting induced local lesions in genomes (TLLING), reviewed in Henikoff et al, 2004. In this method, seeds are mutagenised with a chemical mutagen, for example EMS. The resulting M1 plants are self-fertilised and the M2 generation of individuals is used to prepare DNA samples for mutational screening. DNA samples are pooled and arrayed on microtiter plates and subjected to gene specific PCR. The PCR amplification products may be screened for mutations in the SOD7 and/or NGAL3 target gene using any method that identifies heteroduplexes between wild type and mutant genes. For example, but not limited to, denaturing high pressure liquid chromatography (dHPLC), constant denaturant capillary electrophoresis (CDCE), temperature gradient capillary electrophoresis (TGCE), or by fragmentation using chemical cleavage. Preferably the PCR amplification products are incubated with an endonuclease that preferentially cleaves mismatches in heteroduplexes between wild type and mutant sequences. Cleavage products are electrophoresed using an automated sequencing gel apparatus, and gel images are analyzed with the aid of a standard commercial image-processing program. Any primer specific to the SOD7 or NGAL3 nucleic acid sequence may be utilized to amplify the SOD7 or NGAL3 nucleic acid sequence within the pooled DNA sample. Preferably, the primer is designed to amplify the regions of the SOD7 and/or NGAL3 gene where useful mutations are most likely to arise, specifically in the areas of the SOD7 and/or NGAL3 gene that are highly conserved and/or confer activity as explained elsewhere. To facilitate detection of PCR products on a gel, the PCR primer may be labelled using any conventional labelling method.

[0114] Rapid high-throughput screening procedures thus allow the analysis of amplification products for identifying a mutation conferring the reduction or inactivation of the expression of the SOD7 and/or NGAL3 gene as compared to a corresponding non-mutagenised wild type plant. Once a mutation is identified in a gene of interest, the seeds of the M2 plant carrying that mutation are grown into adult M3 plants and screened for the phenotypic characteristics associated with the target gene SOD7 or NGAL3. Loss of function or reduced function mutants with increased seed size compared to a control can thus be identified.

[0115] Plants obtained or obtainable by such method which carry a functional mutation in the endogenous SOD7 and/or NGAL3 locus are also within the scope of the invention

[0116] In another embodiment, RNA-mediated gene suppression or RNA silencing may be used to achieve silencing of the SOD7 and/or NGAL3 nucleic acid sequence. “Gene silencing” is a term generally used to refer to suppression of expression of a gene via sequence-specific interactions that are mediated by RNA molecules. The degree of reduction may be so as to totally abolish production of the encoded gene product, but more usually the abolition of expression is partial, with some degree of expression remaining. The term should not therefore be taken to require complete “silencing” of expression.

[0117] Transgenes may be used to suppress endogenous plant genes. This was discovered originally when chalcone synthase transgenes in *petunia* caused suppression of the endogenous chalcone synthase genes and indicated by easily visible pigmentation changes. Subsequently it has been described how many, if not all plant genes can be “silenced” by transgenes. Gene silencing requires sequence similarity between the transgene and the gene that becomes silenced. This sequence homology may involve promoter regions or coding regions of the silenced target gene. When coding regions are involved, the transgene able to cause gene silencing may have been constructed with a promoter that would transcribe either the sense or the antisense orientation of the coding sequence RNA. It is likely that the various examples of gene silencing involve different mechanisms that are not well understood. In different examples there may be transcriptional or post-transcriptional gene silencing and both may be used according to the methods of the invention.

[0118] The mechanisms of gene silencing and their application in genetic engineering, which were first discovered in plants in the early 1990s and then shown in *Caenorhabditis elegans* are extensively described in the literature.

[0119] RNA-mediated gene suppression or RNA silencing according to the methods of the invention includes co-suppression wherein over-expression of the target sense RNA or mRNA, that is the SOD7 and/or NGAL3 sense RNA or mRNA, leads to a reduction in the level of expression of the genes concerned. RNAs of the transgene and homologous endogenous gene are coordinately suppressed. Other techniques used in the methods of the invention include antisense RNA to reduce transcript levels of the endogenous target gene in a plant. In this method, RNA silencing does not affect the transcription of a gene locus, but only causes sequence-specific degradation of target mRNAs. An “antisense” nucleic acid sequence comprises a nucleotide sequence that is complementary to a “sense” nucleic acid sequence encoding a NGAL2 and/or NGAL3 protein, or a part of the protein, i.e. complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA transcript sequence. The antisense nucleic acid sequence is preferably complementary to the endogenous SOD7 and/or NGAL3 gene to be silenced. The complementarity may be located in the "coding region" and/or in the "non-coding region" of a gene. The term "coding region" refers to a region of the nucleotide sequence comprising codons that are translated into amino acid residues. The term "non-coding region" refers to 5' and 3' sequences that flank the coding region that are transcribed but not translated into amino acids (also referred to as 5' and 3' untranslated regions).

[0120] Antisense nucleic acid sequences can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid sequence may be complementary to the entire SOD7 and/or NGAL3 nucleic acid sequence, but may also be an oligonucleotide that is antisense to only a part of the nucleic acid sequence (including the mRNA 5' and 3' UTR). For example, the antisense oligonucleotide sequence may be complementary to the region surrounding the translation start site of an mRNA transcript encoding a polypeptide. The length of a suitable antisense oligonucleotide sequence is known in the art and may start from about 50, 45, 40, 35, 30, 25, 20, 15 or 10 nucleotides in length or less. An antisense nucleic acid sequence according to the invention may be constructed using chemical synthesis and enzymatic ligation reactions using methods known in the art. For example, an antisense nucleic acid sequence (e.g., an antisense oligonucleotide sequence) may be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acid sequences, e.g., phosphorothioate derivatives and acridine-substituted nucleotides may be used. Examples of modified nucleotides that may be used to generate the antisense nucleic acid sequences are well known in the art. The antisense nucleic acid sequence can be produced biologically using an expression vector into which a nucleic acid sequence has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest). Preferably, production of antisense nucleic acid sequences in plants occurs by means of a stably integrated nucleic acid construct comprising a promoter, an operably linked antisense oligonucleotide, and a terminator.

[0121] The nucleic acid molecules used for silencing in the methods of the invention hybridize with or bind to mRNA transcripts and/or insert into genomic DNA encoding a polypeptide to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid sequence which binds to DNA duplexes, through specific interactions in the major groove of the double helix. Antisense nucleic acid sequences may be introduced into a plant by transformation or direct injection at a specific tissue site. Alternatively, antisense nucleic acid sequences can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense nucleic acid sequences can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid sequence to peptides or antibodies which bind to cell surface receptors or antigens. The antisense nucleic acid sequences can also be delivered to cells using vectors.

[0122] RNA interference (RNAi) is another post-transcriptional gene-silencing phenomenon which may be used according to the methods of the invention. This is induced by double-stranded RNA in which mRNA that is homologous to the dsRNA is specifically degraded. It refers to the process of sequence-specific post-transcriptional gene silencing mediated by short interfering RNAs (siRNA). The process of RNAi begins when the enzyme, DICER, encounters dsRNA and chops it into pieces called small-interfering RNAs (siRNA). This enzyme belongs to the RNase III nuclease family. A complex of proteins gathers up these RNA remains and uses their code as a guide to search out and destroy any RNAs in the cell with a matching sequence, such as target mRNA.

[0123] Artificial and/or natural microRNAs (miRNAs) may be used to knock out gene expression and/or mRNA translation. MicroRNAs (miRNAs) miRNAs are typically single stranded small RNAs typically 19-24 nucleotides long. Most plant miRNAs have perfect or near-perfect complementarity with their target sequences. However, there are natural targets with up to five mismatches. They are processed from longer non-coding RNAs with characteristic fold-back structures by double-strand specific RNases of the Dicer family. Upon processing, they are incorporated in the RNA-induced silencing complex (RISC) by binding to its main component, an Argonaute protein. miRNAs serve as the specificity components of RISC, since they base-pair to target nucleic acids, mostly mRNAs, in the cytoplasm. Subsequent regulatory events include target mRNA cleavage and destruction and/or translational inhibition. Effects of miRNA overexpression are thus often reflected in decreased mRNA levels of target genes. Artificial microRNA (amiRNA) technology has been applied in *Arabidopsis thaliana* and other plants to efficiently silence target genes of interest. The design principles for amiRNAs have been generalized and integrated into a Web-based tool (wmd.weigelworld.org).

[0124] Thus, according to the various aspects of the invention a plant may be transformed to introduce a RNAi, shRNA, snRNA, dsRNA, siRNA, miRNA, ta-siRNA, amiRNA or cosuppression molecule that has been designed to target the expression of an SOD7 and/or NGAL3 nucleic acid sequence and selectively decreases or inhibits the expression of the gene or stability of its transcript. Preferably, the RNAi, snRNA, dsRNA, shRNA siRNA, miRNA, amiRNA, to-siRNA or cosuppression molecule used according to the various aspects of the invention comprises a fragment of at least 17 nt, preferably 22 to 26 nt and can be designed on the basis of the information shown in SEQ ID NO: 1. Guidelines for designing effective siRNAs are known to the skilled person. Briefly, a short fragment of the target gene sequence (e.g., 19-40 nucleotides in length) is chosen as the target sequence of the siRNA of the invention. The short fragment of target gene sequence is a fragment of the target gene mRNA. In preferred embodiments, the criteria for choosing a sequence fragment from the target gene mRNA to be a candidate siRNA molecule include 1) a sequence from the target gene mRNA that is at least 50-100 nucleotides from the 5' or 3' end of the native mRNA molecule, 2) a sequence from the target gene mRNA that has a G/C content of between 30% and 70%, most preferably around 50%, 3) a sequence from the target gene mRNA that does not contain repetitive sequences (e.g., AAA, CCC, GGG, TTT, AAAA, CCCC, GGGG, TTTT), 4) a sequence from the target gene mRNA that is accessible in the mRNA, 5) a sequence from the target gene mRNA that is unique to the target gene, 6) avoids regions within 75 bases of a start codon. The sequence fragment from the target gene mRNA may meet one or more of the criteria identified above. The selected gene is introduced as a nucleotide sequence in a prediction program that takes into account all the variables described above for the design of optimal oligonucleotides. This program scans any mRNA nucleotide sequence for regions susceptible to be targeted by siRNAs. The output of this analysis is a score of possible siRNA oligonucleotides. The highest scores are used to design double stranded RNA oligonucleotides that are typically made by chemical synthesis. In addition to siRNA which is complementary to the mRNA target region, degenerate siRNA sequences may be used to target homologous regions. siRNAs according to the invention can be synthesized by any method known in the art. RNAs are preferably chemically synthesized using appropriately protected ribonucleoside phosphoramidites and a conventional DNA/RNA synthesizer. Additionally, siRNAs can be obtained from commercial RNA oligonucleotide synthesis suppliers.

[0125] siRNA molecules according to the aspects of the invention may be double stranded. In one embodiment, double stranded siRNA molecules comprise blunt ends. In another embodiment, double stranded siRNA molecules comprise overhanging nucleotides (e.g., 1-5 nucleotide overhangs, preferably 2 nucleotide overhangs). In some embodiments, the siRNA is a short hairpin RNA (shRNA); and the two strands of the siRNA molecule may be connected by a linker region (e.g., a nucleotide linker or a non-nucleotide linker). The siRNAs of the invention may contain one or more modified nucleotides and/or non-phosphodiester linkages. Chemical modifications well known in the art are capable of increasing stability, availability, and/or cell uptake of the siRNA. The skilled person will be aware of other types of chemical modification which may be incorporated into RNA molecules.

[0126] In one embodiment, recombinant DNA constructs as described in U.S. Pat. No. 6,635,805, incorporated herein by reference, may be used.

[0127] The silencing RNA molecule is introduced into the plant using conventional methods, for example a vector and *Agrobacterium*-mediated transformation. Stably transformed plants are generated and expression of the SOD7 and/or NGAL3 gene compared to a wild type control plant is analysed.

[0128] Silencing of the SOD7 and/or NGAL3 nucleic acid sequence may also be achieved using virus-induced gene silencing.

[0129] Thus, in one embodiment of the invention, the plant expresses a nucleic acid construct comprising a RNAi, shRNA snRNA, dsRNA, siRNA, miRNA, ta-siRNA, amiRNA or co-suppression molecule that targets the SOD7 or NGAL3 nucleic acid sequence as described herein and reduces expression of the endogenous SOD7 or NGAL3 nucleic acid sequence. A gene is targeted when, for example, the RNAi, snRNA, dsRNA, siRNA, shRNA miRNA, ta-siRNA, amiRNA or cosuppression molecule selectively decreases or inhibits the expression of the gene compared to a control plant. Alternatively, a RNAi, snRNA, dsRNA, siRNA, miRNA, ta-siRNA, amiRNA or cosuppression molecule targets A SOD7 or NGAL3 nucleic acid sequence when the RNAi, shRNA snRNA, dsRNA, siRNA, miRNA, ta-siRNA, amiRNA or cosuppression molecule hybridises under stringent conditions to the gene transcript.

[0130] Gene silencing may also occur if there is a mutation on an endogenous gene and/or a mutation on an isolated gene/nucleic acid subsequently introduced into a plant. The reduction or substantial elimination may be caused by a non-functional polypeptide. For example, the polypeptide may bind to various interacting proteins; one or more mutation(s) and/or truncation(s) may therefore provide for a polypeptide that is still able to bind interacting proteins (such as receptor proteins) but that cannot exhibit its normal function (such as signalling ligand).

[0131] A further approach to gene silencing is by targeting nucleic acid sequences complementary to the regulatory region of the gene (e.g., the promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. Other methods, such as the use of antibodies directed to an endogenous polypeptide for inhibiting its function in planta, or interference in the signalling pathway in which a polypeptide is involved, will be well known to the skilled man. In particular, it can be envisaged that manmade molecules may be useful for inhibiting the biological function of a target polypeptide, or for interfering with the signalling pathway in which the target polypeptide is involved.

[0132] In one embodiment, the suppressor nucleic acids may be anti-sense suppressors of expression of the NGAL2 or NGAL3 polypeptides. In using anti-sense sequences to down-regulate gene expression, a nucleotide sequence is placed under the control of a promoter in a “reverse orientation” such that transcription yields RNA which is complementary to normal mRNA transcribed from the “sense” strand of the target gene.

[0133] An anti-sense suppressor nucleic acid may comprise an anti-sense sequence of at least 10 nucleotides from the target nucleotide sequence. It may be preferable that there is complete sequence identity in the sequence used for down-regulation of expression of a target sequence, and the target sequence, although total complementarity or similarity of sequence is not essential. One or more nucleotides may differ in the sequence used from the target gene. Thus, a sequence employed in a down-regulation of gene expression in accordance with the present invention may be a wild-type sequence (e.g. gene) selected from those available, or a variant of such a sequence.

[0134] The sequence need not include an open reading frame or specify an RNA that would be translatable. It may be preferred for there to be sufficient homology for the respective anti-sense and sense RNA molecules to hybridise. There may be down regulation of gene expression even where there is about 5%, 10%, 15% or 20% or more mismatch between the sequence used and the target gene. Effectively, the homology should be sufficient for the down-regulation of gene expression to take place.

[0135] Suppressor nucleic acids may be operably linked to tissue-specific or inducible promoters. For example, integument and seed specific promoters can be used to specifically down-regulate a SOD7 or NGAL3 nucleic acids in developing ovules and seeds to increase final seed size.

[0136] Nucleic acid which suppresses expression of a NGAL2 or NGAL3 polypeptide as described herein may be operably linked to a heterologous regulatory sequence, such as a promoter, for example a constitutive, inducible, tissue-specific or developmental specific promoter. The construct or vector may be transformed into plant cells and expressed as described herein. Plant cells comprising such vectors are also within the scope of the invention.

[0137] In another aspect, the invention relates to a silencing construct to silence expression of NGAL2 or NGAL3 obtainable or obtained by a method as described herein and to a plant cell comprising such construct. Accordingly, the invention also relates to the use of a nucleic acid sequence comprising or consisting of SEQ ID NO: 1, 2 or 3 or a part thereof or a homologue of SEQ ID NO: 1, 2 or 3 or a part thereof in silencing expression of NGAL2 or NGAL3. Host cells transformed with such construct are also within the scope of the invention.

[0138] Recently, genome editing techniques have emerged as alternative methods to conventional mutagenesis methods (such as physical and chemical mutagenesis) or methods using the expression of transgenes in plants to produce mutant plants with improved phenotypes that are important in agriculture. These techniques employ sequence-specific nucleases (SSNs) including zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and the RNA-guided nuclease Cas9 (CRISPR/Cas9), which generate targeted DNA double-strand breaks (DSBs), which are then repaired mainly by either error-prone non-homologous end joining (NHEJ) or high-fidelity homologous recombination (HR). The SSNs have been used to create targeted knockout plants in various species ranging from the model plants, *Arabidopsis* and tobacco, to important crops, such as barley, soybean, rice and maize. Heritable gene modification has been demonstrated in *Arabidopsis* and rice using the CRISPR/Cas9 system and TALENs.

[0139] Targeted genome modification or targeted genome editing is a genome engineering technique that uses targeted DNA double-strand breaks (DSBs) to stimulate genome editing through homologous recombination (HR)-mediated recombination events. To achieve effective genome editing via introduction of site-specific DNA DSBs, four major classes of customizable DNA binding proteins can be used: meganucleases derived from microbial mobile genetic elements, ZF nucleases based on eukaryotic transcription factors, transcription activator-like effectors (TALEs) from *Xanthomonas* bacteria, and the RNA-guided DNA endonuclease Cas9 from the type II bacterial adaptive immune system CRISPR (clustered regularly interspaced short palindromic repeats). Meganuclease, ZF, and TALE proteins all recognize specific DNA sequences through protein-DNA interactions. Although meganucleases integrate its nuclease and DNA-binding domains, ZF and TALE proteins consist of individual modules targeting 3 or 1 nucleotides (nt) of DNA, respectively. ZFs and TALEs can be assembled in desired combinations and attached to the nuclease domain of Fokl to direct nucleolytic activity toward specific genomic loci.

[0140] Upon delivery into host cells via the bacterial type III secretion system, TAL effectors enter the nucleus, bind to effector-specific sequences in host gene promoters and activate transcription. Their targeting specificity is determined by a central domain of tandem, 33-35 amino acid repeats. This is followed by a single truncated repeat of 20 amino acids. The majority of naturally occurring TAL effectors examined have between 12 and 27 full repeats.

[0141] These repeats only differ from each other by two adjacent amino acids, their repeat-variable di-residue (RVD). The RVD that determines which single nucleotide the TAL effector will recognize: one RVD corresponds to one nucleotide, with the four most common RVDs each preferentially associating with one of the four bases. Naturally occurring recognition sites are uniformly preceded by a T that is required for TAL effector activity. TAL effectors can be fused to the catalytic domain of the Fokl nuclease to create a TAL effector nuclease (TALEN) which makes targeted DNA double-strand breaks (DSBs) in vivo for genome editing. The use of this technology in genome editing is well described in the art, for example in U.S. Pat. Nos. 8,440,431, 8,440,432 and 8,450,471. Reference 30 describes a set of customized plasmids that can be used with the Golden Gate cloning method to assemble multiple DNA fragments. As described therein, the Golden Gate method uses Type IIS restriction endonucleases, which cleave outside their recognition sites to create unique 4 bp overhangs. Cloning is expedited by digesting and ligating in the same reaction mixture because correct assembly eliminates the enzyme recognition site. Assembly of a custom TALEN or TAL effector construct and involves two steps: (i) assembly of repeat modules into intermediary arrays of 1-10 repeats and (ii) joining of the intermediary arrays into a backbone to make the final construct.

[0142] Another genome editing method that can be used according to the various aspects of the invention is CRISPR. The use of this technology in genome editing is well described in the art, for example in U.S. Pat. No. 8,697,359 and references cited herein. In short, CRISPR is a microbial nuclease system involved in defense against invading phages and plasmids. CRISPR loci in microbial hosts contain a combination of CRISPR-associated (Cas) genes as well as non-coding RNA elements capable of programming the specificity of the CRISPR-mediated nucleic acid cleavage (sgRNA). Three types (I-III) of CRISPR systems have been identified across a wide range of bacterial hosts. One key feature of each CRISPR locus is the presence of an array of repetitive sequences (direct repeats) interspaced by short stretches of non-repetitive sequences (spacers). The non-coding CRISPR array is transcribed and cleaved within direct repeats into short crRNAs containing individual spacer sequences, which direct Cas nucleases to the target site (protospacer). The Type II CRISPR is one of the most well characterized systems and carries out targeted DNA double-strand break in four sequential steps. First, two non-coding RNA, the pre-crRNA array and tracrRNA, are transcribed from the CRISPR locus. Second, tracrRNA hybridizes to the repeat regions of the pre-crRNA and mediates the processing of pre-crRNA into mature crRNAs containing individual spacer sequences. Third, the mature crRNA:tracrRNA complex directs Cas9 to the target DNA via Watson-Crick base-pairing between the spacer on the crRNA and the protospacer on the target DNA next to the protospacer adjacent motif (PAM), an additional requirement for target recognition. Finally, Cas9 mediates cleavage of target DNA to create a double-stranded break within the protospacer.

[0143] Cas9 is thus the hallmark protein of the type II CRISPR-Cas system, and a large monomeric DNA nuclease guided to a DNA target sequence adjacent to the PAM (protospacer adjacent motif) sequence motif by a complex of two noncoding RNAs: CRIPSR RNA (crRNA) and transactivating crRNA (tracrRNA). The Cas9 protein contains two nuclease domains homologous to RuvC and HNH nucleases. The HNH nuclease domain cleaves the complementary DNA strand whereas the RuvC-like domain cleaves the non-complementary strand and, as a result, a blunt cut is introduced in the target DNA. Heterologous expression of Cas9 together with an sgRNA can introduce site-specific double strand breaks (DSBs) into genomic DNA of live cells from various organisms. For applications in eukaryotic organisms, codon optimized versions of Cas9, which is originally from the bacterium *Streptococcus pyogenes*, have been used.

[0144] The single guide RNA (sgRNA) is the second component of the CRISPR/Cas system that forms a complex with the Cas9 nuclease. sgRNA is a synthetic RNA chimera created by fusing crRNA with tracrRNA. The sgRNA guide sequence located at its 5' end confers DNA target specificity. Therefore, by modifying the guide sequence, it is possible to create sgRNAs with different target specificities. The canonical length of the guide sequence is 20 bp. In plants, sgRNAs have been expressed using plant RNA polymerase III promoters, such as U6 and U3.

[0145] Using these techniques, it is possible to specifically target conserved domains to abolish the function of the NGAL2 and/or NGAL3 polypeptide.

[0146] For example, the conserved B3 domain or repression motif may be targeted.

[0147] Thus, in another embodiment of the invention directed to a mutant plant, plant cell, plant or a part thereof characterised in that the activity of a NGAL2 polypeptide is altered and said plant expresses a nucleic acid comprising a mutant SEQ ID NO. 1 or 2 and encoding a mutant NGAL2 polypeptide, a functional homologue or variant thereof, for example one which carries a mutation in the B3 or repressor domain.

[0148] Thus, in another embodiment of the invention directed to a mutant plant, plant cell, plant or a part thereof characterised in that the activity of a NGAL3 polypeptide is altered and said plant expresses a nucleic acid comprising a mutant SEQ ID NO. 4 and encoding a mutant NGAL3 polypeptide, a functional homologue or variant thereof which carries a mutation in the B3 or repressor domain.

[0149] In a preferred embodiment, the invention directed to a mutant plant, plant cell, plant or a part thereof characterised in that the activity of a NGAL2 and a NGAL3 polypeptide is altered and said plant expresses a nucleic acid comprising a mutant SEQ ID NO. 1 or 2 and encoding a mutant NGAL2 polypeptide, a functional homologue or variant thereof, for example one which carries a mutation in the B3 or repressor domain and said plant expresses a nucleic acid comprising a mutant SEQ ID NO. 4 and encoding a mutant NGAL3 polypeptide which carries a mutation in the B3 or repressor domain.

[0150] Mutations in the promoter region of SOD7 and/or NGAL3 resulting in a loss of function are also within the scope of the invention.

[0151] Constructs designed using the genome editing technologies to knock out or knock down NGAL2 or NGAL3, for example as shown herein, are also within the scope of the invention as well as host cells comprising these constructs. In one embodiment, the constructs comprise or consist of a sequence selected from SEQ ID NO: 155, 156, 157 or 158. Accordingly, in a further aspect of the invention, there is provided a nucleic acid construct comprising a sequence selected from SEQ ID NO: 155, 156, 157 or 158. In a further aspect of the invention, there is provided a nucleic acid construct comprising at least one CRISPR target sequence, wherein the target sequence is selected from SEQ ID Nos 150, 160, 161, 162 and 163. Preferably, the target sequence comprises at least two CRISPR target sequences, preferably SEQ ID No 159 and 160 or SEQ ID No 161 and 162, or SEQ ID No 161 and 163 or SEQ ID No 159 and 163.

[0152] In another embodiment of the methods of the invention, inactivating, repressing or down-regulating the activity of NGAL2 and/or NGAL3 can be achieved by manipulating the expression of SOD7 and/or NGAL3 inhibitors in a plant, for example transgenic plant. For example, a gene expressing a protein that inhibits the expression of the SOD7 and/or NGAL3 gene or activity of the SOD7 and/or NGAL3 protein can be introduced into a plant and overexpressed. The inhibitor may interact with the regulatory sequences that direct SOD7 and/or NGAL3 gene expression to down-regulate or repress SOD7 and/or NGAL3 gene expression. For example, the inhibitor may be a transcriptional repressor. Alternatively, it may interact and repress transcriptional regulators, for example transcription factors, that positively regulate expression of the SOD7 and/or NGAL3 gene. Alternatively, the inhibitor it may directly interact with the NGAL2 and/or NGAL3 protein to inhibit its activity or interact with modulators of the NGAL2 and/or NGAL3 protein. For example, the activity of the NGAL2 and/or NGAL3 protein may be inactivated, repressed or down-regulated by manipulating post-transcriptional modifications, of the NGAL2 and/or NGAL3 protein resulting in a reduced or lost activity.

[0153] In one embodiment, the methods of the invention comprise comparing the activity of the NGAL2 and/or NGAL3 polypeptide and/or expression of the SOD7 and/or NGAL3 gene with the activity of the NGAL2 and/or NGAL3 polypeptide and/or expression of the SOD7 and/or NGAL3 gene in a control plant.

[0154] In another aspect, the invention relates to a plant obtainable or obtained by a method as described herein.

[0155] In another aspect, the invention relates to an expression cassette comprising an isolated nucleic acid sequence comprising or consisting of a sequence as shown in SEQ ID NO: 1 or 2 a functional part, variant, homologue or orthologue thereof operably linked to a regulatory element. In another aspect, the invention relates to an expression cassette comprising an isolated nucleic acid sequence comprising or consisting of a sequence as shown in SEQ ID NO: 4 or a functional part, variant, homologue or orthologue thereof operably linked to a regulatory element. The regulatory element may be a promoter. The invention also relates to a vector comprising such expression cassette. The invention also relates to a composition comprising the two expression cassettes above.

[0156] In the methods described here, plants can be regenerated from plants transformed or genetically altered as described above and the phenotype, specifically the seed phenotype is analysed by known methods.

[0157] Transformation methods are known in the art. The nucleic acid sequence is introduced into said plant through a process called transformation. The term "introduction" or "transformation" as referred to herein encompasses the transfer of an exogenous polynucleotide into a host cell, irrespective of the method used for transfer. Plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a genetic construct of the present invention and a whole plant regenerated there from. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristem, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem). The polynucleotide may be transiently or stably introduced into a host cell and may be maintained non-integrated, for example, as a plasmid. Alternatively, it may be integrated into the host genome. The resulting transformed plant cell may then be used to regenerate a transformed plant in a manner known to persons skilled in the art.

[0158] The transfer of foreign genes into the genome of a plant is called transformation. Transformation of plants is now a routine technique in many species. Advantageously, any of several transformation methods may be used to introduce the gene of interest into a suitable ancestor cell. The methods described for the transformation and regeneration of plants from plant tissues or plant cells may be utilized for transient or for stable transformation. Transformation methods include the use of liposomes, electroporation, chemicals that increase free DNA uptake, injection of the DNA directly into the plant, particle gun bombardment, transformation using viruses or pollen and microprojection. Methods may be selected from the calcium/polyethylene glycol method for protoplasts, electroporation of protoplasts, microinjection into plant material, DNA or RNA-coated particle bombardment, infection with (non-integrative) viruses and the like. Transgenic plants, including transgenic crop plants, are preferably produced via *Agrobacterium tumefaciens* mediated transformation.

[0159] To select transformed plants, the plant material obtained in the transformation is, as a rule, subjected to selective conditions so that transformed plants can be distinguished from untransformed plants. For example, the seeds obtained in the above-described manner can be planted and, after an initial growing period, subjected to a suitable selection by spraying. A further possibility is growing the seeds, if appropriate after sterilization, on agar plates using a suitable selection agent so that only the transformed seeds can grow into plants. Alternatively, the transformed plants are screened for the presence of a selectable marker such as the ones described above. Following DNA transfer and regeneration, putatively transformed plants may also be evaluated, for instance using Southern analysis, for the presence of the gene of interest, copy number and/or genomic organisation. Alternatively or additionally, expression levels of the newly introduced DNA may be monitored using Northern and/or Western analysis, both techniques being well known to persons having ordinary skill in the art.

[0160] The generated transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plant may be selfed and homozygous second-generation (or T2) transformants selected, and the T2 plants may then further be propagated through classical breeding techniques. The generated transformed organisms may take a variety of forms. For example, they may be chimeras of transformed cells and non-transformed cells; clonal transformants (e.g., all cells transformed to contain the expression cassette); grafts of transformed and untransformed tissues (e.g., in plants, a transformed rootstock grafted to an untransformed scion).

[0161] The various aspects of the invention described herein clearly extend to any plant cell or any plant produced, obtained or obtainable by any of the methods described herein, and to all plant parts and propagules thereof unless otherwise specified. The present invention extends further to encompass the progeny of a primary transformed or transfected cell, tissue, organ or whole plant that has been produced by any of the aforementioned methods, the only requirement being that progeny exhibit the same genotypic and/or phenotypic characteristic(s) as those produced by the parent in the methods according to the invention.

[0162] The invention also extends to harvestable parts of a plant of the invention as described above such as, but not limited to seeds, leaves, fruits, flowers, stems, roots, rhizomes, tubers and bulbs. The invention furthermore relates to products derived, preferably directly derived, from a harvestable part of such a plant, such as dry pellets or powders, oil, fat and fatty acids, starch or proteins. The invention also relates to food products and food supplements comprising the plant of the invention or parts thereof.

[0163] While the foregoing disclosure provides a general description of the subject matter encompassed within the scope of the present invention, including methods, as well as the best mode thereof, of making and using this invention, the following examples are provided to further enable those skilled in the art to practice this invention and to provide a complete written description thereof. However, those skilled in the art will appreciate that the specifics of these examples should not be read as limiting on the invention, the scope of which should be apprehended from the claims and equivalents thereof appended to this disclosure. Various further aspects and embodiments of the present invention will be apparent to those skilled in the art in view of the present disclosure.

[0164] All documents mentioned in this specification are incorporated herein by reference in their entirety, including references to gene and protein accession numbers.

[0165] "and/or" where used herein is to be taken as specific disclosure of each of the multiple specified features or components with or without the other at each combination unless otherwise dictated. For example "A, B and/or C" is to be taken as specific disclosure of each of (i) A, (ii) B, (iii) C, (iv) A and B, (v) B and C or (vi) A and B and C, just as if each is set out individually herein.

[0166] Unless context dictates otherwise, the descriptions and definitions of the features set out above are not limited to any particular aspect or embodiment of the invention and apply equally to all aspects and embodiments which are described.

[0167] The invention is further described in the following non-limiting examples.

EXAMPLES

[0168] Methods

[0169] Plant Materials and Growth Conditions

[0170] *Arabidopsis thaliana* Columbia (Col-0) was used as wild-type line. The da1-1, sod7-1D, sod7-ko1 and ngal3-ko1 were in the Col-0 background. sod7-1D was identified as a suppressor of da1-1 by using T-DNA activation tagging method. The sod7-ko1 (SM_3_34191) and ngal3-ko1 (SM_3_36641) were identified in AtIDB (atidb.org) and obtained from *Arabidopsis* Stock Centre NASC collection. T-DNA insertions were confirmed by PCR and sequencing by using the primers described in Table 1. *Arabidopsis* plants were grown under long-day conditions (16 h light/8 h dark) at 22° C. Activation tagging screening The activation tagging plasmid pJFAT260 was introduced into the da1-1 mutant plants using *Agrobacterium tumefaciens* strain GV3101 (Fan et al., 2009; Fang et al., 2012), and T1 plants were selected by using the herbicide Basta. Seeds produced from T1 plants were used to isolate modifiers of da1-1.

[0171] Morphological and Cellular Analysis

[0172] To measure seed size, we photographed dry seeds of the wild type and mutants under a Leica microscope (LEICA S8APO) using Leica CCD (DFC420). The projective area of wild-type and mutant seeds was measured by using Image J software. Average seed weight was determined by weighing mature dry seeds in batches of 100 using an electronic analytical balance (METTLER TOLEDO AL104, China). The weights of five sample batches were measured for each seed lot. Fully expanded cotyledons, petals (stage 14) and leaves were scanned to produce digital images for area measurement. To measure cell number and cell size, petals, leaves, ovules and seeds were placed in a drop of clearing solution [30 ml H2O, 80 g Chloral hydrate (Sigma, C8383), 10 ml 100% Glycerol (Sigma, G6279)]. Cleared Samples were imaged under a Leica microscope (LEICA DM2500) with differential interference contrast (DIC) optics and photographed with a SPOT FLEX Cooled CCD Digital Imaging System. Area measurement was made by using Image J software.

[0173] Cloning of the SOD7 Gene

[0174] The flanking sequences of the T-DNA insertion of the sod7-1D mutant were identified by the thermal asymmetric interlaced PCR (TAIL-PCR) according to a previously reported method (Liu et al., 1995). Briefly, TAIL-PCR utilizes three nested specific primers (OJF22, OJF23 and OJF24) within the T-DNA region of the pJFAT260 vector and a shorter arbitrary degenerate primer (AD1). Thus, the relative amplification efficiencies of specific and non-specific products can be thermally controlled. TAIL-PCR products were sequenced using the primer OJF24. The specific primers OJF22, OJF23 and OJF24 and an arbitrary degenerate (AD1) primer are described in Table 1.

[0175] Constructs and Plant Transformation

[0176] The 35S:GFP-SOD7, pSOD7:SOD7-GFP and pSOD7:GUS constructs were made using a PCR-based Gateway system. The coding sequence (CDS) of SOD7 was amplified using the primers SOD7CDS-F and SOD7CDS-R (Table 1). PCR products were cloned into pCR8/TOPO TA cloning vector. The SOD7 CDS was then subcloned into the binary vector pMDC43 with the GFP gene to generate the transformation plasmid 35S:GFP-SOD7. The SOD7 genomic sequence containing 2040-bp promoter sequence and 2104-bp SOD7 gene was amplified using the primers SOD7G-F and SOD7G-R (Table 1). PCR products were cloned into pCR8/TOPO TA cloning vector. The SOD7 genomic sequence was then subcloned into the binary vectors pMDC107 with the GFP gene to generate the transformation plasmid pSOD7:SOD7-GFP. The 2262-bp SOD7 promoter sequence was amplified using the primers SOD7P-F and SOD7P-R (Table 1). PCR products were cloned into pCR8/TOPO TA cloning vector. The SOD7 promoter was then subcloned into the binary vectors pGWB3 with the GUS gene to generate the transformation plasmid pSOD7:GUS. The plasmids 35S:GFP-SOD7, pSOD7:SOD7-GFP and pSOD7:GUS were introduced into Col-0 or sod7-ko1 ngal3ko1 plants using *Agrobacterium tumefaciens* GV3101, respectively, and transformants were selected on hygromycin (30 μg/ml)-containing medium. The SOD7 cDNA was cloned into the Apal and Spel sites of the binary vector pER8 to generate a chemically inducible construct pER8-SOD7. The specific primers for the pER8-SOD7 construct were SOP7ER-F and SOD7ER-R. The plasmid pER8-SOD7 was introduced into Col-0 plants using *Agrobacterium tumefaciens* GV3101, and transformants were selected on hygromycin (30 μg/ml)-containing medium. GUS staining Samples (pSOD7:GUS) were stained in a GUS staining solution (1 mM X-gluc, 50 Mm NaPO4 buffer, 0.4 mM each K3Fe(CN)6/K4Fe(CN)6, and 0.1% (v/v) Triton X-100) and incubated at 37° C. for 3 hours. After GUS staining, chlorophyll was removed by 70% ethanol. RT-PCR and quantitative real-time RT-PCR. Total RNA was extracted from *Arabidopsis* seedlings using an RNAprep pure Plant kit (TIANGEN). mRNA was reverse transcribed into cDNA using SuperScriptIII reverse transcriptase (Invitrogen). cDNA samples were standardized on ACTIN2 transcript amount using the primers ACTIN2-F and ACTIN2-R (Table 1). Quantitative real-time RT-PCR analysis was performed with a Lightcycler 480 machine (Roche) using the Lightcycler 480 SYBR Green I Master (Roche). ACTIN2 mRNA was used as an internal control, and relative amounts of mRNA were calculated using the comparative threshold cycle method. The primers used for RT-PCR and quantitative real-time RT-PCR are described in Table 1.

[0177] The Chromatin Immunoprecipitation (ChIP) Assay

[0178] The chromatin immunoprecipitation (ChIP) assay was performed as described previously with minor modifications (Gendrel et al., 2005). Briefly, 35S:GFP and 35S:GFP-SOD7 transgenic seeds were grown on ½ MS plates for 10 days. The seedlings were cross-linked by 1% formaldehyde for 15 min in vacuum and stopped by 0.125 M Glycine. Samples were ground in liquid nitrogen, and nuclei were isolated. Chromatin was immunoprecipitated by anti-GFP (Roche, 11814460001) and protein A+G beads (Millpore Magna ChIP Protein A+G Magnetic Beads, 16-663). DNA was precipitated by glycogen, NaOAc and ethanol, washed by 70% ethanol, and dissolved in 60 μl of water. Gene-specific primers (PF1-F, PF1-R, PF-2F, PF2-R, ACTIN7-ChIP-F, and ACTIN7-ChIP-R) were used to quantify the enrichment of each fragment (Table 1).

[0179] The DNA Electrophoretic Mobility Shift Assay (EMSA)

[0180] The coding sequence of SOD7 was cloned into the NdeI and BamHI sites of the pMAL-C2 vector to generate the construct MBP-SOD7. MBP-SOD7 fusion proteins were expressed in *Escherichia coli* BL21 (DE3) (Biomed) and purified by Amylose resins(New England Biolabs). The biotin-labeled and unlabeled probes were synthesized as forward and reverse strands. The forward and reverse strands were then incubated in a solution (50 mM Tris-HCl, 5 mM EDTA and 250 mM NaCl) at 95° C. for 10 min and renatured to double stranded probes at room temperature. The gel-shift assay was performed according to the method described previously (Smaczniak et al., 2012).

[0181] Results

[0182] sod7-1D Suppresses the Seed Size Phenotype of Dal-1

[0183] We previously identified the ubiquitin receptor DA1 as a negative regulator of seed size in *Arabidopsis* (Li et al., 2008). The da1-1 mutant formed large seeds due to increased cell proliferation in the maternal integuments (Li et al., 2008; Xia et al., 2013). To identify novel components in the DA1 pathway or other seed size regulators, we initiated a T-DNA activation tagging screen for modifiers of da1-1 (Fang et al., 2012). A dominant suppressor of da1-1 (sod7-1D) was isolated from seeds produced from approximate 16,000 T1 plants (FIG. **1**A). Seeds of the sod7-1D da1-1 double mutant were significantly smaller and lighter than da1-1 seeds (FIGS. **1**A, E and F). The embryo constitutes the major volume of a mature seed in *Arabidopsis*. sod7-1D da1-1 embryos were smaller than da1-1 embryos (FIG. **1**B). The size of sod7-1D da1-1 cotyledons was significantly reduced, compared with that of da1-1 cotyledons (FIG. **1**G). In addition, sod7-1D da1-1 double mutant formed smaller leaves and flowers than da1-1 (FIGS. **1**C and **1**D). Thus, these results show that the sod7-1D mutation suppressed the seed and organ size phenotypes of da1-1.

[0184] sod7-1D Produces Small Seeds

[0185] We isolated the single sod7-1D mutant among F2 progeny derived from a cross between the wild type (Col-0) and sod7-1D da1-1. The sod7-1D seeds were significantly smaller and lighter than wild-type seeds (FIGS. **2**A, B, G and H). We further isolated and visualized embryos from mature wild-type and sod7-1D seeds. The sod7-1D embryos were obviously smaller than wild-type embryos (FIGS. **2**C and D). The changes in seed size were also reflected in the size of seedlings (FIGS. **2**E and F). The 10-d old sod7-1D cotyledons were significantly smaller than wild-type cotyledons (FIGS. **2**E, F and I). In addition, the sod7-1D mutants exhibited small leaves and flowers compared with the wild type. The decreased size of sod7-1D leaves and petals was not caused by smaller cells, indicating that the sod7-1D mutation results in a decrease in cell number. In fact, the average area of epidermal cells in sod7-1D petals was larger than that in wild-type petals, suggesting a possible compensation mechanism between cell number and cell size.

[0186] SOD7 Encodes a B3 Domain Transcriptional Repressor NGAL2

[0187] To determine whether the seed and organ size phenotypes of sod7-1D was caused by the T-DNA insertion, we firstly analyzed the genetic linkage of the mutant phenotypes with Basta resistance, which is conferred by the selectable marker of the activation tagging vector (Fan et al., 2009). In a T2 population, 181 plants with sod7-1D da1-1 phenotypes were resistant, whereas 55 plants with da1-1 phenotypes were sensitive, indicating that the insertion is cosegregated with the sod7-1D phenotypes. To clone the SOD7 gene, we isolated the T-DNA flanking sequences using thermal asymmetric interlaced PCR (Liu et al., 1995). DNA sequencing revealed that the T-DNA had inserted approximately 5.6 kb upstream of the At3g11580 and about 3.7 kb upstream of the At3g11590 gene (FIG. **3**A). To determine which gene is responsible for the sod7-1D phenotypes, we examined the mRNA levels of these two genes. The mRNA of the At3g11590 gene accumulated at a similar level in sod7-1D da1-1 and da1-1, suggesting that At3g11590 is not the SOD7 gene (FIG. **3**B). By contrast, expression level of the At3g11580 gene in sod7-1D da1-1 plants was dramatically higher than that in da1-1 plants, suggesting that At3g11580 is the SOD7 gene (FIG. **3**B). To further confirm whether the sod7-1D phenotypes were caused by ectopic At3g11580 expression, we overexpressed the At3g11580 gene (35S:GFP-SOD7) in wild-type plants (Col-0) and isolated 37 transgenic plants. Most transgenic lines showed small seeds and organs (FIGS. **3**D-F), similar to those observed in the sod7-1D single mutant, indicating that At3g11580 is the SOD7 gene. The SOD7 gene encodes a NGATHA like protein (NGAL2) containing a B3 DNA-binding domain and a transcriptional repression motif (FIG. **3**C) (Alvarez et al., 2009; Ikeda and Ohme-Takagi, 2009; Trigueros et al., 2009). SOD7 belongs to the RAV gene family that consists of 13 members in *Arabidopsis* (FIG. **10**) (Swaminathan et al., 2008). Several members of the RAV family contain the putative transcriptional repression motifs, including NGA1, NGA2, NGA3, NGA4, NGAL1, NGAL2/SOD7 and NGAL3 (FIG. **10**) (Ikeda and Ohme-Takagi, 2009). The transcriptional repression motifs in NGA1, NGAL1 and NGAL2/SOD7 have been known to possess the repressive activity (Ikeda and Ohme-Takagi, 2009), indicating that they are transcriptional repressors. SOD7 exhibits the highest similarity to *Arabidopsis* NGAL3/DEVELOPMENT-RELATED PcG TARGET IN THE APEX 4 (DPA4) (FIG. **10**), which has known roles in the regulation of leaf serrations (Engelhorn et al., 2012), but no previously identified function in seed size control.

[0188] Expression Pattern and Subcellular Localization of SOD7

[0189] To monitor SOD7 expression pattern during development, the pSOD7:GUS and pSOD7:SOD7-GFP vectors were constructed and transformed to wild-type plants, respectively. The tissue-specific expression patterns of SOD7 were examined using a histochemical assay for GUS activity. In seedlings, relatively higher GUS activity was detected in younger leaves than in older leaves (FIGS. **4**A-C). In flowers, GUS activity was observed in sepals, petals, stamens and carpels (FIGS. **4**D-K). GUS activity was stronger in younger floral organs than in older ones (FIGS. **4**D-K). Expression of SOD7 was also detected in ovules (FIG. **4**L). Thus, these analyses indicate that SOD7 is a temporally and spatially expressed gene. As SOD7 encodes a B3 domain transcriptional repressor, we speculated that SOD7 is localized in the nucleus. To determine subcellular localization of SOD7, we observed GFP inflorescence in pSOD7:SOD7-GFP transgenic plants. As shown in FIGS. **4**M-O, GFP signal was only detected in nuclei. We also expressed a GFP-SOD7 fusion protein under the control of the 35S promoter in wild-type plants. Transgenic lines overexpressing GFP-SOD7 formed smaller seeds than the wild type (FIG. **3**D), indicating that the GFP-SOD7 fusion protein is functional. As shown in FIGS. **4**P-R, GFP fluorescence in 35S:GFP-SOD7 transgenic plants was exclusively observed in nuclei. Thus, these results show that SOD7 is a nuclear-localized protein.

[0190] SOD7/NGAL2 Acts Redundantly with NGAL3 to Control Seed Size

[0191] In order to further investigate the function of SOD7 in seed size control, we isolated T-DNA inserted loss-of-function mutants for SOD7 and NGAL3, the most closely related family member. sod7-ko1 (SM_3_34191) was identified with T-DNA insertion in the first exon of the SOD7 gene (FIG. **5**A). ngal3-ko1 (SM_3_36641) had T-DNA insertion in the first exon of the NGAL3 gene (FIG. **5**B). The

T-DNA insertion sites were confirmed by PCR using T-DNA specific and flanking primers and sequencing PCR products. sod7-ko1 and ngal3-ko1 mutants had no detectable full-length transcripts of SOD7 and NGAL3, respectively. Seeds from sod7-ko1 and ngal3-ko1 mutants were slightly larger and heavier than seeds from wild-type plants (FIGS. **5**C, G and H). The cotyledon area of sod7-ko1 and ngal3-ko1 mutants was increased, compared with that of the wild type (FIG. **5**I). Considering that SOD7 shares the highest similarity with NGAL3, we speculated that SOD7 may act redundantly with NGAL3 to influence seed size. To test this, we generated the sod7-ko1 ngal3-ko1 double mutant. As shown in FIGS. **5**C, D, G and H, the seed size and weight phenotypes of sod7-ko1 mutant were synergistically enhanced by the disruption of NGAL3, indicating that SOD7 functions redundantly with NGAL3 to control seed size. We further measured the cotyledon area of 10-d-old seedlings. A synergistic enhancement of cotyledon size of sod7-ko1 by the ngal3-ko1 mutation was also observed (FIG. **5**I). In addition, the sod7-ko1 ngal3-ko1 double mutant formed larger leaves and flowers than their parental lines (FIGS. **5**E and F; 11). Thus, these results indicate that SOD7 and NGAL3 act redundantly to control seed and organ growth.

[0192] SOD7 Acts Maternally to Control Seed Size

[0193] As the size of a seed is determined by the zygotic and/or maternal tissues (Garcia et al., 2005; Xia et al., 2013; Du et al., 2014), we asked whether SOD7 functions maternally or zygotically. We therefore performed reciprocal cross experiments between the wild type and sod7-ko1 ngal3-ko1. The effect of sod7-ko1 ngal3-ko1 on seed size was observed only when sod7-ko1 ngal3-ko1 was used as maternal plants (FIG. **6**A). The size of seeds from sod7-ko1 ngal3-ko1 plants pollinated with wild-type pollen was similar to that from the self-pollinated sod7-ko1 ngal3-ko1 plants (FIG. **6**A). By contrast, the size of seeds from wild-type plants pollinated with sod7-ko1 ngal3-ko1 mutant pollen was similar to that from the self-pollinated wild-type plants (FIG. **6**A). These results indicate that sod7-ko1 ngal3-ko1 acts maternally to influence seed size. We further investigated the size of Col-0/Col-0 F2, Col-0/sod7-ko1 ngal3-ko1 F2, sod7-ko1 ngal3-ko1/Col-0 F2 and sod7-ko1 ngal3-ko1/sod7-ko1 ngal3-ko1 F2 seeds. As shown in FIG. **6**B, sod7-ko1 ngal3-ko1/sod7-ko1 ngal3-ko1 F2 seeds were larger than wild-type seeds, while the size of Col-0/sod7-ko1 ngal3-ko1 F2 and sod7-ko1 ngal3-ko1/Col-0 F2 seeds was similar to that of wild-type seeds. Thus, these results indicate that the embryo and endosperm genotypes for SOD7 do not determine seed size, and SOD7 is required in the sporophytic tissue of the mother plant to control seed growth.

[0194] SOD7 Regulates Cell Proliferation in the Maternal Integuments

[0195] The reciprocal crosses showed that SOD7 functions maternally to influence seed size. The integuments surrounding the ovule are maternal tissues, which could set the growth potential of the seed coat after fertilization. Consistent with this idea, several studies showed that the integument size influences the final size of seeds in *Arabidopsis* (Garcia et al., 2005; Schruff et al., 2006; Adamski et al., 2009; Xia et al., 2013; Du et al., 2014). We therefore asked whether SOD7 acts through the maternal integuments to determine seed size. To test this, we characterized mature ovules of the wild type and sod7-ko1 ngal3-ko1. As shown in FIGS. **6**C and D, the sod7-ko1 ngal3-ko1 ovules were obviously larger than wild-type ovules. The outer integument length of sod7-ko1 ngal3-ko1 ovules was significantly increased, compared with that of wild-type ovules (FIG. **6**E). As the size of the integument is determined by cell proliferation and cell expansion, we examined the number and size of outer integument cells in wild-type and sod7-ko1 ngal3-ko1 ovules. As shown in FIG. **6**F, the number of outer integument cells in sod7-ko1 ngal3-ko1 ovules was increased, compared with that in wild-type ovules. By contrast, the length of outer integument cells in sod7-ko1 ngal3-ko1 ovules was similar to that in wild-type ovules (FIG. **6**G). These results showed that SOD7 is required for cell proliferation in the maternal integuments of ovules. After fertilization, cells in the integument mainly undergo expansion but still have division. We further examined the number and size of outer integument cells in wild-type and sod7-ko1 ngal3-ko1 seeds at 6 and 8 day after pollination (DAP). In wild-type seeds, the number of outer integument cells at 6 DAP was comparable with that at 8 DAP (FIG. **6**F), indicating that cells in the outer integuments of wild-type seeds completely stop dividing by 6 DAP. Similarly, cells in the outer integuments of sod7-ko1 ngal3-ko1 seeds also cease division by 6 DAP. The number of outer integument cells in sod7-ko1 ngal3-ko1 seeds was significantly increased, compared with that in wild-type seeds (FIG. **6**F). By contrast, the length of outer integument cells in sod7-ko1 ngal3-ko1 seeds was not increased in comparison to that in wild-type seeds (FIG. **6**G). Thus, these analyses indicate that SOD7 is required for cell proliferation in the maternal integuments of ovules and developing seeds.

[0196] SOD7 Acts in a Common Pathway with KLU to Control Seed Size, but does so Independently of DA1

[0197] The *Arabidopsis* klu mutants formed small seeds due to the decreased cell proliferation in the integuments, while plants overexpressing KLU/CYP78A5 produced large seeds as a result of the increased cell proliferation in the integuments (Adamski et al., 2009), suggesting that SOD7 and KLU could function antagonistically in a common pathway to control seed growth. To test for genetic interactions between SOD7 and KLU, we generated the klu-4 sod7-ko1 ngal3-ko1 triple mutant and measured the size of seeds from wild-type, klu-4, sod7-ko1 ngal3-ko1 and klu-4 sod7-ko1 ngal3-ko1 plants. As shown in FIGS. **7**A and B, the average size and weight of klu-4 sod7-ko1 ngal3-ko1 seeds were similar to those of the klu-4 single mutant, indicating that klu-4 is epistatic to sod7-ko1 ngal3-ko1 with respect to seed size and weight. We further investigated the mature ovules from wild-type, klu-4, sod7-ko1 ngal3-ko1 and klu-4 sod7-ko1 ngal3-ko1 plants. The outer integument length of klu-4 sod7-ko1 ngal3-ko1 ovules was comparable with that of klu-4 ovules (FIG. **7**C). Similarly, the outer integument length of klu-4 sod7-ko1 ngal3-ko1 seeds was indistinguishable from that of klu-4 seeds at 8 DAP (FIG. **7**C). In addition, the size of klu-4 sod7-ko1 ngal3-ko1 petals was similar to that of klu-4 petals).

[0198] Thus, these genetic analyses show that klu-4 is epistatic to sod7-ko1 ngal3-ko1 with respect to seed and organ size, indicating that SOD7 and KLU act antagonistically in a common pathway to control seed and organ growth. To further understand the cellular basis of epistatic interactions between SOD7 and KLU, we investigated the outer integument cell number of ovules and developing seeds from wild-type, klu-4, sod7-ko1 ngal3-ko1 and klu-4 sod7-ko1 ngal3-ko1 plants. The number of outer integument cells in klu-4 sod7-ko1 ngal3-ko1 ovules was similar to that in klu-4 ovules (FIG. **7**D). Similarly, the number of outer integument cells in klu-4 sod7-ko1 ngal3-ko1 seeds was comparable with that in klu-4 seeds (FIG. **7**D). These results indicate that klu-4 is epistatic to sod7-ko1 ngal3-ko1 with respect to the number of outer integument cells. We also observed that cells in the outer integuments of klu-4 and klu-4 sod7-ko1 ngal3-ko1 seeds were slightly longer than those in wild-type seeds, suggesting a possible compensation mechanism between cell proliferation and cell expansion. Together, these findings show that SOD7 functions antagonistically in a common pathway with KLU to control cell proliferation in the maternal integuments.

[0199] Considering that sod7-1D was identified as a suppressor of da1-1 in seed size, we further asked whether SOD7 and DA1 could act in the same genetic pathway. To test this, we measured the size of wild-type, da1-1, sod7-1D and sod7-1D da1-1 seeds. The genetic interaction between sod7-1D and da1-1 was essentially additive for seed size, compared with that of sod7-1D and da1-1 single mutants, indicating that SOD7 might function independently of DA1 to control seed size. We further crossed sod7-ko1 ngal3-ko1 with da1-1 and generated the sod7-ko1 ngal3-ko1 da1-1 triple mutant and measured its seed size. The genetic interaction between sod7-ko1 ngal3-ko1 and da1-1 was also additive for seed size, compared with their parental lines, further supporting that SOD7 functions to control seed growth separately from DA1.

[0200] SOD7 Directly Binds to the Promoter of KLU and Represses the Expression of KLU

[0201] Considering that SOD7 acts antagonistically in a common pathway with KLU to control seed size, we asked whether the transcription repressor SOD7 could repress the expression of KLU. We therefore investigated the expression of KLU in the chemically-inducible SOD7 (pER8-SOD7) transgenic plants. After the pER8-SOD7 transgenic plants were treated with the inducer (β-estradiol), the expression of SOD7 was strongly induced at 4 and 8 hours (FIG. **8**A). As expected, the expression of KLU was dramatically repressed at 4 and 8 hours (FIG. **8**A). Thus, these results indicate that SOD7 represses the expression of KLU and also suggest that KLU might be a direct target of SOD7.

[0202] To determine whether SOD7 can directly bind to the promoter of the KLU gene, we performed a chromatin immunoprecipitation (ChIP) assay with 35S:GFP and 35:GFP-SOD7 transgenic plants. It has been reported that the CACCTG sequence is recognized by the B3 domain of RAV1, one member of the RAV family (Kagaya et al., 1999; Yamasaki et al., 2004). We therefore analyzed the promoter sequence of KLU and did not find an intact CACCTG sequence within 2 kb promoter region of KLU. However, we found a similar sequence (CACTTG) in the promoter region of KLU (FIG. **8**B), which could be the potential SOD7-binding site. To test this, we examined the enrichment of a KLU promoter fragment (PF1) containing the CACTTG sequence by ChIP analyses and found that the fragment PF1 was strongly enriched in the chromatin-immunoprecipitated DNA with anti-GFP antibody (FIGS. **8**B and C). By contrast, we did not detect significant enrichment of an ACTIN7 promoter sequence and the KLU promoter fragment PF2, which do not contain the CACTTG sequence (FIGS. **8**B and C). This result shows that SOD7 associates with the promoter of KLU in vivo. We further expressed SOD7 as a MBP fusion protein (MBP-SOD7) and performed the DNA electrophoretic mobility shift assays (EMSA). As shown in FIGS. **8**B and D, MBP-SOD7 was able to bind to the biotin-labeled probe A containing the CACTTG sequence, and the binding was reduced by the addition of an unlabeled probe A. By contrast, MBP-SOD7 failed to bind to a probe A-m with mutations in the CACTTG sequence (FIGS. **8**B and D). Taken together, these results show that SOD7 directly binds to the promoter of KLU and represses KLU expression.

[0203] Discussion

[0204] Seed size is crucial for plant fitness and agricultural purposes, but little is known about the genetic and molecular mechanisms that set the final size of seeds in plants. In this study, we show that SOD7 acts maternally to control seed size by restricting cell proliferation in the integuments of ovules and developing seeds. SOD7 encodes a B3 domain transcriptional repressor NGAL2 and acts redundantly with its closest homolog NGAL3 to control seed size. Genetic analyses indicate that SOD7 functions in a common pathway with the maternal factor KLU to control seed growth, but does so independently of DA1. Further results reveal that SOD7 directly binds to the promoter region of KLU and represses KLU expression. Thus, our findings identify SOD7 as a negative factor for seed size and define the genetic and molecular mechanisms of SOD7 and KLU in seed size control.

[0205] SOD7 Acts Maternally to Regulate Seed Size

[0206] The sod7-1D gain-of-function mutant was identified as a suppressor of the large seed phenotype of da1-1. However, genetic analyses showed that SOD7 functions independently of DA1 to control seed growth. The sod7-1D single mutant produced small seeds and organs (FIG. **2**), while the simultaneous disruption of SOD7 and the closely related family member NGAL3 resulted in large seeds and organs (FIG. **5**), indicating that SOD7 is a negative regulator of seed and organ size. Several previous studies suggest that there is a possible link between seed size and organ growth. For instance, arf2, da1-1, da2-1 and eod3-1D mutants produced large seeds and organs (Schruff et al., 2006; Li et al., 2008; Fang et al., 2012; Xia et al., 2013), whereas klu and sod2/ubp15 mutants formed small seeds and organs (Anastasiou et al., 2007; Adamski et al., 2009; Du et al., 2014). However, seed size is not invariably associated with organ size. For example, eod8/med25 mutants with large organs formed normal-sized seeds (Xu and Li, 2011), while ap2 mutants with normal-sized organs produced large seeds (Jofuku et al., 2005; Ohto et al., 2005). Thus, these findings suggest that seeds and organs not only share common mechanisms but also possess distinct pathways to control their respective size.

[0207] Reciprocal cross experiments showed that SOD7 acts maternally to restrict seed growth, and the endosperm and embryo genotypes for SOD7 do not determine seed size (FIG. **6**). The integuments surrounding the ovule are maternal tissues and form the seed coat after fertilization. *Arabidopsis* arf2, ap2, da1-1, da2-1 and eod3-1D mutants with large integuments formed large seeds (Jofuku et al., 2005; Ohto et al., 2005; Schruff et al., 2006; Li et al., 2008; Fang et al., 2012; Xia et al., 2013), while klu-4 and ubp15/sod2 mutants with small integuments produced small seeds (Adamski et al., 2009; Du et al., 2014), indicating that the maternal integuments are crucial for determining seed size in *Arabidopsis*. Consistent with this notion, mature eod7-ko1 ngal3-ko1 ovules were larger than wild-type ovules

(FIGS. **6**C and D). The outer integument length of eod7-ko1 ngal3-ko1 ovules and developing seeds was significantly increased, compared with that of wild-type ovules and seeds (FIGS. **6**E and **7**C). Considering that the maternal integument or seed coat not only acts as a protective structure but also restricts seed growth, the regulation of maternal integument size is one of important mechanisms for seed size control. The size of the integument is determined by cell proliferation and cell expansion; these two processes are assumed to be coordinated. The number of outer integument cells in sod7-ko1 ngal3-ko1 ovules and seeds was significantly increased, compared with that in wild-type ovules and seeds (FIG. **6**F), indicating that SOD7 controls seed growth by limiting cell proliferation in the maternal integuments. Similarly, several mutants with the increased number of cells in the maternal integuments produced large seeds in *Arabidopsis* (Schruff et al., 2006; Li et al., 2008; Xia et al., 2013). By contrast, several other mutants with the decreased number of cells in the maternal integuments formed

[0208] small seeds in *Arabidopsis* (Adamski et al., 2009; Du et al., 2014). Considering that cells in the integuments mainly undergo expansion after fertilization (Garcia et al., 2005), it is possible that the number of cells in the integuments determines the growth potential of the seed coat after fertilization.

[0209] The Genetic and Molecular Mechanisms of SOD7 and KLU in Seed Size Control

[0210] The sod7-1D mutant had small seeds and organs (FIG. **2**), as had been seen in klu mutants (Anastasiou et al., 2007; Adamski et al., 2009). KLU encodes a cytochrome P450 CYP78A5 that has been proposed to generate mobile plant-growth substances (Anastasiou et al., 2007; Adamski et al., 2009). KLU regulates seed size by promoting cell proliferation in the maternal integuments of ovules (Anastasiou et al., 2007; Adamski et al., 2009). By contrast, SOD7 acts maternally to control seed size by limiting cell proliferation in the integuments of ovules and developing seeds (FIG. **6**). These results suggest that SOD7 could function antagonistically in a common pathway with KLU to control seed size. In our growth conditions, klu-4 formed slightly smaller seeds than the wild type due to the decreased cell number and the slightly increased cell length in the integuments of developing seeds (FIGS. **7**A and D), suggesting a possible compensation mechanism between cell proliferation and cell expansion in klu-4 integuments. Importantly, our genetic analyses showed that klu-4 is epistatic to sod7-ko1 ngal3-ko1 with respect to seed and organ size (FIGS. **7**A and B). klu-4 is also epistatic to sod7-ko1 ngal3-ko1 for the outer integument length (FIG. **7**C). Further results revealed that the number of cells in the outer integuments of klu-4 sod7-ko1 ngal3-ko1 ovules and developing seeds was similar to that of *k/u*-4 ovules and developing seeds (FIG. **7**D). Thus, these genetic results demonstrate that SOD7 act in a common pathway with KLU to control seed size by regulating cell proliferation in the maternal integuments.

[0211] SOD7 encodes a B3 domain transcriptional repressor NGAL2 that is localized in nuclei of *Arabidopsis* cells (FIGS. **4**M-R). Thus, it is possible that SOD7 could directly bind to the promoter of KLU and repress KLU expression. Supporting this idea, the inducible expression of SOD7 resulted in a strong reduction of KLU expression (FIG. **8**A). Our ChIP-qPCR data showed that SOD7 associates with the promoter region of KLU in vivo (FIGS. **8**B and C). EMSA experiments revealed that SOD7 directly binds to the CACTTG sequence in the promoter of the KLU gene (FIGS. **8**B and D). Thus, these results illustrate that SOD7 directly targets the promoter region of KLU and represses the expression of KLU, thereby determining seed size. Taken together, these findings reveal the genetic and molecular mechanisms of SOD7 and KLU in regulating *Arabidopsis* seed size.

[0212] For many plants, the seeds are the main product to be harvested, and an increase in seed size would be beneficial for growers. In this study, we identify SOD7 as a negative regulator of seed size, and demonstrate that SOD7 acts in a common genetic pathway with KLU to control seed size. Our current knowledge of SOD7 functions suggests that the SOD7 gene (and its homologs in other plant species) could be used to engineer large seed size in crops. Considering that crop plants have undergone selection for large seed size during domestication (Fan et al., 2006; Song et al., 2007; Gegas et al., 2010), it will be a worthwhile challenge to know whether beneficial alleles of the SOD7 gene have already been utilized by plant breeders.

[0213] Knockout Experiments in Rice Using Genome Editing

[0214] Genome editing experiments to knock out os11g01560000 and/or Os12g0157000 in rice are being carried out using the crisper-cas9 system. Four vectors, each with two recognition (CRISPR target) sites, have been constructed, to achieve these knock outs, as described in FIG. **14**. In summary, the vectors were obtained as follows:

[0215] 1. The target sites were identified. The target site should be (or approximately so) 20 nucleotides before a NGG sequence, N being for any nucleotide. The target sequence was then evaluated using the website: http://cbi.hzau.edu.cn/crispr/help.php (incorporated herein by reference). Of note, the target site should be unique in the genome.

[0216] 2. Using overlap PCR, the target sequence is linked with the U6 sequence, as shown in FIG. **14**. U6 is for transcriptional activity.

[0217] 3. Using infusion technology we connected the U6-guide-gRNA scaffold fragment to the vector pMDC99-cas9 to obtain the pMDC99-cas9-U6-guide-gRNA scaffold constructs. These constructs were named zyy1,zyy2, zyy3, zyy4. The full sequences of these constructs are represented in SEQ ID NO: 155, 156, 157 and 158 respectively. Each construct contains two recognition sites, which are highlighted in the sequence information, and are represented separately as SEQ ID Nos 159, 160, 161, 162 and 163.

[0218] 4. We then transformed these constructs into Agrobacteria and used an Agrobacteria mediated method to transform rice and obtain gene-edited rice. Transformation of plants is a routine technique that is well known to the skilled person. Nonetheless, a brief outline of transformation techniques is provided above.

[0219] Knock out lines are being analysed to assess the phenotype.

TABLE 1

Primers used in this study	
Promer Name	Promer Sequences
Primers tor T-DNA tdentttcatton	
SM_3_34191-LP	ACCATGACATTCGAGGTTCAC (SEQ ID NO. 8)
SM_3_34191-RP	ATCACCACCAAAACGACGTAG (SEQ ID NO. 9)
SM_3_36641-RP	TACGTCATGCTTCAAATCGTG (SEQ ID NO. 10)
SM_3_36641-RP	AGGACACGAACAATTCATTCG (SEQ ID NO. 11)
Spm32	TACGAATAAGAGCGTCCATTTTAGAGTGA (SEQ ID NO. 12)
SM_3_39145-LP	ACCCAAAGAACAGCAATCATG (SEQ ID NO. 13)
SM_3_39145-RP	AAAACACTCCGCCATTAAACC (SEQ ID NO. 14)
Primers tor TAIL-PCR	
OJF22	CGAGTATCAATGGAAACTTAACCG (SEQ ID NO.15)
OJF23	AACGGAGAGTGGCTTGAGAT (SEQ ID NO. 16)
OJF24	TGGCCCTTATGGTTTCTGCA (SEQ ID NO. 17)
AD1	NTCGA(G/C)T(NT)T(G/C)G(A/T)GTT (SEQ ID NO. 18)
Primers tor Constructs	
SOD7CDS-F	ATGTCAGTCAACCATTACCAC (SEQ ID NO. 19)
SOD7CDS-R	CAGGTAGGAGATGGACGAGGTTGA (SEQ ID NO. 20)
SOD7G-F	TGAGAGGAACCATTTCTTAGAGG (SEQ ID NO. 21)
SOD7G-R	ACCTCGTCCATCTCCTACCTGC (SEQ ID NO. 22)
SOD7P-F	AAACACGTCAAATATAACGAAT (SEQ ID NO. 23)
SOD7P-R	CTTTTTTTTGGTTTCTTGGAGTGAGAGAGAGAG (SEQ ID NO. 24)
SOD7-ER-F	AGTCTGGGCCCATGTCAGTCAACCATTAC (SEQ ID NO. 25)
SOD7-ER-R	GCGACTAGTTTATAAAAGAGTTAAAATTA (SEQ ID NO. 25)
MBP-SOD7-FP	CGGGATCCTCAGTCAACCATTACC (SEQ ID NO. 27)
MBP-SOD7-RP	ACTAGTCGACTCAACCTCGTCCATCTCC (SEQ ID NO. 28)
Primers tor RT-PCR and qRT-PCR	
ACTIN2-F	GAAATCACAGCACTTGCACC (SEQ ID NO. 29)
ACTIN2-R	AAGCCTTTGATCTTGAGAGC (SEQ ID NO. 30)
SOD7-EX-F	GCGACGACGGAGAAAGGG (SEQ ID NO. 31)
SOD7-EX-R	ACGACGGCGCCATAGTGT (SEQ ID NO. 32)
NGAL3-EX-F	TTTGAAGACGAGTCAGGCAAGT (SEQ ID NO. 33)
NGAL3-EX-R	TACGGCGGCTCCATAGTGGG (SEQ ID NO. 34)
SOD7-q-FP	GTATTGGAGCGGCTTGACTACACC (SEQ ID NO. 35)
SOD7-q-RP	GACGGCATCACCATGACATTCG (SEQ ID NO. 36)
KLU-q-FP	TGATTCTGACATGATTGCTGTTCT (SEQ ID NO. 37)
KLU-q-RP	TCGCAACTGTATCTGTCCCTCTA (SEQ ID NO. 38)
Primers tor ChIP assay	
ACTIN7-ChIP-FP	CGTTTCGCTTTCCTTAGTGTTAGCT (SEQ ID NO. 29)
ACTIN7-ChIP-RP	AGCGAACGGATCTAGAGACTCACCTTG (SEQ ID NO. 40)
PF1-F	CAGGCCTAAGCCTAACAGTAGAC (SEQ ID NO. 41)
PF1-R	TGTACTAGGATTTATTTACGTAG (SEQ ID NO. 42)
PF2-F	TATTGTTCATAGAAACCCTGCAAA (SEQ ID NO. 43)
PF2-R	AGTCAATGGTTTAATGGCGGAGTG (SEQ ID NO. 44)
Probes tor EMSA	
A-Btottn-FP	TTCTACTACACTTGCTCTCTGTA (SEQ ID NO. 45)
A-Btottn-RP	TACAGAGAGCAAGTGTAGTAGAA (SEQ ID NO. 46)
A-Btottn-m-FP	TTCTACTAACACCTCTCTCTGTA (SEQ ID NO. 47)
A-Btottn-m-RP	TACAGAGAGAGGTGTTAGTAGAA (SEQ ID NO. 48)

REFERENCES

[0220] Adamski, N. M., Anastasiou, E., Eriksson, S., O'Neill, C. M., and Lenhard, M. (2009). mLocal maternal control of seed size by KLUH/CYP78A5-dependent growth signaling. Proceedings of the National Academy of Sciences of the United States of America 106, 20115-20120.

[0221] Alvarez, J. P., Goldshmidt, A., Efroni, I., Bowman, J. L., and Eshed, Y. (2009). Th NGATHA distal organ development genes are essential for style specification in *Arabidopsis*. Plant Cell 21, 1373-1393.

[0222] Anastasiou, E., Kenz, S., Gerstung, M., MacLean, D., Timmer, J., Fleck, C., and Lenhard, M. (2007). Control of plant organ size by KLUH/CYP78A5-dependent intercellular signaling. Developmental cell 13, 843-856.

[0223] Cheng, Z. J., Zhao, X. Y., Shao, X. X., Wang, F., Zhou, C., Liu, Y. G., Zhang, Y., and Zhang, X. S. (2014). Abscisic Acid Regulates Early Seed Development in

Arabidopsis by AB15-Mediated Transcription of SHORT HYPOCOTYL UNDER BLUE1. Plant Cell 26, 1053-1068.

[0224] Du, L., Li, N., Chen, L., Xu, Y., Li, Y., Zhang, Y., and Li, C. (2014). The Ubiquitin Receptor DA1 Regulates Seed and Organ Size by Modulating the Stability of the Ubiquitin-Specific Protease UBP15/SOD2 in *Arabidopsis*. Plant Cell 26, 665-677.

[0225] Engelhorn, J., Reimer, J. J., Leuz, I., Gobel, U., Huettel, B., Farrona, S., and Turck, F. (2012). Development-related PcG target in the apex 4 controls leaf margin architecture in *Arabidopsis thaliana*. Development 139, 2566-2575.

[0226] Fan, C., Xing, Y., Mao, H., Lu, T., Han, B., Xu, C., Li, X., and Zhang, Q. (2006). GS3, a major QTL for grain length and weight and minor QTL for grain width and thickness in rice, encodes a putative transmembrane protein. Theor Appl Genet 112, 1164-1171.

[0227] Fan, J., Hill, L., Crooks, C., Doerner, P., and Lamb, C. (2009). Abscisic acid has a key role in modulating diverse plant-pathogen interactions. Plant physiology 150, 1750-1761.

[0228] Fang, W., Wang, Z., Cui, R., Li, J., and Li, Y. (2012). Maternal control of seed size by EOD3/CYP78A6 in *Arabidopsis thaliana*. Plant J 70, 929-939.

[0229] Garcia, D., Fitz Gerald, J. N., and Berger, F. (2005). Maternal control of integument cell elongation and zygotic control of endosperm growth are coordinated to determine seed size in *Arabidopsis*. Plant Cell 17, 52-60.

[0230] Garcia, D., Saingery, V., Chambrier, P., Mayer, U., Jurgens, G., and Berger, F. (2003). *Arabidopsis* haiku mutants reveal new controls of seed size by endosperm. Plant physiology 131, 1661-1670.

[0231] Gegas, V. C., Nazari, A., Griffiths, S., Simmonds, J., Fish, L., Orford, S., Sayers, L., Doonan, J. H., and Snape, J. W. (2010). A genetic framework for grain size and shape variation in wheat. Plant Cell 22, 1046-1056.

[0232] Gendrel, A. V., Lippman, Z., Martienssen, R., and Colot, V. (2005). Profiling histone modification patterns in plants using genomic tiling microarrays. Nat Methods 2, 213-218.

[0233] Harper, J. L., Lovell, P. H., and Moore, K. G. (1970). The Shapes and Sizes of Seeds. Annual Review of Ecology and Systematics 1, 327-356

[0234] Ikeda, M., and Ohme-Takagi, M. (2009). A novel group of transcriptional repressors in *Arabidopsis*. Plant & cell physiology 50, 970-975.

[0235] Jofuku, K. D., Omidyar, P. K., Gee, Z., and Okamuro, J. K. (2005). Control of seed mass and seed yield by the floral homeotic gene APETALA2. Proceedings of the National Academy of Sciences of the United States of America 102, 3117-3122.

[0236] Kagaya, Y., Ohmiya, K., and Hattori, T. (1999). RAV1, a novel DNA-binding protein, binds to bipartite recognition sequence through two distinct DNA-binding domains uniquely found in higher plants. Nucleic Acids Res 27, 470-478.

[0237] Kang, X., Li, W., Zhou, Y., and Ni, M. (2013). A WRKY transcription factor recruits the SYG1-like protein SHB1 to activate gene expression and seed cavity enlargement. PLoS Genet 9, e1003347.

[0238] Li, J., Nie, X., Tan, J. L., and Berger, F. (2013). Integration of epigenetic and genetic controls of seed size by cytokinin in *Arabidopsis*. Proceedings of the National Academy of Sciences of the United States of America 110, 15479-15484.

[0239] Li, Y., Zheng, L., Corke, F., Smith, C., and Bevan, M. W. (2008). Control of final seed and organ size by the DA1 gene family in *Arabidopsis thaliana*. Genes Dev 22, 1331-1336.

[0240] Liu, Y. G., Mitsukawa, N., Oosumi, T., and Whittier, R. F. (1995). Efficient isolation and mapping of *Arabidopsis thaliana* T-DNA insert junctions by thermal asymmetric interlaced PCR. Plant J 8, 457-463.

[0241] Lopes, M. A., and Larkins, B. A. (1993). Endosperm origin, development, and function. Plant Cell 5, 1383-1399.

[0242] Luo, M., Dennis, E. S., Berger, F., Peacock, W. J., and Chaudhury, A. (2005). MINISEED3 (MINI3), a WRKY family gene, and HAIKU2 (IKU2), a leucine-rich repeat (LRR) KINASE gene, are regulators of seed size in *Arabidopsis*. Proceedings of the National Academy of Sciences of the United States of America 102, 17531-17536.

[0243] Moles, A. T., Ackerly, D. D., Webb, C. O., Tweddle, J. C., Dickie, J. B., and Westoby, M. (2005). A brief history of seed size. Science 307, 576-580.

[0244] Ohto, M. A., Fischer, R. L., Goldberg, R. B., Nakamura, K., and Harada, J. J. (2005). Control of seed mass by APETALA2. Proceedings of the National Academy of Sciences of the United States of America 102, 3123-3128.

[0245] Ohto, M. A., Floyd, S. K., Fischer, R. L., Goldberg, R. B., and Harada, J. J. (2009). Effects of APETALA2 on embryo, endosperm, and seed coat development determine seed size in *Arabidopsis*. Sex Plant Reprod 22, 277-289.

[0246] Orsi, C. H., and Tanksley, S. D. (2009). Natural variation in an ABC transporter gene associated with seed size evolution in tomato species. PLoS Genet 5, e1000347.

[0247] Schruff, M. C., Spielman, M., Tiwari, S., Adams, S., Fenby, N., and Scott, R. J. (2006). The AUXIN RESPONSE FACTOR 2 gene of *Arabidopsis* links auxin signalling, cell division, and the size of seeds and other organs. Development 133, 251-261. Scott, R. J., Spielman, M., Bailey, J., and Dickinson, H. G. (1998). Parent-of-origin effects on seed development in *Arabidopsis thaliana*. Development 125, 3329-3341.

[0248] Smaczniak, C., Immink, R. G., Muino, J. M., Blanvillain, R., Busscher, M., Busscher-Lange, J., Dinh, Q. D., Liu, S., Westphal, A. H., Boeren, S., Percy, F., Xu, L., Caries, C. C., Angenent, G. C., and Kaufmann, K. (2012). Characterization of MADS-domain transcription factor complexes in *Arabidopsis* flower development. Proceedings of the National Academy of Sciences of the United States of America 109, 1560-1565.

[0249] Song, X. J., Huang, W., Shi, M., Zhu, M. Z., and Lin, H. X. (2007). A QTL for rice grain width and weight encodes a previously unknown RING-type E3 ubiquitin ligase. Nat Genet 39, 623-630.

[0250] Swaminathan, K., Peterson, K., and Jack, T. (2008). The plant B3 superfamily. Trends Plant Sci 13, 647-655.

[0251] Trigueros, M., Navarrete-Gomez, M., Sato, S., Christensen, S. K., Pelaz, S., Weigel, D., Yanofsky, M. F., and Ferrandiz, C. (2009). The NGATHA genes direct style development in the *Arabidopsis gynoecium*. Plant Cell 21, 1394-1409.

[0252] Wang, A., Garcia, D., Zhang, H., Feng, K., Chaudhury, A., Berger, F., Peacock, W. J., Dennis, E. S., and Luo, M. (2010). The VQ motif protein IKU1 regulates endosperm growth and seed size in *Arabidopsis*. Plant J 64, 670-679.

[0253] Westoby, M., Falster, D. S., Moles, A. T., Vesk, P. A., and Wright, I. J. (2002). PLANT ECOLOGICAL STRATEGIES: Some Leading Dimensions of Variation Between Species. Annual Review of Ecology and Systematics 33, 125-159.

[0254] Xia, T., Li, N., Dumenil, J., Li, J., Kamenski, A., Bevan, M. W., Gao, F., and Li, Y. (2013). The Ubiquitin Receptor DA1 Interacts with the E3 Ubiquitin Ligase DA2 to Regulate Seed and Organ Size in *Arabidopsis*. Plant Cell 25, 3347-3359.

[0255] Xiao, W., Brown, R. C., Lemmon, B. E., Harada, J. J., Goldberg, R. B., and Fischer, R. L. (2006). Regulation of seed size by hypomethylation of maternal and paternal genomes. Plant physiology 142, 1160-1168.

[0256] Xu, R., and Li, Y. (2011). Control of final organ size by Mediator complex subunit 25 in *Arabidopsis thaliana*. Development 138, 4545-4554.

[0257] Yamasaki, K., Kigawa, T., Inoue, M., Tateno, M., Yamasaki, T., Yabuki, T., Aoki, M., Seki, E., Matsuda, T., Tomo, Y., Hayami, N., Terada, T., Shirouzu, M., Osanai, T., Tanaka, A., Seki, M., Shinozaki, K., and Yokoyama, S. (2004). Solution structure of the B3 DNA binding domain of the *Arabidopsis* cold-responsive transcription factor RAV1. Plant Cell 16, 3448-3459.

[0258] Zhou, Y., Zhang, X., Kang, X., Zhao, X., and Ni, M. (2009). SHORT HYPOCOTYL UNDER BLUE1 associates with MINISEED3 and HAIKU2 promoters in vivo to regulate *Arabidopsis* seed development. Plant Cell 21, 106-117.

SEQUENCE INFORMATION

[0259]

Identtty of homologs to NGAL2 is tndtcated

```
AtSOD7 nucleic acid SEQ ID NO. 1 (cDNA) At3g11580
ATGTCAGTCAACCATTACCACAACACTCTCTCGTTGCATCATCACCACCAAAACGACGTAGCTATAGCACAACGAGAGTCTTTGTTC
GAGAAATCACTCACACCAAGCGACGTCGGAAAGCTAAACCGCTTAGTCATACCAAAACAACACGCCGAGAAATACTTCCCTCTCAAT
AATAATAATAATAATGGCGGCAGCGGAGATGACGTGGCGACGACGGAGAAAGGGATGCTTCTTAGCTTCGAGGATGAGTCAGGCAAG
TGTTGGAAATTCAGATACTCTTATTGGAACAGTAGCCAAAGCTACGTGTTGACCAAAGGATGGAGCAGGTACGTCAAAGACAAACAC
CTCGACGCAGGCGACGTTGTTTTCTTTCAACGTCACCGTTTTGATCTCCATAGACTCTTCATTGGCTGGCGGAGACGCGGTGAAGCT
TCTTCCTCTCCCGCTGTCTCCGTTGTGTCTCAAGAAGCTCTAGTTAATACGACGGCGTATTGGAGCGGCTTGACTACACCTTATCGT
CAAGTACACGCGTCAACTACTTACCCTAATATTCACCAAGAGTATTCACACTATGGCGCCGTCGTTGATCATGCTCAGTCGATACCA
CCGGTGGTCGCAGGTAGCTCGAGGACGGTGAGGCTTTTTGGCGTGAACCTCGAATGTCATGGTGATGCCGTCGAGCCACCACCGCGT
CCTGATGTCTATAATGACCAACACATTTACTATTACTCAACTCCTCATCCCATGAATATATCATTTGCTGGGAAGCATTGGAGCAG
GTAGGAGATGGACGAGGTTGA

AtSOD7 nucleic acid SEQ ID NO. 2 (genomic DNA).
ttgtttcggctatttgttatactattgttataacagtcacaagacttgacctcaacgaaaacttttacaaaacgtgaattggaaatt
tttacaaaatatgctcttaatcgttaatgcttcccaattaggtgagttaaattgtgagaggaaccatttcttagaggaaatggttca
tgaaaacaaatatgaaatagtatcactagtcttagttttgcgagaaaattaggaaaaatagaaacgtgtaagcaccaatgatattcc
tgaaagcacgtgacagatatttcatgatcctataattaacaagtgataaagatattaaataaaattaacgatacttgagaaattcgt
caaataaaatagaagaggaccactcacgtaaccatttgcacgtcccattgatttttgtggtagacttggtatgttatattacttata
ttcacagaattatatacgaaactcacgacttaagatgcacggtaataactacagatggaaatttacccatcaaacaagaaaacaaca
tttactcaagcatctagctagaccaaaatgtttgtttacttgttgacttgcgatccatagatatattagttagaactttttcttcta
caattgatcaaatgtttcacactgttctcaatttctcatctagattcatgacttatatgtttggtcaaatatcacagcttgatgagc
attaaatagcgtcgaagtataggatggttacgttgttcaatattgtaaaggaaaaaaagagaaagagtgccaaaaggtcaagtcgat
ttcacaaataaatcttgaagtctttatccctctcgattataaaatgattaggaaaagaaaaagagagaataaaatgtagataaagag
aaagagaaagagagagaggaacataagggatggtatgaagtagaagtgaagatgcatgcgatggtgtgtcggaaaggcaaagcacat
gctacacaacttgagcttctcacttgcgtcagggataagtatcctctgtaccttcttacttttgcgtaatatgtaccacctcacttc
tcaaccgtttgatctttaatccttcattatttcttcattaccttctctttttgtttttgttttcgttttcaatttctcatagattca
tttacaaactaaatatcataggaaggtgttatctctagttaatttcttatcctactttaacaaaatttaattgtcaaaagattattt
ttacgtttatagacaaaagatactgacacatcaattccacgaaccaaatggttgagaaaaacaaaacgactatctttgtcttgcaaa
taaattaatggcagttagtaagattctcagctgaaaattcatacaagagtaaatgatcaaataaccatttatgagagaaatttaatc
cttcagaaaccaatgaggatctgatcaagtaattgcaaaccacatgagtccatgataaaggattgtttgacttacgcaatccacata
tttatggctgcttgatatgtaaggtttatctgctttgacagtctatagaatcttgctaatcaatacgtcatatccggtgaatactga
aactttttaattaagaaaacacaaatcatcttttctccggaggatttcgaatttagttccggcaatgctgaaataacatatgttga
acttataacattccaagacatcaaattttactaatatataaataattacatattcttcttctacatgatcaaaacctttcaacttt
aattaaagggttacgtcgcggcgttttgtgtggcttactctttttttacactataactatagaacactcgtggatccaatgccgttt
aggacaagatttatcagacgagaaaaaaaaaacaataccacattttaaatatatatggattatggactgcaacaacaatataga
aaagaagagaaaaaaataaaaataatgattgaaaggaaatatcatcacgcaaaaccttaaaagtactatcggtatcgtgtcgtcctc
tcctcatcaaatagttcccacagttttcacatcaatttaaccattttcaatttttttcactctctgtctctctcctttgtataatac
tatattagtaccattacccatctctctttcaccaccaaaccaacacctgcaaatcctctctctctctctcactccaagaaaccaaaa
aaaaagATGTCAGTCAACCATTACCACAACACTCTCTCGTTGCATCATCACCACCAAAACGACGTAGCTATAGCACAACGAGAGTCT
TTGTTCGAGAAATCACTCACACCAAGCGACGTCGGAAAGCTAAACCGCTTAGTCATACCAAAACAACACGCCGAGAAATACTTCCCT
CTCAATAATAATAATAATAATGGCGGCAGCGGAGATGACGTGGCGACGACGGAGAAAGGGATGCTTCTTAGCTTCGAGGATGAGTCA
GGCAAGTGTTGGAAATTCAGATACTCTTATTGGAACAGTAGCCAAAGCTACGTGTTGACCAAAGGATGGAGCAGGTACGTCAAAGAC
AAACACCTCGACGCAGGCGACGTTGTTTTCTTTCAACGTCACCGTTTTGATCTCCATAGACTCTTCATTGGCTGGCGGAGACGCGGT
GAAGCTTCTTCCTCTCCCGCTGTCTCCGTTGTGTCTCAAGAAGCTCTAGTTAATACGACGGCGTATTGGAGCGGCTTGACTACACCT
TATCGTCAAGTACACGCGTCAACTACTTACCCTAATATTCACCAAGAGTATTCACACTATGgtaaattcaaaccctttatttcctct
tttgtttttctttctctcttatctatatgtcagatttatactcctctctgttctcttttaagatttgtctttttcataaaaataga
tgattcgtaatttgtattgcatatttacatgttctcttaaaaaaagtaatagagattaatattttatgcatggtattttagattatc
tgcctactttatatggtagtaaacaagaacattcatcthatttg0ttataaacaaaatatgagaatttttaaaggttagggcaagca
cttggaaagctcaaccattttagttagctggtggaatatctttcttataaaaagcaaatgagttatctaaaactatatgacaattat
tttagttgcgtgtgtaatgtatataaaataacaacatgaaataacattttgtcttttatttttgtcattcttattatttaattttgg
```

-continued

Identtty of homologs to NGAL2 is tndtcated

acccgacaatttcaaataatcttctccaagttgtaactaatccgttacatgcgcgtgaggagaaccgtccaatccacttagactaac
gtgccctttatttcttccttttaattctatgttaaaaaaacaatttaactaaaagatgcgcacgtgtcttgacggtggaaaaaaatt
gtagGCGCCGTCGTTGATCATGCTCAGTCGATACCACCGGTGGTCGCAGGTAGCTCGAGGACGGTGAGGCTTTTTGGCGTGAACCTC
GAATGTCATGGTGATGCCGTCGAGCCACCACCGCGTCCTGATGTCTATAATGACCAACACATTTACTATTACTCAACTCCTCATCCC
ATGgtaaatattttttttttttacatttttgtcagattcaaatttttgcttacgtatgatataattattaaacagatgtcgtggctg
tttctcgagacgagacagatgaaaattagtaattttaaaatagacctgaaagagatttttatgtttaataaattatataaaggagga
atcagagagaataatactatacacttgactgtaaaaccacatggccaatttggtttttatttgattactttgatttgttttgtttac
tcttttgtctctgtagcctccttttgttcattaattaatatcagccgtaagtatatagtttcctgtgaaaacagtctctattttggt
tttactattctaatttgttaggcaccgtcagtttttttttgtgaaaccaaattattgactaataagctggaaagcaaaactgactaaa
agcattacaaacttatcaatgacataagttttgaatttattaccatgttttgtaatgttcagatataatttgaaatgcttagaatta
tatatttgtatacttaaattaatgaaataaagtgaatactaaagatagttttatttttcatattattctatacaattcggtgtacaa
tttgtttttgatgataataaaaataataaaattgcgtgttggaattgtgaaacagAATATATCATTTGCTGGGGAAGCATTGGAGCA
GGTAGGAGATGGACGAGGT

AtNGAL2 SEQ ID NO.3 (protein encoded by AtSOD7)..
MSVNHYHNTLSLHHHHQNDVAIAQRESLFEKSLTPSDVGKLNRLVIPKQHAEKYFPLNNNNNNGGSGDDVATTEKGMLLSFEDESGK
CWKFRYSYWNSSQSYVLTKGWSRYVKDKHLDAGDVVFFQRHRFDLHRLFIGWRRRGEASSSPAVSVVSQEALVNTTAYWSGLTTPYR
QVHASTTYPNIHQEYSHYGAVVDHAQSIPPVVAGSSRTVRLFGVNLECHGDAVEPPPRPDVYNDQHIYYYSTPHPMNISFAGEALEQ
VGDGRG

AtNGAL3 nucleic acid sequence SEQ ID NO. 4 (cDNA) at5g06250
ATGTCAGTCAACCATTACTCCACAGACCACCACCACACTCTCTTGTGGCAGCAACAGCAACACCGCCACACCACCGACACATCGGAG
ACAACCACCACCGCCACATGGCTCCACGACGACCTAAAAGAGTCACTCTTCGAGAAGTCTCTCACACCAAGCGACGTCGGGAAACTC
AACCGCCTCGTCATACCAAAACAACACGCAGAGAAATACTTCCCTCTCAATGCCGTCCTAGTCTCCTCTGCTGCTGCTGACACGTCA
TCTTCGGAGAAAGGGATGCTTCTAAGCTTTGAAGACGAGTCAGGCAAGTCATGGAGGTTCAGATACTCTTACTGGAACAGCAGTCAA
AGCTATGTCTTGACTAAAGGATGGAGCAGATTTGTCAAAGACAAACAGCTCGATCCAGGCGACGTTGTTTTCTTCCAACGACACCGT
TCTGATTCTAGGAGACTCTTCATTGGCTGGCGCAGACGTGGACAAGGCTCCTCATCCTCCGTCGCGGCCACTAACTCCGCCGTGAAT
ACGAGTTCTATGGGAGCTCTTTCTTATCATCAAATCCACGCCACTAGTAATTACTCTAATCCTCCCTCTCACTCAGAGTATTCCCAC
TATGGAGCCGCCGTAGCAACAGCGGCTGAGACTCACAGCACACCGTCGTCTTCCGTCGTCGGGAGCTCAAGGACGGTGAGGCTTTTC
GGTGTGAATCTGGAGTGTCAAATGGATGAAAACGACGGAGATGATTCTGTTGCAGTTGCCACCACCGTTGAATCTCCCGACGGTTAC
TACGGCCAAAACATGTACTATTATTACTCTCATCCTCATAACATGGTAATTTTAACTCTTTTATAA

AtNGAL3 amtno acid SEQ ID NO. 5
MSVNHYSTDHHHTLLWQQQQHRHTTDTSETTTTATWLHDDLKESLFEKSLTPSDVGKLNRLVIPKQHAEKYFPLNAVLVSSAAADTS
SSEKGMLLSFEDESGKSWRFRYSYWNSSQSYVLTKGWSRFVKDKQLDPGDWFFQRHRSDSRRLFIGWRRRGQGSSSSVAATNSAVNT
SSMGALSYHQIHATSNYSNPPSHSEYSHYGAAVATAAETHSTPSSSWGSSRTVRLFGVNLECQMDENDGDDSVAVATTVESPDGYYG
QNMYYYYSHPHNMVILTLL

Oryza sativa
Os12g0157000 LOC_Os12g06080.1
Cover 73% identity 53%

SEQ ID NO: 49
MAMHAGHAWWGVAMYTNHYHHHYRHKTSDVGKNRVKHARYGGGDSGKGSDSGKWRRYSYWTSSSYVTKGWSRYVKKRDAGDVVHRVR
GGAADRGCRRRGSAAAVRVTANGGWSMCYSTSGSSYDTSANSYAYHRSVDDHSDHAGSRADAKSSSAASASRRRGVNDCGADATAMY
GYMHHSYAAVSTVNYWSV

CDS SEQ ID NO: 50
ATGGCCATGCACCCTCTCGCCCAGGGGCACCCCCAGGCGTGGCCATGGGGTGTAGCCATGTACACCAACCTGCACTACCACCACCAC
TACGAGAGGGAGCACCTGTTCGAGAAGCCGCTGACGCCGAGCGACGTCGGCAAGCTCAACAGGCTGGTGATCCCCAAGCAGCACGCC
GAGAGGTACTTCCCGCTCGGCGGCGGCGACTCCGGTGAGAAGGGCCTCCTCCTCTCCTTCGAGGACGAGTCCGGCAAGCCATGGCGG
TTCCGCTACTCCTACTGGACCAGCAGCCAGAGCTACGTGCTCACCAAGGGCTGGAGCCGCTACGTCAAGGAGAAGCGCCTCGACGCC
GGCGACGTCGTCCACTTCGAGCGCGTCCGCGGCCTCGGCGCCGCCGACCGCCTCTTCATCGGCTGCAGGCGCCGCGGCGAGAGCGCG
CCCGCGCCGCCGCCCGCCGTTCGCGTCACGCCGCAGCCGCCTGCCCTCAACGGCGGCGAGCAGCAGCCGTGGAGCCCAATGTGTTAC
AGCACGTCGGGCTCGTCCTACGACCCTACCAGCCCTGCCAATTCATATGCCTACCATCGCTCCGTAGACCAAGATCACAGCGACATA
CTACACGCAGGAGAGTCGCAGAGAGAAGCAGACGCCAAGAGCAGCAGCGCGGCGTCGGCGCCGCCGCCGTCGAGGCGGCTCAGGCTG
TTCGGCGTTAACCTCGACTGCGGCCCGGAGCCGGAGGCGGATCAGGCGACGGCAATGTACGGCTACATGCACCACCAGAGCCCCTAC
GCCGCAGTGTCTACAGTGCCAAATTACTGGTCAGTATTTTTTCAGTTTTAA

Os11g0156000
LOC_Os11g05740.1
Cover 81% identity 47%

SEQ ID NO: 51
MAMNHPLFSQEQPQSWPWGVAMYANFHYHHHYEKEHMFEKPLTPSDVGKLNRLVIPKQHAERYFPLGAGDAADKGLILSFEDEAGAP
WRFRYSYVVTSSQSYVLTKGWSRYVKEKRLDAGDVVHFERVRGSFGVGDRLFIGCRRRGDAAAAQTPAPPPAVRVAPAAQNAGEQQP
WSPMCYSTSGGGSYPTSPANSYAYRRAADHDHGDMHHADESPRDTDSPSFSAGSAPSRRLRLFGVNLDCGPEPEADTTAAATMYGYM
HQQSSYAAMSAVPSYWGNS

CDS SEQ ID NO: 52
ATGGCCATGAACCACCCTCTCTTCTCCCAGGAGCAACCCCAGTCCTGGCCATGGGGTGTGGCCATGTACGCCAACTTCCACTACCAC
CACCACTACGAGAAGGAGCACATGTTTGAGAAGCCCCTGACGCCCAGTGACGTGGGGAAGCTGAACCGGCTGGTGATCCCCAAGCAG
CACGCCGAGAGGTACTTCCCCCTCGGCGCCGGCGACGCCGCCGACAAGGGCCTGATCCTGTCGTTCGAGGACGAGGCCGGCGCGCCG
TGGCGGTTCAGGTACTCCTACTGGACGAGCAGCCAGAGCTACGTGCTCACCAAGGGCTGGAGCCGCTACGTCAAGGAGAAGCGCCTC

-continued

Identtty of homologs to NGAL2 is tndtcated

GACGCCGGCGACGTCGTGCACTTCGAGAGGGTGCGCGGCTCCTTCGGCGTCGGCGACCGTCTCTTCATCGGCTGCAGGCGCCGCGGC
GACGCCGCCGCCGCGCAAACACCCGCACCGCCGCCCGCCGTGCGCGTCGCCCCGGCTGCACAGAACGCCGGCGAGCAGCAGCCGTGG
AGCCCAATGTGTTACAGCACGTCGGGCGGCGGCTCATACCCTACCAGCCCAGCCAACTCCTACGCCTACCGCCGCGCAGCAGATCAT
GATCACGGGGACATGCACCATGCAGACGAGTCTCCGCGCGACACGGACAGCCCAAGCTTCAGTGCAGGCTCGGCGCCATCGAGGCGG
CTCAGGCTGTTCGGCGTCAACCTCGACTGCGGGCCAGAGCCGGAGGCAGACACCACGGCAGCGGCAACAATGTACGGCTACATGCAC
CAGCAGAGCTCCTATGCTGCCATGTCTGCAGTACCCAGTTACTGGGGCAATTCATAA

Os02g0683500 LOC_Os02g45850
Cover 47% identity 62%

SEQ ID NO: 53
MEFTTSSRFSKEEEDEEQDEAGRREIPFMTATAEAAPAPTSSSSSPAHHAASASASASASGSSTPFRSDDGAGASGSGGGGGGGGEA
EVVEKEHMFDKVVTPSDVGKLNRLVIPKQYAEKYFPLDAAANEKGLLLNFEDRAGKPWRFRYSYWNSSQSYVMTKGWSRFVKEKRLD
AGDTVSFSRGIGDEAARHRLFIDWKRRADTRDPLRLPRGLPLPMPLTSHYAPWGIGGGGGFFVQPSPPATLYEHRLRQGLDFRAFNP
AAAMGRQVLLFGSARIPPQAPLLARAPSPLHHHYTLQPSGDGVRAAGSPVVLDSVPVIESPTTAAKRVRLFGVNLDNPHAGGGGGAA
AGESSNHGNALSLQTPAWMRRDPTLRLLELPPHHHHGAESSAASSPSSSSSSKRDAHSALDLDL

CDS SEQ ID NO: 54
ATGGAGTTCACTACAAGCAGTAGGTTTTCTAAAGAAGAGGAGGACGAGGAGCAGGATGAGGCGGGAAGGCGAGAGATCCCCTTCATG
ACGGCCACGGCCGAAGCCGCGCCTGCGCCCACGTCGTCGTCGTCGTCTCCTGCTCATCACGCGGCTTCCGCGTCGGCGTCGGCGTCT
GCGTCAGGGAGCAGCACTCCCTTTCGCTCCGACGATGGCGCCGGGGCGTCTGGGAGCGGCGGCGGCGGCGGCGGCGGCGGAGAAGCG
GAGGTGGTGGAGAAGGAGCACATGTTCGACAAGGTGGTGACGCCGAGCGACGTTGGGAAGCTGAACCGGCTGGTGATCCCGAAGCAG
TACGCCGAGAAGTACTTCCCGCTGGACGCGGCGGCGAACGAGAAGGGCCTCCTGCTCAACTTCGAGGACCGCGCGGGGAAGCCATGG
CGGTTCCGCTACTCCTACTGGAACAGCAGCCAGAGCTACGTGATGACCAAGGGGTGGAGCCGCTTCGTCAAGGAGAAGCGCCTCGAC
GCCGGGGACACCGTCTCCTTCTCCCGCGGCATCGGCGACGAGGCGGCGCGGCACCGCCTCTTCATCGACTGGAAGCGCCGCGCCGAC
ACCCGCGACCCGCTCCGGCTGCCCCGCGGGCTGCCGCTCCCGATGCCGCTCACGTCGCACTACGCCCCGTGGGGGATCGGCGGCGGA
GGGGGATTCTTCGTGCAGCCCTCGCCGCCGGCCACGCTCTACGAGCACCGCCTCAGGCAAGGCCTCGACTTCCGCGCCTTCAACCCC
GCCGCCGCGATGGGGAGGCAGGTCCTCCTGTTCGGCTCGGCGAGGATTCCTCCGCAAGCACCACTGCTGGCGCGCGCGCCGTCGCCG
CTGCACCACCACTACACGCTGCAGCCGAGCGGCGATGGTGTAAGGGCGGCGGGCTCACCGGTGGTGCTCGACTCGGTTCCGGTCATC
GAGAGCCCCACGACGGCCGCGAAGCGCGTGCGGCTGTTCGGCGTGAACCTCGACAACCCGCATGCCGGCGGCGGCGGCGGCGCCGCC
GCCGGCGAGTCGAGCAATCATGGCAATGCACTGTCATTGCAGACGCCCGCGTGGATGAGGAGGGATCCAACACTGCGGCTGCTGGAA
TTGCCTCCTCACCACCACCATGGCGCCGAGTCGTCCGCTGCATCGTCTCCGTCGTCGTCGTCTTCCTCCAAGAGGGACGCGCATTCG
GCCTTGGATCTCGATCTGTAG

os04g0581400 LOC_Os04g49230
Cover 46% identity 64%

CDS SEQ ID NO: 55
ATGGAGTTTGCTACAACGAGTAGTAGGTTTTCCAAGGAAGAGGAGGAGGAGGAGGAAGGGGAACAGGAGATGGAGCAGGAGCAGGAT
GAAGAGGAGGAGGAGGCGGAGGCCTCGCCCCGCGAGATCCCCTTCATGACGTCGGCGGCGGCGGCGGCCACCGCCTCATCGTCCTCC
CCGACATCGGTCTCCCCTTCCGCCACCGCTTCCGCGGCGGCGTCCACGTCGGCGTCGGGCTCTCCCTTCCGGTCGAGCGACGGTGCG
GGAGCGTCGGGGAGTGGCGGCGGCGGTGGCGGCGAGGACGTGGAGGTGATCGAGAAGGAGCACATGTTCGACAAGGTGGTGACGCCG
AGCGACGTGGGGAAGCTGAACCGGCTGGTGATCCCGAAGCAGCACGCCGAGAAGTACTTCCCGCTGGACTCGGCGGCGAACGAGAAG
GGCCTTCTCCTCAGCTTCGAGGACCGAACCGGCAAGCTATGGCGCTTCCGCTACTCCTACTGGAACAGCAGCCAGAGCTACGTCATG
ACCAAGGGTTGGAGCCGCTTCGTCAAGGAGAAGCGCCTCGACGCCGGGGACACCGTCTCCTTCTGCCGCGGCGCCGCCGAGGCCACC
CGCGACCGCCTCTTCATCGACTGGAAGCGCCGCGCCGACGTCCGCGACCCGCACCGCTTCCAGCGCCTACCGCTCCCCATGACCTCG
CCCTACGGCCCGTGGGGCGGCGGCGCGGGCGCTTCTTCATGCCGCCCGCGCCGCCCGCCACGCTCTACGAGCATCACCGCTTTCGCC
AGGGCTTCGACTTCCGCAACATCAACCCCGCTGTGCCGGCGAGGCAGCTCGTCTTCTTCGGCTCCCCAGGGACGGGGATTCATCAGC
ACCCGCCCTTGCCACCGCCGCCGTCGCCACCTCCGCCTCCTCACCAACTCCACATTACGGTGCACCACCCGAGCCCCGTAG

SEQ ID NO: 56
MEFATTSSRFSKEEEEEEEGEQEMEQEQDEEEEEAEASPREIPFMTSAAAAATASSSSPTSVSPSATASAAASTSASGSPFRSSDGA
GASGSGGGGGGEDVEVIEKEHMFDKVVTPSDVGKLNRLVIPKQHAEKYFPLDSAANEKGLLLSFEDRTGKLWRFRYSYWNSSQSYVM
TKGWSRFVKEKRLDAGDTVSFCRGAAEATRDRLFIDWKRRADVRDPHRFQRLPLPMTSPYGPWGGGAGASSCRPRRPPRSTSITAFA
RASTSATSTPLCRRGSSSSSAPQGRGFISTRPCHRRRRHLRLLTNSTLRCTTRAP

Os03g0120900 LOC_Os03g02900
Cover 47% identity 63%

CDS SEQ ID NO: 57
ATGGAGTTCATCACGCCAATCGTGAGGCCGGCATCGGCGGCGGCGGGCGGCGGCGAGGTGCAGGAGAGTGGTGGGAGGAGCTTGGCG
GCGGTGGAGAAGGAGCACATGTTCGACAAGGTGGTGACGCCGAGCGACGTGGGGAAGCTGAACCGGCTGGTGATCCCGAAGCAGCAC
GCGGAGAAGTACTTCCCGCTGGACGCGGCGTCCAACGAGAAGGGGCTCCTGCTCAGCTTCGAGGACCGCACGGGGAAGCCATGGCGG
TTCCGCTACTCCTACTGGAACAGCAGCCAGAGCTACGTGATGACCAAGGGGTGGAGCCGCTTCGTCAAGGAGAAGCGACTCGACGCC
GGGGACACCGTCTCCTTCGGCCGCGGCGTCGGCGAGGCCGCGCGCGGGAGGCTCTTCATCGACTGGCGCCGCCGCCCCGACGTCGTC
GCCGCGCTCCAGCCGCCCACGCACCGCTTCGCCCACCACCTCCCTTCCTCCATCCCCTTCGCTCCCTGGGCGCACCACCACGGACAC
GGAGCCGCCGCCGCCGCCGCCGCCGCCGCCGGCGCCAGGTTTCTCCTGCCTCCCTCCTCGACTCCCATCTACGACCACCACCGCCGA
CACGCCCACGCCGTCGGGTACGACGCGTACGCCGCGGCCACCAGCAGGCAGGTGCTGTTCTACCGGCCGTTGCCGCCGCAGCAGCAG
CATCATCCCGCGGTGGTGCTGGAGTCGGTGCCGGTGCGCATGACGGCGGGGCACGCGGAGCCGCCGTCGGCTCCGTCGAAGCGAGTT
CGGCTGTTCGGGGTGAACCTCGACTGCGCGAATTCCGAACAAGACCACGCCGGCGTGGTCGGGAAGACGGCGCCGCCGCCGCTGCCA
TCGCCGCCGTCATCATCGTCATCTTCCTCCGGGAAAGCGAGGTGCTCCTTGAACCTTGACTTGTGA

-continued

Identtty of homologs to NGAL2 is tndtcated

SEQ ID NO: 58
MEFITPIVRPASAAAGGGEVQESGGRSLAAVEKEHMFDKVVTPSDVGKLNRLVIPKQHAEKYFPLDAASNEKGLLLSFEDRTGKPWR
FRYSYWNSSQSYVMTKGWSRFVKEKRLDAGDTVSFGRGVGEAARGRLFIDWRRRPDVVAALQPPTHRFAHHLPSSIPFAPWAHHHGH
GAAAAAAAAAGARFLLPPSSTPIYDHHRRHAHAVGYDAYAAATSRQVLFYRPLPPQQQHHPAVVLESVPVRMTAGHAEPPSAPSKRV
RLFGVNLDCANSEQDHAGVVGKTAPPPLPSPPSSSSSSSGKARCSLNLDL

Os01g0693400
Cover 47%   identity 63%

CDS SEQ ID NO: 59
ATGGACAGCTCCAGCTGCCTGGTGGATGATACCAACAGCGGCGGCTCGTCCACGGACAAGCTGAGGGCGTTGGCCGCCGCGGCGGCG
GAGACGGCGCCGCTGGAGCGCATGGGGAGCGGGGCGAGCGCGGTGGTGGACGCGGCCGAGCCTGGCGCGGAGGCGGACTCCGGGTCC
GGGGGACGTGTGTGCGGCGGCGGCGGCGGCGGTGCCGGCGGTGCGGGAGGGAAGCTGCCGTCGTCCAAGTTCAAGGGCGTCGTGCCG
CAGCCCAACGGGAGGTGGGGCGCGCAGATCTACGAGCGGCACCAGCGGGTGTGGCTCGGCACGTTCGCCGGGGAGGACGACGCCGCG
CGCGCCTACGACGTCGCCGCGCAGCGCTTCCGCGGCCGCGACGCCGTCACCAACTTCCGCCCGCTCGCCGAGGCCGACCCGGACGCC
GCCGCCGAGCTTCGCTTCCTCGCCACGCGCTCCAAGGCCGAGGTCGTCGACATGCTCCGCAAGCACACCTACTTCGACGAGCTCGCG
CAGAGCAAGCGCACCTTCGCCGCCTCCACGCCGTCGGCCGCGACCACCACCGCCTCCCTCTCCAACGGCCACCTCTCGTCGCCCCGC
TCCCCCTTCGCGCCCGCCGCGGCGCGCGACCACCTGTTCGACAAGACGGTCACCCCGAGCGACGTGGGCAAGCTGAACAGGCTCGTC
ATACCGAAGCAGCACGCCGAGAAGCACTTCCCGCTACAGCTCCCGTCCGCCGGCGGCGAGAGCAAGGGTGTCCTCCTCAACTTCGAG
GACGCCGCCGGCAAGGTGTGGCGGTTCCGGTACTCGTACTGGAACAGCAGCCAGAGCTACGTGCTAACCAAGGGCTGGAGCCGCTTC
GTCAAGGAGAAGGGTCTCCACGCCGGCGACGTCGTCGGCTTCTACCGCTCCGCCGCCAGTGCCGGCGACGACGGCAAGCTCTTCATC
GACTGCAAGTTAGTACGGTCGACCGGCGCCGCCCTCGCGTCGCCCGCTGATCAGCCAGCGCCGTCGCCGGTGAAGGCCGTCAGGCTC
TTCGGCGTGGACCTGCTCACGGCGCCGGCGCCGGTCGAACAGATGGCCGGGTGCAAGAGAGCCAGGGACTTGGCGGCGACGACGCCT
CCACAAGCGGCGGCGTTCAAGAAGCAATGCATAGAGCTGGCACTAGTATAG

SEQ ID NO: 49
60MDSSSCLVDDTNSGGSSTDKLRALAAAAAETAPLERMGSGASAVVDAAEPGAEADSGSGGRVCGGGGGGAGGAGGKLPSSKFKGV
VPQPNGRWGAQIYERHQRVWLGTFAGEDDAARAYDVAAQRFRGRDAVTNFRPLAEADPDAAAELRFLATRSKAEVVDMLRKHTYFDE
LAQSKRTFAASTPSAATTTASLSNGHLSSPRSPFAPAAARDHLFDKTVTPSDVGKLNRLVIPKQHAEKHFPLQLPSAGGESKGVLLN
FEDAAGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKGLHAGDVVGFYRSAASAGDDGKLFIDCKLVRSTGAALASPADQPAPSPVKAV
RLFGVDLLTAPAPVEQMAGCKRARDLAATTPPQAAAFKKQCIELALV

Os10g0537100   LOC_Os10g39190
Cover 47%   identity 60%

CDS SEQ ID NO: 61
ATGGAGTTCACCCCAATTTCGCCGCCGACGAGGGTCGCCGGCGGTGAGGAGGATTCCGAGAGGGGGGCGGCGGCGTGGGCGGTGGTG
GAGAAGGAGCACATGTTTGAGAAGGTCGTGACGCCGAGCGACGTGGGGAAGCTGAACCGATTGGTCATCCCCAAGCAGCACGCCGAG
AGGTACTTCCCGCTCGACGCCGCGGCGGGCGCCGGCGGCGGCGGTGGTGGCGGCGGTGGCGGCGGCGGGGGGAAGGGGCTGGTGCTG
AGCTTCGAGGACAGGACGGGGAAGGCGTGGAGGTTCCGGTACTCGTACTGGAACAGCAGCCAGAGCTACGTGATGACCAAAGGGTGG
AGCCGCTTCGTCAAGGAGAAGCGCCTCGGCGCCGGCGACACCGTGTCGTTCGGCCGCGGCCTCGGCGACGCCGCCCGCGGCCGCCTC
TTCATCGACTTCCGCCGCCGCCGCCAGGACGCCGGCAGCTTCATGTTCCCGCCGACGGCGGCGCCGCCGTCGCACTCGCACCACCAT
CATCAGCGACACCACCCGCCGCTCCCGTCCGTGCCCCTTTGCCCGTGGCGAGACTACACCACCGCCTATGGCGGCGGCTACGGCTAC
GGCTACGGCGGCGGCTCCACCCCGGCGTCCAGCCGCCACGTGCTGTTCCTCCGGCCGCAGGTGCCGGCCGCTGTGGTGCTCAAGTCG
GTGCCGGTGCACGTCGCGGCCACCTCGGCGGTGCAGGAGGCGGCGACGACGACAAGGCCGAAGCGTGTCCGGCTGTTCGGGGTGAAC
CTCGACTGCCCGGCGGCCATGGACGACGACGACGACATCGCCGGAGCGGCGAGCCGGACGGCAGCGTCGTCTCTCCTGCAGCTCCCC
TCGCCGTCGTCCTCGACGTCGTCGTCGACGGCGGGGAAGAAGATGTGCTCCTTGGATCTTGGGTTGTGA

SEQ ID NO: 62
MEFTPISPPTRVAGGEEDSERGAAAWAVVEKEHMFEKVVTPSDVGKLNRLVIPKQHAERYFPLDAAAGAGGGGGGGGGGGGKGLVL
SFEDRTGKAWRFRYSYWNSSQSYVMTKGWSRFVKEKRLGAGDTVSFGRGLGDAARGRLFIDFRRRRQDAGSFMFPPTAAPPSHSHHH
HQRHHPPLPSVPLCPWRDYTTAYGGGYGYGYGGGSTPASSRHVLFLRPQVPAAVVLKSVPVHVAATSAVQEAATTTRPKRVRLFGVN
LDCPAAMDDDDDIAGAASRTAASSLLQLPSPSSSTSSSTAGKKMCSLDLGL

Glycine max

Loc100795470
Cover 75%   identity 53%

SEQ ID NO: 63
Msinhysmdlpeptlwwphphhqqqqltlmdpdplrlnlnsddgngndndndenqttttggeqeilddkepmfekpltpsdvgklnr
lvipkqhaekyfplsgdsggseckglllsfedesgkcwrfrysywnssqsyvltkgwsryvkdkrldagdvvlferhrvdaqrlfig
wrrrrqsdaalpphavssrksgggdgnsnknegwtrgfysahhpypthhlhhhqpspyqqqhdclhagrgsqgqnqrmrpvgnnsss
sssssrvlrlfgvdmecqpehddsgpstpqcsynsnnmlpstqgtdhshhnfyqqqpsnsnpsphhmmvhhqpyyy

CDS SEQ ID NO: 64
ATGTCCATAAACCACTACTCCATGGACCTTCCCGAACCGACACTCTGGTGGCCACACCCACACCACCAACAACAACAACTAACCTTA
ATGGATCCTGACCCTCTCCGTCTCAACCTCAATAGCGACGATGGCAATGGCAATGACAACGACAACGACGAAAATCAAACAACCACA
ACAGGAGGAGAACAAGAAATATTAGACGATAAAGAACCGATGTTCGAGAAGCCCTTAACCCCGAGCGACGTGGGGAAGCTGAACCGT
CTCGTAATCCCGAAGCAGCACGCGGAGAAGTACTTCCCACTGAGTGGTGACTCGGGCGGGAGCGAGTGCAAGGGGCTGTTACTGAGT
TTCGAGGACGAGTCGGGGAAGTGTTGGCGCTTCCGCTACTCGTACTGGAACAGCAGCCAGAGCTACGTGCTCACCAAAGGGTGGAGC
CGCTACGTCAAGGACAAGCGCCTTGACGCGGGCGACGTCGTTTTGTTCGAGCGTCACCGCGTCGACGCGCAGCGCCTCTTCATCGGG
TGGAGGCGCAGGCGGCAGAGCGATGCCGCCTTGCCGCCTGCGCACGTTAGCAGTAGGAAGAGTGGTGGTGGTGATGGGAATAGTAAT

-continued

Identtty of homologs to NGAL2 is tndtcated

AAGAATGAGGGGTGGACCAGAGGGTTCTATTCTGCGCATCATCCTTATCCTACGCATCATCTTCATCATCATCAGCCCTCGCCATAC
CAACAACAACATGACTGTCTTCATGCAGGTAGAGGGTCCCAAGGTCAGAACCAAAGGATGAGACCAGTGGGAAACAACAGTTCTAGC
TCTAGTTCGAGTTCAAGGGTACTTAGGCTGTTCGGGGTCGACATGGAATGCCAACCCGAACATGATGATTCTGGTCCCTCCACACCC
CAATGCTCCTACAATAGTAACAACATGTTGCCATCAACACAGGGCACAGATCATTCCCATCACAATTTCTACCAACAGCAACCTTCT
AATTCCAATCCTTCCCCTCATCACATGATGGTACATCACCAACCATACTACTACTAG

Loc100818164
Cover 50%   identity 73%

SEQ ID NO: 65
MSTNHYTMDLPEPTLWWPHPHQQQLTLIDPDPLPLNLNNDDNDNGDDNDNDENQTVTTTTTGGEEEIINNKEPMFEKPLTPSDVGKL
NRLVIPKQHAEKYFPLSGGDSGSSECKGLLLSFEDESGKCWRFRYSYWNSSQSYVLTKGWSRYVKDKRLDAGDVVLFQRHRADAQRL
FIGWRRRRQSDALPPPAHVSSRKSGGDGNSSKNEGDVGVGWTRGFYPAHHPYPTHHHHPSPYHHQQDDSLHAVRGSQGQNQRTRPVG
NSSSSSSSSSRVLRLFGVNMECQPEHDDSGPSTPQCSYNTNNILPSTQGTDIHSHLNFYQQQQTSNSKPPPHHMMIRHQPYYY

SEQ ID NO: 66
ATGTCGACAAACCACTACACCATGGACCTTCCCGAACCAACACTCTGGTGGCCACACCCACACCAACAACAACTAACCTTAATAGAT
CCAGACCCTCTCCCTCTGAACCTCAACAACGACGACAACGACAATGGCGACGACAACGACAACGACGAAAACCAAACAGTTACAACA
ACCACAACAGGAGGAGAAGAAGAAATAATAAACAATAAAGAACCGATGTTCGAGAAGCCGCTAACCCCGAGCGACGTGGGGAAGCTG
AACCGCCTCGTAATCCCGAAGCAGCACGCTGAGAAGTACTTTCCACTGAGTGGTGGTGACTCGGGCAGTAGCGAGTGCAAGGGGCTG
TTACTGAGTTTCGAGGACGAGTCGGGGAAGTGCTGGCGCTTCCGCTACTCGTACTGGAACAGCAGCCAGAGCTACGTGCTCACCAAA
GGGTGGAGCCGTTACGTGAAGGACAAGCGCCTCGATGCGGGAGATGTCGTTTTATTCCAGCGCCACCGCGCCGACGCGCAGCGCCTC
TTCATCGGCTGGAGGCGCAGGCGGCAGAGCGACGCCCTGCCGCCGCCTGCGCACGTTAGCAGCAGGAAGAGTGGTGGTGATGGGAAT
AGTAGTAAGAATGAGGGTGATGTGGGCGTGGGCTGGACCAGAGGGTTCTATCCTGCGCATCATCCTTATCCTACGCATCATCATCAT
CCCTCGCCATACCATCACCAACAAGATGACTCTCTTCATGCAGTTAGAGGGTCCCAAGGTCAGAACCAAAGGACGAGACCAGTGGGA
AACAGCAGTTCTAGTTCGAGTTCGAGTTCAAGGGTACTTAGGCTATTCGGGGTCAACATGGAATGCCAACCCGAACATGATGATTCT
GGACCCTCCACACCCCAATGCTCCTACAATACTAACAACATATTGCCATCCACACAGGGCACAGATATTCATTCCCATCTCAATTTC
TACCAACAACAACAAACTTCTAATTCCAAGCCTCCCCCTCATCACATGATGATACGTCACCAACCATACTACTACTAG

Loc100802734
Cover 77%   identity 53%

SEQ ID NO: 67
MSSINHYSPETTLYWTNDQQQQAAMWLSNSHTPRFNLNDEEEEEEDDVIVSDKATNNLTQEEEKVAMFEKPLTPSDVGKLNRLVIPK
QHAEKHFPLDSSAAKGLLLSFEDESGKCWRFRYSYWNSSQSYVLTKGWSRYVKDKRLHAGDVVLFHRHRSLPQRFFISCSRRQPNPV
PAHVSTTRSSASFYSAHPPYPAHHFPFPYQPHSLHAPGGGSQGQNETTPGGNSSSSGSGRVLRLFGVNMECQPDNHNDSQNSTPECS
YTHLYHHQTSSYSSSSNPHHHMVPQQP

SEQ ID NO: 68
ATGTCATCGATAAACCACTATTCACCGGAAACAACACTATACTGGACCAACGACCAACAGCAACAAGCCGCCATGTGGCTGAGTAAT
TCCCACACCCCGCGTTTCAATCTGAACGACGAGGAGGAGGAGGAGGAAGACGACGTTATCGTTTCGGACAAGGCTACTAATAACTTG
ACGCAAGAGGAGGAGAAGGTAGCCATGTTCGAGAAGCCGTTGACGCCGAGCGACGTCGGGAAGCTGAACCGGCTCGTGATTCCGAAA
CAGCACGCGGAGAAGCACTTCCCTCTCGACTCGTCGGCGGCGAAGGGGCTGTTGCTGAGTTTCGAGGACGAGTCCGGGAAGTGTTGG
CGCTTCCGTTACTCTTATTGGAACAGTAGCCAGAGTTACGTTTTGACCAAAGGATGGAGCCGTTACGTCAAAGACAAACGCCTCCAC
GCTGGCGACGTCGTTTTGTTCCACAGACACCGCTCCCTCCCTCAACGCTTCTTCATCTCCTGCAGCCGCCGCCAACCCAACCCGGTC
CCCGCTCACGTTAGCACCACCAGATCCTCCGCTTCCTTCTACTCTGCGCACCCACCTTATCCTGCGCACCACTTCCCCTTCCCATAC
CAACCTCACTCTCTTCATGCACCAGGTGGAGGGTCCCAAGGACAGAACGAAACGACACCGGGAGGGAACAGTAGTTCAAGTGGCAGT
GGCAGGGTGCTGAGGCTCTTTGGTGTGAACATGGAATGCCAACCTGATAATCATAATGATTCCCAGAACTCCACACCAGAATGCTCC
TACACCCACTTATACCACCATCAAACCTCTTCTTATTCTTCTTCTTCAAACCCTCACCATCACATGGTACCTCAACAACCATAA

Loc100781489
Cover 49%   identity 64%

SEQ ID NO: 69
MELMQQVKGNYSDSREEEEEEEAAAITRESESSRLHQQDTASNFGKKLDLMDLSLGSSKEEEEEGNLQQGGGGVVHHAHQVVEKEHM
FEKVATPSDVGKLNRLVIPKQHAEKYFPLDSSTNEKGLLLNFEDRNGKVWRFRYSYWNSSQSYVMTKGWSRFVKEKKLDAGDIVSFQ
RGLGDLYRHRLYIDWKRRPDHAHAHPPHHHDPLFLPSIRLYSLPPTMPPRYHHDHHFHHHLNYNNLFTFQQHQYQQLGAATTTHHNN
YGYQNSGSGSLYYLRSSMSMGGGDQNLQGRGSNIVPMIIDSVPVNVAHHNNNRHGNGGITSGGTNCSGKRLRLFGVNMECASSAEDS
KELSSGSAAHVTTAASSSSLHHQRLRVPVPVPLEDPLSSSAAAAARFGDHKGASTGTSLLFDLDPSLQYHRH

CDS SEQ ID NO: 70
ATGGAGTTGATGCAACAAGTTAAAGGTAATTATTCTGATAGCAGGGAGGAAGAGGAGGAAGAGGAAGCTGCAGCAATCACAAGGGAA
TCAGAAAGCAGCAGGTTACACCAACAAGATACAGCATCCAATTTTGGAAAGAAGCTAGACTTGATGGACTTGTCACTAGGGAGCAGC
AAGGAAGAGGAAGAGGAAGGGAATTTGCAACAAGGAGGAGGAGGAGTGGTTCATCATGCTCACCAAGTAGTGGAGAAAGAACACATG
TTTGAGAAAGTGGCGACACCGAGCGACGTAGGGAAGCTGAACAGGCTGGTGATACCGAAGCAGCACGCGGAGAAGTACTTCCCCCTT
GACTCCTCAACCAACGAGAAGGGTCTGCTCCTGAATTTCGAGGACAGGAATGGGAAGGTGTGGCGATTCAGGTATTCCTATTGGAAC
AGCAGCCAGAGCTATGTGATGACAAAAGGGTGGAGCCGCTTTGTTAAGGAGAAGAAGCTGGATGCCGGTGACATTGTCTCCTTCCAG
CGTGGCCTTGGGGATTTGTATAGACATCGGTTGTATATAGATTGGAAGAGAAGGCCCGATCATGCTCATGCTCATCCACCTCATCAT
CACGATCCTTTGTTTCTTCCCTCTATCAGATTGTACTCTCTCCCTCCCACCATGCCACCTCGCTACCACCACGATCATCACTTTCAC
CACCATCTCAATTACAACAACCTCTTCACTTTTCAGCAACACCAGTACCAGCAGCTTGGTGCTGCCACTACCACTCATCACAACAAC
TATGGTTACCAGAATTCGGGATCTGGTTCACTCTATTACCTAAGGTCCTCTATGTCAATGGGTGGTGGTGATCAAAACTTGCAAGGG
AGAGGGAGCAACATTGTCCCCATGATCATTGATTCTGTGCCGGTTAACGTTGCTCATCACAACAACAATCGCCATGGGAATGGGGGC

-continued

Identtty of homologs to NGAL2 is tndtcated

ATCACGAGTGGTGGTACTAATTGTAGTGGAAAACGACTAAGGCTATTTGGGGTGAACATGGAATGCGCTTCTTCGGCAGAAGATTCC
AAAGAATTGTCCTCGGGTTCGGCAGCACACGTGACGACAGCTGCTTCTTCTTCTCTTCATCATCAGCGCTTGAGGGTGCCAGTG
CCAGTGCCACTTGAAGATCCACTTTCGTCGTCAGCAGCAGCAGCAGCAAGGTTTGGGGATCACAAAGGGGCCAGTACTGGGACTTCG
CTGCTGTTTGATTTGGATCCCTCTTTGCAGTATCATCGCCACTGA

Loc100776987
Cover 46%   identity 62%

SEQ ID NO: 71
MDAISCLDESTTTESLSISQAKPSSTIMSSEKASPSPPPPNRLCRVGSGASAVVDSDGGGGGGSTEVESRKLPSSKYKGVVPQPNGR
WGSQIYEKHQRVWLGTFNEEDEAARAYDVAVQRFRGKDAVTNFKPLSGTDDDDGESEFLNSHSKSEIVDMLRKHTYNDELEQSKRSR
GFVRRRGSAAGAGNGNSISGACVMKAREQLFQKAVTPSDVGKLNRLVIPKQHAEKHFPLQSAANGVSATATAAKGVLLNFEDVGGKV
WRFRYSYWNSSQSYVLTKGWSRFVKEKNLKAGDTVCFQRSTGPDRQLYIDWKTRNVVNEVALFGPVVEPIQMVRLFGVNILKLPGSD
SIANNNNASGCCNGKRREMELFSLECSKKPKIIGAL

CDS SEQ ID NO: 72
ATGGATGCAATTAGTTGCCTGGATGAGAGCACCACCACCGAGTCACTCTCCATAAGTCAGGCGAAGCCTTCTTCGACGATTATGTCG
TCCGAGAAGGCTTCTCCTTCCCCGCCGCCGCCGAACAGGCTGTGCCGCGTCGGTAGCGGTGCTAGCGCAGTCGTGGATTCCGACGGC
GGCGGCGGGGGTGGCAGCACCGAGGTGGAGTCGCGGAAGCTCCCCTCGTCCAAGTATAAGGGCGTCGTGCCCCAGCCCAACGGCCGC
TGGGGCTCGCAGATTTACGAGAAGCACCAGCGCGTGTGGCTGGGAACGTTCAACGAGGAAGACGAGGCGGCGCGTGCGTACGACGTC
GCCGTGCAGCGATTCCGCGGCAAGGACGCCGTCACAAACTTCAAGCCGCTCTCCGGCACCGACGACGACGACGGGGAATCGGAGTTT
CTCAACTCGCATTCGAAATCCGAGATCGTCGACATGCTGCGTAAGCATACGTACAATGACGAGCTGGAACAAAGCAAGCGCAGCCGC
GGCTTCGTACGTCGGCGCGGCTCCGCCGCCGGCGCCGGAAACGGAAACTCAATCTCCGGCGCGTGTGTTATGAAGGCGCGTGAGCAG
CTATTCCAGAAGGCCGTTACGCCGAGCGACGTTGGGAAACTGAACCGTTTGGTGATACCGAAGCAGCACGCGGAGAAGCACTTTCCT
TTACAGAGCGCTGCTAACGGCGTTAGCGCGACGGCGACGGCGGCGAAGGGCGTTTTGTTGAACTTCGAAGACGTTGGAGGGAAAGTG
TGGCGGTTTCGTTACTCGTATTGGAACAGTAGCCAGAGTTACGTCTTGACCAAAGGTTGGAGCCGGTTCGTTAAGGAGAAGAATCTG
AAAGCCGGTGACACGGTTTGTTTTCAACGGTCCACTGGACCGGACAGGCAGCTTTACATCGATTGGAAGACGAGGAATGTTGTTAAC
GAGGTCGCGTTGTTCGGACCGGTTGTCGAACCGATCCAGATGGTTCGGCTCTTTGGTGTTAACATTTTGAAACTACCCGGTTCAGAT
TCTATCGCCAATAACAATAATGCAAGTGGGTGCTGCAATGGCAAGAGAAGAGAAATGGAACTCTTTTCATTAGAGTGTAGCAAGAAA
CCTAAGATTATTGGTGCTTTGTAG

Loc100778733
Cover 44%   identity 64%

SEQ ID NO: 73
MELMQEVKGYSDGREEEEEEEEAAEEIITREESSRLLHQHQEAAGSNFIINNNHHHHQHHHHHTTKQLDFMDLSLGSSKDEGNLQGS
SSSVYAHHHHAASASSSANGNNNNSSSSNLQQQQQQPAEKEHMFDKVVTPSDVGKLNRLVIPKQHAEKYFPLDSSANEKGLLLNFED
RNGKLWRFRYSYWNSSQSYVMTKGWSRFVKEKKLDAGDMVSFQRGVGELYRHRLYIDWWRRPDHHHHHHHGPDHSTTLFTPFLIPNQ
PHHLMSIRWGATGRLYSLPSPTPPRHHENLNYNNNAMYHPFHHHGAGSGINATTHHYNNYHEMSSTTTSGSAGSVFYHRSTPPISMP
LADHQTLNTRQQQQQQQQQEGAGNVSLSPMIIDSVPVAHHLHHQQHHGGKSSGPSSTSTSPSTAGKRLRLFGVNMECASSTSEDPKC
FSLLSSSSMANSNSQPPLQLLREDTLSSSSARFGDQRGVGEPSMLFDLDPSLQYRQ

SEQ ID NO: 74
ATGGAGTTGATGCAAGAAGTGAAAGGGTATTCTGATGGCAGAGAGGAGGAGGAGGAGGAAGAGGAAGCAGCAGAAGAAATCATCACA
AGAGAAGAAAGCAGCAGGTTGTTACACCAGCACCAGGAGGCAGCAGGTTCCAATTTCATCATCAACAATAATCATCATCATCATCAA
CATCACCACCACCACACAACAAAGCAGCTAGACTTCATGGACTTGTCACTTGGTAGCAGCAAGGATGAAGGGAATTTGCAAGGATCA
TCTTCTTCTGTCTATGCTCATCATCATCATGCAGCAAGTGCTAGTTCTTCTGCCAATGGTAACAACAACAACAGCAGCAGCAGCAAC
TTGCAGCAACAGCAGCAGCAGCCTGCTGAGAAGGAGCACATGTTTGATAAAGTAGTGACACCAAGTGATGTGGGGAAGCTGAACCGG
TTGGTGATACCAAAGCAGCATGCTGAGAAGTATTTCCCTCTTGATTCCTCAGCCAATGAGAAGGGTCTGTTGCTGAATTTTGAGGAC
AGGAATGGTAAGTTGTGGAGGTTCAGGTACTCCTATTGGAACAGCAGCCAGAGCTATGTGATGACCAAAGGTTGGAGCCGTTTTGTT
AAGGAGAAGAAGCTTGATGCTGGTGACATGGTGTCCTTCCAGCGTGGTGTTGGGGAGTTGTATAGGCATAGGTTGTACATAGATTGG
TGGAGAAGGCCTGATCATCATCACCATCACCATCATGGCCCTGACCATTCAACCACACTCTTCACACCTTTCTTAATTCCCAATCAG
CCTCATCACTTAATGTCCATCAGATGGGGTGCCACTGGCAGATTGTACTCCCTCCCTTCCCCAACCCCACCACGCCACCATGAACAC
CTCAATTACAACAATAACGCCATGTATCATCCCTTTCATCACCATGGTGCTGGAAGTGGAATTAATGCTACTACTCATCACTACAAC
AACTATCATGAGATGAGTAGTACTACTACTTCAGGATCTGCAGGCTCAGTCTTTTACCACAGGTCAACACCCCCAATATCAATGCCA
TTGGCTGACCACCAAACCTTGAACACAAGGCAGCAGCAACAACAACAACAACAACAAGAGGGAGCTGGCAATGTTTCTCTTTCCCCT
ATGATCATTGATTCTGTTCCAGTTGCTCACCACCTCCATCATCAACAACACCATGGTGGCAAGAGTAGTGGTCCTAGTAGTACTAGT
ACTAGTCCTAGCACTGCAGGGAAAAGACTAAGGCTATTTGGGGTCAACATGGAATGTGCTTCTTCAACATCAGAAGACCCCAAATGC
TTCAGCTTGTTGTCCTCATCTTCAATGGCTAATTCCAATTCACAACCACCACTTCAGCTTTTGAGGGAAGATACACTTTCGTCATCA
TCGGCAAGGTTTGGGGATCAGAGAGGAGTAGGGGAACCTTCAATGCTTTTTGATCTGGACCCTTCTTTGCAATACCGGCAGTGA

Loc732601
Cover 44%   identity 62%

SEQ ID NO: 75
MDGGCVTDETTTSSDSLSVPPPSRVGSVASAVVDPDGCCVSGEAESRKLPSSKYKGVVPQPNGRWGAQIYEKHQRVWLGTFNEEDEA
ARAYDIAALRFRGPDAVTNFKPPAASDDAESEFLNSHSKFEIVDMLRKHTYDDELQQSTRGGRRRLDADTASSGVFDAKAREQLFEK
TVTPSDVGKLNRLVIPKQHAEKHFPLSGSGDESSPCVAGASAAKGMLLNFEDVGGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKNLR
AGDAVQFFKSTGPDRQLYIDCKARSGEVNNNAGGLFVPIGPVVEPVQMVRLFGVNLLKLPVPGSDGVGKRKEMELFAFECCKKLKVI
GAL

-continued

Identtty of homologs to NGAL2 is tndtcated

CDS SEQ ID NO: 76
ATGGATGGAGGCTGTGTCACAGACGAAACCACCACATCCAGCGACTCTCTTTCCGTTCCGCCGCCCAGCCGCGTCGGCAGCGTTGCA
AGCGCCGTCGTCGACCCCGACGGTTGTTGCGTTTCCGGCGAGGCCGAATCCCGGAAACTCCCTTCGTCGAAATACAAAGGCGTGGTG
CCGCAACCGAACGGTCGCTGGGGAGCTCAGATTTACGAGAAGCACCAGCGCGTGTGGCTCGGCACTTTCAACGAGGAAGACGAAGCC
GCCAGAGCCTACGACATCGCCGCGCTGCGCTTCCGCGGCCCCGACGCCGTCACCAACTTCAAGCCTCCCGCCGCCTCCGACGACGCC
GAGTCCGAGTTCCTCAACTCGCATTCCAAGTTCGAGATCGTCGACATGCTCCGCAAGCACACCTACGACGACGAGCTCCAGCAGAGC
ACGCGCGGTGGTAGGCGCCGCCTCGACGCTGACACCGCGTCGAGCGGTGTGTTCGACGCGAAAGCGCGTGAGCAGCTGTTCGAGAAA
ACGGTTACGCCGAGCGACGTCGGGAAGCTGAATCGATTAGTGATACCGAAGCAGCACGCGGAGAAGCACTTTCCGTTAAGCGGATCC
GGCGACGAAAGCTCGCCGTGCGTGGCGGGGGCTTCGGCGGCGAAGGGAATGTTGTTGAACTTTGAGGACGTTGGAGGGAAAGTGTGG
CGGTTTCGTTACTCTTATTGGAACAGTAGCCAGAGCTACGTGCTTACCAAAGGATGGAGCCGGTTCGTTAAGGAGAAGAATCTTCGA
GCCGGTGACGCGGTTCAGTTCTTCAAGTCGACCGGACCGGACCGGCAGCTATATATAGACTGCAAGGCGAGGAGTGGTGAGGTTAAC
AATAATGCTGGCGGTTTGTTTGTTCCGATTGGACCGGTCGTTGAGCCGGTTCAGATGGTTCGGCTTTTCGGGGTCAACCTTTTGAAA
CTACCCGTACCCGGTTCGGATGGTGTAGGGAAGAGAAAAGAGATGGAACTGTTTGCATTTGAATGTTGCAAGAAGTTAAAAGTAATT
GGAGCTTTGTAA

Loc100801107
Cover 44%   identity 61%

SEQ ID NO: 77
MDAISCMDESTTTESLSISLSPTSSSEKAKPSSMITSSEKVSLSPPPSNRLCRVGSGASAVVDPDGGGSGAEVESRKLPSSKYKGVV
PQPNGRWGAQIYEKHQRVWLGTFNEEDEAARAYDIAAQRFRGKDAVTNFKPLAGADDDDGESEFLNSHSKPEIVDMLRKHTYNDELE
QSKRSRGVVRRRGSAAAGTANSISGACFTKAREQLFEKAVTPSDVGKLNRLVIPKQHAEKHFPLQSSNGVSATTIAAVTATPTAAKG
VLLNFEDVGGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKNLKAGDTVCFHRSTGPDKQLYIDWKTRNVVNNEVALFGPVGPVVEPIQ
MVRLFGVNILKLPGSDTIVGNNNNASGCCNGKRREMELFSLECSKKPKIIGAL

CDS SEQ ID NO: 78
ATGGATGCAATTAGTTGCATGGATGAGAGCACCACCACTGAGTCACTCTCTATAAGTCTTTCTCCGACGTCATCGTCGGAGAAAGCG
AAGCCTTCTTCGATGATTACATCGTCGGAGAAGGTTTCTCTGTCCCCGCCGCCGTCAAACAGACTATGCCGTGTTGGAAGCGGCGCG
AGCGCAGTCGTGGATCCTGATGGCGGCGGCAGCGGCGCTGAGGTAGAGTCGCGGAAACTCCCCTCGTCGAAGTACAAGGGCGTGGTG
CCCCAGCCCAACGGCCGCTGGGGTGCGCAGATTTACGAGAAGCACCAGCGCGTGTGGCTTGGAACGTTCAACGAGGAAGACGAGGCG
GCGCGTGCGTACGACATCGCCGCGCAGCGGTTCCGCGGCAAGGACGCCGTCACGAACTTCAAGCCGCTCGCCGGCGCCGACGACGAC
GACGGAGAATCGGAGTTTCTCAACTCGCATTCCAAACCCGAGATCGTCGACATGCTGCGAAAGCACACGTACAATGACGAGCTGGAG
CAGAGCAAGCGCAGCCGCGGCGTCGTCCGGCGGCGAGGCTCCGCCGCCGCCGGCACCGCAAACTCAATTTCCGGCGCGTGCTTTACT
AAGGCACGTGAGCAGCTATTCGAGAAGGCTGTTACGCCGAGCGACGTTGGGAAATTGAACCGTTTGGTGATACCGAAGCAGCACGCG
GAGAAGCACTTTCCGTTACAGAGCTCTAACGGCGTTAGCGCGACGACGATAGCGGCGGTGACGGCGACGCCGACGGCGGCGAAGGGC
GTTTTGTTGAACTTCGAAGACGTTGGAGGGAAAGTGTGGCGGTTTCGTTACTCGTATTGGAACAGTAGCCAGAGTTACGTCTTAACC
AAAGGTTGGAGCCGGTTCGTTAAGGAGAAGAATCTGAAAGCTGGTGACACGGTTTGTTTTCACCGGTCCACTGGACCGGACAAGCAG
CTTTACATCGATTGGAAGACGAGGAATGTTGTTAACAACGAGGTCGCGTTGTTCGGACCGGTCGGACCGGTTGTCGAACCGATCCAG
ATGGTTCGGCTCTTTGGGGTTAACATTTTGAAACTACCCGGTTCAGATACTATTGTTGGCAATAACAATAATGCAAGTGGGTGCTGC
AATGGCAAGAGAAGAGAAATGGAACTGTTCTCGTTAGAGTGTAGCAAGAAACCTAAGATTATTGGTGCTTTGTAA

Loc100789009
Cover 44%   identity 62%

SEQ ID NO: 79
MDGGSVTDETTTTSNSLSVPANLSPPPLSLVGSGATAVVYPDGCCVSGEAESRKLPSSKYKGVVPQPNGRWGAQIYEKHQRVWLGTF
NEEDEAARAYDIAAHRFRGRDAVTNFKPLAGADDAEAEFLSTHSKSEIVDMLRKHTYDNELQQSTRGGRRRRDAETASSGAFDAKAR
EQLFEKTVTQSDVGKLNRLVIPKQHAEKHFPLSGSGGGALPCMAAAAGAKGMLLNFEDVGGKVWRFRYSYWNSSQSYVLTKGWSRFV
KEKNLRAGDAVQFFKSTGLDRQLYIDCKARSGKVNNNAAGLFIPVGPVVEPVQMVRLFGVDLLKLPVPGSDGIGVGCDGKRKEMELF
AFECSKKLKVIGAL

SEQ ID NO: 80
ATGGATGGAGGCAGTGTCACAGACGAAACCACCACAACCAGCAACTCTCTTTCGGTTCCGGCGAATCTATCTCCGCCGCCTCTCAGC
CTTGTCGGCAGCGGCGCAACCGCCGTCGTCTACCCCGACGGTTGTTGCGTCTCCGGCGAAGCCGAATCCCGGAAACTCCCGTCCTCG
AAATACAAAGGCGTGGTGCCGCAACCGAACGGTCGTTGGGGAGCTCAGATTTACGAGAAGCACCAGCGCGTGTGGCTCGGCACCTTC
AACGAGGAAGACGAAGCCGCCAGAGCCTACGACATCGCCGCGCATCGCTTCCGCGGCCGCGACGCCGTCACTAACTTCAAGCCTCTC
GCCGGCGCCGACGACGCCGAAGCCGAGTTCCTCAGCACGCATTCCAAGTCCGAGATCGTCGACATGCTCCGCAAGCACACCTACGAC
AACGAGCTCCAGCAGAGCACCCGCGGCGGCAGGCGCCGCCGGGACGCCGAAACCGCGTCGAGCGGCGCGTTCGACGCGAAGGCGCGT
GAGCAGCTGTTCGAGAAAACCGTTACGCAGAGCGACGTCGGGAAGCTGAACCGATTAGTGATACCAAAGCAGCACGCGGAGAAGCAC
TTTCCGTTAAGCGGATCCGGCGGCGGAGCCTTGCCGTGCATGGCGGCGGCTGCGGGGGCGAAGGGAATGTTGCTGAACTTTGAGGAC
GTTGGAGGGAAAGTGTGGCGGTTCCGTTACTCGTATTGGAACAGTAGCCAGAGCTACGTGCTTACCAAAGGATGGAGCCGGTTCGTT
AAGGAGAAGAATCTTCGAGCTGGTGACGCGGTTCAGTTCTTCAAGTCGACCGGACTGGACCGGCAACTATATATAGACTGCAAGGCG
AGGAGTGGTAAGGTTAACAATAATGCTGCCGGTTTGTTTATTCCGGTTGGACCGGTTGTTGAGCCGGTTCAGATGGTACGGCTTTTC
GGGGTCGACCTTTTGAAACTACCCGTACCCGGTTCGGATGGTATTGGGGTTGGCTGTGACGGGAAGAGAAAAGAGATGGAGCTGTTT
GCATTTGAATGTAGCAAGAAGTTAAAAGTAATTGGAGCTTTGTAA

-continued

Identtty of homologs to NGAL2 is tndtcated

Loc102660503
Cover 36% identity 57%

SEQ ID NO: 81
migvekvticmrievntegrralmdcwqisgvhessdcseikfafdavvkrarheennaaaqkfkgvvsqqngnwgaqiyahqqriw
lgtfksereaamaydsasiklrsgechrnfpwndqtvqepqfqshysaetvlnmirdgtypskfatflktrqtqkgvakhiglkgdd
eeqfcctqlfqkeltpsdvgklnrlvipkkhavsyfpyvggsadesgsvdveavfydklmrlwkfrycywkssqsyvftrgwnrfvk
dkklkakdviafftwgksggegeafalidviynnnaeedskgdtkqvlgnqlqlagseegededanigkdfnaqkglrlfgvcit

CDS SEQ ID NO: 82
atgattggagttgagaaagtgacaatttgtatgagaatagaggtgaatactgaaaagggaagaagggctttaatggactgttggcaa
atatcaggagttcatgaaagttcagattgtagcgaaatcaaatttgcattcgacgcagtagtaaaacgcgcgaggcatgaagagaat
aatgcagcagcacagaagttcaaaggcgttgtgtctcaacaaaatgggaactggggtgcacagatatatgcacaccagcagagaatc
tggttggggaccttcaaatctgaaagagaggctgcaatggcttatgacagcgccagcataaaacttagaagcggagagtgccacaga
aactttccatggaacgaccaaacagttcaagagcctcagttccaaagccattacagcgcagaaacagtgctaaacatgattagagat
ggcacctatccatcaaaatttgctacatttctcaaaactcgtcaaacccaaaaaggcgttgcgaaacacataggtctgaagggtgat
gacgaggaacagttttgttgcacccaactttttcagaaggaattaacaccaagtgatgtgggcaagctcaacaggcttgtcatccca
aagaagcatgcagttagctattttccttacgttggtggcagtgctgatgagagtggtagtgttgacgtggaggctgtgttttatgac
aaactcatgcgattgtggaagttccgatactgctattggaagagcagccaaagttacgtgttcaccagaggctggaatcggtttgtg
aaggataagaagttgaaggctaaagatgtcattgcgtttttttacgtggggaaaaagtggaggagagggagaagcttttgcattgatc
gatgtaatttataataataatgcagaagaagacagcaagggagacaccaaacaagttttgggaaaccaattacaattagctggcagt
gaagaaggtgaagatgaagatgcaaacattggaaaggatttcaatgcacaaaagggtctgaggctctttggtgtgtgtatcacctaa

Hordeum vulgare

MLOC_66387
Cover 47% identity 64%

SEQ ID NO: 83
MEFTATSSRFSKGEEEVEEEQEEASMREIPFMTPAAATCAAAPPSASASASTPASASGSSPPFRSGDDAGASGSGAGDGSRSNVAEA
VEKEHMFDKVVTPSDVGKLNRLVIPKQYAEKYFPLDSAANEKGLLLNFEDSAGKPWRFRYSYWNSSQSYVMTKGWSRFVKEKRLDAG
DTVSFSRGAGEAARHRLFIDWKRRADTRDPLRLPRLPLPMPLTSHYSPWGLGAGARGFFMPPSPPATLYEHRLRQGFDFRGMNPSYP
TMGRQVILFGSAARMPPHGPAPLLVPRPPPPLHFTVQQQGSDAGGSVTAGSPVVLDSVPVIESPTTATKKRVRLFGVNLDNPQHPGD
GGGESSNYGSALPLQMPASAWRPRDHTLRLLEFPSHGAEASSPSSSSSSKREAHSGLDLDL

SEQ ID NO: 84
ATGGAGTTTACTGCGACAAGCAGTAGGTTTTCTAAAGGAGAGGAGGAGGTGGAGGAGGAGCAGGAGGAGGCGTCGATGCGCGAGATC
CCTTTCATGACGCCCGCGGCCGCCACCTGCGCCGCGGCGCCGCCTTCTGCTTCTGCGTCGGCCTCGACACCCGCGTCAGCGTCTGGA
AGTAGCCCTCCCTTTCGATCTGGGGATGACGCCGGAGCGTCGGGGAGCGGGGCCGGCGACGGCAGCCGCAGCAACGTGGCGGAGGCC
GTGGAGAAGGAGCACATGTTCGACAAAGTGGTGACGCCGAGCGACGTGGGGAAGCTTAACCGGCTGGTCATCCCCAAGCAGTACGCC
GAGAAGTACTTCCCGCTGGACTCGGCGGCCAACGAGAAGGGCCTTCTGCTCAACTTCGAGGACAGCGCCGGGAAGCCATGGCGCTTC
CGCTATTCCTACTGGAACAGCAGCCAGAGCTACGTCATGACCAAAGGCTGGAGCCGCTTCGTCAAGGAGAAGCGCCTCGACGCTGGG
GACACCGTCTCCTTCTCCCGCGGCGCCGGTGAGGCCGCGCGCCACCGCCTCTTCATCGACTGGAAGCGCCGAGCCGACACCAGAGAC
CCGCTCCGCTTGCCCCGCCTCCCGCTCCCGATGCCGCTGACGTCGCACTACAGCCCGTGGGGCCTCGGCGCCGGCGCCAGAGGATTC
TTCATGCCTCCCTCGCCGCCAGCCACGCTCTACGAGCACCGTCTCCGTCAAGGCTTCGACTTCCGCGGCATGAACCCCAGTTACCCC
ACAATGGGGAGACAGGTCATCCTTTTCGGCTCGGCCGCCAGGATGCCTCCGCACGGACCAGCACCACTCCTCGTGCCGCGCCCGCCG
CCGCCGCTGCACTTCACGGTGCAGCAACAAGGCAGCGACGCCGGCGGAAGTGTAACCGCAGGATCCCCAGTGGTGCTCGACTCAGTG
CCGGTAATCGAAAGCCCCACGACGGCAACGAAGAAGCGCGTGCGCTTGTTCGGCGTGAACTTGGACAACCCGCAGCATCCCGGTGAT
GGCGGGGGCGAATCGAGCAATTATGGCAGTGCACTGCCATTGCAGATGCCCGCATCAGCATGGCGGCCAAGGGACCATACGCTGAGG
CTGCTCGAATTCCCCTCGCACGGTGCCGAGGCGTCGTCTCCATCGTCGTCGTCGTCTTCCAAGAGGGAGGCGCATTCGGGCTTGGAT
CTCGATCTGTGA

MLOC44012
Cover 55% identity 63%

SEQ ID NO: 85
MLRKHTYFDELAQSKRAFAASAALSAPTTSGDAGGSASPPSPAAVREHLFDKTVTPSDVGKLNRLVIPKQNAEKHFPLQLPAGGGES
KGLLLNFEDDAGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKGLGAGDVVGFYRSAAGRTGEDSKFFIDCRLRPNTNTAAEADPVDQS
SAPVQKAVRLFGVDLLAAPEQGMPGGCKRARDLVKPPPPKVAFKKQCIELALA

SEQ ID NO: 86
ATGCTCCGCAAGCACACCTACTTCGACGAGCTCGCCCAGAGCAAGCGCGCCTTCGCCGCGTCGGCCGCGCTCTCCGCGCCCACCACC
TCGGGCGACGCCGGCGGCAGCGCCTCGCCGCCCTCCCCGGCCGCCGTGCGCGAGCACCTCTTCGACAAGACCGTCACGCCCAGCGAC
GTCGGCAAGCTGAACAGGCTGGTGATACCGAAGCAGAACGCCGAGAAGCACTTCCCGCTGCAGCTCCCGGCCGGCGGCGGCGAGAGC
AAGGGCCTGCTCCTCAACTTCGAGGACGATGCGGGCAAGGTGTGGCGGTTCCGCTACTCGTACTGGAACAGCAGCCAGAGCTACGTC
CTCACCAAGGGCTGGAGCCGCTTCGTGAAGGAGAAGGGCCTCGGCGCCGGAGACGTCGTCGGGTTCTACCGCTCCGCCGCCGGGAGG

-continued

Identtty of homologs to NGAL2 is tndtcated

ACCGGCGAAGACAGCAAGTTCTTCATTGACTGCAGGCTGCGGCCGAACACCAACACCGCCGCCGAAGCAGACCCCGTGGACCAGTCG
TCGGCGCCCGTGCAGAAGGCCGTGAGACTCTTCGGCGTCGATCTTCTCGCGGCGCCGGAGCAGGGCATGCCGGGCGGGTGCAAGAGG
GCCAGAGACTTGGTGAAGCCGCCGCCTCCGAAAGTGGCGTTCAAGAAGCAATGCATAGAGCTGGCGCTAGCGTAG

MLOC_57250
Cover 50%   identity 57%

SEQ ID NO: 87
MYCSRGRIDPAEEGQVMGGLGVRDASWALFKVLEQSDVQVGQNRLLLTKEAVWGGPIPKLFPELEELRGDGLNAENRVAVKILDADG
CEGDANFRYLNSSKAYRVMGPQWSRLVKETGMCKGDRLDLYAATATAASSCSGARAAVAPAIPPGAIVKAAGF

CDS SEQ ID NO: 88
ATGTATTGTTCCCGCGGCCGCATCGATCCCGCGGAAGAAGGGCAGGTGATGGGCGGCCTCGGCGTGCGCGACGCCAGCTGGGCGCTG
TTCAAGGTGTTGGAGCAGTCCGACGTCCAGGTGGGGCAGAACCGGCTGCTCCTCACCAAGGAGGCGGTGTGGGGCGGCCCTATCCCC
AAGCTTTTCCCGGAGCTGGAGGAGCTCCGCGGCGACGGCCTCAACGCCGAGAACAGGGTCGCGGTCAAGATCCTCGACGCCGACGGC
TGCGAGGGGGACGCCAACTTCCGCTACCTCAACTCCAGCAAGGCGTACCGGGTCATGGGGCCTCAGTGGAGCCGGCTCGTGAAGGAG
ACCGGCATGTGCAAGGGAGACCGCCTCGATCTGTACGCGGCAACGGCGACCGCTGCCTCTTCGTGTTCTGGAGCCAGGGCGGCTGTG
GCGCCGGCGATACCTCCCGGAGCAATCGTGAAGGCAGCCGGGTTCTAA

MLOC_38822
Cover 47%   identity 56%

SEQ ID NO: 89
MLRKHIYPDELAQHKRAFFFAAASSPTSSSSPLASPAPSAAAARREHLFDKTVTPSDVGKLNRLVIPKQHAEKHFPLQLPSASAAVP
GECKGVLLNFDDATGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKGLHAGDAVEFYRAASGNNQLFIDCKLRSKSTTTTTSVNSEAAP
SPAPVTRTVRLFGVDLLIAPAARHAHEHEDYGMAKTNKRTMEASVAAPTPAHAVWKKRCVDFALTYRLATTPQCPRSRDQLEGVQAA
GSTFAL

CDS SEQ ID NO: 90
ATGCTGCGCAAGCACATCTATCCCGACGAGCTCGCGCAGCACAAGCGCGCCTTCTTCTTCGCCGCGGCGTCGTCCCCTACGTCGTCG
TCGTCACCTCTCGCCTCGCCGGCTCCTTCAGCCGCGGCGGCGCGGCGCGAGCACCTGTTCGACAAGACGGTCACGCCCAGCGACGTG
GGGAAGCTGAACCGGCTGGTGATCCCCAAGCAGCACGCCGAGAAGCACTTCCCGCTGCAGCTCCCTTCTGCCAGCGCCGCCGTGCCA
GGCGAGTGCAAGGGCGTGCTGCTCAACTTCGATGACGCGACCGGCAAGGTGTGGAGGTTCCGGTACTCCTACTGGAACAGCAGCCAG
AGCTACGTGCTCACCAAGGGGTGGAGCCGCTTCGTGAAGGAGAAGGGCCTTCACGCCGGCGACGCCGTCGAGTTCTACCGCGCCGCC
TCCGGCAACAACCAGCTCTTCATCGACTGCAAGCTCCGGTCCAAGAGCACCACGACGACGACCTCCGTCAACTCGGAGGCCGCCCCA
TCGCCGGCACCCGTGACGAGGACAGTGCGACTCTTCGGGGTCGACCTTCTCATCGCGCCGGCGGCGAGGCACGCGCATGAGCACGAG
GACTACGGCATGGCCAAGACAAACAAGAGAACCATGGAGGCCAGCGTAGCGGCGCCTACTCCGGCGCACGCGGTGTGGAAGAAGCGG
TGCGTAGACTTCGCGCTGACCTACCGACTTGCCACCACCCCACAGTGCCCGAGGTCAAGAGATCAACTAGAAGGAGTACAAGCAGCT
GGGAGTACATTTGCTCTATAG

MLOC_7940
Cover 49%   identity 52%

SEQ ID NO: 91
MGVEILSSTGEHSSQYSSGAASTATTESGVGGRPPTAPSLPVSIADESATSRSASAQSTSSRFKGVVPQPNGRWGAQIYERHARVWL
GTFPDEDSAARAYDVAALRYRGREAATNFPCAAAEAELAFLAAHSKAEIVDMLRKHTYTDELRQGLRRGRGMGARAQPTPSWAREPL
FEKAVTPSDVGKLNRLVVPKQHAEKHFPLKRTPETTTTTGKGVLLNFEDGEGKVWRFRYSYWNSSQSYVLTKGWSRFVREKGLGAGD
SIVFSCSAYGQEKQFFIDCKKNKTMTSCPADDRGAATASPPVSEPTKGEQVRVVRLFGVDIAGEKRGRAAPVEQELFKRQCVAHSQH
SPALGAFVL

CDS SEQ ID NO: 92
ATGGGGGTGGAGATCCTGAGCTCAACGGGGGAACACTCCTCCCAGTACTCTTCCGGAGCCGCGTCCACGGCGACGACGGAGTCAGGC
GTGGGCGGACGGCCGCCGACTGCGCCGAGCCTACCTGTTTCCATCGCCGACGAGTCGGCGACCTCGCGGTCGGCATCGGCGCAGTCG
ACGTCGTCGCGGTTCAAGGGCGTGGTGCCGCAGCCCAACGGGCGGTGGGGCGCCCAGATCTACGAGCGCCACGCCCGCGTCTGGCTC
GGCACGTTCCCGGACGAAGACTCTGCGGCGCGCGCCTACGACGTGGCCGCGCTCCGGTACCGGGGCCGCGAGGCCGCCACCAACTTC
CCGTGCGCGGCCGCCGAGGCGGAGCTCGCCTTCCTGGCGGCACACTCCAAGGCCGAGATCGTCGACATGCTCCGGAAGCACACCTAC
ACCGACGAGCTCCGCCAGGGCCTGCGGCGCGGCCGCGGCATGGGGGCGCGCGCGCAGCCGACGCCGTCGTGGGCGCGGGAGCCCCTT
TTCGAGAAGGCCGTGACCCCGAGCGACGTGGGCAAGCTCAACCGCCTCGTTGTGCCGAAGCAGCACGCCGAGAAGCACTTCCCCCTG
AAACGCACGCCGGAGACGACAACGACCACCGGCAAGGGGGTGCTTCTCAACTTCGAGGATGGCGAGGGGAAAGTGTGGAGGTTCCGG
TACTCGTATTGGAACAGCAGCCAGAGCTACGTGCTCACCAAGGGATGGAGCCGCTTCGTTCGGGAGAAGGGCCTCGGTGCCGGCGAC
TCCATCGTGTTCTCCTGCTCGGCGTACGGTCAGGAGAAGCAGTTCTTCATCGACTGCAAGAAGAACAAGACGATGACGAGCTGCCCC
GCCGATGACCGCGGCGCCGCAACAGCGTCGCCGCCAGTGTCAGAGCCAACAAAAGGAGAACAAGTCCGTGTTGTGAGGCTGTTCGGC
GTCGACATCGCCGGAGAGAAGAGGGGGCGAGCGGCGCCGGTGGAGCAGGAGTTGTTCAAGAGGCAATGCGTGGCACACAGCCAGCAC
TCTCCAGCCCTAGGTGCCTTCGTCTTATAG

MLOC_56567
Cover 42%   identity 59%

SEQ ID NO: 93
MGVEILSSMVEHSFQYSSGASSATAESGAVGTPPRHLSLPVAIADESLTSRSASSRFKGVVPQPNGRWGAQIYERHARVWLGTFPDQ
DSAARAYDVASLRYRGGDAAFNFPCVVVEAELAFLAAHSKAEIVDMLRKQTYADELRQGLRRGRGMGVRAQPMPSWARVPLFEKAVT
PSDVGKLNRLVVPKQHAEKHFPLKRSPETTTTTGNGVLLNFEDGQGKVWRFRYSYWNSSQSYVLTKGWSRFVREKGLGAGDSIMFSC
SAYGQEKQFFIDCKKNTTVNGGKSASPLQVMEIAKAEQVRVVRLFGVDIAGVKRERAATAEQGPQGWFKRQCMAHGQHSPALGDFAL

-continued

Identtty of homologs to NGAL2 is tndtcated

SEQ ID NO: 94
ATGGGGGTGGAGATCCTGAGCTCCATGGTGGAGCACTCCTTCCAGTACTCTTCGGGCGCGTCCTCGGCCACCGCGGAGTCAGGCGCC
GTCGGAACACCGCCGAGGCATCTGAGCCTACCTGTCGCCATCGCCGACGAGTCCCTGACCTCACGGTCGGCGTCGTCTCGGTTCAAG
GGCGTGGTGCCGCAGCCCAACGGGCGGTGGGGCGCCCAGATCTACGAGCGCCACGCTCGCGTCTGGCTCGGCACGTTCCCAGACCAG
GACTCGGCGGCGCGCGCCTACGACGTTGCCTCGCTCAGGTACCGCGGCGGCGACGCCGCCTTCAACTTCCCGTGCGTGGTGGTGGAG
GCGGAGCTCGCCTTCCTGGCGGCGCACTCCAAGGCTGAGATCGTTGACATGCTCCGGAAGCAGACCTACGCCGATGAACTCCGCCAG
GGACTACGGCGCGGCCGTGGCATGGGGGTGCGCGCGCAGCCGATGCCGTCGTGGGCGCGGGTTCCCCTTTTCGAGAAGGCCGTGACC
CCTAGCGATGTCGGCAAGCTCAATCGCCTGGTGGTGCCGAAGCAGCACGCCGAGAAGCACTTCCCCCTGAAGCGCAGCCCGGAGACG
ACGACCACCACCGGCAACGGCGTACTGCTCAACTTTGAGGACGGCCAGGGAAAAGTGTGGAGGTTCCGGTACTCATATTGGAACAGC
AGCCAGAGCTACGTGCTCACCAAAGGCTGGAGCCGCTTCGTCCGGGAGAAGGGCCTCGGCGCCGGTGACTCCATCATGTTCTCCTGC
TCGGCGTACGGGCAGGAGAAGCAGTTCTTCATCGACTGCAAGAAGAACACGACCGTGAACGGAGGCAAATCGGCGTCGCCGCTGCAG
GTGATGGAGATTGCCAAAGCAGAACAAGTCCGCGTCGTTAGACTGTTCGGTGTCGACATCGCCGGGGTGAAGAGGGAGCGAGCGGCG
ACGGCGGAGCAAGGCCCGCAGGGGTGGTTCAAGAGGCAATGCATGGCACACGGCCAGCACTCTCCTGCCCTAGGTGACTTCGCCTTA
TAG

MLOC_75135
Cover 43%   identity 57%

SEQ ID NO: 95
MGMEILSSTVEHCSQYSSSASTATTESGAAGRSTTALSLPVAITDESVTSRSASAQPASSRFKGVVPQPNGRWGSQIYERHARVWLG
TFPDQDSAARAYDVASLRYRGRDAATNFPCAAAEAELAFLTAHSKAEIVDMLRKHTYADELRQGLRRGRGMGARAQPTPSWARVPLF
EKAVTPSDVGKLNRLVVPKQHAEKHFPLKCTAETTTTTGNGVLLNFEDGEGKVWRFRYSYWNSSQSYVLTKGWSSFVREKGLGAGDS
IVFSSSAYGQEKQLFINCKKNTTMNGGKTALPLPVVETAKGEQDHVVKLFGVDIAGVKRVRAATGELGPPELFKRQSVAHGCGRMNY
ICYSIGTIGPLMLN

SEQ ID NO: 96
ATGGGGATGGAAATCCTGAGCTCCACGGTGGAGCACTGCTCCCAGTACTCTTCCAGCGCGTCCACGGCCACAACGGAGTCAGGCGCC
GCCGGAAGATCGACGACGGCTCTGAGCCTACCAGTTGCCATCACCGACGAGTCCGTTACCTCGCGGTCGGCATCGGCGCAGCCGGCG
TCATCACGGTTCAAGGGCGTGGTGCCGCAGCCCAACGGGCGGTGGGGCTCCCAGATCTACGAGCGCCACGCTCGCGTCTGGCTCGGC
ACCTTCCCGGATCAGGACTCGGCGGCGCGTGCCTACGACGTTGCCTCGCTCAGGTACCGGGGCCGCGATGCCGCCACCAACTTCCCG
TGCGCCGCTGCGGAAGCGGAGCTCGCCTTCCTGACCGCGCACTCCAAGGCCGAGATCGTCGACATGCTCCGGAAGCACACCTACGCC
GACGAACTCCGCCAGGGCCTGCGGCGCGGCCGCGGCATGGGTGCGCGCGCGCAGCCGACGCCGTCGTGGGCGCGGGTTCCCCTTTTC
GAGAAGGCTGTGACCCCTAGCGATGTCGGCAAGCTCAATCGCCTGGTGGTGCCGAAGCAGCACGCCGAGAAGCACTTCCCCCTGAAG
TGCACCGCAGAGACGACGACCACCACCGGCAACGGCGTGCTGCTAAACTTCGAGGATGGTGAGGGGAAGGTGTGGAGGTTCCGGTAC
TCGTATTGGAACAGTAGCCAGAGCTACGTGCTCACCAAAGGCTGGAGCAGCTTCGTCCGGGAGAAGGGCCTCGGCGCAGGCGACTCC
ATCGTCTTCTCCTCCTCGGCGTACGGGCAGGAGAAGCAGTTATTCATCAACTGCAAAAAGAACACGACTATGAACGGCGGCAAAACA
GCGTTGCCGCTGCCAGTGGTGGAGACTGCCAAAGGAGAACAAGACCACGTCGTTAAGTTGTTCGGTGTTGACATCGCCGGTGTGAAG
AGGGTGCGAGCGGCGACGGGGGAGCTAGGCCCGCCGGAGTTGTTCAAGAGACAATCCGTGGCACACGGATGCGGAAGGATGAACTAC
ATTTGCTACTCCATAGGGACAATAGGACCTCTTATGCTCAACTGA

MLOC_63261
Cover 49%   identity 51%

SEQ ID NO: 97
MASSKPTNPEVDNDMECSSPESGAEDAVESSSPVAAPSSRFKGVVPQPNGRWGAQIYEKHSRVWLGTFGDEEAAACAYDVAALRFRG
RDAVTNHQRLPAAEGAGWSSTSELAFLADHSKAEIVDMLRKHTYDDELRQGLRRGHGRAQPTPAWAREFLFEKALTPSDVGKLNRLV
VPKQHAEKHFPPTTAAAAGSDGKGLLLNFEDGQGKVWRFRYSYWNSSQSYVLTKGWSRFVQEKGLCAGDTVTFSRSAYVMNDTDEQL
FIDYKQSSKNDEAADVATADENEAGHVAVKLFGVDIGWAGMAGSSGG

SEQ ID NO: 98
ATGGCGTCTAGCAAGCCGACAAACCCCGAGGTAGACAATGACATGGAGTGCTCCTCCCCGGAATCGGGTGCCGAGGACGCCGTGGAG
TCGTCGTCGCCGGTGGCAGCGCCATCTTCGCGGTTCAAGGGCGTCGTGCCGCAGCCTAACGGGCGCTGGGGCGCGCAGATCTACGAG
AAGCACTCGCGGGTGTGGCTTGGCACGTTCGGGGACGAGGAAGCCGCCGCGTGCGCCTACGACGTGGCCGCGCTCCGCTTCCGCGGC
CGCGACGCCGTCACCAACCACCAGCGCCTGCCGGCGGCGGAGGGGGCCGGCTGGTCGTCCACGAGCGAGCTCGCCTTCCTCGCCGAC
CACTCCAAGGCCGAGATCGTCGACATGCTCCGGAAGCACACCTACGACGACGAGCTCCGGCAGGGCCTGCGCCGCGGCCACGGGCGC
GCGCAGCCCACGCCGGCGTGGGCGCGAGAGTTCCTCTTCGAGAAGGCCCTGACCCCGAGCGACGTCGGCAAGCTCAACCGCCTGGTC
GTTCCGAAGCAGCACGCCGAGAAGCACTTCCCCCCGACGACGGCGGCGGCCGCCGGAAGCGACGGCAAGGGCTTGCTGCTCAACTTC
GAGGACGGCCAAGGGAAGGTGTGGAGGTTCCGGTACTCATACTGGAACAGCAGCCAGAGCTACGTGCTCACCAAGGGCTGGAGCCGC
TTCGTCCAAGAAAAGGGCCTCTGCGCCGGCGACACCGTGACGTTCTCCCGGTCGGCGTACGTGATGAATGACACGGATGAGCAGCTC
TTCATCGACTACAAGCAGAGTAGCAAGAACGACGAAGCGGCCGACGTAGCCACTGCCGATGAGAATGAGGCCGGCCATGTCGCCGTG
AAGCTCTTCGGGGTCGACATTGGCTGGGCTGGGATGGCGGGATCATCAGGTGGGTGA

MLOC_64708
Cover 49%   identity 51%

SEQ ID NO: 99
MLFDSSVSASLGTMRPLVKKLDMLLAPARGYSTLCKRIKEVMHLLKHDVEEISSYLDELTEVEDPPPMAKCWMNEARDLSYDMEDYI
DSLLFVPPGHFIKKKKKKKKGKKKMVIKKRLKWCKQIVFTKQVSDHGIKTSKIIHVNVPRLPNKPKVAKIILQFRIYVQEAIERYD
KYRLHHCSTLRRRLLSTGSMLSVPIPYEEAAQIVTDGRMNEFISSLAANNAADQQQLKVVSVLGSGCLGKTTLANVLYDRIGMQFEC
RAFIRVSKKPDMKRLFRDLLSQFHQKQPLPTSCNELGISDNIIKHLQDKRYLIVIDDLWDLSVWDIIKYAFPKGNHGSRIIITTQIE
DVALTCCCDHSEHVFEMKPLNIGHSRELFFNRLFGSESDCLEEFKRVSNEIVDICGGLPLATINIASHLANQETEVSLDLLTDTRDL
LRSCLWSNSTSERTKQVLNLSYSNLPDYLKTCLLYLHMYPVGSIIWKDDLVKQLVAEGFIATREGKDQDQEMIEKAAGLCFDALIDR
RFIQPIYTKYNNKVLSCTVHEVVHDLIAQKSAEENFIVVADHNRKNIALSHKVRRLSLIFGDTIYAKTPANITKSQIRSFRFFGLFE
CMPCITEFKVLRVLNLQLSGHRGDNDPIDLTGISELFQLRYLKITSDVCIKLPNQMQKLQYLETLDIMDAPRVTAVPWDIINLPHLL

-continued

Identtty of homologs to NGAL2 is tndtcated

HLTLPVDTYLLDWISSMTDSVISLWTLGKLNYLQHLHLTSSSTRPSYHLERSVEALGYLIGGHGKLKTIVVAHVSSAQNTVVRGAPE
VTISWDRMSPPPLLQRFECPHSCFIFYRIPKWVTELGNLCILKIAVKELHMICLGTLRGLHALTDLSLYVETAPIDKIIFDKAGFSV
LKYCKLRFAAGIAWLKFEADAMPSLWKLMLVFNAIPRMDQNLVFFHHSRPAMHQRGGAVIIVEHMPGLRVISAKFGGAASDLEYASR
TVVSNHPSNPTINMQLVCYSSNGKRSRKRKQQPYDVVKGQPDEYAKRLERPAEKRISTPTKSSLRLHVPEITPKPMQITDNNVCIRR
EHMFDTVLTRGDVGMLNRLVVPKKHAEKYFPLDSSSTRTSKAIVLSFEDPAGKSWFFHYSYRSSSQNYVMFKGWTGFVKEKFLEAGD
TVSFSRGVGEATRGRLFIDCQNEQRYMFERVLTASDMESDGCSLMVPVNLVWPHPGLRKTIKGRHAVLQFEDGSGNGKVWPFQFEAS
GQYYLMKGLNYFVNDRDLAAGYTVSFYRAGTRLFVDSGRKDDKVALGTRSRERIYPKIVRSQ

Brassica rapa

LOC103849927
Cover 99%   ident 80%

CDS SEQ ID NO: 100
ATGTTGTTTGATAGTTCAGTGAGTGCTTCGTTGGGCACCATGAGACCACTTGTCAAGAAGCTCGACATGCTGCTAGCTCCTGCTCGG
GGATACAGTACCTTGTGCAAGAGGATCAAGGAAGTGATGCACCTTCTCAAACATGATGTTGAAGAGATAAGCTCCTACCTTGATGAA
CTTACAGAGGTGGAGGACCCTCCACCAATGGCCAAGTGCTGGATGAACGAGGCACGCGACCTGTCTTATGATATGGAGGATTACATT
GATAGCTTGTTATTTGTGCCACCTGGCCATTTCATCAAGAAGAAGAAGAAGAAGAAGAAGAAGGGAAAGAAGAAGATGGTGATAAAG
AAGAGGCTCAAGTGGTGCAAACAGATCGTATTCACAAAGCAAGTGTCAGACCATGGTATCAAGACCAGTAAAATCATTCATGTTAAT
GTCCCTCGTCTTCCCAATAAGCCCAAGGTTGCAAAAATAATATTACAGTTCAGGATCTATGTCCAGGAGGCTATTGAACGGTATGAC
AAGTATAGGCTTCACCATTGCAGCACCTTGAGGCGTAGATTGTTGTCCACTGGTAGTATGCTTTCAGTGCCAATACCCTATGAAGAA
GCTGCCCAAATTGTAACTGATGGCCGGATGAATGAGTTTATCAGCTCACTGGCTGCTAATAATGCAGCAGATCAGCAGCAGCTCAAG
GTGGTATCTGTTCTTGGATCTGGGTGTCTAGGTAAAACTACGCTTGCGAATGTGTTGTACGACAGAATTGGGATGCAATTCGAATGC
AGAGCTTTCATTCGAGTGTCCAAAAAGCCTGATATGAAGAGACTTTTCCGTGACTTGCTCTCGCAATTCCACCAGAAGCAGCCACTG
CCTACCAGTTGTAATGAGCTTGGCATAAGTGACAATATCATCAAACATCTGCAAGATAAAAGGTATCTAATTGTTATTGATGATTTG
TGGGATTTATCAGTATGGGATATTATTAAATATGCTTTTCCAAAGGGAAACCATGGAAGCAGAATAATAATAACTACACAGATTGAA
GATGTTGCATTAACTTGTTGCTGTGATCACTCGGAGCATGTTTTCGAGATGAAACCTCTCAACATTGGTCACTCAAGAGAGCTATTT
TTTAATAGACTTTTTGGTTCTGAAAGTGACTGTCTTGAAGAATTCAAACGAGTTTCAAACGAAATTGTTGATATATGTGGTGGTTTA
CCGCTAGCAACAATCAACATAGCTAGTCATTTGGCAAACCAGGAGACAGAAGTATCATTGGATTTGCTAACAGACACACGTGATTTG
TTGAGGTCCTGTTTGTGGTCAAATTCTACTTCAGAAAGAACAAAACAAGTACTGAACCTCAGCTACAGTAATCTTCCTGATTATCTG
AAGACATGTTTGCTGTATCTTCATATGTATCCAGTGGGCTCCATAATCTGGAAGGATGATCTGGTGAAGCAATTGGTGGCTGAAGGG
TTTATTGCTACAAGAGAAGGGAAAGACCAAGACCAAGAAATGATAGAGAAAGCTGCAGGACTCTGTTTCGATGCACTTATTGATAGA
AGATTCATCCAGCCTATATATACCAAGTACAACAATAAGGTGTTGTCCTGCACGGTTCATGAGGTGGTACATGATCTTATTGCCCAA
AAGTCTGCTGAAGAGAATTTCATTGTGGTAGCAGACCACAATCGAAAGAATATAGCACTTTCTCATAAGGTTCGTCGACTATCTCTC
ATCTTTGGCGACACAATATATGCCAAGACACCAGCAAACATCACAAAGTCACAAATTCGGTCATTCAGATTTTTTGGATTATTCGAG
TGTATGCCTTGTATTACAGAGTTCAAGGTTCTCCGTGTTCTAAACCTTCAACTATCTGGTCATCGTGGGGACAATGACCCTATAGAC
CTCACTGGGATTTCAGAACTGTTTCAGCTGAGATATTTAAAGATTACAAGTGATGTGTGCATAAAACTACCAAATCAAATGCAAAAA
CTGCAATATTTGGAAACGTTGGACATTATGGATGCACCAAGAGTCACTGCTGTTCCATGGGATATTATAAATCTCCCACACCTGTTG
CACCTGACTCTTCCTGTTGATACATATCTGCTGGATTGGATTAGCAGCATGACTGACTCCGTCATCAGTCTGTGGACCCTTGGCAAG
CTGAACTACCTGCAGCATCTTCATCTTACTAGTTCTTCTACACGTCCTTCATACCATCTGGAGAGAAGTGTGGAGGCTCTGGGTTAT
TTGATCGGAGGACATGGCAAGCTGAAAACTATAGTAGTCGCTCATGTCTCCTCTGCTCAAAATACTGTGGTTCGTGGCGCCCCAGAA
GTAACCATTTCATGGGATCGTATGTCACCTCCCCCCCTTCTCCAGAGATTCGAATGCCCACACAGCTGCTTCATATTTTACCGAATT
CCTAAGTGGGTTACAGAACTTGGCAACCTGTGCATTTTGAAGATTGCAGTGAAGGAGCTTCATATGATTTGTCTTGGTACTCTCAGA
GGATTGCATGCCCTCACTGATCTGTCGCTGTATGTGGAGACAGCGCCCATTGACAAGATCATCTTTGACAAGGCCGGGTTCTCAGTT
CTCAAGTACTGCAAATTGCGCTTCGCGGCTGGTATAGCTTGGCTGAAATTTGAGGCTGATGCAATGCCTAGTCTATGGAAACTGATG
CTAGTTTTCAACGCCATCCCACGAATGGACCAAAATCTTGTTTTCTTTCACCACAGCCGACCGGCGATGCATCAACGTGGTGGTGCA
GTAATCATTGTCGAGCATATGCCAGGGCTTAGAGTGATCTCCGCAAAATTTGGGGGCGCAGCTTCTGATCTAGAGTATGCTTCGAGG
ACCGTCGTTAGTAACCATCCAAGCAATCCTACAATCAACATGCAATTGGTGTGTTATAGTTCCAATGGTAAGAGAAGCAGAAAAAGG
AAACAACAACCTTACGACGTTGTGAAGGGACAACCAGATGAATACGCCAAGAGATTGGAGAGACCAGCTGAGAAAAGGATTTCAACG
CCGACAAAGTCTTCTTTGCGTCTGCATGTTCCAGAAATTACACCAAAACCTATGCAGATTACAGACAACAATGTTCAGAGGAGGGAG
CACATGTTCGATACGGTTCTGACTCGGGGGGACGTGGGGATGCTGAACCGGCTGGTGGTACCGAAGAAGCACGCGGAGAAGTACTTC
CCGCTGGACAGTTCCTCCACCCGCACCAGCAAGGCCATCGTACTCAGCTTTGAGGACCCTGCTGGGAAGTCATGGTTCTTCCACTAC
TCCTACCGGAGCAGCAGCCAGAACTACGTCATGTTCAAGGGGTGGACTGGCTTCGTCAAGGAGAAGTTTCTCGAAGCCGGCGACACC
GTCTCCTTCAGCCGCGGCGTCGGGGAGGCCACGAGGGGGAGGCTCTTCATCGACTGTCAAAATGAGCAGAGGTACATGTTCGAGCGA
GTGCTGACGGCGAGTGATATGGAGTCGGATGGCTGCTCGCTGATGGTCCCAGTGAACTTGGTGTGGCCGCACCCCGGCCTCCGCAAG
ACGATCAAGGGGAGGCACGCCGTGCTGCAGTTTGAGGACGGCAGCGGCAACGGGAAGGTGTGGCCATTTCAGTTTGAGGCCTCCGGC
CAATACTATCTCATGAAGGGCTTGAACTACTTTGTTAACGACCGCGACCTTGCGGCTGGCTATACCGTCTCCTTCTACCGCGCCGGC
ACGCGGTTGTTCGTCGACTCCGGGCGTAAAGATGACAAAGTAGCCTTGGGAACCAGAAGCCGCGAAAGGATCTATCCTAAGATCGTG
CGGTCGCAGTAG

LOC103849927

SEQ ID NO: 101
msgnhysrdihhntpsvhhhqnyavvdreylfeksltpsdvgklnrlvipkqhaekhfplnnagddvaaaettekgmlltfedesgk
cwkfrysywnssqsyvltkgwsryvkdkhlhagdvvffqrhrfdlhrvfigwrkrgevssptavsvvsqearvnttaywsglttpyr
qvhastssypnihqeyshygavaeiptvvtgssrtvrlfgvnlechgdvvetppcpdgyngqhfyyystpdpmnisfageameqvgd
grr

-continued

Identtty of homologs to NGAL2 is tndtcated

Bra034828
Cover 100%   identity 79%

SEQ ID NO: 102
MSVNHYSNTLSSHNHHNEHKESLFEKSLTPSDVGKLNRLVIPKQHAERYLPLNNCGGGGDVTAESTEKGVLLSFEDESGKSWKFRYS
YWNSSQSYVLTKGWSRYVKDKHLNAGDVVLFQRHRFDIHRLFIGWRRRGEASSSSAVSAVTQDPRANTTAYWNGLTTPYRQVHASTS
SYPNNIHQEYSHYGPVAETPTVAAGSSKTVRLFGVNLECHSDVVEPPPCPDAYNGQHIYYYSTPHPMNISFAGEAMEQVGDGRG

CDS SEQ ID NO: 103
ATGTCAGTCAACCATTACTCAAACACTCTCTCGTCGCACAATCACCACAACGAACATAAAGAGTCTTTGTTCGAGAAGTCACTCACG
CCAAGCGATGTTGGAAAGCTAAACCGTTTAGTCATACCAAAACAACACGCCGAGAGATACCTCCCTCTCAATAATTGCGGCGGCGGC
GGCGACGTGACGGCGGAGTCGACGGAGAAAGGGGTGCTTCTCAGCTTCGAGGACGAGTCGGGAAAATCTTGGAAATTCAGATACTCA
TATTGGAACAGTAGTCAAAGCTACGTGTTGACCAAAGGATGGAGCAGGTACGTCAAAGACAAGCACCTCAACGCAGGGGACGTCGTT
TTATTTCAACGGCACCGTTTTGATATTCATAGACTCTTCATTGGCTGGAGGAGACGCGGAGAGGCTTCTTCCTCTTCCGCCGTTTCC
GCCGTGACTCAAGATCCTCGAGCTAACACGACGGCGTACTGGAACGGTTTGACTACACCTTATCGTCAAGTACACGCGTCAACTAGT
TCTTACCCTAACAACATCCACCAAGAGTATTCACATTATGGCCCTGTTGCTGAGACACCGACGGTAGCTGCAGGGAGCTCGAAGACG
GTGAGGCTATTTGGAGTTAACCTCGAATGTCACAGTGACGTTGTGGAGCCACCACCGTGTCCTGACGCCTACAACGGCCAACACATT
TACTATTACTCAACTCCACATCCCATGAATATCTCATTTGCTGGAGAAGCAATGGAGCAGGTAGGAGATGGACGAGGTTGA

Bra005886
Cover 100%   identity 79%

SEQ ID NO: 104
MSVNHYSTDHHQVHHHHTLFLQNLHTTDTSEPTTTAATSLREDQKEYLFEKSLTPSDVGKLNRLVIPKQHAEKYFPLNTIISNNAEE
KGMLLSFEDESGKCWRFRYSYWNSSQSYVLTKGWSRYVKDKQLDPADVVFFQRQRSDSRRLFIGWRRRGQGSSSAANTTSYSSSMTA
PPYSNYSNRPAHSEYSHYGAAVATATETHFIPSSSAVGSSRTVRLFGVNLECQMDEDEGDDSVATAAAAECPRQDSYYDQNMYNYYT
PHSSAS

CDS 105
ATGTCAGTCAACCATTACTCCACGGACCACCACCAGGTCCACCACCACCACACTCTCTTCTTGCAGAACCTCCACACCACCGACACA
TCGGAGCCAACCACAACCGCCGCCACATCACTCCGCGAAGACCAGAAAGAGTATCTCTTCGAGAAATCTCTCACACCAAGCGACGTT
GGCAAACTCAACCGTCTCGTTATACCAAAACAGCACGCGGAGAAGTACTTCCCTCTCAACACCATCATCTCCAATAATGCTGAGGAG
AAAGGGATGCTTCTAAGCTTCGAAGACGAGTCAGGCAAGTGCTGGAGGTTCAGATACTCTTACTGGAACAGCAGTCAAAGCTACGTG
TTGACTAAAGGATGGAGCAGATACGTCAAAGACAAACAGCTCGACCCAGCCGATGTTGTTTTCTTCCAACGTCAACGTTCTGATTCC
CGGAGACTCTTTATTGGCTGGCGTAGACGCGGTCAAGGCTCCTCCTCCGCCGCGAATACGACGTCGTATTCTAGTTCCATGACTGCT
CCACCGTATAGTAATTACTCTAATCGTCCTGCTCACTCAGAGTATTCCCACTATGGCGCCGCCGTAGCAACAGCGACGGAGACGCAC
TTCATACCATCGTCTTCCGCCGTCGGGAGCTCGAGGACGGTGAGGCTTTTTGGTGTGAATTTGGAGTGTCAAATGGATGAAGACGAA
GGAGATGATTCGGTTGCCACGGCAGCCGCCGCTGAGTGTCCTCGTCAGGACAGCTACTACGACCAAAACATGTACAATTATTACACT
CCTCACTCCTCAGCCTCATAA

Bra005301
Cover 100%   identity 58%

SEQ ID NO: 106
MSINQYSSDFNYHSLMWQQQQHRHHHHQNDVAEEKEALFEKPLTPSDVGKLNRLVIPKQHAERYFPLAAAAADAMEKGLLLCFEDEE
GKPWRFRYSYWNSSQSYVLTKGWSRYVKEKQLDAGDVILFHRHRVDGGRFFIGWRRRGNSSSSSDSYRHLQSNASLQYYPHAGVQAV
ESQRGNSKTLRLFGVNMECQLDSDLPDPSTPDGSTICPTSHDQFHLYPQQHYPPPYYMDISFTGDVHQTRSPQG

CDS SEQ ID NO: 107
ATGTCAATAAACCAATACTCAAGCGATTTCAACTACCACTCTCTCATGTGGCAACAACAGCAGCACCGCCACCACCACCATCAAAAC
GACGTCGCGGAGGAAAAAGAAGCTCTTTTCGAGAAACCCTTAACCCCAAGTGACGTCGGAAAACTCAACCGCCTCGTCATCCCAAAA
CAGCACGCCGAGAGATACTTCCCTCTCGCAGCAGCCGCCGCAGACGCGATGGAGAAGGGATTACTTCTCTGCTTCGAGGACGAGGAA
GGTAAGCCATGGAGATTCAGATACTCGTATTGGAACAGTAGCCAGAGTTATGTCTTGACCAAAGGATGGAGCAGATACGTCAAGGAG
AAGCAGCTCGACGCCGGTGACGTCATTCTCTTCCACCGCCACCGTGTTGACGGAGGAAGATTCTTCATTGGCTGGAGAAGACGCGGC
AACTCTTCCTCCTCTTCCGACTCTTATCGCCATCTTCAGTCCAATGCCTCGCTCCAATATTATCCTCATGCAGGAGTTCAAGCGGTG
GAGAGCCAGAGAGGGAATTCGAAGACATTAAGACTGTTCGGAGTGAACATGGAGTGTCAGCTAGACTCCGACTTGCCCGATCCATCT
ACACCAGACGGTTCCACCATATGTCCGACCAGTCACGACCAGTTTCATCTCTACCCTCAACAACACTATCCTCCTCCGTACTACATG
GACATAAGTTTCACAGGAGATGTGCACCAGACGAGAAGCCCACAAGGATAA

Bra017262
Cover 92%   identity 56%

SEQ ID NO: 108
MSINQYSSEFYYHSLMWQQQQQHHHQNEVVEEKEALFEKPLTPSDVGKLNRLVIPKQHAERYFPLAAAAVDAVEKGLLLCFEDEEGK
PWRFRYSYWNSSQSYVLTKGWSRYVKEKQLDAGDVVLFHRHRADGGRFFIGWRRRGDSSSSSDSYRNLQSNSSLQYYPHAGAQAVEN
QRGNSKTLRLFGVNMECQIDSDWSEPSTPDGFTTCPTNHDQFPIYPEHFPPPYYMDVSFTGDVHQTSSQQG

CDS SEQ ID NO: 109
ATGTCAATAAATCAATATTCAAGCGAGTTCTACTACCATTCTCTCATGTGGCAACAACAGCAGCAACACCACCATCAAAACGAAGTC
GTGGAGGAAAAAGAAGCTCTTTTCGAGAAACCCTTAACCCCAAGTGACGTCGGAAAACTAAACCGCCTAGTCATCCCTAAACAGCAC
GCCGAGAGATACTTCCCTCTCGCCGCCGCCGCGGTAGACGCCGTGGAGAAGGGATTACTCCTCTGCTTCGAGGACGAGGAAGGTAAG
CCATGGAGATTCAGATACTCTTATTGGAATAGTAGCCAGAGTTACGTCTTGACCAAAGGATGGAGCAGATATGTTAAAGAGAAGCAA
CTTGACGCCGGCGACGTTGTTCTCTTTCATCGCCACCGTGCTGACGGTGGAAGATTCTTCATTGGCTGGAGAAGACGCGGCGACTCT

-continued

Identtty of homologs to NGAL2 is tndtcated

TCCTCCTCCTCCGACTCTTATCGCAATCTTCAATCTAATTCCTCGCTCCAATATTATCCTCATGCAGGGGCTCAAGCGGTGGAGAAC
CAGAGAGGTAACTCCAAGACATTGAGACTTTTTGGAGTGAACATGGAGTGCCAGATAGACTCAGACTGGTCCGAGCCATCCACACCT
GACGGTTTTACCACATGTCCAACCAATCACGACCAGTTTCCTATCTACCCTGAACACTTTCCTCCTCCGTACTACATGGACGTAAGT
TTCACAGGAGATGTGCACCAGACGAGTAGCCAACAAGGATAG

Bra000434
Cover 96%   identity 47%

SEQ ID NO: 110
MMTNLSLAREGEEEEEEAGAKKPTEEVEREHMFDKVVTPSDVGKLNRLVIPKQHAERYFPLDSSTNEKGLILNFEDLTGKSWRFRYS
YWNSSQSYVMTKGWSRFVKDKKLDAGDIVSFLRCVGDTGRDSRLFIDWRRRPKVPDYTTSTSHFPAGAMFPRFYSFQTATTSTSYNP
YNHQQPRHHHSGYCYPQIPREFGYGYVVRSVDQRAVVADPLVIESVPVMMHGGARVNQAAVGTAGKRLRLFGVDMECGESGGTNSTE
EESSSSGGSLPRGGASPSSSMFQLRLGNSSEDDHLFKKGKSSLPFNLDQ

SEQ ID NO: 111
ATGATGACAAATTTGTCTCTTGCAAGAGAAGGAGAAGAAGAAGAAGAAGAGGCAGGAGCAAAGAAGCCCACAGAAGAAGTGGAGAGA
GAGCACATGTTCGACAAAGTGGTGACTCCAAGTGACGTCGGGAAACTAAACCGACTCGTGATCCCAAAGCAACACGCGGAGAGATAC
TTCCCTTTAGATTCATCCACAAACGAGAAGGGTTTGATTCTAAACTTCGAAGATCTCACGGGAAAGTCATGGAGGTTCCGTTACTCT
TACTGGAACAGCAGTCAGAGCTATGTCATGACTAAAGGTTGGAGCCGTTTCGTTAAAGACAAGAAGCTAGACGCTGGAGATATTGTC
TCTTTCCTGAGATGTGTCGGAGACACAGGAAGGGACAGCCGCTTGTTTATCGATTGGAGGAGACGACCTAAAGTCCCTGACTACACG
ACATCGACTTCTCACTTTCCTGCCGGAGCTATGTTCCCTAGGTTTTACAGTTTTCAGACAGCAACTACTTCCACAAGTTACAATCCC
TATAATCATCAGCAGCCACGTCATCATCACAGTGGTTACTGTTATCCTCAAATCCCGAGAGAATTTGGATATGGGTATGTCGTTAGG
TCAGTAGATCAGAGGGCGGTGGTGGCTGATCCGTTAGTGATCGAATCTGTGCCGGTGATGATGCACGGAGGAGCTCGAGTGAACCAG
GCGGCTGTTGGAACGGCCGGGAAAAGGCTGAGGCTTTTTGGAGTCGATATGGAATGTGGCGAGAGTGGAGGAACAAACAGTACGGAG
GAAGAATCTTCATCTTCCGGTGGGAGTTTGCCACGTGGCGGTGCTTCTCCGTCTTCCTCTATGTTTCAGCTGAGGCTTGGAAACAGC
AGTGAAGATGATCACTTATTTAAGAAAGGAAAGTCTTCATTGCCTTTTAATTTGGATCAATAA

Bra040478
Cover 96%   identity 48%

SEQ ID NO: 112
MMTNLSLAREGEAQVKKPIEEVEREHMFDKVVTPSDVGKLNRLVIPKQHAERYFPLDSSSNEKGLLLNFEDLTGKSWRFRYSYWNSS
QSYVMTKGWSRFVKDKKLDAGDIVSFQRCVGDSRLFIDWRRRPKVPDYPTSTAHFAAGAMFPRFYSFPTATTSTCYDLYNHQPPRHH
HIGYGYPCLIPREFGYGYFVRSVDQRAVVADPLVIESVPVMMRGGARVSQEVVGTAGKRLRLFGVDMEEESSSSGGSLPRAGGGGAS
SSSSLFQLRLGSSCEDDHFSKKGKSSLPFDLDQ

SEQ ID NO: 113
ATGATGACCAACTTGTCTCTTGCAAGGGAAGGAGAAGCACAAGTAAAGAAGCCCATAGAAGAAGTTGAGAGAGAGCACATGTTCGAC
AAAGTGGTGACTCCAAGCGACGTAGGGAAACTAAACAGACTCGTGATCCCAAAGCAACACGCAGAGAGATACTTCCCTCTAGATTCA
TCCTCAAACGAGAAAGGTTTGCTTCTAAACTTTGAAGATCTAACAGGAAAGTCATGGAGGTTCCGTTACTCTTACTGGAACAGTAGC
CAGAGCTATGTCATGACTAAAGGTTGGAGTCGTTTCGTTAAAGACAAGAAGCTTGACGCCGGAGATATTGTCTCTTTCCAGAGATGT
GTCGGAGACAGCCGCTTGTTTATCGATTGGAGGAGACGACCTAAAGTCCCTGACTATCCGACATCGACTGCTCACTTTGCTGCAGGA
GCTATGTTCCCTAGGTTTTACAGTTTTCCGACAGCAACTACTTCGACATGTTACGATCTGTACAATCATCAGCCGCCACGTCATCAT
CACATTGGTTACGGTTATCCACAGATTCCGAGAGAATTTGGATACGGGTATTTCGTTAGGTCAGTGGACCAGAGAGCGGTGGTGGCT
GATCCGTTGGTGATCGAATCTGTGCCGGTGATGATGCGCGGAGGAGCTCGAGTTAGTCAGGAGGTTGTTGGAACGGCCGGGAAGAGG
CTGAGGCTTTTTGGAGTCGATATGGAGGAAGAATCTTCATCTTCCGGTGGGAGTTTGCCGCGTGCCGGAGGTGGCGGTGCTTCTTCA
TCTTCCTCTTTGTTTCAGCTGAGACTTGGGAGCAGCTGTGAAGATGATCACTTCTCTAAGAAAGGAAAGTCTTCATTGCCTTTTGAT
TTGGATCAATAA

Bra004501
Cover 74%   identity 45%

SEQ ID NO: 114
MMMTNLSLSREGEEEEEEEQEEAKKPMEEVEREHMFDKVVTPSDVGKLNRLVIPKQYAERYFPLDSSTNEKGLLLNFEDLAGKSWRF
RYSYWNSSQSYVMTKGWSRFVKDKKLDAGDIVSFQRCVGDSGRDSRLFIDWRRRPKVPDHPTSIAHFAAGSMFPRFYSFPTATSYNL
YNYQQPRHHHHSGYNYPQIPREFGYGYLVDQRAVVADPLVIESVPVMMHGGAQVSQAVVGTAGKRLRLFGVDMEEESSSSGGSLPRG
DASPSSSLFQLRLGSSSEDDHFSKKGKSSLPFDLDQ

SEQ ID NO: 133
ATGATGATGACAAACTTGTCTCTTTCAAGAGAAGGAGAAGAGGAGGAAGAAGAAGAACAAGAAGAGGCCAAGAAGCCCATGGAAGAA
GTAGAGAGAGAGCACATGTTCGACAAAGTGGTGACTCCAAGCGATGTTGGTAAACTAAACCGGCTCGTGATCCCAAAGCAATACGCA
GAGAGATACTTCCCTTTAGATTCATCCACAAACGAGAAAGGTTTGCTTCTAAACTTCGAAGATCTCGCAGGAAAGTCATGGAGGTTC
CGTTACTCTTACTGGAACAGTAGTCAGAGCTATGTCATGACTAAAGGTTGGAGCCGTTTCGTTAAAGACAAAAAGCTAGACGCCGGA
GATATTGTCTCTTTCCAGAGATGTGTCGGAGATTCAGGAAGAGACAGCCGCTTGTTTATTGATTGGAGGAGAAGACCTAAAGTTCCT
GACCATCCGACATCGATTGCTCACTTTGCTGCCGGATCTATGTTTCCTAGGTTTTACAGTTTTCCGACAGCAACTAGTTACAATCTT
TACAACTATCAGCAGCCACGTCATCATCATCACAGTGGTTATAATTATCCTCAAATTCCGAGAGAATTTGGATACGGGTACTTGGTG
GATCAAAGAGCCGTGGTGGCTGATCCGTTGGTGATTGAATCTGTGCCGGTGATGATGCACGGAGGAGCTCAAGTTAGTCAGGCGGTT

-continued

Identtty of homologs to NGAL2 is tndtcated

GTTGGAACGGCCGGGAAGAGGCTGAGGCTTTTTGGAGTCGATATGGAGGAAGAATCTTCATCTTCCGGTGGGAGTTTGCCACGTGGT
GACGCTTCTCCGTCTTCCTCTTTGTTTCAGCTGAGACTTGGAAGCAGCAGTGAAGATGATCACTTCTCTAAGAAAGGAAAGTCCTCA
TTGCCTTTTGATTTGGATCAATAA

Bra003482
Cover 79%   identity 44%

SEQ ID NO: 115
MNQEEENPVEKASSMEREHMFEKVVTPSDVGKLNRLVIPKQHAERYFPLDNNSDSSKGLLLNFEDRTGNSWRFRYSYWNSSQSYVMT
KGWSRFVKDKKLDAGDIVSFQRDPGNKDKLFIDWRRRPKIPDHHHQFAGAMFPRFYSFSHPQNLYHRYQQDLGIGYYVSSMERNDPT
AVIESVPLIMQRRAAHVAAIPSSRGEKRLRLFGVDMECGGGGGSVNSTEEESSSSGGGGGVSMASVGSLLQLRLVSSDDESLVAMEA
ASVDEDHHLFTKKGKSSLSFDLDRK

SEQ ID NO: 116
ATGAATCAAGAAGAAGAGAATCCTGTGGAAAAAGCCTCTTCAATGGAGAGAGAGCACATGTTTGAAAAAGTAGTAACACCAAGCGAC
GTAGGCAAACTAAACCGACTCGTGATCCCAAAGCAACACGCGGAGAGATACTTCCCTTTAGACAACAATTCTGACAGCAGCAAAGGT
TTGCTTCTAAACTTCGAAGACCGAACAGGAAACTCATGGAGATTCCGTTACTCTTACTGGAACAGTAGCCAGAGTTATGTCATGACA
AAAGGTTGGAGCCGCTTCGTCAAAGACAAGAAGCTTGATGCTGGCGACATCGTTTCTTTTCAGAGAGATCCTGGTAATAAAGACAAG
CTTTTCATTGATTGGAGGAGACGACCAAAGATTCCAGATCATCATCATCAATTCGCTGGAGCTATGTTCCCTAGGTTTTACTCTTTC
TCTCATCCTCAGAACCTTTATCATCGATATCAACAAGATCTTGGAATTGGGTATTATGTGAGTTCAATGGAGAGAAATGATCCAACG
GCTGTAATTGAATCTGTGCCGTTGATAATGCAAAGGAGAGCAGCACACGTGGCTGCTATACCTTCATCAAGAGGAGAGAAGAGGTTA
AGGCTGTTTGGAGTGGACATGGAGTGCGGCGGCGGCGGAGGAAGTGTGAATAGCACGGAGGAAGAGTCGTCGTCTTCCGGTGGTGGC
GGCGGCGTTTCTATGGCTAGTGTTGGTTCTCTTCTCCAATTGAGGCTAGTGAGCAGTGATGATGAGTCTTTGGTAGCAATGGAAGCT
GCAAGTGTCGATGAGGATCATCACTTGTTTACAAAGAAAGGAAAGTCTTCTTTGTCTTTCGATTTGGATAGAAAATGA

Bra007646
Cover 74%   identity 45%

SEQ ID NO: 117
MNQENKKPLEEASTSMERENMFDKVVTPSDVGKLNRLVIPKQHAERYFPLDNSSTNNKGLLLDFEDRTGSSWRFRYSYWNSSQSYVM
TKGWSRFVKDKKLDAGDIVSFQRDPCNKDKLYIDWRRRPKIPDHHQFAGAMFPRFYSFPHPQMPTSFESSHNLYHHRFQRDLGIGYY
PTAVIESVPVIMQRREAQVANMASSRGEKRLRLFGVDVECGGGGGGSVNSTEEESSSSGGSMSRGGVSMAGVGSLLQLRLVSSDDES
LVAMEGATVDEDHHLFTTKKGKSSLSFDLDI

CDS SEQ ID NO: 118
ATGAATCAAGAAAACAAGAAGCCTTTGGAAGAAGCTTCGACTTCAATGGAGAGAGAGAACATGTTCGACAAAGTAGTAACACCAAGC
GACGTAGGGAAACTAAACCGACTCGTGATCCCAAAGCAACACGCAGAGAGATACTTCCCTTTAGACAACTCCTCAACAAACAACAAA
GGGTTGCTTCTAGACTTCGAAGACCGTACAGGAAGCTCATGGAGATTCCGTTACTCTTACTGGAACAGTAGCCAAAGTTATGTCATG
ACAAAAGGTTGGAGCCGTTTTGTCAAAGACAAGAAGCTTGATGCTGGTGACATCGTGTCTTTTCAAAGAGATCCCTGTAATAAAGAC
AAGCTTTACATAGATTGGAGGAGACGACCAAAGATTCCAGATCATCATCAGTTCGCCGGAGCTATGTTCCCTAGGTTTTACTCTTTC
CCTCACCCTCAGATGCCGACAAGTTTTGAAAGTAGTCACAACCTTTATCATCATCGGTTTCAACGAGATCTTGGAATTGGGTATTAT
CCAACGGCTGTGATTGAATCTGTGCCGGTGATAATGCAAAGGAGAGAAGCACAAGTGGCTAATATGGCTTCATCAAGAGGAGAGAAG
AGGTTAAGGCTGTTTGGAGTGGACGTGGAGTGCGGCGGCGGAGGAGGAGGAAGTGTGAATAGCACGGAGGAAGAGTCGTCGTCTTCC
GGTGGTAGTATGTCACGTGGCGGCGTTTCTATGGCTGGTGTTGGTTCTCTCCTTCAGTTGAGGTTAGTGAGCAGTGATGATGAGTCT
TTAGTAGCGATGGAAGGTGCTACTGTCGATGAGGATCATCACTTGTTTACAACTAAGAAAGGAAAGTCTTCTTTGTCTTTCGATTTG
GATATATGA

Bra014415
Cover 48%   identity 60%

SEQ ID NO: 119
MERKSNDLERSENIDSQNKKMNLEEERPVQEASSMEREHMFDKVVTPSDVGKLNRLVIPKQHAERYFPLDNNSSDNNKGLLLNFEDR
IGILWSFRYSYWNSSQSYVMTKGWSRFVKDKKLDAGDIVSFHRGSCNKDKLFIDWKRRPKIPDHQVVGAMFPRFYSYPYPQIQASYE
RHNLYHRYQRDIGIGYYVRSMERYDPTAVIESVPVIMQRRAHVATMASSRGEKRLRLFGVDMECVRGGRGGGGSVNSTEEESSTSGG
SISRGGVSMAGVGSPLQLRLVSSDGDDQSLVARGAARVDEDHHLFTKKGKSSLSFDLDK

CDS SEQ ID NO: 120
ATGGAGAGGAAGTCCAATGATCTTGAGAGATCTGAGAATATTGATTCTCAAAACAAGAAGATGAATCTAGAAGAAGAGAGGCCTGTA
CAAGAAGCTTCTTCGATGGAGAGAGAGCACATGTTCGACAAAGTAGTAACACCAAGCGACGTTGGGAAACTAAACCGGCTGGTGATC
CCAAAGCAACACGCAGAGCGATACTTCCCTTTAGACAATAATTCCTCAGACAACAACAAAGGTTTGCTTCTAAACTTCGAAGATCGA
ATAGGAATCTTATGGAGTTTCCGTTACTCCTACTGGAACAGTAGCCAAAGTTATGTAATGACTAAAGGCTGGAGCCGTTTCGTCAAA
GACAAGAAGCTTGATGCTGGCGACATAGTTTCTTTTCATAGAGGTTCTTGTAATAAAGACAAGCTTTTCATTGATTGGAAGAGACGA
CCAAAGATTCCTGATCACCAAGTCGTCGGAGCTATGTTCCCTAGGTTTTACTCTTACCCTTATCCTCAGATACAGGCTAGTTATGAA
CGTCACAACCTTTATCATCGATATCAACGAGATATAGGAATTGGGTATTATGTGAGGTCAATGGAGAGATATGATCCAACGGCTGTA
ATTGAATCTGTGCCGGTGATAATGCAAAGGAGAGCACATGTGGCTACTATGGCTTCATCAAGAGGAGAGAAGAGGTTAAGGCTTTTT
GGAGTGGATATGGAGTGCGTCAGAGGCGGCCGAGGAGGAGGAGGAAGTGTGAATAGCACGGAGGAAGAGTCTTCGACTTCCGGTGGT

-continued

Identtty of homologs to NGAL2 is tndtcated

AGTATCTCACGTGGCGGCGTTTCTATGGCTGGTGTTGGCTCTCCACTCCAGTTGAGGTTAGTGAGCAGTGACGGTGATGATCAGTCT
CTAGTAGCTAGGGGAGCTGCTAGGGTTGATGAGGATCATCACTTGTTTACAAAGAAAGGAAAGTCTTCTTTGTCTTTCGATTTGGAT
AAATGA

Bra038346
Cover 51%   identity 57%

SEQ ID NO: 121
MVFSCIDESSSTSESFSPATATATATATKFSAPPLPPLRLNRMRSGGSNVVLDSKNGVDIDSRKLSSSKYKGVVPQPNGRWGAQIYV
KHQRVWLGTFCDEEEAAHSYDIAARKFRGRDAVVNFKTFLASEDDNGELCFLEAHSKAEIVDMLRKHTYADELAQSNKRSGANTNTN
TTQSHTVSRTREVLFEKVVTPSDVGKLNRLVIPKQHAEKYFPLPSLSVTKGVLINFEDVTGKVWRFRYSYWNSSQSYVLTKGWSRFV
KEKNLRAGDVVTFERSTGSDRQLYIDWKIRSGPSKNPVQVVVRLFGVDIFNVTSAKPSNVVDACGGKRSRDVDMFALRCSKKHAIIN
AL

CDS SEQ ID NO: 122
ATGGTATTCAGTTGCATAGACGAGAGCTCTTCCACTTCAGAATCTTTTTCACCCGCAACCGCAACCGCAACCGCAACCGCCACAAAG
TTCTCTGCTCCTCCGCTTCCACCGTTACGCCTCAACCGGATGAGAAGCGGTGGAAGCAACGTCGTGTTGGATTCAAAGAATGGCGTA
GATATTGATTCACGGAAGCTATCGTCGTCAAAGTACAAAGGCGTGGTTCCTCAGCCCAACGGAAGATGGGGAGCTCAGATTTACGTG
AAGCACCAGCGAGTTTGGCTGGGCACTTTCTGCGATGAAGAGGAAGCTGCTCACTCCTACGACATAGCCGCCCGTAAATTCCGTGGC
CGTGACGCCGTTGTCAACTTCAAAACCTTCCTCGCCTCAGAGGACGACAACGGCGAGTTATGTTTCCTTGAAGCTCACTCCAAGGCC
GAGATCGTCGACATGTTGAGGAAACACACTTACGCTGACGAGCTTGCGCAGAGCAATAAACGCAGCGGAGCGAATACGAATACGAAT
ACGACTCAAAGCCACACCGTTTCGAGAACACGTGAAGTGCTTTTCGAGAAGGTTGTCACGCCTAGCGACGTTGGTAAGCTAAACCGC
CTCGTGATACCTAAACAGCACGCGGAGAAATATTTTCCGTTACCGTCACTGTCGGTGACTAAAGGCGTTCTGATCAACTTCGAAGAC
GTGACGGGTAAGGTGTGGCGGTTCCGTTACTCATACTGGAACAGTAGTCAAAGTTACGTGTTGACCAAGGGATGGAGTCGGTTCGTT
AAGGAGAAGAATCTCCGAGCCGGTGATGTCGTTACTTTCGAGAGATCGACCGGTTCAGACCGGCAGCTTTATATTGATTGGAAAATC
CGGTCTGGTCCGAGCAAAAACCCTGTTCAGGTTGTGGTTAGGCTTTTCGGAGTTGACATCTTCAACGTGACAAGCGCGAAGCCGAGC
AACGTTGTAGACGCGTGCGGTGGAAAGAGATCTCGGGATGTTGATATGTTTGCGCTACGGTGTTCCAAAAAACACGCTATAATCAAT
GCTTTGTGA

Zea mays

GRMZM2G053008
Cover 74%   identity 47%

SEQ ID NO: 123
MAASPSSPLTAPPEPVTPPSPWTITDGAISGTLPAAEAFAVHYPGYPSSPARAARTLGGLPGLAKVRSSDPGARLELRFRPEDPYCH
PAFGQSRASTGLLLRLSKRKGAAAPCAHVVARVRTAYYFEGMADFQHVVPVHAAQTRKRKHSDSQNDNENFGSDKTGHDEADGDVMM
LVPPLFSVKDRPTKIALVPSSNAISKTMHRGVVQERWEMNVGPTLALPFNTQVVPEKINWEDHIRKNSVEWGWQMAVCKLFDERPVW
PRQSLYERFLDDNVHVSQNQFKRLLFRAGYYFSTGPFGKFWIRRGYDPRKDSESQIYQRIDFRMPPELRYLLRLKNSESRKWADMCK
LETMPSQSFIYLQLYELKDDFIQAEIRKPSYQSVCSRSTGWFSKPMIKTLRLQVSIRLLSLLHNEEAKNLLRNAHELIERSKKQEAL
SRSELSIEYNDADQVSAAHTGTEDQVGPNNSDSEDVDDEEEEEELEGYDSPPMADDIHEFTLGDSYAFGEGFSNGYLEEVLRSLPLQ
EDGQKKLCDAPINADASD

CDS SEQ ID NO: 124
ATGGCCGCCTCGCCCTCTTCACCCTTGACAGCGCCGCCAGAGCCGGTGACCCCGCCGTCCCCATGGACCATCACAGACGGAGCCATC
TCTGGCACGCTCCCAGCAGCCGAGGCCTTCGCAGTGCACTACCCGGGCTACCCCTCCTCTCCCGCCCGCGCCGCCCGCACCCTCGGC
GGTCTCCCCGGCCTCGCCAAGGTCCGGAGTTCCGATCCCGGCGCCCGCCTCGAGCTCCGCTTCCGCCCCGAGGACCCCTACTGCCAT
CCAGCCTTTGGCCAGTCCCGCGCCTCCACTGGCCTTCTGCTGCGCCTCTCCAAGCGCAAAGGAGCTGCGGCACCTTGTGCCCATGTG
GTCGCTCGTGTCCGGACTGCTTACTACTTCGAAGGTATGGCAGATTTTCAACATGTTGTTCCAGTGCATGCTGCACAAACAAGAAAA
AGAAAACACTCAGATTCTCAAAATGATAATGAGAATTTTGGTAGTGATAAGACAGGACATGATGAAGCAGATGGAGATGTCATGATG
TTGGTACCCCCTCTCTTTTCAGTGAAGGATAGGCCAACAAAGATAGCGCTTGTACCATCGTCCAATGCCATATCTAAAACCATGCAC
AGGGGAGTTGTACAAGAACGGTGGGAGATGAATGTTGGACCAACTCTGGCGCTTCCGTTCAACACTCAAGTTGTCCCGGAGAAGATT
AATTGGGAAGACCACATTAGAAAGAATTCTGTAGAATGGGGTTGGCAAATGGCTGTTTGCAAATTGTTTGATGAGCGCCCTGTGTGG
CCAAGGCAATCACTTTATGAGCGGTTCCTTGATGATAATGTGCATGTCTCTCAAAACCAATTCAAAAGGCTTCTGTTTAGAGCTGGA
TACTACTTCTCTACTGGACCCTTTGGAAAATTTTGGATCAGAAGAGGATATGACCCTCGTAAAGACTCTGAGTCACAAATATATCAG
AGAATTGATTTTCGCATGCCTCCCGAGCTACGATATCTTCTAAGGCTGAAGAATTCTGAGTCTCGAAAGTGGGCAGATATGTGCAAG
CTTGAAACAATGCCATCACAGAGTTTCATCTACCTGCAATTATATGAACTGAAGGATGATTTTATTCAAGCAGAAATTCGAAAACCT
TCTTATCAATCAGTTTGTTCACGTTCTACAGGATGGTTTTCTAAGCCAATGATCAAAACCCTGAGGTTGCAAGTGAGCATAAGGCTC
CTCTCTTTATTGCATAATGAAGAGGCTAAAAACTTGTTGAGGAATGCCCATGAGCTTATTGAAAGGTCCAAGAAGCAGGAAGCCCTT
TCGAGATCTGAGCTGTCAATAGAATATAATGATGCTGATCAAGTTTCTGCCGCACATACTGGAACTGAGGATCAAGTCGGCCCTAAC
AACTCTGATAGTGAAGATGTGGATGATGAAGAAGAGGAAGAGGAATTGGAGGGTTATGATTCTCCACCTATGGCAGATGATATTCAT
GAGTTCACCTTAGGTGATTCCTATGCATTTGGTGAAGGCTTCTCGAATGGATACCTCGAAGAAGTACTGCGCAGCTTGCCATTGCAG
GAAGACGGCCAAAAGAAATTATGTGATGCTCCTATCAACGCTGATGCAAGTGATGGAGAGTTTGAAATTTACGAACAGCCCAGTGAT
GATGAAGATTCTGATGGCTAG

GRMZM2G102059_T01
Cover 47%   identity 62%

SEQ ID NO: 125
MEFASSSSRFSREEDEEEQEEEEEEEEASPREIPFMTAAATADTGAAASSSSPSAAASSGPAAAPRSSDGAGASGSGGGGSDDVQV
IEKEHMFDKVVTPSDVGKLNRLVIPKQHAEKYFPLDAAANEKGQLLSFEDRAGKLWRFRYSYWNSSQSYVMTKGWSRFVKEKRLDAG
DTVSFCRGAGDTARDRLFIDWKRRADSRDPHRMPRLPLPMAPVASPYGPWGGGGGGGAGGFFMPPAPPATLYEHHRFRQALDFRNIN
AAAAPARQLLFFGSAGMPPRASMPQQQQPPPPPHPPLHSIMLVQPSPAPPTASVPMLLDSVPLVNSPTAASKRVRLFGVNLDNPQPG
TSAESSQDANALSLRTPGWQRPGPLRFFESPQRGAESSAASSPSSSSSSKREAHSSLDLDL

-continued

Identtty of homologs to NGAL2 is tndtcated

CDS SEQ ID NO: 126
ATGGAGTTCGCGAGCTCTTCGAGTAGGTTTTCCAGGGAGGAGGACGAGGAGGAAGAGCAGGAGGAAGAGGAGGAGGAGGAGGAGGCG
TCTCCGCGCGAGATCCCCTTCATGACAGCGGCAGCGACGGCCGACACCGGAGCCGCCGCCTCCTCGTCCTCGCCTTCCGCGGCGGCC
TCATCGGGTCCTGCTGCTGCCCCCCGCTCGAGCGACGGCGCCGGGGCGTCCGGGAGCGGCGGCGGCGGGAGCGACGACGTGCAGGTG
ATCGAGAAGGAGCACATGTTCGACAAGGTGGTGACGCCCAGCGACGTGGGGAAGCTCAACCGGCTGGTGATCCCGAAGCAGCACGCG
GAGAAGTACTTCCCGCTGGACGCGGCGGCCAACGAGAAGGGCCAGCTGCTCAGCTTCGAGGACCGCGCCGGTAAGCTCTGGCGCTTC
CGCTACTCCTACTGGAACAGCAGCCAGAGCTACGTCATGACCAAGGGCTGGAGCCGCTTCGTCAAGGAGAAGCGCCTCGACGCCGGC
GACACCGTCTCCTTCTGCCGCGGCGCCGGCGACACCGCGCGGGACCGCCTCTTCATCGACTGGAAGCGCCGCGCCGACTCCCGCGAC
CCGCACCGCATGCCGCGCCTCCCGCTCCCCATGGCGCCCGTCGCGTCGCCCTACGGCCCCTGGGGCGGCGGCGGCGGCGGCGGCGCG
GGCGGTTTCTTCATGCCGCCCGCGCCGCCCGCCACACTCTACGAGCACCACCGCTTCCGCCAGGCCCTCGACTTCCGCAACATCAAC
GCCGCGGCCGCGCCGGCCAGGCAGCTCCTCTTCTTCGGCTCAGCCGGCATGCCCCCGCGCGCGTCCATGCCGCAGCAGCAGCAGCCG
CCTCCGCCCCCGCACCCGCCTCTGCACAGCATTATGTTGGTGCAACCCAGCCCCGCGCCGCCCACGGCCAGCGTGCCCATGCTTCTC
GACTCGGTACCGCTCGTCAACAGCCCAACGGCAGCGTCGAAGCGCGTCCGCCTGTTTGGGGTCAACCTCGACAACCCGCAACCAGGC
ACAAGTGCGGAGTCAAGCCAAGATGCCAACGCATTGTCGCTGAGGACACCGGGATGGCAAAGGCCGGGGCCGTTGAGGTTCTTCGAA
TCGCCTCAACGCGGCGCCGAGTCATCTGCAGCCTCCTCGCCGTCGTCATCGTCGTCCTCCAAGAGAGAAGCGCACTCGTCCTTGGAT
CTCGATCTGTGA

GRMZM2G098443_T01
Cover 47% identity 63%

SEQ ID NO: 127
MEFTTPPPATRSGGGEERAAAEHNQHHQQQHATVEKEHMFDKVVTPSDVGKLNRLVIPKQHAEKYFPLDAAANEKGLLLSFEDRTGK
PWRFRYSYWNSSQSYVMTKGWSRFVKEKRLDAGDTVSFGRGISEAARDRLFIDWRCRPDPPVVHHQYHHRLPLPSAVVPYAPWAAHA
HHHHYPADGHTEPVTPCLCATLVATEMRASSSQLSLTRSNLSRPPQPRIARVDGAQPRPSSSPRQPQSLWCRSCQPQPRRTADVP

CDS SEQ ID NO: 128
ATGGAGTTCACCACTCCCCCGCCCGCGACCCGGTCGGGCGGCGGAGAGGAGAGGGCGGCTGCTGAGCACAACCAGCACCACCAGCAG
CAGCATGCGACGGTGGAGAAGGAGCACATGTTCGACAAGGTGGTGACGCCGAGCGACGTCGGGAAGCTGAACCGGCTGGTGATCCCG
AAGCAGCACGCGGAGAAGTACTTCCCGCTGGACGCGGCGGCGAACGAGAAGGGCCTCCTGCTCAGCTTCGAGGACCGCACGGGGAAG
CCCTGGCGCTTCCGCTACTCCTACTGGAACAGTAGCCAGAGCTACGTGATGACCAAGGGCTGGAGCCGCTTCGTCAAGGAGAAGCGC
CTCGACGCCGGGGACACAGTCTCCTTCGGCCGCGGCATCAGCGAGGCGGCGCGCGACAGGCTTTTCATCGACTGGCGGTGCCGACCC
GACCCGCCCGTCGTGCACCACCAGTACCACCACCGCCTCCCTCTCCCCTCCGCCGTCGTCCCCTACGCGCCGTGGGCGGCGCACGCG
CACCACCACCACTACCCAGCAGATGGGCACACGGAACCAGTAACACCTTGCCTGTGCGCCACACTCGTTGCCACTGAAATGAGAGCA
TCATCTTCGCAACTGTCACTCACACGCTCCAACCTCTCCAGGCCGCCACAACCTAGAATAGCCAGAGTCGATGGCGCCCAGCCACGG
CCGTCGTCGTCACCACGCCAGCCACAGTCGTTGTGGTGCCGGTCGTGCCAACCGCAACCACGGCGAACGGCCGACGTTCCTTGA

GRMZM2G082227_T01
Cover 45% identity 64%

SEQ ID NO: 129
MEFTAPPPATRSGGGEERAAAEHHQQQQQATVEKEHMFDKVVTPSDVGKLNRLVIPKQHAERYFPLDAAANDKGLLLSFEDRAGKPW
RFRYSYWNSSQSYVMTKGWSRFVKEKRLDAGDTVSFGRGVGEAARGRLFIDWRRRPDPPVVHHQYHHHRLPLPSAVVPYAPWAAAAH
AHHHHYPAAGVGAARTTTTTTTVLHHLPPSPSPLYLDTRRRHVGYDAYGAGTRQLLFYRPHQQPSTTVMLDSVPVRLPPTPGQHAE
PPPPAVASSASKRVRLFGVNLDCAAAAGSEEENVGGWRTSAPPTQQASSSSSYSSGKARCSLNLDL

CDS SEQ ID NO: 130
ATGGAGTTCACCGCTCCCCCGCCCGCGACCCGGTCGGGCGGCGGCGAGGAGAGGGCGGCTGCTGAGCACCACCAGCAGCAGCAGCAG
GCGACGGTGGAGAAGGAGCACATGTTCGACAAGGTGGTGACGCCGAGCGACGTCGGGAAGCTGAACCGGCTGGTGATCCCGAAGCAG
CACGCGGAGAGGTACTTCCCGCTGGACGCGGCGGCGAACGACAAGGGCCTGCTGCTCAGCTTCGAGGACCGCGCGGGGAAGCCCTGG
CGCTTCCGCTACTCCTACTGGAACAGCAGCCAGAGCTACGTGATGACCAAGGGCTGGAGCCGCTTCGTCAAGGAGAAGCGCCTCGAC
GCCGGGGACACCGTCTCCTTCGGCCGCGGCGTCGGCGAGGCGGCGCGCGGCAGGCTCTTCATCGACTGGCGGCGCCGACCCGACCCG
CCCGTCGTGCACCACCAGTACCACCACCACCGCCTCCCTCTCCCCTCCGCCGTCGTCCCCTACGCGCCGTGGGCGGCGGCGGCGCAC
GCGCACCACCACCACTACCCAGCAGCTGGGGTCGGTGCCGCCAGGACGACGACGACGACGACGACGACGGTGCTCCACCACCTGCCG
CCCTCGCCCTCCCCGCTCTACCTTGACACCCGCCGCCGCCACGTCGGCTACGACGCCTACGGGGCCGGCACCAGGCAACTTCTCTTC
TACAGGCCGCACCAGCAGCCCTCCACGACGGTGATGCTGGACTCCGTGCCGGTACGGTTACCGCCAACGCCAGGGCAGCACGCCGAG
CCGCCGCCCCCCGCCGTGGCGTCGTCAGCCTCGAAGCGGGTGCGCCTGTTCGGGGTGAACCTCGACTGCGCCGCCGCCGCCGGCTCA
GAGGAGGAGAACGTCGGCGGGTGGAGGACTAGTGCGCCGCCGACGCAGCAGGCGTCCTCCTCCTCATCCTACTCTTCCGGGAAAGCG
AGGTGCTCCTTGAACCTTGACTTGTGA

GRMZM2G024948_T01
Cover 46% identity 63%

SEQ ID NO: 131
MDQFAASGRFSREEEADEEQEDASNSMREISFMPPAAASSSSAAASASASASTSASACASGSSSAPFRSASASGDAAGASGSGGPAD
ADAEAEAVEKEHMFDKVVTPSDVGKLNRLVIPKQYAEKYFPLDAAANEKGLLLSFEDSAGKHWRFRYSYWNSSQSYVMTKGWSRFVK
EKRLVAGDTVSFSRAAAEDARHRLFIDWKRRVDTRGPLRFSGLALPMPLPSSHYGGPHHYSPWGFGGGGGGGGFFMPPSPPATLYE
HRLRQGLDFRSMTTTYPAPTVGRQLLFFGSARMPPHHAPPPQPRPFSLPLHHYTVQPSAAGVTAASRPVLLDSVPVIESPTTAAKRV
RLFGVNLDNNPDGGGEASHQGDALSLQMPGWQQRTPTLRLLELPRHGGESSAASSPSSSSSSKREARSALDLDL

CDS SEQ ID NO: 132
ATGGACCAGTTCGCCGCGAGCGGGAGGTTCTCTAGAGAGGAGGAGGCGGACGAGGAGCAGGAGGATGCGTCCAATTCCATGCGCGAG
ATCTCCTTCATGCCGCCGGCTGCGGCCTCGTCATCTTCGGCGGCTGCTTCCGCGTCCGCGTCCGCCTCCACCAGCGCATCCGCGTGT
GCATCGGGAAGCAGCAGCGCCCCCTTCCGCTCCGCCTCCGCGTCGGGGGATGCCGCCGGAGCGTCGGGGAGCGGCGGCCCAGCGGAC

-continued

Identtty of homologs to NGAL2 is tndtcated

GCGGACGCGGAGGCGGAGGCGGTGGAGAAGGAGCACATGTTCGACAAGGTGGTCACGCCGAGCGACGTGGGGAAGCTCAACCGGCTG
GTGATCCCGAAGCAGTACGCGGAGAAGTACTTCCCGCTGGACGCGGCGGCCAACGAGAAGGGCCTCCTCCTCAGCTTCGAGGACAGC
GCCGGCAAGCACTGGCGCTTCCGCTACTCCTACTGGAACAGCAGCCAGAGCTACGTCATGACCAAGGGCTGGAGCCGCTTCGTCAAG
GAGAAGCGCCTCGTCGCCGGGGACACCGTCTCCTTCTCCCGCGCCGCCGCCGAGGACGCGCGCCACCGCCTCTTCATCGACTGGAAG
CGCCGGGTCGACACCCGCGGCCCGCTTCGTTTCTCCGGCCTCGCGCTGCCGATGCCGCTGCCGTCGTCGCACTACGGCGGGCCCCAC
CACTACAGCCCGTGGGGCTTCGGCGGCGGCGGCGGCGGCGGCGGCGGATTCTTCATGCCGCCCTCGCCGCCCGCCACGCTCTACGAG
CACCGCCTCAGACAGGGCCTCGACTTCCGCAGCATGACGACGACCTACCCCGCGCCGACCGTGGGGAGGCAGCTCCTGTTTTTCGGC
TCGGCCAGGATGCCTCCTCATCACGCGCCGCCGCCCCAGCCGCGCCCGTTCTCGCTGCCGCTGCATCACTACACGGTGCAACCGAGC
GCCGCCGGCGTCACCGCCGCGTCACGGCCGGTCCTTCTTGACTCGGTGCCGGTCATCGAGAGCCCGACGACCGCCGCGAAGCGCGTG
CGGCTGTTCGGCGTCAACCTGGACAACAACCCAGATGGCGGCGGCGAGGCTAGCCATCAGGGCGATGCATTGTCATTGCAGATGCCC
GGGTGGCAGCAAAGGACTCCAACTCTAAGGCTACTAGAATTGCCTCGCCATGGCGGGGAGTCCTCCGCGGCGTCGTCTCCGTCGTCG
TCGTCTTCCTCCAAGAGGGAGGCGCGTTCAGCTTTGGATCTCGATCTGTGA

GRMZM2G328742_T01
Cover 55%   identity 64%

SEQ ID NO: 134
MATNHLSQGQHQHPQAWPWGVAMYTNLHYHHQQHHHYEKEHLFEKPLTPSDVGKLNRLVIPKQHAERYFPLSSSGAGDKGLILCFED
DDDDEAAAANKPWRFRYSYWTSSQSYVLTKGWSRYVKEKQLDAGDVVRFQRMRGFGMPDRLFISHSRRGETTATAATTVPPAAAAVR
VVVAPAQSAGADHQQQQQPSPWSPMCYSTSGSYSYPTSSPANSQHAYHRHSADHDHSNNMQHAGESQSDRDNRSCSAASAPPPPSRR
LRLFGVNLDCGPGPEPETPTAMYGYMHQSPYAYNNWGSPYQHDEEI

CDS 135
ATGGCCACGAACCATCTCTCCCAAGGGCAGCACCAGCACCCGCAGGCCTGGCCCTGGGGCGTGGCCATGTACACCAACCTACACTAC
CACCACCAGCAGCACCACCACTACGAGAAGGAGCACCTGTTCGAGAAGCCGCTGACGCCGAGCGACGTGGGCAAGCTCAACAGGCTG
GTGATCCCCAAGCAGCACGCCGAGAGGTACTTCCCTCTCAGCAGCAGCGGCGCCGGCGACAAAGGCCTCATCCTGTGCTTCGAGGAC
GACGACGACGACGAGGCTGCCGCCGCCAACAAGCCGTGGCGGTTCCGCTACTCGTACTGGACCAGCAGCCAGAGCTACGTGCTCACC
AAGGGCTGGAGCCGCTACGTCAAGGAGAAGCAGCTTGACGCCGGCGACGTCGTGCGCTTCCAGAGGATGCGTGGTTTCGGCATGCCC
GACCGCCTGTTCATCAGCCACAGCCGCCGCGGCGAGACTACTGCTACTGCTGCAACAACAGTGCCCCCCGCTGCTGCTGCCGTGCGC
GTAGTAGTGGCACCTGCACAGAGCGCTGGCGCAGACCACCAGCAGCAGCAGCAGCCGTCGCCTTGGAGCCCAATGTGCTACAGCACA
TCAGGCTCGTACTCGTACCCCACCAGCAGCCCAGCCAATTCCCAGCATGCCTACCACCGCCACTCAGCTGACCATGACCACAGCAAC
AACATGCAACATGCAGGAGAATCTCAGTCCGACAGAGACAACAGGAGCTGCAGTGCAGCTTCGGCACCGCCGCCACCGTCGCGGCGG
CTCCGGCTGTTCGGCGTAAACCTCGACTGCGGCCCGGGGCCGGAGCCGGAGACACCAACGGCGATGTACGGCTACATGCACCAAAGC
CCCTACGCTTACAACAACTGGGGCAGTCCATACCAGCATGACGAGGAGATTTAA

GRMZM2G142999_T01
Cover 44%   identity 64%

SEQ ID NO: 136
MEFTPAHAHARVVEDSERPRGGVAWVEKEHMFEKVVTPSDVGKLNRLVIPKQHAERYFPALDASSAAAAAAAAAAGGGKGLVLSFED
RAGKAWRFRYSYWNSSQSYVMTKGWSRFVKEKRLGAGDTVLFARGAGGARGRFFIDFRRRRQDLAFLQPTLASAQRLLPLPSVPICP
WQDYGASAPAPNRHVLFLRPQVPAAVVLKSVPVHVAASAVEATMSKRVRLFGVNLDCPPDAEDSATVPRGRAASTTLLQLPSPSSST
SSSTAGKDVCCLDLGL

CDS SEQ ID NO: 137
ATGGAGTTCACGCCCGCGCATGCGCATGCCCGTGTCGTTGAGGATTCCGAGAGGCCTCGCGGCGGCGTGGCCTGGGTGGAGAAGGAG
CACATGTTCGAGAAGGTGGTCACCCCGAGCGACGTGGGGAAGCTCAATCGCCTGGTCATCCCAAAGCAGCACGCGGAGCGCTACTTC
CCCGCGCTGGACGCCTCGTCCGCCGCGGCGGCGGCGGCGGCAGCAGCCGCGGGAGGCGGGAAGGGGCTGGTGCTCAGCTTCGAGGAC
CGGGCGGGGAAGGCGTGGCGCTTCCGCTACTCGTACTGGAACAGCAGCCAGAGCTACGTGATGACCAAAGGTTGGAGCCGCTTCGTG
AAGGAGAAGCGCCTCGGTGCCGGGGACACAGTCTTGTTCGCGCGCGGCGCGGGCGGCGCGCGCGGCCGCTTCTTCATCGATTTCCGC
CGCCGTCGCCAGGATCTCGCGTTCCTGCAGCCGACGCTGGCGTCTGCGCAGCGACTCCTGCCGCTGCCGTCGGTGCCCATCTGCCCG
TGGCAGGACTACGGCGCCTCGGCTCCGGCGCCCAACCGGCACGTGCTGTTCCTGCGGCCGCAGGTGCCGGCCGCCGTAGTGCTCAAG
TCGGTCCCCGTGCACGTTGCTGCATCCGCGGTGGAGGCGACCATGTCGAAGCGCGTCCGCCTGTTCGGGGTGAACCTCGACTGCCCG
CCGGACGCCGAAGACAGCGCCACAGTCCCCCGGGGCCGGGCGGCGTCGACGACGCTTCTGCAACTGCCCTCGCCATCGTCGTCAACA
TCCTCCTCGACGGCAGGGAAGGACGTGTGCTGTTTGGATCTTGGACTGTGA

GRMZM2G125095_T01
Cover 85%   identity 40%

SEQ ID NO: 138
MEFRPAHARVFEDSERPRGGVAWLEKEHMFEKVVTPSDVGKLNRLVIPKQHAERYFPALDASAAAASASASAGGGKAGLVLSFEDRA
GKAWRFRYSYWNSSQSYVMTKGWSRFVKEKRLGAGDTVLFARGAGATRGRFFIDFRRRRHELAFLQPPLASAQRLLPLPSVPICPWQ
GYGASAPAPSRHVLFLRPQVPAAVVLTSVPVRVAASAVEEATRSKRVRLFGVNLDCPPDAEDGATATRTPSTLLQLPSPSSSTSSST
GGKDVRSLDLGL

CDS SEQ ID NO: 139
ATGGAGTTCAGGCCCGCGCATGCCCGTGTCTTCGAGGATTCCGAGAGGCCTCGCGGCGGCGTGGCGTGGCTGGAGAAGGAGCACATG
TTCGAGAAAGTGGTCACCCCGAGCGACGTGGGGAAGCTCAATCGCCTGGTCATCCCGAAGCAGCACGCCGAGCGCTACTTCCCCGCG
CTGGACGCCTCGGCCGCCGCGGCGTCGGCATCGGCGTCGGCGGGCGGCGGGAAGGCGGGGCTGGTGCTCAGCTTCGAGGACCGGGCG
GGGAAGGCGTGGCGCTTCCGCTACTCGTACTGGAACAGCAGCCAGAGCTACGTGATGACCAAGGGATGGAGCCGCTTCGTGAAAGAG
AAGCGCCTCGGTGCCGGGGACACGGTATTGTTCGCGCGCGGCGCGGGCGCCACGCGCGGCCGCTTCTTCATCGATTTCCGCCGCCGC
CGCCACGAGCTCGCGTTCCTGCAGCCGCCGCTGGCGTCTGCGCAGCGCCTCCTGCCGCTCCCGTCGGTGCCCATCTGCCCGTGGCAG

-continued

Identtty of homologs to NGAL2 is tndtcated

GGCTACGGCGCCTCCGCTCCGGCGCCAAGCCGGCACGTGCTGTTCCTGCGGCCGCAGGTGCCGGCCGCCGTAGTGCTCACGTCGGTG
CCCGTGCGCGTCGCCGCATCCGCGGTGGAGGAGGCGACGAGGTCGAAGCGCGTCCGCCTGTTCGGGGTGAACCTCGACTGCCCGCCG
GACGCCGAAGACGGTGCCACAGCCACCCGGACGCCGTCGACGCTTCTGCAGCTGCCCTCGCCATCGTCGTCAACATCCTCCTCCACG
GGAGGCAAGGATGTGCGTTCTTTGGATCTTGGACTTTGA

Tricum aeseirum

TRAES3BF098300010CFD_ t1
Cover: 42%   ident 60%

SEQ ID NO: 140
MGVEILSSMVEHSFQYSSGVSTATTESGTAGTPPRPLSLPVAIADESVTSRSASSRFKGVVPQPNGRWGAQIYERHARVWLGTFPDQ
DSAARAYDVASLRYRGRDVAFNFPCAAVEGELAFLAAHSKAEIVDMLRKQTYADELRQGLRRGRGMGARAQPTPSWAREPLFEKAVT
PSDVGKLNRLVVPKQHAEKHFPLKRTPETPTTTGKGVLLNFEDGEGKVWRFRYSYWNSSQSYVLTKGWSRFVREKGLGAGDSILFSC
SLYEQEKQFFIDCKKNTSMNGGKSASPLPVGVTTKGEQVRVVRLFGVDISGVKRGRAATATAEQGLQELFKRQCVAPGQHSPALGAF
AL

CDS SEQ ID NO: 141
ATGGGGGTGGAAATCCTGAGCTCCATGGTGGAGCACTCCTTCCAGTACTCTTCCGGCGTGTCCACGGCCACGACGGAGTCAGGCACC
GCCGGAACACCGCCGAGGCCTTTGAGCCTACCTGTCGCCATCGCCGACGAGTCCGTGACCTCGCGGTCGGCGTCGTCTCGGTTCAAG
GGCGTGGTGCCGCAGCCAAACGGGCGATGGGGCGCCCAGATCTACGAGCGCCACGCTCGCGTCTGGCTCGGCACGTTCCCAGACCAG
GACTCGGCGGCGCGCGCCTACGACGTAGCCTCGCTCAGGTACCGCGGCCGCGACGTCGCCTTCAACTTCCCGTGCGCGGCCGTGGAG
GGGGAGCTCGCCTTCCTGGCGGCGCACTCCAAGGCTGAGATAGTGGACATGCTCCGGAAGCAGACCTACGCCGATGAACTCCGCCAG
GGCCTGCGGCGCGGCCGTGGCATGGGGGCGCGCGCGCAGCCGACGCCGTCGTGGGCGCGGGAGCCCCTTTTCGAGAAGGCCGTGACC
CCTAGCGATGTCGGCAAGCTCAATCGCCTCGTAGTGCCGAAGCAGCACGCCGAGAAGCACTTCCCCCTGAAGCGCACGCCGGAGACG
CCGACCACCACCGGCAAGGGCGTGCTGCTCAACTTCGAGGACGGCGAGGGGAAGGTGTGGAGGTTCCGGTACTCGTACTGGAACAGC
AGCCAGAGCTACGTGCTCACCAAAGGCTGGAGCCGCTTCGTCCGGGAGAAGGGCCTAGGTGCCGGCGACTCCATCCTATTCTCGTGC
TCGCTGTACGAACAGGAGAAGCAGTTCTTCATCGACTGCAAGAAGAACACTAGCATGAACGGAGGCAAATCGGCGTCGCCGCTGCCA
GTGGGGGTGACTACCAAAGGAGAACAAGTTCGCGTCGTTAGGCTATTCGGTGTCGACATCTCGGGAGTGAAGAGGGGGCGAGCGGCG
ACGGCAACGGCGGAGCAAGGCCTGCAGGAGTTGTTCAAGAGGCAATGCGTGGCACCCGGCCAGCACTCTCCTGCCCTAGGTGCCTTC
GCCTTATAG

TRAES3BF062700040CFD_t1
Cover 47%   ident 55%

SEQ ID NO: 142
MASGKPTNHGMEDDNDMEYSSAESGAEDAAEPSSSPVLAPPRAAPSSRFKGVVPQPNGRWGAQIYEKHSRVWLGTFPDEDAAVRAYD
VAALRFRGPDAVINHQRPTAAEEAGSSSSRSELDPELGFLADHSKAEIVDMLRKHTYDDELRQGLRRGRGRAQPTPAWARELLFEKA
VTPSDVGKLNRLVVPKQQAEKHFPPTTAAATGSNGKGVLLNFEDGEGKVWRFRYSYWNSSQSYVLTKGWSRFVKETGLRAGDTVAFY
RSAYGNDTEDQLFIDYKKMNKNDDAADAAISDENETGHVAVKLFGVDIAGGGMAGSSGG

CDS SEQ ID NO: 143
ATGGCATCTGGCAAGCCGACAAACCACGGGATGGAGGACGACAACGACATGGAGTACTCCTCCGCGGAATCGGGGGCCGAGGACGCG
GCGGAGCCGTCGTCGTCGCCGGTGCTGGCGCCGCCCCGGGCGGCTCCATCGTCGCGGTTCAAGGGCGTCGTGCCGCAGCCCAACGGG
CGGTGGGGAGCGCAGATCTACGAGAAGCACTCGCGGGTGTGGCTCGGAACGTTCCCCGACGAGGACGCCGCCGTGCGCGCCTACGAC
GTGGCCGCGCTCCGCTTCCGCGGCCCGGACGCCGTCATCAACCACCAGCGACCGACGGCCGCGGAGGAGGCCGGCTCGTCGTCGTCC
AGGAGCGAGCTGGATCCAGAGCTCGGCTTCCTTGCCGACCACTCCAAGGCCGAGATCGTCGACATGCTCCGGAAGCACACCTACGAC
GACGAGCTCCGTCAGGGCCTGCGCCGCGGCCGCGGGCGCGCGCAGCCGACGCCGGCGTGGGCACGAGAGCTCCTCTTCGAGAAGGCC
GTGACCCCGAGCGACGTCGGCAAGCTCAACCGCCTCGTGGTGCCGAAGCAGCAGGCCGAGAAGCACTTCCCTCCGACCACTGCGGCG
GCCACCGGCAGCAACGGCAAGGGCGTGCTGCTCAACTTCGAGGACGGCGAAGGGAAGGTGTGGCGCTTCCGGTACTCGTACTGGAAC
AGCAGCCAGAGCTACGTGCTCACCAAGGGCTGGAGCCGCTTCGTCAAGGAGACGGGCCTCCGCGCCGGCGACACCGTGGCGTTCTAC
CGGTCGGCGTACGGGAATGACACGGAGGATCAGCTCTTCATCGACTACAAGAAGATGAACAAGAATGACGATGCTGCGGACGCGGCG
ATTTCCGATGAGAATGAGACAGGCCATGTCGCCGTCAAGCTCTTCGGCGTTGACATTGCCGGTGGAGGGATGGCGGGATCATCAGGT
GGCTGA

TRAES3BF062600010CFD_t1
Cover 43%   ident 58%

SEQ ID NO: 144
MASGKPTNHGMEDDNDMEYSSAESGAEDAAEPSSSPVLAPPRAAPSSRFKGVVPQPNGRWGAQIYEKHSRVWLGTFPDEDAAARAYD
VAALRFRGPDAVINHQRPTAAEEAGSSSSRSELDPELGFLADHSKAEIVDMLRKHTYDDELRQGLRRGRGRAQPTPAWARELLFEKA
VTPSDVGKLNRLVVPKQQAEKHFPPTTAAATGSNGKGVLLNFEDGEGKVWRFRYSYWNSSQSYVLTKGWSRFVKETGLRAGDTVAFY
RSAYGNDTEDQLFIDYKKMNKNDDAADAAISDENETGHVAVKLFGVDIAGGGMAGSSGG

CDS SEQ ID NO: 145
ATGGCATCTGGCAAGCCGACAAACCACGGGATGGAGGACGACAACGACATGGAGTACTCCTCCGCGGAATCGGGGGCCGAGGACGCG
GCGGAGCCGTCGTCGTCGCCGGTGCTGGCGCCGCCCCGGGCGGCTCCATCGTCGCGGTTCAAGGGCGTCGTGCCGCAGCCCAACGGG
CGGTGGGGAGCGCAGATCTACGAGAAGCACTCGCGGGTGTGGCTCGGAACGTTCCCCGACGAGGACGCCGCCGCGCGCGCCTACGAC
GTGGCCGCGCTCCGCTTCCGCGGCCCGGACGCCGTCATCAACCACCAGCGACCGACGGCCGCGGAGGAGGCCGGCTCGTCGTCGTCC
AGGAGCGAGCTGGATCCAGAGCTCGGCTTCCTCGCCGACCACTCCAAGGCCGAGATCGTCGACATGCTCCGGAAGCACACCTACGAC
GACGAGCTCCGTCAGGGCCTGCGCCGCGGCCGCGGGCGCGCGCAGCCGACGCCGGCGTGGGCACGAGAGCTCCTCTTCGAGAAGGCC
GTGACCCCGAGCGACGTCGGCAAGCTCAACCGCCTCGTGGTGCCGAAGCAGCAGGCCGAGAAGCACTTCCCTCCGACCACTGCGGCG
GCCACCGGCAGCAACGGCAAGGGCGTGCTGCTCAACTTCGAGGACGGCGAAGGGAAGGTGTGGCGCTTCCGGTACTCGTACTGGAAC
AGCAGCCAGAGCTACGTGCTCACCAAGGGCTGGAGCCGCTTCGTCAAGGAGACGGGCCTCCGCGCCGGCGACACCGTGGCGTTCTAC

-continued

Identtty of homologs to NGAL2 is tndtcated
CGGTCGGCGTACGGGAATGACACGGAGGATCAGCTCTTCATCGACTACAAGAAGATGAACAAGAATGACGATGCTGCGGACGCGGCGATTTCCGATGAGAATGAGACAGGCCATGTCGCCGTCAAGCTCTTCGGCGTTGACATTGCCGGTGGAGGGATGGCGGGATCATCAGGTGGCTGA

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 272

<210> SEQ ID NO 1
<211> LENGTH: 804
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: cDNA

<400> SEQUENCE: 1

atgtcagtca accattacca caacactctc tcgttgcatc atcaccacca aaacgacgta 60

gctatagcac aacgagagtc tttgttcgag aaatcactca caccaagcga cgtcggaaag 120

ctaaaccgct tagtcatacc aaaacaacac gccgagaaat acttccctct caataataat 180

aataataatg gcggcagcgg agatgacgtg gcgacgacgg agaaagggat gcttcttagc 240

ttcgaggatg agtcaggcaa gtgttggaaa ttcagatact cttattggaa cagtagccaa 300

agctacgtgt tgaccaaagg atggagcagg tacgtcaaag acaaacacct cgacgcaggc 360

gacgttgttt tctttcaacg tcaccgtttt gatctccata gactcttcat tggctggcgg 420

agacgcggtg aagcttcttc ctctcccgct gtctccgttg tgtctcaaga agctctagtt 480

aatacgacgg cgtattggag cggcttgact acaccttatc gtcaagtaca cgcgtcaact 540

acttacccta atattcacca agagtattca cactatggcg ccgtcgttga tcatgctcag 600

tcgataccac cggtggtcgc aggtagctcg aggacggtga ggctttttgg cgtgaacctc 660

gaatgtcatg gtgatgccgt cgagccacca ccgcgtcctg atgtctataa tgaccaacac 720

atttactatt actcaactcc tcatcccatg aatatatcat ttgctgggga agcattggag 780

caggtaggag atggacgagg ttga 804

<210> SEQ ID NO 2
<211> LENGTH: 4285
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 2

ttgtttcggc tatttgttat actattgtta taacagtcac aagacttgac ctcaacgaaa 60

acttttacaa aacgtgaatt ggaaattttt acaaaatatg ctcttaatcg ttaatgcttc 120

ccaattaggt gagttaaatt gtgagaggaa ccatttctta gaggaaatgg ttcatgaaaa 180

caaatatgaa atagtatcac tagtcttagt tttgcgagaa aattaggaaa aatagaaacg 240

tgtaagcacc aatgatattc ctgaaagcac gtgacagata tttcatgatc ctataattaa 300

caagtgataa agatattaaa taaaattaac gatacttgag aaattcgtca aataaaatag 360

aagaggacca ctcacgtaac catttgcacg tcccattgat ttttgtggta gacttggtat 420

gttatattac ttatattcac agaattatat acgaaactca cgacttaaga tgcacggtaa 480

taactacaga tggaaattta cccatcaaac aagaaaacaa catttactca agcatctagc 540

-continued

tagaccaaaa tgtttgttta cttgttgact tgcgatccat agatatatta gttagaactt 600

tttcttctac aattgatcaa atgtttcaca ctgttctcaa tttctcatct agattcatga 660

cttatatgtt tggtcaaata tcacagcttg atgagcatta aatagcgtcg aagtatagga 720

tggttacgtt gttcaatatt gtaaaggaaa aaaagagaaa gagtgccaaa aggtcaagtc 780

gatttcacaa ataaatcttg aagtctttat ccctctcgat tataaaatga ttaggaaaag 840

aaaaagagag aataaaatgt agataaagag aaagagaaag agagagagga acataaggga 900

tggtatgaag tagaagtgaa gatgcatgcg atggtgtgtc ggaaaggcaa agcacatgct 960

acacaacttg agcttctcac ttgcgtcagg gataagtatc ctctgtacct tcttactttt 1020

gcgtaatatg taccacctca cttctcaacc gtttgatctt taatccttca ttatttcttc 1080

attaccttct ctttttgttt ttgttttcgt tttcaatttc tcatagattc atttacaaac 1140

taaatatcat aggaaggtgt tatctctagt taatttctta tcctacttta acaaaattta 1200

attgtcaaaa gattattttt acgtttatag acaaaagata ctgacacatc aattccacga 1260

accaaatggt tgagaaaaac aaaacgacta tctttgtctt gcaaataaat taatggcagt 1320

tagtaagatt ctcagctgaa aattcataca agagtaaatg atcaaataac catttatgag 1380

agaaatttaa tccttcagaa accaatgagg atctgatcaa gtaattgcaa accacatgag 1440

tccatgataa aggattgttt gacttacgca atccacatat ttatggctgc ttgatatgta 1500

aggtttatct gctttgacag tctatagaat cttgctaatc aatacgtcat atccggtgaa 1560

tactgaaact tttttaatta agaaaacaca aatcatcttt tctccggagg atttcgaatt 1620

tagttccggc aatgctgaaa taacatatgt tgaacttata acattccaag acatcaaatt 1680

ttactaatat ataaataatt acatattctt cttctacatg atcaaaacct tttcaacttt 1740

aattaaaggg ttacgtcgcg gcgttttgtg tggcttactc tttttttaca ctataactat 1800

agaacactcg tggatccaat gccgtttagg acaagatttt atcagacgag aaaaaaaaaa 1860

acaataccac atttttaaat atatatggat tatggactgc aacaacaata tagaaaagaa 1920

gagaaaaaaa taaaaataat gattgaaagg aaatatcatc acgcaaaacc ttaaaagtac 1980

tatcggtatc gtgtcgtcct ctcctcatca aatagttccc acagttttca catcaattta 2040

accattttca atttttttca ctctctgtct ctctcctttg tataatacta tattagtacc 2100

attacccatc tctctttcac caccaaacca acacctgcaa atcctctctc tctctctcac 2160

tccaagaaac caaaaaaaaa gatgtcagtc aaccattacc acaacactct ctcgttgcat 2220

catcaccacc aaaacgacgt agctatagca caacgagagt ctttgttcga gaaatcactc 2280

acaccaagcg acgtcggaaa gctaaaccgc ttagtcatac caaaacaaca cgccgagaaa 2340

tacttccctc tcaataataa taataataat ggcggcagcg gagatgacgt ggcgacgacg 2400

gagaaaggga tgcttcttag cttcgaggat gagtcaggca agtgttggaa attcagatac 2460

tcttattgga acagtagcca aagctacgtg ttgaccaaag gatggagcag gtacgtcaaa 2520

gacaaacacc tcgacgcagg cgacgttgtt ttctttcaac gtcaccgttt tgatctccat 2580

agactcttca ttggctggcg gagacgcggt gaagcttctt cctctcccgc tgtctccgtt 2640

gtgtctcaag aagctctagt taatacgacg gcgtattgga gcggcttgac tacaccttat 2700

cgtcaagtac acgcgtcaac tacttaccct aatattcacc aagagtattc acactatggt 2760

aaattcaaac cctttatttc ctcttttgtt ttttctttct ctcttatcta tatgtcagat 2820

-continued

```
ttatactcct ctctgttctc ttttaagatt tgtctttttc ataaaaatag atgattcgta   2880

atttgtattg catatttaca tgttctctta aaaaaagtaa tagagattaa tattttatgc   2940

atggtatttt agattatctg cctactttat atggtagtaa acaagaacat tcatctttat   3000

ttggttttat aaacaaaata tgagaatttt taaaggttag ggcaagcact tggaaagctc   3060

aaccatttta gttagctggt ggaatatctt tcttataaaa agcaaatgag ttatctaaaa   3120

ctatatgaca attattttag ttgcgtgtgt aatgtatata aaataacaac atgaaataac   3180

attttgtctt ttatttttgt cattcttatt atttaatttt ggacccgaca atttcaaata   3240

atcttctcca agttgtaact aatccgttac atgcgcgtga ggagaaccgt ccaatccact   3300

tagactaacg tgccctttat ttcttccttt taattctatg ttaaaaaaac aatttaacta   3360

aaagatgcgc acgtgtcttg acggtggaaa aaaattgtag gcgccgtcgt tgatcatgct   3420

cagtcgatac caccggtggt cgcaggtagc tcgaggacgg tgaggctttt tggcgtgaac   3480

ctcgaatgtc atggtgatgc cgtcgagcca ccaccgcgtc ctgatgtcta taatgaccaa   3540

cacatttact attactcaac tcctcatccc atggtaaata ttttttttt ttacattttt   3600

gtcagattca aatttttgct tacgtatgat ataattatta aacagatgtc gtggctgttt   3660

ctcgagacga gacagatgaa aattagtaat tttaaaatag acctgaaaga gatttttatg   3720

tttaataaat tatataaagg aggaatcaga gagaataata ctatacactt gactgtaaaa   3780

ccacatggcc aatttggttt ttatttgatt actttgattt gttttgttta ctcttttgtc   3840

tctgtagcct ccttttgttc attaattaat atcagccgta agtatatagt ttcctgtgaa   3900

aacagtctct attttggttt tactattcta atttgttagg caccgtcagt ttttttgtg   3960

aaaccaaatt attgactaat aagctggaaa gcaaaactga ctaaaagcat tacaaactta   4020

tcaatgacat aagttttgaa tttattacca tgttttgtaa tgttcagata taatttgaaa   4080

tgcttagaat tatatatttg tatacttaaa ttaatgaaat aaagtgaata ctaaagatag   4140

ttttattttt catattattc tatacaattc ggtgtacaat ttgtttttga tgataataaa   4200

aataataaaa ttgcgtgttg gaattgtgaa acagaatata tcatttgctg ggaagcatt   4260

ggagcaggta ggagatggac gaggt                                         4285

<210> SEQ ID NO 3
<211> LENGTH: 267
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 3

Met Ser Val Asn His Tyr His Asn Thr Leu Ser Leu His His His His
1               5                   10                  15

Gln Asn Asp Val Ala Ile Ala Gln Arg Glu Ser Leu Phe Glu Lys Ser
            20                  25                  30

Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys
        35                  40                  45

Gln His Ala Glu Lys Tyr Phe Pro Leu Asn Asn Asn Asn Asn Asn Gly
    50                  55                  60

Gly Ser Gly Asp Asp Val Ala Thr Thr Glu Lys Gly Met Leu Leu Ser
65                  70                  75                  80

Phe Glu Asp Glu Ser Gly Lys Cys Trp Lys Phe Arg Tyr Ser Tyr Trp
                85                  90                  95
```

-continued

```
Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val
            100                 105                 110

Lys Asp Lys His Leu Asp Ala Gly Asp Val Val Phe Phe Gln Arg His
        115                 120                 125

Arg Phe Asp Leu His Arg Leu Phe Ile Gly Trp Arg Arg Arg Gly Glu
    130                 135                 140

Ala Ser Ser Ser Pro Ala Val Ser Val Val Ser Gln Glu Ala Leu Val
145                 150                 155                 160

Asn Thr Thr Ala Tyr Trp Ser Gly Leu Thr Thr Pro Tyr Arg Gln Val
                165                 170                 175

His Ala Ser Thr Thr Tyr Pro Asn Ile His Gln Glu Tyr Ser His Tyr
            180                 185                 190

Gly Ala Val Val Asp His Ala Gln Ser Ile Pro Pro Val Val Ala Gly
        195                 200                 205

Ser Ser Arg Thr Val Arg Leu Phe Gly Val Asn Leu Glu Cys His Gly
    210                 215                 220

Asp Ala Val Glu Pro Pro Pro Arg Pro Asp Val Tyr Asn Asp Gln His
225                 230                 235                 240

Ile Tyr Tyr Tyr Ser Thr Pro His Pro Met Asn Ile Ser Phe Ala Gly
                245                 250                 255

Glu Ala Leu Glu Gln Val Gly Asp Gly Arg Gly
            260                 265


<210> SEQ ID NO 4
<211> LENGTH: 849
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: cDNA

<400> SEQUENCE: 4

atgtcagtca accattactc cacagaccac caccacactc tcttgtggca gcaacagcaa      60

caccgccaca ccaccgacac atcggagaca accaccaccg ccacatggct ccacgacgac     120

ctaaaagagt cactcttcga gaagtctctc acaccaagcg acgtcgggaa actcaaccgc     180

ctcgtcatac caaaacaaca cgcagagaaa tacttccctc tcaatgccgt cctagtctcc     240

tctgctgctg ctgacacgtc atcttcggag aaagggatgc ttctaagctt tgaagacgag     300

tcaggcaagt catggaggtt cagatactct tactggaaca gcagtcaaag ctatgtcttg     360

actaaaggat ggagcagatt tgtcaaagac aaacagctcg atccaggcga cgttgttttc     420

ttccaacgac accgttctga ttctaggaga ctcttcattg gctggcgcag acgtggacaa     480

ggctcctcat cctccgtcgc ggccactaac tccgccgtga atacgagttc tatgggagct     540

ctttcttatc atcaaatcca cgccactagt aattactcta atcctccctc tcactcagag     600

tattcccact atggagccgc cgtagcaaca gcggctgaga ctcacagcac accgtcgtct     660

tccgtcgtcg ggagctcaag gacggtgagg cttttcggtg tgaatctgga gtgtcaaatg     720

gatgaaaacg acggagatga ttctgttgca gttgccacca ccgttgaatc tcccgacggt     780

tactacggcc aaaacatgta ctattattac tctcatcctc ataacatggt aattttaact     840

cttttataa                                                             849


<210> SEQ ID NO 5
```

-continued

```
<211> LENGTH: 282
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 5

Met Ser Val Asn His Tyr Ser Thr Asp His His His Thr Leu Leu Trp
1               5                   10                  15

Gln Gln Gln Gln His Arg His Thr Thr Asp Thr Ser Glu Thr Thr Thr
            20                  25                  30

Thr Ala Thr Trp Leu His Asp Asp Leu Lys Glu Ser Leu Phe Glu Lys
        35                  40                  45

Ser Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro
    50                  55                  60

Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asn Ala Val Leu Val Ser
65                  70                  75                  80

Ser Ala Ala Ala Asp Thr Ser Ser Ser Glu Lys Gly Met Leu Leu Ser
                85                  90                  95

Phe Glu Asp Glu Ser Gly Lys Ser Trp Arg Phe Arg Tyr Ser Tyr Trp
            100                 105                 110

Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val
        115                 120                 125

Lys Asp Lys Gln Leu Asp Pro Gly Asp Val Val Phe Phe Gln Arg His
    130                 135                 140

Arg Ser Asp Ser Arg Arg Leu Phe Ile Gly Trp Arg Arg Arg Gly Gln
145                 150                 155                 160

Gly Ser Ser Ser Ser Val Ala Ala Thr Asn Ser Ala Val Asn Thr Ser
                165                 170                 175

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

Ser Asn Pro Pro Ser His Ser Glu Tyr Ser His Tyr Gly Ala Ala Val
        195                 200                 205

Ala Thr Ala Ala Glu Thr His Ser Thr Pro Ser Ser Ser Val Val Gly
    210                 215                 220

Ser Ser Arg Thr Val Arg Leu Phe Gly Val Asn Leu Glu Cys Gln Met
225                 230                 235                 240

Asp Glu Asn Asp Gly Asp Asp Ser Val Ala Val Ala Thr Thr Val Glu
                245                 250                 255

Ser Pro Asp Gly Tyr Tyr Gly Gln Asn Met Tyr Tyr Tyr Tyr Ser His
            260                 265                 270

Pro His Asn Met Val Ile Leu Thr Leu Leu
        275                 280


<210> SEQ ID NO 6
<211> LENGTH: 33
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: domain

<400> SEQUENCE: 6

Ser Asn Asn Asn Asn Asn Asn Gly Gly Ser Gly Asp Asp Val Ala Cys
1               5                   10                  15

His Phe Gln Arg Phe Asp Leu His Arg Leu Phe Ile Gly Trp Arg Gly
            20                  25                  30
```

-continued

```
Glu


<210> SEQ ID NO 7
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: domain

<400> SEQUENCE: 7

Val Arg Leu Phe Gly Val Asn Leu Glu
1               5


<210> SEQ ID NO 8
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 8

accatgacat tcgaggttca c                                            21


<210> SEQ ID NO 9
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 9

atcaccacca aaacgacgta g                                            21


<210> SEQ ID NO 10
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 10

tacgtcatgc ttcaaatcgt g                                            21


<210> SEQ ID NO 11
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 11

aggacacgaa caattcattc g                                            21


<210> SEQ ID NO 12
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 12

tacgaataag agcgtccatt ttagagtga                                    29
```

-continued

```
<210> SEQ ID NO 13
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 13

acccaaagaa cagcaatcat g                                            21


<210> SEQ ID NO 14
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 14

aaaacactcc gccattaaac c                                            21


<210> SEQ ID NO 15
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 15

cgagtatcaa tggaaactta accg                                         24


<210> SEQ ID NO 16
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 16

aacggagagt ggcttgagat                                              20


<210> SEQ ID NO 17
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 17

tggcccttat ggtttctgca                                              20


<210> SEQ ID NO 18
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
```

-continued

```
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 18

ntcgantntn gngtt                                                    15


<210> SEQ ID NO 19
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 19

atgtcagtca accattacca c                                             21


<210> SEQ ID NO 20
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 20

caggtaggag atggacgagg ttga                                          24


<210> SEQ ID NO 21
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 21

tgagaggaac catttcttag agg                                           23


<210> SEQ ID NO 22
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 22

acctcgtcca tctcctacct gc                                            22


<210> SEQ ID NO 23
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 23

aaacacgtca aatataacga at                                            22
```

-continued

```
<210> SEQ ID NO 24
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 24

ctttttttg gtttcttgga gtgagagaga gag                                33


<210> SEQ ID NO 25
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 25

agtctgggcc catgtcagtc aaccattac                                    29


<210> SEQ ID NO 26
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 26

gcgactagtt tataaaagag ttaaaatta                                    29


<210> SEQ ID NO 27
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 27

cgggatcctc agtcaaccat tacc                                         24


<210> SEQ ID NO 28
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 28

actagtcgac tcaacctcgt ccatctcc                                     28


<210> SEQ ID NO 29
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 29

gaaatcacag cacttgcacc                                              20


<210> SEQ ID NO 30
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
```

-continued

```
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 30

aagcctttga tcttgagagc                                                    20


<210> SEQ ID NO 31
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 31

gcgacgacgg agaaaggg                                                      18


<210> SEQ ID NO 32
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 32

acgacggcgc catagtgt                                                      18


<210> SEQ ID NO 33
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 33

tttgaagacg agtcaggcaa gt                                                 22


<210> SEQ ID NO 34
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 34

tacggcggct ccatagtggg                                                    20


<210> SEQ ID NO 35
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 35

gtattggagc ggcttgacta cacc                                               24


<210> SEQ ID NO 36
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 36
```

-continued

```
gacggcatca ccatgacatt cg                                            22


<210> SEQ ID NO 37
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 37

tgattctgac atgattgctg ttct                                          24


<210> SEQ ID NO 38
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 38

tcgcaactgt atctgtccct cta                                           23


<210> SEQ ID NO 39
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 39

cgtttcgctt tccttagtgt tagct                                         25


<210> SEQ ID NO 40
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 40

agcgaacgga tctagagact caccttg                                       27


<210> SEQ ID NO 41
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 41

caggcctaag cctaacagta gac                                           23


<210> SEQ ID NO 42
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 42

tgtactagga tttatttacg tag                                           23
```

-continued

```
<210> SEQ ID NO 43
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 43

tattgttcat agaaaccctg caaa                                              24


<210> SEQ ID NO 44
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 44

agtcaatggt ttaatggcgg agtg                                              24


<210> SEQ ID NO 45
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 45

ttctactaca cttgctctct gta                                               23


<210> SEQ ID NO 46
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 46

tacagagagc aagtgtagta gaa                                               23


<210> SEQ ID NO 47
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 47

ttctactaac acctctctct gta                                               23


<210> SEQ ID NO 48
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 48

tacagagaga ggtgttagta gaa                                               23


<210> SEQ ID NO 49
<211> LENGTH: 192
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa
```

-continued

```
<400> SEQUENCE: 49

Met Ala Met His Ala Gly His Ala Trp Trp Gly Val Ala Met Tyr Thr
1               5                   10                  15

Asn His Tyr His His His Tyr Arg His Lys Thr Ser Asp Val Gly Lys
            20                  25                  30

Asn Arg Val Lys His Ala Arg Tyr Gly Gly Gly Asp Ser Gly Lys Gly
        35                  40                  45

Ser Asp Ser Gly Lys Trp Arg Arg Tyr Ser Tyr Trp Thr Ser Ser Ser
    50                  55                  60

Tyr Val Thr Lys Gly Trp Ser Arg Tyr Val Lys Lys Arg Asp Ala Gly
65                  70                  75                  80

Asp Val Val His Arg Val Arg Gly Gly Ala Ala Asp Arg Gly Cys Arg
                85                  90                  95

Arg Arg Gly Ser Ala Ala Ala Val Arg Val Thr Ala Asn Gly Gly Trp
            100                 105                 110

Ser Met Cys Tyr Ser Thr Ser Gly Ser Ser Tyr Asp Thr Ser Ala Asn
        115                 120                 125

Ser Tyr Ala Tyr His Arg Ser Val Asp Asp His Ser Asp His Ala Gly
    130                 135                 140

Ser Arg Ala Asp Ala Lys Ser Ser Ser Ala Ala Ser Ala Ser Arg Arg
145                 150                 155                 160

Arg Gly Val Asn Asp Cys Gly Ala Asp Ala Thr Ala Met Tyr Gly Tyr
                165                 170                 175

Met His His Ser Tyr Ala Ala Val Ser Thr Val Asn Tyr Trp Ser Val
            180                 185                 190


<210> SEQ ID NO 50
<211> LENGTH: 834
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 50

atggccatgc accctctcgc ccaggggcac ccccaggcgt ggccatgggg tgtagccatg      60

tacaccaacc tgcactacca ccaccactac gagagggagc acctgttcga gaagccgctg     120

acgccgagcg acgtcggcaa gctcaacagg ctggtgatcc ccaagcagca cgccgagagg     180

tacttcccgc tcggcggcgg cgactccggt gagaagggcc tcctcctctc cttcgaggac     240

gagtccggca agccatggcg gttccgctac tcctactgga ccagcagcca gagctacgtg     300

ctcaccaagg gctggagccg ctacgtcaag gagaagcgcc tcgacgccgg cgacgtcgtc     360

cacttcgagc gcgtccgcgg cctcggcgcc gccgaccgcc tcttcatcgg ctgcaggcgc     420

cgcggcgaga gcgcgcccgc gccgccgccc gccgttcgcg tcacgccgca gccgcctgcc     480

ctcaacggcg gcgagcagca gccgtggagc ccaatgtgtt acagcacgtc gggctcgtcc     540

tacgacccta ccagccctgc caattcatat gcctaccatc gctccgtaga ccaagatcac     600

agcgacatac tacacgcagg agagtcgcag agagaagcag acgccaagag cagcagcgcg     660

gcgtcggcgc cgccgccgtc gaggcggctc aggctgttcg gcgttaacct cgactgcggc     720

ccggagccgg aggcggatca ggcgacggca atgtacggct acatgcacca ccagagcccc     780

tacgccgcag tgtctacagt gccaaattac tggtcagtat tttttcagtt ttaa           834
```

-continued

```
<210> SEQ ID NO 51
<211> LENGTH: 279
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 51

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

Pro Trp Gly Val Ala Met Tyr Ala Asn Phe His Tyr His His His Tyr
            20                  25                  30

Glu Lys Glu His Met Phe Glu Lys Pro Leu Thr Pro Ser Asp Val Gly
        35                  40                  45

Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe
    50                  55                  60

Pro Leu Gly Ala Gly Asp Ala Ala Asp Lys Gly Leu Ile Leu Ser Phe
65                  70                  75                  80

Glu Asp Glu Ala Gly Ala Pro Trp Arg Phe Arg Tyr Ser Tyr Trp Thr
                85                  90                  95

Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys
            100                 105                 110

Glu Lys Arg Leu Asp Ala Gly Asp Val Val His Phe Glu Arg Val Arg
        115                 120                 125

Gly Ser Phe Gly Val Gly Asp Arg Leu Phe Ile Gly Cys Arg Arg Arg
    130                 135                 140

Gly Asp Ala Ala Ala Ala Gln Thr Pro Ala Pro Pro Pro Ala Val Arg
145                 150                 155                 160

Val Ala Pro Ala Ala Gln Asn Ala Gly Glu Gln Gln Pro Trp Ser Pro
                165                 170                 175

Met Cys Tyr Ser Thr Ser Gly Gly Gly Ser Tyr Pro Thr Ser Pro Ala
            180                 185                 190

Asn Ser Tyr Ala Tyr Arg Arg Ala Ala Asp His Asp His Gly Asp Met
        195                 200                 205

His His Ala Asp Glu Ser Pro Arg Asp Thr Asp Ser Pro Ser Phe Ser
    210                 215                 220

Ala Gly Ser Ala Pro Ser Arg Arg Leu Arg Leu Phe Gly Val Asn Leu
225                 230                 235                 240

Asp Cys Gly Pro Glu Pro Glu Ala Asp Thr Thr Ala Ala Ala Thr Met
                245                 250                 255

Tyr Gly Tyr Met His Gln Gln Ser Ser Tyr Ala Ala Met Ser Ala Val
            260                 265                 270

Pro Ser Tyr Trp Gly Asn Ser
        275


<210> SEQ ID NO 52
<211> LENGTH: 840
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 52

atggccatga accaccctct cttctcccag gagcaacccc agtcctggcc atggggtgtg      60

gccatgtacg ccaacttcca ctaccaccac cactacgaga aggagcacat gtttgagaag     120

cccctgacgc ccagtgacgt ggggaagctg aaccggctgg tgatccccaa gcagcacgcc     180

gagaggtact tcccccctcgg cgccggcgac gccgccgaca agggcctgat cctgtcgttc    240
```

-continued

```
gaggacgagg ccggcgcgcc gtggcggttc aggtactcct actggacgag cagccagagc    300

tacgtgctca ccaagggctg gagccgctac gtcaaggaga agcgcctcga cgccggcgac    360

gtcgtgcact tcgagagggt gcgcggctcc ttcggcgtcg gcgaccgtct cttcatcggc    420

tgcaggcgcc gcggcgacgc cgccgccgcg caaacacccg caccgccgcc cgccgtgcgc    480

gtcgccccgg ctgcacagaa cgccggcgag cagcagccgt ggagcccaat gtgttacagc    540

acgtcgggcg gcggctcata ccctaccagc ccagccaact cctacgccta ccgccgcgca    600

gcagatcatg atcacgggga catgcaccat gcagacgagt ctccgcgcga cacggacagc    660

ccaagcttca gtgcaggctc ggcgccatcg aggcggctca ggctgttcgg cgtcaacctc    720

gactgcgggc cagagccgga ggcagacacc acggcagcgg caacaatgta cggctacatg    780

caccagcaga gctcctatgc tgccatgtct gcagtaccca gttactgggg caattcataa    840


<210> SEQ ID NO 53
<211> LENGTH: 412
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 53

Met Glu Phe Thr Thr Ser Ser Arg Phe Ser Lys Glu Glu Glu Asp Glu
1               5                   10                  15

Glu Gln Asp Glu Ala Gly Arg Arg Glu Ile Pro Phe Met Thr Ala Thr
            20                  25                  30

Ala Glu Ala Ala Pro Ala Pro Thr Ser Ser Ser Ser Ser Pro Ala His
        35                  40                  45

His Ala Ala Ser Ala Ser Ala Ser Ala Ser Ala Ser Gly Ser Ser Thr
    50                  55                  60

Pro Phe Arg Ser Asp Asp Gly Ala Gly Ala Ser Gly Ser Gly Gly Gly
65                  70                  75                  80

Gly Gly Gly Gly Gly Glu Ala Glu Val Val Glu Lys Glu His Met Phe
                85                  90                  95

Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val
            100                 105                 110

Ile Pro Lys Gln Tyr Ala Glu Lys Tyr Phe Pro Leu Asp Ala Ala Ala
        115                 120                 125

Asn Glu Lys Gly Leu Leu Leu Asn Phe Glu Asp Arg Ala Gly Lys Pro
    130                 135                 140

Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met
145                 150                 155                 160

Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Asp Ala Gly
                165                 170                 175

Asp Thr Val Ser Phe Ser Arg Gly Ile Gly Asp Glu Ala Ala Arg His
            180                 185                 190

Arg Leu Phe Ile Asp Trp Lys Arg Arg Ala Asp Thr Arg Asp Pro Leu
        195                 200                 205

Arg Leu Pro Arg Gly Leu Pro Leu Pro Met Pro Leu Thr Ser His Tyr
    210                 215                 220

Ala Pro Trp Gly Ile Gly Gly Gly Gly Gly Phe Phe Val Gln Pro Ser
225                 230                 235                 240

Pro Pro Ala Thr Leu Tyr Glu His Arg Leu Arg Gln Gly Leu Asp Phe
                245                 250                 255
```

-continued

```
Arg Ala Phe Asn Pro Ala Ala Ala Met Gly Arg Gln Val Leu Leu Phe
            260                 265                 270

Gly Ser Ala Arg Ile Pro Pro Gln Ala Pro Leu Leu Ala Arg Ala Pro
        275                 280                 285

Ser Pro Leu His His His Tyr Thr Leu Gln Pro Ser Gly Asp Gly Val
    290                 295                 300

Arg Ala Ala Gly Ser Pro Val Val Leu Asp Ser Val Pro Val Ile Glu
305                 310                 315                 320

Ser Pro Thr Thr Ala Ala Lys Arg Val Arg Leu Phe Gly Val Asn Leu
                325                 330                 335

Asp Asn Pro His Ala Gly Gly Gly Gly Gly Ala Ala Ala Gly Glu Ser
            340                 345                 350

Ser Asn His Gly Asn Ala Leu Ser Leu Gln Thr Pro Ala Trp Met Arg
        355                 360                 365

Arg Asp Pro Thr Leu Arg Leu Leu Glu Leu Pro Pro His His His His
    370                 375                 380

Gly Ala Glu Ser Ser Ala Ala Ser Ser Pro Ser Ser Ser Ser Ser Ser
385                 390                 395                 400

Lys Arg Asp Ala His Ser Ala Leu Asp Leu Asp Leu
                405                 410


<210> SEQ ID NO 54
<211> LENGTH: 1239
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 54

atggagttca ctacaagcag taggttttct aaagaagagg aggacgagga gcaggatgag      60

gcgggaaggc gagagatccc cttcatgacg gccacggccg aagccgcgcc tgcgcccacg     120

tcgtcgtcgt cgtctcctgc tcatcacgcg gcttccgcgt cggcgtcggc gtctgcgtca     180

gggagcagca ctccctttcg ctccgacgat ggcgccgggg cgtctgggag cggcggcggc     240

ggcggcggcg gcggagaagc ggaggtggtg gagaaggagc acatgttcga caaggtggtg     300

acgccgagcg acgttgggaa gctgaaccgg ctggtgatcc cgaagcagta cgccgagaag     360

tacttcccgc tggacgcggc ggcgaacgag aagggcctcc tgctcaactt cgaggaccgc     420

gcggggaagc catggcggtt ccgctactcc tactggaaca gcagccagag ctacgtgatg     480

accaaggggt ggagccgctt cgtcaaggag aagcgcctcg acgccgggga caccgtctcc     540

ttctcccgcg gcatcggcga cgaggcggcg cggcaccgcc tcttcatcga ctggaagcgc     600

cgcgccgaca cccgcgaccc gctccggctg ccccgcgggc tgccgctccc gatgccgctc     660

acgtcgcact acgccccgtg gggatcggc ggcggagggg gattcttcgt gcagccctcg     720

ccgccggcca cgctctacga gcaccgcctc aggcaaggcc tcgacttccg cgccttcaac     780

cccgccgccg cgatggggag gcaggtcctc ctgttcggct cggcgaggat tcctccgcaa     840

gcaccactgc tggcgcgcgc gccgtcgccg ctgcaccacc actacacgct gcagccgagc     900

ggcgatggtg taagggcggc gggctcaccg gtggtgctcg actcggttcc ggtcatcgag     960

agccccacga cggccgcgaa gcgcgtgcgg ctgttcggcg tgaacctcga caacccgcat    1020

gccggcggcg gcggcggcgc cgccgccggc gagtcgagca atcatggcaa tgcactgtca    1080

ttgcagacgc ccgcgtggat gaggagggat ccaacactgc ggctgctgga attgcctcct    1140
```

-continued

```
caccaccacc atggcgccga gtcgtccgct gcatcgtctc cgtcgtcgtc gtcttcctcc   1200

aagagggacg cgcattcggc cttggatctc gatctgtag                           1239


<210> SEQ ID NO 55
<211> LENGTH: 951
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 55

atggagtttg ctacaacgag tagtaggttt tccaaggaag aggaggagga ggaggaaggg     60

gaacaggaga tggagcagga gcaggatgaa gaggaggagg aggcggaggc ctcgccccgc    120

gagatcccct tcatgacgtc ggcggcggcg gcggccaccg cctcatcgtc ctccccgaca    180

tcggtctccc cttccgccac cgcttccgcg gcggcgtcca cgtcggcgtc gggctctccc    240

ttccggtcga gcgacggtgc gggagcgtcg gggagtggcg gcggcggtgg cggcgaggac    300

gtggaggtga tcgagaagga gcacatgttc gacaaggtgg tgacgccgag cgacgtgggg    360

aagctgaacc ggctggtgat cccgaagcag cacgccgaga agtacttccc gctggactcg    420

gcggcgaacg agaagggcct tctcctcagc ttcgaggacc gaaccggcaa gctatggcgc    480

ttccgctact cctactggaa cagcagccag agctacgtca tgaccaaggg ttggagccgc    540

ttcgtcaagg agaagcgcct cgacgccggg gacaccgtct ccttctgccg cggcgccgcc    600

gaggccaccc gcgaccgcct cttcatcgac tggaagcgcc gcgccgacgt ccgcgacccg    660

caccgcttcc agcgcctacc gctccccatg acctcgccct acggcccgtg gggcggcggc    720

gcgggcgctt cttcatgccg cccgcgccgc ccgccacgct ctacgagcat caccgctttc    780

gccagggctt cgacttccgc aacatcaacc ccgctgtgcc ggcgaggcag ctcgtcttct    840

tcggctcccc agggacgggg attcatcagc acccgccctt gccaccgccg ccgtcgccac    900

ctccgcctcc tcaccaactc cacattacgg tgcaccaccc gagccccgta g             951


<210> SEQ ID NO 56
<211> LENGTH: 316
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 56

Met Glu Phe Ala Thr Thr Ser Ser Arg Phe Ser Lys Glu Glu Glu Glu
1               5                   10                  15

Glu Glu Glu Gly Glu Gln Glu Met Glu Gln Glu Gln Asp Glu Glu Glu
            20                  25                  30

Glu Glu Ala Glu Ala Ser Pro Arg Glu Ile Pro Phe Met Thr Ser Ala
        35                  40                  45

Ala Ala Ala Ala Thr Ala Ser Ser Ser Ser Pro Thr Ser Val Ser Pro
    50                  55                  60

Ser Ala Thr Ala Ser Ala Ala Ala Ser Thr Ser Ala Ser Gly Ser Pro
65                  70                  75                  80

Phe Arg Ser Ser Asp Gly Ala Gly Ala Ser Gly Ser Gly Gly Gly Gly
                85                  90                  95

Gly Gly Glu Asp Val Glu Val Ile Glu Lys Glu His Met Phe Asp Lys
            100                 105                 110

Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro
        115                 120                 125
```

-continued

```
Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asp Ser Ala Ala Asn Glu
    130                 135                 140

Lys Gly Leu Leu Leu Ser Phe Glu Asp Arg Thr Gly Lys Leu Trp Arg
145                 150                 155                 160

Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys
                165                 170                 175

Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Asp Ala Gly Asp Thr
            180                 185                 190

Val Ser Phe Cys Arg Gly Ala Ala Glu Ala Thr Arg Asp Arg Leu Phe
        195                 200                 205

Ile Asp Trp Lys Arg Arg Ala Asp Val Arg Asp Pro His Arg Phe Gln
    210                 215                 220

Arg Leu Pro Leu Pro Met Thr Ser Pro Tyr Gly Pro Trp Gly Gly Gly
225                 230                 235                 240

Ala Gly Ala Ser Ser Cys Arg Pro Arg Arg Pro Pro Arg Ser Thr Ser
                245                 250                 255

Ile Thr Ala Phe Ala Arg Ala Ser Thr Ser Ala Thr Ser Thr Pro Leu
            260                 265                 270

Cys Arg Arg Gly Ser Ser Ser Ser Ser Ala Pro Gln Gly Arg Gly Phe
        275                 280                 285

Ile Ser Thr Arg Pro Cys His Arg Arg Arg Arg His Leu Arg Leu Leu
    290                 295                 300

Thr Asn Ser Thr Leu Arg Cys Thr Thr Arg Ala Pro
305                 310                 315
```

```
<210> SEQ ID NO 57
<211> LENGTH: 936
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 57

atggagttca tcacgccaat cgtgaggccg gcatcggcgg cggcgggcgg cggcgaggtg      60

caggagagtg gtgggaggag cttggcggcg gtggagaagg agcacatgtt cgacaaggtg     120

gtgacgccga gcgacgtggg gaagctgaac cggctggtga tcccgaagca gcacgcggag     180

aagtacttcc cgctggacgc ggcgtccaac gagaaggggc tcctgctcag cttcgaggac     240

cgcacgggga agccatggcg gttccgctac tcctactgga acagcagcca gagctacgtg     300

atgaccaagg ggtggagccg cttcgtcaag gagaagcgac tcgacgccgg ggacaccgtc     360

tccttcggcc gcggcgtcgg cgaggccgcg cgcgggaggc tcttcatcga ctggcgccgc     420

cgccccgacg tcgtcgccgc gctccagccg cccacgcacc gcttcgccca ccacctccct     480

tcctccatcc ccttcgctcc ctgggcgcac caccacggac acggagccgc cgccgccgcc     540

gccgccgccg ccggcgccag gtttctcctg cctccctcct cgactcccat ctacgaccac     600

caccgccgac acgcccacgc cgtcgggtac gacgcgtacg ccgcggccac cagcaggcag     660

gtgctgttct accggccgtt gccgccgcag cagcagcatc atcccgcggt ggtgctggag     720

tcggtgccgg tgcgcatgac ggcggggcac gcggagccgc cgtcggctcc gtcgaagcga     780

gttcggctgt tcggggtgaa cctcgactgc gcgaattccg aacaagacca cgccggcgtg     840

gtcgggaaga cggcgccgcc gccgctgcca tcgccgccgt catcatcgtc atcttcctcc     900

gggaaagcga ggtgctcctt gaaccttgac ttgtga                               936
```

-continued

```
<210> SEQ ID NO 58
<211> LENGTH: 311
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 58

Met Glu Phe Ile Thr Pro Ile Val Arg Pro Ala Ser Ala Ala Ala Gly
1               5                   10                  15

Gly Gly Glu Val Gln Glu Ser Gly Gly Arg Ser Leu Ala Ala Val Glu
            20                  25                  30

Lys Glu His Met Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys
        35                  40                  45

Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro
    50                  55                  60

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

Arg Thr Gly Lys Pro Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser
                85                  90                  95

Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys
            100                 105                 110

Arg Leu Asp Ala Gly Asp Thr Val Ser Phe Gly Arg Gly Val Gly Glu
        115                 120                 125

Ala Ala Arg Gly Arg Leu Phe Ile Asp Trp Arg Arg Arg Pro Asp Val
    130                 135                 140

Val Ala Ala Leu Gln Pro Pro Thr His Arg Phe Ala His His Leu Pro
145                 150                 155                 160

Ser Ser Ile Pro Phe Ala Pro Trp Ala His His His Gly His Gly Ala
                165                 170                 175

Ala Ala Ala Ala Ala Ala Ala Ala Gly Ala Arg Phe Leu Leu Pro Pro
            180                 185                 190

Ser Ser Thr Pro Ile Tyr Asp His His Arg Arg His Ala His Ala Val
        195                 200                 205

Gly Tyr Asp Ala Tyr Ala Ala Ala Thr Ser Arg Gln Val Leu Phe Tyr
    210                 215                 220

Arg Pro Leu Pro Pro Gln Gln Gln His His Pro Ala Val Val Leu Glu
225                 230                 235                 240

Ser Val Pro Val Arg Met Thr Ala Gly His Ala Glu Pro Pro Ser Ala
                245                 250                 255

Pro Ser Lys Arg Val Arg Leu Phe Gly Val Asn Leu Asp Cys Ala Asn
            260                 265                 270

Ser Glu Gln Asp His Ala Gly Val Val Gly Lys Thr Ala Pro Pro Pro
        275                 280                 285

Leu Pro Ser Pro Pro Ser Ser Ser Ser Ser Ser Ser Gly Lys Ala Arg
    290                 295                 300

Cys Ser Leu Asn Leu Asp Leu
305                 310


<210> SEQ ID NO 59
<211> LENGTH: 1182
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 59
```

-continued

```
atggacagct ccagctgcct ggtggatgat accaacagcg gcggctcgtc cacggacaag     60

ctgagggcgt tggccgccgc ggcggcggag acggcgccgc tggagcgcat ggggagcggg    120

gcgagcgcgg tggtggacgc ggccgagcct ggcgcggagg cggactccgg gtccggggga    180

cgtgtgtgcg gcggcggcgg cggcggtgcc ggcggtgcgg gagggaagct gccgtcgtcc    240

aagttcaagg gcgtcgtgcc gcagcccaac gggaggtggg gcgcgcagat ctacgagcgg    300

caccagcggg tgtggctcgg cacgttcgcc ggggaggacg acgccgcgcg cgcctacgac    360

gtcgccgcgc agcgcttccg cggccgcgac gccgtcacca acttccgccc gctcgccgag    420

gccgacccgg acgccgccgc cgagcttcgc ttcctcgcca cgcgctccaa ggccgaggtc    480

gtcgacatgc tccgcaagca cacctacttc gacgagctcg cgcagagcaa gcgcaccttc    540

gccgcctcca cgccgtcggc cgcgaccacc accgcctccc tctccaacgg ccacctctcg    600

tcgccccgct ccccccttcgc gcccgccgcg gcgcgcgacc acctgttcga caagacggtc    660

accccgagcg acgtgggcaa gctgaacagg ctcgtcatac cgaagcagca cgccgagaag    720

cacttcccgc tacagctccc gtccgccggc ggcgagagca agggtgtcct cctcaacttc    780

gaggacgccg ccggcaaggt gtggcggttc cggtactcgt actggaacag cagccagagc    840

tacgtgctaa ccaagggctg gagccgcttc gtcaaggaga agggtctcca cgccggcgac    900

gtcgtcggct tctaccgctc cgccgccagt gccggcgacg acggcaagct cttcatcgac    960

tgcaagttag tacggtcgac cggcgccgcc ctcgcgtcgc ccgctgatca gccagcgccg   1020

tcgccggtga aggccgtcag gctcttcggc gtggacctgc tcacggcgcc ggcgccggtc   1080

gaacagatgg ccgggtgcaa gagagccagg gacttggcgg cgacgacgcc tccacaagcg   1140

gcggcgttca agaagcaatg catagagctg gcactagtat ag                      1182
```

<210> SEQ ID NO 60
<211> LENGTH: 393
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 60

```
Met Asp Ser Ser Ser Cys Leu Val Asp Asp Thr Asn Ser Gly Gly Ser
1               5                   10                  15

Ser Thr Asp Lys Leu Arg Ala Leu Ala Ala Ala Ala Ala Glu Thr Ala
            20                  25                  30

Pro Leu Glu Arg Met Gly Ser Gly Ala Ser Ala Val Val Asp Ala Ala
        35                  40                  45

Glu Pro Gly Ala Glu Ala Asp Ser Gly Ser Gly Gly Arg Val Cys Gly
    50                  55                  60

Gly Gly Gly Gly Gly Ala Gly Gly Ala Gly Gly Lys Leu Pro Ser Ser
65                  70                  75                  80

Lys Phe Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln
                85                  90                  95

Ile Tyr Glu Arg His Gln Arg Val Trp Leu Gly Thr Phe Ala Gly Glu
            100                 105                 110

Asp Asp Ala Ala Arg Ala Tyr Asp Val Ala Ala Gln Arg Phe Arg Gly
        115                 120                 125

Arg Asp Ala Val Thr Asn Phe Arg Pro Leu Ala Glu Ala Asp Pro Asp
    130                 135                 140
```

-continued

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

Val Asp Met Leu Arg Lys His Thr Tyr Phe Asp Glu Leu Ala Gln Ser
165 170 175

Lys Arg Thr Phe Ala Ala Ser Thr Pro Ser Ala Ala Thr Thr Thr Ala
180 185 190

Ser Leu Ser Asn Gly His Leu Ser Ser Pro Arg Ser Pro Phe Ala Pro
195 200 205

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

Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys
225 230 235 240

His Phe Pro Leu Gln Leu Pro Ser Ala Gly Gly Glu Ser Lys Gly Val
245 250 255

Leu Leu Asn Phe Glu Asp Ala Ala Gly Lys Val Trp Arg Phe Arg Tyr
260 265 270

Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
275 280 285

Arg Phe Val Lys Glu Lys Gly Leu His Ala Gly Asp Val Val Gly Phe
290 295 300

Tyr Arg Ser Ala Ala Ser Ala Gly Asp Asp Gly Lys Leu Phe Ile Asp
305 310 315 320

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

Gln Pro Ala Pro Ser Pro Val Lys Ala Val Arg Leu Phe Gly Val Asp
340 345 350

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

Ala Arg Asp Leu Ala Ala Thr Thr Pro Pro Gln Ala Ala Ala Phe Lys
370 375 380

Lys Gln Cys Ile Glu Leu Ala Leu Val
385 390

<210> SEQ ID NO 61
<211> LENGTH: 939
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 61

atggagttca ccccaatttc gccgccgacg agggtcgccg gcggtgagga ggattccgag 60

agggggggcgg cggcgtgggc ggtggtggag aaggagcaca tgtttgagaa ggtcgtgacg 120

ccgagcgacg tggggaagct gaaccgattg gtcatcccca agcagcacgc cgagaggtac 180

ttcccgctcg acgccgcggc gggcgccggc ggcggcggtg gtggcggcgg tggcggcggc 240

ggggggaagg ggctggtgct gagcttcgag gacaggacgg ggaaggcgtg gaggttccgg 300

tactcgtact ggaacagcag ccagagctac gtgatgacca aagggtggag ccgcttcgtc 360

aaggagaagc gcctcggcgc cggcgacacc gtgtcgttcg gccgcggcct cggcgacgcc 420

gcccgcggcc gcctcttcat cgacttccgc cgccgccgcc aggacgccgg cagcttcatg 480

ttcccgccga cggcggcgcc gccgtcgcac tcgcaccacc atcatcagcg acaccacccg 540

ccgctcccgt ccgtgcccct ttgcccgtgg cgagactaca ccaccgccta tggcggcggc 600

-continued

```
tacggctacg gctacggcgg cggctccacc ccggcgtcca gccgccacgt gctgttcctc     660

cggccgcagg tgccggccgc tgtggtgctc aagtcggtgc cggtgcacgt cgcggccacc     720

tcggcggtgc aggaggcggc gacgacgaca aggccgaagc gtgtccggct gttcggggtg     780

aacctcgact gcccggcggc catggacgac gacgacgaca tcgccggagc ggcgagccgg     840

acggcagcgt cgtctctcct gcagctcccc tcgccgtcgt cctcgacgtc gtcgtcgacg     900

gcggggaaga agatgtgctc cttggatctt gggttgtga                            939


<210> SEQ ID NO 62
<211> LENGTH: 312
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 62

Met Glu Phe Thr Pro Ile Ser Pro Pro Thr Arg Val Ala Gly Gly Glu
1               5                   10                  15

Glu Asp Ser Glu Arg Gly Ala Ala Ala Trp Ala Val Val Glu Lys Glu
            20                  25                  30

His Met Phe Glu Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn
        35                  40                  45

Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe Pro Leu Asp
    50                  55                  60

Ala Ala Ala Gly Ala Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
65                  70                  75                  80

Gly Gly Lys Gly Leu Val Leu Ser Phe Glu Asp Arg Thr Gly Lys Ala
                85                  90                  95

Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met
            100                 105                 110

Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Gly Ala Gly
        115                 120                 125

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

Leu Phe Ile Asp Phe Arg Arg Arg Arg Gln Asp Ala Gly Ser Phe Met
145                 150                 155                 160

Phe Pro Pro Thr Ala Ala Pro Pro Ser His Ser His His His His Gln
                165                 170                 175

Arg His His Pro Pro Leu Pro Ser Val Pro Leu Cys Pro Trp Arg Asp
            180                 185                 190

Tyr Thr Thr Ala Tyr Gly Gly Gly Tyr Gly Tyr Gly Tyr Gly Gly Gly
        195                 200                 205

Ser Thr Pro Ala Ser Ser Arg His Val Leu Phe Leu Arg Pro Gln Val
    210                 215                 220

Pro Ala Ala Val Val Leu Lys Ser Val Pro Val His Val Ala Ala Thr
225                 230                 235                 240

Ser Ala Val Gln Glu Ala Ala Thr Thr Thr Arg Pro Lys Arg Val Arg
                245                 250                 255

Leu Phe Gly Val Asn Leu Asp Cys Pro Ala Ala Met Asp Asp Asp Asp
            260                 265                 270

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

Leu Pro Ser Pro Ser Ser Ser Thr Ser Ser Ser Thr Ala Gly Lys Lys
    290                 295                 300
```

-continued

```
Met Cys Ser Leu Asp Leu Gly Leu
305                 310


<210> SEQ ID NO 63
<211> LENGTH: 337
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 63

Met Ser Ile Asn His Tyr Ser Met Asp Leu Pro Glu Pro Thr Leu Trp
1               5                   10                  15

Trp Pro His Pro His His Gln Gln Gln Gln Leu Thr Leu Met Asp Pro
            20                  25                  30

Asp Pro Leu Arg Leu Asn Leu Asn Ser Asp Asp Gly Asn Gly Asn Asp
        35                  40                  45

Asn Asp Asn Asp Glu Asn Gln Thr Thr Thr Thr Gly Gly Glu Gln Glu
    50                  55                  60

Ile Leu Asp Asp Lys Glu Pro Met Phe Glu Lys Pro Leu Thr Pro Ser
65                  70                  75                  80

Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu
                85                  90                  95

Lys Tyr Phe Pro Leu Ser Gly Asp Ser Gly Gly Ser Glu Cys Lys Gly
            100                 105                 110

Leu Leu Leu Ser Phe Glu Asp Glu Ser Gly Lys Cys Trp Arg Phe Arg
        115                 120                 125

Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp
    130                 135                 140

Ser Arg Tyr Val Lys Asp Lys Arg Leu Asp Ala Gly Asp Val Val Leu
145                 150                 155                 160

Phe Glu Arg His Arg Val Asp Ala Gln Arg Leu Phe Ile Gly Trp Arg
                165                 170                 175

Arg Arg Arg Gln Ser Asp Ala Ala Leu Pro Pro Ala His Val Ser Ser
            180                 185                 190

Arg Lys Ser Gly Gly Gly Asp Gly Asn Ser Asn Lys Asn Glu Gly Trp
        195                 200                 205

Thr Arg Gly Phe Tyr Ser Ala His His Pro Tyr Pro Thr His His Leu
    210                 215                 220

His His His Gln Pro Ser Pro Tyr Gln Gln Gln His Asp Cys Leu His
225                 230                 235                 240

Ala Gly Arg Gly Ser Gln Gly Gln Asn Gln Arg Met Arg Pro Val Gly
                245                 250                 255

Asn Asn Ser Ser Ser Ser Ser Ser Ser Ser Arg Val Leu Arg Leu Phe
            260                 265                 270

Gly Val Asp Met Glu Cys Gln Pro Glu His Asp Asp Ser Gly Pro Ser
        275                 280                 285

Thr Pro Gln Cys Ser Tyr Asn Ser Asn Asn Met Leu Pro Ser Thr Gln
    290                 295                 300

Gly Thr Asp His Ser His His Asn Phe Tyr Gln Gln Gln Pro Ser Asn
305                 310                 315                 320

Ser Asn Pro Ser Pro His His Met Met Val His His Gln Pro Tyr Tyr
                325                 330                 335

Tyr
```

```
<210> SEQ ID NO 64
<211> LENGTH: 1014
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 64

atgtccataa accactactc catggacctt cccgaaccga cactctggtg gccacaccca      60

caccaccaac aacaacaact aaccttaatg gatcctgacc ctctccgtct caacctcaat     120

agcgacgatg gcaatggcaa tgacaacgac aacgacgaaa atcaaacaac cacaacagga     180

ggagaacaag aaatattaga cgataaagaa ccgatgttcg agaagccctt aaccccgagc     240

gacgtgggga agctgaaccg tctcgtaatc ccgaagcagc acgcggagaa gtacttccca     300

ctgagtggtg actcgggcgg gagcgagtgc aaggggctgt tactgagttt cgaggacgag     360

tcggggaagt gttggcgctt ccgctactcg tactggaaca gcagccagag ctacgtgctc     420

accaaagggt ggagccgcta cgtcaaggac aagcgccttg acgcgggcga cgtcgttttg     480

ttcgagcgtc accgcgtcga cgcgcagcgc ctcttcatcg ggtggaggcg caggcggcag     540

agcgatgccg ccttgccgcc tgcgcacgtt agcagtagga agagtggtgg tggtgatggg     600

aatagtaata agaatgaggg gtggaccaga gggttctatt ctgcgcatca tccttatcct     660

acgcatcatc ttcatcatca tcagccctcg ccataccaac aacaacatga ctgtcttcat     720

gcaggtagag ggtcccaagg tcagaaccaa aggatgagac cagtgggaaa caacagttct     780

agctctagtt cgagttcaag ggtacttagg ctgttcgggg tcgacatgga atgccaaccc     840

gaacatgatg attctggtcc ctccacaccc caatgctcct acaatagtaa caacatgttg     900

ccatcaacac agggcacaga tcattcccat cacaatttct accaacagca accttctaat     960

tccaatcctt cccctcatca catgatggta catcaccaac catactacta ctag          1014


<210> SEQ ID NO 65
<211> LENGTH: 344
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 65

Met Ser Thr Asn His Tyr Thr Met Asp Leu Pro Glu Pro Thr Leu Trp
1               5                   10                  15

Trp Pro His Pro His Gln Gln Gln Leu Thr Leu Ile Asp Pro Asp Pro
            20                  25                  30

Leu Pro Leu Asn Leu Asn Asn Asp Asp Asn Asp Asn Gly Asp Asp Asn
        35                  40                  45

Asp Asn Asp Glu Asn Gln Thr Val Thr Thr Thr Thr Thr Gly Gly Glu
    50                  55                  60

Glu Glu Ile Ile Asn Asn Lys Glu Pro Met Phe Glu Lys Pro Leu Thr
65                  70                  75                  80

Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His
                85                  90                  95

Ala Glu Lys Tyr Phe Pro Leu Ser Gly Gly Asp Ser Gly Ser Ser Glu
            100                 105                 110

Cys Lys Gly Leu Leu Leu Ser Phe Glu Asp Glu Ser Gly Lys Cys Trp
        115                 120                 125

Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr
```

-continued

130 135 140

Lys Gly Trp Ser Arg Tyr Val Lys Asp Lys Arg Leu Asp Ala Gly Asp
145 150 155 160

Val Val Leu Phe Gln Arg His Arg Ala Asp Ala Gln Arg Leu Phe Ile
165 170 175

Gly Trp Arg Arg Arg Gln Ser Asp Ala Leu Pro Pro Pro Ala His
180 185 190

Val Ser Ser Arg Lys Ser Gly Gly Asp Gly Asn Ser Ser Lys Asn Glu
195 200 205

Gly Asp Val Gly Val Gly Trp Thr Arg Gly Phe Tyr Pro Ala His His
210 215 220

Pro Tyr Pro Thr His His His His Pro Ser Pro Tyr His His Gln Gln
225 230 235 240

Asp Asp Ser Leu His Ala Val Arg Gly Ser Gln Gly Gln Asn Gln Arg
245 250 255

Thr Arg Pro Val Gly Asn Ser Ser Ser Ser Ser Ser Ser Ser Ser Arg
260 265 270

Val Leu Arg Leu Phe Gly Val Asn Met Glu Cys Gln Pro Glu His Asp
275 280 285

Asp Ser Gly Pro Ser Thr Pro Gln Cys Ser Tyr Asn Thr Asn Asn Ile
290 295 300

Leu Pro Ser Thr Gln Gly Thr Asp Ile His Ser His Leu Asn Phe Tyr
305 310 315 320

Gln Gln Gln Gln Thr Ser Asn Ser Lys Pro Pro Pro His His Met Met
325 330 335

Ile Arg His Gln Pro Tyr Tyr Tyr
340

<210> SEQ ID NO 66
<211> LENGTH: 1035
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 66

atgtcgacaa accactacac catggacctt cccgaaccaa cactctggtg gccacaccca 60

caccaacaac aactaacctt aatagatcca gaccctctcc ctctgaacct caacaacgac 120

gacaacgaca atggcgacga caacgacaac gacgaaaacc aaacagttac aacaaccaca 180

acaggaggag aagaagaaat aataaacaat aaagaaccga tgttcgagaa gccgctaacc 240

ccgagcgacg tggggaagct gaaccgcctc gtaatcccga agcagcacgc tgagaagtac 300

tttccactga gtggtggtga ctcgggcagt agcgagtgca aggggctgtt actgagtttc 360

gaggacgagt cggggaagtg ctggcgcttc cgctactcgt actggaacag cagccagagc 420

tacgtgctca ccaaagggtg gagccgttac gtgaaggaca agcgcctcga tgcgggagat 480

gtcgttttat tccagcgcca ccgcgccgac gcgcagcgcc tcttcatcgg ctggaggcgc 540

aggcggcaga gcgacgccct gccgccgcct gcgcacgtta gcagcaggaa gagtggtggt 600

gatgggaata gtagtaagaa tgagggtgat gtgggcgtgg gctggaccag agggttctat 660

cctgcgcatc atccttatcc tacgcatcat catcatccct cgccatacca tcaccaacaa 720

gatgactctc ttcatgcagt tagagggtcc caaggtcaga accaaaggac gagaccagtg 780

ggaaacagca gttctagttc gagttcgagt tcaagggtac ttaggctatt cggggtcaac 840

-continued

```
atggaatgcc aacccgaaca tgatgattct ggaccctcca caccccaatg ctcctacaat    900

actaacaaca tattgccatc cacacagggc acagatattc attcccatct caatttctac    960

caacaacaac aaacttctaa ttccaagcct ccccctcatc acatgatgat acgtcaccaa   1020

ccatactact actag                                                    1035


<210> SEQ ID NO 67
<211> LENGTH: 288
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 67

Met Ser Ser Ile Asn His Tyr Ser Pro Glu Thr Thr Leu Tyr Trp Thr
1               5                   10                  15

Asn Asp Gln Gln Gln Gln Ala Ala Met Trp Leu Ser Asn Ser His Thr
            20                  25                  30

Pro Arg Phe Asn Leu Asn Asp Glu Glu Glu Glu Glu Glu Asp Asp Val
        35                  40                  45

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

Val Ala Met Phe Glu Lys Pro Leu Thr Pro Ser Asp Val Gly Lys Leu
65                  70                  75                  80

Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu
                85                  90                  95

Asp Ser Ser Ala Ala Lys Gly Leu Leu Leu Ser Phe Glu Asp Glu Ser
            100                 105                 110

Gly Lys Cys Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser
        115                 120                 125

Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys Asp Lys Arg Leu
    130                 135                 140

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

Arg Phe Phe Ile Ser Cys Ser Arg Arg Gln Pro Asn Pro Val Pro Ala
                165                 170                 175

His Val Ser Thr Thr Arg Ser Ser Ala Ser Phe Tyr Ser Ala His Pro
            180                 185                 190

Pro Tyr Pro Ala His His Phe Pro Phe Pro Tyr Gln Pro His Ser Leu
        195                 200                 205

His Ala Pro Gly Gly Gly Ser Gln Gly Gln Asn Glu Thr Thr Pro Gly
    210                 215                 220

Gly Asn Ser Ser Ser Ser Gly Ser Gly Arg Val Leu Arg Leu Phe Gly
225                 230                 235                 240

Val Asn Met Glu Cys Gln Pro Asp Asn His Asn Asp Ser Gln Asn Ser
                245                 250                 255

Thr Pro Glu Cys Ser Tyr Thr His Leu Tyr His His Gln Thr Ser Ser
            260                 265                 270

Tyr Ser Ser Ser Ser Asn Pro His His His Met Val Pro Gln Gln Pro
        275                 280                 285


<210> SEQ ID NO 68
<211> LENGTH: 867
<212> TYPE: DNA
<213> ORGANISM: Glycine max
```

-continued

```
<400> SEQUENCE: 68

atgtcatcga taaaccacta ttcaccggaa acaacactat actggaccaa cgaccaacag      60

caacaagccg ccatgtggct gagtaattcc cacaccccgc gtttcaatct gaacgacgag     120

gaggaggagg aggaagacga cgttatcgtt tcggacaagg ctactaataa cttgacgcaa     180

gaggaggaga aggtagccat gttcgagaag ccgttgacgc cgagcgacgt cgggaagctg     240

aaccggctcg tgattccgaa acagcacgcg gagaagcact tccctctcga ctcgtcggcg     300

gcgaaggggc tgttgctgag tttcgaggac gagtccggga agtgttggcg cttccgttac     360

tcttattgga acagtagcca gagttacgtt ttgaccaaag gatggagccg ttacgtcaaa     420

gacaaacgcc tccacgctgg cgacgtcgtt ttgttccaca gacaccgctc cctccctcaa     480

cgcttcttca tctcctgcag ccgccgccaa cccaacccgg tccccgctca cgttagcacc     540

accagatcct ccgcttcctt ctactctgcg cacccacctt atcctgcgca ccacttcccc     600

ttcccatacc aacctcactc tcttcatgca ccaggtggag ggtcccaagg acagaacgaa     660

acgacaccgg gagggaacag tagttcaagt ggcagtggca gggtgctgag gctctttggt     720

gtgaacatgg aatgccaacc tgataatcat aatgattccc agaactccac accagaatgc     780

tcctacaccc acttatacca ccatcaaacc tcttcttatt cttcttcttc aaaccctcac     840

catcacatgg tacctcaaca accataa                                         867


<210> SEQ ID NO 69
<211> LENGTH: 420
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 69

Met Glu Leu Met Gln Gln Val Lys Gly Asn Tyr Ser Asp Ser Arg Glu
1               5                   10                  15

Glu Glu Glu Glu Glu Glu Ala Ala Ala Ile Thr Arg Glu Ser Glu Ser
            20                  25                  30

Ser Arg Leu His Gln Gln Asp Thr Ala Ser Asn Phe Gly Lys Lys Leu
        35                  40                  45

Asp Leu Met Asp Leu Ser Leu Gly Ser Ser Lys Glu Glu Glu Glu Glu
    50                  55                  60

Gly Asn Leu Gln Gln Gly Gly Gly Gly Val Val His His Ala His Gln
65                  70                  75                  80

Val Val Glu Lys Glu His Met Phe Glu Lys Val Ala Thr Pro Ser Asp
                85                  90                  95

Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys
            100                 105                 110

Tyr Phe Pro Leu Asp Ser Ser Thr Asn Glu Lys Gly Leu Leu Leu Asn
        115                 120                 125

Phe Glu Asp Arg Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp
    130                 135                 140

Asn Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val
145                 150                 155                 160

Lys Glu Lys Lys Leu Asp Ala Gly Asp Ile Val Ser Phe Gln Arg Gly
                165                 170                 175

Leu Gly Asp Leu Tyr Arg His Arg Leu Tyr Ile Asp Trp Lys Arg Arg
            180                 185                 190
```

-continued

```
Pro Asp His Ala His Ala His Pro Pro His His His Asp Pro Leu Phe
        195                 200                 205

Leu Pro Ser Ile Arg Leu Tyr Ser Leu Pro Pro Thr Met Pro Pro Arg
    210                 215                 220

Tyr His His Asp His His Phe His His His Leu Asn Tyr Asn Asn Leu
225                 230                 235                 240

Phe Thr Phe Gln Gln His Gln Tyr Gln Gln Leu Gly Ala Ala Thr Thr
                245                 250                 255

Thr His His Asn Asn Tyr Gly Tyr Gln Asn Ser Gly Ser Gly Ser Leu
            260                 265                 270

Tyr Tyr Leu Arg Ser Ser Met Ser Met Gly Gly Gly Asp Gln Asn Leu
        275                 280                 285

Gln Gly Arg Gly Ser Asn Ile Val Pro Met Ile Ile Asp Ser Val Pro
    290                 295                 300

Val Asn Val Ala His His Asn Asn Asn Arg His Gly Asn Gly Gly Ile
305                 310                 315                 320

Thr Ser Gly Gly Thr Asn Cys Ser Gly Lys Arg Leu Arg Leu Phe Gly
                325                 330                 335

Val Asn Met Glu Cys Ala Ser Ser Ala Glu Asp Ser Lys Glu Leu Ser
            340                 345                 350

Ser Gly Ser Ala Ala His Val Thr Thr Ala Ala Ser Ser Ser Ser Leu
        355                 360                 365

His His Gln Arg Leu Arg Val Pro Val Pro Val Pro Leu Glu Asp Pro
    370                 375                 380

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

Ala Ser Thr Gly Thr Ser Leu Leu Phe Asp Leu Asp Pro Ser Leu Gln
                405                 410                 415

Tyr His Arg His
            420


<210> SEQ ID NO 70
<211> LENGTH: 1263
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 70

atggagttga tgcaacaagt taaaggtaat tattctgata gcagggagga agaggaggaa     60

gaggaagctg cagcaatcac aagggaatca gaaagcagca ggttacacca acaagataca    120

gcatccaatt ttggaaagaa gctagacttg atggacttgt cactagggag cagcaaggaa    180

gaggaagagg aagggaattt gcaacaagga ggaggaggag tggttcatca tgctcaccaa    240

gtagtggaga aagaacacat gtttgagaaa gtggcgacac cgagcgacgt agggaagctg    300

aacaggctgg tgataccgaa gcagcacgcg gagaagtact tcccccttga ctcctcaacc    360

aacgagaagg gtctgctcct gaatttcgag gacaggaatg ggaaggtgtg gcgattcagg    420

tattcctatt ggaacagcag ccagagctat gtgatgacaa aagggtggag ccgctttgtt    480

aaggagaaga agctggatgc cggtgacatt gtctccttcc agcgtggcct tggggatttg    540

tatagacatc ggttgtatat agattggaag agaaggcccg atcatgctca tgctcatcca    600

cctcatcatc acgatccttt gtttcttccc tctatcagat tgtactctct ccctcccacc    660
```

-continued

```
atgccacctc gctaccacca cgatcatcac tttcaccacc atctcaatta caacaacctc    720

ttcacttttc agcaacacca gtaccagcag cttggtgctg ccactaccac tcatcacaac    780

aactatggtt accagaattc gggatctggt tcactctatt acctaaggtc ctctatgtca    840

atgggtggtg gtgatcaaaa cttgcaaggg agagggagca acattgtccc catgatcatt    900

gattctgtgc cggttaacgt tgctcatcac aacaacaatc gccatgggaa tgggggcatc    960

acgagtggtg gtactaattg tagtggaaaa cgactaaggc tatttggggt gaacatggaa   1020

tgcgcttctt cggcagaaga ttccaaagaa ttgtcctcgg gttcggcagc acacgtgacg   1080

acagctgctt cttcttcttc tcttcatcat cagcgcttga gggtgccagt gccagtgcca   1140

cttgaagatc cactttcgtc gtcagcagca gcagcagcaa ggtttgggga tcacaaaggg   1200

gccagtactg ggacttcgct gctgtttgat ttggatccct ctttgcagta tcatcgccac   1260

tga                                                                 1263
```

```
<210> SEQ ID NO 71
<211> LENGTH: 384
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 71

Met Asp Ala Ile Ser Cys Leu Asp Glu Ser Thr Thr Thr Glu Ser Leu
1               5                   10                  15

Ser Ile Ser Gln Ala Lys Pro Ser Ser Thr Ile Met Ser Ser Glu Lys
            20                  25                  30

Ala Ser Pro Ser Pro Pro Pro Pro Asn Arg Leu Cys Arg Val Gly Ser
        35                  40                  45

Gly Ala Ser Ala Val Val Asp Ser Asp Gly Gly Gly Gly Gly Gly Ser
    50                  55                  60

Thr Glu Val Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val
65                  70                  75                  80

Val Pro Gln Pro Asn Gly Arg Trp Gly Ser Gln Ile Tyr Glu Lys His
                85                  90                  95

Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala Arg
            100                 105                 110

Ala Tyr Asp Val Ala Val Gln Arg Phe Arg Gly Lys Asp Ala Val Thr
        115                 120                 125

Asn Phe Lys Pro Leu Ser Gly Thr Asp Asp Asp Asp Gly Glu Ser Glu
    130                 135                 140

Phe Leu Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys
145                 150                 155                 160

His Thr Tyr Asn Asp Glu Leu Glu Gln Ser Lys Arg Ser Arg Gly Phe
                165                 170                 175

Val Arg Arg Arg Gly Ser Ala Ala Gly Ala Gly Asn Gly Asn Ser Ile
            180                 185                 190

Ser Gly Ala Cys Val Met Lys Ala Arg Glu Gln Leu Phe Gln Lys Ala
        195                 200                 205

Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys
    210                 215                 220

Gln His Ala Glu Lys His Phe Pro Leu Gln Ser Ala Ala Asn Gly Val
225                 230                 235                 240

Ser Ala Thr Ala Thr Ala Ala Lys Gly Val Leu Leu Asn Phe Glu Asp
```

-continued

```
                245                 250                 255

Val Gly Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser
            260                 265                 270

Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys
        275                 280                 285

Asn Leu Lys Ala Gly Asp Thr Val Cys Phe Gln Arg Ser Thr Gly Pro
    290                 295                 300

Asp Arg Gln Leu Tyr Ile Asp Trp Lys Thr Arg Asn Val Val Asn Glu
305                 310                 315                 320

Val Ala Leu Phe Gly Pro Val Val Glu Pro Ile Gln Met Val Arg Leu
                325                 330                 335

Phe Gly Val Asn Ile Leu Lys Leu Pro Gly Ser Asp Ser Ile Ala Asn
            340                 345                 350

Asn Asn Asn Ala Ser Gly Cys Cys Asn Gly Lys Arg Arg Glu Met Glu
        355                 360                 365

Leu Phe Ser Leu Glu Cys Ser Lys Lys Pro Lys Ile Ile Gly Ala Leu
    370                 375                 380
```

<210> SEQ ID NO 72
<211> LENGTH: 1155
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 72

```
atggatgcaa ttagttgcct ggatgagagc accaccaccg agtcactctc cataagtcag     60

gcgaagcctt cttcgacgat tatgtcgtcc gagaaggctt ctccttcccc gccgccgccg    120

aacaggctgt gccgcgtcgg tagcggtgct agcgcagtcg tggattccga cggcggcggc    180

gggggtggca gcaccgaggt ggagtcgcgg aagctcccct cgtccaagta taagggcgtc    240

gtgccccagc ccaacggccg ctggggctcg cagatttacg agaagcacca gcgcgtgtgg    300

ctgggaacgt tcaacgagga agacgaggcg gcgcgtgcgt acgacgtcgc cgtgcagcga    360

ttccgcggca aggacgccgt cacaaacttc aagccgctct ccggcaccga cgacgacgac    420

ggggaatcgg agtttctcaa ctcgcattcg aaatccgaga tcgtcgacat gctgcgtaag    480

catacgtaca atgacgagct ggaacaaagc aagcgcagcc gcggcttcgt acgtcggcgc    540

ggctccgccg ccggcgccgg aaacggaaac tcaatctccg gcgcgtgtgt tatgaaggcg    600

cgtgagcagc tattccagaa ggccgttacg ccgagcgacg ttgggaaact gaaccgtttg    660

gtgataccga agcagcacgc ggagaagcac tttcctttac agagcgctgc taacggcgtt    720

agcgcgacgg cgacggcggc gaagggcgtt ttgttgaact tcgaagacgt tggagggaaa    780

gtgtggcggt ttcgttactc gtattggaac agtagccaga gttacgtctt gaccaaaggt    840

tggagccggt tcgttaagga gaagaatctg aaagccggtg acacggtttg ttttcaacgg    900

tccactggac cggacaggca gctttacatc gattggaaga cgaggaatgt tgttaacgag    960

gtcgcgttgt tcggaccggt tgtcgaaccg atccagatgg ttcggctctt tggtgttaac   1020

attttgaaac tacccggttc agattctatc gccaataaca ataatgcaag tgggtgctgc   1080

aatggcaaga gaagagaaat ggaactcttt tcattagagt gtagcaagaa acctaagatt   1140

attggtgctt tgtag                                                     1155
```

<210> SEQ ID NO 73

-continued

<211> LENGTH: 491
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 73

Met Glu Leu Met Gln Glu Val Lys Gly Tyr Ser Asp Gly Arg Glu Glu
1 5 10 15

Glu Glu Glu Glu Glu Glu Ala Ala Glu Glu Ile Ile Thr Arg Glu Glu
20 25 30

Ser Ser Arg Leu Leu His Gln His Gln Glu Ala Ala Gly Ser Asn Phe
35 40 45

Ile Ile Asn Asn Asn His His His His Gln His His His His His Thr
50 55 60

Thr Lys Gln Leu Asp Phe Met Asp Leu Ser Leu Gly Ser Ser Lys Asp
65 70 75 80

Glu Gly Asn Leu Gln Gly Ser Ser Ser Ser Val Tyr Ala His His His
85 90 95

His Ala Ala Ser Ala Ser Ser Ser Ala Asn Gly Asn Asn Asn Asn Ser
100 105 110

Ser Ser Ser Asn Leu Gln Gln Gln Gln Gln Gln Pro Ala Glu Lys Glu
115 120 125

His Met Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn
130 135 140

Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asp
145 150 155 160

Ser Ser Ala Asn Glu Lys Gly Leu Leu Leu Asn Phe Glu Asp Arg Asn
165 170 175

Gly Lys Leu Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser
180 185 190

Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Lys Leu
195 200 205

Asp Ala Gly Asp Met Val Ser Phe Gln Arg Gly Val Gly Glu Leu Tyr
210 215 220

Arg His Arg Leu Tyr Ile Asp Trp Trp Arg Arg Pro Asp His His His
225 230 235 240

His His His His Gly Pro Asp His Ser Thr Thr Leu Phe Thr Pro Phe
245 250 255

Leu Ile Pro Asn Gln Pro His His Leu Met Ser Ile Arg Trp Gly Ala
260 265 270

Thr Gly Arg Leu Tyr Ser Leu Pro Ser Pro Thr Pro Pro Arg His His
275 280 285

Glu His Leu Asn Tyr Asn Asn Asn Ala Met Tyr His Pro Phe His His
290 295 300

His Gly Ala Gly Ser Gly Ile Asn Ala Thr Thr His His Tyr Asn Asn
305 310 315 320

Tyr His Glu Met Ser Ser Thr Thr Thr Ser Gly Ser Ala Gly Ser Val
325 330 335

Phe Tyr His Arg Ser Thr Pro Pro Ile Ser Met Pro Leu Ala Asp His
340 345 350

Gln Thr Leu Asn Thr Arg Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu
355 360 365

Gly Ala Gly Asn Val Ser Leu Ser Pro Met Ile Ile Asp Ser Val Pro

-continued

```
    370                 375                 380

Val Ala His His Leu His His Gln Gln His His Gly Gly Lys Ser Ser
385                 390                 395                 400

Gly Pro Ser Ser Thr Ser Thr Ser Pro Ser Thr Ala Gly Lys Arg Leu
                405                 410                 415

Arg Leu Phe Gly Val Asn Met Glu Cys Ala Ser Ser Thr Ser Glu Asp
            420                 425                 430

Pro Lys Cys Phe Ser Leu Leu Ser Ser Ser Ser Met Ala Asn Ser Asn
        435                 440                 445

Ser Gln Pro Pro Leu Gln Leu Leu Arg Glu Asp Thr Leu Ser Ser Ser
    450                 455                 460

Ser Ala Arg Phe Gly Asp Gln Arg Gly Val Gly Glu Pro Ser Met Leu
465                 470                 475                 480

Phe Asp Leu Asp Pro Ser Leu Gln Tyr Arg Gln
                485                 490


<210> SEQ ID NO 74
<211> LENGTH: 1476
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 74

atggagttga tgcaagaagt gaaagggtat tctgatggca gagaggagga ggaggaggaa     60

gaggaagcag cagaagaaat catcacaaga gaagaaagca gcaggttgtt acaccagcac    120

caggaggcag caggttccaa tttcatcatc aacaataatc atcatcatca tcaacatcac    180

caccaccaca caacaaagca gctagacttc atggacttgt cacttggtag cagcaaggat    240

gaagggaatt tgcaaggatc atcttcttct gtctatgctc atcatcatca tgcagcaagt    300

gctagttctt ctgccaatgg taacaacaac aacagcagca gcagcaactt gcagcaacag    360

cagcagcagc ctgctgagaa ggagcacatg tttgataaag tagtgacacc aagtgatgtg    420

gggaagctga accggttggt gataccaaag cagcatgctg agaagtattt ccctcttgat    480

tcctcagcca atgagaaggg tctgttgctg aattttgagg acaggaatgg taagttgtgg    540

aggttcaggt actcctattg gaacagcagc cagagctatg tgatgaccaa aggttggagc    600

cgttttgtta aggagaagaa gcttgatgct ggtgacatgg tgtccttcca gcgtggtgtt    660

ggggagttgt ataggcatag gttgtacata gattggtgga gaaggcctga tcatcatcac    720

catcaccatc atggccctga ccattcaacc acactcttca cacctttctt aattcccaat    780

cagcctcatc acttaatgtc catcagatgg ggtgccactg gcagattgta ctccctccct    840

tccccaaccc caccacgcca ccatgaacac ctcaattaca acaataacgc catgtatcat    900

ccctttcatc accatggtgc tggaagtgga attaatgcta ctactcatca ctacaacaac    960

tatcatgaga tgagtagtac tactacttca ggatctgcag gctcagtctt ttaccacagg   1020

tcaacacccc caatatcaat gccattggct gaccaccaaa ccttgaacac aaggcagcag   1080

caacaacaac aacaacaaca agagggagct ggcaatgttt ctctttcccc tatgatcatt   1140

gattctgttc cagttgctca ccacctccat catcaacaac accatggtgg caagagtagt   1200

ggtcctagta gtactagtac tagtcctagc actgcaggga aaagactaag gctatttggg   1260

gtcaacatgg aatgtgcttc ttcaacatca gaagacccca aatgcttcag cttgttgtcc   1320

tcatcttcaa tggctaattc caattcacaa ccaccacttc agcttttgag ggaagataca   1380
```

-continued

```
ctttcgtcat catcggcaag gtttggggat cagagaggag taggggaacc ttcaatgctt   1440

tttgatctgg acccttcttt gcaataccgg cagtga                             1476


<210> SEQ ID NO 75
<211> LENGTH: 351
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 75

Met Asp Gly Gly Cys Val Thr Asp Glu Thr Thr Thr Ser Ser Asp Ser
1               5                   10                  15

Leu Ser Val Pro Pro Pro Ser Arg Val Gly Ser Val Ala Ser Ala Val
            20                  25                  30

Val Asp Pro Asp Gly Cys Cys Val Ser Gly Glu Ala Glu Ser Arg Lys
        35                  40                  45

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

Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr
65                  70                  75                  80

Phe Asn Glu Glu Asp Glu Ala Ala Arg Ala Tyr Asp Ile Ala Ala Leu
                85                  90                  95

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

Ser Asp Asp Ala Glu Ser Glu Phe Leu Asn Ser His Ser Lys Phe Glu
        115                 120                 125

Ile Val Asp Met Leu Arg Lys His Thr Tyr Asp Asp Glu Leu Gln Gln
    130                 135                 140

Ser Thr Arg Gly Gly Arg Arg Arg Leu Asp Ala Asp Thr Ala Ser Ser
145                 150                 155                 160

Gly Val Phe Asp Ala Lys Ala Arg Glu Gln Leu Phe Glu Lys Thr Val
                165                 170                 175

Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln
            180                 185                 190

His Ala Glu Lys His Phe Pro Leu Ser Gly Ser Gly Asp Glu Ser Ser
        195                 200                 205

Pro Cys Val Ala Gly Ala Ser Ala Ala Lys Gly Met Leu Leu Asn Phe
    210                 215                 220

Glu Asp Val Gly Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn
225                 230                 235                 240

Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys
                245                 250                 255

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

Gly Pro Asp Arg Gln Leu Tyr Ile Asp Cys Lys Ala Arg Ser Gly Glu
        275                 280                 285

Val Asn Asn Asn Ala Gly Gly Leu Phe Val Pro Ile Gly Pro Val Val
    290                 295                 300

Glu Pro Val Gln Met Val Arg Leu Phe Gly Val Asn Leu Leu Lys Leu
305                 310                 315                 320

Pro Val Pro Gly Ser Asp Gly Val Gly Lys Arg Lys Glu Met Glu Leu
                325                 330                 335
```

-continued

Phe Ala Phe Glu Cys Cys Lys Lys Leu Lys Val Ile Gly Ala Leu
340 345 350

<210> SEQ ID NO 76
<211> LENGTH: 1056
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 76

atggatggag gctgtgtcac agacgaaacc accacatcca gcgactctct ttccgttccg 60

ccgcccagcc gcgtcggcag cgttgcaagc gccgtcgtcg accccgacgg ttgttgcgtt 120

tccggcgagg ccgaatcccg gaaactccct tcgtcgaaat acaaaggcgt ggtgccgcaa 180

ccgaacggtc gctggggagc tcagatttac gagaagcacc agcgcgtgtg gctcggcact 240

ttcaacgagg aagacgaagc cgccagagcc tacgacatcg ccgcgctgcg cttccgcggc 300

cccgacgccg tcaccaactt caagcctccc gccgcctccg acgacgccga gtccgagttc 360

ctcaactcgc attccaagtt cgagatcgtc gacatgctcc gcaagcacac ctacgacgac 420

gagctccagc agagcacgcg cggtggtagg cgccgcctcg acgctgacac cgcgtcgagc 480

ggtgtgttcg acgcgaaagc gcgtgagcag ctgttcgaga aaacggttac gccgagcgac 540

gtcgggaagc tgaatcgatt agtgataccg aagcagcacg cggagaagca ctttccgtta 600

agcggatccg gcgacgaaag ctcgccgtgc gtggcggggg cttcggcggc gaagggaatg 660

ttgttgaact ttgaggacgt tggagggaaa gtgtggcggt ttcgttactc ttattggaac 720

agtagccaga gctacgtgct taccaaagga tggagccggt tcgttaagga gaagaatctt 780

cgagccggtg acgcggttca gttcttcaag tcgaccggac cggaccggca gctatatata 840

gactgcaagg cgaggagtgg tgaggttaac aataatgctg gcggtttgtt tgttccgatt 900

ggaccggtcg ttgagccggt tcagatggtt cggcttttcg gggtcaacct tttgaaacta 960

cccgtacccg gttcggatgg tgtagggaag agaaaagaga tggaactgtt tgcatttgaa 1020

tgttgcaaga agttaaaagt aattggagct ttgtaa 1056

<210> SEQ ID NO 77
<211> LENGTH: 401
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 77

Met Asp Ala Ile Ser Cys Met Asp Glu Ser Thr Thr Thr Glu Ser Leu
1 5 10 15

Ser Ile Ser Leu Ser Pro Thr Ser Ser Ser Glu Lys Ala Lys Pro Ser
20 25 30

Ser Met Ile Thr Ser Ser Glu Lys Val Ser Leu Ser Pro Pro Pro Ser
35 40 45

Asn Arg Leu Cys Arg Val Gly Ser Gly Ala Ser Ala Val Val Asp Pro
50 55 60

Asp Gly Gly Gly Ser Gly Ala Glu Val Glu Ser Arg Lys Leu Pro Ser
65 70 75 80

Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala
85 90 95

Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu
100 105 110

-continued

Glu Asp Glu Ala Ala Arg Ala Tyr Asp Ile Ala Ala Gln Arg Phe Arg
115 120 125

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

Asp Asp Gly Glu Ser Glu Phe Leu Asn Ser His Ser Lys Pro Glu Ile
145 150 155 160

Val Asp Met Leu Arg Lys His Thr Tyr Asn Asp Glu Leu Glu Gln Ser
165 170 175

Lys Arg Ser Arg Gly Val Val Arg Arg Arg Gly Ser Ala Ala Ala Gly
180 185 190

Thr Ala Asn Ser Ile Ser Gly Ala Cys Phe Thr Lys Ala Arg Glu Gln
195 200 205

Leu Phe Glu Lys Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg
210 215 220

Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Gln Ser
225 230 235 240

Ser Asn Gly Val Ser Ala Thr Thr Ile Ala Ala Val Thr Ala Thr Pro
245 250 255

Thr Ala Ala Lys Gly Val Leu Leu Asn Phe Glu Asp Val Gly Gly Lys
260 265 270

Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val
275 280 285

Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Lys Ala
290 295 300

Gly Asp Thr Val Cys Phe His Arg Ser Thr Gly Pro Asp Lys Gln Leu
305 310 315 320

Tyr Ile Asp Trp Lys Thr Arg Asn Val Val Asn Asn Glu Val Ala Leu
325 330 335

Phe Gly Pro Val Gly Pro Val Val Glu Pro Ile Gln Met Val Arg Leu
340 345 350

Phe Gly Val Asn Ile Leu Lys Leu Pro Gly Ser Asp Thr Ile Val Gly
355 360 365

Asn Asn Asn Asn Ala Ser Gly Cys Cys Asn Gly Lys Arg Arg Glu Met
370 375 380

Glu Leu Phe Ser Leu Glu Cys Ser Lys Lys Pro Lys Ile Ile Gly Ala
385 390 395 400

Leu

<210> SEQ ID NO 78
<211> LENGTH: 1206
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 78

atggatgcaa ttagttgcat ggatgagagc accaccactg agtcactctc tataagtctt 60

tctccgacgt catcgtcgga gaaagcgaag ccttcttcga tgattacatc gtcggagaag 120

gtttctctgt ccccgccgcc gtcaaacaga ctatgccgtg ttggaagcgg cgcgagcgca 180

gtcgtggatc ctgatggcgg cggcagcggc gctgaggtag agtcgcggaa actcccctcg 240

tcgaagtaca agggcgtggt gccccagccc aacggccgct ggggtgcgca gatttacgag 300

aagcaccagc gcgtgtggct tggaacgttc aacgaggaag acgaggcggc gcgtgcgtac 360

-continued

```
gacatcgccg cgcagcggtt ccgcggcaag gacgccgtca cgaacttcaa gccgctcgcc    420

ggcgccgacg acgacgacgg agaatcggag tttctcaact cgcattccaa acccgagatc    480

gtcgacatgc tgcgaaagca cacgtacaat gacgagctgg agcagagcaa gcgcagccgc    540

ggcgtcgtcc ggcggcgagg ctccgccgcc gccggcaccg caaactcaat ttccggcgcg    600

tgctttacta aggcacgtga gcagctattc gagaaggctg ttacgccgag cgacgttggg    660

aaattgaacc gtttggtgat accgaagcag cacgcggaga agcactttcc gttacagagc    720

tctaacggcg ttagcgcgac gacgatagcg gcggtgacgg cgacgccgac ggcggcgaag    780

ggcgttttgt tgaacttcga agacgttgga gggaaagtgt ggcggtttcg ttactcgtat    840

tggaacagta gccagagtta cgtcttaacc aaaggttgga gccggttcgt taaggagaag    900

aatctgaaag ctggtgacac ggtttgtttt caccggtcca ctggaccgga caagcagctt    960

tacatcgatt ggaagacgag gaatgttgtt aacaacgagg tcgcgttgtt cggaccggtc   1020

ggaccggttg tcgaaccgat ccagatggtt cggctctttg ggttaacat tttgaaacta   1080

cccggttcag atactattgt tggcaataac aataatgcaa gtgggtgctg caatggcaag   1140

agaagagaaa tggaactgtt ctcgttagag tgtagcaaga aacctaagat tattggtgct   1200

ttgtaa                                                               1206
```

```
<210> SEQ ID NO 79
<211> LENGTH: 362
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 79

Met Asp Gly Gly Ser Val Thr Asp Glu Thr Thr Thr Thr Ser Asn Ser
1               5                   10                  15

Leu Ser Val Pro Ala Asn Leu Ser Pro Pro Pro Leu Ser Leu Val Gly
            20                  25                  30

Ser Gly Ala Thr Ala Val Val Tyr Pro Asp Gly Cys Cys Val Ser Gly
        35                  40                  45

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

Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln
65                  70                  75                  80

Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala Arg Ala
                85                  90                  95

Tyr Asp Ile Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val Thr Asn
            100                 105                 110

Phe Lys Pro Leu Ala Gly Ala Asp Asp Ala Glu Ala Glu Phe Leu Ser
        115                 120                 125

Thr His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
    130                 135                 140

Asp Asn Glu Leu Gln Gln Ser Thr Arg Gly Gly Arg Arg Arg Arg Asp
145                 150                 155                 160

Ala Glu Thr Ala Ser Ser Gly Ala Phe Asp Ala Lys Ala Arg Glu Gln
                165                 170                 175

Leu Phe Glu Lys Thr Val Thr Gln Ser Asp Val Gly Lys Leu Asn Arg
            180                 185                 190

Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Ser Gly
        195                 200                 205
```

-continued

```
Ser Gly Gly Gly Ala Leu Pro Cys Met Ala Ala Ala Ala Gly Ala Lys
    210                 215                 220

Gly Met Leu Leu Asn Phe Glu Asp Val Gly Gly Lys Val Trp Arg Phe
225                 230                 235                 240

Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly
                245                 250                 255

Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Ala Val
            260                 265                 270

Gln Phe Phe Lys Ser Thr Gly Leu Asp Arg Gln Leu Tyr Ile Asp Cys
        275                 280                 285

Lys Ala Arg Ser Gly Lys Val Asn Asn Asn Ala Ala Gly Leu Phe Ile
    290                 295                 300

Pro Val Gly Pro Val Val Glu Pro Val Gln Met Val Arg Leu Phe Gly
305                 310                 315                 320

Val Asp Leu Leu Lys Leu Pro Val Pro Gly Ser Asp Gly Ile Gly Val
                325                 330                 335

Gly Cys Asp Gly Lys Arg Lys Glu Met Glu Leu Phe Ala Phe Glu Cys
            340                 345                 350

Ser Lys Lys Leu Lys Val Ile Gly Ala Leu
        355                 360


<210> SEQ ID NO 80
<211> LENGTH: 1089
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 80

atggatggag gcagtgtcac agacgaaacc accacaacca gcaactctct ttcggttccg     60

gcgaatctat ctccgccgcc tctcagcctt gtcggcagcg gcgcaaccgc cgtcgtctac    120

cccgacggtt gttgcgtctc cggcgaagcc gaatcccgga aactcccgtc ctcgaaatac    180

aaaggcgtgg tgccgcaacc gaacggtcgt tggggagctc agatttacga gaagcaccag    240

cgcgtgtggc tcggcacctt caacgaggaa gacgaagccg ccagagccta cgacatcgcc    300

gcgcatcgct tccgcggccg cgacgccgtc actaacttca agcctctcgc cggcgccgac    360

gacgccgaag ccgagttcct cagcacgcat tccaagtccg agatcgtcga catgctccgc    420

aagcacacct acgacaacga gctccagcag agcacccgcg gcggcaggcg ccgccgggac    480

gccgaaaccg cgtcgagcgg cgcgttcgac gcgaaggcgc gtgagcagct gttcgagaaa    540

accgttacgc agagcgacgt cgggaagctg aaccgattag tgataccaaa gcagcacgcg    600

gagaagcact ttccgttaag cggatccggc ggcggagcct tgccgtgcat ggcggcggct    660

gcgggggcga agggaatgtt gctgaacttt gaggacgttg gagggaaagt gtggcggttc    720

cgttactcgt attggaacag tagccagagc tacgtgctta ccaaaggatg gagccggttc    780

gttaaggaga agaatcttcg agctggtgac gcggttcagt tcttcaagtc gaccggactg    840

gaccggcaac tatatataga ctgcaaggcg aggagtggta aggttaacaa taatgctgcc    900

ggtttgttta ttccggttgg accggttgtt gagccggttc agatggtacg gcttttcggg    960

gtcgaccttt tgaaactacc cgtacccggt tcggatggta ttggggttgg ctgtgacggg   1020

aagagaaaag agatggagct gtttgcattt gaatgtagca agaagttaaa agtaattgga   1080

gctttgtaa                                                           1089
```

```
<210> SEQ ID NO 81
<211> LENGTH: 347
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 81

Met Ile Gly Val Glu Lys Val Thr Ile Cys Met Arg Ile Glu Val Asn
1               5                   10                  15

Thr Glu Lys Gly Arg Arg Ala Leu Met Asp Cys Trp Gln Ile Ser Gly
            20                  25                  30

Val His Glu Ser Ser Asp Cys Ser Glu Ile Lys Phe Ala Phe Asp Ala
        35                  40                  45

Val Val Lys Arg Ala Arg His Glu Glu Asn Asn Ala Ala Ala Gln Lys
    50                  55                  60

Phe Lys Gly Val Val Ser Gln Gln Asn Gly Asn Trp Gly Ala Gln Ile
65                  70                  75                  80

Tyr Ala His Gln Gln Arg Ile Trp Leu Gly Thr Phe Lys Ser Glu Arg
                85                  90                  95

Glu Ala Ala Met Ala Tyr Asp Ser Ala Ser Ile Lys Leu Arg Ser Gly
            100                 105                 110

Glu Cys His Arg Asn Phe Pro Trp Asn Asp Gln Thr Val Gln Glu Pro
        115                 120                 125

Gln Phe Gln Ser His Tyr Ser Ala Glu Thr Val Leu Asn Met Ile Arg
    130                 135                 140

Asp Gly Thr Tyr Pro Ser Lys Phe Ala Thr Phe Leu Lys Thr Arg Gln
145                 150                 155                 160

Thr Gln Lys Gly Val Ala Lys His Ile Gly Leu Lys Gly Asp Asp Glu
                165                 170                 175

Glu Gln Phe Cys Cys Thr Gln Leu Phe Gln Lys Glu Leu Thr Pro Ser
            180                 185                 190

Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Lys His Ala Val
        195                 200                 205

Ser Tyr Phe Pro Tyr Val Gly Gly Ser Ala Asp Glu Ser Gly Ser Val
    210                 215                 220

Asp Val Glu Ala Val Phe Tyr Asp Lys Leu Met Arg Leu Trp Lys Phe
225                 230                 235                 240

Arg Tyr Cys Tyr Trp Lys Ser Ser Gln Ser Tyr Val Phe Thr Arg Gly
                245                 250                 255

Trp Asn Arg Phe Val Lys Asp Lys Lys Leu Lys Ala Lys Asp Val Ile
            260                 265                 270

Ala Phe Phe Thr Trp Gly Lys Ser Gly Gly Glu Gly Glu Ala Phe Ala
        275                 280                 285

Leu Ile Asp Val Ile Tyr Asn Asn Asn Ala Glu Glu Asp Ser Lys Gly
    290                 295                 300

Asp Thr Lys Gln Val Leu Gly Asn Gln Leu Gln Leu Ala Gly Ser Glu
305                 310                 315                 320

Glu Gly Glu Asp Glu Asp Ala Asn Ile Gly Lys Asp Phe Asn Ala Gln
                325                 330                 335

Lys Gly Leu Arg Leu Phe Gly Val Cys Ile Thr
            340                 345
```

-continued

```
<210> SEQ ID NO 82
<211> LENGTH: 1044
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 82

atgattggag ttgagaaagt gacaatttgt atgagaatag aggtgaatac tgaaaaggga      60

agaagggctt taatggactg ttggcaaata tcaggagttc atgaaagttc agattgtagc     120

gaaatcaaat ttgcattcga cgcagtagta aaacgcgcga ggcatgaaga gaataatgca     180

gcagcacaga agttcaaagg cgttgtgtct caacaaaatg ggaactgggg tgcacagata     240

tatgcacacc agcagagaat ctggttgggg accttcaaat ctgaaagaga ggctgcaatg     300

gcttatgaca gcgccagcat aaaacttaga agcggagagt gccacagaaa ctttccatgg     360

aacgaccaaa cagttcaaga gcctcagttc caaagccatt acagcgcaga aacagtgcta     420

aacatgatta gagatggcac ctatccatca aaatttgcta catttctcaa aactcgtcaa     480

acccaaaaag gcgttgcgaa acacataggt ctgaagggtg atgacgagga acagttttgt     540

tgcacccaac tttttcagaa ggaattaaca ccaagtgatg tgggcaagct caacaggctt     600

gtcatcccaa agaagcatgc agttagctat tttccttacg ttggtggcag tgctgatgag     660

agtggtagtg ttgacgtgga ggctgtgttt tatgacaaac tcatgcgatt gtggaagttc     720

cgatactgct attggaagag cagccaaagt tacgtgttca ccagaggctg gaatcggttt     780

gtgaaggata agaagttgaa ggctaaagat gtcattgcgt tttttacgtg ggaaaaaagt     840

ggaggagagg gagaagcttt tgcattgatc gatgtaattt ataataataa tgcagaagaa     900

gacagcaagg gagacaccaa acaagttttg ggaaaccaat tacaattagc tggcagtgaa     960

gaaggtgaag atgaagatgc aaacattgga aaggatttca atgcacaaaa gggtctgagg    1020

ctctttggtg tgtgtatcac ctaa                                           1044


<210> SEQ ID NO 83
<211> LENGTH: 409
<212> TYPE: PRT
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 83

Met Glu Phe Thr Ala Thr Ser Ser Arg Phe Ser Lys Gly Glu Glu Glu
1               5                   10                  15

Val Glu Glu Glu Gln Glu Glu Ala Ser Met Arg Glu Ile Pro Phe Met
            20                  25                  30

Thr Pro Ala Ala Ala Thr Cys Ala Ala Ala Pro Pro Ser Ala Ser Ala
        35                  40                  45

Ser Ala Ser Thr Pro Ala Ser Ala Ser Gly Ser Ser Pro Pro Phe Arg
    50                  55                  60

Ser Gly Asp Asp Ala Gly Ala Ser Gly Ser Gly Ala Gly Asp Gly Ser
65                  70                  75                  80

Arg Ser Asn Val Ala Glu Ala Val Glu Lys Glu His Met Phe Asp Lys
                85                  90                  95

Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro
            100                 105                 110

Lys Gln Tyr Ala Glu Lys Tyr Phe Pro Leu Asp Ser Ala Ala Asn Glu
        115                 120                 125

Lys Gly Leu Leu Leu Asn Phe Glu Asp Ser Ala Gly Lys Pro Trp Arg
```

-continued

```
    130                 135                 140

Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys
145                 150                 155                 160

Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Asp Ala Gly Asp Thr
                165                 170                 175

Val Ser Phe Ser Arg Gly Ala Gly Glu Ala Ala Arg His Arg Leu Phe
            180                 185                 190

Ile Asp Trp Lys Arg Arg Ala Asp Thr Arg Asp Pro Leu Arg Leu Pro
        195                 200                 205

Arg Leu Pro Leu Pro Met Pro Leu Thr Ser His Tyr Ser Pro Trp Gly
    210                 215                 220

Leu Gly Ala Gly Ala Arg Gly Phe Phe Met Pro Pro Ser Pro Pro Ala
225                 230                 235                 240

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

Asn Pro Ser Tyr Pro Thr Met Gly Arg Gln Val Ile Leu Phe Gly Ser
            260                 265                 270

Ala Ala Arg Met Pro Pro His Gly Pro Ala Pro Leu Leu Val Pro Arg
        275                 280                 285

Pro Pro Pro Pro Leu His Phe Thr Val Gln Gln Gln Gly Ser Asp Ala
    290                 295                 300

Gly Gly Ser Val Thr Ala Gly Ser Pro Val Val Leu Asp Ser Val Pro
305                 310                 315                 320

Val Ile Glu Ser Pro Thr Thr Ala Thr Lys Lys Arg Val Arg Leu Phe
                325                 330                 335

Gly Val Asn Leu Asp Asn Pro Gln His Pro Gly Asp Gly Gly Gly Glu
            340                 345                 350

Ser Ser Asn Tyr Gly Ser Ala Leu Pro Leu Gln Met Pro Ala Ser Ala
        355                 360                 365

Trp Arg Pro Arg Asp His Thr Leu Arg Leu Leu Glu Phe Pro Ser His
    370                 375                 380

Gly Ala Glu Ala Ser Ser Pro Ser Ser Ser Ser Ser Ser Lys Arg Glu
385                 390                 395                 400

Ala His Ser Gly Leu Asp Leu Asp Leu
                405


<210> SEQ ID NO 84
<211> LENGTH: 1230
<212> TYPE: DNA
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 84

atggagttta ctgcgacaag cagtaggttt tctaaaggag aggaggaggt ggaggaggag      60

caggaggagg cgtcgatgcg cgagatccct ttcatgacgc ccgcggccgc cacctgcgcc     120

gcggcgccgc cttctgcttc tgcgtcggcc tcgacacccg cgtcagcgtc tggaagtagc     180

cctccctttc gatctgggga tgacgccgga gcgtcgggga gcggggccgg cgacggcagc     240

cgcagcaacg tggcggaggc cgtggagaag gagcacatgt tcgacaaagt ggtgacgccg     300

agcgacgtgg ggaagcttaa ccggctggtc atccccaagc agtacgccga gaagtacttc     360

ccgctggact cggcggccaa cgagaagggc cttctgctca acttcgagga cagcgccggg     420

aagccatggc gcttccgcta ttcctactgg aacagcagcc agagctacgt catgaccaaa     480
```

-continued

```
ggctggagcc gcttcgtcaa ggagaagcgc ctcgacgctg ggacaccgt ctccttctcc    540

cgcggcgccg gtgaggccgc gcgccaccgc ctcttcatcg actggaagcg ccgagccgac    600

accagagacc cgctccgctt gccccgcctc ccgctcccga tgccgctgac gtcgcactac    660

agcccgtggg gcctcggcgc cggcgccaga ggattcttca tgcctccctc gccgccagcc    720

acgctctacg agcaccgtct ccgtcaaggc ttcgacttcc gcggcatgaa ccccagttac    780

cccacaatgg ggagacaggt catccttttc ggctcggccg ccaggatgcc tccgcacgga    840

ccagcaccac tcctcgtgcc gcgcccgccg ccgccgctgc acttcacggt gcagcaacaa    900

ggcagcgacg ccggcggaag tgtaaccgca ggatccccag tggtgctcga ctcagtgccg    960

gtaatcgaaa gccccacgac ggcaacgaag aagcgcgtgc gcttgttcgg cgtgaacttg   1020

gacaacccgc agcatcccgg tgatggcggg ggcgaatcga gcaattatgg cagtgcactg   1080

ccattgcaga tgcccgcatc agcatggcgg ccaagggacc atacgctgag gctgctcgaa   1140

ttcccctcgc acggtgccga ggcgtcgtct ccatcgtcgt cgtcgtcttc caagagggag   1200

gcgcattcgg gcttggatct cgatctgtga                                     1230
```

<210> SEQ ID NO 85
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 85

```
Met Leu Arg Lys His Thr Tyr Phe Asp Glu Leu Ala Gln Ser Lys Arg
1               5                   10                  15

Ala Phe Ala Ala Ser Ala Ala Leu Ser Ala Pro Thr Thr Ser Gly Asp
            20                  25                  30

Ala Gly Gly Ser Ala Ser Pro Pro Ser Pro Ala Ala Val Arg Glu His
        35                  40                  45

Leu Phe Asp Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg
    50                  55                  60

Leu Val Ile Pro Lys Gln Asn Ala Glu Lys His Phe Pro Leu Gln Leu
65              70                  75                  80

Pro Ala Gly Gly Gly Glu Ser Lys Gly Leu Leu Leu Asn Phe Glu Asp
                85                  90                  95

Asp Ala Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser
            100                 105                 110

Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys
        115                 120                 125

Gly Leu Gly Ala Gly Asp Val Val Gly Phe Tyr Arg Ser Ala Ala Gly
    130                 135                 140

Arg Thr Gly Glu Asp Ser Lys Phe Phe Ile Asp Cys Arg Leu Arg Pro
145             150                 155                 160

Asn Thr Asn Thr Ala Ala Glu Ala Asp Pro Val Asp Gln Ser Ser Ala
                165                 170                 175

Pro Val Gln Lys Ala Val Arg Leu Phe Gly Val Asp Leu Leu Ala Ala
            180                 185                 190

Pro Glu Gln Gly Met Pro Gly Gly Cys Lys Arg Ala Arg Asp Leu Val
        195                 200                 205

Lys Pro Pro Pro Pro Lys Val Ala Phe Lys Lys Gln Cys Ile Glu Leu
    210                 215                 220
```

-continued

```
Ala Leu Ala
225


<210> SEQ ID NO 86
<211> LENGTH: 684
<212> TYPE: DNA
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 86

atgctccgca agcacaccta cttcgacgag ctcgcccaga gcaagcgcgc cttcgccgcg      60

tcggccgcgc tctccgcgcc caccacctcg ggcgacgccg gcggcagcgc ctcgccgccc     120

tccccggccg ccgtgcgcga gcacctcttc gacaagaccg tcacgcccag cgacgtcggc     180

aagctgaaca ggctggtgat accgaagcag aacgccgaga agcacttccc gctgcagctc     240

ccggccggcg gcggcgagag caagggcctg ctcctcaact tcgaggacga tgcgggcaag     300

gtgtggcggt tccgctactc gtactggaac agcagccaga gctacgtcct caccaagggc     360

tggagccgct tcgtgaagga gaagggcctc ggcgccggag acgtcgtcgg gttctaccgc     420

tccgccgccg ggaggaccgg cgaagacagc aagttcttca ttgactgcag gctgcggccg     480

aacaccaaca ccgccgccga agcagacccc gtggaccagt cgtcggcgcc cgtgcagaag     540

gccgtgagac tcttcggcgt cgatcttctc gcggcgccgg agcagggcat gccgggcggg     600

tgcaagaggg ccagagactt ggtgaagccg ccgcctccga aagtggcgtt caagaagcaa     660

tgcatagagc tggcgctagc gtag                                            684


<210> SEQ ID NO 87
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 87

Met Tyr Cys Ser Arg Gly Arg Ile Asp Pro Ala Glu Glu Gly Gln Val
1               5                   10                  15

Met Gly Gly Leu Gly Val Arg Asp Ala Ser Trp Ala Leu Phe Lys Val
            20                  25                  30

Leu Glu Gln Ser Asp Val Gln Val Gly Gln Asn Arg Leu Leu Leu Thr
        35                  40                  45

Lys Glu Ala Val Trp Gly Gly Pro Ile Pro Lys Leu Phe Pro Glu Leu
    50                  55                  60

Glu Glu Leu Arg Gly Asp Gly Leu Asn Ala Glu Asn Arg Val Ala Val
65                  70                  75                  80

Lys Ile Leu Asp Ala Asp Gly Cys Glu Gly Asp Ala Asn Phe Arg Tyr
                85                  90                  95

Leu Asn Ser Ser Lys Ala Tyr Arg Val Met Gly Pro Gln Trp Ser Arg
            100                 105                 110

Leu Val Lys Glu Thr Gly Met Cys Lys Gly Asp Arg Leu Asp Leu Tyr
        115                 120                 125

Ala Ala Thr Ala Thr Ala Ala Ser Ser Cys Ser Gly Ala Arg Ala Ala
    130                 135                 140

Val Ala Pro Ala Ile Pro Pro Gly Ala Ile Val Lys Ala Ala Gly Phe
145                 150                 155                 160


<210> SEQ ID NO 88
```

-continued

<211> LENGTH: 483
<212> TYPE: DNA
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 88

atgtattgtt cccgcggccg catcgatccc gcggaagaag ggcaggtgat gggcggcctc 60

ggcgtgcgcg acgccagctg ggcgctgttc aaggtgttgg agcagtccga cgtccaggtg 120

gggcagaacc ggctgctcct caccaaggag gcggtgtggg gcggccctat ccccaagctt 180

ttcccggagc tggaggagct ccgcggcgac ggcctcaacg ccgagaacag ggtcgcggtc 240

aagatcctcg acgccgacgg ctgcgagggg gacgccaact tccgctacct caactccagc 300

aaggcgtacc gggtcatggg gcctcagtgg agccggctcg tgaaggagac cggcatgtgc 360

aagggagacc gcctcgatct gtacgcggca acggcgaccg ctgcctcttc gtgttctgga 420

gccagggcgg ctgtggcgcc ggcgatacct cccggagcaa tcgtgaaggc agccgggttc 480

taa 483

<210> SEQ ID NO 89
<211> LENGTH: 267
<212> TYPE: PRT
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 89

Met Leu Arg Lys His Ile Tyr Pro Asp Glu Leu Ala Gln His Lys Arg
1 5 10 15

Ala Phe Phe Phe Ala Ala Ala Ser Ser Pro Thr Ser Ser Ser Ser Pro
20 25 30

Leu Ala Ser Pro Ala Pro Ser Ala Ala Ala Ala Arg Arg Glu His Leu
35 40 45

Phe Asp Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
50 55 60

Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Gln Leu Pro
65 70 75 80

Ser Ala Ser Ala Ala Val Pro Gly Glu Cys Lys Gly Val Leu Leu Asn
85 90 95

Phe Asp Asp Ala Thr Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp
100 105 110

Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val
115 120 125

Lys Glu Lys Gly Leu His Ala Gly Asp Ala Val Glu Phe Tyr Arg Ala
130 135 140

Ala Ser Gly Asn Asn Gln Leu Phe Ile Asp Cys Lys Leu Arg Ser Lys
145 150 155 160

Ser Thr Thr Thr Thr Thr Ser Val Asn Ser Glu Ala Ala Pro Ser Pro
165 170 175

Ala Pro Val Thr Arg Thr Val Arg Leu Phe Gly Val Asp Leu Leu Ile
180 185 190

Ala Pro Ala Ala Arg His Ala His Glu His Glu Asp Tyr Gly Met Ala
195 200 205

Lys Thr Asn Lys Arg Thr Met Glu Ala Ser Val Ala Ala Pro Thr Pro
210 215 220

Ala His Ala Val Trp Lys Lys Arg Cys Val Asp Phe Ala Leu Thr Tyr
225 230 235 240

-continued

```
Arg Leu Ala Thr Thr Pro Gln Cys Pro Arg Ser Arg Asp Gln Leu Glu
                245                 250                 255

Gly Val Gln Ala Ala Gly Ser Thr Phe Ala Leu
            260                 265


<210> SEQ ID NO 90
<211> LENGTH: 804
<212> TYPE: DNA
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 90

atgctgcgca agcacatcta tcccgacgag ctcgcgcagc acaagcgcgc cttcttcttc      60

gccgcggcgt cgtcccctac gtcgtcgtcg tcacctctcg cctcgccggc tccttcagcc     120

gcggcggcgc ggcgcgagca cctgttcgac aagacggtca cgcccagcga cgtggggaag     180

ctgaaccggc tggtgatccc caagcagcac gccgagaagc acttcccgct gcagctccct     240

tctgccagcg ccgccgtgcc aggcgagtgc aagggcgtgc tgctcaactt cgatgacgcg     300

accggcaagg tgtggaggtt ccggtactcc tactggaaca gcagccagag ctacgtgctc     360

accaaggggt ggagccgctt cgtgaaggag aagggccttc acgccggcga cgccgtcgag     420

ttctaccgcg ccgcctccgg caacaaccag ctcttcatcg actgcaagct ccggtccaag     480

agcaccacga cgacgacctc cgtcaactcg gaggccgccc catcgccggc acccgtgacg     540

aggacagtgc gactcttcgg ggtcgacctt ctcatcgcgc cggcggcgag gcacgcgcat     600

gagcacgagg actacggcat ggccaagaca aacaagagaa ccatggaggc cagcgtagcg     660

gcgcctactc cggcgcacgc ggtgtggaag aagcggtgcg tagacttcgc gctgacctac     720

cgacttgcca ccacccccaca gtgcccgagg tcaagagatc aactagaagg agtacaagca     780

gctgggagta catttgctct atag                                            804


<210> SEQ ID NO 91
<211> LENGTH: 357
<212> TYPE: PRT
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 91

Met Gly Val Glu Ile Leu Ser Ser Thr Gly Glu His Ser Ser Gln Tyr
1               5                   10                  15

Ser Ser Gly Ala Ala Ser Thr Ala Thr Thr Glu Ser Gly Val Gly Gly
            20                  25                  30

Arg Pro Pro Thr Ala Pro Ser Leu Pro Val Ser Ile Ala Asp Glu Ser
        35                  40                  45

Ala Thr Ser Arg Ser Ala Ser Ala Gln Ser Thr Ser Ser Arg Phe Lys
    50                  55                  60

Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu
65                  70                  75                  80

Arg His Ala Arg Val Trp Leu Gly Thr Phe Pro Asp Glu Asp Ser Ala
                85                  90                  95

Ala Arg Ala Tyr Asp Val Ala Ala Leu Arg Tyr Arg Gly Arg Glu Ala
            100                 105                 110

Ala Thr Asn Phe Pro Cys Ala Ala Ala Glu Ala Glu Leu Ala Phe Leu
        115                 120                 125

Ala Ala His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr
```

-continued

```
    130                 135                 140

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

Ala Arg Ala Gln Pro Thr Pro Ser Trp Ala Arg Glu Pro Leu Phe Glu
                165                 170                 175

Lys Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Val
            180                 185                 190

Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Lys Arg Thr Pro Glu
        195                 200                 205

Thr Thr Thr Thr Thr Gly Lys Gly Val Leu Leu Asn Phe Glu Asp Gly
    210                 215                 220

Glu Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln
225                 230                 235                 240

Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Arg Glu Lys Gly
                245                 250                 255

Leu Gly Ala Gly Asp Ser Ile Val Phe Ser Cys Ser Ala Tyr Gly Gln
            260                 265                 270

Glu Lys Gln Phe Phe Ile Asp Cys Lys Lys Asn Lys Thr Met Thr Ser
        275                 280                 285

Cys Pro Ala Asp Asp Arg Gly Ala Ala Thr Ala Ser Pro Pro Val Ser
    290                 295                 300

Glu Pro Thr Lys Gly Glu Gln Val Arg Val Val Arg Leu Phe Gly Val
305                 310                 315                 320

Asp Ile Ala Gly Glu Lys Arg Gly Arg Ala Ala Pro Val Glu Gln Glu
                325                 330                 335

Leu Phe Lys Arg Gln Cys Val Ala His Ser Gln His Ser Pro Ala Leu
            340                 345                 350

Gly Ala Phe Val Leu
        355


<210> SEQ ID NO 92
<211> LENGTH: 1074
<212> TYPE: DNA
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 92

atgggggtgg agatcctgag ctcaacgggg gaacactcct cccagtactc ttccggagcc     60

gcgtccacgg cgacgacgga gtcaggcgtg ggcggacggc cgccgactgc gccgagccta    120

cctgtttcca tcgccgacga gtcggcgacc tcgcggtcgg catcggcgca gtcgacgtcg    180

tcgcggttca agggcgtggt gccgcagccc aacgggcggt ggggcgccca gatctacgag    240

cgccacgccc gcgtctggct cggcacgttc ccggacgaag actctgcggc gcgcgcctac    300

gacgtggccg cgctccggta ccggggccgc gaggccgcca ccaacttccc gtgcgcggcc    360

gccgaggcgg agctcgcctt cctggcggca cactccaagg ccgagatcgt cgacatgctc    420

cggaagcaca cctacaccga cgagctccgc cagggcctgc ggcgcggccg cggcatgggg    480

gcgcgcgcgc agccgacgcc gtcgtgggcg cgggagcccc ttttcgagaa ggccgtgacc    540

ccgagcgacg tgggcaagct caaccgcctc gttgtgccga agcagcacgc cgagaagcac    600

ttcccccctga aacgcacgcc ggagacgaca acgaccaccg gcaagggggt gcttctcaac    660

ttcgaggatg gcgaggggaa agtgtggagg ttccggtact cgtattggaa cagcagccag    720
```

-continued

```
agctacgtgc tcaccaaggg atggagccgc ttcgttcggg agaagggcct cggtgccggc     780

gactccatcg tgttctcctg ctcggcgtac ggtcaggaga agcagttctt catcgactgc     840

aagaagaaca agacgatgac gagctgcccc gccgatgacc gcggcgccgc aacagcgtcg     900

ccgccagtgt cagagccaac aaaaggagaa caagtccgtg ttgtgaggct gttcggcgtc     960

gacatcgccg gagagaagag ggggcgagcg gcgccggtgg agcaggagtt gttcaagagg    1020

caatgcgtgg cacacagcca gcactctcca gccctaggtg ccttcgtctt atag          1074


<210> SEQ ID NO 93
<211> LENGTH: 348
<212> TYPE: PRT
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 93

Met Gly Val Glu Ile Leu Ser Ser Met Val Glu His Ser Phe Gln Tyr
1               5                   10                  15

Ser Ser Gly Ala Ser Ser Ala Thr Ala Glu Ser Gly Ala Val Gly Thr
            20                  25                  30

Pro Pro Arg His Leu Ser Leu Pro Val Ala Ile Ala Asp Glu Ser Leu
        35                  40                  45

Thr Ser Arg Ser Ala Ser Ser Arg Phe Lys Gly Val Val Pro Gln Pro
    50                  55                  60

Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Arg His Ala Arg Val Trp
65                  70                  75                  80

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

Ala Ser Leu Arg Tyr Arg Gly Gly Asp Ala Ala Phe Asn Phe Pro Cys
            100                 105                 110

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

Glu Ile Val Asp Met Leu Arg Lys Gln Thr Tyr Ala Asp Glu Leu Arg
    130                 135                 140

Gln Gly Leu Arg Arg Gly Arg Gly Met Gly Val Arg Ala Gln Pro Met
145                 150                 155                 160

Pro Ser Trp Ala Arg Val Pro Leu Phe Glu Lys Ala Val Thr Pro Ser
                165                 170                 175

Asp Val Gly Lys Leu Asn Arg Leu Val Val Pro Lys Gln His Ala Glu
            180                 185                 190

Lys His Phe Pro Leu Lys Arg Ser Pro Glu Thr Thr Thr Thr Thr Gly
        195                 200                 205

Asn Gly Val Leu Leu Asn Phe Glu Asp Gly Gln Gly Lys Val Trp Arg
    210                 215                 220

Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys
225                 230                 235                 240

Gly Trp Ser Arg Phe Val Arg Glu Lys Gly Leu Gly Ala Gly Asp Ser
                245                 250                 255

Ile Met Phe Ser Cys Ser Ala Tyr Gly Gln Glu Lys Gln Phe Phe Ile
            260                 265                 270

Asp Cys Lys Lys Asn Thr Thr Val Asn Gly Gly Lys Ser Ala Ser Pro
        275                 280                 285

Leu Gln Val Met Glu Ile Ala Lys Ala Glu Gln Val Arg Val Val Arg
    290                 295                 300
```

-continued

```
Leu Phe Gly Val Asp Ile Ala Gly Val Lys Arg Glu Arg Ala Ala Thr
305                 310                 315                 320

Ala Glu Gln Gly Pro Gln Gly Trp Phe Lys Arg Gln Cys Met Ala His
                325                 330                 335

Gly Gln His Ser Pro Ala Leu Gly Asp Phe Ala Leu
            340                 345


<210> SEQ ID NO 94
<211> LENGTH: 1047
<212> TYPE: DNA
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 94

atgggggtgg agatcctgag ctccatggtg gagcactcct tccagtactc ttcgggcgcg      60

tcctcggcca ccgcggagtc aggcgccgtc ggaacaccgc cgaggcatct gagcctacct     120

gtcgccatcg ccgacgagtc cctgacctca cggtcggcgt cgtctcggtt caagggcgtg     180

gtgccgcagc ccaacgggcg gtggggcgcc cagatctacg agcgccacgc tcgcgtctgg     240

ctcggcacgt tcccagacca ggactcggcg gcgcgcgcct acgacgttgc ctcgctcagg     300

taccgcggcg gcgacgccgc cttcaacttc ccgtgcgtgg tggtggaggc ggagctcgcc     360

ttcctggcgg cgcactccaa ggctgagatc gttgacatgc tccggaagca gacctacgcc     420

gatgaactcc gccagggact acggcgcggc cgtggcatgg gggtgcgcgc gcagccgatg     480

ccgtcgtggg cgcgggttcc ccttttcgag aaggccgtga cccctagcga tgtcggcaag     540

ctcaatcgcc tggtggtgcc gaagcagcac gccgagaagc acttcccccct gaagcgcagc     600

ccggagacga cgaccaccac cggcaacggc gtactgctca actttgagga cggccaggga     660

aaagtgtgga ggttccggta ctcatattgg aacagcagcc agagctacgt gctcaccaaa     720

ggctggagcc gcttcgtccg ggagaagggc ctcggcgccg gtgactccat catgttctcc     780

tgctcggcgt acgggcagga gaagcagttc ttcatcgact gcaagaagaa cacgaccgtg     840

aacggaggca aatcggcgtc gccgctgcag gtgatggaga ttgccaaagc agaacaagtc     900

cgcgtcgtta gactgttcgg tgtcgacatc gccggggtga agagggagcg agcggcgacg     960

gcggagcaag gcccgcaggg gtggttcaag aggcaatgca tggcacacgg ccagcactct    1020

cctgccctag gtgacttcgc cttatag                                       1047


<210> SEQ ID NO 95
<211> LENGTH: 362
<212> TYPE: PRT
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 95

Met Gly Met Glu Ile Leu Ser Ser Thr Val Glu His Cys Ser Gln Tyr
1               5                   10                  15

Ser Ser Ser Ala Ser Thr Ala Thr Thr Glu Ser Gly Ala Ala Gly Arg
            20                  25                  30

Ser Thr Thr Ala Leu Ser Leu Pro Val Ala Ile Thr Asp Glu Ser Val
        35                  40                  45

Thr Ser Arg Ser Ala Ser Ala Gln Pro Ala Ser Ser Arg Phe Lys Gly
    50                  55                  60

Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ser Gln Ile Tyr Glu Arg
65                  70                  75                  80
```

-continued

```
His Ala Arg Val Trp Leu Gly Thr Phe Pro Asp Gln Asp Ser Ala Ala
                85                  90                  95

Arg Ala Tyr Asp Val Ala Ser Leu Arg Tyr Arg Gly Arg Asp Ala Ala
            100                 105                 110

Thr Asn Phe Pro Cys Ala Ala Ala Glu Ala Glu Leu Ala Phe Leu Thr
        115                 120                 125

Ala His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
    130                 135                 140

Ala Asp Glu Leu Arg Gln Gly Leu Arg Arg Gly Arg Gly Met Gly Ala
145                 150                 155                 160

Arg Ala Gln Pro Thr Pro Ser Trp Ala Arg Val Pro Leu Phe Glu Lys
                165                 170                 175

Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Val Pro
            180                 185                 190

Lys Gln His Ala Glu Lys His Phe Pro Leu Lys Cys Thr Ala Glu Thr
        195                 200                 205

Thr Thr Thr Thr Gly Asn Gly Val Leu Leu Asn Phe Glu Asp Gly Glu
    210                 215                 220

Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser
225                 230                 235                 240

Tyr Val Leu Thr Lys Gly Trp Ser Ser Phe Val Arg Glu Lys Gly Leu
                245                 250                 255

Gly Ala Gly Asp Ser Ile Val Phe Ser Ser Ser Ala Tyr Gly Gln Glu
            260                 265                 270

Lys Gln Leu Phe Ile Asn Cys Lys Lys Asn Thr Thr Met Asn Gly Gly
        275                 280                 285

Lys Thr Ala Leu Pro Leu Pro Val Val Glu Thr Ala Lys Gly Glu Gln
    290                 295                 300

Asp His Val Val Lys Leu Phe Gly Val Asp Ile Ala Gly Val Lys Arg
305                 310                 315                 320

Val Arg Ala Ala Thr Gly Glu Leu Gly Pro Pro Glu Leu Phe Lys Arg
                325                 330                 335

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

Ile Gly Thr Ile Gly Pro Leu Met Leu Asn
        355                 360
```

<210> SEQ ID NO 96
<211> LENGTH: 1089
<212> TYPE: DNA
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 96

```
atggggatgg aaatcctgag ctccacggtg gagcactgct cccagtactc ttccagcgcg      60

tccacggcca caacggagtc aggcgccgcc ggaagatcga cgacggctct gagcctacca     120

gttgccatca ccgacgagtc cgttacctcg cggtcggcat cggcgcagcc ggcgtcatca     180

cggttcaagg gcgtggtgcc gcagcccaac gggcggtggg gctcccagat ctacgagcgc     240

cacgctcgcg tctggctcgg caccttcccg gatcaggact cggcggcgcg tgcctacgac     300

gttgcctcgc tcaggtaccg gggccgcgat gccgccacca acttcccgtg cgccgctgcg     360

gaagcggagc tcgccttcct gaccgcgcac tccaaggccg agatcgtcga catgctccgg     420
```

-continued

```
aagcacacct acgccgacga actccgccag ggcctgcggc gcggccgcgg catgggtgcg    480

cgcgcgcagc cgacgccgtc gtgggcgcgg gttccccttt tcgagaaggc tgtgacccct    540

agcgatgtcg gcaagctcaa tcgcctggtg gtgccgaagc agcacgccga gaagcacttc    600

cccctgaagt gcaccgcaga gacgacgacc accaccggca acggcgtgct gctaaacttc    660

gaggatggtg aggggaaggt gtggaggttc cggtactcgt attggaacag tagccagagc    720

tacgtgctca ccaaaggctg gagcagcttc gtccgggaga agggcctcgg cgcaggcgac    780

tccatcgtct tctcctcctc ggcgtacggg caggagaagc agttattcat caactgcaaa    840

aagaacacga ctatgaacgg cggcaaaaca gcgttgccgc tgccagtggt ggagactgcc    900

aaaggagaac aagaccacgt cgttaagttg ttcggtgttg acatcgccgg tgtgaagagg    960

gtgcgagcgg cgacggggga gctaggcccg ccggagttgt tcaagagaca atccgtggca   1020

cacggatgcg gaaggatgaa ctacatttgc tactccatag ggacaatagg acctcttatg   1080

ctcaactga                                                           1089
```

```
<210> SEQ ID NO 97
<211> LENGTH: 308
<212> TYPE: PRT
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 97

Met Ala Ser Ser Lys Pro Thr Asn Pro Glu Val Asp Asn Asp Met Glu
1               5                   10                  15

Cys Ser Ser Pro Glu Ser Gly Ala Glu Asp Ala Val Glu Ser Ser Ser
            20                  25                  30

Pro Val Ala Ala Pro Ser Ser Arg Phe Lys Gly Val Val Pro Gln Pro
        35                  40                  45

Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Ser Arg Val Trp
    50                  55                  60

Leu Gly Thr Phe Gly Asp Glu Glu Ala Ala Ala Cys Ala Tyr Asp Val
65                  70                  75                  80

Ala Ala Leu Arg Phe Arg Gly Arg Asp Ala Val Thr Asn His Gln Arg
                85                  90                  95

Leu Pro Ala Ala Glu Gly Ala Gly Trp Ser Ser Thr Ser Glu Leu Ala
            100                 105                 110

Phe Leu Ala Asp His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys
        115                 120                 125

His Thr Tyr Asp Asp Glu Leu Arg Gln Gly Leu Arg Arg Gly His Gly
    130                 135                 140

Arg Ala Gln Pro Thr Pro Ala Trp Ala Arg Glu Phe Leu Phe Glu Lys
145                 150                 155                 160

Ala Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Val Pro
                165                 170                 175

Lys Gln His Ala Glu Lys His Phe Pro Pro Thr Thr Ala Ala Ala Ala
            180                 185                 190

Gly Ser Asp Gly Lys Gly Leu Leu Leu Asn Phe Glu Asp Gly Gln Gly
        195                 200                 205

Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr
    210                 215                 220

Val Leu Thr Lys Gly Trp Ser Arg Phe Val Gln Glu Lys Gly Leu Cys
```

-continued

225 230 235 240

Ala Gly Asp Thr Val Thr Phe Ser Arg Ser Ala Tyr Val Met Asn Asp
245 250 255

Thr Asp Glu Gln Leu Phe Ile Asp Tyr Lys Gln Ser Ser Lys Asn Asp
260 265 270

Glu Ala Ala Asp Val Ala Thr Ala Asp Glu Asn Glu Ala Gly His Val
275 280 285

Ala Val Lys Leu Phe Gly Val Asp Ile Gly Trp Ala Gly Met Ala Gly
290 295 300

Ser Ser Gly Gly
305

<210> SEQ ID NO 98
<211> LENGTH: 927
<212> TYPE: DNA
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 98

atggcgtcta gcaagccgac aaaccccgag gtagacaatg acatggagtg ctcctccccg 60

gaatcgggtg ccgaggacgc cgtggagtcg tcgtcgccgg tggcagcgcc atcttcgcgg 120

ttcaagggcg tcgtgccgca gcctaacggg cgctggggcg cgcagatcta cgagaagcac 180

tcgcgggtgt ggcttggcac gttcggggac gaggaagccg ccgcgtgcgc ctacgacgtg 240

gccgcgctcc gcttccgcgg ccgcgacgcc gtcaccaacc accagcgcct gccggcggcg 300

gagggggccg gctggtcgtc cacgagcgag ctcgccttcc tcgccgacca ctccaaggcc 360

gagatcgtcg acatgctccg gaagcacacc tacgacgacg agctccggca gggcctgcgc 420

cgcggccacg ggcgcgcgca gcccacgccg gcgtgggcgc gagagttcct cttcgagaag 480

gccctgaccc cgagcgacgt cggcaagctc aaccgcctgg tcgttccgaa gcagcacgcc 540

gagaagcact tccccccgac gacggcggcg gccgccggaa gcgacggcaa gggcttgctg 600

ctcaacttcg aggacggcca agggaaggtg tggaggttcc ggtactcata ctggaacagc 660

agccagagct acgtgctcac caagggctgg agccgcttcg tccaagaaaa gggcctctgc 720

gccggcgaca ccgtgacgtt ctcccggtcg gcgtacgtga tgaatgacac ggatgagcag 780

ctcttcatcg actacaagca gagtagcaag aacgacgaag cggccgacgt agccactgcc 840

gatgagaatg aggccggcca tgtcgccgtg aagctcttcg ggtcgacat tggctgggct 900

gggatggcgg gatcatcagg tgggtga 927

<210> SEQ ID NO 99
<211> LENGTH: 1279
<212> TYPE: PRT
<213> ORGANISM: Hordeum vulgare

<400> SEQUENCE: 99

Met Leu Phe Asp Ser Ser Val Ser Ala Ser Leu Gly Thr Met Arg Pro
1 5 10 15

Leu Val Lys Lys Leu Asp Met Leu Leu Ala Pro Ala Arg Gly Tyr Ser
20 25 30

Thr Leu Cys Lys Arg Ile Lys Glu Val Met His Leu Leu Lys His Asp
35 40 45

Val Glu Glu Ile Ser Ser Tyr Leu Asp Glu Leu Thr Glu Val Glu Asp
50 55 60

-continued

```
Pro Pro Pro Met Ala Lys Cys Trp Met Asn Glu Ala Arg Asp Leu Ser
65                  70                  75                  80

Tyr Asp Met Glu Asp Tyr Ile Asp Ser Leu Leu Phe Val Pro Pro Gly
                85                  90                  95

His Phe Ile Lys Lys Lys Lys Lys Lys Lys Lys Lys Gly Lys Lys Lys
            100                 105                 110

Met Val Ile Lys Lys Arg Leu Lys Trp Cys Lys Gln Ile Val Phe Thr
        115                 120                 125

Lys Gln Val Ser Asp His Gly Ile Lys Thr Ser Lys Ile Ile His Val
    130                 135                 140

Asn Val Pro Arg Leu Pro Asn Lys Pro Lys Val Ala Lys Ile Ile Leu
145                 150                 155                 160

Gln Phe Arg Ile Tyr Val Gln Glu Ala Ile Glu Arg Tyr Asp Lys Tyr
                165                 170                 175

Arg Leu His His Cys Ser Thr Leu Arg Arg Arg Leu Leu Ser Thr Gly
            180                 185                 190

Ser Met Leu Ser Val Pro Ile Pro Tyr Glu Glu Ala Ala Gln Ile Val
        195                 200                 205

Thr Asp Gly Arg Met Asn Glu Phe Ile Ser Ser Leu Ala Ala Asn Asn
    210                 215                 220

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

Cys Leu Gly Lys Thr Thr Leu Ala Asn Val Leu Tyr Asp Arg Ile Gly
                245                 250                 255

Met Gln Phe Glu Cys Arg Ala Phe Ile Arg Val Ser Lys Lys Pro Asp
            260                 265                 270

Met Lys Arg Leu Phe Arg Asp Leu Leu Ser Gln Phe His Gln Lys Gln
        275                 280                 285

Pro Leu Pro Thr Ser Cys Asn Glu Leu Gly Ile Ser Asp Asn Ile Ile
    290                 295                 300

Lys His Leu Gln Asp Lys Arg Tyr Leu Ile Val Ile Asp Asp Leu Trp
305                 310                 315                 320

Asp Leu Ser Val Trp Asp Ile Ile Lys Tyr Ala Phe Pro Lys Gly Asn
                325                 330                 335

His Gly Ser Arg Ile Ile Ile Thr Thr Gln Ile Glu Asp Val Ala Leu
            340                 345                 350

Thr Cys Cys Cys Asp His Ser Glu His Val Phe Glu Met Lys Pro Leu
        355                 360                 365

Asn Ile Gly His Ser Arg Glu Leu Phe Phe Asn Arg Leu Phe Gly Ser
    370                 375                 380

Glu Ser Asp Cys Leu Glu Glu Phe Lys Arg Val Ser Asn Glu Ile Val
385                 390                 395                 400

Asp Ile Cys Gly Gly Leu Pro Leu Ala Thr Ile Asn Ile Ala Ser His
                405                 410                 415

Leu Ala Asn Gln Glu Thr Glu Val Ser Leu Asp Leu Leu Thr Asp Thr
            420                 425                 430

Arg Asp Leu Leu Arg Ser Cys Leu Trp Ser Asn Ser Thr Ser Glu Arg
        435                 440                 445

Thr Lys Gln Val Leu Asn Leu Ser Tyr Ser Asn Leu Pro Asp Tyr Leu
    450                 455                 460
```

-continued

```
Lys Thr Cys Leu Leu Tyr Leu His Met Tyr Pro Val Gly Ser Ile Ile
465                 470                 475                 480

Trp Lys Asp Asp Leu Val Lys Gln Leu Val Ala Glu Gly Phe Ile Ala
                485                 490                 495

Thr Arg Glu Gly Lys Asp Gln Asp Gln Glu Met Ile Glu Lys Ala Ala
            500                 505                 510

Gly Leu Cys Phe Asp Ala Leu Ile Asp Arg Arg Phe Ile Gln Pro Ile
        515                 520                 525

Tyr Thr Lys Tyr Asn Asn Lys Val Leu Ser Cys Thr Val His Glu Val
    530                 535                 540

Val His Asp Leu Ile Ala Gln Lys Ser Ala Glu Glu Asn Phe Ile Val
545                 550                 555                 560

Val Ala Asp His Asn Arg Lys Asn Ile Ala Leu Ser His Lys Val Arg
                565                 570                 575

Arg Leu Ser Leu Ile Phe Gly Asp Thr Ile Tyr Ala Lys Thr Pro Ala
            580                 585                 590

Asn Ile Thr Lys Ser Gln Ile Arg Ser Phe Arg Phe Phe Gly Leu Phe
        595                 600                 605

Glu Cys Met Pro Cys Ile Thr Glu Phe Lys Val Leu Arg Val Leu Asn
    610                 615                 620

Leu Gln Leu Ser Gly His Arg Gly Asp Asn Asp Pro Ile Asp Leu Thr
625                 630                 635                 640

Gly Ile Ser Glu Leu Phe Gln Leu Arg Tyr Leu Lys Ile Thr Ser Asp
                645                 650                 655

Val Cys Ile Lys Leu Pro Asn Gln Met Gln Lys Leu Gln Tyr Leu Glu
            660                 665                 670

Thr Leu Asp Ile Met Asp Ala Pro Arg Val Thr Ala Val Pro Trp Asp
        675                 680                 685

Ile Ile Asn Leu Pro His Leu Leu His Leu Thr Leu Pro Val Asp Thr
    690                 695                 700

Tyr Leu Leu Asp Trp Ile Ser Ser Met Thr Asp Ser Val Ile Ser Leu
705                 710                 715                 720

Trp Thr Leu Gly Lys Leu Asn Tyr Leu Gln His Leu His Leu Thr Ser
                725                 730                 735

Ser Ser Thr Arg Pro Ser Tyr His Leu Glu Arg Ser Val Glu Ala Leu
            740                 745                 750

Gly Tyr Leu Ile Gly Gly His Gly Lys Leu Lys Thr Ile Val Val Ala
        755                 760                 765

His Val Ser Ser Ala Gln Asn Thr Val Val Arg Gly Ala Pro Glu Val
    770                 775                 780

Thr Ile Ser Trp Asp Arg Met Ser Pro Pro Pro Leu Leu Gln Arg Phe
785                 790                 795                 800

Glu Cys Pro His Ser Cys Phe Ile Phe Tyr Arg Ile Pro Lys Trp Val
                805                 810                 815

Thr Glu Leu Gly Asn Leu Cys Ile Leu Lys Ile Ala Val Lys Glu Leu
            820                 825                 830

His Met Ile Cys Leu Gly Thr Leu Arg Gly Leu His Ala Leu Thr Asp
        835                 840                 845

Leu Ser Leu Tyr Val Glu Thr Ala Pro Ile Asp Lys Ile Ile Phe Asp
    850                 855                 860

Lys Ala Gly Phe Ser Val Leu Lys Tyr Cys Lys Leu Arg Phe Ala Ala
```

-continued

```
865                 870                 875                 880

Gly Ile Ala Trp Leu Lys Phe Glu Ala Asp Ala Met Pro Ser Leu Trp
                885                 890                 895

Lys Leu Met Leu Val Phe Asn Ala Ile Pro Arg Met Asp Gln Asn Leu
            900                 905                 910

Val Phe Phe His His Ser Arg Pro Ala Met His Gln Arg Gly Gly Ala
        915                 920                 925

Val Ile Ile Val Glu His Met Pro Gly Leu Arg Val Ile Ser Ala Lys
    930                 935                 940

Phe Gly Gly Ala Ala Ser Asp Leu Glu Tyr Ala Ser Arg Thr Val Val
945                 950                 955                 960

Ser Asn His Pro Ser Asn Pro Thr Ile Asn Met Gln Leu Val Cys Tyr
                965                 970                 975

Ser Ser Asn Gly Lys Arg Ser Arg Lys Arg Lys Gln Gln Pro Tyr Asp
            980                 985                 990

Val Val Lys Gly Gln Pro Asp Glu  Tyr Ala Lys Arg Leu  Glu Arg Pro
        995                 1000                 1005

Ala Glu  Lys Arg Ile Ser Thr  Pro Thr Lys Ser Ser  Leu Arg Leu
    1010                 1015                 1020

His Val  Pro Glu Ile Thr Pro  Lys Pro Met Gln Ile  Thr Asp Asn
    1025                 1030                 1035

Asn Val  Gln Arg Arg Glu His  Met Phe Asp Thr Val  Leu Thr Arg
    1040                 1045                 1050

Gly Asp  Val Gly Met Leu Asn  Arg Leu Val Val Pro  Lys Lys His
    1055                 1060                 1065

Ala Glu  Lys Tyr Phe Pro Leu  Asp Ser Ser Ser Thr  Arg Thr Ser
    1070                 1075                 1080

Lys Ala  Ile Val Leu Ser Phe  Glu Asp Pro Ala Gly  Lys Ser Trp
    1085                 1090                 1095

Phe Phe  His Tyr Ser Tyr Arg  Ser Ser Ser Gln Asn  Tyr Val Met
    1100                 1105                 1110

Phe Lys  Gly Trp Thr Gly Phe  Val Lys Glu Lys Phe  Leu Glu Ala
    1115                 1120                 1125

Gly Asp  Thr Val Ser Phe Ser  Arg Gly Val Gly Glu  Ala Thr Arg
    1130                 1135                 1140

Gly Arg  Leu Phe Ile Asp Cys  Gln Asn Glu Gln Arg  Tyr Met Phe
    1145                 1150                 1155

Glu Arg  Val Leu Thr Ala Ser  Asp Met Glu Ser Asp  Gly Cys Ser
    1160                 1165                 1170

Leu Met  Val Pro Val Asn Leu  Val Trp Pro His Pro  Gly Leu Arg
    1175                 1180                 1185

Lys Thr  Ile Lys Gly Arg His  Ala Val Leu Gln Phe  Glu Asp Gly
    1190                 1195                 1200

Ser Gly  Asn Gly Lys Val Trp  Pro Phe Gln Phe Glu  Ala Ser Gly
    1205                 1210                 1215

Gln Tyr  Tyr Leu Met Lys Gly  Leu Asn Tyr Phe Val  Asn Asp Arg
    1220                 1225                 1230

Asp Leu  Ala Ala Gly Tyr Thr  Val Ser Phe Tyr Arg  Ala Gly Thr
    1235                 1240                 1245

Arg Leu  Phe Val Asp Ser Gly  Arg Lys Asp Asp Lys  Val Ala Leu
    1250                 1255                 1260
```

-continued

```
Gly Thr Arg Ser Arg Glu Arg Ile Tyr Pro Lys Ile Val Arg Ser
    1265                1270                1275

Gln


<210> SEQ ID NO 100
<211> LENGTH: 3840
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 100

atgttgtttg atagttcagt gagtgcttcg ttgggcacca tgagaccact tgtcaagaag      60

ctcgacatgc tgctagctcc tgctcgggga tacagtacct tgtgcaagag gatcaaggaa     120

gtgatgcacc ttctcaaaca tgatgttgaa gagataagct cctaccttga tgaacttaca     180

gaggtggagg accctccacc aatggccaag tgctggatga acgaggcacg cgacctgtct     240

tatgatatgg aggattacat tgatagcttg ttatttgtgc cacctggcca tttcatcaag     300

aagaagaaga agaagaagaa gaagggaaag aagaagatgg tgataaagaa gaggctcaag     360

tggtgcaaac agatcgtatt cacaaagcaa gtgtcagacc atggtatcaa gaccagtaaa     420

atcattcatg ttaatgtccc tcgtcttccc aataagccca aggttgcaaa aataatatta     480

cagttcagga tctatgtcca ggaggctatt gaacggtatg acaagtatag gcttcaccat     540

tgcagcacct tgaggcgtag attgttgtcc actggtagta tgctttcagt gccaataccc     600

tatgaagaag ctgcccaaat tgtaactgat ggccggatga atgagtttat cagctcactg     660

gctgctaata atgcagcaga tcagcagcag ctcaaggtgg tatctgttct tggatctggg     720

tgtctaggta aaactacgct tgcgaatgtg ttgtacgaca gaattgggat gcaattcgaa     780

tgcagagctt tcattcgagt gtccaaaaag cctgatatga agagactttt ccgtgacttg     840

ctctcgcaat tccaccagaa gcagccactg cctaccagtt gtaatgagct tggcataagt     900

gacaatatca tcaaacatct gcaagataaa aggtatctaa ttgttattga tgatttgtgg     960

gatttatcag tatgggatat tattaaatat gcttttccaa agggaaacca tggaagcaga    1020

ataataataa ctacacagat tgaagatgtt gcattaactt gttgctgtga tcactcggag    1080

catgttttcg agatgaaacc tctcaacatt ggtcactcaa gagagctatt ttttaataga    1140

ctttttggtt ctgaaagtga ctgtcttgaa gaattcaaac gagtttcaaa cgaaattgtt    1200

gatatatgtg gtggtttacc gctagcaaca atcaacatag ctagtcattt ggcaaaccag    1260

gagacagaag tatcattgga tttgctaaca gacacacgtg atttgttgag gtcctgtttg    1320

tggtcaaatt ctacttcaga aagaacaaaa caagtactga acctcagcta cagtaatctt    1380

cctgattatc tgaagacatg tttgctgtat cttcatatgt atccagtggg ctccataatc    1440

tggaaggatg atctggtgaa gcaattggtg gctgaagggt ttattgctac aagagaaggg    1500

aaagaccaag accaagaaat gatagagaaa gctgcaggac tctgtttcga tgcacttatt    1560

gatagaagat tcatccagcc tatatatacc aagtacaaca ataaggtgtt gtcctgcacg    1620

gttcatgagg tggtacatga tcttattgcc caaaagtctg ctgaagagaa tttcattgtg    1680

gtagcagacc acaatcgaaa gaatatagca ctttctcata aggttcgtcg actatctctc    1740

atctttggcg acacaatata tgccaagaca ccagcaaaca tcacaaagtc acaaattcgg    1800

tcattcagat tttttggatt attcgagtgt atgccttgta ttacagagtt caaggttctc    1860
```

-continued

cgtgttctaa accttcaact atctggtcat cgtggggaca atgaccctat agacctcact 1920

gggatttcag aactgtttca gctgagatat ttaaagatta caagtgatgt gtgcataaaa 1980

ctaccaaatc aaatgcaaaa actgcaatat ttggaaacgt tggacattat ggatgcacca 2040

agagtcactg ctgttccatg ggatattata aatctcccac acctgttgca cctgactctt 2100

cctgttgata catatctgct ggattggatt agcagcatga ctgactccgt catcagtctg 2160

tggacccttg gcaagctgaa ctacctgcag catcttcatc ttactagttc ttctacacgt 2220

ccttcatacc atctggagag aagtgtggag gctctgggtt atttgatcgg aggacatggc 2280

aagctgaaaa ctatagtagt cgctcatgtc tcctctgctc aaaatactgt ggttcgtggc 2340

gccccagaag taaccatttc atgggatcgt atgtcacctc cccccttct ccagagattc 2400

gaatgcccac acagctgctt catattttac cgaattccta agtgggttac agaacttggc 2460

aacctgtgca ttttgaagat tgcagtgaag gagcttcata tgatttgtct tggtactctc 2520

agaggattgc atgccctcac tgatctgtcg ctgtatgtgg agacagcgcc cattgacaag 2580

atcatctttg acaaggccgg gttctcagtt ctcaagtact gcaaattgcg cttcgcggct 2640

ggtatagctt ggctgaaatt tgaggctgat gcaatgccta gtctatggaa actgatgcta 2700

gttttcaacg ccatcccacg aatggaccaa aatcttgttt tctttcacca cagccgaccg 2760

gcgatgcatc aacgtggtgg tgcagtaatc attgtcgagc atatgccagg gcttagagtg 2820

atctccgcaa aatttggggg cgcagcttct gatctagagt atgcttcgag gaccgtcgtt 2880

agtaaccatc caagcaatcc tacaatcaac atgcaattgg tgtgttatag ttccaatggt 2940

aagagaagca gaaaaaggaa acaacaacct tacgacgttg tgaagggaca accagatgaa 3000

tacgccaaga gattggagag accagctgag aaaaggattt caacgccgac aaagtcttct 3060

ttgcgtctgc atgttccaga aattacacca aaacctatgc agattacaga caacaatgtt 3120

cagaggaggg agcacatgtt cgatacggtt ctgactcggg gggacgtggg gatgctgaac 3180

cggctggtgg taccgaagaa gcacgcggag aagtacttcc cgctggacag ttcctccacc 3240

cgcaccagca aggccatcgt actcagcttt gaggaccctg ctgggaagtc atggttcttc 3300

cactactcct accggagcag cagccagaac tacgtcatgt tcaaggggtg gactggcttc 3360

gtcaaggaga agtttctcga agccggcgac accgtctcct tcagccgcgg cgtcggggag 3420

gccacgaggg ggaggctctt catcgactgt caaaatgagc agaggtacat gttcgagcga 3480

gtgctgacgg cgagtgatat ggagtcggat ggctgctcgc tgatggtccc agtgaacttg 3540

gtgtggccgc accccggcct ccgcaagacg atcaagggga ggcacgccgt gctgcagttt 3600

gaggacggca gcggcaacgg gaaggtgtgg ccatttcagt ttgaggcctc cggccaatac 3660

tatctcatga agggcttgaa ctactttgtt aacgaccgcg accttgcggc tggctatacc 3720

gtctccttct accgcgccgg cacgcggttg ttcgtcgact ccgggcgtaa agatgacaaa 3780

gtagccttgg gaaccagaag ccgcgaaagg atctatccta agatcgtgcg gtcgcagtag 3840

<210> SEQ ID NO 101
<211> LENGTH: 264
<212> TYPE: PRT
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 101

Met Ser Gly Asn His Tyr Ser Arg Asp Ile His His Asn Thr Pro Ser
1 5 10 15

-continued

```
Val His His His Gln Asn Tyr Ala Val Val Asp Arg Glu Tyr Leu Phe
            20                  25                  30

Glu Lys Ser Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val
    35                  40                  45

Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Asn Asn Ala Gly
    50                  55                  60

Asp Asp Val Ala Ala Ala Glu Thr Thr Glu Lys Gly Met Leu Leu Thr
65                  70                  75                  80

Phe Glu Asp Glu Ser Gly Lys Cys Trp Lys Phe Arg Tyr Ser Tyr Trp
                85                  90                  95

Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val
            100                 105                 110

Lys Asp Lys His Leu His Ala Gly Asp Val Val Phe Phe Gln Arg His
    115                 120                 125

Arg Phe Asp Leu His Arg Val Phe Ile Gly Trp Arg Lys Arg Gly Glu
    130                 135                 140

Val Ser Ser Pro Thr Ala Val Ser Val Val Ser Gln Glu Ala Arg Val
145                 150                 155                 160

Asn Thr Thr Ala Tyr Trp Ser Gly Leu Thr Thr Pro Tyr Arg Gln Val
                165                 170                 175

His Ala Ser Thr Ser Ser Tyr Pro Asn Ile His Gln Glu Tyr Ser His
            180                 185                 190

Tyr Gly Ala Val Ala Glu Ile Pro Thr Val Val Thr Gly Ser Ser Arg
    195                 200                 205

Thr Val Arg Leu Phe Gly Val Asn Leu Glu Cys His Gly Asp Val Val
    210                 215                 220

Glu Thr Pro Pro Cys Pro Asp Gly Tyr Asn Gly Gln His Phe Tyr Tyr
225                 230                 235                 240

Tyr Ser Thr Pro Asp Pro Met Asn Ile Ser Phe Ala Gly Glu Ala Met
                245                 250                 255

Glu Gln Val Gly Asp Gly Arg Arg
            260


<210> SEQ ID NO 102
<211> LENGTH: 258
<212> TYPE: PRT
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 102

Met Ser Val Asn His Tyr Ser Asn Thr Leu Ser Ser His Asn His His
1               5                   10                  15

Asn Glu His Lys Glu Ser Leu Phe Glu Lys Ser Leu Thr Pro Ser Asp
            20                  25                  30

Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg
    35                  40                  45

Tyr Leu Pro Leu Asn Asn Cys Gly Gly Gly Gly Asp Val Thr Ala Glu
    50                  55                  60

Ser Thr Glu Lys Gly Val Leu Leu Ser Phe Glu Asp Glu Ser Gly Lys
65                  70                  75                  80

Ser Trp Lys Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val
                85                  90                  95

Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys Asp Lys His Leu Asn Ala
```

-continued

```
            100                 105                 110

Gly Asp Val Val Leu Phe Gln Arg His Arg Phe Asp Ile His Arg Leu
        115                 120                 125

Phe Ile Gly Trp Arg Arg Arg Gly Glu Ala Ser Ser Ser Ser Ala Val
    130                 135                 140

Ser Ala Val Thr Gln Asp Pro Arg Ala Asn Thr Thr Ala Tyr Trp Asn
145                 150                 155                 160

Gly Leu Thr Thr Pro Tyr Arg Gln Val His Ala Ser Thr Ser Ser Tyr
                165                 170                 175

Pro Asn Asn Ile His Gln Glu Tyr Ser His Tyr Gly Pro Val Ala Glu
            180                 185                 190

Thr Pro Thr Val Ala Ala Gly Ser Ser Lys Thr Val Arg Leu Phe Gly
        195                 200                 205

Val Asn Leu Glu Cys His Ser Asp Val Val Glu Pro Pro Pro Cys Pro
    210                 215                 220

Asp Ala Tyr Asn Gly Gln His Ile Tyr Tyr Tyr Ser Thr Pro His Pro
225                 230                 235                 240

Met Asn Ile Ser Phe Ala Gly Glu Ala Met Glu Gln Val Gly Asp Gly
                245                 250                 255

Arg Gly
```

<210> SEQ ID NO 103
<211> LENGTH: 777
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 103

```
atgtcagtca accattactc aaacactctc tcgtcgcaca atcaccacaa cgaacataaa     60

gagtctttgt tcgagaagtc actcacgcca agcgatgttg gaaagctaaa ccgtttagtc    120

ataccaaaac aacacgccga gagatacctc cctctcaata attgcggcgg cggcggcgac    180

gtgacggcgg agtcgacgga gaaaggggtg cttctcagct tcgaggacga gtcgggaaaa    240

tcttggaaat tcagatactc atattggaac agtagtcaaa gctacgtgtt gaccaaagga    300

tggagcaggt acgtcaaaga caagcacctc aacgcagggg acgtcgtttt atttcaacgg    360

caccgttttg atattcatag actcttcatt ggctggagga gacgcggaga ggcttcttcc    420

tcttccgccg tttccgccgt gactcaagat cctcgagcta acacgacggc gtactggaac    480

ggtttgacta caccttatcg tcaagtacac gcgtcaacta gttcttaccc taacaacatc    540

caccaagagt attcacatta tggccctgtt gctgagacac cgacggtagc tgcagggagc    600

tcgaagacgg tgaggctatt tggagttaac ctcgaatgtc acagtgacgt tgtggagcca    660

ccaccgtgtc ctgacgccta caacggccaa cacatttact attactcaac tccacatccc    720

atgaatatct catttgctgg agaagcaatg gagcaggtag gagatggacg aggttga       777
```

<210> SEQ ID NO 104
<211> LENGTH: 267
<212> TYPE: PRT
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 104

```
Met Ser Val Asn His Tyr Ser Thr Asp His His Gln Val His His His
1               5                   10                  15
```

-continued

```
His Thr Leu Phe Leu Gln Asn Leu His Thr Thr Asp Thr Ser Glu Pro
            20                  25                  30

Thr Thr Thr Ala Ala Thr Ser Leu Arg Glu Asp Gln Lys Glu Tyr Leu
        35                  40                  45

Phe Glu Lys Ser Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
    50                  55                  60

Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asn Thr Ile
65                  70                  75                  80

Ile Ser Asn Asn Ala Glu Glu Lys Gly Met Leu Leu Ser Phe Glu Asp
                85                  90                  95

Glu Ser Gly Lys Cys Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser
            100                 105                 110

Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys Asp Lys
        115                 120                 125

Gln Leu Asp Pro Ala Asp Val Val Phe Phe Gln Arg Gln Arg Ser Asp
    130                 135                 140

Ser Arg Arg Leu Phe Ile Gly Trp Arg Arg Arg Gly Gln Gly Ser Ser
145                 150                 155                 160

Ser Ala Ala Asn Thr Thr Ser Tyr Ser Ser Ser Met Thr Ala Pro Pro
                165                 170                 175

Tyr Ser Asn Tyr Ser Asn Arg Pro Ala His Ser Glu Tyr Ser His Tyr
            180                 185                 190

Gly Ala Ala Val Ala Thr Ala Thr Glu Thr His Phe Ile Pro Ser Ser
        195                 200                 205

Ser Ala Val Gly Ser Ser Arg Thr Val Arg Leu Phe Gly Val Asn Leu
    210                 215                 220

Glu Cys Gln Met Asp Glu Asp Glu Gly Asp Asp Ser Val Ala Thr Ala
225                 230                 235                 240

Ala Ala Ala Glu Cys Pro Arg Gln Asp Ser Tyr Tyr Asp Gln Asn Met
                245                 250                 255

Tyr Asn Tyr Tyr Thr Pro His Ser Ser Ala Ser
            260                 265
```

<210> SEQ ID NO 105
<211> LENGTH: 804
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 105

```
atgtcagtca accattactc cacggaccac caccaggtcc accaccacca cactctcttc      60

ttgcagaacc tccacaccac cgacacatcg gagccaacca caaccgccgc cacatcactc     120

cgcgaagacc agaaagagta tctcttcgag aaatctctca caccaagcga cgttggcaaa     180

ctcaaccgtc tcgttatacc aaaacagcac gcggagaagt acttccctct caacaccatc     240

atctccaata atgctgagga gaaagggatg cttctaagct tcgaagacga gtcaggcaag     300

tgctggaggt tcagatactc ttactggaac agcagtcaaa gctacgtgtt gactaaagga     360

tggagcagat acgtcaaaga caaacagctc gacccagccg atgttgtttt cttccaacgt     420

caacgttctg attcccggag actctttatt ggctggcgta gacgcggtca aggctcctcc     480

tccgccgcga atacgacgtc gtattctagt tccatgactg ctccaccgta tagtaattac     540

tctaatcgtc ctgctcactc agagtattcc cactatggcg ccgccgtagc aacagcgacg     600
```

-continued

```
gagacgcact tcataccatc gtcttccgcc gtcgggagct cgaggacggt gaggcttttt    660

ggtgtgaatt tggagtgtca aatggatgaa gacgaaggag atgattcggt tgccacggca    720

gccgccgctg agtgtcctcg tcaggacagc tactacgacc aaaacatgta caattattac    780

actcctcact cctcagcctc ataa                                            804


<210> SEQ ID NO 106
<211> LENGTH: 248
<212> TYPE: PRT
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 106

Met Ser Ile Asn Gln Tyr Ser Ser Asp Phe Asn Tyr His Ser Leu Met
1               5                   10                  15

Trp Gln Gln Gln Gln His Arg His His His His Gln Asn Asp Val Ala
            20                  25                  30

Glu Glu Lys Glu Ala Leu Phe Glu Lys Pro Leu Thr Pro Ser Asp Val
        35                  40                  45

Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr
    50                  55                  60

Phe Pro Leu Ala Ala Ala Ala Ala Asp Ala Met Glu Lys Gly Leu Leu
65                  70                  75                  80

Leu Cys Phe Glu Asp Glu Glu Gly Lys Pro Trp Arg Phe Arg Tyr Ser
                85                  90                  95

Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg
            100                 105                 110

Tyr Val Lys Glu Lys Gln Leu Asp Ala Gly Asp Val Ile Leu Phe His
        115                 120                 125

Arg His Arg Val Asp Gly Gly Arg Phe Phe Ile Gly Trp Arg Arg Arg
    130                 135                 140

Gly Asn Ser Ser Ser Ser Ser Asp Ser Tyr Arg His Leu Gln Ser Asn
145                 150                 155                 160

Ala Ser Leu Gln Tyr Tyr Pro His Ala Gly Val Gln Ala Val Glu Ser
                165                 170                 175

Gln Arg Gly Asn Ser Lys Thr Leu Arg Leu Phe Gly Val Asn Met Glu
            180                 185                 190

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

Thr Ile Cys Pro Thr Ser His Asp Gln Phe His Leu Tyr Pro Gln Gln
    210                 215                 220

His Tyr Pro Pro Pro Tyr Tyr Met Asp Ile Ser Phe Thr Gly Asp Val
225                 230                 235                 240

His Gln Thr Arg Ser Pro Gln Gly
                245


<210> SEQ ID NO 107
<211> LENGTH: 747
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 107

atgtcaataa accaatactc aagcgatttc aactaccact ctctcatgtg gcaacaacag     60

cagcaccgcc accaccacca tcaaaacgac gtcgcggagg aaaaagaagc tcttttcgag    120
```

-continued

```
aaacccttaa ccccaagtga cgtcggaaaa ctcaaccgcc tcgtcatccc aaaacagcac    180

gccgagagat acttccctct cgcagcagcc gccgcagacg cgatggagaa gggattactt    240

ctctgcttcg aggacgagga aggtaagcca tggagattca gatactcgta ttggaacagt    300

agccagagtt atgtcttgac caaaggatgg agcagatacg tcaaggagaa gcagctcgac    360

gccggtgacg tcattctctt ccaccgccac cgtgttgacg gaggaagatt cttcattggc    420

tggagaagac gcggcaactc ttcctcctct tccgactctt atcgccatct tcagtccaat    480

gcctcgctcc aatattatcc tcatgcagga gttcaagcgg tggagagcca gagagggaat    540

tcgaagacat taagactgtt cggagtgaac atggagtgtc agctagactc cgacttgccc    600

gatccatcta caccagacgg ttccaccata tgtccgacca gtcacgacca gtttcatctc    660

taccctcaac aacactatcc tcctccgtac tacatggaca taagtttcac aggagatgtg    720

caccagacga gaagcccaca aggataa                                        747


<210> SEQ ID NO 108
<211> LENGTH: 245
<212> TYPE: PRT
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 108

Met Ser Ile Asn Gln Tyr Ser Ser Glu Phe Tyr Tyr His Ser Leu Met
1               5                   10                  15

Trp Gln Gln Gln Gln Gln His His His Gln Asn Glu Val Val Glu Glu
            20                  25                  30

Lys Glu Ala Leu Phe Glu Lys Pro Leu Thr Pro Ser Asp Val Gly Lys
        35                  40                  45

Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe Pro
    50                  55                  60

Leu Ala Ala Ala Ala Val Asp Ala Val Glu Lys Gly Leu Leu Leu Cys
65                  70                  75                  80

Phe Glu Asp Glu Glu Gly Lys Pro Trp Arg Phe Arg Tyr Ser Tyr Trp
                85                  90                  95

Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val
            100                 105                 110

Lys Glu Lys Gln Leu Asp Ala Gly Asp Val Val Leu Phe His Arg His
        115                 120                 125

Arg Ala Asp Gly Gly Arg Phe Phe Ile Gly Trp Arg Arg Arg Gly Asp
    130                 135                 140

Ser Ser Ser Ser Ser Asp Ser Tyr Arg Asn Leu Gln Ser Asn Ser Ser
145                 150                 155                 160

Leu Gln Tyr Tyr Pro His Ala Gly Ala Gln Ala Val Glu Asn Gln Arg
                165                 170                 175

Gly Asn Ser Lys Thr Leu Arg Leu Phe Gly Val Asn Met Glu Cys Gln
            180                 185                 190

Ile Asp Ser Asp Trp Ser Glu Pro Ser Thr Pro Asp Gly Phe Thr Thr
        195                 200                 205

Cys Pro Thr Asn His Asp Gln Phe Pro Ile Tyr Pro Glu His Phe Pro
    210                 215                 220

Pro Pro Tyr Tyr Met Asp Val Ser Phe Thr Gly Asp Val His Gln Thr
225                 230                 235                 240

Ser Ser Gln Gln Gly
```

-continued

```
                245


<210> SEQ ID NO 109
<211> LENGTH: 738
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 109

atgtcaataa atcaatattc aagcgagttc tactaccatt ctctcatgtg gcaacaacag      60

cagcaacacc accatcaaaa cgaagtcgtg gaggaaaaag aagctctttt cgagaaaccc     120

ttaaccccaa gtgacgtcgg aaaactaaac cgcctagtca tccctaaaca gcacgccgag     180

agatacttcc ctctcgccgc cgccgcggta gacgccgtgg agaagggatt actcctctgc     240

ttcgaggacg aggaaggtaa gccatggaga ttcagatact cttattggaa tagtagccag     300

agttacgtct tgaccaaagg atggagcaga tatgttaaag agaagcaact tgacgccggc     360

gacgttgttc tctttcatcg ccaccgtgct gacggtggaa gattcttcat tggctggaga     420

agacgcggcg actcttcctc ctcctccgac tcttatcgca atcttcaatc taattcctcg     480

ctccaatatt atcctcatgc aggggctcaa gcggtggaga accagagagg taactccaag     540

acattgagac tttttggagt gaacatggag tgccagatag actcagactg gtccgagcca     600

tccacacctg acggttttac cacatgtcca accaatcacg accagtttcc tatctaccct     660

gaacactttc ctcctccgta ctacatggac gtaagtttca caggagatgt gcaccagacg     720

agtagccaac aaggatag                                                   738


<210> SEQ ID NO 110
<211> LENGTH: 310
<212> TYPE: PRT
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 110

Met Met Thr Asn Leu Ser Leu Ala Arg Glu Gly Glu Glu Glu Glu Glu
1               5                   10                  15

Glu Ala Gly Ala Lys Lys Pro Thr Glu Glu Val Glu Arg Glu His Met
            20                  25                  30

Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
        35                  40                  45

Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe Pro Leu Asp Ser Ser
    50                  55                  60

Thr Asn Glu Lys Gly Leu Ile Leu Asn Phe Glu Asp Leu Thr Gly Lys
65                  70                  75                  80

Ser Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val
                85                  90                  95

Met Thr Lys Gly Trp Ser Arg Phe Val Lys Asp Lys Lys Leu Asp Ala
            100                 105                 110

Gly Asp Ile Val Ser Phe Leu Arg Cys Val Gly Asp Thr Gly Arg Asp
        115                 120                 125

Ser Arg Leu Phe Ile Asp Trp Arg Arg Arg Pro Lys Val Pro Asp Tyr
    130                 135                 140

Thr Thr Ser Thr Ser His Phe Pro Ala Gly Ala Met Phe Pro Arg Phe
145                 150                 155                 160

Tyr Ser Phe Gln Thr Ala Thr Thr Ser Thr Ser Tyr Asn Pro Tyr Asn
                165                 170                 175
```

-continued

```
His Gln Gln Pro Arg His His His Ser Gly Tyr Cys Tyr Pro Gln Ile
            180                 185                 190

Pro Arg Glu Phe Gly Tyr Gly Tyr Val Val Arg Ser Val Asp Gln Arg
        195                 200                 205

Ala Val Val Ala Asp Pro Leu Val Ile Glu Ser Val Pro Val Met Met
    210                 215                 220

His Gly Gly Ala Arg Val Asn Gln Ala Ala Val Gly Thr Ala Gly Lys
225                 230                 235                 240

Arg Leu Arg Leu Phe Gly Val Asp Met Glu Cys Gly Glu Ser Gly Gly
                245                 250                 255

Thr Asn Ser Thr Glu Glu Glu Ser Ser Ser Ser Gly Gly Ser Leu Pro
            260                 265                 270

Arg Gly Gly Ala Ser Pro Ser Ser Ser Met Phe Gln Leu Arg Leu Gly
        275                 280                 285

Asn Ser Ser Glu Asp Asp His Leu Phe Lys Lys Gly Lys Ser Ser Leu
    290                 295                 300

Pro Phe Asn Leu Asp Gln
305                 310


<210> SEQ ID NO 111
<211> LENGTH: 933
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 111

atgatgacaa atttgtctct tgcaagagaa ggagaagaag aagaagaaga ggcaggagca      60

aagaagccca cagaagaagt ggagagagag cacatgttcg acaaagtggt gactccaagt     120

gacgtcggga aactaaaccg actcgtgatc ccaaagcaac acgcggagag atacttccct     180

ttagattcat ccacaaacga gaagggtttg attctaaact tcgaagatct cacgggaaag     240

tcatggaggt tccgttactc ttactggaac agcagtcaga gctatgtcat gactaaaggt     300

tggagccgtt tcgttaaaga caagaagcta gacgctggag atattgtctc tttcctgaga     360

tgtgtcggag acacaggaag ggacagccgc ttgtttatcg attggaggag acgacctaaa     420

gtccctgact acacgacatc gacttctcac tttcctgccg gagctatgtt ccctaggttt     480

tacagttttc agacagcaac tacttccaca agttacaatc cctataatca tcagcagcca     540

cgtcatcatc acagtggtta ctgttatcct caaatcccga gagaatttgg atatgggtat     600

gtcgttaggt cagtagatca gagggcggtg gtggctgatc cgttagtgat cgaatctgtg     660

ccggtgatga tgcacggagg agctcgagtg aaccaggcgg ctgttggaac ggccgggaaa     720

aggctgaggc tttttggagt cgatatggaa tgtggcgaga gtggaggaac aaacagtacg     780

gaggaagaat cttcatcttc cggtgggagt ttgccacgtg gcggtgcttc tccgtcttcc     840

tctatgtttc agctgaggct tggaaacagc agtgaagatg atcacttatt taagaaagga     900

aagtcttcat tgccttttaa tttggatcaa taa                                 933


<210> SEQ ID NO 112
<211> LENGTH: 293
<212> TYPE: PRT
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 112
```

-continued

```
Met Met Thr Asn Leu Ser Leu Ala Arg Glu Gly Glu Ala Gln Val Lys
1               5                   10                  15

Lys Pro Ile Glu Glu Val Glu Arg Glu His Met Phe Asp Lys Val Val
            20                  25                  30

Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln
        35                  40                  45

His Ala Glu Arg Tyr Phe Pro Leu Asp Ser Ser Ser Asn Glu Lys Gly
    50                  55                  60

Leu Leu Leu Asn Phe Glu Asp Leu Thr Gly Lys Ser Trp Arg Phe Arg
65                  70                  75                  80

Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp
                85                  90                  95

Ser Arg Phe Val Lys Asp Lys Lys Leu Asp Ala Gly Asp Ile Val Ser
            100                 105                 110

Phe Gln Arg Cys Val Gly Asp Ser Arg Leu Phe Ile Asp Trp Arg Arg
        115                 120                 125

Arg Pro Lys Val Pro Asp Tyr Pro Thr Ser Thr Ala His Phe Ala Ala
    130                 135                 140

Gly Ala Met Phe Pro Arg Phe Tyr Ser Phe Pro Thr Ala Thr Thr Ser
145                 150                 155                 160

Thr Cys Tyr Asp Leu Tyr Asn His Gln Pro Pro Arg His His His Ile
                165                 170                 175

Gly Tyr Gly Tyr Pro Gln Ile Pro Arg Glu Phe Gly Tyr Gly Tyr Phe
            180                 185                 190

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

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

Val Val Gly Thr Ala Gly Lys Arg Leu Arg Leu Phe Gly Val Asp Met
225                 230                 235                 240

Glu Glu Glu Ser Ser Ser Ser Gly Gly Ser Leu Pro Arg Ala Gly Gly
                245                 250                 255

Gly Gly Ala Ser Ser Ser Ser Ser Leu Phe Gln Leu Arg Leu Gly Ser
            260                 265                 270

Ser Cys Glu Asp Asp His Phe Ser Lys Lys Gly Lys Ser Ser Leu Pro
        275                 280                 285

Phe Asp Leu Asp Gln
    290


<210> SEQ ID NO 113
<211> LENGTH: 882
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 113

atgatgacca acttgtctct tgcaagggaa ggagaagcac aagtaaagaa gcccatagaa      60

gaagttgaga gagagcacat gttcgacaaa gtggtgactc caagcgacgt agggaaacta     120

aacagactcg tgatcccaaa gcaacacgca gagagatact tccctctaga ttcatcctca     180

aacgagaaag gtttgcttct aaactttgaa gatctaacag gaaagtcatg gaggttccgt     240

tactcttact ggaacagtag ccagagctat gtcatgacta aaggttggag tcgtttcgtt     300

aaagacaaga agcttgacgc cggagatatt gtctctttcc agagatgtgt cggagacagc     360
```

-continued

```
cgcttgttta tcgattggag gagacgacct aaagtccctg actatccgac atcgactgct    420

cactttgctg caggagctat gttccctagg ttttacagtt ttccgacagc aactacttcg    480

acatgttacg atctgtacaa tcatcagccg ccacgtcatc atcacattgg ttacggttat    540

ccacagattc cgagagaatt tggatacggg tatttcgtta ggtcagtgga ccagagagcg    600

gtggtggctg atccgttggt gatcgaatct gtgccggtga tgatgcgcgg aggagctcga    660

gttagtcagg aggttgttgg aacggccggg aagaggctga ggctttttgg agtcgatatg    720

gaggaagaat cttcatcttc cggtgggagt ttgccgcgtg ccggaggtgg cggtgcttct    780

tcatcttcct ctttgtttca gctgagactt gggagcagct gtgaagatga tcacttctct    840

aagaaaggaa agtcttcatt gccttttgat ttggatcaat aa                       882
```

```
<210> SEQ ID NO 114
<211> LENGTH: 297
<212> TYPE: PRT
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 114

Met Met Met Thr Asn Leu Ser Leu Ser Arg Glu Gly Glu Glu Glu Glu
1               5                   10                  15

Glu Glu Glu Gln Glu Glu Ala Lys Lys Pro Met Glu Glu Val Glu Arg
            20                  25                  30

Glu His Met Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu
        35                  40                  45

Asn Arg Leu Val Ile Pro Lys Gln Tyr Ala Glu Arg Tyr Phe Pro Leu
    50                  55                  60

Asp Ser Ser Thr Asn Glu Lys Gly Leu Leu Leu Asn Phe Glu Asp Leu
65                  70                  75                  80

Ala Gly Lys Ser Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln
                85                  90                  95

Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys Asp Lys Lys
            100                 105                 110

Leu Asp Ala Gly Asp Ile Val Ser Phe Gln Arg Cys Val Gly Asp Ser
        115                 120                 125

Gly Arg Asp Ser Arg Leu Phe Ile Asp Trp Arg Arg Arg Pro Lys Val
    130                 135                 140

Pro Asp His Pro Thr Ser Ile Ala His Phe Ala Ala Gly Ser Met Phe
145                 150                 155                 160

Pro Arg Phe Tyr Ser Phe Pro Thr Ala Thr Ser Tyr Asn Leu Tyr Asn
                165                 170                 175

Tyr Gln Gln Pro Arg His His His His Ser Gly Tyr Asn Tyr Pro Gln
            180                 185                 190

Ile Pro Arg Glu Phe Gly Tyr Gly Tyr Leu Val Asp Gln Arg Ala Val
        195                 200                 205

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

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

Arg Leu Phe Gly Val Asp Met Glu Glu Glu Ser Ser Ser Ser Gly Gly
                245                 250                 255

Ser Leu Pro Arg Gly Asp Ala Ser Pro Ser Ser Ser Leu Phe Gln Leu
```

-continued

```
            260                 265                 270

Arg Leu Gly Ser Ser Ser Glu Asp Asp His Phe Ser Lys Lys Gly Lys
        275                 280                 285

Ser Ser Leu Pro Phe Asp Leu Asp Gln
    290                 295


<210> SEQ ID NO 115
<211> LENGTH: 894
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 115

atgatgatga caaacttgtc tctttcaaga gaaggagaag aggaggaaga agaagaacaa      60

gaagaggcca agaagcccat ggaagaagta gagagagagc acatgttcga caaagtggtg     120

actccaagcg atgttggtaa actaaaccgg ctcgtgatcc caaagcaata cgcagagaga     180

tacttccctt tagattcatc cacaaacgag aaaggtttgc ttctaaactt cgaagatctc     240

gcaggaaagt catggaggtt ccgttactct tactggaaca gtagtcagag ctatgtcatg     300

actaaaggtt ggagccgttt cgttaaagac aaaaagctag acgccggaga tattgtctct     360

ttccagagat gtgtcggaga ttcaggaaga gacagccgct tgtttattga ttggaggaga     420

agacctaaag ttcctgacca tccgacatcg attgctcact ttgctgccgg atctatgttt     480

cctaggtttt acagttttcc gacagcaact agttacaatc tttacaacta tcagcagcca     540

cgtcatcatc atcacagtgg ttataattat cctcaaattc cgagagaatt tggatacggg     600

tacttggtgg atcaaagagc cgtggtggct gatccgttgg tgattgaatc tgtgccggtg     660

atgatgcacg gaggagctca agttagtcag gcggttgttg gaacggccgg gaagaggctg     720

aggctttttg gagtcgatat ggaggaagaa tcttcatctt ccggtgggag tttgccacgt     780

ggtgacgctt ctccgtcttc ctctttgttt cagctgagac ttggaagcag cagtgaagat     840

gatcacttct ctaagaaagg aaagtcctca ttgccttttg atttggatca ataa           894


<210> SEQ ID NO 116
<211> LENGTH: 286
<212> TYPE: PRT
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 116

Met Asn Gln Glu Glu Glu Asn Pro Val Glu Lys Ala Ser Ser Met Glu
1               5                   10                  15

Arg Glu His Met Phe Glu Lys Val Val Thr Pro Ser Asp Val Gly Lys
            20                  25                  30

Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe Pro
        35                  40                  45

Leu Asp Asn Asn Ser Asp Ser Ser Lys Gly Leu Leu Leu Asn Phe Glu
    50                  55                  60

Asp Arg Thr Gly Asn Ser Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser
65                  70                  75                  80

Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys Asp
                85                  90                  95

Lys Lys Leu Asp Ala Gly Asp Ile Val Ser Phe Gln Arg Asp Pro Gly
            100                 105                 110

Asn Lys Asp Lys Leu Phe Ile Asp Trp Arg Arg Arg Pro Lys Ile Pro
```

-continued

```
        115                 120                 125

Asp His His His Gln Phe Ala Gly Ala Met Phe Pro Arg Phe Tyr Ser
    130                 135                 140

Phe Ser His Pro Gln Asn Leu Tyr His Arg Tyr Gln Gln Asp Leu Gly
145                 150                 155                 160

Ile Gly Tyr Tyr Val Ser Ser Met Glu Arg Asn Asp Pro Thr Ala Val
                165                 170                 175

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

Ala Ile Pro Ser Ser Arg Gly Glu Lys Arg Leu Arg Leu Phe Gly Val
        195                 200                 205

Asp Met Glu Cys Gly Gly Gly Gly Gly Ser Val Asn Ser Thr Glu Glu
    210                 215                 220

Glu Ser Ser Ser Ser Gly Gly Gly Gly Gly Val Ser Met Ala Ser Val
225                 230                 235                 240

Gly Ser Leu Leu Gln Leu Arg Leu Val Ser Ser Asp Asp Glu Ser Leu
                245                 250                 255

Val Ala Met Glu Ala Ala Ser Val Asp Glu Asp His His Leu Phe Thr
            260                 265                 270

Lys Lys Gly Lys Ser Ser Leu Ser Phe Asp Leu Asp Arg Lys
        275                 280                 285


<210> SEQ ID NO 117
<211> LENGTH: 861
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 117

atgaatcaag aagaagagaa tcctgtggaa aaagcctctt caatggagag agagcacatg     60

tttgaaaaag tagtaacacc aagcgacgta ggcaaactaa accgactcgt gatcccaaag    120

caacacgcgg agagatactt ccctttagac aacaattctg acagcagcaa aggtttgctt    180

ctaaacttcg aagaccgaac aggaaactca tggagattcc gttactctta ctggaacagt    240

agccagagtt atgtcatgac aaaaggttgg agccgcttcg tcaaagacaa gaagcttgat    300

gctggcgaca tcgtttcttt tcagagagat cctggtaata aagacaagct tttcattgat    360

tggaggagac gaccaaagat tccagatcat catcatcaat tcgctggagc tatgttccct    420

aggttttact ctttctctca tcctcagaac ctttatcatc gatatcaaca agatcttgga    480

attgggtatt atgtgagttc aatggagaga aatgatccaa cggctgtaat tgaatctgtg    540

ccgttgataa tgcaaaggag agcagcacac gtggctgcta taccttcatc aagaggagag    600

aagaggttaa ggctgtttgg agtggacatg gagtgcggcg gcggcggagg aagtgtgaat    660

agcacggagg aagagtcgtc gtcttccggt ggtggcggcg gcgtttctat ggctagtgtt    720

ggttctcttc tccaattgag gctagtgagc agtgatgatg agtctttggt agcaatggaa    780

gctgcaagtg tcgatgagga tcatcacttg tttacaaaga aaggaaagtc ttctttgtct    840

ttcgatttgg atagaaaatg a                                              861


<210> SEQ ID NO 118
<211> LENGTH: 292
<212> TYPE: PRT
<213> ORGANISM: Brassica rapa
```

-continued

<400> SEQUENCE: 118

Met Asn Gln Glu Asn Lys Lys Pro Leu Glu Glu Ala Ser Thr Ser Met
1 5 10 15

Glu Arg Glu Asn Met Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly
20 25 30

Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe
35 40 45

Pro Leu Asp Asn Ser Ser Thr Asn Asn Lys Gly Leu Leu Leu Asp Phe
50 55 60

Glu Asp Arg Thr Gly Ser Ser Trp Arg Phe Arg Tyr Ser Tyr Trp Asn
65 70 75 80

Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys
85 90 95

Asp Lys Lys Leu Asp Ala Gly Asp Ile Val Ser Phe Gln Arg Asp Pro
100 105 110

Cys Asn Lys Asp Lys Leu Tyr Ile Asp Trp Arg Arg Arg Pro Lys Ile
115 120 125

Pro Asp His His Gln Phe Ala Gly Ala Met Phe Pro Arg Phe Tyr Ser
130 135 140

Phe Pro His Pro Gln Met Pro Thr Ser Phe Glu Ser Ser His Asn Leu
145 150 155 160

Tyr His His Arg Phe Gln Arg Asp Leu Gly Ile Gly Tyr Tyr Pro Thr
165 170 175

Ala Val Ile Glu Ser Val Pro Val Ile Met Gln Arg Arg Glu Ala Gln
180 185 190

Val Ala Asn Met Ala Ser Ser Arg Gly Glu Lys Arg Leu Arg Leu Phe
195 200 205

Gly Val Asp Val Glu Cys Gly Gly Gly Gly Gly Gly Ser Val Asn Ser
210 215 220

Thr Glu Glu Glu Ser Ser Ser Ser Gly Gly Ser Met Ser Arg Gly Gly
225 230 235 240

Val Ser Met Ala Gly Val Gly Ser Leu Leu Gln Leu Arg Leu Val Ser
245 250 255

Ser Asp Asp Glu Ser Leu Val Ala Met Glu Gly Ala Thr Val Asp Glu
260 265 270

Asp His His Leu Phe Thr Thr Lys Lys Gly Lys Ser Ser Leu Ser Phe
275 280 285

Asp Leu Asp Ile
290

<210> SEQ ID NO 119
<211> LENGTH: 879
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 119

atgaatcaag aaaacaagaa gcctttggaa gaagcttcga cttcaatgga gagagagaac 60

atgttcgaca aagtagtaac accaagcgac gtagggaaac taaaccgact cgtgatccca 120

aagcaacacg cagagagata cttcccttta gacaactcct caacaaacaa caaagggttg 180

cttctagact tcgaagaccg tacaggaagc tcatggagat tccgttactc ttactggaac 240

agtagccaaa gttatgtcat gacaaaaggt tggagccgtt ttgtcaaaga caagaagctt 300

-continued

```
gatgctggtg acatcgtgtc ttttcaaaga gatccctgta ataaagacaa gctttacata    360

gattggagga gacgaccaaa gattccagat catcatcagt tcgccggagc tatgttccct    420

aggttttact ctttccctca ccctcagatg ccgacaagtt ttgaaagtag tcacaacctt    480

tatcatcatc ggtttcaacg agatcttgga attgggtatt atccaacggc tgtgattgaa    540

tctgtgccgg tgataatgca aaggagagaa gcacaagtgg ctaatatggc ttcatcaaga    600

ggagagaaga ggttaaggct gtttggagtg gacgtggagt gcggcggcgg aggaggagga    660

agtgtgaata gcacggagga agagtcgtcg tcttccggtg gtagtatgtc acgtggcggc    720

gtttctatgg ctggtgttgg ttctctcctt cagttgaggt tagtgagcag tgatgatgag    780

tctttagtag cgatggaagg tgctactgtc gatgaggatc atcacttgtt tacaactaag    840

aaaggaaagt cttctttgtc tttcgatttg gatatatga                           879
```

```
<210> SEQ ID NO 120
<211> LENGTH: 320
<212> TYPE: PRT
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 120

Met Glu Arg Lys Ser Asn Asp Leu Glu Arg Ser Glu Asn Ile Asp Ser
1               5                   10                  15

Gln Asn Lys Lys Met Asn Leu Glu Glu Glu Arg Pro Val Gln Glu Ala
            20                  25                  30

Ser Ser Met Glu Arg Glu His Met Phe Asp Lys Val Val Thr Pro Ser
        35                  40                  45

Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu
    50                  55                  60

Arg Tyr Phe Pro Leu Asp Asn Asn Ser Ser Asp Asn Asn Lys Gly Leu
65                  70                  75                  80

Leu Leu Asn Phe Glu Asp Arg Ile Gly Ile Leu Trp Ser Phe Arg Tyr
                85                  90                  95

Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser
            100                 105                 110

Arg Phe Val Lys Asp Lys Lys Leu Asp Ala Gly Asp Ile Val Ser Phe
        115                 120                 125

His Arg Gly Ser Cys Asn Lys Asp Lys Leu Phe Ile Asp Trp Lys Arg
    130                 135                 140

Arg Pro Lys Ile Pro Asp His Gln Val Val Gly Ala Met Phe Pro Arg
145                 150                 155                 160

Phe Tyr Ser Tyr Pro Tyr Pro Gln Ile Gln Ala Ser Tyr Glu Arg His
                165                 170                 175

Asn Leu Tyr His Arg Tyr Gln Arg Asp Ile Gly Ile Gly Tyr Tyr Val
            180                 185                 190

Arg Ser Met Glu Arg Tyr Asp Pro Thr Ala Val Ile Glu Ser Val Pro
        195                 200                 205

Val Ile Met Gln Arg Arg Ala His Val Ala Thr Met Ala Ser Ser Arg
    210                 215                 220

Gly Glu Lys Arg Leu Arg Leu Phe Gly Val Asp Met Glu Cys Val Arg
225                 230                 235                 240

Gly Gly Arg Gly Gly Gly Gly Ser Val Asn Ser Thr Glu Glu Glu Ser
                245                 250                 255
```

-continued

Ser Thr Ser Gly Gly Ser Ile Ser Arg Gly Gly Val Ser Met Ala Gly
260 265 270

Val Gly Ser Pro Leu Gln Leu Arg Leu Val Ser Ser Asp Gly Asp Asp
275 280 285

Gln Ser Leu Val Ala Arg Gly Ala Ala Arg Val Asp Glu Asp His His
290 295 300

Leu Phe Thr Lys Lys Gly Lys Ser Ser Leu Ser Phe Asp Leu Asp Lys
305 310 315 320

<210> SEQ ID NO 121
<211> LENGTH: 963
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 121

atggagagga agtccaatga tcttgagaga tctgagaata ttgattctca aaacaagaag 60

atgaatctag aagaagagag gcctgtacaa gaagcttctt cgatggagag agagcacatg 120

ttcgacaaag tagtaacacc aagcgacgtt gggaaactaa accggctggt gatcccaaag 180

caacacgcag agcgatactt ccctttagac aataattcct cagacaacaa caaaggtttg 240

cttctaaact tcgaagatcg aataggaatc ttatggagtt tccgttactc ctactggaac 300

agtagccaaa gttatgtaat gactaaaggc tggagccgtt tcgtcaaaga caagaagctt 360

gatgctggcg acatagtttc ttttcataga ggttcttgta ataaagacaa gcttttcatt 420

gattggaaga gacgaccaaa gattcctgat caccaagtcg tcggagctat gttccctagg 480

ttttactctt acccttatcc tcagatacag gctagttatg aacgtcacaa cctttatcat 540

cgatatcaac gagatatagg aattgggtat tatgtgaggt caatggagag atatgatcca 600

acggctgtaa ttgaatctgt gccggtgata atgcaaagga gagcacatgt ggctactatg 660

gcttcatcaa gaggagagaa gaggttaagg ctttttggag tggatatgga gtgcgtcaga 720

ggcggccgag gaggaggagg aagtgtgaat agcacggagg aagagtcttc gacttccggt 780

ggtagtatct cacgtggcgg cgtttctatg gctggtgttg gctctccact ccagttgagg 840

ttagtgagca gtgacggtga tgatcagtct ctagtagcta ggggagctgc tagggttgat 900

gaggatcatc acttgtttac aaagaaagga aagtcttctt tgtctttcga tttggataaa 960

tga 963

<210> SEQ ID NO 122
<211> LENGTH: 350
<212> TYPE: PRT
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 122

Met Val Phe Ser Cys Ile Asp Glu Ser Ser Ser Thr Ser Glu Ser Phe
1 5 10 15

Ser Pro Ala Thr Ala Thr Ala Thr Ala Thr Ala Thr Lys Phe Ser Ala
20 25 30

Pro Pro Leu Pro Pro Leu Arg Leu Asn Arg Met Arg Ser Gly Gly Ser
35 40 45

Asn Val Val Leu Asp Ser Lys Asn Gly Val Asp Ile Asp Ser Arg Lys
50 55 60

Leu Ser Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg

-continued

```
65                  70                  75                  80

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

Phe Cys Asp Glu Glu Glu Ala Ala His Ser Tyr Asp Ile Ala Ala Arg
            100                 105                 110

Lys Phe Arg Gly Arg Asp Ala Val Val Asn Phe Lys Thr Phe Leu Ala
        115                 120                 125

Ser Glu Asp Asp Asn Gly Glu Leu Cys Phe Leu Glu Ala His Ser Lys
    130                 135                 140

Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Leu
145                 150                 155                 160

Ala Gln Ser Asn Lys Arg Ser Gly Ala Asn Thr Asn Thr Asn Thr Thr
                165                 170                 175

Gln Ser His Thr Val Ser Arg Thr Arg Glu Val Leu Phe Glu Lys Val
            180                 185                 190

Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys
        195                 200                 205

Gln His Ala Glu Lys Tyr Phe Pro Leu Pro Ser Leu Ser Val Thr Lys
    210                 215                 220

Gly Val Leu Ile Asn Phe Glu Asp Val Thr Gly Lys Val Trp Arg Phe
225                 230                 235                 240

Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly
                245                 250                 255

Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val
            260                 265                 270

Thr Phe Glu Arg Ser Thr Gly Ser Asp Arg Gln Leu Tyr Ile Asp Trp
        275                 280                 285

Lys Ile Arg Ser Gly Pro Ser Lys Asn Pro Val Gln Val Val Val Arg
    290                 295                 300

Leu Phe Gly Val Asp Ile Phe Asn Val Thr Ser Ala Lys Pro Ser Asn
305                 310                 315                 320

Val Val Asp Ala Cys Gly Gly Lys Arg Ser Arg Asp Val Asp Met Phe
                325                 330                 335

Ala Leu Arg Cys Ser Lys Lys His Ala Ile Ile Asn Ala Leu
            340                 345                 350


<210> SEQ ID NO 123
<211> LENGTH: 1053
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 123

atggtattca gttgcataga cgagagctct tccacttcag aatctttttc acccgcaacc      60

gcaaccgcaa ccgcaaccgc cacaaagttc tctgctcctc cgcttccacc gttacgcctc     120

aaccggatga gaagcggtgg aagcaacgtc gtgttggatt caaagaatgg cgtagatatt     180

gattcacgga agctatcgtc gtcaaagtac aaaggcgtgg ttcctcagcc caacggaaga     240

tggggagctc agatttacgt gaagcaccag cgagtttggc tgggcacttt ctgcgatgaa     300

gaggaagctg ctcactccta cgacatagcc gcccgtaaat tccgtggccg tgacgccgtt     360

gtcaacttca aaaccttcct cgcctcagag gacgacaacg gcgagttatg tttccttgaa     420

gctcactcca aggccgagat cgtcgacatg ttgaggaaac acacttacgc tgacgagctt     480
```

-continued

```
gcgcagagca ataaacgcag cggagcgaat acgaatacga atacgactca aagccacacc    540

gtttcgagaa cacgtgaagt gcttttcgag aaggttgtca cgcctagcga cgttggtaag    600

ctaaaccgcc tcgtgatacc taaacagcac gcggagaaat attttccgtt accgtcactg    660

tcggtgacta aaggcgttct gatcaacttc gaagacgtga cgggtaaggt gtggcggttc    720

cgttactcat actggaacag tagtcaaagt tacgtgttga ccaagggatg gagtcggttc    780

gttaaggaga agaatctccg agccggtgat gtcgttactt tcgagagatc gaccggttca    840

gaccggcagc tttatattga ttggaaaatc cggtctggtc cgagcaaaaa ccctgttcag    900

gttgtggtta ggcttttcgg agttgacatc ttcaacgtga caagcgcgaa gccgagcaac    960

gttgtagacg cgtgcggtgg aaagagatct cgggatgttg atatgtttgc gctacggtgt   1020

tccaaaaaac acgctataat caatgctttg tga                                1053


<210> SEQ ID NO 124
<211> LENGTH: 540
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 124

Met Ala Ala Ser Pro Ser Ser Pro Leu Thr Ala Pro Pro Glu Pro Val
1               5                   10                  15

Thr Pro Pro Ser Pro Trp Thr Ile Thr Asp Gly Ala Ile Ser Gly Thr
            20                  25                  30

Leu Pro Ala Ala Glu Ala Phe Ala Val His Tyr Pro Gly Tyr Pro Ser
        35                  40                  45

Ser Pro Ala Arg Ala Ala Arg Thr Leu Gly Gly Leu Pro Gly Leu Ala
    50                  55                  60

Lys Val Arg Ser Ser Asp Pro Gly Ala Arg Leu Glu Leu Arg Phe Arg
65                  70                  75                  80

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

Thr Gly Leu Leu Leu Arg Leu Ser Lys Arg Lys Gly Ala Ala Ala Pro
            100                 105                 110

Cys Ala His Val Val Ala Arg Val Arg Thr Ala Tyr Tyr Phe Glu Gly
        115                 120                 125

Met Ala Asp Phe Gln His Val Val Pro Val His Ala Ala Gln Thr Arg
    130                 135                 140

Lys Arg Lys His Ser Asp Ser Gln Asn Asp Asn Glu Asn Phe Gly Ser
145                 150                 155                 160

Asp Lys Thr Gly His Asp Glu Ala Asp Gly Asp Val Met Met Leu Val
                165                 170                 175

Pro Pro Leu Phe Ser Val Lys Asp Arg Pro Thr Lys Ile Ala Leu Val
            180                 185                 190

Pro Ser Ser Asn Ala Ile Ser Lys Thr Met His Arg Gly Val Val Gln
        195                 200                 205

Glu Arg Trp Glu Met Asn Val Gly Pro Thr Leu Ala Leu Pro Phe Asn
    210                 215                 220

Thr Gln Val Val Pro Glu Lys Ile Asn Trp Glu Asp His Ile Arg Lys
225                 230                 235                 240

Asn Ser Val Glu Trp Gly Trp Gln Met Ala Val Cys Lys Leu Phe Asp
                245                 250                 255
```

-continued

```
Glu Arg Pro Val Trp Pro Arg Gln Ser Leu Tyr Glu Arg Phe Leu Asp
            260                 265                 270

Asp Asn Val His Val Ser Gln Asn Gln Phe Lys Arg Leu Leu Phe Arg
        275                 280                 285

Ala Gly Tyr Tyr Phe Ser Thr Gly Pro Phe Gly Lys Phe Trp Ile Arg
    290                 295                 300

Arg Gly Tyr Asp Pro Arg Lys Asp Ser Glu Ser Gln Ile Tyr Gln Arg
305                 310                 315                 320

Ile Asp Phe Arg Met Pro Pro Glu Leu Arg Tyr Leu Leu Arg Leu Lys
                325                 330                 335

Asn Ser Glu Ser Arg Lys Trp Ala Asp Met Cys Lys Leu Glu Thr Met
            340                 345                 350

Pro Ser Gln Ser Phe Ile Tyr Leu Gln Leu Tyr Glu Leu Lys Asp Asp
        355                 360                 365

Phe Ile Gln Ala Glu Ile Arg Lys Pro Ser Tyr Gln Ser Val Cys Ser
    370                 375                 380

Arg Ser Thr Gly Trp Phe Ser Lys Pro Met Ile Lys Thr Leu Arg Leu
385                 390                 395                 400

Gln Val Ser Ile Arg Leu Leu Ser Leu Leu His Asn Glu Glu Ala Lys
                405                 410                 415

Asn Leu Leu Arg Asn Ala His Glu Leu Ile Glu Arg Ser Lys Lys Gln
            420                 425                 430

Glu Ala Leu Ser Arg Ser Glu Leu Ser Ile Glu Tyr Asn Asp Ala Asp
        435                 440                 445

Gln Val Ser Ala Ala His Thr Gly Thr Glu Asp Gln Val Gly Pro Asn
    450                 455                 460

Asn Ser Asp Ser Glu Asp Val Asp Asp Glu Glu Glu Glu Glu Glu Leu
465                 470                 475                 480

Glu Gly Tyr Asp Ser Pro Pro Met Ala Asp Asp Ile His Glu Phe Thr
                485                 490                 495

Leu Gly Asp Ser Tyr Ala Phe Gly Glu Gly Phe Ser Asn Gly Tyr Leu
            500                 505                 510

Glu Glu Val Leu Arg Ser Leu Pro Leu Gln Glu Asp Gly Gln Lys Lys
        515                 520                 525

Leu Cys Asp Ala Pro Ile Asn Ala Asp Ala Ser Asp
    530                 535                 540


<210> SEQ ID NO 125
<211> LENGTH: 1674
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 125

atggccgcct cgccctcttc acccttgaca gcgccgccag agccggtgac cccgccgtcc      60

ccatggacca tcacagacgg agccatctct ggcacgctcc cagcagccga ggccttcgca     120

gtgcactacc cgggctaccc ctcctctccc gcccgcgccg cccgcaccct cggcggtctc     180

cccggcctcg ccaaggtccg gagttccgat cccggcgccc gcctcgagct ccgcttccgc     240

cccgaggacc cctactgcca tccagccttt ggccagtccc gcgcctccac tggccttctg     300

ctgcgcctct ccaagcgcaa aggagctgcg gcaccttgtg cccatgtggt cgctcgtgtc     360

cggactgctt actacttcga aggtatggca gattttcaac atgttgttcc agtgcatgct     420
```

-continued

```
gcacaaacaa gaaaaagaaa acactcagat tctcaaaatg ataatgagaa ttttggtagt    480

gataagacag gacatgatga agcagatgga gatgtcatga tgttggtacc ccctctcttt    540

tcagtgaagg ataggccaac aaagatagcg cttgtaccat cgtccaatgc catatctaaa    600

accatgcaca ggggagttgt acaagaacgg tgggagatga atgttggacc aactctggcg    660

cttccgttca acactcaagt tgtcccggag aagattaatt gggaagacca cattagaaag    720

aattctgtag aatggggttg gcaaatggct gtttgcaaat tgtttgatga gcgccctgtg    780

tggccaaggc aatcacttta tgagcggttc cttgatgata atgtgcatgt ctctcaaaac    840

caattcaaaa ggcttctgtt tagagctgga tactacttct ctactggacc ctttggaaaa    900

ttttggatca gaagaggata tgaccctcgt aaagactctg agtcacaaat atatcagaga    960

attgattttc gcatgcctcc cgagctacga tatcttctaa ggctgaagaa ttctgagtct   1020

cgaaagtggg cagatatgtg caagcttgaa acaatgccat cacagagttt catctacctg   1080

caattatatg aactgaagga tgattttatt caagcagaaa ttcgaaaacc ttcttatcaa   1140

tcagtttgtt cacgttctac aggatggttt tctaagccaa tgatcaaaac cctgaggttg   1200

caagtgagca taaggctcct ctctttattg cataatgaag aggctaaaaa cttgttgagg   1260

aatgcccatg agcttattga aaggtccaag aagcaggaag ccctttcgag atctgagctg   1320

tcaatagaat ataatgatgc tgatcaagtt tctgccgcac atactggaac tgaggatcaa   1380

gtcggcccta acaactctga tagtgaagat gtggatgatg aagaagagga agaggaattg   1440

gagggttatg attctccacc tatggcagat gatattcatg agttcacctt aggtgattcc   1500

tatgcatttg gtgaaggctt ctcgaatgga tacctcgaag aagtactgcg cagcttgcca   1560

ttgcaggaag acggccaaaa gaaattatgt gatgctccta tcaacgctga tgcaagtgat   1620

ggagagtttg aaatttacga acagcccagt gatgatgaag attctgatgg ctag          1674


<210> SEQ ID NO 126
<211> LENGTH: 409
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 126

Met Glu Phe Ala Ser Ser Ser Ser Arg Phe Ser Arg Glu Glu Asp Glu
1               5                   10                  15

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

Glu Ile Pro Phe Met Thr Ala Ala Ala Thr Ala Asp Thr Gly Ala Ala
        35                  40                  45

Ala Ser Ser Ser Ser Pro Ser Ala Ala Ala Ser Ser Gly Pro Ala Ala
    50                  55                  60

Ala Pro Arg Ser Ser Asp Gly Ala Gly Ala Ser Gly Ser Gly Gly Gly
65                  70                  75                  80

Gly Ser Asp Asp Val Gln Val Ile Glu Lys Glu His Met Phe Asp Lys
                85                  90                  95

Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro
            100                 105                 110

Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asp Ala Ala Ala Asn Glu
        115                 120                 125

Lys Gly Gln Leu Leu Ser Phe Glu Asp Arg Ala Gly Lys Leu Trp Arg
```

-continued

```
    130                 135                 140

Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys
145                 150                 155                 160

Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Asp Ala Gly Asp Thr
                165                 170                 175

Val Ser Phe Cys Arg Gly Ala Gly Asp Thr Ala Arg Asp Arg Leu Phe
            180                 185                 190

Ile Asp Trp Lys Arg Arg Ala Asp Ser Arg Asp Pro His Arg Met Pro
        195                 200                 205

Arg Leu Pro Leu Pro Met Ala Pro Val Ala Ser Pro Tyr Gly Pro Trp
    210                 215                 220

Gly Gly Gly Gly Gly Gly Gly Ala Gly Gly Phe Phe Met Pro Pro Ala
225                 230                 235                 240

Pro Pro Ala Thr Leu Tyr Glu His His Arg Phe Arg Gln Ala Leu Asp
                245                 250                 255

Phe Arg Asn Ile Asn Ala Ala Ala Ala Pro Ala Arg Gln Leu Leu Phe
            260                 265                 270

Phe Gly Ser Ala Gly Met Pro Pro Arg Ala Ser Met Pro Gln Gln Gln
        275                 280                 285

Gln Pro Pro Pro Pro Pro His Pro Pro Leu His Ser Ile Met Leu Val
    290                 295                 300

Gln Pro Ser Pro Ala Pro Pro Thr Ala Ser Val Pro Met Leu Leu Asp
305                 310                 315                 320

Ser Val Pro Leu Val Asn Ser Pro Thr Ala Ala Ser Lys Arg Val Arg
                325                 330                 335

Leu Phe Gly Val Asn Leu Asp Asn Pro Gln Pro Gly Thr Ser Ala Glu
            340                 345                 350

Ser Ser Gln Asp Ala Asn Ala Leu Ser Leu Arg Thr Pro Gly Trp Gln
        355                 360                 365

Arg Pro Gly Pro Leu Arg Phe Phe Glu Ser Pro Gln Arg Gly Ala Glu
    370                 375                 380

Ser Ser Ala Ala Ser Ser Pro Ser Ser Ser Ser Ser Ser Lys Arg Glu
385                 390                 395                 400

Ala His Ser Ser Leu Asp Leu Asp Leu
                405


<210> SEQ ID NO 127
<211> LENGTH: 259
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 127

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

Glu Arg Ala Ala Ala Glu His Asn Gln His His Gln Gln Gln His Ala
            20                  25                  30

Thr Val Glu Lys Glu His Met Phe Asp Lys Val Val Thr Pro Ser Asp
        35                  40                  45

Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys
    50                  55                  60

Tyr Phe Pro Leu Asp Ala Ala Ala Asn Glu Lys Gly Leu Leu Leu Ser
65                  70                  75                  80
```

-continued

```
Phe Glu Asp Arg Thr Gly Lys Pro Trp Arg Phe Arg Tyr Ser Tyr Trp
                85                  90                  95

Asn Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val
            100                 105                 110

Lys Glu Lys Arg Leu Asp Ala Gly Asp Thr Val Ser Phe Gly Arg Gly
        115                 120                 125

Ile Ser Glu Ala Ala Arg Asp Arg Leu Phe Ile Asp Trp Arg Cys Arg
    130                 135                 140

Pro Asp Pro Pro Val Val His His Gln Tyr His His Arg Leu Pro Leu
145                 150                 155                 160

Pro Ser Ala Val Val Pro Tyr Ala Pro Trp Ala Ala His Ala His His
                165                 170                 175

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

Cys Ala Thr Leu Val Ala Thr Glu Met Arg Ala Ser Ser Ser Gln Leu
        195                 200                 205

Ser Leu Thr Arg Ser Asn Leu Ser Arg Pro Pro Gln Pro Arg Ile Ala
    210                 215                 220

Arg Val Asp Gly Ala Gln Pro Arg Pro Ser Ser Ser Pro Arg Gln Pro
225                 230                 235                 240

Gln Ser Leu Trp Cys Arg Ser Cys Gln Pro Gln Pro Arg Arg Thr Ala
                245                 250                 255

Asp Val Pro
```

<210> SEQ ID NO 128
<211> LENGTH: 780
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 128

```
atggagttca ccactccccc gcccgcgacc cggtcgggcg gcggagagga gagggcggct      60

gctgagcaca accagcacca ccagcagcag catgcgacgg tggagaagga gcacatgttc     120

gacaaggtgg tgacgccgag cgacgtcggg aagctgaacc ggctggtgat cccgaagcag     180

cacgcggaga agtacttccc gctggacgcg gcggcgaacg agaagggcct cctgctcagc     240

ttcgaggacc gcacggggaa gccctggcgc ttccgctact cctactggaa cagtagccag     300

agctacgtga tgaccaaggg ctggagccgc ttcgtcaagg agaagcgcct cgacgccggg     360

gacacagtct ccttcggccg cggcatcagc gaggcggcgc gcgacaggct tttcatcgac     420

tggcggtgcc gacccgaccc gcccgtcgtg caccaccagt accaccaccg cctccctctc     480

ccctccgccg tcgtccccta cgcgccgtgg gcggcgcacg cgcaccacca ccactaccca     540

gcagatgggc acacggaacc agtaacacct tgcctgtgcg ccacactcgt tgccactgaa     600

atgagagcat catcttcgca actgtcactc acacgctcca acctctccag gccgccacaa     660

cctagaatag ccagagtcga tggcgcccag ccacggccgt cgtcgtcacc acgccagcca     720

cagtcgttgt ggtgccggtc gtgccaaccg caaccacggc gaacggccga cgttccttga     780
```

<210> SEQ ID NO 129
<211> LENGTH: 327
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 129

-continued

```
Met Glu Phe Thr Ala Pro Pro Pro Ala Thr Arg Ser Gly Gly Gly Glu
1               5                   10                  15

Glu Arg Ala Ala Ala Glu His His Gln Gln Gln Gln Ala Thr Val
            20                  25                  30

Glu Lys Glu His Met Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly
        35                  40                  45

Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe
    50                  55                  60

Pro Leu Asp Ala Ala Ala Asn Asp Lys Gly Leu Leu Leu Ser Phe Glu
65                  70                  75                  80

Asp Arg Ala Gly Lys Pro Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser
                85                  90                  95

Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys Glu
            100                 105                 110

Lys Arg Leu Asp Ala Gly Asp Thr Val Ser Phe Gly Arg Gly Val Gly
        115                 120                 125

Glu Ala Ala Arg Gly Arg Leu Phe Ile Asp Trp Arg Arg Arg Pro Asp
    130                 135                 140

Pro Pro Val Val His His Gln Tyr His His His Arg Leu Pro Leu Pro
145                 150                 155                 160

Ser Ala Val Val Pro Tyr Ala Pro Trp Ala Ala Ala Ala His Ala His
                165                 170                 175

His His His Tyr Pro Ala Ala Gly Val Gly Ala Ala Arg Thr Thr Thr
            180                 185                 190

Thr Thr Thr Thr Thr Val Leu His His Leu Pro Pro Ser Pro Ser Pro
        195                 200                 205

Leu Tyr Leu Asp Thr Arg Arg Arg His Val Gly Tyr Asp Ala Tyr Gly
    210                 215                 220

Ala Gly Thr Arg Gln Leu Leu Phe Tyr Arg Pro His Gln Gln Pro Ser
225                 230                 235                 240

Thr Thr Val Met Leu Asp Ser Val Pro Val Arg Leu Pro Pro Thr Pro
                245                 250                 255

Gly Gln His Ala Glu Pro Pro Pro Pro Ala Val Ala Ser Ser Ala Ser
            260                 265                 270

Lys Arg Val Arg Leu Phe Gly Val Asn Leu Asp Cys Ala Ala Ala Ala
        275                 280                 285

Gly Ser Glu Glu Glu Asn Val Gly Gly Trp Arg Thr Ser Ala Pro Pro
    290                 295                 300

Thr Gln Gln Ala Ser Ser Ser Ser Ser Tyr Ser Ser Gly Lys Ala Arg
305                 310                 315                 320

Cys Ser Leu Asn Leu Asp Leu
                325


<210> SEQ ID NO 130
<211> LENGTH: 984
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 130

atggagttca ccgctccccc gcccgcgacc cggtcgggcg gcggcgagga gagggcggct      60

gctgagcacc accagcagca gcagcaggcg acggtggaga aggagcacat gttcgacaag     120
```

-continued

```
gtggtgacgc cgagcgacgt cgggaagctg aaccggctgg tgatcccgaa gcagcacgcg    180

gagaggtact tcccgctgga cgcggcggcg aacgacaagg gcctgctgct cagcttcgag    240

gaccgcgcgg ggaagccctg gcgcttccgc tactcctact ggaacagcag ccagagctac    300

gtgatgacca agggctggag ccgcttcgtc aaggagaagc gcctcgacgc cggggacacc    360

gtctccttcg gccgcggcgt cggcgaggcg gcgcgcggca ggctcttcat cgactggcgg    420

cgccgacccg acccgcccgt cgtgcaccac cagtaccacc accaccgcct ccctctcccc    480

tccgccgtcg tcccctacgc gccgtgggcg gcggcggcgc acgcgcacca ccaccactac    540

ccagcagctg ggtcggtgc cgccaggacg acgacgacga cgacgacgac ggtgctccac    600

cacctgccgc cctcgccctc cccgctctac cttgacaccc gccgccgcca cgtcggctac    660

gacgcctacg gggccggcac caggcaactt ctcttctaca ggccgcacca gcagccctcc    720

acgacggtga tgctggactc cgtgccggta cggttaccgc caacgccagg gcagcacgcc    780

gagccgccgc cccccgccgt ggcgtcgtca gcctcgaagc gggtgcgcct gttcggggtg    840

aacctcgact gcgccgccgc cgccggctca gaggaggaga acgtcggcgg gtggaggact    900

agtgcgccgc cgacgcagca ggcgtcctcc tcctcatcct actcttccgg gaaagcgagg    960

tgctccttga accttgactt gtga                                           984
```

```
<210> SEQ ID NO 131
<211> LENGTH: 422
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 131

Met Asp Gln Phe Ala Ala Ser Gly Arg Phe Ser Arg Glu Glu Glu Ala
1               5                   10                  15

Asp Glu Glu Gln Glu Asp Ala Ser Asn Ser Met Arg Glu Ile Ser Phe
            20                  25                  30

Met Pro Pro Ala Ala Ala Ser Ser Ser Ser Ala Ala Ala Ser Ala Ser
    35                  40                  45

Ala Ser Ala Ser Thr Ser Ala Ser Ala Cys Ala Ser Gly Ser Ser Ser
    50                  55                  60

Ala Pro Phe Arg Ser Ala Ser Ala Ser Gly Asp Ala Ala Gly Ala Ser
65                  70                  75                  80

Gly Ser Gly Gly Pro Ala Asp Ala Asp Ala Glu Ala Glu Ala Val Glu
                85                  90                  95

Lys Glu His Met Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys
            100                 105                 110

Leu Asn Arg Leu Val Ile Pro Lys Gln Tyr Ala Glu Lys Tyr Phe Pro
        115                 120                 125

Leu Asp Ala Ala Ala Asn Glu Lys Gly Leu Leu Leu Ser Phe Glu Asp
    130                 135                 140

Ser Ala Gly Lys His Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser
145                 150                 155                 160

Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys
                165                 170                 175

Arg Leu Val Ala Gly Asp Thr Val Ser Phe Ser Arg Ala Ala Ala Glu
            180                 185                 190

Asp Ala Arg His Arg Leu Phe Ile Asp Trp Lys Arg Arg Val Asp Thr
        195                 200                 205
```

-continued

```
Arg Gly Pro Leu Arg Phe Ser Gly Leu Ala Leu Pro Met Pro Leu Pro
    210                 215                 220

Ser Ser His Tyr Gly Gly Pro His His Tyr Ser Pro Trp Gly Phe Gly
225                 230                 235                 240

Gly Gly Gly Gly Gly Gly Gly Gly Phe Phe Met Pro Pro Ser Pro Pro
                245                 250                 255

Ala Thr Leu Tyr Glu His Arg Leu Arg Gln Gly Leu Asp Phe Arg Ser
            260                 265                 270

Met Thr Thr Thr Tyr Pro Ala Pro Thr Val Gly Arg Gln Leu Leu Phe
        275                 280                 285

Phe Gly Ser Ala Arg Met Pro Pro His His Ala Pro Pro Pro Gln Pro
    290                 295                 300

Arg Pro Phe Ser Leu Pro Leu His His Tyr Thr Val Gln Pro Ser Ala
305                 310                 315                 320

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

Val Ile Glu Ser Pro Thr Thr Ala Ala Lys Arg Val Arg Leu Phe Gly
            340                 345                 350

Val Asn Leu Asp Asn Asn Pro Asp Gly Gly Gly Glu Ala Ser His Gln
        355                 360                 365

Gly Asp Ala Leu Ser Leu Gln Met Pro Gly Trp Gln Gln Arg Thr Pro
    370                 375                 380

Thr Leu Arg Leu Leu Glu Leu Pro Arg His Gly Gly Glu Ser Ser Ala
385                 390                 395                 400

Ala Ser Ser Pro Ser Ser Ser Ser Ser Ser Lys Arg Glu Ala Arg Ser
                405                 410                 415

Ala Leu Asp Leu Asp Leu
            420


<210> SEQ ID NO 132
<211> LENGTH: 1269
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 132

atggaccagt tcgccgcgag cgggaggttc tctagagagg aggaggcgga cgaggagcag     60

gaggatgcgt ccaattccat gcgcgagatc tccttcatgc cgccggctgc ggcctcgtca    120

tcttcggcgg ctgcttccgc gtccgcgtcc gcctccacca gcgcatccgc gtgtgcatcg    180

ggaagcagca gcgccccctt ccgctccgcc tccgcgtcgg gggatgccgc cggagcgtcg    240

gggagcggcg gcccagcgga cgcggacgcg gaggcggagg cggtggagaa ggagcacatg    300

ttcgacaagg tggtcacgcc gagcgacgtg gggaagctca accggctggt gatcccgaag    360

cagtacgcgg agaagtactt cccgctggac gcggcggcca acgagaaggg cctcctcctc    420

agcttcgagg acagcgccgg caagcactgg cgcttccgct actcctactg gaacagcagc    480

cagagctacg tcatgaccaa gggctggagc cgcttcgtca aggagaagcg cctcgtcgcc    540

ggggacaccg tctccttctc ccgcgccgcc gccgaggacg cgcgccaccg cctcttcatc    600

gactggaagc gccgggtcga cacccgcggc ccgcttcgtt tctccggcct cgcgctgccg    660

atgccgctgc cgtcgtcgca ctacggcggg ccccaccact acagcccgtg gggcttcggc    720

ggcggcggcg gcggcggcgg cggattcttc atgccgccct cgccgcccgc cacgctctac    780
```

gagcaccgcc tcagacaggg cctcgacttc cgcagcatga cgacgaccta ccccgcgccg 840

accgtgggga ggcagctcct gtttttcggc tcggccagga tgcctcctca tcacgcgccg 900

ccgccccagc cgcgcccgtt ctcgctgccg ctgcatcact acacggtgca accgagcgcc 960

gccggcgtca ccgccgcgtc acggccggtc cttcttgact cggtgccggt catcgagagc 1020

ccgacgaccg ccgcgaagcg cgtgcggctg ttcggcgtca acctggacaa caacccagat 1080

ggcggcggcg aggctagcca tcagggcgat gcattgtcat tgcagatgcc cgggtggcag 1140

caaaggactc caactctaag gctactagaa ttgcctcgcc atggcgggga gtcctccgcg 1200

gcgtcgtctc cgtcgtcgtc gtcttcctcc aagagggagg cgcgttcagc tttggatctc 1260

gatctgtga 1269

<210> SEQ ID NO 133
<211> LENGTH: 894
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 133

atgatgatga caaacttgtc tctttcaaga gaaggagaag aggaggaaga agaagaacaa 60

gaagaggcca agaagcccat ggaagaagta gagagagagc acatgttcga caaagtggtg 120

actccaagcg atgttggtaa actaaaccgg ctcgtgatcc caaagcaata cgcagagaga 180

tacttccctt tagattcatc cacaaacgag aaaggtttgc ttctaaactt cgaagatctc 240

gcaggaaagt catggaggtt ccgttactct tactggaaca gtagtcagag ctatgtcatg 300

actaaaggtt ggagccgttt cgttaaagac aaaaagctag acgccggaga tattgtctct 360

ttccagagat gtgtcggaga ttcaggaaga gacagccgct tgtttattga ttggaggaga 420

agacctaaag ttcctgacca tccgacatcg attgctcact ttgctgccgg atctatgttt 480

cctaggtttt acagttttcc gacagcaact agttacaatc tttacaacta tcagcagcca 540

cgtcatcatc atcacagtgg ttataattat cctcaaattc cgagagaatt tggatacggg 600

tacttggtgg atcaaagagc cgtggtggct gatccgttgg tgattgaatc tgtgccggtg 660

atgatgcacg gaggagctca agttagtcag gcggttgttg gaacggccgg gaagaggctg 720

aggctttttg gagtcgatat ggaggaagaa tcttcatctt ccggtgggag tttgccacgt 780

ggtgacgctt ctccgtcttc ctctttgttt cagctgagac ttggaagcag cagtgaagat 840

gatcacttct ctaagaaagg aaagtcctca ttgccttttg atttggatca ataa 894

<210> SEQ ID NO 134
<211> LENGTH: 307
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 134

```
Met Ala Thr Asn His Leu Ser Gln Gly Gln His Gln His Pro Gln Ala
1               5                   10                  15

Trp Pro Trp Gly Val Ala Met Tyr Thr Asn Leu His Tyr His His Gln
            20                  25                  30

Gln His His His Tyr Glu Lys Glu His Leu Phe Glu Lys Pro Leu Thr
        35                  40                  45

Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His
    50                  55                  60
```

-continued

```
Ala Glu Arg Tyr Phe Pro Leu Ser Ser Ser Gly Ala Gly Asp Lys Gly
65                  70                  75                  80

Leu Ile Leu Cys Phe Glu Asp Asp Asp Asp Asp Glu Ala Ala Ala Ala
                85                  90                  95

Asn Lys Pro Trp Arg Phe Arg Tyr Ser Tyr Trp Thr Ser Ser Gln Ser
            100                 105                 110

Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys Glu Lys Gln Leu
        115                 120                 125

Asp Ala Gly Asp Val Val Arg Phe Gln Arg Met Arg Gly Phe Gly Met
    130                 135                 140

Pro Asp Arg Leu Phe Ile Ser His Ser Arg Arg Gly Glu Thr Thr Ala
145                 150                 155                 160

Thr Ala Ala Thr Thr Val Pro Pro Ala Ala Ala Ala Val Arg Val Val
                165                 170                 175

Val Ala Pro Ala Gln Ser Ala Gly Ala Asp His Gln Gln Gln Gln Gln
            180                 185                 190

Pro Ser Pro Trp Ser Pro Met Cys Tyr Ser Thr Ser Gly Ser Tyr Ser
        195                 200                 205

Tyr Pro Thr Ser Ser Pro Ala Asn Ser Gln His Ala Tyr His Arg His
    210                 215                 220

Ser Ala Asp His Asp His Ser Asn Asn Met Gln His Ala Gly Glu Ser
225                 230                 235                 240

Gln Ser Asp Arg Asp Asn Arg Ser Cys Ser Ala Ala Ser Ala Pro Pro
                245                 250                 255

Pro Pro Ser Arg Arg Leu Arg Leu Phe Gly Val Asn Leu Asp Cys Gly
            260                 265                 270

Pro Gly Pro Glu Pro Glu Thr Pro Thr Ala Met Tyr Gly Tyr Met His
        275                 280                 285

Gln Ser Pro Tyr Ala Tyr Asn Asn Trp Gly Ser Pro Tyr Gln His Asp
    290                 295                 300

Glu Glu Ile
305


<210> SEQ ID NO 135
<211> LENGTH: 924
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 135

atggccacga accatctctc ccaagggcag caccagcacc cgcaggcctg gccctggggc      60

gtggccatgt acaccaacct acactaccac caccagcagc accaccacta cgagaaggag     120

cacctgttcg agaagccgct gacgccgagc gacgtgggca agctcaacag gctggtgatc     180

cccaagcagc acgccgagag gtacttccct ctcagcagca gcggcgccgg cgacaaaggc     240

ctcatcctgt gcttcgagga cgacgacgac gacgaggctg ccgccgccaa caagccgtgg     300

cggttccgct actcgtactg gaccagcagc cagagctacg tgctcaccaa gggctggagc     360

cgctacgtca aggagaagca gcttgacgcc ggcgacgtcg tgcgcttcca gaggatgcgt     420

ggtttcggca tgcccgaccg cctgttcatc agccacagcc gccgcggcga gactactgct     480

actgctgcaa caacagtgcc ccccgctgct gctgccgtgc gcgtagtagt ggcacctgca     540

cagagcgctg gcgcagacca ccagcagcag cagcagccgt cgccttggag cccaatgtgc     600
```

-continued

```
tacagcacat caggctcgta ctcgtacccc accagcagcc cagccaattc ccagcatgcc    660

taccaccgcc actcagctga ccatgaccac agcaacaaca tgcaacatgc aggagaatct    720

cagtccgaca gagacaacag gagctgcagt gcagcttcgg caccgccgcc accgtcgcgg    780

cggctccggc tgttcggcgt aaacctcgac tgcggcccgg ggccggagcc ggagacacca    840

acggcgatgt acggctacat gcaccaaagc ccctacgctt acaacaactg gggcagtcca    900

taccagcatg acgaggagat ttaa                                            924
```

```
<210> SEQ ID NO 136
<211> LENGTH: 277
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 136

Met Glu Phe Thr Pro Ala His Ala His Ala Arg Val Val Glu Asp Ser
1               5                   10                  15

Glu Arg Pro Arg Gly Gly Val Ala Trp Val Glu Lys Glu His Met Phe
            20                  25                  30

Glu Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val
        35                  40                  45

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

Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Lys Gly
65                  70                  75                  80

Leu Val Leu Ser Phe Glu Asp Arg Ala Gly Lys Ala Trp Arg Phe Arg
                85                  90                  95

Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp
            100                 105                 110

Ser Arg Phe Val Lys Glu Lys Arg Leu Gly Ala Gly Asp Thr Val Leu
        115                 120                 125

Phe Ala Arg Gly Ala Gly Gly Ala Arg Gly Arg Phe Phe Ile Asp Phe
    130                 135                 140

Arg Arg Arg Arg Gln Asp Leu Ala Phe Leu Gln Pro Thr Leu Ala Ser
145                 150                 155                 160

Ala Gln Arg Leu Leu Pro Leu Pro Ser Val Pro Ile Cys Pro Trp Gln
                165                 170                 175

Asp Tyr Gly Ala Ser Ala Pro Ala Pro Asn Arg His Val Leu Phe Leu
            180                 185                 190

Arg Pro Gln Val Pro Ala Ala Val Val Leu Lys Ser Val Pro Val His
        195                 200                 205

Val Ala Ala Ser Ala Val Glu Ala Thr Met Ser Lys Arg Val Arg Leu
    210                 215                 220

Phe Gly Val Asn Leu Asp Cys Pro Pro Asp Ala Glu Asp Ser Ala Thr
225                 230                 235                 240

Val Pro Arg Gly Arg Ala Ala Ser Thr Thr Leu Leu Gln Leu Pro Ser
                245                 250                 255

Pro Ser Ser Ser Thr Ser Ser Ser Thr Ala Gly Lys Asp Val Cys Cys
            260                 265                 270

Leu Asp Leu Gly Leu
        275
```

-continued

```
<210> SEQ ID NO 137
<211> LENGTH: 834
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 137

atggagttca cgcccgcgca tgcgcatgcc cgtgtcgttg aggattccga gaggcctcgc      60

ggcggcgtgg cctgggtgga gaaggagcac atgttcgaga aggtggtcac cccgagcgac     120

gtggggaagc tcaatcgcct ggtcatccca aagcagcacg cggagcgcta cttccccgcg     180

ctggacgcct cgtccgccgc ggcggcggcg gcggcagcag ccgcgggagg cgggaagggg     240

ctggtgctca gcttcgagga ccgggcgggg aaggcgtggc gcttccgcta ctcgtactgg     300

aacagcagcc agagctacgt gatgaccaaa ggttggagcc gcttcgtgaa ggagaagcgc     360

ctcggtgccg gggacacagt cttgttcgcg cgcggcgcgg gcggcgcgcg cggccgcttc     420

ttcatcgatt tccgccgccg tcgccaggat ctcgcgttcc tgcagccgac gctggcgtct     480

gcgcagcgac tcctgccgct gccgtcggtg cccatctgcc cgtggcagga ctacggcgcc     540

tcggctccgg cgcccaaccg gcacgtgctg ttcctgcggc cgcaggtgcc ggccgccgta     600

gtgctcaagt cggtccccgt gcacgttgct gcatccgcgg tggaggcgac catgtcgaag     660

cgcgtccgcc tgttcggggt gaacctcgac tgcccgccgg acgccgaaga cagcgccaca     720

gtcccccggg gccgggcggc gtcgacgacg cttctgcaac tgccctcgcc atcgtcgtca     780

acatcctcct cgacggcagg gaaggacgtg tgctgtttgg atcttggact gtga           834


<210> SEQ ID NO 138
<211> LENGTH: 273
<212> TYPE: PRT
<213> ORGANISM: Zea mays

<400> SEQUENCE: 138

Met Glu Phe Arg Pro Ala His Ala Arg Val Phe Glu Asp Ser Glu Arg
1               5                   10                  15

Pro Arg Gly Gly Val Ala Trp Leu Glu Lys Glu His Met Phe Glu Lys
            20                  25                  30

Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro
        35                  40                  45

Lys Gln His Ala Glu Arg Tyr Phe Pro Ala Leu Asp Ala Ser Ala Ala
    50                  55                  60

Ala Ala Ser Ala Ser Ala Ser Ala Gly Gly Gly Lys Ala Gly Leu Val
65                  70                  75                  80

Leu Ser Phe Glu Asp Arg Ala Gly Lys Ala Trp Arg Phe Arg Tyr Ser
                85                  90                  95

Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg
            100                 105                 110

Phe Val Lys Glu Lys Arg Leu Gly Ala Gly Asp Thr Val Leu Phe Ala
        115                 120                 125

Arg Gly Ala Gly Ala Thr Arg Gly Arg Phe Phe Ile Asp Phe Arg Arg
    130                 135                 140

Arg Arg His Glu Leu Ala Phe Leu Gln Pro Pro Leu Ala Ser Ala Gln
145                 150                 155                 160

Arg Leu Leu Pro Leu Pro Ser Val Pro Ile Cys Pro Trp Gln Gly Tyr
                165                 170                 175
```

-continued

```
Gly Ala Ser Ala Pro Ala Pro Ser Arg His Val Leu Phe Leu Arg Pro
            180                 185                 190

Gln Val Pro Ala Ala Val Val Leu Thr Ser Val Pro Val Arg Val Ala
        195                 200                 205

Ala Ser Ala Val Glu Glu Ala Thr Arg Ser Lys Arg Val Arg Leu Phe
    210                 215                 220

Gly Val Asn Leu Asp Cys Pro Pro Asp Ala Glu Asp Gly Ala Thr Ala
225                 230                 235                 240

Thr Arg Thr Pro Ser Thr Leu Leu Gln Leu Pro Ser Pro Ser Ser Ser
                245                 250                 255

Thr Ser Ser Ser Thr Gly Gly Lys Asp Val Arg Ser Leu Asp Leu Gly
            260                 265                 270

Leu


<210> SEQ ID NO 139
<211> LENGTH: 822
<212> TYPE: DNA
<213> ORGANISM: Zea mays

<400> SEQUENCE: 139

atggagttca ggcccgcgca tgcccgtgtc ttcgaggatt ccgagaggcc tcgcggcggc      60

gtggcgtggc tggagaagga gcacatgttc gagaaagtgg tcaccccgag cgacgtgggg     120

aagctcaatc gcctggtcat cccgaagcag cacgccgagc gctacttccc cgcgctggac     180

gcctcggccg ccgcggcgtc ggcatcggcg tcggcgggcg gcgggaaggc ggggctggtg     240

ctcagcttcg aggaccgggc ggggaaggcg tggcgcttcc gctactcgta ctggaacagc     300

agccagagct acgtgatgac caagggatgg agccgcttcg tgaaagagaa gcgcctcggt     360

gccggggaca cggtattgtt cgcgcgcggc gcgggcgcca cgcgcggccg cttcttcatc     420

gatttccgcc gccgccgcca cgagctcgcg ttcctgcagc cgccgctggc gtctgcgcag     480

cgcctcctgc cgctcccgtc ggtgcccatc tgcccgtggc agggctacgg cgcctccgct     540

ccggcgccaa gccggcacgt gctgttcctg cggccgcagg tgccggccgc cgtagtgctc     600

acgtcggtgc ccgtgcgcgt cgccgcatcc gcggtggagg aggcgacgag gtcgaagcgc     660

gtccgcctgt tcggggtgaa cctcgactgc ccgccggacg ccgaagacgg tgccacagcc     720

acccggacgc cgtcgacgct tctgcagctg ccctcgccat cgtcgtcaac atcctcctcc     780

acgggaggca aggatgtgcg ttctttggat cttggacttt ga                       822


<210> SEQ ID NO 140
<211> LENGTH: 350
<212> TYPE: PRT
<213> ORGANISM: Triticum aestivum

<400> SEQUENCE: 140

Met Gly Val Glu Ile Leu Ser Ser Met Val Glu His Ser Phe Gln Tyr
1               5                   10                  15

Ser Ser Gly Val Ser Thr Ala Thr Thr Glu Ser Gly Thr Ala Gly Thr
            20                  25                  30

Pro Pro Arg Pro Leu Ser Leu Pro Val Ala Ile Ala Asp Glu Ser Val
        35                  40                  45

Thr Ser Arg Ser Ala Ser Ser Arg Phe Lys Gly Val Val Pro Gln Pro
    50                  55                  60
```

-continued

```
Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Arg His Ala Arg Val Trp
65                  70                  75                  80

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

Ala Ser Leu Arg Tyr Arg Gly Arg Asp Val Ala Phe Asn Phe Pro Cys
            100                 105                 110

Ala Ala Val Glu Gly Glu Leu Ala Phe Leu Ala Ala His Ser Lys Ala
        115                 120                 125

Glu Ile Val Asp Met Leu Arg Lys Gln Thr Tyr Ala Asp Glu Leu Arg
    130                 135                 140

Gln Gly Leu Arg Arg Gly Arg Gly Met Gly Ala Arg Ala Gln Pro Thr
145                 150                 155                 160

Pro Ser Trp Ala Arg Glu Pro Leu Phe Glu Lys Ala Val Thr Pro Ser
                165                 170                 175

Asp Val Gly Lys Leu Asn Arg Leu Val Val Pro Lys Gln His Ala Glu
            180                 185                 190

Lys His Phe Pro Leu Lys Arg Thr Pro Glu Thr Pro Thr Thr Thr Gly
        195                 200                 205

Lys Gly Val Leu Leu Asn Phe Glu Asp Gly Glu Gly Lys Val Trp Arg
    210                 215                 220

Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys
225                 230                 235                 240

Gly Trp Ser Arg Phe Val Arg Glu Lys Gly Leu Gly Ala Gly Asp Ser
                245                 250                 255

Ile Leu Phe Ser Cys Ser Leu Tyr Glu Gln Glu Lys Gln Phe Phe Ile
            260                 265                 270

Asp Cys Lys Lys Asn Thr Ser Met Asn Gly Gly Lys Ser Ala Ser Pro
        275                 280                 285

Leu Pro Val Gly Val Thr Thr Lys Gly Glu Gln Val Arg Val Val Arg
    290                 295                 300

Leu Phe Gly Val Asp Ile Ser Gly Val Lys Arg Gly Arg Ala Ala Thr
305                 310                 315                 320

Ala Thr Ala Glu Gln Gly Leu Gln Glu Leu Phe Lys Arg Gln Cys Val
                325                 330                 335

Ala Pro Gly Gln His Ser Pro Ala Leu Gly Ala Phe Ala Leu
            340                 345                 350


<210> SEQ ID NO 141
<211> LENGTH: 1053
<212> TYPE: DNA
<213> ORGANISM: Triticum aestivum

<400> SEQUENCE: 141

atgggggtgg aaatcctgag ctccatggtg gagcactcct tccagtactc ttccggcgtg      60

tccacggcca cgacggagtc aggcaccgcc ggaacaccgc cgaggccttt gagcctacct     120

gtcgccatcg ccgacgagtc cgtgacctcg cggtcggcgt cgtctcggtt caagggcgtg     180

gtgccgcagc caaacgggcg atggggcgcc cagatctacg agcgccacgc tcgcgtctgg     240

ctcggcacgt tcccagacca ggactcggcg gcgcgcgcct acgacgtagc ctcgctcagg     300

taccgcggcc gcgacgtcgc cttcaacttc ccgtgcgcgg ccgtggaggg ggagctcgcc     360

ttcctggcgg cgcactccaa ggctgagata gtggacatgc tccggaagca gacctacgcc     420
```

-continued

```
gatgaactcc gccagggcct gcggcgcggc cgtggcatgg gggcgcgcgc gcagccgacg    480

ccgtcgtggg cgcgggagcc ccttttcgag aaggccgtga cccctagcga tgtcggcaag    540

ctcaatcgcc tcgtagtgcc gaagcagcac gccgagaagc acttcccccct gaagcgcacg    600

ccggagacgc cgaccaccac cggcaagggc gtgctgctca acttcgagga cggcgagggg    660

aaggtgtgga ggttccggta ctcgtactgg aacagcagcc agagctacgt gctcaccaaa    720

ggctggagcc gcttcgtccg ggagaagggc ctaggtgccg gcgactccat cctattctcg    780

tgctcgctgt acgaacagga gaagcagttc ttcatcgact gcaagaagaa cactagcatg    840

aacggaggca aatcggcgtc gccgctgcca gtgggggtga ctaccaaagg agaacaagtt    900

cgcgtcgtta ggctattcgg tgtcgacatc tcgggagtga agagggggcg agcggcgacg    960

gcaacggcgg agcaaggcct gcaggagttg ttcaagaggc aatgcgtggc acccggccag   1020

cactctcctg ccctaggtgc cttcgcctta tag                                1053


<210> SEQ ID NO 142
<211> LENGTH: 320
<212> TYPE: PRT
<213> ORGANISM: Triticum aestivum

<400> SEQUENCE: 142

Met Ala Ser Gly Lys Pro Thr Asn His Gly Met Glu Asp Asp Asn Asp
1               5                   10                  15

Met Glu Tyr Ser Ser Ala Glu Ser Gly Ala Glu Asp Ala Ala Glu Pro
            20                  25                  30

Ser Ser Ser Pro Val Leu Ala Pro Pro Arg Ala Ala Pro Ser Ser Arg
        35                  40                  45

Phe Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile
    50                  55                  60

Tyr Glu Lys His Ser Arg Val Trp Leu Gly Thr Phe Pro Asp Glu Asp
65                  70                  75                  80

Ala Ala Val Arg Ala Tyr Asp Val Ala Ala Leu Arg Phe Arg Gly Pro
                85                  90                  95

Asp Ala Val Ile Asn His Gln Arg Pro Thr Ala Ala Glu Glu Ala Gly
            100                 105                 110

Ser Ser Ser Ser Arg Ser Glu Leu Asp Pro Glu Leu Gly Phe Leu Ala
        115                 120                 125

Asp His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
    130                 135                 140

Asp Asp Glu Leu Arg Gln Gly Leu Arg Arg Gly Arg Gly Arg Ala Gln
145                 150                 155                 160

Pro Thr Pro Ala Trp Ala Arg Glu Leu Leu Phe Glu Lys Ala Val Thr
                165                 170                 175

Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Val Pro Lys Gln Gln
            180                 185                 190

Ala Glu Lys His Phe Pro Pro Thr Thr Ala Ala Ala Thr Gly Ser Asn
        195                 200                 205

Gly Lys Gly Val Leu Leu Asn Phe Glu Asp Gly Glu Gly Lys Val Trp
    210                 215                 220

Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr
225                 230                 235                 240

Lys Gly Trp Ser Arg Phe Val Lys Glu Thr Gly Leu Arg Ala Gly Asp
```

-continued

245 250 255

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

Leu Phe Ile Asp Tyr Lys Lys Met Asn Lys Asn Asp Asp Ala Ala Asp
275 280 285

Ala Ala Ile Ser Asp Glu Asn Glu Thr Gly His Val Ala Val Lys Leu
290 295 300

Phe Gly Val Asp Ile Ala Gly Gly Gly Met Ala Gly Ser Ser Gly Gly
305 310 315 320

<210> SEQ ID NO 143
<211> LENGTH: 963
<212> TYPE: DNA
<213> ORGANISM: Triticum aestivum

<400> SEQUENCE: 143

atggcatctg gcaagccgac aaaccacggg atggaggacg acaacgacat ggagtactcc 60

tccgcggaat cgggggccga ggacgcggcg gagccgtcgt cgtcgccggt gctggcgccg 120

ccccgggcgg ctccatcgtc gcggttcaag ggcgtcgtgc cgcagcccaa cgggcggtgg 180

ggagcgcaga tctacgagaa gcactcgcgg gtgtggctcg gaacgttccc cgacgaggac 240

gccgccgtgc gcgcctacga cgtggccgcg ctccgcttcc gcggcccgga cgccgtcatc 300

aaccaccagc gaccgacggc cgcggaggag gccggctcgt cgtcgtccag gagcgagctg 360

gatccagagc tcggcttcct tgccgaccac tccaaggccg agatcgtcga catgctccgg 420

aagcacacct acgacgacga gctccgtcag ggcctgcgcc gcggccgcgg gcgcgcgcag 480

ccgacgccgg cgtgggcacg agagctcctc ttcgagaagg ccgtgacccc gagcgacgtc 540

ggcaagctca accgcctcgt ggtgccgaag cagcaggccg agaagcactt ccctccgacc 600

actgcggcgg ccaccggcag caacggcaag ggcgtgctgc tcaacttcga ggacggcgaa 660

gggaaggtgt ggcgcttccg gtactcgtac tggaacagca gccagagcta cgtgctcacc 720

aagggctgga gccgcttcgt caaggagacg ggcctccgcg ccggcgacac cgtggcgttc 780

taccggtcgg cgtacgggaa tgacacggag gatcagctct tcatcgacta caagaagatg 840

aacaagaatg acgatgctgc ggacgcggcg atttccgatg agaatgagac aggccatgtc 900

gccgtcaagc tcttcggcgt tgacattgcc ggtggaggga tggcgggatc atcaggtggc 960

tga 963

<210> SEQ ID NO 144
<211> LENGTH: 320
<212> TYPE: PRT
<213> ORGANISM: Triticum aestivum

<400> SEQUENCE: 144

Met Ala Ser Gly Lys Pro Thr Asn His Gly Met Glu Asp Asp Asn Asp
1 5 10 15

Met Glu Tyr Ser Ser Ala Glu Ser Gly Ala Glu Asp Ala Ala Glu Pro
20 25 30

Ser Ser Ser Pro Val Leu Ala Pro Pro Arg Ala Ala Pro Ser Ser Arg
35 40 45

Phe Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile
50 55 60

-continued

```
Tyr Glu Lys His Ser Arg Val Trp Leu Gly Thr Phe Pro Asp Glu Asp
65                  70                  75                  80

Ala Ala Ala Arg Ala Tyr Asp Val Ala Ala Leu Arg Phe Arg Gly Pro
                85                  90                  95

Asp Ala Val Ile Asn His Gln Arg Pro Thr Ala Ala Glu Glu Ala Gly
            100                 105                 110

Ser Ser Ser Ser Arg Ser Glu Leu Asp Pro Glu Leu Gly Phe Leu Ala
        115                 120                 125

Asp His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
    130                 135                 140

Asp Asp Glu Leu Arg Gln Gly Leu Arg Arg Gly Arg Gly Arg Ala Gln
145                 150                 155                 160

Pro Thr Pro Ala Trp Ala Arg Glu Leu Leu Phe Glu Lys Ala Val Thr
                165                 170                 175

Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Val Pro Lys Gln Gln
            180                 185                 190

Ala Glu Lys His Phe Pro Pro Thr Thr Ala Ala Ala Thr Gly Ser Asn
        195                 200                 205

Gly Lys Gly Val Leu Leu Asn Phe Glu Asp Gly Glu Gly Lys Val Trp
    210                 215                 220

Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr
225                 230                 235                 240

Lys Gly Trp Ser Arg Phe Val Lys Glu Thr Gly Leu Arg Ala Gly Asp
                245                 250                 255

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

Leu Phe Ile Asp Tyr Lys Lys Met Asn Lys Asn Asp Asp Ala Ala Asp
        275                 280                 285

Ala Ala Ile Ser Asp Glu Asn Glu Thr Gly His Val Ala Val Lys Leu
    290                 295                 300

Phe Gly Val Asp Ile Ala Gly Gly Gly Met Ala Gly Ser Ser Gly Gly
305                 310                 315                 320
```

<210> SEQ ID NO 145
<211> LENGTH: 963
<212> TYPE: DNA
<213> ORGANISM: Triticum aestivum

<400> SEQUENCE: 145

```
atggcatctg gcaagccgac aaaccacggg atggaggacg acaacgacat ggagtactcc      60

tccgcggaat cgggggccga ggacgcggcg gagccgtcgt cgtcgccggt gctggcgccg     120

ccccgggcgg ctccatcgtc gcggttcaag ggcgtcgtgc cgcagcccaa cgggcggtgg     180

ggagcgcaga tctacgagaa gcactcgcgg gtgtggctcg gaacgttccc cgacgaggac     240

gccgccgcgc gcgcctacga cgtggccgcg ctccgcttcc gcggcccgga cgccgtcatc     300

aaccaccagc gaccgacggc cgcggaggag gccggctcgt cgtcgtccag gagcgagctg     360

gatccagagc tcggcttcct cgccgaccac tccaaggccg agatcgtcga catgctccgg     420

aagcacacct acgacgacga gctccgtcag ggcctgcgcc gcggccgcgg gcgcgcgcag     480

ccgacgccgg cgtgggcacg agagctcctc ttcgagaagg ccgtgacccc gagcgacgtc     540

ggcaagctca accgcctcgt ggtgccgaag cagcaggccg agaagcactt ccctccgacc     600
```

-continued

actgcggcgg ccaccggcag caacggcaag ggcgtgctgc tcaacttcga ggacggcgaa 660

gggaaggtgt ggcgcttccg gtactcgtac tggaacagca gccagagcta cgtgctcacc 720

aagggctgga gccgcttcgt caaggagacg ggcctccgcg ccggcgacac cgtggcgttc 780

taccggtcgg cgtacgggaa tgacacggag gatcagctct tcatcgacta caagaagatg 840

aacaagaatg acgatgctgc ggacgcggcg atttccgatg agaatgagac aggccatgtc 900

gccgtcaagc tcttcggcgt tgacattgcc ggtggaggga tggcgggatc atcaggtggc 960

tga 963

<210> SEQ ID NO 146
<211> LENGTH: 488
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: gRNA sequence

<400> SEQUENCE: 146

gacggccagt gccaagcttc tcggatccac tagtaacggc cgccagtgtg ctggaattgc 60

ccttggatca tgaaccaacg gcctggctgt atttggtggt tgtgtaggga gatggggaga 120

agaaaagccc gattctcttc gctgtgatgg gctggatgca tgcgggggag cgggaggccc 180

aagtacgtgc acggtgagcg gcccacaggg cgagtgtgag cgcgagaggc gggaggaaca 240

gtttagtacc acattgccca gctaactcga acgcgaccaa cttataaacc cgcgcgctgt 300

cgcttgtgtg ggaaggaaga gacagattgg ttttagagct agaaatagca agttaaaata 360

aggctagtcc gttatcaact tgaaaaagtg gcaccgagtc ggtgcttttt ttgtcccttc 420

gaagggcaat tctgcagata tccatcacac tggcggccgc tcgaggtcga agcttgcatg 480

cctgcagg 488

<210> SEQ ID NO 147
<211> LENGTH: 41
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 147

ggactggggt tgctcctggg acacaagcga cagcgcgcgg g 41

<210> SEQ ID NO 148
<211> LENGTH: 41
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 148

cccaggagca accccagtcc gttttagagc tagaaatagc a 41

<210> SEQ ID NO 149
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 149

```
tgctatttct agctctaaaa cacacaagcg acagcgcgcg gg                          42


<210> SEQ ID NO 150
<211> LENGTH: 41
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 150

gcccctgacg cccagtgacg gttttagagc tagaaatagc a                           41


<210> SEQ ID NO 151
<211> LENGTH: 41
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 151

gggggtgccc ctgggcgaga acacaagcga cagcgcgcgg g                           41


<210> SEQ ID NO 152
<211> LENGTH: 41
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 152

tctcgcccag ggcacccccc gttttagagc tagaaatagc a                           41


<210> SEQ ID NO 153
<211> LENGTH: 41
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 153

ctcgtagtgg tggtggtagt acacaagcga cagcgcgcgg g                           41


<210> SEQ ID NO 154
<211> LENGTH: 41
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 154

actaccacca ccactacgag gttttagagc tagaaatagc a                           41


<210> SEQ ID NO 155
<211> LENGTH: 15681
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: vector
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5964)..(5984)
<223> OTHER INFORMATION: /note="target sequence"
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6617)..(6637)
```

-continued

<223> OTHER INFORMATION: /note="target sequence"

<400> SEQUENCE: 155

aattcccgat ctagtaacat agatgacacc gcgcgcgata atttatccta gtttgcgcgc 60

tatattttgt tttctatcgc gtattaaatg tataattgcg ggactctaat cataaaaacc 120

catctcataa ataacgtcat gcattacatg ttaattatta catgcttaac gtaattcaac 180

agaaattata tgataatcat cgcaagaccg gcaacaggat tcaatcttaa gaaactttat 240

tgccaaatgt ttgaacgatc ggggaaattc gagctctatc gatcaatcag gatccttact 300

ttttcttttt tgcctggccg gcctttttcg tggccgccgg ccttttgtcg cctcccagct 360

gagacaggtc gatccgtgtc tcgtacaggc cggtgatgct ctggtggatc agggtggcgt 420

ccagcacctc tttggtgctg gtgtacctct tccggtcgat ggtggtgtca aagtacttga 480

aggcggcagg ggctcccaga ttggtcaggg taaacaggtg gatgatattc tcggcctgct 540

ctctgatggg cttatcccgg tgcttgttgt aggcggacag cactttgtcc agattagcgt 600

cggccaggat cactctcttg gagaactcgc tgatctgctc gatgatctcg tccaggtagt 660

gcttgtgctg ttccacaaac agctgtttct gctcattatc ctcgggggag cccttcagct 720

tctcatagtg gctggccagg tacaggaagt tcacatattt ggagggcagg gccagttcgt 780

ttcccttctg cagttcgccg gcagaggcca gcattctctt ccggccgttt tccagctcga 840

acagggagta cttaggcagc ttgatgatca ggtccttttt cacttctttg tagcccttgg 900

cttccagaaa gtcgatggga ttcttctcga agctgcttct ttccatgatg gtgatcccca 960

gcagctcttt cacactcttc agtttcttgg acttgccctt ttccactttg gccaccacca 1020

gcacagaata ggccacggtg gggctgtcga agccgccgta cttcttaggg tcccagtcct 1080

tctttctggc gatcagctta tcgctgttcc tcttgggcag gatagactct ttgctgaagc 1140

cgcctgtctg cacctcggtc tttttcacga tattcacttg ggcatgctc agcactttcc 1200

gcacggtggc aaaatcccgg cccttatccc acacgatctc cccggtttcg ccgtttgtct 1260

cgatcagagg ccgcttccgg atctcgccgt tggccagggt aatctcggtc ttgaaaaagt 1320

tcatgatgtt gctgtagaag aagtacttgg cggtagcctt gccgatttcc tgctcgctct 1380

tggcgatcat cttccgcacg tcgtacacct tgtagtcgcc gtacacgaac tcgctttcca 1440

gcttagggta ctttttgatc agggcggttc ccacgacggc gttcaggtag gcgtcgtggg 1500

cgtggtggta gttgttgatc tcgcgcactt tgtaaaactg gaaatccttc cggaaatcgg 1560

acaccagctt ggacttcagg gtgatcactt tcacttcccg gatcagcttg tcattctcgt 1620

cgtacttagt gttcatccgg gagtccagga tctgtgccac gtgctttgtg atctgccggg 1680

tttccaccag ctgtctcttg atgaagccgg ccttatccag ttcgctcagg ccgcctctct 1740

cggccttggt cagattgtcg aactttctct gggtaatcag cttggcgttc agcagctgcc 1800

gccagtagtt cttcatcttc ttcacgacct cttcggaggg cacgttgtcg ctcttgcccc 1860

ggttcttgtc gcttctggtc agcaccttgt tgtcgatgga gtcgtccttc agaaagctct 1920

gaggcacgat atggtccaca tcgtagtcgg acagccggtt gatgtccagt tcctggtcca 1980

cgtacatatc ccgcccattc tgcaggtagt acaggtacag cttctcgttc tgcagctggg 2040

tgttttccac ggggtgttct ttcaggatct ggctgcccag ctctttgatg ccctcttcga 2100

tccgcttcat tctctcgcgg ctgttcttct gtcccttctg ggtggtctgg ttctctctgg 2160

-continued

```
ccatttcgat cacgatgttc tcgggcttgt gccggcccat cactttcacg agctcgtcca   2220

ccaccttcac tgtctgcagg atgcccttct taatggcggg gctgccggcc agattggcaa   2280

tgtgctcgtg caggctatcg ccctggccgg acacctgggc tttctggatg tcctctttaa   2340

aggtcaggct gtcgtcgtgg atcagctgca tgaagtttct gttggcgaag ccgtcggact   2400

tcaggaaatc caggattgtc ttgccggact gcttgtcccg gatgccgttg atcagcttcc   2460

ggctcagcct gccccagccg gtgtatctcc gccgcttcag ctgcttcatc actttgtcgt   2520

cgaacaggtg ggcataggtt ttcagccgtt cctcgatcat ctctctgtcc tcaaacagtg   2580

tcagggtcag cacgatatct tccagaatgt cctcgttttc ctcattgtcc aggaagtcct   2640

tgtccttgat aattttcagc agatcgtggt atgtgcccag ggaggcgttg aaccgatctt   2700

ccacgccgga gatttccacg gagtcgaagc actcgatttt cttgaagtag tcctctttca   2760

gctgcttcac ggtcactttc cggttggtct tgaacagcag gtccacgatg gcctttttct   2820

gctcgccgct caggaaggcg ggctttctca ttccctcggt cacgtatttc actttggtca   2880

gctcgttata cacggtgaag tactcgtaca gcaggctgtg cttgggcagc accttctcgt   2940

tgggcaggtt cttatcgaag ttggtcatcc gctcgatgaa gctctgggcg gaagcgccct   3000

tgtccaccac ttcctcgaag ttccaggggg tgatggtttc ctcgctcttt ctggtcatcc   3060

aggcgaatct gctgtttccc ctggccagag ggcccacgta gtaggggatg cggaaggtca   3120

ggatcttctc gatcttttcc cggttgtcct tcaggaatgg gtaaaaatct tcctgccgcc   3180

gcagaatggc gtgcagctct cccaggtgga tctggtgggg gatgctgccg ttgtcgaagg   3240

tccgctgctt ccgcagcagg tcctctctgt tcagcttcac gagcagttcc tcggtgccgt   3300

ccatcttttc caggatgggc ttgatgaact tgtagaactc ttcctggctg gctccgccgt   3360

caatgtagcc ggcgtagccg ttcttgctct ggtcgaagaa aatctctttg tacttctcag   3420

gcagctgctg ccgcacgaga gctttcagca gggtcaggtc ctggtggtgc tcgtcgtatc   3480

tcttgatcat agaggcgctc agggggggcct tggtgatctc ggtgttcact ctcaggatgt   3540

cgctcagcag gatggcgtcg gacaggttct tggcggccag aaacaggtcg gcgtactggt   3600

cgccgatctg ggccagcagg ttgtccaggt cgtcgtcgta ggtgtccttg ctcagctgca   3660

gtttggcatc ctcggccagg tcgaagttgc tcttgaagtt gggggtcagg cccaggctca   3720

gggcaatcag gtttccgaac aggccattct tcttctcgcc gggcagctgg gcgatcagat   3780

tttccagccg tctgctcttg ctcagtctgg cagacaggat ggccttggcg tccacgccgc   3840

tggcgttgat ggggttttcc tcgaacagct ggttgtaggt ctgcaccagc tggatgaaca   3900

gcttgtccac gtcgctgttg tcggggttca ggtcgccctc gatcaggaag tggccccgga   3960

acttgatcat gtgggccagg gccagataga tcagccgcag gtcggccttg tcggtgctgt   4020

ccaccagttt ctttctcagg tggtagatgg tggggtactt ctcgtggtag gccacctcgt   4080

ccacgatgtt gccgaagatg gggtgccgct cgtgcttctt atcctcttcc accaggaagg   4140

actcttccag tctgtggaag aagctgtcgt ccaccttggc catctcgttg ctgaagatct   4200

cttgcagata gcagatccgg ttcttccgtc tggtgtatct tcttctggcg gttctcttca   4260

gccgggtggc ctcggctgtt tcgccgctgt cgaacagcag ggctccgatc aggttcttct   4320

tgatgctgtg ccggtcggtg ttgcccagca ccttgaattt cttgctgggc accttgtact   4380

cgtcggtgat cacggcccag cccacagagt tggtgccgat gtccaggccg atgctgtact   4440
```

-continued

```
tcttgtcggc tgctgggact ccgtggatac cgaccttccg cttcttcttt ggggccatct   4500

tatcgtcatc gtctttgtaa tcaatatcat gatccttgta gtctccgtcg tggtccttat   4560

agtccatctc gagtatcgtt cgtaaatggt gaaaattttc agaaaattgc ttttgcttta   4620

aaagaaatga tttaaattgc tgcaatagaa gtagaatgct tgattgcttg agattcgttt   4680

gttttgtata tgttgtgttg aggtcgaggt cctctccaaa tgaaatgaac ttccttatat   4740

agaggaaggg tcttgcgaag gatagtggga ttgtgcgtca tcccttacgt cagtggagat   4800

atcacatcaa tccacttgct ttgaagacgt ggttggaacg tcttcttttt ccacgatgct   4860

cctcgtgggt gggggtccat ctttgggacc actgtcggca gaggcatctt caacgatggc   4920

ctttccttta tcgcaatgat ggcatttgta ggagccacct tccttttcca ctatcttcac   4980

aataaagtga cagatagctg ggcaatggaa tccgaggagg tttccggata tcaccctttg   5040

ttgaaaagtc tcaattgccc tttggtcttc tgagactgta tctttgatat ttttggagta   5100

gacaagtgtg tcgtgctcca ccatgttatc acatcaatcc acttgctttg aagacgtggt   5160

tggaacgtct tctttttcca cgatgctcct cgtgggtggg ggtccatctt tgggaccact   5220

gtcggcagag gcatcttcaa cgatggcctt tcctttatcg caatgatggc atttgtagga   5280

gccaccttcc ttttccacta tcttcacaat aaagtgacag atagctgggc aatggaatcc   5340

gaggaggttt ccggatatta ccctttgttg aaaagtctca attgcccttt ggtcttctga   5400

gactgtatct ttgatatttt tggagtagac aagtgtgtcg tgctccacca tgttgacctg   5460

caggcatgcc tcggatccac tagtaacggc cgccagtgtg ctggaattgc ccttaagctt   5520

cgttgaacaa cggaaactcg acttgccttc cgcacaatac atcatttctt cttagctttt   5580

tttcttcttc ttcgttcata cagttttttt ttgtttatca gcttacattt tcttgaaccg   5640

tagctttcgt tttcttcttt ttaactttcc attcggagtt tttgtatctt gtttcatagt   5700

ttgtcccagg attagaatga ttaggcatcg aaccttcaag aatttgattg aataaaacat   5760

cttcattctt aagatatgaa gataatcttc aaaaggcccc tgggaatctg aaagaagaga   5820

agcaggccca tttatatggg aaagaacaat agtatttctt atataggccc atttaagttg   5880

aaaacaatct tcaaaagtcc cacatcgctt agataagaaa acgaagctga gtttatatac   5940

agctagagtc gaagtagtga tttccccacg tcactgggcg tcgttttaga gctagaaata   6000

gcaagttaaa ataaggctag tccgttatca acttgaaaaa gtggcaccga gtcggtgctt   6060

tttttgtccc ttcgaagggc ctttctcaga tatccatcac actggcggcc gctcgaggtc   6120

gctcggatcc actagtaacg gccgccagtg tgctggaatt gcccttaagc ttcgttgaac   6180

aacggaaact cgacttgcct tccgcacaat acatcatttc ttcttagctt tttttcttct   6240

tcttcgttca tacagttttt ttttgtttat cagcttacat tttcttgaac cgtagctttc   6300

gttttcttct ttttaacttt ccattcggag tttttgtatc ttgtttcata gtttgtccca   6360

ggattagaat gattaggcat cgaaccttca agaatttgat tgaataaaac atcttcattc   6420

ttaagatatg aagataatct tcaaaaggcc cctgggaatc tgaaagaaga gaagcaggcc   6480

catttatatg ggaaagaaca atagtatttc ttatataggc ccatttaagt tgaaaacaat   6540

cttcaaaagt cccacatcgc ttagataaga aaacgaagct gagtttatat acagctagag   6600

tcgaagtagt gattcacacc ccatggccag gactgtttta gagctagaaa tagcaagtta   6660

aaataaggct agtccgttat caacttgaaa aagtggcacc gagtcggtgc tttttttgtc   6720
```

-continued

ccttcgaagg gcctttctca gatatccatc acactggcgg ccgctcgagg tcgaagcttg 6780

gcactggccg tcgttttaca acgtcgtgac tgggaaaacc ctggcgttac ccaacttaat 6840

cgccttgcag cacatccccc tttcgccagc tggcgtaata gcgaagaggc ccgcaccgat 6900

cgcccttccc aacagttgcg cagcctgaat ggcgaatgct agagcagctt gagcttggat 6960

cagattgtcg tttcccgcct tcagtttaaa ctatcagtgt ttgacaggat atattggcgg 7020

gtaaacctaa gagaaaagag cgtttattag aataacggat atttaaaagg gcgtgaaaag 7080

gtttatccgt tcgtccattt gtatgtgcat gccaaccaca gggttcccct cgggatcaaa 7140

gtactttgat ccaacccctc cgctgctata gtgcagtcgg cttctgacgt tcagtgcagc 7200

cgtcttctga aaacgacatg tcgcacaagt cctaagttac gcgacaggct gccgccctgc 7260

ccttttcctg gcgttttctt gtcgcgtgtt ttagtcgcat aaagtagaat acttgcgact 7320

agaaccggag acattacgcc atgaacaaga gcgccgccgc tggcctgctg ggctatgccc 7380

gcgtcagcac cgacgaccag gacttgacca accaacgggc cgaactgcac gcggccggct 7440

gcaccaagct gttttccgag aagatcaccg gcaccaggcg cgaccgcccg gagctggcca 7500

ggatgcttga ccacctacgc cctggcgacg ttgtgacagt gaccaggcta gaccgcctgg 7560

cccgcagcac ccgcgaccta ctggacattg ccgagcgcat ccaggaggcc ggcgcgggcc 7620

tgcgtagcct ggcagagccg tgggccgaca ccaccacgcc ggccggccgc atggtgttga 7680

ccgtgttcgc cggcattgcc gagttcgagc gttccctaat catcgaccgc acccggagcg 7740

ggcgcgaggc cgccaaggcc cgaggcgtga agtttggccc ccgccctacc ctcaccccgg 7800

cacagatcgc gcacgcccgc gagctgatcg accaggaagg ccgcaccgtg aaagaggcgg 7860

ctgcactgct tggcgtgcat cgctcgaccc tgtaccgcgc acttgagcgc agcgaggaag 7920

tgacgcccac cgaggccagg cggcgcggtg ccttccgtga ggacgcattg accgaggccg 7980

acgccctggc ggccgccgag aatgaacgcc aagaggaaca agcatgaaac cgcaccagga 8040

cggccaggac gaaccgtttt tcattaccga agagatcgag gcggagatga tcgcggccgg 8100

gtacgtgttc gagccgcccg cgcacgtctc aaccgtgcgg ctgcatgaaa tcctggccgg 8160

tttgtctgat gccaagctgg cggcctggcc ggccagcttg gccgctgaag aaaccgagcg 8220

ccgccgtcta aaaaggtgat gtgtatttga gtaaaacagc ttgcgtcatg cggtcgctgc 8280

gtatatgatg cgatgagtaa ataaacaaat acgcaagggg aacgcatgaa ggttatcgct 8340

gtacttaacc agaaaggcgg gtcaggcaag acgaccatcg caacccatct agcccgcgcc 8400

ctgcaactcg ccggggccga tgttctgtta gtcgattccg atccccaggg cagtgcccgc 8460

gattgggcgg ccgtgcggga agatcaaccg ctaaccgttg tcggcatcga ccgcccgacg 8520

attgaccgcg acgtgaaggc catcggccgg cgcgacttcg tagtgatcga cggagcgccc 8580

caggcggcgg acttggctgt gtccgcgatc aaggcagccg acttcgtgct gattccggtg 8640

cagccaagcc cttacgacat atgggccacc gccgacctgg tggagctggt taagcagcgc 8700

attgaggtca cggatggaag gctacaagcg gcctttgtcg tgtcgcgggc gatcaaaggc 8760

acgcgcatcg gcggtgaggt tgccgaggcg ctggccgggt acgagctgcc cattcttgag 8820

tcccgtatca cgcagcgcgt gagctaccca ggcactgccg ccgccggcac aaccgttctt 8880

gaatcagaac ccgagggcga cgctgcccgc gaggtccagg cgctggccgc tgaaattaaa 8940

tcaaaactca tttgagttaa tgaggtaaag agaaaatgag caaaagcaca aacacgctaa 9000

-continued

gtgccggccg tccgagcgca cgcagcagca aggctgcaac gttggccagc ctggcagaca 9060

cgccagccat gaagcgggtc aactttcagt tgccggcgga ggatcacacc aagctgaaga 9120

tgtacgcggt acgccaaggc aagaccatta ccgagctgct atctgaatac atcgcgcagc 9180

taccagagta aatgagcaaa tgaataaatg agtagatgaa ttttagcggc taaaggaggc 9240

ggcatggaaa atcaagaaca accaggcacc gacgccgtgg aatgccccat gtgtggagga 9300

acgggcggtt ggccaggcgt aagcggctgg gttgtctgcc ggccctgcaa tggcactgga 9360

acccccaagc ccgaggaatc ggcgtgacgg tcgcaaacca tccggcccgg tacaaatcgg 9420

cgcggcgctg ggtgatgacc tggtggagaa gttgaaggcc gcgcaggccg cccagcggca 9480

acgcatcgag gcagaagcac gccccggtga atcgtggcaa gcggccgctg atcgaatccg 9540

caaagaatcc cggcaaccgc cggcagccgg tgcgccgtcg attaggaagc cgcccaaggg 9600

cgacgagcaa ccagattttt tcgttccgat gctctatgac gtgggcaccc gcgatagtcg 9660

cagcatcatg gacgtggccg ttttccgtct gtcgaagcgt gaccgacgag ctggcgaggt 9720

gatccgctac gagcttccag acgggcacgt agaggtttcc gcagggccgg ccggcatggc 9780

cagtgtgtgg gattacgacc tggtactgat ggcggtttcc catctaaccg aatccatgaa 9840

ccgataccgg gaagggaagg gagacaagcc cggccgcgtg ttccgtccac acgttgcgga 9900

cgtactcaag ttctgccggc gagccgatgg cggaaagcag aaagacgacc tggtagaaac 9960

ctgcattcgg ttaaacacca cgcacgttgc catgcagcgt acgaagaagg ccaagaacgg 10020

ccgcctggtg acggtatccg agggtgaagc cttgattagc cgctacaaga tcgtaaagag 10080

cgaaaccggg cggccggagt acatcgagat cgagctagct gattggatgt accgcgagat 10140

cacagaaggc aagaacccgg acgtgctgac ggttcacccc gattactttt tgatcgatcc 10200

cggcatcggc cgttttctct accgcctggc acgccgcgcc gcaggcaagg cagaagccag 10260

atggttgttc aagacgatct acgaacgcag tggcagcgcc ggagagttca agaagttctg 10320

tttcaccgtg cgcaagctga tcgggtcaaa tgacctgccg gagtacgatt tgaaggagga 10380

ggcggggcag gctggcccga tcctagtcat gcgctaccgc aacctgatcg agggcgaagc 10440

atccgccggt tcctaatgta cggagcagat gctagggcaa attgccctag caggggaaaa 10500

aggtcgaaaa ggtctctttc ctgtggatag cacgtacatt gggaacccaa agccgtacat 10560

tgggaaccgg aacccgtaca ttgggaaccc aaagccgtac attgggaacc ggtcacacat 10620

gtaagtgact gatataaaag agaaaaaagg cgatttttcc gcctaaaact ctttaaaact 10680

tattaaaact cttaaaaccc gcctggcctg tgcataactg tctggccagc gcacagccga 10740

agagctgcaa aaagcgccta cccttcggtc gctgcgctcc ctacgccccg ccgcttcgcg 10800

tcggcctatc gcggccgctg gccgctcaaa aatggctggc ctacggccag gcaatctacc 10860

agggcgcgga caagccgcgc cgtcgccact cgaccgccgg cgcccacatc aaggcaccct 10920

gcctcgcgcg tttcggtgat gacggtgaaa acctctgaca catgcagctc ccggagacgg 10980

tcacagcttg tctgtaagcg gatgccggga gcagacaagc ccgtcagggc gcgtcagcgg 11040

gtgttggcgg gtgtcggggc gcagccatga cccagtcacg tagcgatagc ggagtgtata 11100

ctggcttaac tatgcggcat cagagcagat tgtactgaga gtgcaccata tgcggtgtga 11160

aataccgcac agatgcgtaa ggagaaaata ccgcatcagg cgctcttccg cttcctcgct 11220

cactgactcg ctgcgctcgg tcgttcggct gcggcgagcg gtatcagctc actcaaaggc 11280

-continued

ggtaatacgg ttatccacag aatcagggga taacgcagga aagaacatgt gagcaaaagg 11340

ccagcaaaag gccaggaacc gtaaaaaggc cgcgttgctg gcgtttttcc ataggctccg 11400

cccccctgac gagcatcaca aaaatcgacg ctcaagtcag aggtggcgaa acccgacagg 11460

actataaaga taccaggcgt ttccccctgg aagctccctc gtgcgctctc ctgttccgac 11520

cctgccgctt accggatacc tgtccgcctt tctcccttcg ggaagcgtgg cgctttctca 11580

tagctcacgc tgtaggtatc tcagttcggt gtaggtcgtt cgctccaagc tgggctgtgt 11640

gcacgaaccc cccgttcagc ccgaccgctg cgccttatcc ggtaactatc gtcttgagtc 11700

caacccggta agacacgact tatcgccact ggcagcagcc actggtaaca ggattagcag 11760

agcgaggtat gtaggcggtg ctacagagtt cttgaagtgg tggcctaact acggctacac 11820

tagaaggaca gtatttggta tctgcgctct gctgaagcca gttaccttcg gaaaaagagt 11880

tggtagctct tgatccggca aacaaaccac cgctggtagc ggtggttttt ttgtttgcaa 11940

gcagcagatt acgcgcagaa aaaaaggatc tcaagaagat cctttgatct tttctacggg 12000

gtctgacgct cagtggaacg aaaactcacg ttaagggatt ttggtcatgc attctaggta 12060

ctaaaacaat tcatccagta aaatataata ttttattttc tcccaatcag gcttgatccc 12120

cagtaagtca aaaaatagct cgacatactg ttcttccccg atatcctccc tgatcgaccg 12180

gacgcagaag gcaatgtcat accacttgtc cgccctgccg cttctcccaa gatcaataaa 12240

gccacttact ttgccatctt tcacaaagat gttgctgtct cccaggtcgc cgtgggaaaa 12300

gacaagttcc tcttcgggct tttccgtctt taaaaaatca tacagctcgc gcggatcttt 12360

aaatggagtg tcttcttccc agttttcgca atccacatcg gccagatcgt tattcagtaa 12420

gtaatccaat tcggctaagc ggctgtctaa gctattcgta tagggacaat ccgatatgtc 12480

gatggagtga aagagcctga tgcactccgc atacagctcg ataatctttt cagggctttg 12540

ttcatcttca tactcttccg agcaaaggac gccatcggcc tcactcatga gcagattgct 12600

ccagccatca tgccgttcaa agtgcaggac ctttggaaca ggcagctttc cttccagcca 12660

tagcatcatg tccttttccc gttccacatc ataggtggtc cctttatacc ggctgtccgt 12720

catttttaaa tataggtttt cattttctcc caccagctta tataccttag caggagacat 12780

tccttccgta tcttttacgc agcggtattt ttcgatcagt tttttcaatt ccggtgatat 12840

tctcatttta gccatttatt atttccttcc tcttttctac agtatttaaa gataccccaa 12900

gaagctaatt ataacaagac gaactccaat tcactgttcc ttgcattcta aaaccttaaa 12960

taccagaaaa cagctttttc aaagttgttt tcaaagttgg cgtataacat agtatcgacg 13020

gagccgattt tgaaaccgcg gtgatcacag gcagcaacgc tctgtcatcg ttacaatcaa 13080

catgctaccc tccgcgagat catccgtgtt tcaaacccgg cagcttagtt gccgttcttc 13140

cgaatagcat cggtaacatg agcaaagtct gccgccttac aacggctctc ccgctgacgc 13200

cgtcccggac tgatgggctg cctgtatcga gtggtgattt tgtgccgagc tgccggtcgg 13260

ggagctgttg gctggctggt ggcaggatat attgtggtgt aaacaaattg acgcttagac 13320

aacttaataa cacattgcgg acgtttttaa tgtactgaat taacgccgaa ttaattcggg 13380

ggatctggat tttagtactg gattttggtt ttaggaatta gaaattttat tgatagaagt 13440

attttacaaa tacaaataca tactaagggt ttcttatatg ctcaacacat gagcgaaacc 13500

ctataggaac cctaattccc ttatctggga actactcaca cattattatg gagaaactcg 13560

-continued

agcttgtcga tcgacagatc cggtcggcat ctactctatt tctttgccct cggacgagtg 13620

ctggggcgtc ggtttccact atcggcgagt acttctacac agccatcggt ccagacggcc 13680

gcgcttctgc gggcgatttg tgtacgcccg acagtcccgg ctccggatcg gacgattgcg 13740

tcgcatcgac cctgcgccca agctgcatca tcgaaattgc cgtcaaccaa gctctgatag 13800

agttggtcaa gaccaatgcg gagcatatac gcccggagtc gtggcgatcc tgcaagctcc 13860

ggatgcctcc gctcgaagta gcgcgtctgc tgctccatac aagccaacca cggcctccag 13920

aagaagatgt tggcgacctc gtattgggaa tccccgaaca tcgcctcgct ccagtcaatg 13980

accgctgtta tgcggccatt gtccgtcagg acattgttgg agccgaaatc cgcgtgcacg 14040

aggtgccgga cttcggggca gtcctcggcc caaagcatca gctcatcgag agcctgcgcg 14100

acggacgcac tgacggtgtc gtccatcaca gtttgccagt gatacacatg gggatcagca 14160

atcgcgcata tgaaatcacg ccatgtagtg tattgaccga ttccttgcgg tccgaatggg 14220

ccgaacccgc tcgtctggct aagatcggcc gcagcgatcg catccatagc ctccgcgacc 14280

ggttgtagaa cagcgggcag ttcggtttca ggcaggtctt gcaacgtgac accctgtgca 14340

cggcgggaga tgcaataggt caggctctcg ctaaactccc caatgtcaag cacttccgga 14400

atcgggagcg cggccgatgc aaagtgccga taaacataac gatctttgta gaaaccatcg 14460

gcgcagctat ttacccgcag gacatatcca cgccctccta catcgaagct gaaagcacga 14520

gattcttcgc cctccgagag ctgcatcagg tcggagacgc tgtcgaactt ttcgatcaga 14580

aacttctcga cagacgtcgc ggtgagttca ggctttttca tatctcattg cccccggga 14640

tctgcgaaag ctcgagagag atagatttgt agagagagac tggtgatttc agcgtgtcct 14700

ctccaaatga aatgaacttc cttatataga ggaaggtctt gcgaaggata gtgggattgt 14760

gcgtcatccc ttacgtcagt ggagatatca catcaatcca cttgctttga agacgtggtt 14820

ggaacgtctt ctttttccac gatgctcctc gtgggtgggg gtccatcttt gggaccactg 14880

tcggcagagg catcttgaac gatagccttt cctttatcgc aatgatggca tttgtaggtg 14940

ccaccttcct tttctactgt ccttttgatg aagtgacaga tagctgggca atggaatccg 15000

aggaggtttc ccgatattac cctttgttga aaagtctcaa tagccctttg gtcttctgag 15060

actgtatctt tgatattctt ggagtagacg agagtgtcgt gctccaccat gttatcacat 15120

caatccactt gctttgaaga cgtggttgga acgtcttctt tttccacgat gctcctcgtg 15180

ggtgggggtc catctttggg accactgtcg gcagaggcat cttgaacgat agcctttcct 15240

ttatcgcaat gatggcattt gtaggtgcca ccttcctttt ctactgtcct tttgatgaag 15300

tgacagatag ctgggcaatg gaatccgagg aggtttcccg atattaccct ttgttgaaaa 15360

gtctcaatag ccctttggtc ttctgagact gtatctttga tattcttgga gtagacgaga 15420

gtgtcgtgct ccaccatgtt ggcaagctgc tctagccaat acgcaaaccg cctctccccg 15480

cgcgttggcc gattcattaa tgcagctggc acgacaggtt tcccgactgg aaagcgggca 15540

gtgagcgcaa cgcaattaat gtgagttagc tcactcatta ggcaccccag gctttacact 15600

ttatgcttcc ggctcgtatg ttgtgtggaa ttgtgagcgg ataacaattt cacacaggaa 15660

acagctatga ccatgattac g 15681

<210> SEQ ID NO 156
<211> LENGTH: 15681
<212> TYPE: DNA

-continued

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: vector
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5964)..(5984)
<223> OTHER INFORMATION: /note="target sequence"
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6617)..(6637)
<223> OTHER INFORMATION: /note="target sequence"

<400> SEQUENCE: 156

aattcccgat ctagtaacat agatgacacc gcgcgcgata atttatccta gtttgcgcgc 60

tatattttgt tttctatcgc gtattaaatg tataattgcg ggactctaat cataaaaacc 120

catctcataa ataacgtcat gcattacatg ttaattatta catgcttaac gtaattcaac 180

agaaattata tgataatcat cgcaagaccg gcaacaggat tcaatcttaa gaaactttat 240

tgccaaatgt ttgaacgatc ggggaaattc gagctctatc gatcaatcag gatccttact 300

ttttcttttt tgcctggccg gcctttttcg tggccgccgg ccttttgtcg cctcccagct 360

gagacaggtc gatccgtgtc tcgtacaggc cggtgatgct ctggtggatc agggtggcgt 420

ccagcacctc tttggtgctg gtgtacctct tccggtcgat ggtggtgtca aagtacttga 480

aggcggcagg ggctcccaga ttggtcaggg taaacaggtg gatgatattc tcggcctgct 540

ctctgatggg cttatcccgg tgcttgttgt aggcggacag cactttgtcc agattagcgt 600

cggccaggat cactctcttg gagaactcgc tgatctgctc gatgatctcg tccaggtagt 660

gcttgtgctg ttccacaaac agctgtttct gctcattatc ctcgggggag cccttcagct 720

tctcatagtg gctggccagg tacaggaagt tcacatattt ggagggcagg gccagttcgt 780

ttcccttctg cagttcgccg gcagaggcca gcattctctt ccggccgttt tccagctcga 840

acagggagta cttaggcagc ttgatgatca ggtccttttt cacttctttg tagcccttgg 900

cttccagaaa gtcgatggga ttcttctcga agctgcttct ttccatgatg gtgatcccca 960

gcagctcttt cacactcttc agtttcttgg acttgccctt ttccactttg gccaccacca 1020

gcacagaata ggccacggtg gggctgtcga agccgccgta cttcttaggg tcccagtcct 1080

tctttctggc gatcagctta tcgctgttcc tcttgggcag gatagactct ttgctgaagc 1140

cgcctgtctg cacctcggtc tttttcacga tattcacttg gggcatgctc agcactttcc 1200

gcacggtggc aaaatcccgg cccttatccc acacgatctc cccggtttcg ccgtttgtct 1260

cgatcagagg ccgcttccgg atctcgccgt tggccagggt aatctcggtc ttgaaaaagt 1320

tcatgatgtt gctgtagaag aagtacttgg cggtagcctt gccgatttcc tgctcgctct 1380

tggcgatcat cttccgcacg tcgtacacct tgtagtcgcc gtacacgaac tcgctttcca 1440

gcttagggta ctttttgatc agggcggttc ccacgacggc gttcaggtag gcgtcgtggg 1500

cgtggtggta gttgttgatc tcgcgcactt tgtaaaactg gaaatccttc cggaaatcgg 1560

acaccagctt ggacttcagg gtgatcactt tcacttcccg gatcagcttg tcattctcgt 1620

cgtacttagt gttcatccgg gagtccagga tctgtgccac gtgctttgtg atctgccggg 1680

tttccaccag ctgtctcttg atgaagccgg ccttatccag ttcgctcagg ccgcctctct 1740

cggccttggt cagattgtcg aactttctct gggtaatcag cttggcgttc agcagctgcc 1800

gccagtagtt cttcatcttc ttcacgacct cttcggaggg cacgttgtcg ctcttgcccc 1860

-continued

ggttcttgtc gcttctggtc agcaccttgt tgtcgatgga gtcgtccttc agaaagctct 1920

gaggcacgat atggtccaca tcgtagtcgg acagccggtt gatgtccagt tcctggtcca 1980

cgtacatatc ccgcccattc tgcaggtagt acaggtacag cttctcgttc tgcagctggg 2040

tgttttccac ggggtgttct ttcaggatct ggctgcccag ctctttgatg ccctcttcga 2100

tccgcttcat tctctcgcgg ctgttcttct gtcccttctg ggtggtctgg ttctctctgg 2160

ccatttcgat cacgatgttc tcgggcttgt gccggcccat cactttcacg agctcgtcca 2220

ccaccttcac tgtctgcagg atgcccttct taatggcggg gctgccggcc agattggcaa 2280

tgtgctcgtg caggctatcg ccctggccgg acacctgggc tttctggatg tcctctttaa 2340

aggtcaggct gtcgtcgtgg atcagctgca tgaagtttct gttggcgaag ccgtcggact 2400

tcaggaaatc caggattgtc ttgccggact gcttgtcccg gatgccgttg atcagcttcc 2460

ggctcagcct gccccagccg gtgtatctcc gccgcttcag ctgcttcatc actttgtcgt 2520

cgaacaggtg ggcataggtt ttcagccgtt cctcgatcat ctctctgtcc tcaaacagtg 2580

tcagggtcag cacgatatct tccagaatgt cctcgttttc ctcattgtcc aggaagtcct 2640

tgtccttgat aattttcagc agatcgtggt atgtgcccag ggaggcgttg aaccgatctt 2700

ccacgccgga gatttccacg gagtcgaagc actcgatttt cttgaagtag tcctctttca 2760

gctgcttcac ggtcactttc cggttggtct tgaacagcag gtccacgatg gccttttct 2820

gctcgccgct caggaaggcg ggctttctca ttccctcggt cacgtatttc actttggtca 2880

gctcgttata cacggtgaag tactcgtaca gcaggctgtg cttgggcagc accttctcgt 2940

tgggcaggtt cttatcgaag ttggtcatcc gctcgatgaa gctctgggcg gaagcgccct 3000

tgtccaccac ttcctcgaag ttccaggggg tgatggtttc ctcgctcttt ctggtcatcc 3060

aggcgaatct gctgtttccc ctggccagag ggcccacgta gtaggggatg cggaaggtca 3120

ggatcttctc gatcttttcc cggttgtcct tcaggaatgg gtaaaaatct tcctgccgcc 3180

gcagaatggc gtgcagctct cccaggtgga tctggtgggg gatgctgccg ttgtcgaagg 3240

tccgctgctt ccgcagcagg tcctctctgt tcagcttcac gagcagttcc tcggtgccgt 3300

ccatcttttc caggatgggc ttgatgaact tgtagaactc ttcctggctg gctccgccgt 3360

caatgtagcc ggcgtagccg ttcttgctct ggtcgaagaa aatctctttg tacttctcag 3420

gcagctgctg ccgcacgaga gctttcagca gggtcaggtc ctggtggtgc tcgtcgtatc 3480

tcttgatcat agaggcgctc agggggcct tggtgatctc ggtgttcact ctcaggatgt 3540

cgctcagcag gatggcgtcg gacaggttct tggcggccag aaacaggtcg gcgtactggt 3600

cgccgatctg ggccagcagg ttgtccaggt cgtcgtcgta ggtgtccttg ctcagctgca 3660

gtttggcatc ctcggccagg tcgaagttgc tcttgaagtt gggggtcagg cccaggctca 3720

gggcaatcag gtttccgaac aggccattct tcttctcgcc gggcagctgg gcgatcagat 3780

tttccagccg tctgctcttg ctcagtctgg cagacaggat ggccttggcg tccacgccgc 3840

tggcgttgat ggggttttcc tcgaacagct ggttgtaggt ctgcaccagc tggatgaaca 3900

gcttgtccac gtcgctgttg tcggggttca ggtcgccctc gatcaggaag tggccccgga 3960

acttgatcat gtgggccagg gccagataga tcagccgcag gtcggccttg tcggtgctgt 4020

ccaccagttt ctttctcagg tggtagatgg tggggtactt ctcgtggtag gccacctcgt 4080

ccacgatgtt gccgaagatg gggtgccgct cgtgcttctt atcctcttcc accaggaagg 4140

-continued

actcttccag tctgtggaag aagctgtcgt ccaccttggc catctcgttg ctgaagatct 4200

cttgcagata gcagatccgg ttcttccgtc tggtgtatct tcttctggcg gttctcttca 4260

gccgggtggc ctcggctgtt tcgccgctgt cgaacagcag ggctccgatc aggttcttct 4320

tgatgctgtg ccggtcggtg ttgcccagca ccttgaattt cttgctgggc accttgtact 4380

cgtcggtgat cacggcccag cccacagagt tggtgccgat gtccaggccg atgctgtact 4440

tcttgtcggc tgctgggact ccgtggatac cgaccttccg cttcttcttt ggggccatct 4500

tatcgtcatc gtctttgtaa tcaatatcat gatccttgta gtctccgtcg tggtccttat 4560

agtccatctc gagtatcgtt cgtaaatggt gaaaattttc agaaaattgc ttttgcttta 4620

aaagaaatga tttaaattgc tgcaatagaa gtagaatgct tgattgcttg agattcgttt 4680

gttttgtata tgttgtgttg aggtcgaggt cctctccaaa tgaaatgaac ttccttatat 4740

agaggaaggg tcttgcgaag gatagtggga ttgtgcgtca tcccttacgt cagtggagat 4800

atcacatcaa tccacttgct ttgaagacgt ggttggaacg tcttcttttt ccacgatgct 4860

cctcgtgggt gggggtccat ctttgggacc actgtcggca gaggcatctt caacgatggc 4920

ctttccttta tcgcaatgat ggcatttgta ggagccacct tccttttcca ctatcttcac 4980

aataaagtga cagatagctg ggcaatggaa tccgaggagg tttccggata tcaccctttg 5040

ttgaaaagtc tcaattgccc tttggtcttc tgagactgta tctttgatat ttttggagta 5100

gacaagtgtg tcgtgctcca ccatgttatc acatcaatcc acttgctttg aagacgtggt 5160

tggaacgtct tctttttcca cgatgctcct cgtgggtggg ggtccatctt tgggaccact 5220

gtcggcagag gcatcttcaa cgatggcctt tcctttatcg caatgatggc atttgtagga 5280

gccaccttcc ttttccacta tcttcacaat aaagtgacag atagctgggc aatggaatcc 5340

gaggaggttt ccggatatta ccctttgttg aaaagtctca attgcccttt ggtcttctga 5400

gactgtatct ttgatatttt tggagtagac aagtgtgtcg tgctccacca tgttgacctg 5460

caggcatgcc tcggatccac tagtaacggc cgccagtgtg ctggaattgc ccttaagctt 5520

cgttgaacaa cggaaactcg acttgccttc cgcacaatac atcatttctt cttagctttt 5580

tttcttcttc ttcgttcata cagttttttt ttgtttatca gcttacattt tcttgaaccg 5640

tagctttcgt tttcttcttt ttaactttcc attcggagtt tttgtatctt gtttcatagt 5700

ttgtcccagg attagaatga ttaggcatcg aaccttcaag aatttgattg aataaaacat 5760

cttcattctt aagatatgaa gataatcttc aaaaggcccc tgggaatctg aaagaagaga 5820

agcaggccca tttatatggg aaagaacaat agtatttctt atataggccc atttaagttg 5880

aaaacaatct tcaaaagtcc cacatcgctt agataagaaa acgaagctga gtttatatac 5940

agctagagtc gaagtagtga ttgcggagac tcgtctacag ttgttttaga gctagaaata 6000

gcaagttaaa ataaggctag tccgttatca acttgaaaaa gtggcaccga gtcggtgctt 6060

tttttgtccc ttcgaagggc ctttctcaga tatccatcac actggcggcc gctcgaggtc 6120

gctcggatcc actagtaacg gccgccagtg tgctggaatt gcccttaagc ttcgttgaac 6180

aacggaaact cgacttgcct tccgcacaat acatcatttc ttcttagctt tttttcttct 6240

tcttcgttca tacagttttt ttttgtttat cagcttacat tttcttgaac cgtagctttc 6300

gttttcttct ttttaacttt ccattcggag tttttgtatc ttgtttcata gtttgtccca 6360

ggattagaat gattaggcat cgaaccttca agaatttgat tgaataaaac atcttcattc 6420

-continued

ttaagatatg aagataatct tcaaaaggcc cctgggaatc tgaaagaaga gaagcaggcc 6480

catttatatg ggaaagaaca atagtatttc ttatataggc ccatttaagt tgaaaacaat 6540

cttcaaaagt cccacatcgc ttagataaga aaacgaagct gagtttatat acagctagag 6600

tcgaagtagt gattatgtgt tacagcacgt cggggtttta gagctagaaa tagcaagtta 6660

aaataaggct agtccgttat caacttgaaa aagtggcacc gagtcggtgc ttttttttgtc 6720

ccttcgaagg gcctttctca gatatccatc acactggcgg ccgctcgagg tcgaagcttg 6780

gcactggccg tcgttttaca acgtcgtgac tgggaaaacc ctggcgttac ccaacttaat 6840

cgccttgcag cacatccccc tttcgccagc tggcgtaata gcgaagaggc ccgcaccgat 6900

cgcccttccc aacagttgcg cagcctgaat ggcgaatgct agagcagctt gagcttggat 6960

cagattgtcg tttcccgcct tcagtttaaa ctatcagtgt ttgacaggat atattggcgg 7020

gtaaacctaa gagaaaagag cgtttattag aataacggat atttaaaagg gcgtgaaaag 7080

gtttatccgt tcgtccattt gtatgtgcat gccaaccaca gggttcccct cgggatcaaa 7140

gtactttgat ccaacccctc cgctgctata gtgcagtcgg cttctgacgt tcagtgcagc 7200

cgtcttctga aaacgacatg tcgcacaagt cctaagttac gcgacaggct gccgccctgc 7260

ccttttcctg gcgttttctt gtcgcgtgtt ttagtcgcat aaagtagaat acttgcgact 7320

agaaccggag acattacgcc atgaacaaga gcgccgccgc tggcctgctg ggctatgccc 7380

gcgtcagcac cgacgaccag gacttgacca accaacgggc cgaactgcac gcggccggct 7440

gcaccaagct gttttccgag aagatcaccg gcaccaggcg cgaccgcccg gagctggcca 7500

ggatgcttga ccacctacgc cctggcgacg ttgtgacagt gaccaggcta gaccgcctgg 7560

cccgcagcac ccgcgaccta ctggacattg ccgagcgcat ccaggaggcc ggcgcgggcc 7620

tgcgtagcct ggcagagccg tgggccgaca ccaccacgcc ggccggccgc atggtgttga 7680

ccgtgttcgc cggcattgcc gagttcgagc gttccctaat catcgaccgc acccggagcg 7740

ggcgcgaggc cgccaaggcc cgaggcgtga agtttggccc ccgccctacc ctcaccccgg 7800

cacagatcgc gcacgcccgc gagctgatcg accaggaagg ccgcaccgtg aaagaggcgg 7860

ctgcactgct tggcgtgcat cgctcgaccc tgtaccgcgc acttgagcgc agcgaggaag 7920

tgacgcccac cgaggccagg cggcgcggtg ccttccgtga ggacgcattg accgaggccg 7980

acgccctggc ggccgccgag aatgaacgcc aagaggaaca agcatgaaac cgcaccagga 8040

cggccaggac gaaccgtttt tcattaccga agagatcgag gcggagatga tcgcggccgg 8100

gtacgtgttc gagccgcccg cgcacgtctc aaccgtgcgg ctgcatgaaa tcctggccgg 8160

tttgtctgat gccaagctgg cggcctggcc ggccagcttg gccgctgaag aaaccgagcg 8220

ccgccgtcta aaaaggtgat gtgtatttga gtaaaacagc ttgcgtcatg cggtcgctgc 8280

gtatatgatg cgatgagtaa ataaacaaat acgcaagggg aacgcatgaa ggttatcgct 8340

gtacttaacc agaaaggcgg gtcaggcaag acgaccatcg caacccatct agcccgcgcc 8400

ctgcaactcg ccggggccga tgttctgtta gtcgattccg atccccaggg cagtgcccgc 8460

gattgggcgg ccgtgcggga agatcaaccg ctaaccgttg tcggcatcga ccgcccgacg 8520

attgaccgcg acgtgaaggc catcggccgg cgcgacttcg tagtgatcga cggagcgccc 8580

caggcggcgg acttggctgt gtccgcgatc aaggcagccg acttcgtgct gattccggtg 8640

cagccaagcc cttacgacat atgggccacc gccgacctgg tggagctggt taagcagcgc 8700

-continued

attgaggtca cggatggaag gctacaagcg gcctttgtcg tgtcgcgggc gatcaaaggc 8760

acgcgcatcg gcggtgaggt tgccgaggcg ctggccgggt acgagctgcc cattcttgag 8820

tcccgtatca cgcagcgcgt gagctaccca ggcactgccg ccgccggcac aaccgttctt 8880

gaatcagaac ccgagggcga cgctgcccgc gaggtccagg cgctggccgc tgaaattaaa 8940

tcaaaactca tttgagttaa tgaggtaaag agaaaatgag caaaagcaca aacacgctaa 9000

gtgccggccg tccgagcgca cgcagcagca aggctgcaac gttggccagc ctggcagaca 9060

cgccagccat gaagcgggtc aactttcagt tgccggcgga ggatcacacc aagctgaaga 9120

tgtacgcggt acgccaaggc aagaccatta ccgagctgct atctgaatac atcgcgcagc 9180

taccagagta aatgagcaaa tgaataaatg agtagatgaa ttttagcggc taaaggaggc 9240

ggcatggaaa atcaagaaca accaggcacc gacgccgtgg aatgccccat gtgtggagga 9300

acgggcggtt ggccaggcgt aagcggctgg gttgtctgcc ggccctgcaa tggcactgga 9360

acccccaagc ccgaggaatc ggcgtgacgg tcgcaaacca tccggcccgg tacaaatcgg 9420

cgcggcgctg ggtgatgacc tggtggagaa gttgaaggcc gcgcaggccg cccagcggca 9480

acgcatcgag gcagaagcac gccccggtga atcgtggcaa gcggccgctg atcgaatccg 9540

caaagaatcc cggcaaccgc cggcagccgg tgcgccgtcg attaggaagc cgcccaaggg 9600

cgacgagcaa ccagattttt tcgttccgat gctctatgac gtgggcaccc gcgatagtcg 9660

cagcatcatg gacgtggccg ttttccgtct gtcgaagcgt gaccgacgag ctggcgaggt 9720

gatccgctac gagcttccag acgggcacgt agaggtttcc gcagggccgg ccggcatggc 9780

cagtgtgtgg gattacgacc tggtactgat ggcggtttcc catctaaccg aatccatgaa 9840

ccgataccgg gaagggaagg gagacaagcc cggccgcgtg ttccgtccac acgttgcgga 9900

cgtactcaag ttctgccggc gagccgatgg cggaaagcag aaagacgacc tggtagaaac 9960

ctgcattcgg ttaaacacca cgcacgttgc catgcagcgt acgaagaagg ccaagaacgg 10020

ccgcctggtg acggtatccg agggtgaagc cttgattagc cgctacaaga tcgtaaagag 10080

cgaaaccggg cggccggagt acatcgagat cgagctagct gattggatgt accgcgagat 10140

cacagaaggc aagaacccgg acgtgctgac ggttcacccc gattactttt tgatcgatcc 10200

cggcatcggc cgttttctct accgcctggc acgccgcgcc gcaggcaagg cagaagccag 10260

atggttgttc aagacgatct acgaacgcag tggcagcgcc ggagagttca agaagttctg 10320

tttcaccgtg cgcaagctga tcgggtcaaa tgacctgccg gagtacgatt tgaaggagga 10380

ggcggggcag gctggcccga tcctagtcat gcgctaccgc aacctgatcg agggcgaagc 10440

atccgccggt tcctaatgta cggagcagat gctagggcaa attgccctag caggggaaaa 10500

aggtcgaaaa ggtctctttc ctgtggatag cacgtacatt gggaacccaa agccgtacat 10560

tgggaaccgg aacccgtaca ttgggaaccc aaagccgtac attgggaacc ggtcacacat 10620

gtaagtgact gatataaaag agaaaaaagg cgatttttcc gcctaaaact ctttaaaact 10680

tattaaaact cttaaaaccc gcctggcctg tgcataactg tctggccagc gcacagccga 10740

agagctgcaa aaagcgccta cccttcggtc gctgcgctcc ctacgccccg ccgcttcgcg 10800

tcggcctatc gcggccgctg gccgctcaaa aatggctggc ctacggccag gcaatctacc 10860

agggcgcgga caagccgcgc cgtcgccact cgaccgccgg cgcccacatc aaggcaccct 10920

gcctcgcgcg tttcggtgat gacggtgaaa acctctgaca catgcagctc ccggagacgg 10980

-continued

```
tcacagcttg tctgtaagcg gatgccggga gcagacaagc ccgtcagggc gcgtcagcgg  11040

gtgttggcgg gtgtcggggc gcagccatga cccagtcacg tagcgatagc ggagtgtata  11100

ctggcttaac tatgcggcat cagagcagat tgtactgaga gtgcaccata tgcggtgtga  11160

aataccgcac agatgcgtaa ggagaaaata ccgcatcagg cgctcttccg cttcctcgct  11220

cactgactcg ctgcgctcgg tcgttcggct gcggcgagcg gtatcagctc actcaaaggc  11280

ggtaatacgg ttatccacag aatcagggga taacgcagga aagaacatgt gagcaaaagg  11340

ccagcaaaag gccaggaacc gtaaaaaggc cgcgttgctg gcgtttttcc ataggctccg  11400

cccccctgac gagcatcaca aaaatcgacg ctcaagtcag aggtggcgaa acccgacagg  11460

actataaaga taccaggcgt ttccccctgg aagctccctc gtgcgctctc ctgttccgac  11520

cctgccgctt accggatacc tgtccgcctt tctcccttcg ggaagcgtgg cgctttctca  11580

tagctcacgc tgtaggtatc tcagttcggt gtaggtcgtt cgctccaagc tgggctgtgt  11640

gcacgaaccc cccgttcagc ccgaccgctg cgccttatcc ggtaactatc gtcttgagtc  11700

caacccggta agacacgact tatcgccact ggcagcagcc actggtaaca ggattagcag  11760

agcgaggtat gtaggcggtg ctacagagtt cttgaagtgg tggcctaact acggctacac  11820

tagaaggaca gtatttggta tctgcgctct gctgaagcca gttaccttcg gaaaaagagt  11880

tggtagctct tgatccggca aacaaaccac cgctggtagc ggtggttttt ttgtttgcaa  11940

gcagcagatt acgcgcagaa aaaaaggatc tcaagaagat cctttgatct tttctacggg  12000

gtctgacgct cagtggaacg aaaactcacg ttaagggatt ttggtcatgc attctaggta  12060

ctaaaacaat tcatccagta aaatataata ttttattttc tcccaatcag gcttgatccc  12120

cagtaagtca aaaaatagct cgacatactg ttcttccccg atatcctccc tgatcgaccg  12180

gacgcagaag gcaatgtcat accacttgtc cgccctgccg cttctcccaa gatcaataaa  12240

gccacttact ttgccatctt tcacaaagat gttgctgtct cccaggtcgc cgtgggaaaa  12300

gacaagttcc tcttcgggct tttccgtctt taaaaaatca tacagctcgc gcggatcttt  12360

aaatggagtg tcttcttccc agttttcgca atccacatcg gccagatcgt tattcagtaa  12420

gtaatccaat tcggctaagc ggctgtctaa gctattcgta tagggacaat ccgatatgtc  12480

gatggagtga aagagcctga tgcactccgc atacagctcg ataatctttt cagggctttg  12540

ttcatcttca tactcttccg agcaaaggac gccatcggcc tcactcatga gcagattgct  12600

ccagccatca tgccgttcaa agtgcaggac ctttggaaca ggcagctttc cttccagcca  12660

tagcatcatg tccttttccc gttccacatc ataggtggtc cctttatacc ggctgtccgt  12720

catttttaaa tataggtttt cattttctcc caccagctta tataccttag caggagacat  12780

tccttccgta tcttttacgc agcggtattt ttcgatcagt tttttcaatt ccggtgatat  12840

tctcatttta gccatttatt atttccttcc tcttttctac agtatttaaa gataccccaa  12900

gaagctaatt ataacaagac gaactccaat tcactgttcc ttgcattcta aaaccttaaa  12960

taccagaaaa cagctttttc aaagttgttt tcaaagttgg cgtataacat agtatcgacg  13020

gagccgattt tgaaaccgcg gtgatcacag gcagcaacgc tctgtcatcg ttacaatcaa  13080

catgctaccc tccgcgagat catccgtgtt tcaaacccgg cagcttagtt gccgttcttc  13140

cgaatagcat cggtaacatg agcaaagtct gccgccttac aacggctctc ccgctgacgc  13200

cgtcccggac tgatgggctg cctgtatcga gtggtgattt tgtgccgagc tgccggtcgg  13260
```

-continued

ggagctgttg gctggctggt ggcaggatat attgtggtgt aaacaaattg acgcttagac 13320

aacttaataa cacattgcgg acgtttttaa tgtactgaat taacgccgaa ttaattcggg 13380

ggatctggat tttagtactg gattttggtt ttaggaatta gaaattttat tgatagaagt 13440

attttacaaa tacaaataca tactaagggt ttcttatatg ctcaacacat gagcgaaacc 13500

ctataggaac cctaattccc ttatctggga actactcaca cattattatg gagaaactcg 13560

agcttgtcga tcgacagatc cggtcggcat ctactctatt tctttgccct cggacgagtg 13620

ctggggcgtc ggtttccact atcggcgagt acttctacac agccatcggt ccagacggcc 13680

gcgcttctgc gggcgatttg tgtacgcccg acagtcccgg ctccggatcg gacgattgcg 13740

tcgcatcgac cctgcgccca agctgcatca tcgaaattgc cgtcaaccaa gctctgatag 13800

agttggtcaa gaccaatgcg gagcatatac gcccggagtc gtggcgatcc tgcaagctcc 13860

ggatgcctcc gctcgaagta gcgcgtctgc tgctccatac aagccaacca cggcctccag 13920

aagaagatgt tggcgacctc gtattgggaa tccccgaaca tcgcctcgct ccagtcaatg 13980

accgctgtta tgcggccatt gtccgtcagg acattgttgg agccgaaatc cgcgtgcacg 14040

aggtgccgga cttcggggca gtcctcggcc caaagcatca gctcatcgag agcctgcgcg 14100

acggacgcac tgacggtgtc gtccatcaca gtttgccagt gatacacatg gggatcagca 14160

atcgcgcata tgaaatcacg ccatgtagtg tattgaccga ttccttgcgg tccgaatggg 14220

ccgaacccgc tcgtctggct aagatcggcc gcagcgatcg catccatagc ctccgcgacc 14280

ggttgtagaa cagcgggcag ttcggtttca ggcaggtctt gcaacgtgac accctgtgca 14340

cggcgggaga tgcaataggt caggctctcg ctaaactccc caatgtcaag cacttccgga 14400

atcgggagcg cggccgatgc aaagtgccga taaacataac gatctttgta gaaaccatcg 14460

gcgcagctat ttacccgcag gacatatcca cgccctccta catcgaagct gaaagcacga 14520

gattcttcgc cctccgagag ctgcatcagg tcggagacgc tgtcgaactt ttcgatcaga 14580

aacttctcga cagacgtcgc ggtgagttca ggctttttca tatctcattg cccccggga 14640

tctgcgaaag ctcgagagag atagatttgt agagagagac tggtgatttc agcgtgtcct 14700

ctccaaatga aatgaacttc cttatataga ggaaggtctt gcgaaggata gtgggattgt 14760

gcgtcatccc ttacgtcagt ggagatatca catcaatcca cttgctttga agacgtggtt 14820

ggaacgtctt ctttttccac gatgctcctc gtgggtgggg gtccatcttt gggaccactg 14880

tcggcagagg catcttgaac gatagccttt cctttatcgc aatgatggca tttgtaggtg 14940

ccaccttcct tttctactgt ccttttgatg aagtgacaga tagctgggca atggaatccg 15000

aggaggtttc ccgatattac cctttgttga aaagtctcaa tagccctttg gtcttctgag 15060

actgtatctt tgatattctt ggagtagacg agagtgtcgt gctccaccat gttatcacat 15120

caatccactt gctttgaaga cgtggttgga acgtcttctt tttccacgat gctcctcgtg 15180

ggtgggggtc catctttggg accactgtcg gcagaggcat cttgaacgat agcctttcct 15240

ttatcgcaat gatggcattt gtaggtgcca ccttcctttt ctactgtcct tttgatgaag 15300

tgacagatag ctgggcaatg gaatccgagg aggtttcccg atattaccct ttgttgaaaa 15360

gtctcaatag ccctttggtc ttctgagact gtatctttga tattcttgga gtagacgaga 15420

gtgtcgtgct ccaccatgtt ggcaagctgc tctagccaat acgcaaaccg cctctccccg 15480

cgcgttggcc gattcattaa tgcagctggc acgacaggtt tcccgactgg aaagcgggca 15540

-continued

gtgagcgcaa cgcaattaat gtgagttagc tcactcatta ggcaccccag gctttacact 15600

ttatgcttcc ggctcgtatg ttgtgtggaa ttgtgagcgg ataacaattt cacacaggaa 15660

acagctatga ccatgattac g 15681

<210> SEQ ID NO 157
<211> LENGTH: 15681
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: vector
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5964)..(5984)
<223> OTHER INFORMATION: /note="target sequence"
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6617)..(6637)
<223> OTHER INFORMATION: /note="target sequence"

<400> SEQUENCE: 157

aattcccgat ctagtaacat agatgacacc gcgcgcgata atttatccta gtttgcgcgc 60

tatattttgt tttctatcgc gtattaaatg tataattgcg ggactctaat cataaaaacc 120

catctcataa ataacgtcat gcattacatg ttaattatta catgcttaac gtaattcaac 180

agaaattata tgataatcat cgcaagaccg gcaacaggat tcaatcttaa gaaactttat 240

tgccaaatgt ttgaacgatc ggggaaattc gagctctatc gatcaatcag gatccttact 300

ttttcttttt tgcctggccg gccttttttcg tggccgccgg ccttttgtcg cctcccagct 360

gagacaggtc gatccgtgtc tcgtacaggc cggtgatgct ctggtggatc agggtggcgt 420

ccagcacctc tttggtgctg gtgtacctct tccggtcgat ggtggtgtca aagtacttga 480

aggcggcagg ggctcccaga ttggtcaggg taaacaggtg gatgatattc tcggcctgct 540

ctctgatggg cttatcccgg tgcttgttgt aggcggacag cactttgtcc agattagcgt 600

cggccaggat cactctcttg gagaactcgc tgatctgctc gatgatctcg tccaggtagt 660

gcttgtgctg ttccacaaac agctgtttct gctcattatc ctcgggggag cccttcagct 720

tctcatagtg gctggccagg tacaggaagt tcacatattt ggagggcagg gccagttcgt 780

ttcccttctg cagttcgccg gcagaggcca gcattctctt ccggccgttt tccagctcga 840

acagggagta cttaggcagc ttgatgatca ggtccttttt cacttctttg tagcccttgg 900

cttccagaaa gtcgatggga ttcttctcga agctgcttct ttccatgatg gtgatcccca 960

gcagctcttt cacactcttc agtttcttgg acttgccctt ttccactttg gccaccacca 1020

gcacagaata ggccacggtg ggctgtcga agccgccgta cttcttaggg tcccagtcct 1080

tctttctggc gatcagctta tcgctgttcc tcttgggcag gatagactct ttgctgaagc 1140

cgcctgtctg cacctcggtc tttttcacga tattcacttg ggcatgctc agcactttcc 1200

gcacggtggc aaaatcccgg cccttatccc acacgatctc cccggtttcg ccgtttgtct 1260

cgatcagagg ccgcttccgg atctcgccgt tggccagggt aatctcggtc ttgaaaaagt 1320

tcatgatgtt gctgtagaag aagtacttgg cggtagcctt gccgatttcc tgctcgctct 1380

tggcgatcat cttccgcacg tcgtacacct tgtagtcgcc gtacacgaac tcgctttcca 1440

gcttagggta ctttttgatc agggcggttc ccacgacggc gttcaggtag gcgtcgtggg 1500

cgtggtggta gttgttgatc tcgcgcactt tgtaaaactg gaaatccttc cggaaatcgg 1560

-continued

acaccagctt ggacttcagg gtgatcactt tcacttcccg gatcagcttg tcattctcgt 1620

cgtacttagt gttcatccgg gagtccagga tctgtgccac gtgctttgtg atctgccggg 1680

tttccaccag ctgtctcttg atgaagccgg ccttatccag ttcgctcagg ccgcctctct 1740

cggccttggt cagattgtcg aactttctct gggtaatcag cttggcgttc agcagctgcc 1800

gccagtagtt cttcatcttc ttcacgacct cttcggaggg cacgttgtcg ctcttgcccc 1860

ggttcttgtc gcttctggtc agcaccttgt tgtcgatgga gtcgtccttc agaaagctct 1920

gaggcacgat atggtccaca tcgtagtcgg acagccggtt gatgtccagt tcctggtcca 1980

cgtacatatc ccgcccattc tgcaggtagt acaggtacag cttctcgttc tgcagctggg 2040

tgttttccac ggggtgttct ttcaggatct ggctgcccag ctctttgatg ccctcttcga 2100

tccgcttcat tctctcgcgg ctgttcttct gtcccttctg ggtggtctgg ttctctctgg 2160

ccatttcgat cacgatgttc tcgggcttgt gccggcccat cactttcacg agctcgtcca 2220

ccaccttcac tgtctgcagg atgcccttct taatggcggg gctgccggcc agattggcaa 2280

tgtgctcgtg caggctatcg ccctggccgg acacctgggc tttctggatg tcctctttaa 2340

aggtcaggct gtcgtcgtgg atcagctgca tgaagtttct gttggcgaag ccgtcggact 2400

tcaggaaatc caggattgtc ttgccggact gcttgtcccg gatgccgttg atcagcttcc 2460

ggctcagcct gccccagccg gtgtatctcc gccgcttcag ctgcttcatc actttgtcgt 2520

cgaacaggtg ggcataggtt ttcagccgtt cctcgatcat ctctctgtcc tcaaacagtg 2580

tcagggtcag cacgatatct tccagaatgt cctcgttttc ctcattgtcc aggaagtcct 2640

tgtccttgat aattttcagc agatcgtggt atgtgcccag ggaggcgttg aaccgatctt 2700

ccacgccgga gatttccacg gagtcgaagc actcgatttt cttgaagtag tcctctttca 2760

gctgcttcac ggtcactttc cggttggtct tgaacagcag gtccacgatg gccttttttct 2820

gctcgccgct caggaaggcg ggctttctca ttccctcggt cacgtatttc actttggtca 2880

gctcgttata cacggtgaag tactcgtaca gcaggctgtg cttgggcagc accttctcgt 2940

tgggcaggtt cttatcgaag ttggtcatcc gctcgatgaa gctctgggcg gaagcgccct 3000

tgtccaccac ttcctcgaag ttccaggggg tgatggtttc ctcgctcttt ctggtcatcc 3060

aggcgaatct gctgtttccc ctggccagag ggcccacgta gtaggggatg cggaaggtca 3120

ggatcttctc gatcttttcc cggttgtcct tcaggaatgg gtaaaaatct tcctgccgcc 3180

gcagaatggc gtgcagctct cccaggtgga tctggtgggg gatgctgccg ttgtcgaagg 3240

tccgctgctt ccgcagcagg tcctctctgt tcagcttcac gagcagttcc tcggtgccgt 3300

ccatcttttc caggatgggc ttgatgaact tgtagaactc ttcctggctg gctccgccgt 3360

caatgtagcc ggcgtagccg ttcttgctct ggtcgaagaa aatctctttg tacttctcag 3420

gcagctgctg ccgcacgaga gctttcagca gggtcaggtc ctggtggtgc tcgtcgtatc 3480

tcttgatcat agaggcgctc agggggggcct tggtgatctc ggtgttcact ctcaggatgt 3540

cgctcagcag gatggcgtcg gacaggttct tggcggccag aaacaggtcg gcgtactggt 3600

cgccgatctg ggccagcagg ttgtccaggt cgtcgtcgta ggtgtccttg ctcagctgca 3660

gtttggcatc ctcggccagg tcgaagttgc tcttgaagtt gggggtcagg cccaggctca 3720

gggcaatcag gtttccgaac aggccattct tcttctcgcc gggcagctgg gcgatcagat 3780

tttccagccg tctgctcttg ctcagtctgg cagacaggat ggccttggcg tccacgccgc 3840

-continued

tggcgttgat ggggttttcc tcgaacagct ggttgtaggt ctgcaccagc tggatgaaca 3900

gcttgtccac gtcgctgttg tcggggttca ggtcgccctc gatcaggaag tggccccgga 3960

acttgatcat gtgggccagg gccagataga tcagccgcag gtcggccttg tcggtgctgt 4020

ccaccagttt ctttctcagg tggtagatgg tggggtactt ctcgtggtag gccacctcgt 4080

ccacgatgtt gccgaagatg gggtgccgct cgtgcttctt atcctcttcc accaggaagg 4140

actcttccag tctgtggaag aagctgtcgt ccaccttggc catctcgttg ctgaagatct 4200

cttgcagata gcagatccgg ttcttccgtc tggtgtatct tcttctggcg gttctcttca 4260

gccgggtggc ctcggctgtt tcgccgctgt cgaacagcag ggctccgatc aggttcttct 4320

tgatgctgtg ccggtcggtg ttgcccagca ccttgaattt cttgctgggc accttgtact 4380

cgtcggtgat cacggcccag cccacagagt tggtgccgat gtccaggccg atgctgtact 4440

tcttgtcggc tgctgggact ccgtggatac cgaccttccg cttcttcttt ggggccatct 4500

tatcgtcatc gtctttgtaa tcaatatcat gatccttgta gtctccgtcg tggtccttat 4560

agtccatctc gagtatcgtt cgtaaatggt gaaaattttc agaaaattgc ttttgcttta 4620

aaagaaatga tttaaattgc tgcaatagaa gtagaatgct tgattgcttg agattcgttt 4680

gttttgtata tgttgtgttg aggtcgaggt cctctccaaa tgaaatgaac ttccttatat 4740

agaggaaggg tcttgcgaag gatagtggga ttgtgcgtca tcccttacgt cagtggagat 4800

atcacatcaa tccacttgct ttgaagacgt ggttggaacg tcttcttttt ccacgatgct 4860

cctcgtgggt gggggtccat ctttgggacc actgtcggca gaggcatctt caacgatggc 4920

ctttccttta tcgcaatgat ggcatttgta ggagccacct tccttttcca ctatcttcac 4980

aataaagtga cagatagctg ggcaatggaa tccgaggagg tttccggata tcaccctttg 5040

ttgaaaagtc tcaattgccc tttggtcttc tgagactgta tctttgatat ttttggagta 5100

gacaagtgtg tcgtgctcca ccatgttatc acatcaatcc acttgctttg aagacgtggt 5160

tggaacgtct tctttttcca cgatgctcct cgtgggtggg ggtccatctt tgggaccact 5220

gtcggcagag gcatcttcaa cgatggcctt tcctttatcg caatgatggc atttgtagga 5280

gccaccttcc ttttccacta tcttcacaat aaagtgacag atagctgggc aatggaatcc 5340

gaggaggttt ccggatatta ccctttgttg aaaagtctca attgcccttt ggtcttctga 5400

gactgtatct ttgatatttt tggagtagac aagtgtgtcg tgctccacca tgttgacctg 5460

caggcatgcc tcggatccac tagtaacggc cgccagtgtg ctggaattgc ccttaagctt 5520

cgttgaacaa cggaaactcg acttgccttc cgcacaatac atcatttctt cttagctttt 5580

tttcttcttc ttcgttcata cagttttttt ttgtttatca gcttacattt tcttgaaccg 5640

tagctttcgt tttcttcttt ttaactttcc attcggagtt tttgtatctt gtttcatagt 5700

ttgtcccagg attagaatga ttaggcatcg aaccttcaag aatttgattg aataaaacat 5760

cttcattctt aagatatgaa gataatcttc aaaaggcccc tgggaatctg aaagaagaga 5820

agcaggccca tttatatggg aaagaacaat agtatttctt atataggccc atttaagttg 5880

aaaacaatct tcaaaagtcc cacatcgctt agataagaaa acgaagctga gtttatatac 5940

agctagagtc gaagtagtga ttgcggagac tcgtctacag ttgttttaga gctagaaata 6000

gcaagttaaa ataaggctag tccgttatca acttgaaaaa gtggcaccga gtcggtgctt 6060

tttttgtccc ttcgaagggc ctttctcaga tatccatcac actggcggcc gctcgaggtc 6120

-continued

gctcggatcc actagtaacg gccgccagtg tgctggaatt gcccttaagc ttcgttgaac 6180

aacggaaact cgacttgcct tccgcacaat acatcatttc ttcttagctt tttttcttct 6240

tcttcgttca tacagttttt ttttgtttat cagcttacat ttcttgaac cgtagctttc 6300

gttttcttct ttttaacttt ccattcggag tttttgtatc ttgtttcata gtttgtccca 6360

ggattagaat gattaggcat cgaaccttca agaatttgat tgaataaaac atcttcattc 6420

ttaagatatg aagataatct tcaaaaggcc cctgggaatc tgaaagaaga gaagcaggcc 6480

catttatatg ggaaagaaca atagtatttc ttatataggc ccatttaagt tgaaaacaat 6540

cttcaaaagt cccacatcgc ttagataaga aaacgaagct gagtttatat acagctagag 6600

tcgaagtagt gattttggtc tacggagcga tggtgtttta gagctagaaa tagcaagtta 6660

aaataaggct agtccgttat caacttgaaa aagtggcacc gagtcggtgc tttttttgtc 6720

ccttcgaagg gcctttctca gatatccatc acactggcgg ccgctcgagg tcgaagcttg 6780

gcactggccg tcgttttaca acgtcgtgac tgggaaaacc ctggcgttac ccaacttaat 6840

cgccttgcag cacatccccc tttcgccagc tggcgtaata gcgaagaggc ccgcaccgat 6900

cgcccttccc aacagttgcg cagcctgaat ggcgaatgct agagcagctt gagcttggat 6960

cagattgtcg tttcccgcct tcagtttaaa ctatcagtgt ttgacaggat atattggcgg 7020

gtaaacctaa gagaaaagag cgtttattag aataacggat atttaaaagg gcgtgaaaag 7080

gtttatccgt tcgtccattt gtatgtgcat gccaaccaca gggttcccct cgggatcaaa 7140

gtactttgat ccaacccctc cgctgctata gtgcagtcgg cttctgacgt tcagtgcagc 7200

cgtcttctga aaacgacatg tcgcacaagt cctaagttac gcgacaggct gccgccctgc 7260

ccttttcctg gcgttttctt gtcgcgtgtt ttagtcgcat aaagtagaat acttgcgact 7320

agaaccggag acattacgcc atgaacaaga gcgccgccgc tggcctgctg ggctatgccc 7380

gcgtcagcac cgacgaccag gacttgacca accaacgggc cgaactgcac gcggccggct 7440

gcaccaagct gttttccgag aagatcaccg gcaccaggcg cgaccgcccg gagctggcca 7500

ggatgcttga ccacctacgc cctggcgacg ttgtgacagt gaccaggcta gaccgcctgg 7560

cccgcagcac ccgcgaccta ctggacattg ccgagcgcat ccaggaggcc ggcgcgggcc 7620

tgcgtagcct ggcagagccg tgggccgaca ccaccacgcc ggccggccgc atggtgttga 7680

ccgtgttcgc cggcattgcc gagttcgagc gttccctaat catcgaccgc acccggagcg 7740

ggcgcgaggc cgccaaggcc cgaggcgtga agtttggccc ccgccctacc ctcaccccgg 7800

cacagatcgc gcacgcccgc gagctgatcg accaggaagg ccgcaccgtg aaagaggcgg 7860

ctgcactgct tggcgtgcat cgctcgaccc tgtaccgcgc acttgagcgc agcgaggaag 7920

tgacgcccac cgaggccagg cggcgcggtg ccttccgtga ggacgcattg accgaggccg 7980

acgccctggc ggccgccgag aatgaacgcc aagaggaaca agcatgaaac cgcaccagga 8040

cggccaggac gaaccgtttt tcattaccga agagatcgag gcggagatga tcgcggccgg 8100

gtacgtgttc gagccgcccg cgcacgtctc aaccgtgcgg ctgcatgaaa tcctggccgg 8160

tttgtctgat gccaagctgg cggcctggcc ggccagcttg gccgctgaag aaaccgagcg 8220

ccgccgtcta aaaaggtgat gtgtatttga gtaaaacagc ttgcgtcatg cggtcgctgc 8280

gtatatgatg cgatgagtaa ataaacaaat acgcaagggg aacgcatgaa ggttatcgct 8340

gtacttaacc agaaaggcgg gtcaggcaag acgaccatcg caacccatct agcccgcgcc 8400

-continued

ctgcaactcg ccggggccga tgttctgtta gtcgattccg atccccaggg cagtgcccgc 8460

gattgggcgg ccgtgcggga agatcaaccg ctaaccgttg tcggcatcga ccgcccgacg 8520

attgaccgcg acgtgaaggc catcggccgg cgcgacttcg tagtgatcga cggagcgccc 8580

caggcggcgg acttggctgt gtccgcgatc aaggcagccg acttcgtgct gattccggtg 8640

cagccaagcc cttacgacat atgggccacc gccgacctgg tggagctggt taagcagcgc 8700

attgaggtca cggatggaag gctacaagcg gcctttgtcg tgtcgcgggc gatcaaaggc 8760

acgcgcatcg gcggtgaggt tgccgaggcg ctggccgggt acgagctgcc cattcttgag 8820

tcccgtatca cgcagcgcgt gagctaccca ggcactgccg ccgccggcac aaccgttctt 8880

gaatcagaac ccgagggcga cgctgcccgc gaggtccagg cgctggccgc tgaaattaaa 8940

tcaaaactca tttgagttaa tgaggtaaag agaaaatgag caaaagcaca aacacgctaa 9000

gtgccggccg tccgagcgca cgcagcagca aggctgcaac gttggccagc ctggcagaca 9060

cgccagccat gaagcgggtc aactttcagt tgccggcgga ggatcacacc aagctgaaga 9120

tgtacgcggt acgccaaggc aagaccatta ccgagctgct atctgaatac atcgcgcagc 9180

taccagagta aatgagcaaa tgaataaatg agtagatgaa ttttagcggc taaaggaggc 9240

ggcatggaaa atcaagaaca accaggcacc gacgccgtgg aatgccccat gtgtggagga 9300

acgggcggtt ggccaggcgt aagcggctgg gttgtctgcc ggccctgcaa tggcactgga 9360

acccccaagc ccgaggaatc ggcgtgacgg tcgcaaacca tccggcccgg tacaaatcgg 9420

cgcggcgctg ggtgatgacc tggtggagaa gttgaaggcc gcgcaggccg cccagcggca 9480

acgcatcgag gcagaagcac gccccggtga atcgtggcaa gcggccgctg atcgaatccg 9540

caaagaatcc cggcaaccgc cggcagccgg tgcgccgtcg attaggaagc cgcccaaggg 9600

cgacgagcaa ccagattttt tcgttccgat gctctatgac gtgggcaccc gcgatagtcg 9660

cagcatcatg gacgtggccg ttttccgtct gtcgaagcgt gaccgacgag ctggcgaggt 9720

gatccgctac gagcttccag acgggcacgt agaggtttcc gcagggccgg ccggcatggc 9780

cagtgtgtgg gattacgacc tggtactgat ggcggtttcc catctaaccg aatccatgaa 9840

ccgataccgg gaagggaagg gagacaagcc cggccgcgtg ttccgtccac acgttgcgga 9900

cgtactcaag ttctgccggc gagccgatgg cggaaagcag aaagacgacc tggtagaaac 9960

ctgcattcgg ttaaacacca cgcacgttgc catgcagcgt acgaagaagg ccaagaacgg 10020

ccgcctggtg acggtatccg agggtgaagc cttgattagc cgctacaaga tcgtaaagag 10080

cgaaaccggg cggccggagt acatcgagat cgagctagct gattggatgt accgcgagat 10140

cacagaaggc aagaacccgg acgtgctgac ggttcacccc gattactttt tgatcgatcc 10200

cggcatcggc cgttttctct accgcctggc acgccgcgcc gcaggcaagg cagaagccag 10260

atggttgttc aagacgatct acgaacgcag tggcagcgcc ggagagttca agaagttctg 10320

tttcaccgtg cgcaagctga tcgggtcaaa tgacctgccg gagtacgatt tgaaggagga 10380

ggcggggcag gctggcccga tcctagtcat gcgctaccgc aacctgatcg agggcgaagc 10440

atccgccggt tcctaatgta cggagcagat gctagggcaa attgccctag caggggaaaa 10500

aggtcgaaaa ggtctctttc ctgtggatag cacgtacatt gggaacccaa agccgtacat 10560

tgggaaccgg aacccgtaca ttgggaaccc aaagccgtac attgggaacc ggtcacacat 10620

gtaagtgact gatataaaag agaaaaaagg cgatttttcc gcctaaaact ctttaaaact 10680

-continued

tattaaaact cttaaaaccc gcctggcctg tgcataactg tctggccagc gcacagccga 10740

agagctgcaa aaagcgccta cccttcggtc gctgcgctcc ctacgccccg ccgcttcgcg 10800

tcggcctatc gcggccgctg gccgctcaaa aatggctggc ctacggccag gcaatctacc 10860

agggcgcgga caagccgcgc cgtcgccact cgaccgccgg cgcccacatc aaggcaccct 10920

gcctcgcgcg tttcggtgat gacggtgaaa acctctgaca catgcagctc ccggagacgg 10980

tcacagcttg tctgtaagcg gatgccggga gcagacaagc ccgtcagggc gcgtcagcgg 11040

gtgttggcgg gtgtcggggc gcagccatga cccagtcacg tagcgatagc ggagtgtata 11100

ctggcttaac tatgcggcat cagagcagat tgtactgaga gtgcaccata tgcggtgtga 11160

aataccgcac agatgcgtaa ggagaaaata ccgcatcagg cgctcttccg cttcctcgct 11220

cactgactcg ctgcgctcgg tcgttcggct gcggcgagcg gtatcagctc actcaaaggc 11280

ggtaatacgg ttatccacag aatcagggga taacgcagga aagaacatgt gagcaaaagg 11340

ccagcaaaag gccaggaacc gtaaaaaggc cgcgttgctg gcgtttttcc ataggctccg 11400

cccccctgac gagcatcaca aaaatcgacg ctcaagtcag aggtggcgaa acccgacagg 11460

actataaaga taccaggcgt ttccccctgg aagctccctc gtgcgctctc ctgttccgac 11520

cctgccgctt accggatacc tgtccgcctt tctcccttcg ggaagcgtgg cgctttctca 11580

tagctcacgc tgtaggtatc tcagttcggt gtaggtcgtt cgctccaagc tgggctgtgt 11640

gcacgaaccc cccgttcagc ccgaccgctg cgccttatcc ggtaactatc gtcttgagtc 11700

caacccggta agacacgact tatcgccact ggcagcagcc actggtaaca ggattagcag 11760

agcgaggtat gtaggcggtg ctacagagtt cttgaagtgg tggcctaact acggctacac 11820

tagaaggaca gtatttggta tctgcgctct gctgaagcca gttaccttcg gaaaaagagt 11880

tggtagctct tgatccggca aacaaaccac cgctggtagc ggtggttttt ttgtttgcaa 11940

gcagcagatt acgcgcagaa aaaaaggatc tcaagaagat cctttgatct tttctacggg 12000

gtctgacgct cagtggaacg aaaactcacg ttaagggatt ttggtcatgc attctaggta 12060

ctaaaacaat tcatccagta aaatataata ttttattttc tcccaatcag gcttgatccc 12120

cagtaagtca aaaaatagct cgacatactg ttcttccccg atatcctccc tgatcgaccg 12180

gacgcagaag gcaatgtcat accacttgtc cgccctgccg cttctcccaa gatcaataaa 12240

gccacttact ttgccatctt tcacaaagat gttgctgtct cccaggtcgc cgtgggaaaa 12300

gacaagttcc tcttcgggct tttccgtctt taaaaaatca tacagctcgc gcggatcttt 12360

aaatggagtg tcttcttccc agttttcgca atccacatcg gccagatcgt tattcagtaa 12420

gtaatccaat tcggctaagc ggctgtctaa gctattcgta tagggacaat ccgatatgtc 12480

gatggagtga aagagcctga tgcactccgc atacagctcg ataatctttt cagggctttg 12540

ttcatcttca tactcttccg agcaaaggac gccatcggcc tcactcatga gcagattgct 12600

ccagccatca tgccgttcaa agtgcaggac ctttggaaca ggcagctttc cttccagcca 12660

tagcatcatg tccttttccc gttccacatc ataggtggtc cctttatacc ggctgtccgt 12720

catttttaaa tataggtttt cattttctcc caccagctta tataccttag caggagacat 12780

tccttccgta tcttttacgc agcggtattt ttcgatcagt tttttcaatt ccggtgatat 12840

tctcatttta gccatttatt atttccttcc tcttttctac agtatttaaa gataccccaa 12900

gaagctaatt ataacaagac gaactccaat tcactgttcc ttgcattcta aaaccttaaa 12960

-continued

taccagaaaa cagctttttc aaagttgttt tcaaagttgg cgtataacat agtatcgacg 13020

gagccgattt tgaaaccgcg gtgatcacag gcagcaacgc tctgtcatcg ttacaatcaa 13080

catgctaccc tccgcgagat catccgtgtt tcaaacccgg cagcttagtt gccgttcttc 13140

cgaatagcat cggtaacatg agcaaagtct gccgccttac aacggctctc ccgctgacgc 13200

cgtcccggac tgatgggctg cctgtatcga gtggtgattt tgtgccgagc tgccggtcgg 13260

ggagctgttg gctggctggt ggcaggatat attgtggtgt aaacaaattg acgcttagac 13320

aacttaataa cacattgcgg acgtttttaa tgtactgaat taacgccgaa ttaattcggg 13380

ggatctggat tttagtactg gattttggtt ttaggaatta gaaattttat tgatagaagt 13440

attttacaaa tacaaataca tactaagggt ttcttatatg ctcaacacat gagcgaaacc 13500

ctataggaac cctaattccc ttatctggga actactcaca cattattatg gagaaactcg 13560

agcttgtcga tcgacagatc cggtcggcat ctactctatt tctttgccct cggacgagtg 13620

ctggggcgtc ggtttccact atcggcgagt acttctacac agccatcggt ccagacggcc 13680

gcgcttctgc gggcgatttg tgtacgcccg acagtcccgg ctccggatcg gacgattgcg 13740

tcgcatcgac cctgcgccca agctgcatca tcgaaattgc cgtcaaccaa gctctgatag 13800

agttggtcaa gaccaatgcg gagcatatac gcccggagtc gtggcgatcc tgcaagctcc 13860

ggatgcctcc gctcgaagta gcgcgtctgc tgctccatac aagccaacca cggcctccag 13920

aagaagatgt tggcgacctc gtattgggaa tccccgaaca tcgcctcgct ccagtcaatg 13980

accgctgtta tgcggccatt gtccgtcagg acattgttgg agccgaaatc cgcgtgcacg 14040

aggtgccgga cttcggggca gtcctcggcc caaagcatca gctcatcgag agcctgcgcg 14100

acggacgcac tgacggtgtc gtccatcaca gtttgccagt gatacacatg gggatcagca 14160

atcgcgcata tgaaatcacg ccatgtagtg tattgaccga ttccttgcgg tccgaatggg 14220

ccgaacccgc tcgtctggct aagatcggcc gcagcgatcg catccatagc ctccgcgacc 14280

ggttgtagaa cagcgggcag ttcggtttca ggcaggtctt gcaacgtgac accctgtgca 14340

cggcgggaga tgcaataggt caggctctcg ctaaactccc caatgtcaag cacttccgga 14400

atcgggagcg cggccgatgc aaagtgccga taaacataac gatctttgta gaaaccatcg 14460

gcgcagctat ttacccgcag gacatatcca cgccctccta catcgaagct gaaagcacga 14520

gattcttcgc cctccgagag ctgcatcagg tcggagacgc tgtcgaactt ttcgatcaga 14580

aacttctcga cagacgtcgc ggtgagttca ggctttttca tatctcattg cccccccgga 14640

tctgcgaaag ctcgagagag atagatttgt agagagagac tggtgatttc agcgtgtcct 14700

ctccaaatga aatgaacttc cttatataga ggaaggtctt gcgaaggata gtgggattgt 14760

gcgtcatccc ttacgtcagt ggagatatca catcaatcca cttgctttga agacgtggtt 14820

ggaacgtctt ctttttccac gatgctcctc gtgggtgggg gtccatcttt gggaccactg 14880

tcggcagagg catcttgaac gatagccttt cctttatcgc aatgatggca tttgtaggtg 14940

ccaccttcct tttctactgt ccttttgatg aagtgacaga tagctgggca atggaatccg 15000

aggaggtttc ccgatattac cctttgttga aaagtctcaa tagccctttg gtcttctgag 15060

actgtatctt tgatattctt ggagtagacg agagtgtcgt gctccaccat gttatcacat 15120

caatccactt gctttgaaga cgtggttgga acgtcttctt tttccacgat gctcctcgtg 15180

ggtgggggtc catctttggg accactgtcg gcagaggcat cttgaacgat agcctttcct 15240

-continued

ttatcgcaat gatggcattt gtaggtgcca ccttcctttt ctactgtcct tttgatgaag 15300

tgacagatag ctgggcaatg gaatccgagg aggtttcccg atattaccct ttgttgaaaa 15360

gtctcaatag ccctttggtc ttctgagact gtatctttga tattcttgga gtagacgaga 15420

gtgtcgtgct ccaccatgtt ggcaagctgc tctagccaat acgcaaaccg cctctccccg 15480

cgcgttggcc gattcattaa tgcagctggc acgacaggtt tcccgactgg aaagcgggca 15540

gtgagcgcaa cgcaattaat gtgagttagc tcactcatta ggcaccccag gctttacact 15600

ttatgcttcc ggctcgtatg ttgtgtggaa ttgtgagcgg ataacaattt cacacaggaa 15660

acagctatga ccatgattac g 15681

<210> SEQ ID NO 158
<211> LENGTH: 15681
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: vector
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5964)..(5984)
<223> OTHER INFORMATION: /note="target sequence"
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6617)..(6637)
<223> OTHER INFORMATION: /note="target sequence"

<400> SEQUENCE: 158

aattcccgat ctagtaacat agatgacacc gcgcgcgata atttatccta gtttgcgcgc 60

tatattttgt tttctatcgc gtattaaatg tataattgcg ggactctaat cataaaaacc 120

catctcataa ataacgtcat gcattacatg ttaattatta catgcttaac gtaattcaac 180

agaaattata tgataatcat cgcaagaccg gcaacaggat tcaatcttaa gaaactttat 240

tgccaaatgt ttgaacgatc ggggaaattc gagctctatc gatcaatcag gatccttact 300

ttttcttttt tgcctggccg gcctttttcg tggccgccgg ccttttgtcg cctcccagct 360

gagacaggtc gatccgtgtc tcgtacaggc cggtgatgct ctggtggatc agggtggcgt 420

ccagcacctc tttggtgctg gtgtacctct tccggtcgat ggtggtgtca aagtacttga 480

aggcggcagg ggctcccaga ttggtcaggg taaacaggtg gatgatattc tcggcctgct 540

ctctgatggg cttatcccgg tgcttgttgt aggcggacag cactttgtcc agattagcgt 600

cggccaggat cactctcttg gagaactcgc tgatctgctc gatgatctcg tccaggtagt 660

gcttgtgctg ttccacaaac agctgtttct gctcattatc ctcgggggag cccttcagct 720

tctcatagtg gctggccagg tacaggaagt tcacatattt ggagggcagg gccagttcgt 780

ttcccttctg cagttcgccg gcagaggcca gcattctctt ccggccgttt tccagctcga 840

acagggagta cttaggcagc ttgatgatca ggtccttttt cacttctttg tagcccttgg 900

cttccagaaa gtcgatggga ttcttctcga agctgcttct ttccatgatg gtgatcccca 960

gcagctcttt cacactcttc agtttcttgg acttgccctt ttccactttg gccaccacca 1020

gcacagaata ggccacggtg gggctgtcga agccgccgta cttcttaggg tcccagtcct 1080

tctttctggc gatcagctta tcgctgttcc tcttgggcag gatagactct ttgctgaagc 1140

cgcctgtctg cacctcggtc tttttcacga tattcacttg gggcatgctc agcactttcc 1200

gcacggtggc aaaatcccgg cccttatccc acacgatctc cccggtttcg ccgtttgtct 1260

-continued

cgatcagagg ccgcttccgg atctcgccgt tggccagggt aatctcggtc ttgaaaaagt 1320

tcatgatgtt gctgtagaag aagtacttgg cggtagcctt gccgatttcc tgctcgctct 1380

tggcgatcat cttccgcacg tcgtacacct tgtagtcgcc gtacacgaac tcgctttcca 1440

gcttagggta ctttttgatc agggcggttc ccacgacggc gttcaggtag gcgtcgtggg 1500

cgtggtggta gttgttgatc tcgcgcactt tgtaaaactg gaaatccttc cggaaatcgg 1560

acaccagctt ggacttcagg gtgatcactt tcacttcccg gatcagcttg tcattctcgt 1620

cgtacttagt gttcatccgg gagtccagga tctgtgccac gtgctttgtg atctgccggg 1680

tttccaccag ctgtctcttg atgaagccgg ccttatccag ttcgctcagg ccgcctctct 1740

cggccttggt cagattgtcg aactttctct gggtaatcag cttggcgttc agcagctgcc 1800

gccagtagtt cttcatcttc ttcacgacct cttcggaggg cacgttgtcg ctcttgcccc 1860

ggttcttgtc gcttctggtc agcaccttgt tgtcgatgga gtcgtccttc agaaagctct 1920

gaggcacgat atggtccaca tcgtagtcgg acagccggtt gatgtccagt tcctggtcca 1980

cgtacatatc ccgcccattc tgcaggtagt acaggtacag cttctcgttc tgcagctggg 2040

tgttttccac ggggtgttct ttcaggatct ggctgcccag ctctttgatg ccctcttcga 2100

tccgcttcat tctctcgcgg ctgttcttct gtcccttctg ggtggtctgg ttctctctgg 2160

ccatttcgat cacgatgttc tcgggcttgt gccggcccat cactttcacg agctcgtcca 2220

ccaccttcac tgtctgcagg atgcccttct taatggcggg gctgccggcc agattggcaa 2280

tgtgctcgtg caggctatcg ccctggccgg acacctgggc tttctggatg tcctctttaa 2340

aggtcaggct gtcgtcgtgg atcagctgca tgaagtttct gttggcgaag ccgtcggact 2400

tcaggaaatc caggattgtc ttgccggact gcttgtcccg gatgccgttg atcagcttcc 2460

ggctcagcct gccccagccg gtgtatctcc gccgcttcag ctgcttcatc actttgtcgt 2520

cgaacaggtg ggcataggtt ttcagccgtt cctcgatcat ctctctgtcc tcaaacagtg 2580

tcagggtcag cacgatatct tccagaatgt cctcgttttc ctcattgtcc aggaagtcct 2640

tgtccttgat aattttcagc agatcgtggt atgtgcccag ggaggcgttg aaccgatctt 2700

ccacgccgga gatttccacg gagtcgaagc actcgatttt cttgaagtag tcctctttca 2760

gctgcttcac ggtcactttc cggttggtct tgaacagcag gtccacgatg gcctttttct 2820

gctcgccgct caggaaggcg ggctttctca ttccctcggt cacgtatttc actttggtca 2880

gctcgttata cacggtgaag tactcgtaca gcaggctgtg cttgggcagc accttctcgt 2940

tgggcaggtt cttatcgaag ttggtcatcc gctcgatgaa gctctgggcg gaagcgccct 3000

tgtccaccac ttcctcgaag ttccaggggg tgatggtttc ctcgctcttt ctggtcatcc 3060

aggcgaatct gctgtttccc ctggccagag ggcccacgta gtaggggatg cggaaggtca 3120

ggatcttctc gatcttttcc cggttgtcct tcaggaatgg gtaaaaatct tcctgccgcc 3180

gcagaatggc gtgcagctct cccaggtgga tctggtgggg gatgctgccg ttgtcgaagg 3240

tccgctgctt ccgcagcagg tcctctctgt tcagcttcac gagcagttcc tcggtgccgt 3300

ccatcttttc caggatgggc ttgatgaact tgtagaactc ttcctggctg gctccgccgt 3360

caatgtagcc ggcgtagccg ttcttgctct ggtcgaagaa aatctctttg tacttctcag 3420

gcagctgctg ccgcacgaga gctttcagca gggtcaggtc ctggtggtgc tcgtcgtatc 3480

tcttgatcat agaggcgctc agggggccct tggtgatctc ggtgttcact ctcaggatgt 3540

-continued

cgctcagcag gatggcgtcg gacaggttct tggcggccag aaacaggtcg gcgtactggt 3600

cgccgatctg ggccagcagg ttgtccaggt cgtcgtcgta ggtgtccttg ctcagctgca 3660

gtttggcatc ctcggccagg tcgaagttgc tcttgaagtt gggggtcagg cccaggctca 3720

gggcaatcag gtttccgaac aggccattct tcttctcgcc gggcagctgg gcgatcagat 3780

tttccagccg tctgctcttg ctcagtctgg cagacaggat ggccttggcg tccacgccgc 3840

tggcgttgat ggggttttcc tcgaacagct ggttgtaggt ctgcaccagc tggatgaaca 3900

gcttgtccac gtcgctgttg tcggggttca ggtcgccctc gatcaggaag tggccccgga 3960

acttgatcat gtgggccagg gccagataga tcagccgcag gtcggccttg tcggtgctgt 4020

ccaccagttt ctttctcagg tggtagatgg tggggtactt ctcgtggtag gccacctcgt 4080

ccacgatgtt gccgaagatg gggtgccgct cgtgcttctt atcctcttcc accaggaagg 4140

actcttccag tctgtggaag aagctgtcgt ccaccttggc catctcgttg ctgaagatct 4200

cttgcagata gcagatccgg ttcttccgtc tggtgtatct tcttctggcg gttctcttca 4260

gccgggtggc ctcggctgtt tcgccgctgt cgaacagcag ggctccgatc aggttcttct 4320

tgatgctgtg ccggtcggtg ttgcccagca ccttgaattt cttgctgggc accttgtact 4380

cgtcggtgat cacggcccag cccacagagt tggtgccgat gtccaggccg atgctgtact 4440

tcttgtcggc tgctgggact ccgtggatac cgaccttccg cttcttcttt ggggccatct 4500

tatcgtcatc gtctttgtaa tcaatatcat gatccttgta gtctccgtcg tggtccttat 4560

agtccatctc gagtatcgtt cgtaaatggt gaaaattttc agaaaattgc ttttgcttta 4620

aaagaaatga tttaaattgc tgcaatagaa gtagaatgct tgattgcttg agattcgttt 4680

gttttgtata tgttgtgttg aggtcgaggt cctctccaaa tgaaatgaac ttccttatat 4740

agaggaaggg tcttgcgaag gatagtggga ttgtgcgtca tcccttacgt cagtggagat 4800

atcacatcaa tccacttgct ttgaagacgt ggttggaacg tcttcttttt ccacgatgct 4860

cctcgtgggt gggggtccat ctttgggacc actgtcggca gaggcatctt caacgatggc 4920

ctttccttta tcgcaatgat ggcatttgta ggagccacct tccttttcca ctatcttcac 4980

aataaagtga cagatagctg ggcaatggaa tccgaggagg tttccggata tcaccctttg 5040

ttgaaaagtc tcaattgccc tttggtcttc tgagactgta tctttgatat ttttggagta 5100

gacaagtgtg tcgtgctcca ccatgttatc acatcaatcc acttgctttg aagacgtggt 5160

tggaacgtct tctttttcca cgatgctcct cgtgggtggg ggtccatctt tgggaccact 5220

gtcggcagag gcatcttcaa cgatggcctt tcctttatcg caatgatggc atttgtagga 5280

gccaccttcc ttttccacta tcttcacaat aaagtgacag atagctgggc aatggaatcc 5340

gaggaggttt ccggatatta ccctttgttg aaaagtctca attgcccttt ggtcttctga 5400

gactgtatct ttgatatttt tggagtagac aagtgtgtcg tgctccacca tgttgacctg 5460

caggcatgcc tcggatccac tagtaacggc cgccagtgtg ctggaattgc ccttaagctt 5520

cgttgaacaa cggaaactcg acttgccttc cgcacaatac atcatttctt cttagctttt 5580

tttcttcttc ttcgttcata cagttttttt ttgtttatca gcttacattt tcttgaaccg 5640

tagctttcgt tttcttcttt ttaactttcc attcggagtt tttgtatctt gtttcatagt 5700

ttgtcccagg attagaatga ttaggcatcg aaccttcaag aatttgattg aataaaacat 5760

cttcattctt aagatatgaa gataatcttc aaaaggcccc tgggaatctg aaagaagaga 5820

-continued

agcaggccca tttatatggg aaagaacaat agtatttctt atataggccc atttaagttg 5880

aaaacaatct tcaaaagtcc cacatcgctt agataagaaa acgaagctga gtttatatac 5940

agctagagtc gaagtagtga tttccccacg tcactgggcg tcgttttaga gctagaaata 6000

gcaagttaaa ataaggctag tccgttatca acttgaaaaa gtggcaccga gtcggtgctt 6060

tttttgtccc ttcgaagggc ctttctcaga tatccatcac actggcggcc gctcgaggtc 6120

gctcggatcc actagtaacg gccgccagtg tgctggaatt gcccttaagc ttcgttgaac 6180

aacggaaact cgacttgcct tccgcacaat acatcatttc ttcttagctt tttttcttct 6240

tcttcgttca tacagttttt ttttgtttat cagcttacat ttcttgaac cgtagctttc 6300

gttttcttct ttttaacttt ccattcggag tttttgtatc ttgtttcata gtttgtccca 6360

ggattagaat gattaggcat cgaaccttca agaatttgat tgaataaaac atcttcattc 6420

ttaagatatg aagataatct tcaaaaggcc cctgggaatc tgaaagaaga gaagcaggcc 6480

catttatatg ggaaagaaca atagtatttc ttatataggc ccatttaagt tgaaaacaat 6540

cttcaaaagt cccacatcgc ttagataaga aaacgaagct gagtttatat acagctagag 6600

tcgaagtagt gattttggtc tacggagcga tggtgtttta gagctagaaa tagcaagtta 6660

aaataaggct agtccgttat caacttgaaa aagtggcacc gagtcggtgc tttttttgtc 6720

ccttcgaagg gcctttctca gatatccatc acactggcgg ccgctcgagg tcgaagcttg 6780

gcactggccg tcgttttaca acgtcgtgac tgggaaaacc ctggcgttac ccaacttaat 6840

cgccttgcag cacatccccc tttcgccagc tggcgtaata gcgaagaggc ccgcaccgat 6900

cgcccttccc aacagttgcg cagcctgaat ggcgaatgct agagcagctt gagcttggat 6960

cagattgtcg tttcccgcct tcagtttaaa ctatcagtgt ttgacaggat atattggcgg 7020

gtaaacctaa gagaaaagag cgtttattag aataacggat atttaaaagg gcgtgaaaag 7080

gtttatccgt tcgtccattt gtatgtgcat gccaaccaca gggttcccct cgggatcaaa 7140

gtactttgat ccaacccctc cgctgctata gtgcagtcgg cttctgacgt tcagtgcagc 7200

cgtcttctga aaacgacatg tcgcacaagt cctaagttac gcgacaggct gccgccctgc 7260

ccttttcctg gcgttttctt gtcgcgtgtt ttagtcgcat aaagtagaat acttgcgact 7320

agaaccggag acattacgcc atgaacaaga gcgccgccgc tggcctgctg ggctatgccc 7380

gcgtcagcac cgacgaccag gacttgacca accaacgggc cgaactgcac gcggccggct 7440

gcaccaagct gttttccgag aagatcaccg gcaccaggcg cgaccgcccg gagctggcca 7500

ggatgcttga ccacctacgc cctggcgacg ttgtgacagt gaccaggcta gaccgcctgg 7560

cccgcagcac ccgcgaccta ctggacattg ccgagcgcat ccaggaggcc ggcgcgggcc 7620

tgcgtagcct ggcagagccg tgggccgaca ccaccacgcc ggccggccgc atggtgttga 7680

ccgtgttcgc cggcattgcc gagttcgagc gttccctaat catcgaccgc acccggagcg 7740

ggcgcgaggc cgccaaggcc cgaggcgtga agtttggccc ccgccctacc ctcaccccgg 7800

cacagatcgc gcacgcccgc gagctgatcg accaggaagg ccgcaccgtg aaagaggcgg 7860

ctgcactgct tggcgtgcat cgctcgaccc tgtaccgcgc acttgagcgc agcgaggaag 7920

tgacgcccac cgaggccagg cggcgcggtg ccttccgtga ggacgcattg accgaggccg 7980

acgccctggc ggccgccgag aatgaacgcc aagaggaaca agcatgaaac cgcaccagga 8040

cggccaggac gaaccgtttt tcattaccga agagatcgag gcggagatga tcgcggccgg 8100

-continued

gtacgtgttc gagccgcccg cgcacgtctc aaccgtgcgg ctgcatgaaa tcctggccgg 8160

tttgtctgat gccaagctgg cggcctggcc ggccagcttg gccgctgaag aaaccgagcg 8220

ccgccgtcta aaaaggtgat gtgtatttga gtaaaacagc ttgcgtcatg cggtcgctgc 8280

gtatatgatg cgatgagtaa ataaacaaat acgcaagggg aacgcatgaa ggttatcgct 8340

gtacttaacc agaaaggcgg gtcaggcaag acgaccatcg caacccatct agcccgcgcc 8400

ctgcaactcg ccggggccga tgttctgtta gtcgattccg atccccaggg cagtgcccgc 8460

gattgggcgg ccgtgcggga agatcaaccg ctaaccgttg tcggcatcga ccgcccgacg 8520

attgaccgcg acgtgaaggc catcggccgg cgcgacttcg tagtgatcga cggagcgccc 8580

caggcggcgg acttggctgt gtccgcgatc aaggcagccg acttcgtgct gattccggtg 8640

cagccaagcc cttacgacat atgggccacc gccgacctgg tggagctggt taagcagcgc 8700

attgaggtca cggatggaag gctacaagcg gcctttgtcg tgtcgcgggc gatcaaaggc 8760

acgcgcatcg gcggtgaggt tgccgaggcg ctggccgggt acgagctgcc cattcttgag 8820

tcccgtatca cgcagcgcgt gagctaccca ggcactgccg ccgccggcac aaccgttctt 8880

gaatcagaac ccgagggcga cgctgcccgc gaggtccagg cgctggccgc tgaaattaaa 8940

tcaaaactca tttgagttaa tgaggtaaag agaaaatgag caaaagcaca aacacgctaa 9000

gtgccggccg tccgagcgca cgcagcagca aggctgcaac gttggccagc ctggcagaca 9060

cgccagccat gaagcgggtc aactttcagt tgccggcgga ggatcacacc aagctgaaga 9120

tgtacgcggt acgccaaggc aagaccatta ccgagctgct atctgaatac atcgcgcagc 9180

taccagagta aatgagcaaa tgaataaatg agtagatgaa ttttagcggc taaaggaggc 9240

ggcatggaaa atcaagaaca accaggcacc gacgccgtgg aatgccccat gtgtggagga 9300

acgggcggtt ggccaggcgt aagcggctgg gttgtctgcc ggccctgcaa tggcactgga 9360

acccccaagc ccgaggaatc ggcgtgacgg tcgcaaacca tccggcccgg tacaaatcgg 9420

cgcggcgctg ggtgatgacc tggtggagaa gttgaaggcc gcgcaggccg cccagcggca 9480

acgcatcgag gcagaagcac gccccggtga atcgtggcaa gcggccgctg atcgaatccg 9540

caaagaatcc cggcaaccgc cggcagccgg tgcgccgtcg attaggaagc cgcccaaggg 9600

cgacgagcaa ccagattttt tcgttccgat gctctatgac gtgggcaccc gcgatagtcg 9660

cagcatcatg gacgtggccg ttttccgtct gtcgaagcgt gaccgacgag ctggcgaggt 9720

gatccgctac gagcttccag acgggcacgt agaggtttcc gcagggccgg ccggcatggc 9780

cagtgtgtgg gattacgacc tggtactgat ggcggtttcc catctaaccg aatccatgaa 9840

ccgataccgg gaagggaagg gagacaagcc cggccgcgtg ttccgtccac acgttgcgga 9900

cgtactcaag ttctgccggc gagccgatgg cggaaagcag aaagacgacc tggtagaaac 9960

ctgcattcgg ttaaacacca cgcacgttgc catgcagcgt acgaagaagg ccaagaacgg 10020

ccgcctggtg acggtatccg agggtgaagc cttgattagc cgctacaaga tcgtaaagag 10080

cgaaaccggg cggccggagt acatcgagat cgagctagct gattggatgt accgcgagat 10140

cacagaaggc aagaacccgg acgtgctgac ggttcacccc gattactttt tgatcgatcc 10200

cggcatcggc cgttttctct accgcctggc acgccgcgcc gcaggcaagg cagaagccag 10260

atggttgttc aagacgatct acgaacgcag tggcagcgcc ggagagttca agaagttctg 10320

tttcaccgtg cgcaagctga tcgggtcaaa tgacctgccg gagtacgatt tgaaggagga 10380

-continued

ggcggggcag gctggcccga tcctagtcat gcgctaccgc aacctgatcg agggcgaagc 10440

atccgccggt tcctaatgta cggagcagat gctagggcaa attgccctag caggggaaaa 10500

aggtcgaaaa ggtctctttc ctgtggatag cacgtacatt gggaacccaa agccgtacat 10560

tgggaaccgg aacccgtaca ttgggaaccc aaagccgtac attgggaacc ggtcacacat 10620

gtaagtgact gatataaaag agaaaaaagg cgatttttcc gcctaaaact ctttaaaact 10680

tattaaaact cttaaaaccc gcctggcctg tgcataactg tctggccagc gcacagccga 10740

agagctgcaa aaagcgccta cccttcggtc gctgcgctcc ctacgccccg ccgcttcgcg 10800

tcggcctatc gcggccgctg gccgctcaaa aatggctggc ctacggccag gcaatctacc 10860

agggcgcgga caagccgcgc cgtcgccact cgaccgccgg cgcccacatc aaggcaccct 10920

gcctcgcgcg tttcggtgat gacggtgaaa acctctgaca catgcagctc ccggagacgg 10980

tcacagcttg tctgtaagcg gatgccggga gcagacaagc ccgtcagggc gcgtcagcgg 11040

gtgttggcgg gtgtcggggc gcagccatga cccagtcacg tagcgatagc ggagtgtata 11100

ctggcttaac tatgcggcat cagagcagat tgtactgaga gtgcaccata tgcggtgtga 11160

aataccgcac agatgcgtaa ggagaaaata ccgcatcagg cgctcttccg cttcctcgct 11220

cactgactcg ctgcgctcgg tcgttcggct gcggcgagcg gtatcagctc actcaaaggc 11280

ggtaatacgg ttatccacag aatcagggga taacgcagga aagaacatgt gagcaaaagg 11340

ccagcaaaag gccaggaacc gtaaaaaggc cgcgttgctg gcgtttttcc ataggctccg 11400

cccccctgac gagcatcaca aaaatcgacg ctcaagtcag aggtggcgaa acccgacagg 11460

actataaaga taccaggcgt ttccccctgg aagctccctc gtgcgctctc ctgttccgac 11520

cctgccgctt accggatacc tgtccgcctt tctcccttcg ggaagcgtgg cgctttctca 11580

tagctcacgc tgtaggtatc tcagttcggt gtaggtcgtt cgctccaagc tgggctgtgt 11640

gcacgaaccc cccgttcagc ccgaccgctg cgccttatcc ggtaactatc gtcttgagtc 11700

caacccggta agacacgact tatcgccact ggcagcagcc actggtaaca ggattagcag 11760

agcgaggtat gtaggcggtg ctacagagtt cttgaagtgg tggcctaact acggctacac 11820

tagaaggaca gtatttggta tctgcgctct gctgaagcca gttaccttcg gaaaaagagt 11880

tggtagctct tgatccggca aacaaaccac cgctggtagc ggtggttttt ttgtttgcaa 11940

gcagcagatt acgcgcagaa aaaaaggatc tcaagaagat cctttgatct tttctacggg 12000

gtctgacgct cagtggaacg aaaactcacg ttaagggatt ttggtcatgc attctaggta 12060

ctaaaacaat tcatccagta aaatataata ttttattttc tcccaatcag gcttgatccc 12120

cagtaagtca aaaaatagct cgacatactg ttcttccccg atatcctccc tgatcgaccg 12180

gacgcagaag gcaatgtcat accacttgtc cgccctgccg cttctcccaa gatcaataaa 12240

gccacttact ttgccatctt tcacaaagat gttgctgtct cccaggtcgc cgtgggaaaa 12300

gacaagttcc tcttcgggct tttccgtctt taaaaaatca tacagctcgc gcggatcttt 12360

aaatggagtg tcttcttccc agttttcgca atccacatcg gccagatcgt tattcagtaa 12420

gtaatccaat tcggctaagc ggctgtctaa gctattcgta tagggacaat ccgatatgtc 12480

gatggagtga aagagcctga tgcactccgc atacagctcg ataatctttt cagggctttg 12540

ttcatcttca tactcttccg agcaaaggac gccatcggcc tcactcatga gcagattgct 12600

ccagccatca tgccgttcaa agtgcaggac ctttggaaca ggcagctttc cttccagcca 12660

-continued

tagcatcatg tccttttccc gttccacatc ataggtggtc cctttatacc ggctgtccgt 12720

catttttaaa tataggtttt cattttctcc caccagctta tataccttag caggagacat 12780

tccttccgta tcttttacgc agcggtattt ttcgatcagt tttttcaatt ccggtgatat 12840

tctcatttta gccatttatt atttccttcc tcttttctac agtatttaaa gataccccaa 12900

gaagctaatt ataacaagac gaactccaat tcactgttcc ttgcattcta aaaccttaaa 12960

taccagaaaa cagctttttc aaagttgttt tcaaagttgg cgtataacat agtatcgacg 13020

gagccgattt tgaaaccgcg gtgatcacag gcagcaacgc tctgtcatcg ttacaatcaa 13080

catgctaccc tccgcgagat catccgtgtt tcaaacccgg cagcttagtt gccgttcttc 13140

cgaatagcat cggtaacatg agcaaagtct gccgccttac aacggctctc ccgctgacgc 13200

cgtcccggac tgatgggctg cctgtatcga gtggtgattt tgtgccgagc tgccggtcgg 13260

ggagctgttg gctggctggt ggcaggatat attgtggtgt aaacaaattg acgcttagac 13320

aacttaataa cacattgcgg acgtttttaa tgtactgaat taacgccgaa ttaattcggg 13380

ggatctggat tttagtactg gattttggtt ttaggaatta gaaattttat tgatagaagt 13440

attttacaaa tacaaataca tactaagggt ttcttatatg ctcaacacat gagcgaaacc 13500

ctataggaac cctaattccc ttatctggga actactcaca cattattatg gagaaactcg 13560

agcttgtcga tcgacagatc cggtcggcat ctactctatt tctttgccct cggacgagtg 13620

ctggggcgtc ggtttccact atcggcgagt acttctacac agccatcggt ccagacggcc 13680

gcgcttctgc gggcgatttg tgtacgcccg acagtcccgg ctccggatcg gacgattgcg 13740

tcgcatcgac cctgcgccca agctgcatca tcgaaattgc cgtcaaccaa gctctgatag 13800

agttggtcaa gaccaatgcg gagcatatac gcccggagtc gtggcgatcc tgcaagctcc 13860

ggatgcctcc gctcgaagta gcgcgtctgc tgctccatac aagccaacca cggcctccag 13920

aagaagatgt tggcgacctc gtattgggaa tccccgaaca tcgcctcgct ccagtcaatg 13980

accgctgtta tgcggccatt gtccgtcagg acattgttgg agccgaaatc cgcgtgcacg 14040

aggtgccgga cttcggggca gtcctcggcc caaagcatca gctcatcgag agcctgcgcg 14100

acggacgcac tgacggtgtc gtccatcaca gtttgccagt gatacacatg gggatcagca 14160

atcgcgcata tgaaatcacg ccatgtagtg tattgaccga ttccttgcgg tccgaatggg 14220

ccgaacccgc tcgtctggct aagatcggcc gcagcgatcg catccatagc ctccgcgacc 14280

ggttgtagaa cagcgggcag ttcggtttca ggcaggtctt gcaacgtgac accctgtgca 14340

cggcgggaga tgcaataggt caggctctcg ctaaactccc caatgtcaag cacttccgga 14400

atcgggagcg cggccgatgc aaagtgccga taaacataac gatctttgta gaaaccatcg 14460

gcgcagctat ttacccgcag gacatatcca cgccctccta catcgaagct gaaagcacga 14520

gattcttcgc cctccgagag ctgcatcagg tcggagacgc tgtcgaactt ttcgatcaga 14580

aacttctcga cagacgtcgc ggtgagttca ggctttttca tatctcattg cccccgggga 14640

tctgcgaaag ctcgagagag atagatttgt agagagagac tggtgatttc agcgtgtcct 14700

ctccaaatga aatgaacttc cttatataga ggaaggtctt gcgaaggata gtgggattgt 14760

gcgtcatccc ttacgtcagt ggagatatca catcaatcca cttgctttga agacgtggtt 14820

ggaacgtctt ctttttccac gatgctcctc gtgggtgggg gtccatcttt gggaccactg 14880

tcggcagagg catcttgaac gatagccttt cctttatcgc aatgatggca tttgtaggtg 14940

-continued

ccaccttcct tttctactgt ccttttgatg aagtgacaga tagctgggca atggaatccg 15000

aggaggtttc ccgatattac cctttgttga aaagtctcaa tagccctttg gtcttctgag 15060

actgtatctt tgatattctt ggagtagacg agagtgtcgt gctccaccat gttatcacat 15120

caatccactt gctttgaaga cgtggttgga acgtcttctt tttccacgat gctcctcgtg 15180

ggtgggggtc catctttggg accactgtcg gcagaggcat cttgaacgat agcctttcct 15240

ttatcgcaat gatggcattt gtaggtgcca ccttcctttt ctactgtcct tttgatgaag 15300

tgacagatag ctgggcaatg gaatccgagg aggtttcccg atattaccct ttgttgaaaa 15360

gtctcaatag ccctttggtc ttctgagact gtatctttga tattcttgga gtagacgaga 15420

gtgtcgtgct ccaccatgtt ggcaagctgc tctagccaat acgcaaaccg cctctccccg 15480

cgcgttggcc gattcattaa tgcagctggc acgacaggtt tcccgactgg aaagcgggca 15540

gtgagcgcaa cgcaattaat gtgagttagc tcactcatta ggcaccccag gctttacact 15600

ttatgcttcc ggctcgtatg ttgtgtggaa ttgtgagcgg ataacaattt cacacaggaa 15660

acagctatga ccatgattac g 15681

<210> SEQ ID NO 159
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: target site

<400> SEQUENCE: 159

tccccacgtc actgggcgtc 20

<210> SEQ ID NO 160
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: target site

<400> SEQUENCE: 160

cacaccccat ggccaggact 20

<210> SEQ ID NO 161
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: target site

<400> SEQUENCE: 161

gcggagactc gtctacagtt 20

<210> SEQ ID NO 162
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: target site

<400> SEQUENCE: 162

atgtgttaca gcacgtcggg 20

<210> SEQ ID NO 163

-continued

```
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: vector

<400> SEQUENCE: 163

ttggtctacg gagcgatggt                                                20


<210> SEQ ID NO 164
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 164

Asp Arg Leu Phe Ile Asp Trp Lys Arg Arg
1               5                   10


<210> SEQ ID NO 165
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 165

Leu Arg Leu Phe Gly Val Asp Val Glu
1               5


<210> SEQ ID NO 166
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 166

Leu Arg Leu Phe Gly Val Asp Met Glu
1               5


<210> SEQ ID NO 167
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 167

Leu Arg Leu Phe Gly Val Asp Met Glu
1               5


<210> SEQ ID NO 168
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 168

Leu Arg Leu Phe Gly Val Asp Met Glu
1               5
```

-continued

```
<210> SEQ ID NO 169
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 169

Leu Arg Leu Phe Gly Val Asp Met Glu
1               5


<210> SEQ ID NO 170
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 170

Leu Arg Leu Phe Gly Val Asp Met Glu
1               5


<210> SEQ ID NO 171
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 171

Leu Arg Leu Phe Gly Val Asp Met Glu
1               5


<210> SEQ ID NO 172
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 172

Leu Arg Leu Phe Gly Val Asn Met Glu
1               5


<210> SEQ ID NO 173
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 173

Leu Arg Leu Phe Gly Val Asn Met Glu
1               5


<210> SEQ ID NO 174
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 174

Leu Arg Leu Phe Gly Val Asn Met Glu
1               5
```

-continued

```
<210> SEQ ID NO 175
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 175

Leu Arg Leu Phe Gly Val Asn Met Glu
1               5


<210> SEQ ID NO 176
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 176

Leu Arg Leu Phe Gly Val Asn Met Glu
1               5


<210> SEQ ID NO 177
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 177

Leu Arg Leu Phe Gly Val Asn Met Glu
1               5


<210> SEQ ID NO 178
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 178

Leu Arg Leu Phe Gly Val Cys Ile Thr
1               5


<210> SEQ ID NO 179
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 179

Val Arg Leu Phe Gly Val Asp Ile Ala
1               5


<210> SEQ ID NO 180
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 180
```

-continued

Val Arg Leu Phe Gly Val Asp Ile Ala
1   5

<210> SEQ ID NO 181
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 181

Val Arg Leu Phe Gly Val Asp Ile Phe
1   5

<210> SEQ ID NO 182
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 182

Val Arg Leu Phe Gly Val Asp Ile Ser
1   5

<210> SEQ ID NO 183
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 183

Val Arg Leu Phe Gly Val Asn Ile Leu
1   5

<210> SEQ ID NO 184
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 184

Val Arg Leu Phe Gly Val Asn Ile Leu
1   5

<210> SEQ ID NO 185
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 185

Val Arg Leu Phe Gly Val Asp Leu Leu
1   5

<210> SEQ ID NO 186
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

-continued

```
<400> SEQUENCE: 186

Val Arg Leu Phe Gly Val Asp Leu Leu
1               5


<210> SEQ ID NO 187
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 187

Val Arg Leu Phe Gly Val Asp Leu Leu
1               5


<210> SEQ ID NO 188
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 188

Val Arg Leu Phe Gly Val Asp Leu Leu
1               5


<210> SEQ ID NO 189
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 189

Val Arg Leu Phe Gly Val Asn Leu Leu
1               5


<210> SEQ ID NO 190
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 190

Val Arg Leu Phe Gly Val Asn Leu Glu
1               5


<210> SEQ ID NO 191
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 191

Val Arg Leu Phe Gly Val Asn Leu Glu
1               5


<210> SEQ ID NO 192
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
```

```
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 192

Val Arg Leu Phe Gly Val Asn Leu Glu
1               5


<210> SEQ ID NO 193
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 193

Val Arg Leu Phe Gly Val Asn Leu Glu
1               5


<210> SEQ ID NO 194
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 194

Val Arg Leu Phe Gly Val Asn Leu Glu
1               5


<210> SEQ ID NO 195
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 195

Leu Arg Leu Phe Gly Val Asn Leu Asp
1               5


<210> SEQ ID NO 196
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 196

Leu Arg Leu Phe Gly Val Asn Leu Asp
1               5


<210> SEQ ID NO 197
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 197

Val Arg Leu Phe Gly Val Asn Leu Asp
1               5


<210> SEQ ID NO 198
<211> LENGTH: 9
<212> TYPE: PRT
```

-continued

```
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 198

Val Arg Leu Phe Gly Val Asn Leu Asp
1               5


<210> SEQ ID NO 199
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 199

Val Arg Leu Phe Gly Val Asn Leu Asp
1               5


<210> SEQ ID NO 200
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 200

Val Arg Leu Phe Gly Val Asn Leu Asp
1               5


<210> SEQ ID NO 201
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 201

Val Arg Leu Phe Gly Val Asn Leu Asp
1               5


<210> SEQ ID NO 202
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 202

Val Arg Leu Phe Gly Val Asn Leu Asp
1               5


<210> SEQ ID NO 203
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 203

Val Arg Leu Phe Gly Val Asn Leu Asp
1               5


<210> SEQ ID NO 204
```

```
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 204

Val Arg Leu Phe Gly Val Asn Leu Asp
1               5


<210> SEQ ID NO 205
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 205

Val Arg Leu Phe Gly Val Asn Leu Asp
1               5


<210> SEQ ID NO 206
<211> LENGTH: 894
<212> TYPE: DNA
<213> ORGANISM: Brassica rapa

<400> SEQUENCE: 206

atgatgatga caaacttgtc tctttcaaga gaaggagaag aggaggaaga agaagaacaa      60

gaagaggcca agaagcccat ggaagaagta gagagagagc acatgttcga caaagtggtg     120

actccaagcg atgttggtaa actaaaccgg ctcgtgatcc caaagcaata cgcagagaga     180

tacttccctt tagattcatc cacaaacgag aaaggtttgc ttctaaactt cgaagatctc     240

gcaggaaagt catggaggtt ccgttactct tactggaaca gtagtcagag ctatgtcatg     300

actaaaggtt ggagccgttt cgttaaagac aaaaagctag acgccggaga tattgtctct     360

ttccagagat gtgtcggaga ttcaggaaga gacagccgct tgtttattga ttggaggaga     420

agacctaaag ttcctgacca tccgacatcg attgctcact ttgctgccgg atctatgttt     480

cctaggtttt acagttttcc gacagcaact agttacaatc tttacaacta tcagcagcca     540

cgtcatcatc atcacagtgg ttataattat cctcaaattc cgagagaatt tggatacggg     600

tacttggtgg atcaaagagc cgtggtggct gatccgttgg tgattgaatc tgtgccggtg     660

atgatgcacg gaggagctca agttagtcag gcggttgttg gaacggccgg gaagaggctg     720

aggctttttg gagtcgatat ggaggaagaa tcttcatctt ccggtgggag tttgccacgt     780

ggtgacgctt ctccgtcttc ctctttgttt cagctgagac ttggaagcag cagtgaagat     840

gatcacttct ctaagaaagg aaagtcctca ttgccttttg atttggatca ataa           894


<210> SEQ ID NO 207
<211> LENGTH: 540
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 207

Met Ala Ala Ser Pro Ser Ser Pro Leu Thr Ala Pro Pro Glu Pro Val
1               5                   10                  15

Thr Pro Pro Ser Pro Trp Thr Ile Thr Asp Gly Ala Ile Ser Gly Thr
```

-continued

```
            20                  25                  30

Leu Pro Ala Ala Glu Ala Phe Ala Val His Tyr Pro Gly Tyr Pro Ser
        35                  40                  45

Ser Pro Ala Arg Ala Ala Arg Thr Leu Gly Gly Leu Pro Gly Leu Ala
    50                  55                  60

Lys Val Arg Ser Ser Asp Pro Gly Ala Arg Leu Glu Leu Arg Phe Arg
65                  70                  75                   80

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

Thr Gly Leu Leu Leu Arg Leu Ser Lys Arg Lys Gly Ala Ala Ala Pro
            100                 105                 110

Cys Ala His Val Val Ala Arg Val Arg Thr Ala Tyr Tyr Phe Glu Gly
        115                 120                 125

Met Ala Asp Phe Gln His Val Val Pro Val His Ala Ala Gln Thr Arg
    130                 135                 140

Lys Arg Lys His Ser Asp Ser Gln Asn Asp Asn Glu Asn Phe Gly Ser
145                 150                 155                 160

Asp Lys Thr Gly His Asp Glu Ala Asp Gly Asp Val Met Met Leu Val
                165                 170                 175

Pro Pro Leu Phe Ser Val Lys Asp Arg Pro Thr Lys Ile Ala Leu Val
            180                 185                 190

Pro Ser Ser Asn Ala Ile Ser Lys Thr Met His Arg Gly Val Val Gln
        195                 200                 205

Glu Arg Trp Glu Met Asn Val Gly Pro Thr Leu Ala Leu Pro Phe Asn
    210                 215                 220

Thr Gln Val Val Pro Glu Lys Ile Asn Trp Glu Asp His Ile Arg Lys
225                 230                 235                 240

Asn Ser Val Glu Trp Gly Trp Gln Met Ala Val Cys Lys Leu Phe Asp
                245                 250                 255

Glu Arg Pro Val Trp Pro Arg Gln Ser Leu Tyr Glu Arg Phe Leu Asp
            260                 265                 270

Asp Asn Val His Val Ser Gln Asn Gln Phe Lys Arg Leu Leu Phe Arg
        275                 280                 285

Ala Gly Tyr Tyr Phe Ser Thr Gly Pro Phe Gly Lys Phe Trp Ile Arg
    290                 295                 300

Arg Gly Tyr Asp Pro Arg Lys Asp Ser Glu Ser Gln Ile Tyr Gln Arg
305                 310                 315                 320

Ile Asp Phe Arg Met Pro Pro Glu Leu Arg Tyr Leu Leu Arg Leu Lys
                325                 330                 335

Asn Ser Glu Ser Arg Lys Trp Ala Asp Met Cys Lys Leu Glu Thr Met
            340                 345                 350

Pro Ser Gln Ser Phe Ile Tyr Leu Gln Leu Tyr Glu Leu Lys Asp Asp
        355                 360                 365

Phe Ile Gln Ala Glu Ile Arg Lys Pro Ser Tyr Gln Ser Val Cys Ser
    370                 375                 380

Arg Ser Thr Gly Trp Phe Ser Lys Pro Met Ile Lys Thr Leu Arg Leu
385                 390                 395                 400

Gln Val Ser Ile Arg Leu Leu Ser Leu Leu His Asn Glu Glu Ala Lys
                405                 410                 415

Asn Leu Leu Arg Asn Ala His Glu Leu Ile Glu Arg Ser Lys Lys Gln
            420                 425                 430
```

-continued

```
Glu Ala Leu Ser Arg Ser Glu Leu Ser Ile Glu Tyr Asn Asp Ala Asp
        435                 440                 445

Gln Val Ser Ala Ala His Thr Gly Thr Glu Asp Gln Val Gly Pro Asn
    450                 455                 460

Asn Ser Asp Ser Glu Asp Val Asp Asp Glu Glu Glu Glu Glu Glu Leu
465                 470                 475                 480

Glu Gly Tyr Asp Ser Pro Pro Met Ala Asp Asp Ile His Glu Phe Thr
                485                 490                 495

Leu Gly Asp Ser Tyr Ala Phe Gly Glu Gly Phe Ser Asn Gly Tyr Leu
            500                 505                 510

Glu Glu Val Leu Arg Ser Leu Pro Leu Gln Glu Asp Gly Gln Lys Lys
        515                 520                 525

Leu Cys Asp Ala Pro Ile Asn Ala Asp Ala Ser Asp
    530                 535                 540


<210> SEQ ID NO 208
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 208

Met Tyr Cys Ser Arg Gly Arg Ile Asp Pro Ala Glu Glu Gly Gln Val
1               5                   10                  15

Met Gly Gly Leu Gly Val Arg Asp Ala Ser Trp Ala Leu Phe Lys Val
            20                  25                  30

Leu Glu Gln Ser Asp Val Gln Val Gly Gln Asn Arg Leu Leu Leu Thr
        35                  40                  45

Lys Glu Ala Val Trp Gly Gly Pro Ile Pro Lys Leu Phe Pro Glu Leu
    50                  55                  60

Glu Glu Leu Arg Gly Asp Gly Leu Asn Ala Glu Asn Arg Val Ala Val
65                  70                  75                  80

Lys Ile Leu Asp Ala Asp Gly Cys Glu Gly Asp Ala Asn Phe Arg Tyr
                85                  90                  95

Leu Asn Ser Ser Lys Ala Tyr Arg Val Met Gly Pro Gln Trp Ser Arg
            100                 105                 110

Leu Val Lys Glu Thr Gly Met Cys Lys Gly Asp Arg Leu Asp Leu Tyr
        115                 120                 125

Ala Ala Thr Ala Thr Ala Ala Ser Ser Cys Ser Gly Ala Arg Ala Ala
    130                 135                 140

Val Ala Pro Ala Ile Pro Pro Gly Ala Ile Val Lys Ala Ala Gly Phe
145                 150                 155                 160


<210> SEQ ID NO 209
<211> LENGTH: 192
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 209

Met Ala Met His Ala Gly His Ala Trp Trp Gly Val Ala Met Tyr Thr
1               5                   10                  15

Asn His Tyr His His His Tyr Arg His Lys Thr Ser Asp Val Gly Lys
```

-continued

```
            20                  25                  30

Asn Arg Val Lys His Ala Arg Tyr Gly Gly Gly Asp Ser Gly Lys Gly
        35                  40                  45

Ser Asp Ser Gly Lys Trp Arg Arg Tyr Ser Tyr Trp Thr Ser Ser Ser
    50                  55                  60

Tyr Val Thr Lys Gly Trp Ser Arg Tyr Val Lys Lys Arg Asp Ala Gly
65                  70                  75                  80

Asp Val Val His Arg Val Arg Gly Gly Ala Ala Asp Arg Gly Cys Arg
                85                  90                  95

Arg Arg Gly Ser Ala Ala Ala Val Arg Val Thr Ala Asn Gly Gly Trp
            100                 105                 110

Ser Met Cys Tyr Ser Thr Ser Gly Ser Ser Tyr Asp Thr Ser Ala Asn
        115                 120                 125

Ser Tyr Ala Tyr His Arg Ser Val Asp Asp His Ser Asp His Ala Gly
    130                 135                 140

Ser Arg Ala Asp Ala Lys Ser Ser Ser Ala Ala Ser Ala Ser Arg Arg
145                 150                 155                 160

Arg Gly Val Asn Asp Cys Gly Ala Asp Ala Thr Ala Met Tyr Gly Tyr
                165                 170                 175

Met His His Ser Tyr Ala Ala Val Ser Thr Val Asn Tyr Trp Ser Val
            180                 185                 190


<210> SEQ ID NO 210
<211> LENGTH: 491
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 210

Met Glu Leu Met Gln Glu Val Lys Gly Tyr Ser Asp Gly Arg Glu Glu
1                   5                   10                  15

Glu Glu Glu Glu Glu Glu Ala Ala Glu Glu Ile Ile Thr Arg Glu Glu
            20                  25                  30

Ser Ser Arg Leu Leu His Gln His Gln Glu Ala Ala Gly Ser Asn Phe
        35                  40                  45

Ile Ile Asn Asn Asn His His His His Gln His His His His His Thr
    50                  55                  60

Thr Lys Gln Leu Asp Phe Met Asp Leu Ser Leu Gly Ser Ser Lys Asp
65                  70                  75                  80

Glu Gly Asn Leu Gln Gly Ser Ser Ser Ser Val Tyr Ala His His His
                85                  90                  95

His Ala Ala Ser Ala Ser Ser Ser Ala Asn Gly Asn Asn Asn Asn Ser
            100                 105                 110

Ser Ser Ser Asn Leu Gln Gln Gln Gln Gln Gln Pro Ala Glu Lys Glu
        115                 120                 125

His Met Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn
    130                 135                 140

Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asp
145                 150                 155                 160

Ser Ser Ala Asn Glu Lys Gly Leu Leu Leu Asn Phe Glu Asp Arg Asn
                165                 170                 175

Gly Lys Leu Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser
```

-continued

```
            180                 185                 190

Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Lys Leu
        195                 200                 205

Asp Ala Gly Asp Met Val Ser Phe Gln Arg Gly Val Gly Glu Leu Tyr
    210                 215                 220

Arg His Arg Leu Tyr Ile Asp Trp Trp Arg Arg Pro Asp His His His
225                 230                 235                 240

His His His His Gly Pro Asp His Ser Thr Thr Leu Phe Thr Pro Phe
                245                 250                 255

Leu Ile Pro Asn Gln Pro His His Leu Met Ser Ile Arg Trp Gly Ala
            260                 265                 270

Thr Gly Arg Leu Tyr Ser Leu Pro Ser Pro Thr Pro Pro Arg His His
        275                 280                 285

Glu His Leu Asn Tyr Asn Asn Asn Ala Met Tyr His Pro Phe His His
    290                 295                 300

His Gly Ala Gly Ser Gly Ile Asn Ala Thr Thr His His Tyr Asn Asn
305                 310                 315                 320

Tyr His Glu Met Ser Ser Thr Thr Thr Ser Gly Ser Ala Gly Ser Val
                325                 330                 335

Phe Tyr His Arg Ser Thr Pro Pro Ile Ser Met Pro Leu Ala Asp His
            340                 345                 350

Gln Thr Leu Asn Thr Arg Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu
        355                 360                 365

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

Val Ala His His Leu His His Gln Gln His His Gly Gly Lys Ser Ser
385                 390                 395                 400

Gly Pro Ser Ser Thr Ser Thr Ser Pro Ser Thr Ala Gly Lys Arg Leu
                405                 410                 415

Arg Leu Phe Gly Val Asn Met Glu Cys Ala Ser Ser Thr Ser Glu Asp
            420                 425                 430

Pro Lys Cys Phe Ser Leu Leu Ser Ser Ser Ser Met Ala Asn Ser Asn
        435                 440                 445

Ser Gln Pro Pro Leu Gln Leu Leu Arg Glu Asp Thr Leu Ser Ser Ser
    450                 455                 460

Ser Ala Arg Phe Gly Asp Gln Arg Gly Val Gly Glu Pro Ser Met Leu
465                 470                 475                 480

Phe Asp Leu Asp Pro Ser Leu Gln Tyr Arg Gln
                485                 490


<210> SEQ ID NO 211
<211> LENGTH: 297
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 211

Met Met Met Thr Asn Leu Ser Leu Ser Arg Glu Gly Glu Glu Glu Glu
1               5                   10                  15

Glu Glu Glu Gln Glu Glu Ala Lys Lys Pro Met Glu Glu Val Glu Arg
            20                  25                  30

Glu His Met Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu
```

-continued

```
        35                  40                  45

Asn Arg Leu Val Ile Pro Lys Gln Tyr Ala Glu Arg Tyr Phe Pro Leu
    50                  55                  60

Asp Ser Ser Thr Asn Glu Lys Gly Leu Leu Leu Asn Phe Glu Asp Leu
65                  70                  75                  80

Ala Gly Lys Ser Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln
                85                  90                  95

Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys Asp Lys Lys
            100                 105                 110

Leu Asp Ala Gly Asp Ile Val Ser Phe Gln Arg Cys Val Gly Asp Ser
        115                 120                 125

Gly Arg Asp Ser Arg Leu Phe Ile Asp Trp Arg Arg Arg Pro Lys Val
    130                 135                 140

Pro Asp His Pro Thr Ser Ile Ala His Phe Ala Ala Gly Ser Met Phe
145                 150                 155                 160

Pro Arg Phe Tyr Ser Phe Pro Thr Ala Thr Ser Tyr Asn Leu Tyr Asn
                165                 170                 175

Tyr Gln Gln Pro Arg His His His His Ser Gly Tyr Asn Tyr Pro Gln
            180                 185                 190

Ile Pro Arg Glu Phe Gly Tyr Gly Tyr Leu Val Asp Gln Arg Ala Val
        195                 200                 205

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

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

Arg Leu Phe Gly Val Asp Met Glu Glu Glu Ser Ser Ser Ser Gly Gly
                245                 250                 255

Ser Leu Pro Arg Gly Asp Ala Ser Pro Ser Ser Ser Leu Phe Gln Leu
            260                 265                 270

Arg Leu Gly Ser Ser Ser Glu Asp Asp His Phe Ser Lys Lys Gly Lys
        275                 280                 285

Ser Ser Leu Pro Phe Asp Leu Asp Gln
    290                 295


<210> SEQ ID NO 212
<211> LENGTH: 310
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 212

Met Met Thr Asn Leu Ser Leu Ala Arg Glu Gly Glu Glu Glu Glu Glu
1               5                   10                  15

Glu Ala Gly Ala Lys Lys Pro Thr Glu Glu Val Glu Arg Glu His Met
            20                  25                  30

Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
        35                  40                  45

Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe Pro Leu Asp Ser Ser
    50                  55                  60

Thr Asn Glu Lys Gly Leu Ile Leu Asn Phe Glu Asp Leu Thr Gly Lys
65                  70                  75                  80

Ser Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val
```

-continued

```
                85                  90                  95

Met Thr Lys Gly Trp Ser Arg Phe Val Lys Asp Lys Lys Leu Asp Ala
            100                 105                 110

Gly Asp Ile Val Ser Phe Leu Arg Cys Val Gly Asp Thr Gly Arg Asp
        115                 120                 125

Ser Arg Leu Phe Ile Asp Trp Arg Arg Arg Pro Lys Val Pro Asp Tyr
    130                 135                 140

Thr Thr Ser Thr Ser His Phe Pro Ala Gly Ala Met Phe Pro Arg Phe
145                 150                 155                 160

Tyr Ser Phe Gln Thr Ala Thr Thr Ser Thr Ser Tyr Asn Pro Tyr Asn
                165                 170                 175

His Gln Gln Pro Arg His His His Ser Gly Tyr Cys Tyr Pro Gln Ile
            180                 185                 190

Pro Arg Glu Phe Gly Tyr Gly Tyr Val Val Arg Ser Val Asp Gln Arg
        195                 200                 205

Ala Val Val Ala Asp Pro Leu Val Ile Glu Ser Val Pro Val Met Met
    210                 215                 220

His Gly Gly Ala Arg Val Asn Gln Ala Ala Val Gly Thr Ala Gly Lys
225                 230                 235                 240

Arg Leu Arg Leu Phe Gly Val Asp Met Glu Cys Gly Glu Ser Gly Gly
                245                 250                 255

Thr Asn Ser Thr Glu Glu Glu Ser Ser Ser Ser Gly Gly Ser Leu Pro
            260                 265                 270

Arg Gly Gly Ala Ser Pro Ser Ser Ser Met Phe Gln Leu Arg Leu Gly
        275                 280                 285

Asn Ser Ser Glu Asp Asp His Leu Phe Lys Lys Gly Lys Ser Ser Leu
    290                 295                 300

Pro Phe Asn Leu Asp Gln
305                 310


<210> SEQ ID NO 213
<211> LENGTH: 293
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 213

Met Met Thr Asn Leu Ser Leu Ala Arg Glu Gly Glu Ala Gln Val Lys
1               5                   10                  15

Lys Pro Ile Glu Glu Val Glu Arg Glu His Met Phe Asp Lys Val Val
            20                  25                  30

Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln
        35                  40                  45

His Ala Glu Arg Tyr Phe Pro Leu Asp Ser Ser Ser Asn Glu Lys Gly
    50                  55                  60

Leu Leu Leu Asn Phe Glu Asp Leu Thr Gly Lys Ser Trp Arg Phe Arg
65                  70                  75                  80

Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp
                85                  90                  95

Ser Arg Phe Val Lys Asp Lys Lys Leu Asp Ala Gly Asp Ile Val Ser
            100                 105                 110

Phe Gln Arg Cys Val Gly Asp Ser Arg Leu Phe Ile Asp Trp Arg Arg
```

-continued

```
        115                 120                 125

Arg Pro Lys Val Pro Asp Tyr Pro Thr Ser Thr Ala His Phe Ala Ala
    130                 135                 140

Gly Ala Met Phe Pro Arg Phe Tyr Ser Phe Pro Thr Ala Thr Thr Ser
145                 150                 155                 160

Thr Cys Tyr Asp Leu Tyr Asn His Gln Pro Pro Arg His His His Ile
                165                 170                 175

Gly Tyr Gly Tyr Pro Gln Ile Pro Arg Glu Phe Gly Tyr Gly Tyr Phe
            180                 185                 190

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

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

Val Val Gly Thr Ala Gly Lys Arg Leu Arg Leu Phe Gly Val Asp Met
225                 230                 235                 240

Glu Glu Glu Ser Ser Ser Ser Gly Gly Ser Leu Pro Arg Ala Gly Gly
                245                 250                 255

Gly Gly Ala Ser Ser Ser Ser Ser Leu Phe Gln Leu Arg Leu Gly Ser
            260                 265                 270

Ser Cys Glu Asp Asp His Phe Ser Lys Lys Gly Lys Ser Ser Leu Pro
        275                 280                 285

Phe Asp Leu Asp Gln
    290


<210> SEQ ID NO 214
<211> LENGTH: 320
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 214

Met Glu Arg Lys Ser Asn Asp Leu Glu Arg Ser Glu Asn Ile Asp Ser
1               5                   10                  15

Gln Asn Lys Lys Met Asn Leu Glu Glu Glu Arg Pro Val Gln Glu Ala
            20                  25                  30

Ser Ser Met Glu Arg Glu His Met Phe Asp Lys Val Val Thr Pro Ser
        35                  40                  45

Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu
    50                  55                  60

Arg Tyr Phe Pro Leu Asp Asn Asn Ser Ser Asp Asn Asn Lys Gly Leu
65                  70                  75                  80

Leu Leu Asn Phe Glu Asp Arg Ile Gly Ile Leu Trp Ser Phe Arg Tyr
                85                  90                  95

Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser
            100                 105                 110

Arg Phe Val Lys Asp Lys Lys Leu Asp Ala Gly Asp Ile Val Ser Phe
        115                 120                 125

His Arg Gly Ser Cys Asn Lys Asp Lys Leu Phe Ile Asp Trp Lys Arg
    130                 135                 140

Arg Pro Lys Ile Pro Asp His Gln Val Val Gly Ala Met Phe Pro Arg
145                 150                 155                 160

Phe Tyr Ser Tyr Pro Tyr Pro Gln Ile Gln Ala Ser Tyr Glu Arg His
```

-continued

```
                165                 170                 175

Asn Leu Tyr His Arg Tyr Gln Arg Asp Ile Gly Ile Gly Tyr Tyr Val
            180                 185                 190

Arg Ser Met Glu Arg Tyr Asp Pro Thr Ala Val Ile Glu Ser Val Pro
        195                 200                 205

Val Ile Met Gln Arg Arg Ala His Val Ala Thr Met Ala Ser Ser Arg
    210                 215                 220

Gly Glu Lys Arg Leu Arg Leu Phe Gly Val Asp Met Glu Cys Val Arg
225                 230                 235                 240

Gly Gly Arg Gly Gly Gly Gly Ser Val Asn Ser Thr Glu Glu Glu Ser
                245                 250                 255

Ser Thr Ser Gly Gly Ser Ile Ser Arg Gly Gly Val Ser Met Ala Gly
            260                 265                 270

Val Gly Ser Pro Leu Gln Leu Arg Leu Val Ser Ser Asp Gly Asp Asp
        275                 280                 285

Gln Ser Leu Val Ala Arg Gly Ala Ala Arg Val Asp Glu Asp His His
    290                 295                 300

Leu Phe Thr Lys Lys Gly Lys Ser Ser Leu Ser Phe Asp Leu Asp Lys
305                 310                 315                 320


<210> SEQ ID NO 215
<211> LENGTH: 286
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 215

Met Asn Gln Glu Glu Glu Asn Pro Val Glu Lys Ala Ser Ser Met Glu
1               5                   10                  15

Arg Glu His Met Phe Glu Lys Val Val Thr Pro Ser Asp Val Gly Lys
            20                  25                  30

Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe Pro
        35                  40                  45

Leu Asp Asn Asn Ser Asp Ser Ser Lys Gly Leu Leu Leu Asn Phe Glu
    50                  55                  60

Asp Arg Thr Gly Asn Ser Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser
65                  70                  75                  80

Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys Asp
                85                  90                  95

Lys Lys Leu Asp Ala Gly Asp Ile Val Ser Phe Gln Arg Asp Pro Gly
            100                 105                 110

Asn Lys Asp Lys Leu Phe Ile Asp Trp Arg Arg Arg Pro Lys Ile Pro
        115                 120                 125

Asp His His His Gln Phe Ala Gly Ala Met Phe Pro Arg Phe Tyr Ser
    130                 135                 140

Phe Ser His Pro Gln Asn Leu Tyr His Arg Tyr Gln Gln Asp Leu Gly
145                 150                 155                 160

Ile Gly Tyr Tyr Val Ser Ser Met Glu Arg Asn Asp Pro Thr Ala Val
                165                 170                 175

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

Ala Ile Pro Ser Ser Arg Gly Glu Lys Arg Leu Arg Leu Phe Gly Val
```

-continued

```
        195                 200                 205

Asp Met Glu Cys Gly Gly Gly Gly Gly Ser Val Asn Ser Thr Glu Glu
    210                 215                 220

Glu Ser Ser Ser Ser Gly Gly Gly Gly Gly Val Ser Met Ala Ser Val
225                 230                 235                 240

Gly Ser Leu Leu Gln Leu Arg Leu Val Ser Ser Asp Asp Glu Ser Leu
                245                 250                 255

Val Ala Met Glu Ala Ala Ser Val Asp Glu Asp His His Leu Phe Thr
            260                 265                 270

Lys Lys Gly Lys Ser Ser Leu Ser Phe Asp Leu Asp Arg Lys
        275                 280                 285


<210> SEQ ID NO 216
<211> LENGTH: 292
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 216

Met Asn Gln Glu Asn Lys Lys Pro Leu Glu Glu Ala Ser Thr Ser Met
1               5                   10                  15

Glu Arg Glu Asn Met Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly
            20                  25                  30

Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe
        35                  40                  45

Pro Leu Asp Asn Ser Ser Thr Asn Asn Lys Gly Leu Leu Leu Asp Phe
    50                  55                  60

Glu Asp Arg Thr Gly Ser Ser Trp Arg Phe Arg Tyr Ser Tyr Trp Asn
65                  70                  75                  80

Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys
                85                  90                  95

Asp Lys Lys Leu Asp Ala Gly Asp Ile Val Ser Phe Gln Arg Asp Pro
            100                 105                 110

Cys Asn Lys Asp Lys Leu Tyr Ile Asp Trp Arg Arg Arg Pro Lys Ile
        115                 120                 125

Pro Asp His His Gln Phe Ala Gly Ala Met Phe Pro Arg Phe Tyr Ser
    130                 135                 140

Phe Pro His Pro Gln Met Pro Thr Ser Phe Glu Ser Ser His Asn Leu
145                 150                 155                 160

Tyr His His Arg Phe Gln Arg Asp Leu Gly Ile Gly Tyr Tyr Pro Thr
                165                 170                 175

Ala Val Ile Glu Ser Val Pro Val Ile Met Gln Arg Arg Glu Ala Gln
            180                 185                 190

Val Ala Asn Met Ala Ser Ser Arg Gly Glu Lys Arg Leu Arg Leu Phe
        195                 200                 205

Gly Val Asp Val Glu Cys Gly Gly Gly Gly Gly Gly Ser Val Asn Ser
    210                 215                 220

Thr Glu Glu Glu Ser Ser Ser Ser Gly Gly Ser Met Ser Arg Gly Gly
225                 230                 235                 240

Val Ser Met Ala Gly Val Gly Ser Leu Leu Gln Leu Arg Leu Val Ser
                245                 250                 255

Ser Asp Asp Glu Ser Leu Val Ala Met Glu Gly Ala Thr Val Asp Glu
```

-continued

```
            260                 265                 270

Asp His His Leu Phe Thr Thr Lys Lys Gly Lys Ser Ser Leu Ser Phe
        275                 280                 285

Asp Leu Asp Ile
    290


<210> SEQ ID NO 217
<211> LENGTH: 420
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 217

Met Glu Leu Met Gln Gln Val Lys Gly Asn Tyr Ser Asp Ser Arg Glu
1               5                   10                  15

Glu Glu Glu Glu Glu Glu Ala Ala Ala Ile Thr Arg Glu Ser Glu Ser
            20                  25                  30

Ser Arg Leu His Gln Gln Asp Thr Ala Ser Asn Phe Gly Lys Lys Leu
        35                  40                  45

Asp Leu Met Asp Leu Ser Leu Gly Ser Ser Lys Glu Glu Glu Glu Glu
    50                  55                  60

Gly Asn Leu Gln Gln Gly Gly Gly Gly Val Val His His Ala His Gln
65                  70                  75                  80

Val Val Glu Lys Glu His Met Phe Glu Lys Val Ala Thr Pro Ser Asp
                85                  90                  95

Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys
            100                 105                 110

Tyr Phe Pro Leu Asp Ser Ser Thr Asn Glu Lys Gly Leu Leu Leu Asn
        115                 120                 125

Phe Glu Asp Arg Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp
    130                 135                 140

Asn Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val
145                 150                 155                 160

Lys Glu Lys Lys Leu Asp Ala Gly Asp Ile Val Ser Phe Gln Arg Gly
                165                 170                 175

Leu Gly Asp Leu Tyr Arg His Arg Leu Tyr Ile Asp Trp Lys Arg Arg
            180                 185                 190

Pro Asp His Ala His Ala His Pro Pro His His His Asp Pro Leu Phe
        195                 200                 205

Leu Pro Ser Ile Arg Leu Tyr Ser Leu Pro Pro Thr Met Pro Pro Arg
    210                 215                 220

Tyr His His Asp His His Phe His His His Leu Asn Tyr Asn Asn Leu
225                 230                 235                 240

Phe Thr Phe Gln Gln His Gln Tyr Gln Gln Leu Gly Ala Ala Thr Thr
                245                 250                 255

Thr His His Asn Asn Tyr Gly Tyr Gln Asn Ser Gly Ser Gly Ser Leu
            260                 265                 270

Tyr Tyr Leu Arg Ser Ser Met Ser Met Gly Gly Gly Asp Gln Asn Leu
        275                 280                 285

Gln Gly Arg Gly Ser Asn Ile Val Pro Met Ile Ile Asp Ser Val Pro
    290                 295                 300

Val Asn Val Ala His His Asn Asn Asn Arg His Gly Asn Gly Gly Ile
```

-continued

```
305                 310                 315                 320

Thr Ser Gly Gly Thr Asn Cys Ser Gly Lys Arg Leu Arg Leu Phe Gly
                325                 330                 335

Val Asn Met Glu Cys Ala Ser Ser Ala Glu Asp Ser Lys Glu Leu Ser
            340                 345                 350

Ser Gly Ser Ala Ala His Val Thr Thr Ala Ala Ser Ser Ser Ser Leu
        355                 360                 365

His His Gln Arg Leu Arg Val Pro Val Pro Val Pro Leu Glu Asp Pro
    370                 375                 380

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

Ala Ser Thr Gly Thr Ser Leu Leu Phe Asp Leu Asp Pro Ser Leu Gln
                405                 410                 415

Tyr His Arg His
            420


<210> SEQ ID NO 218
<211> LENGTH: 422
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 218

Met Asp Gln Phe Ala Ala Ser Gly Arg Phe Ser Arg Glu Glu Glu Ala
1               5                   10                  15

Asp Glu Glu Gln Glu Asp Ala Ser Asn Ser Met Arg Glu Ile Ser Phe
            20                  25                  30

Met Pro Pro Ala Ala Ala Ser Ser Ser Ser Ala Ala Ala Ser Ala Ser
        35                  40                  45

Ala Ser Ala Ser Thr Ser Ala Ser Ala Cys Ala Ser Gly Ser Ser Ser
    50                  55                  60

Ala Pro Phe Arg Ser Ala Ser Ala Ser Gly Asp Ala Ala Gly Ala Ser
65                  70                  75                  80

Gly Ser Gly Gly Pro Ala Asp Ala Asp Ala Glu Ala Glu Ala Val Glu
                85                  90                  95

Lys Glu His Met Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys
            100                 105                 110

Leu Asn Arg Leu Val Ile Pro Lys Gln Tyr Ala Glu Lys Tyr Phe Pro
        115                 120                 125

Leu Asp Ala Ala Ala Asn Glu Lys Gly Leu Leu Leu Ser Phe Glu Asp
    130                 135                 140

Ser Ala Gly Lys His Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser
145                 150                 155                 160

Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys
                165                 170                 175

Arg Leu Val Ala Gly Asp Thr Val Ser Phe Ser Arg Ala Ala Ala Glu
            180                 185                 190

Asp Ala Arg His Arg Leu Phe Ile Asp Trp Lys Arg Arg Val Asp Thr
        195                 200                 205

Arg Gly Pro Leu Arg Phe Ser Gly Leu Ala Leu Pro Met Pro Leu Pro
    210                 215                 220

Ser Ser His Tyr Gly Gly Pro His His Tyr Ser Pro Trp Gly Phe Gly
```

-continued

```
225                 230                 235                 240

Gly Gly Gly Gly Gly Gly Gly Gly Phe Phe Met Pro Pro Ser Pro Pro
                245                 250                 255

Ala Thr Leu Tyr Glu His Arg Leu Arg Gln Gly Leu Asp Phe Arg Ser
            260                 265                 270

Met Thr Thr Thr Tyr Pro Ala Pro Thr Val Gly Arg Gln Leu Leu Phe
        275                 280                 285

Phe Gly Ser Ala Arg Met Pro Pro His His Ala Pro Pro Pro Gln Pro
    290                 295                 300

Arg Pro Phe Ser Leu Pro Leu His His Tyr Thr Val Gln Pro Ser Ala
305                 310                 315                 320

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

Val Ile Glu Ser Pro Thr Thr Ala Ala Lys Arg Val Arg Leu Phe Gly
            340                 345                 350

Val Asn Leu Asp Asn Asn Pro Asp Gly Gly Gly Glu Ala Ser His Gln
        355                 360                 365

Gly Asp Ala Leu Ser Leu Gln Met Pro Gly Trp Gln Gln Arg Thr Pro
    370                 375                 380

Thr Leu Arg Leu Leu Glu Leu Pro Arg His Gly Gly Glu Ser Ser Ala
385                 390                 395                 400

Ala Ser Ser Pro Ser Ser Ser Ser Ser Ser Lys Arg Glu Ala Arg Ser
                405                 410                 415

Ala Leu Asp Leu Asp Leu
            420


<210> SEQ ID NO 219
<211> LENGTH: 412
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 219

Met Glu Phe Thr Thr Ser Ser Arg Phe Ser Lys Glu Glu Glu Asp Glu
1               5                   10                  15

Glu Gln Asp Glu Ala Gly Arg Arg Glu Ile Pro Phe Met Thr Ala Thr
            20                  25                  30

Ala Glu Ala Ala Pro Ala Pro Thr Ser Ser Ser Ser Ser Pro Ala His
        35                  40                  45

His Ala Ala Ser Ala Ser Ala Ser Ala Ser Ala Ser Gly Ser Ser Thr
    50                  55                  60

Pro Phe Arg Ser Asp Asp Gly Ala Gly Ala Ser Gly Ser Gly Gly Gly
65                  70                  75                  80

Gly Gly Gly Gly Gly Glu Ala Glu Val Val Glu Lys Glu His Met Phe
                85                  90                  95

Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val
            100                 105                 110

Ile Pro Lys Gln Tyr Ala Glu Lys Tyr Phe Pro Leu Asp Ala Ala Ala
        115                 120                 125

Asn Glu Lys Gly Leu Leu Leu Asn Phe Glu Asp Arg Ala Gly Lys Pro
    130                 135                 140

Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met
```

-continued

```
145                 150                 155                 160

Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Asp Ala Gly
                165                 170                 175

Asp Thr Val Ser Phe Ser Arg Gly Ile Gly Asp Glu Ala Ala Arg His
            180                 185                 190

Arg Leu Phe Ile Asp Trp Lys Arg Arg Ala Asp Thr Arg Asp Pro Leu
        195                 200                 205

Arg Leu Pro Arg Gly Leu Pro Leu Pro Met Pro Leu Thr Ser His Tyr
    210                 215                 220

Ala Pro Trp Gly Ile Gly Gly Gly Gly Gly Phe Phe Val Gln Pro Ser
225                 230                 235                 240

Pro Pro Ala Thr Leu Tyr Glu His Arg Leu Arg Gln Gly Leu Asp Phe
                245                 250                 255

Arg Ala Phe Asn Pro Ala Ala Ala Met Gly Arg Gln Val Leu Leu Phe
            260                 265                 270

Gly Ser Ala Arg Ile Pro Pro Gln Ala Pro Leu Leu Ala Arg Ala Pro
        275                 280                 285

Ser Pro Leu His His His Tyr Thr Leu Gln Pro Ser Gly Asp Gly Val
    290                 295                 300

Arg Ala Ala Gly Ser Pro Val Val Leu Asp Ser Val Pro Val Ile Glu
305                 310                 315                 320

Ser Pro Thr Thr Ala Ala Lys Arg Val Arg Leu Phe Gly Val Asn Leu
                325                 330                 335

Asp Asn Pro His Ala Gly Gly Gly Gly Gly Ala Ala Ala Gly Glu Ser
            340                 345                 350

Ser Asn His Gly Asn Ala Leu Ser Leu Gln Thr Pro Ala Trp Met Arg
        355                 360                 365

Arg Asp Pro Thr Leu Arg Leu Leu Glu Leu Pro Pro His His His His
    370                 375                 380

Gly Ala Glu Ser Ser Ala Ala Ser Ser Pro Ser Ser Ser Ser Ser Ser
385                 390                 395                 400

Lys Arg Asp Ala His Ser Ala Leu Asp Leu Asp Leu
                405                 410


<210> SEQ ID NO 220
<211> LENGTH: 409
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 220

Met Glu Phe Thr Ala Thr Ser Ser Arg Phe Ser Lys Gly Glu Glu Glu
1               5                   10                  15

Val Glu Glu Glu Gln Glu Glu Ala Ser Met Arg Glu Ile Pro Phe Met
            20                  25                  30

Thr Pro Ala Ala Ala Thr Cys Ala Ala Ala Pro Pro Ser Ala Ser Ala
        35                  40                  45

Ser Ala Ser Thr Pro Ala Ser Ala Ser Gly Ser Ser Pro Pro Phe Arg
    50                  55                  60

Ser Gly Asp Asp Ala Gly Ala Ser Gly Ser Gly Ala Gly Asp Gly Ser
65                  70                  75                  80

Arg Ser Asn Val Ala Glu Ala Val Glu Lys Glu His Met Phe Asp Lys
```

-continued

```
                85                  90                  95

Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro
            100                 105                 110

Lys Gln Tyr Ala Glu Lys Tyr Phe Pro Leu Asp Ser Ala Ala Asn Glu
        115                 120                 125

Lys Gly Leu Leu Leu Asn Phe Glu Asp Ser Ala Gly Lys Pro Trp Arg
    130                 135                 140

Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys
145                 150                 155                 160

Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Asp Ala Gly Asp Thr
                165                 170                 175

Val Ser Phe Ser Arg Gly Ala Gly Glu Ala Ala Arg His Arg Leu Phe
            180                 185                 190

Ile Asp Trp Lys Arg Arg Ala Asp Thr Arg Asp Pro Leu Arg Leu Pro
        195                 200                 205

Arg Leu Pro Leu Pro Met Pro Leu Thr Ser His Tyr Ser Pro Trp Gly
    210                 215                 220

Leu Gly Ala Gly Ala Arg Gly Phe Phe Met Pro Pro Ser Pro Pro Ala
225                 230                 235                 240

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

Asn Pro Ser Tyr Pro Thr Met Gly Arg Gln Val Ile Leu Phe Gly Ser
            260                 265                 270

Ala Ala Arg Met Pro Pro His Gly Pro Ala Pro Leu Leu Val Pro Arg
        275                 280                 285

Pro Pro Pro Pro Leu His Phe Thr Val Gln Gln Gln Gly Ser Asp Ala
    290                 295                 300

Gly Gly Ser Val Thr Ala Gly Ser Pro Val Val Leu Asp Ser Val Pro
305                 310                 315                 320

Val Ile Glu Ser Pro Thr Thr Ala Thr Lys Lys Arg Val Arg Leu Phe
                325                 330                 335

Gly Val Asn Leu Asp Asn Pro Gln His Pro Gly Asp Gly Gly Gly Glu
            340                 345                 350

Ser Ser Asn Tyr Gly Ser Ala Leu Pro Leu Gln Met Pro Ala Ser Ala
        355                 360                 365

Trp Arg Pro Arg Asp His Thr Leu Arg Leu Leu Glu Phe Pro Ser His
    370                 375                 380

Gly Ala Glu Ala Ser Ser Pro Ser Ser Ser Ser Ser Ser Lys Arg Glu
385                 390                 395                 400

Ala His Ser Gly Leu Asp Leu Asp Leu
                405


<210> SEQ ID NO 221
<211> LENGTH: 316
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 221

Met Glu Phe Ala Thr Thr Ser Ser Arg Phe Ser Lys Glu Glu Glu Glu
1               5                   10                  15

Glu Glu Glu Gly Glu Gln Glu Met Glu Gln Glu Gln Asp Glu Glu Glu
```

-continued

20 25 30

Glu Glu Ala Glu Ala Ser Pro Arg Glu Ile Pro Phe Met Thr Ser Ala
35 40 45

Ala Ala Ala Ala Thr Ala Ser Ser Ser Ser Pro Thr Ser Val Ser Pro
50 55 60

Ser Ala Thr Ala Ser Ala Ala Ala Ser Thr Ser Ala Ser Gly Ser Pro
65 70 75 80

Phe Arg Ser Ser Asp Gly Ala Gly Ala Ser Gly Ser Gly Gly Gly Gly
85 90 95

Gly Gly Glu Asp Val Glu Val Ile Glu Lys Glu His Met Phe Asp Lys
100 105 110

Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro
115 120 125

Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asp Ser Ala Ala Asn Glu
130 135 140

Lys Gly Leu Leu Leu Ser Phe Glu Asp Arg Thr Gly Lys Leu Trp Arg
145 150 155 160

Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys
165 170 175

Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Asp Ala Gly Asp Thr
180 185 190

Val Ser Phe Cys Arg Gly Ala Ala Glu Ala Thr Arg Asp Arg Leu Phe
195 200 205

Ile Asp Trp Lys Arg Arg Ala Asp Val Arg Asp Pro His Arg Phe Gln
210 215 220

Arg Leu Pro Leu Pro Met Thr Ser Pro Tyr Gly Pro Trp Gly Gly Gly
225 230 235 240

Ala Gly Ala Ser Ser Cys Arg Pro Arg Arg Pro Pro Arg Ser Thr Ser
245 250 255

Ile Thr Ala Phe Ala Arg Ala Ser Thr Ser Ala Thr Ser Thr Pro Leu
260 265 270

Cys Arg Arg Gly Ser Ser Ser Ser Ser Ala Pro Gln Gly Arg Gly Phe
275 280 285

Ile Ser Thr Arg Pro Cys His Arg Arg Arg Arg His Leu Arg Leu Leu
290 295 300

Thr Asn Ser Thr Leu Arg Cys Thr Thr Arg Ala Pro
305 310 315

<210> SEQ ID NO 222
<211> LENGTH: 409
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 222

Met Glu Phe Ala Ser Ser Ser Ser Arg Phe Ser Arg Glu Glu Asp Glu
1 5 10 15

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

Glu Ile Pro Phe Met Thr Ala Ala Ala Thr Ala Asp Thr Gly Ala Ala
35 40 45

Ala Ser Ser Ser Ser Pro Ser Ala Ala Ala Ser Ser Gly Pro Ala Ala

-continued

```
    50                  55                  60

Ala Pro Arg Ser Ser Asp Gly Ala Gly Ala Ser Gly Ser Gly Gly Gly
65                  70                  75                  80

Gly Ser Asp Asp Val Gln Val Ile Glu Lys Glu His Met Phe Asp Lys
                85                  90                  95

Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro
            100                 105                 110

Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asp Ala Ala Ala Asn Glu
        115                 120                 125

Lys Gly Gln Leu Leu Ser Phe Glu Asp Arg Ala Gly Lys Leu Trp Arg
    130                 135                 140

Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys
145                 150                 155                 160

Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Asp Ala Gly Asp Thr
                165                 170                 175

Val Ser Phe Cys Arg Gly Ala Gly Asp Thr Ala Arg Asp Arg Leu Phe
            180                 185                 190

Ile Asp Trp Lys Arg Arg Ala Asp Ser Arg Asp Pro His Arg Met Pro
        195                 200                 205

Arg Leu Pro Leu Pro Met Ala Pro Val Ala Ser Pro Tyr Gly Pro Trp
    210                 215                 220

Gly Gly Gly Gly Gly Gly Gly Ala Gly Gly Phe Phe Met Pro Pro Ala
225                 230                 235                 240

Pro Pro Ala Thr Leu Tyr Glu His His Arg Phe Arg Gln Ala Leu Asp
                245                 250                 255

Phe Arg Asn Ile Asn Ala Ala Ala Ala Pro Ala Arg Gln Leu Leu Phe
            260                 265                 270

Phe Gly Ser Ala Gly Met Pro Pro Arg Ala Ser Met Pro Gln Gln Gln
        275                 280                 285

Gln Pro Pro Pro Pro Pro His Pro Pro Leu His Ser Ile Met Leu Val
    290                 295                 300

Gln Pro Ser Pro Ala Pro Pro Thr Ala Ser Val Pro Met Leu Leu Asp
305                 310                 315                 320

Ser Val Pro Leu Val Asn Ser Pro Thr Ala Ala Ser Lys Arg Val Arg
                325                 330                 335

Leu Phe Gly Val Asn Leu Asp Asn Pro Gln Pro Gly Thr Ser Ala Glu
            340                 345                 350

Ser Ser Gln Asp Ala Asn Ala Leu Ser Leu Arg Thr Pro Gly Trp Gln
        355                 360                 365

Arg Pro Gly Pro Leu Arg Phe Phe Glu Ser Pro Gln Arg Gly Ala Glu
    370                 375                 380

Ser Ser Ala Ala Ser Ser Pro Ser Ser Ser Ser Ser Ser Lys Arg Glu
385                 390                 395                 400

Ala His Ser Ser Leu Asp Leu Asp Leu
                405


<210> SEQ ID NO 223
<211> LENGTH: 312
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment
```

-continued

```
<400> SEQUENCE: 223

Met Glu Phe Thr Pro Ile Ser Pro Pro Thr Arg Val Ala Gly Gly Glu
1               5                   10                  15

Glu Asp Ser Glu Arg Gly Ala Ala Ala Trp Ala Val Val Glu Lys Glu
            20                  25                  30

His Met Phe Glu Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn
        35                  40                  45

Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe Pro Leu Asp
    50                  55                  60

Ala Ala Ala Gly Ala Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
65                  70                  75                  80

Gly Gly Lys Gly Leu Val Leu Ser Phe Glu Asp Arg Thr Gly Lys Ala
                85                  90                  95

Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met
            100                 105                 110

Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Gly Ala Gly
        115                 120                 125

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

Leu Phe Ile Asp Phe Arg Arg Arg Arg Gln Asp Ala Gly Ser Phe Met
145                 150                 155                 160

Phe Pro Pro Thr Ala Ala Pro Pro Ser His Ser His His His His Gln
                165                 170                 175

Arg His His Pro Pro Leu Pro Ser Val Pro Leu Cys Pro Trp Arg Asp
            180                 185                 190

Tyr Thr Thr Ala Tyr Gly Gly Gly Tyr Gly Tyr Gly Tyr Gly Gly Gly
        195                 200                 205

Ser Thr Pro Ala Ser Ser Arg His Val Leu Phe Leu Arg Pro Gln Val
    210                 215                 220

Pro Ala Ala Val Val Leu Lys Ser Val Pro Val His Val Ala Ala Thr
225                 230                 235                 240

Ser Ala Val Gln Glu Ala Ala Thr Thr Thr Arg Pro Lys Arg Val Arg
                245                 250                 255

Leu Phe Gly Val Asn Leu Asp Cys Pro Ala Ala Met Asp Asp Asp Asp
            260                 265                 270

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

Leu Pro Ser Pro Ser Ser Ser Thr Ser Ser Ser Thr Ala Gly Lys Lys
    290                 295                 300

Met Cys Ser Leu Asp Leu Gly Leu
305                 310


<210> SEQ ID NO 224
<211> LENGTH: 277
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 224

Met Glu Phe Thr Pro Ala His Ala His Ala Arg Val Val Glu Asp Ser
1               5                   10                  15

Glu Arg Pro Arg Gly Gly Val Ala Trp Val Glu Lys Glu His Met Phe
```

-continued

```
            20                  25                  30

Glu Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val
        35                  40                  45

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

Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Lys Gly
65                  70                  75                  80

Leu Val Leu Ser Phe Glu Asp Arg Ala Gly Lys Ala Trp Arg Phe Arg
                85                  90                  95

Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp
            100                 105                 110

Ser Arg Phe Val Lys Glu Lys Arg Leu Gly Ala Gly Asp Thr Val Leu
        115                 120                 125

Phe Ala Arg Gly Ala Gly Gly Ala Arg Gly Arg Phe Phe Ile Asp Phe
    130                 135                 140

Arg Arg Arg Arg Gln Asp Leu Ala Phe Leu Gln Pro Thr Leu Ala Ser
145                 150                 155                 160

Ala Gln Arg Leu Leu Pro Leu Pro Ser Val Pro Ile Cys Pro Trp Gln
                165                 170                 175

Asp Tyr Gly Ala Ser Ala Pro Ala Pro Asn Arg His Val Leu Phe Leu
            180                 185                 190

Arg Pro Gln Val Pro Ala Ala Val Val Leu Lys Ser Val Pro Val His
        195                 200                 205

Val Ala Ala Ser Ala Val Glu Ala Thr Met Ser Lys Arg Val Arg Leu
    210                 215                 220

Phe Gly Val Asn Leu Asp Cys Pro Pro Asp Ala Glu Asp Ser Ala Thr
225                 230                 235                 240

Val Pro Arg Gly Arg Ala Ala Ser Thr Thr Leu Leu Gln Leu Pro Ser
                245                 250                 255

Pro Ser Ser Ser Thr Ser Ser Ser Thr Ala Gly Lys Asp Val Cys Cys
            260                 265                 270

Leu Asp Leu Gly Leu
        275


<210> SEQ ID NO 225
<211> LENGTH: 273
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 225

Met Glu Phe Arg Pro Ala His Ala Arg Val Phe Glu Asp Ser Glu Arg
1               5                   10                  15

Pro Arg Gly Gly Val Ala Trp Leu Glu Lys Glu His Met Phe Glu Lys
            20                  25                  30

Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro
        35                  40                  45

Lys Gln His Ala Glu Arg Tyr Phe Pro Ala Leu Asp Ala Ser Ala Ala
    50                  55                  60

Ala Ala Ser Ala Ser Ala Ser Ala Gly Gly Gly Lys Ala Gly Leu Val
65                  70                  75                  80

Leu Ser Phe Glu Asp Arg Ala Gly Lys Ala Trp Arg Phe Arg Tyr Ser
```

-continued

```
                85                  90                  95

Tyr Trp Asn Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg
            100                 105                 110

Phe Val Lys Glu Lys Arg Leu Gly Ala Gly Asp Thr Val Leu Phe Ala
        115                 120                 125

Arg Gly Ala Gly Ala Thr Arg Gly Arg Phe Phe Ile Asp Phe Arg Arg
    130                 135                 140

Arg Arg His Glu Leu Ala Phe Leu Gln Pro Pro Leu Ala Ser Ala Gln
145                 150                 155                 160

Arg Leu Leu Pro Leu Pro Ser Val Pro Ile Cys Pro Trp Gln Gly Tyr
                165                 170                 175

Gly Ala Ser Ala Pro Ala Pro Ser Arg His Val Leu Phe Leu Arg Pro
            180                 185                 190

Gln Val Pro Ala Ala Val Val Leu Thr Ser Val Pro Val Arg Val Ala
        195                 200                 205

Ala Ser Ala Val Glu Glu Ala Thr Arg Ser Lys Arg Val Arg Leu Phe
    210                 215                 220

Gly Val Asn Leu Asp Cys Pro Pro Asp Ala Glu Asp Gly Ala Thr Ala
225                 230                 235                 240

Thr Arg Thr Pro Ser Thr Leu Leu Gln Leu Pro Ser Pro Ser Ser Ser
                245                 250                 255

Thr Ser Ser Ser Thr Gly Gly Lys Asp Val Arg Ser Leu Asp Leu Gly
            260                 265                 270

Leu


<210> SEQ ID NO 226
<211> LENGTH: 282
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 226

Met Glu Phe Ile Thr Pro Ile Val Arg Pro Ala Ser Ala Ala Ala Gly
1               5                   10                  15

Gly Gly Glu Val Gln Glu Ser Glu Arg Pro Arg Gly Gly Val Ala Trp
            20                  25                  30

Leu Glu Lys Glu His Met Phe Glu Lys Val Val Thr Pro Ser Asp Val
        35                  40                  45

Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr
    50                  55                  60

Phe Pro Ala Leu Asp Ala Ser Ala Ala Ala Ala Ser Ala Ser Ala Ser
65                  70                  75                  80

Ala Gly Gly Gly Lys Ala Gly Leu Val Leu Ser Phe Glu Asp Arg Ala
                85                  90                  95

Gly Lys Ala Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser
            100                 105                 110

Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu
        115                 120                 125

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

Gly Arg Phe Phe Ile Asp Phe Arg Arg Arg Arg His Glu Leu Ala Phe
145                 150                 155                 160
```

-continued

```
Leu Gln Pro Pro Leu Ala Ser Ala Gln Arg Leu Leu Pro Leu Pro Ser
                165                 170                 175

Val Pro Ile Cys Pro Trp Gln Gly Tyr Gly Ala Ser Ala Pro Ala Pro
            180                 185                 190

Ser Arg His Val Leu Phe Leu Arg Pro Gln Val Pro Ala Ala Val Val
        195                 200                 205

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

Thr Arg Ser Lys Arg Val Arg Leu Phe Gly Val Asn Leu Asp Cys Pro
225                 230                 235                 240

Pro Asp Ala Glu Asp Gly Ala Thr Ala Thr Arg Thr Pro Ser Thr Leu
                245                 250                 255

Leu Gln Leu Pro Ser Pro Ser Ser Ser Thr Ser Ser Ser Thr Gly Gly
            260                 265                 270

Lys Asp Val Arg Ser Leu Asp Leu Gly Leu
        275                 280


<210> SEQ ID NO 227
<211> LENGTH: 259
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 227

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

Glu Arg Ala Ala Ala Glu His Asn Gln His His Gln Gln Gln His Ala
            20                  25                  30

Thr Val Glu Lys Glu His Met Phe Asp Lys Val Val Thr Pro Ser Asp
        35                  40                  45

Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys
    50                  55                  60

Tyr Phe Pro Leu Asp Ala Ala Ala Asn Glu Lys Gly Leu Leu Leu Ser
65                  70                  75                  80

Phe Glu Asp Arg Thr Gly Lys Pro Trp Arg Phe Arg Tyr Ser Tyr Trp
                85                  90                  95

Asn Ser Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val
            100                 105                 110

Lys Glu Lys Arg Leu Asp Ala Gly Asp Thr Val Ser Phe Gly Arg Gly
        115                 120                 125

Ile Ser Glu Ala Ala Arg Asp Arg Leu Phe Ile Asp Trp Arg Cys Arg
    130                 135                 140

Pro Asp Pro Pro Val Val His His Gln Tyr His His Arg Leu Pro Leu
145                 150                 155                 160

Pro Ser Ala Val Val Pro Tyr Ala Pro Trp Ala Ala His Ala His His
                165                 170                 175

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

Cys Ala Thr Leu Val Ala Thr Glu Met Arg Ala Ser Ser Ser Gln Leu
        195                 200                 205

Ser Leu Thr Arg Ser Asn Leu Ser Arg Pro Pro Gln Pro Arg Ile Ala
    210                 215                 220
```

-continued

```
Arg Val Asp Gly Ala Gln Pro Arg Pro Ser Ser Ser Pro Arg Gln Pro
225                 230                 235                 240

Gln Ser Leu Trp Cys Arg Ser Cys Gln Pro Gln Pro Arg Arg Thr Ala
                245                 250                 255

Asp Val Pro


<210> SEQ ID NO 228
<211> LENGTH: 327
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 228

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

Glu Arg Ala Ala Ala Glu His His Gln Gln Gln Gln Gln Ala Thr Val
            20                  25                  30

Glu Lys Glu His Met Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly
        35                  40                  45

Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe
    50                  55                  60

Pro Leu Asp Ala Ala Ala Asn Asp Lys Gly Leu Leu Leu Ser Phe Glu
65                  70                  75                  80

Asp Arg Ala Gly Lys Pro Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser
                85                  90                  95

Ser Gln Ser Tyr Val Met Thr Lys Gly Trp Ser Arg Phe Val Lys Glu
            100                 105                 110

Lys Arg Leu Asp Ala Gly Asp Thr Val Ser Phe Gly Arg Gly Val Gly
        115                 120                 125

Glu Ala Ala Arg Gly Arg Leu Phe Ile Asp Trp Arg Arg Arg Pro Asp
    130                 135                 140

Pro Pro Val Val His His Gln Tyr His His His Arg Leu Pro Leu Pro
145                 150                 155                 160

Ser Ala Val Val Pro Tyr Ala Pro Trp Ala Ala Ala Ala His Ala His
                165                 170                 175

His His His Tyr Pro Ala Ala Gly Val Gly Ala Ala Arg Thr Thr Thr
            180                 185                 190

Thr Thr Thr Thr Thr Val Leu His His Leu Pro Pro Ser Pro Ser Pro
        195                 200                 205

Leu Tyr Leu Asp Thr Arg Arg Arg His Val Gly Tyr Asp Ala Tyr Gly
    210                 215                 220

Ala Gly Thr Arg Gln Leu Leu Phe Tyr Arg Pro His Gln Gln Pro Ser
225                 230                 235                 240

Thr Thr Val Met Leu Asp Ser Val Pro Val Arg Leu Pro Pro Thr Pro
                245                 250                 255

Gly Gln His Ala Glu Pro Pro Pro Pro Ala Val Ala Ser Ser Ala Ser
            260                 265                 270

Lys Arg Val Arg Leu Phe Gly Val Asn Leu Asp Cys Ala Ala Ala Ala
        275                 280                 285

Gly Ser Glu Glu Glu Asn Val Gly Gly Trp Arg Thr Ser Ala Pro Pro
    290                 295                 300
```

```
Thr Gln Gln Ala Ser Ser Ser Ser Ser Tyr Ser Ser Gly Lys Ala Arg
305                 310                 315                 320

Cys Ser Leu Asn Leu Asp Leu
                325


<210> SEQ ID NO 229
<211> LENGTH: 279
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 229

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

Pro Trp Gly Val Ala Met Tyr Ala Asn Phe His Tyr His His His Tyr
            20                  25                  30

Glu Lys Glu His Met Phe Glu Lys Pro Leu Thr Pro Ser Asp Val Gly
        35                  40                  45

Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe
    50                  55                  60

Pro Leu Gly Ala Gly Asp Ala Ala Asp Lys Gly Leu Ile Leu Ser Phe
65                  70                  75                  80

Glu Asp Glu Ala Gly Ala Pro Trp Arg Phe Arg Tyr Ser Tyr Trp Thr
                85                  90                  95

Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys
            100                 105                 110

Glu Lys Arg Leu Asp Ala Gly Asp Val Val His Phe Glu Arg Val Arg
        115                 120                 125

Gly Ser Phe Gly Val Gly Asp Arg Leu Phe Ile Gly Cys Arg Arg Arg
    130                 135                 140

Gly Asp Ala Ala Ala Ala Gln Thr Pro Ala Pro Pro Pro Ala Val Arg
145                 150                 155                 160

Val Ala Pro Ala Ala Gln Asn Ala Gly Glu Gln Gln Pro Trp Ser Pro
                165                 170                 175

Met Cys Tyr Ser Thr Ser Gly Gly Gly Ser Tyr Pro Thr Ser Pro Ala
            180                 185                 190

Asn Ser Tyr Ala Tyr Arg Arg Ala Ala Asp His Asp His Gly Asp Met
        195                 200                 205

His His Ala Asp Glu Ser Pro Arg Asp Thr Asp Ser Pro Ser Phe Ser
    210                 215                 220

Ala Gly Ser Ala Pro Ser Arg Arg Leu Arg Leu Phe Gly Val Asn Leu
225                 230                 235                 240

Asp Cys Gly Pro Glu Pro Glu Ala Asp Thr Thr Ala Ala Ala Thr Met
                245                 250                 255

Tyr Gly Tyr Met His Gln Gln Ser Ser Tyr Ala Ala Met Ser Ala Val
            260                 265                 270

Pro Ser Tyr Trp Gly Asn Ser
        275


<210> SEQ ID NO 230
<211> LENGTH: 307
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
```

-continued

```
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 230

Met Ala Thr Asn His Leu Ser Gln Gly Gln His Gln His Pro Gln Ala
1               5                   10                  15

Trp Pro Trp Gly Val Ala Met Tyr Thr Asn Leu His Tyr His His Gln
            20                  25                  30

Gln His His His Tyr Glu Lys Glu His Leu Phe Glu Lys Pro Leu Thr
        35                  40                  45

Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His
    50                  55                  60

Ala Glu Arg Tyr Phe Pro Leu Ser Ser Ser Gly Ala Gly Asp Lys Gly
65                  70                  75                  80

Leu Ile Leu Cys Phe Glu Asp Asp Asp Asp Asp Glu Ala Ala Ala Ala
                85                  90                  95

Asn Lys Pro Trp Arg Phe Arg Tyr Ser Tyr Trp Thr Ser Ser Gln Ser
            100                 105                 110

Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys Glu Lys Gln Leu
        115                 120                 125

Asp Ala Gly Asp Val Val Arg Phe Gln Arg Met Arg Gly Phe Gly Met
    130                 135                 140

Pro Asp Arg Leu Phe Ile Ser His Ser Arg Arg Gly Glu Thr Thr Ala
145                 150                 155                 160

Thr Ala Ala Thr Thr Val Pro Pro Ala Ala Ala Ala Val Arg Val Val
                165                 170                 175

Val Ala Pro Ala Gln Ser Ala Gly Ala Asp His Gln Gln Gln Gln Gln
            180                 185                 190

Pro Ser Pro Trp Ser Pro Met Cys Tyr Ser Thr Ser Gly Ser Tyr Ser
        195                 200                 205

Tyr Pro Thr Ser Ser Pro Ala Asn Ser Gln His Ala Tyr His Arg His
    210                 215                 220

Ser Ala Asp His Asp His Ser Asn Asn Met Gln His Ala Gly Glu Ser
225                 230                 235                 240

Gln Ser Asp Arg Asp Asn Arg Ser Cys Ser Ala Ala Ser Ala Pro Pro
                245                 250                 255

Pro Pro Ser Arg Arg Leu Arg Leu Phe Gly Val Asn Leu Asp Cys Gly
            260                 265                 270

Pro Gly Pro Glu Pro Glu Thr Pro Thr Ala Met Tyr Gly Tyr Met His
        275                 280                 285

Gln Ser Pro Tyr Ala Tyr Asn Asn Trp Gly Ser Pro Tyr Gln His Asp
    290                 295                 300

Glu Glu Ile
305


<210> SEQ ID NO 231
<211> LENGTH: 288
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 231

Met Ser Ser Ile Asn His Tyr Ser Pro Glu Thr Thr Leu Tyr Trp Thr
1               5                   10                  15
```

-continued

```
Asn Asp Gln Gln Gln Gln Ala Ala Met Trp Leu Ser Asn Ser His Thr
            20                  25                  30

Pro Arg Phe Asn Leu Asn Asp Glu Glu Glu Glu Glu Asp Asp Val
        35                  40                  45

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

Val Ala Met Phe Glu Lys Pro Leu Thr Pro Ser Asp Val Gly Lys Leu
65                  70                  75                  80

Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu
                85                  90                  95

Asp Ser Ser Ala Ala Lys Gly Leu Leu Leu Ser Phe Glu Asp Glu Ser
            100                 105                 110

Gly Lys Cys Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser
        115                 120                 125

Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys Asp Lys Arg Leu
    130                 135                 140

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

Arg Phe Phe Ile Ser Cys Ser Arg Arg Gln Pro Asn Pro Val Pro Ala
                165                 170                 175

His Val Ser Thr Thr Arg Ser Ser Ala Ser Phe Tyr Ser Ala His Pro
            180                 185                 190

Pro Tyr Pro Ala His His Phe Pro Phe Pro Tyr Gln Pro His Ser Leu
        195                 200                 205

His Ala Pro Gly Gly Gly Ser Gln Gly Gln Asn Glu Thr Thr Pro Gly
    210                 215                 220

Gly Asn Ser Ser Ser Ser Gly Ser Gly Arg Val Leu Arg Leu Phe Gly
225                 230                 235                 240

Val Asn Met Glu Cys Gln Pro Asp Asn His Asn Asp Ser Gln Asn Ser
                245                 250                 255

Thr Pro Glu Cys Ser Tyr Thr His Leu Tyr His His Gln Thr Ser Ser
            260                 265                 270

Tyr Ser Ser Ser Ser Asn Pro His His His Met Val Pro Gln Gln Pro
        275                 280                 285


<210> SEQ ID NO 232
<211> LENGTH: 337
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 232

Met Ser Ile Asn His Tyr Ser Met Asp Leu Pro Glu Pro Thr Leu Trp
1               5                   10                  15

Trp Pro His Pro His His Gln Gln Gln Gln Leu Thr Leu Met Asp Pro
            20                  25                  30

Asp Pro Leu Arg Leu Asn Leu Asn Ser Asp Asp Gly Asn Gly Asn Asp
        35                  40                  45

Asn Asp Asn Asp Glu Asn Gln Thr Thr Thr Thr Gly Gly Glu Gln Glu
    50                  55                  60

Ile Leu Asp Asp Lys Glu Pro Met Phe Glu Lys Pro Leu Thr Pro Ser
65                  70                  75                  80
```

-continued

```
Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu
                85                  90                  95

Lys Tyr Phe Pro Leu Ser Gly Asp Ser Gly Gly Ser Glu Cys Lys Gly
            100                 105                 110

Leu Leu Leu Ser Phe Glu Asp Glu Ser Gly Lys Cys Trp Arg Phe Arg
        115                 120                 125

Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp
    130                 135                 140

Ser Arg Tyr Val Lys Asp Lys Arg Leu Asp Ala Gly Asp Val Val Leu
145                 150                 155                 160

Phe Glu Arg His Arg Val Asp Ala Gln Arg Leu Phe Ile Gly Trp Arg
                165                 170                 175

Arg Arg Arg Gln Ser Asp Ala Ala Leu Pro Pro Ala His Val Ser Ser
            180                 185                 190

Arg Lys Ser Gly Gly Gly Asp Gly Asn Ser Asn Lys Asn Glu Gly Trp
        195                 200                 205

Thr Arg Gly Phe Tyr Ser Ala His His Pro Tyr Pro Thr His His Leu
    210                 215                 220

His His His Gln Pro Ser Pro Tyr Gln Gln Gln His Asp Cys Leu His
225                 230                 235                 240

Ala Gly Arg Gly Ser Gln Gly Gln Asn Gln Arg Met Arg Pro Val Gly
                245                 250                 255

Asn Asn Ser Ser Ser Ser Ser Ser Ser Ser Arg Val Leu Arg Leu Phe
            260                 265                 270

Gly Val Asp Met Glu Cys Gln Pro Glu His Asp Asp Ser Gly Pro Ser
        275                 280                 285

Thr Pro Gln Cys Ser Tyr Asn Ser Asn Asn Met Leu Pro Ser Thr Gln
    290                 295                 300

Gly Thr Asp His Ser His His Asn Phe Tyr Gln Gln Gln Pro Ser Asn
305                 310                 315                 320

Ser Asn Pro Ser Pro His His Met Met Val His His Gln Pro Tyr Tyr
                325                 330                 335

Tyr


<210> SEQ ID NO 233
<211> LENGTH: 344
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 233

Met Ser Thr Asn His Tyr Thr Met Asp Leu Pro Glu Pro Thr Leu Trp
1               5                   10                  15

Trp Pro His Pro His Gln Gln Gln Leu Thr Leu Ile Asp Pro Asp Pro
            20                  25                  30

Leu Pro Leu Asn Leu Asn Asn Asp Asp Asn Asp Asn Gly Asp Asp Asn
        35                  40                  45

Asp Asn Asp Glu Asn Gln Thr Val Thr Thr Thr Thr Thr Gly Gly Glu
    50                  55                  60

Glu Glu Ile Ile Asn Asn Lys Glu Pro Met Phe Glu Lys Pro Leu Thr
65                  70                  75                  80
```

-continued

```
Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His
                85                  90                  95

Ala Glu Lys Tyr Phe Pro Leu Ser Gly Gly Asp Ser Gly Ser Ser Glu
            100                 105                 110

Cys Lys Gly Leu Leu Leu Ser Phe Glu Asp Glu Ser Gly Lys Cys Trp
        115                 120                 125

Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr
    130                 135                 140

Lys Gly Trp Ser Arg Tyr Val Lys Asp Lys Arg Leu Asp Ala Gly Asp
145                 150                 155                 160

Val Val Leu Phe Gln Arg His Arg Ala Asp Ala Gln Arg Leu Phe Ile
                165                 170                 175

Gly Trp Arg Arg Arg Arg Gln Ser Asp Ala Leu Pro Pro Pro Ala His
            180                 185                 190

Val Ser Ser Arg Lys Ser Gly Gly Asp Gly Asn Ser Ser Lys Asn Glu
        195                 200                 205

Gly Asp Val Gly Val Gly Trp Thr Arg Gly Phe Tyr Pro Ala His His
    210                 215                 220

Pro Tyr Pro Thr His His His His Pro Ser Pro Tyr His His Gln Gln
225                 230                 235                 240

Asp Asp Ser Leu His Ala Val Arg Gly Ser Gln Gly Gln Asn Gln Arg
                245                 250                 255

Thr Arg Pro Val Gly Asn Ser Ser Ser Ser Ser Ser Ser Ser Ser Arg
            260                 265                 270

Val Leu Arg Leu Phe Gly Val Asn Met Glu Cys Gln Pro Glu His Asp
        275                 280                 285

Asp Ser Gly Pro Ser Thr Pro Gln Cys Ser Tyr Asn Thr Asn Asn Ile
    290                 295                 300

Leu Pro Ser Thr Gln Gly Thr Asp Ile His Ser His Leu Asn Phe Tyr
305                 310                 315                 320

Gln Gln Gln Gln Thr Ser Asn Ser Lys Pro Pro Pro His His Met Met
                325                 330                 335

Ile Arg His Gln Pro Tyr Tyr Tyr
            340


<210> SEQ ID NO 234
<211> LENGTH: 245
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 234

Met Ser Ile Asn Gln Tyr Ser Ser Glu Phe Tyr Tyr His Ser Leu Met
1               5                   10                  15

Trp Gln Gln Gln Gln Gln His His His Gln Asn Glu Val Val Glu Glu
            20                  25                  30

Lys Glu Ala Leu Phe Glu Lys Pro Leu Thr Pro Ser Asp Val Gly Lys
        35                  40                  45

Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe Pro
    50                  55                  60

Leu Ala Ala Ala Ala Val Asp Ala Val Glu Lys Gly Leu Leu Leu Cys
65                  70                  75                  80
```

-continued

```
Phe Glu Asp Glu Glu Gly Lys Pro Trp Arg Phe Arg Tyr Ser Tyr Trp
                85                  90                  95

Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val
            100                 105                 110

Lys Glu Lys Gln Leu Asp Ala Gly Asp Val Val Leu Phe His Arg His
        115                 120                 125

Arg Ala Asp Gly Gly Arg Phe Phe Ile Gly Trp Arg Arg Arg Gly Asp
    130                 135                 140

Ser Ser Ser Ser Ser Asp Ser Tyr Arg Asn Leu Gln Ser Asn Ser Ser
145                 150                 155                 160

Leu Gln Tyr Tyr Pro His Ala Gly Ala Gln Ala Val Glu Asn Gln Arg
                165                 170                 175

Gly Asn Ser Lys Thr Leu Arg Leu Phe Gly Val Asn Met Glu Cys Gln
            180                 185                 190

Ile Asp Ser Asp Trp Ser Glu Pro Ser Thr Pro Asp Gly Phe Thr Thr
        195                 200                 205

Cys Pro Thr Asn His Asp Gln Phe Pro Ile Tyr Pro Glu His Phe Pro
    210                 215                 220

Pro Pro Tyr Tyr Met Asp Val Ser Phe Thr Gly Asp Val His Gln Thr
225                 230                 235                 240

Ser Ser Gln Gln Gly
                245
```

<210> SEQ ID NO 235
<211> LENGTH: 244
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 235

```
Met Ser Ile Asn Gln Tyr Ser Ser Asp Phe His Tyr His Ser Leu Met
1               5                   10                  15

Trp Gln Gln Gln Gln Gln Gln Gln Gln His Gln Asn Asp Val Val Glu
            20                  25                  30

Glu Lys Glu Ala Leu Phe Glu Lys Pro Leu Thr Pro Ser Asp Val Gly
        35                  40                  45

Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe
    50                  55                  60

Pro Leu Ala Ala Ala Ala Ala Asp Ala Val Glu Lys Gly Leu Leu Leu
65                  70                  75                  80

Cys Phe Glu Asp Glu Glu Gly Lys Pro Trp Arg Phe Arg Tyr Ser Tyr
                85                  90                  95

Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr
            100                 105                 110

Val Lys Glu Lys His Leu Asp Ala Gly Asp Val Val Leu Phe His Arg
        115                 120                 125

His Arg Ser Asp Gly Gly Arg Phe Phe Ile Gly Trp Arg Arg Arg Gly
    130                 135                 140

Asp Ser Ser Ser Ser Ser Asp Ser Tyr Arg His Val Gln Ser Asn Ala
145                 150                 155                 160

Ser Leu Gln Tyr Tyr Pro His Ala Gly Ala Gln Ala Val Glu Ser Gln
                165                 170                 175
```

-continued

```
Arg Gly Asn Ser Lys Thr Leu Arg Leu Phe Gly Val Asn Met Glu Cys
            180                 185                 190

Gln Leu Asp Ser Asp Trp Ser Glu Pro Ser Thr Pro Asp Gly Ser Asn
        195                 200                 205

Thr Tyr Thr Thr Asn His Asp Gln Phe His Phe Tyr Pro Gln Gln Gln
    210                 215                 220

His Tyr Pro Pro Pro Tyr Tyr Met Asp Ile Ser Phe Thr Gly Asp Met
225                 230                 235                 240

Asn Arg Thr Ser


<210> SEQ ID NO 236
<211> LENGTH: 248
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 236

Met Ser Ile Asn Gln Tyr Ser Ser Asp Phe Asn Tyr His Ser Leu Met
1               5                   10                  15

Trp Gln Gln Gln Gln His Arg His His His His Gln Asn Asp Val Ala
            20                  25                  30

Glu Glu Lys Glu Ala Leu Phe Glu Lys Pro Leu Thr Pro Ser Asp Val
        35                  40                  45

Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg Tyr
    50                  55                  60

Phe Pro Leu Ala Ala Ala Ala Ala Asp Ala Met Glu Lys Gly Leu Leu
65                  70                  75                  80

Leu Cys Phe Glu Asp Glu Glu Gly Lys Pro Trp Arg Phe Arg Tyr Ser
                85                  90                  95

Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg
            100                 105                 110

Tyr Val Lys Glu Lys Gln Leu Asp Ala Gly Asp Val Ile Leu Phe His
        115                 120                 125

Arg His Arg Val Asp Gly Gly Arg Phe Phe Ile Gly Trp Arg Arg Arg
    130                 135                 140

Gly Asn Ser Ser Ser Ser Ser Asp Ser Tyr Arg His Leu Gln Ser Asn
145                 150                 155                 160

Ala Ser Leu Gln Tyr Tyr Pro His Ala Gly Val Gln Ala Val Glu Ser
                165                 170                 175

Gln Arg Gly Asn Ser Lys Thr Leu Arg Leu Phe Gly Val Asn Met Glu
            180                 185                 190

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

Thr Ile Cys Pro Thr Ser His Asp Gln Phe His Leu Tyr Pro Gln Gln
    210                 215                 220

His Tyr Pro Pro Pro Tyr Tyr Met Asp Ile Ser Phe Thr Gly Asp Val
225                 230                 235                 240

His Gln Thr Arg Ser Pro Gln Gly
                245


<210> SEQ ID NO 237
<211> LENGTH: 267
<212> TYPE: PRT
```

-continued

```
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 237

Met Ser Val Asn His Tyr His Asn Thr Leu Ser Leu His His His His
1               5                   10                  15

Gln Asn Asp Val Ala Ile Ala Gln Arg Glu Ser Leu Phe Glu Lys Ser
            20                  25                  30

Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys
        35                  40                  45

Gln His Ala Glu Lys Tyr Phe Pro Leu Asn Asn Asn Asn Asn Asn Gly
    50                  55                  60

Gly Ser Gly Asp Asp Val Ala Thr Thr Glu Lys Gly Met Leu Leu Ser
65                  70                  75                  80

Phe Glu Asp Glu Ser Gly Lys Cys Trp Lys Phe Arg Tyr Ser Tyr Trp
                85                  90                  95

Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val
            100                 105                 110

Lys Asp Lys His Leu Asp Ala Gly Asp Val Val Phe Phe Gln Arg His
        115                 120                 125

Arg Phe Asp Leu His Arg Leu Phe Ile Gly Trp Arg Arg Arg Gly Glu
    130                 135                 140

Ala Ser Ser Ser Pro Ala Val Ser Val Val Ser Gln Glu Ala Leu Val
145                 150                 155                 160

Asn Thr Thr Ala Tyr Trp Ser Gly Leu Thr Thr Pro Tyr Arg Gln Val
                165                 170                 175

His Ala Ser Thr Thr Tyr Pro Asn Ile His Gln Glu Tyr Ser His Tyr
            180                 185                 190

Gly Ala Val Val Asp His Ala Gln Ser Ile Pro Pro Val Val Ala Gly
        195                 200                 205

Ser Ser Arg Thr Val Arg Leu Phe Gly Val Asn Leu Glu Cys His Gly
    210                 215                 220

Asp Ala Val Glu Pro Pro Pro Arg Pro Asp Val Tyr Asn Asp Gln His
225                 230                 235                 240

Ile Tyr Tyr Tyr Ser Thr Pro His Pro Met Asn Ile Ser Phe Ala Gly
                245                 250                 255

Glu Ala Leu Glu Gln Val Gly Asp Gly Arg Gly
            260                 265


<210> SEQ ID NO 238
<211> LENGTH: 264
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 238

Met Ser Gly Asn His Tyr Ser Arg Asp Ile His His Asn Thr Pro Ser
1               5                   10                  15

Val His His His Gln Asn Tyr Ala Val Val Asp Arg Glu Tyr Leu Phe
            20                  25                  30

Glu Lys Ser Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val
        35                  40                  45
```

-continued

```
Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Asn Asn Ala Gly
    50                  55                  60

Asp Asp Val Ala Ala Ala Glu Thr Thr Glu Lys Gly Met Leu Leu Thr
65                  70                  75                  80

Phe Glu Asp Glu Ser Gly Lys Cys Trp Lys Phe Arg Tyr Ser Tyr Trp
                85                  90                  95

Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val
            100                 105                 110

Lys Asp Lys His Leu His Ala Gly Asp Val Val Phe Phe Gln Arg His
        115                 120                 125

Arg Phe Asp Leu His Arg Val Phe Ile Gly Trp Arg Lys Arg Gly Glu
    130                 135                 140

Val Ser Ser Pro Thr Ala Val Ser Val Val Ser Gln Glu Ala Arg Val
145                 150                 155                 160

Asn Thr Thr Ala Tyr Trp Ser Gly Leu Thr Thr Pro Tyr Arg Gln Val
                165                 170                 175

His Ala Ser Thr Ser Ser Tyr Pro Asn Ile His Gln Glu Tyr Ser His
            180                 185                 190

Tyr Gly Ala Val Ala Glu Ile Pro Thr Val Val Thr Gly Ser Ser Arg
        195                 200                 205

Thr Val Arg Leu Phe Gly Val Asn Leu Glu Cys His Gly Asp Val Val
    210                 215                 220

Glu Thr Pro Pro Cys Pro Asp Gly Tyr Asn Gly Gln His Phe Tyr Tyr
225                 230                 235                 240

Tyr Ser Thr Pro Asp Pro Met Asn Ile Ser Phe Ala Gly Glu Ala Met
                245                 250                 255

Glu Gln Val Gly Asp Gly Arg Arg
            260


<210> SEQ ID NO 239
<211> LENGTH: 258
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 239

Met Ser Val Asn His Tyr Ser Asn Thr Leu Ser Ser His Asn His His
1               5                   10                  15

Asn Glu His Lys Glu Ser Leu Phe Glu Lys Ser Leu Thr Pro Ser Asp
            20                  25                  30

Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Arg
        35                  40                  45

Tyr Leu Pro Leu Asn Asn Cys Gly Gly Gly Gly Asp Val Thr Ala Glu
    50                  55                  60

Ser Thr Glu Lys Gly Val Leu Leu Ser Phe Glu Asp Glu Ser Gly Lys
65                  70                  75                  80

Ser Trp Lys Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val
                85                  90                  95

Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys Asp Lys His Leu Asn Ala
            100                 105                 110

Gly Asp Val Val Leu Phe Gln Arg His Arg Phe Asp Ile His Arg Leu
        115                 120                 125
```

-continued

```
Phe Ile Gly Trp Arg Arg Arg Gly Glu Ala Ser Ser Ser Ser Ala Val
    130                 135                 140

Ser Ala Val Thr Gln Asp Pro Arg Ala Asn Thr Thr Ala Tyr Trp Asn
145                 150                 155                 160

Gly Leu Thr Thr Pro Tyr Arg Gln Val His Ala Ser Thr Ser Ser Tyr
                165                 170                 175

Pro Asn Asn Ile His Gln Glu Tyr Ser His Tyr Gly Pro Val Ala Glu
            180                 185                 190

Thr Pro Thr Val Ala Ala Gly Ser Ser Lys Thr Val Arg Leu Phe Gly
        195                 200                 205

Val Asn Leu Glu Cys His Ser Asp Val Val Glu Pro Pro Pro Cys Pro
    210                 215                 220

Asp Ala Tyr Asn Gly Gln His Ile Tyr Tyr Tyr Ser Thr Pro His Pro
225                 230                 235                 240

Met Asn Ile Ser Phe Ala Gly Glu Ala Met Glu Gln Val Gly Asp Gly
                245                 250                 255

Arg Gly


<210> SEQ ID NO 240
<211> LENGTH: 278
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 240

Met Ser Val Asn His Tyr Ser Thr Asp His His His Thr Leu Leu Trp
1               5                   10                  15

Gln Gln Gln Gln His Arg His Thr Thr Asp Thr Ser Glu Thr Thr Thr
            20                  25                  30

Thr Ala Thr Trp Leu His Asp Asp Leu Lys Glu Ser Leu Phe Glu Lys
        35                  40                  45

Ser Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro
    50                  55                  60

Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asn Ala Val Leu Val Ser
65                  70                  75                  80

Ser Ala Ala Ala Asp Thr Ser Ser Ser Leu Leu Ser Phe Glu Asp Glu
                85                  90                  95

Ser Gly Lys Ser Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln
            100                 105                 110

Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Asp Lys Gln
        115                 120                 125

Leu Asp Pro Gly Asp Val Val Phe Phe Gln Arg His Arg Ser Asp Ser
    130                 135                 140

Arg Arg Leu Phe Ile Gly Trp Arg Arg Arg Gly Gln Gly Ser Ser Ser
145                 150                 155                 160

Ser Val Ala Ala Thr Asn Ser Ala Val Asn Thr Ser Ser Met Gly Ala
                165                 170                 175

Leu Ser Tyr His Gln Ile His Ala Thr Ser Asn Tyr Ser Asn Pro Pro
            180                 185                 190

Ser His Ser Glu Tyr Ser His Tyr Gly Ala Ala Val Ala Thr Ala Ala
        195                 200                 205

Glu Thr His Ser Thr Pro Ser Ser Ser Val Val Gly Ser Ser Arg Thr
```

-continued

```
    210                 215                 220

Val Arg Leu Phe Gly Val Asn Leu Glu Cys Gln Met Asp Glu Asn Asp
225                 230                 235                 240

Gly Asp Asp Ser Val Ala Val Ala Thr Thr Val Glu Ser Pro Asp Gly
                245                 250                 255

Tyr Tyr Gly Gln Asn Met Tyr Tyr Tyr Tyr Ser His Pro His Asn Met
            260                 265                 270

Val Ile Leu Thr Leu Leu
        275


<210> SEQ ID NO 241
<211> LENGTH: 267
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 241

Met Ser Val Asn His Tyr Ser Thr Asp His His Gln Val His His His
1               5                   10                  15

His Thr Leu Phe Leu Gln Asn Leu His Thr Thr Asp Thr Ser Glu Pro
            20                  25                  30

Thr Thr Thr Ala Ala Thr Ser Leu Arg Glu Asp Gln Lys Glu Tyr Leu
        35                  40                  45

Phe Glu Lys Ser Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
    50                  55                  60

Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asn Thr Ile
65                  70                  75                  80

Ile Ser Asn Asn Ala Glu Glu Lys Gly Met Leu Leu Ser Phe Glu Asp
                85                  90                  95

Glu Ser Gly Lys Cys Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser
            100                 105                 110

Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys Asp Lys
        115                 120                 125

Gln Leu Asp Pro Ala Asp Val Val Phe Phe Gln Arg Gln Arg Ser Asp
    130                 135                 140

Ser Arg Arg Leu Phe Ile Gly Trp Arg Arg Arg Gly Gln Gly Ser Ser
145                 150                 155                 160

Ser Ala Ala Asn Thr Thr Ser Tyr Ser Ser Ser Met Thr Ala Pro Pro
                165                 170                 175

Tyr Ser Asn Tyr Ser Asn Arg Pro Ala His Ser Glu Tyr Ser His Tyr
            180                 185                 190

Gly Ala Ala Val Ala Thr Ala Thr Glu Thr His Phe Ile Pro Ser Ser
        195                 200                 205

Ser Ala Val Gly Ser Ser Arg Thr Val Arg Leu Phe Gly Val Asn Leu
    210                 215                 220

Glu Cys Gln Met Asp Glu Asp Glu Gly Asp Asp Ser Val Ala Thr Ala
225                 230                 235                 240

Ala Ala Ala Glu Cys Pro Arg Gln Asp Ser Tyr Tyr Asp Gln Asn Met
                245                 250                 255

Tyr Asn Tyr Tyr Thr Pro His Ser Ser Ala Ser
            260                 265
```

-continued

```
<210> SEQ ID NO 242
<211> LENGTH: 347
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 242

Met Ile Gly Val Glu Lys Val Thr Ile Cys Met Arg Ile Glu Val Asn
1               5                   10                  15

Thr Glu Lys Gly Arg Arg Ala Leu Met Asp Cys Trp Gln Ile Ser Gly
            20                  25                  30

Val His Glu Ser Ser Asp Cys Ser Glu Ile Lys Phe Ala Phe Asp Ala
        35                  40                  45

Val Val Lys Arg Ala Arg His Glu Glu Asn Asn Ala Ala Ala Gln Lys
    50                  55                  60

Phe Lys Gly Val Val Ser Gln Gln Asn Gly Asn Trp Gly Ala Gln Ile
65                  70                  75                  80

Tyr Ala His Gln Gln Arg Ile Trp Leu Gly Thr Phe Lys Ser Glu Arg
                85                  90                  95

Glu Ala Ala Met Ala Tyr Asp Ser Ala Ser Ile Lys Leu Arg Ser Gly
            100                 105                 110

Glu Cys His Arg Asn Phe Pro Trp Asn Asp Gln Thr Val Gln Glu Pro
        115                 120                 125

Gln Phe Gln Ser His Tyr Ser Ala Glu Thr Val Leu Asn Met Ile Arg
    130                 135                 140

Asp Gly Thr Tyr Pro Ser Lys Phe Ala Thr Phe Leu Lys Thr Arg Gln
145                 150                 155                 160

Thr Gln Lys Gly Val Ala Lys His Ile Gly Leu Lys Gly Asp Asp Glu
                165                 170                 175

Glu Gln Phe Cys Cys Thr Gln Leu Phe Gln Lys Glu Leu Thr Pro Ser
            180                 185                 190

Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Lys His Ala Val
        195                 200                 205

Ser Tyr Phe Pro Tyr Val Gly Gly Ser Ala Asp Glu Ser Gly Ser Val
    210                 215                 220

Asp Val Glu Ala Val Phe Tyr Asp Lys Leu Met Arg Leu Trp Lys Phe
225                 230                 235                 240

Arg Tyr Cys Tyr Trp Lys Ser Ser Gln Ser Tyr Val Phe Thr Arg Gly
                245                 250                 255

Trp Asn Arg Phe Val Lys Asp Lys Lys Leu Lys Ala Lys Asp Val Ile
            260                 265                 270

Ala Phe Phe Thr Trp Gly Lys Ser Gly Gly Glu Gly Glu Ala Phe Ala
        275                 280                 285

Leu Ile Asp Val Ile Tyr Asn Asn Asn Ala Glu Glu Asp Ser Lys Gly
    290                 295                 300

Asp Thr Lys Gln Val Leu Gly Asn Gln Leu Gln Leu Ala Gly Ser Glu
305                 310                 315                 320

Glu Gly Glu Asp Glu Asp Ala Asn Ile Gly Lys Asp Phe Asn Ala Gln
                325                 330                 335

Lys Gly Leu Arg Leu Phe Gly Val Cys Ile Thr
            340                 345
```

-continued

```
<210> SEQ ID NO 243
<211> LENGTH: 267
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 243

Met Leu Arg Lys His Ile Tyr Pro Asp Glu Leu Ala Gln His Lys Arg
1               5                   10                  15

Ala Phe Phe Phe Ala Ala Ala Ser Ser Pro Thr Ser Ser Ser Ser Pro
            20                  25                  30

Leu Ala Ser Pro Ala Pro Ser Ala Ala Ala Ala Arg Arg Glu His Leu
        35                  40                  45

Phe Asp Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
    50                  55                  60

Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Gln Leu Pro
65                  70                  75                  80

Ser Ala Ser Ala Ala Val Pro Gly Glu Cys Lys Gly Val Leu Leu Asn
                85                  90                  95

Phe Asp Asp Ala Thr Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp
            100                 105                 110

Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val
        115                 120                 125

Lys Glu Lys Gly Leu His Ala Gly Asp Ala Val Glu Phe Tyr Arg Ala
    130                 135                 140

Ala Ser Gly Asn Asn Gln Leu Phe Ile Asp Cys Lys Leu Arg Ser Lys
145                 150                 155                 160

Ser Thr Thr Thr Thr Thr Ser Val Asn Ser Glu Ala Ala Pro Ser Pro
                165                 170                 175

Ala Pro Val Thr Arg Thr Val Arg Leu Phe Gly Val Asp Leu Leu Ile
            180                 185                 190

Ala Pro Ala Ala Arg His Ala His Glu His Glu Asp Tyr Gly Met Ala
        195                 200                 205

Lys Thr Asn Lys Arg Thr Met Glu Ala Ser Val Ala Ala Pro Thr Pro
    210                 215                 220

Ala His Ala Val Trp Lys Lys Arg Cys Val Asp Phe Ala Leu Thr Tyr
225                 230                 235                 240

Arg Leu Ala Thr Thr Pro Gln Cys Pro Arg Ser Arg Asp Gln Leu Glu
                245                 250                 255

Gly Val Gln Ala Ala Gly Ser Thr Phe Ala Leu
            260                 265


<210> SEQ ID NO 244
<211> LENGTH: 393
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 244

Met Asp Ser Ser Ser Cys Leu Val Asp Asp Thr Asn Ser Gly Gly Ser
1               5                   10                  15

Ser Thr Asp Lys Leu Arg Ala Leu Ala Ala Ala Ala Ala Glu Thr Ala
            20                  25                  30
```

-continued

```
Pro Leu Glu Arg Met Gly Ser Gly Ala Ser Ala Val Val Asp Ala Ala
        35                  40                  45

Glu Pro Gly Ala Glu Ala Asp Ser Gly Ser Gly Gly Arg Val Cys Gly
    50                  55                  60

Gly Gly Gly Gly Gly Ala Gly Gly Ala Gly Gly Lys Leu Pro Ser Ser
65                  70                  75                  80

Lys Phe Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln
                85                  90                  95

Ile Tyr Glu Arg His Gln Arg Val Trp Leu Gly Thr Phe Ala Gly Glu
            100                 105                 110

Asp Asp Ala Ala Arg Ala Tyr Asp Val Ala Ala Gln Arg Phe Arg Gly
        115                 120                 125

Arg Asp Ala Val Thr Asn Phe Arg Pro Leu Ala Glu Ala Asp Pro Asp
    130                 135                 140

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

Val Asp Met Leu Arg Lys His Thr Tyr Phe Asp Glu Leu Ala Gln Ser
                165                 170                 175

Lys Arg Thr Phe Ala Ala Ser Thr Pro Ser Ala Ala Thr Thr Thr Ala
            180                 185                 190

Ser Leu Ser Asn Gly His Leu Ser Ser Pro Arg Ser Pro Phe Ala Pro
        195                 200                 205

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

Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys
225                 230                 235                 240

His Phe Pro Leu Gln Leu Pro Ser Ala Gly Gly Glu Ser Lys Gly Val
                245                 250                 255

Leu Leu Asn Phe Glu Asp Ala Ala Gly Lys Val Trp Arg Phe Arg Tyr
            260                 265                 270

Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
        275                 280                 285

Arg Phe Val Lys Glu Lys Gly Leu His Ala Gly Asp Val Val Gly Phe
    290                 295                 300

Tyr Arg Ser Ala Ala Ser Ala Gly Asp Asp Gly Lys Leu Phe Ile Asp
305                 310                 315                 320

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

Gln Pro Ala Pro Ser Pro Val Lys Ala Val Arg Leu Phe Gly Val Asp
            340                 345                 350

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

Ala Arg Asp Leu Ala Ala Thr Thr Pro Pro Gln Ala Ala Ala Phe Lys
    370                 375                 380

Lys Gln Cys Ile Glu Leu Ala Leu Val
385                 390


<210> SEQ ID NO 245
<211> LENGTH: 254
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment
```

-continued

```
<400> SEQUENCE: 245

Met Leu Arg Lys His Thr Tyr Phe Asp Glu Leu Ala Gln Ser Lys Arg
1               5                   10                  15

Ala Phe Ala Ala Ser Ala Ala Leu Ser Ala Pro Thr Thr Ser Gly Asp
            20                  25                  30

Ala Gly Gly Ser Ala Ser Pro Pro Ser Pro Ala Ala Val Arg Glu His
        35                  40                  45

Leu Phe Asp Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg
    50                  55                  60

Leu Val Ile Pro Lys Gln Asn Ala Glu Lys His Phe Pro Leu Gln Leu
65                  70                  75                  80

Pro Ala Gly Gly Gly Glu Ser Lys Gly Leu Leu Leu Asn Phe Glu Asp
                85                  90                  95

Asp Ala Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser
            100                 105                 110

Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys
        115                 120                 125

Gly Leu Gly Ala Gly Asp Val Val Gly Phe Tyr Arg Ser Ala Ala Gly
    130                 135                 140

Arg Thr Gly Glu Asp Ser Lys Phe Phe Ile Asp Cys Arg Leu Arg Pro
145                 150                 155                 160

Asn Thr Asn Thr Ala Ala Glu Ala Asp Pro Val Tyr Gly Asn Asp Thr
                165                 170                 175

Glu Asp Gln Leu Phe Ile Asp Tyr Lys Lys Met Asn Lys Asn Asp Asp
            180                 185                 190

Ala Ala Asp Ala Ala Ile Asp Gln Ser Ser Ala Pro Val Gln Lys Ala
        195                 200                 205

Val Arg Leu Phe Gly Val Asp Leu Leu Ala Ala Pro Glu Gln Gly Met
    210                 215                 220

Pro Gly Gly Cys Lys Arg Ala Arg Asp Leu Val Lys Pro Pro Pro Pro
225                 230                 235                 240

Lys Val Ala Phe Lys Lys Gln Cys Ile Glu Leu Ala Leu Ala
                245                 250


<210> SEQ ID NO 246
<211> LENGTH: 357
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 246

Met Gly Val Glu Ile Leu Ser Ser Thr Gly Glu His Ser Ser Gln Tyr
1               5                   10                  15

Ser Ser Gly Ala Ala Ser Thr Ala Thr Thr Glu Ser Gly Val Gly Gly
            20                  25                  30

Arg Pro Pro Thr Ala Pro Ser Leu Pro Val Ser Ile Ala Asp Glu Ser
        35                  40                  45

Ala Thr Ser Arg Ser Ala Ser Ala Gln Ser Thr Ser Ser Arg Phe Lys
    50                  55                  60

Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu
65                  70                  75                  80
```

-continued

```
Arg His Ala Arg Val Trp Leu Gly Thr Phe Pro Asp Glu Asp Ser Ala
                85                  90                  95

Ala Arg Ala Tyr Asp Val Ala Ala Leu Arg Tyr Arg Gly Arg Glu Ala
            100                 105                 110

Ala Thr Asn Phe Pro Cys Ala Ala Ala Glu Ala Glu Leu Ala Phe Leu
        115                 120                 125

Ala Ala His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr
    130                 135                 140

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

Ala Arg Ala Gln Pro Thr Pro Ser Trp Ala Arg Glu Pro Leu Phe Glu
                165                 170                 175

Lys Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Val
            180                 185                 190

Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Lys Arg Thr Pro Glu
        195                 200                 205

Thr Thr Thr Thr Thr Gly Lys Gly Val Leu Leu Asn Phe Glu Asp Gly
    210                 215                 220

Glu Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln
225                 230                 235                 240

Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Arg Glu Lys Gly
                245                 250                 255

Leu Gly Ala Gly Asp Ser Ile Val Phe Ser Cys Ser Ala Tyr Gly Gln
            260                 265                 270

Glu Lys Gln Phe Phe Ile Asp Cys Lys Lys Asn Lys Thr Met Thr Ser
        275                 280                 285

Cys Pro Ala Asp Asp Arg Gly Ala Ala Thr Ala Ser Pro Pro Val Ser
    290                 295                 300

Glu Pro Thr Lys Gly Glu Gln Val Arg Val Val Arg Leu Phe Gly Val
305                 310                 315                 320

Asp Ile Ala Gly Glu Lys Arg Gly Arg Ala Ala Pro Val Glu Gln Glu
                325                 330                 335

Leu Phe Lys Arg Gln Cys Val Ala His Ser Gln His Ser Pro Ala Leu
            340                 345                 350

Gly Ala Phe Val Leu
        355


<210> SEQ ID NO 247
<211> LENGTH: 362
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 247

Met Gly Met Glu Ile Leu Ser Ser Thr Val Glu His Cys Ser Gln Tyr
1               5                   10                  15

Ser Ser Ser Ala Ser Thr Ala Thr Thr Glu Ser Gly Ala Ala Gly Arg
            20                  25                  30

Ser Thr Thr Ala Leu Ser Leu Pro Val Ala Ile Thr Asp Glu Ser Val
        35                  40                  45

Thr Ser Arg Ser Ala Ser Ala Gln Pro Ala Ser Ser Arg Phe Lys Gly
    50                  55                  60
```

-continued

```
Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ser Gln Ile Tyr Glu Arg
65                  70                  75                  80

His Ala Arg Val Trp Leu Gly Thr Phe Pro Asp Gln Asp Ser Ala Ala
                85                  90                  95

Arg Ala Tyr Asp Val Ala Ser Leu Arg Tyr Arg Gly Arg Asp Ala Ala
            100                 105                 110

Thr Asn Phe Pro Cys Ala Ala Ala Glu Ala Glu Leu Ala Phe Leu Thr
        115                 120                 125

Ala His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
    130                 135                 140

Ala Asp Glu Leu Arg Gln Gly Leu Arg Arg Gly Arg Gly Met Gly Ala
145                 150                 155                 160

Arg Ala Gln Pro Thr Pro Ser Trp Ala Arg Val Pro Leu Phe Glu Lys
                165                 170                 175

Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Val Pro
            180                 185                 190

Lys Gln His Ala Glu Lys His Phe Pro Leu Lys Cys Thr Ala Glu Thr
        195                 200                 205

Thr Thr Thr Thr Gly Asn Gly Val Leu Leu Asn Phe Glu Asp Gly Glu
    210                 215                 220

Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser
225                 230                 235                 240

Tyr Val Leu Thr Lys Gly Trp Ser Ser Phe Val Arg Glu Lys Gly Leu
                245                 250                 255

Gly Ala Gly Asp Ser Ile Val Phe Ser Ser Ser Ala Tyr Gly Gln Glu
            260                 265                 270

Lys Gln Leu Phe Ile Asn Cys Lys Lys Asn Thr Thr Met Asn Gly Gly
        275                 280                 285

Lys Thr Ala Leu Pro Leu Pro Val Val Glu Thr Ala Lys Gly Glu Gln
    290                 295                 300

Asp His Val Val Lys Leu Phe Gly Val Asp Ile Ala Gly Val Lys Arg
305                 310                 315                 320

Val Arg Ala Ala Thr Gly Glu Leu Gly Pro Pro Glu Leu Phe Lys Arg
                325                 330                 335

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

Ile Gly Thr Ile Gly Pro Leu Met Leu Asn
        355                 360


<210> SEQ ID NO 248
<211> LENGTH: 351
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 248

Met Gly Val Glu Ile Leu Ser Ser Met Val Glu Asp Ser Ser Gln Tyr
1               5                   10                  15

Ser Ser Gly Ala Ser Thr Ala Thr Thr Glu Ser Gly Thr Thr Gly Arg
            20                  25                  30

Ala Leu Thr Ala Leu Ser Leu Pro Val Ala Ile Ala Asp Glu Ser Val
        35                  40                  45
```

-continued

```
Thr Ser Ala Gln Ser Ala Pro Ser Arg Phe Lys Gly Val Val Pro Gln
    50                  55                  60

Pro Asn Gly Arg Trp Gly Ser Gln Ile Tyr Glu Arg His Ala Arg Val
65                  70                  75                  80

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

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

Cys Ala Ala Ala Glu Ala Glu Leu Ala Phe Leu Gly Ala His Ser Lys
        115                 120                 125

Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Leu
    130                 135                 140

Arg Gln Gly Leu Arg Arg Gly Arg Gly Met Gly Ala Arg Ala Gln Pro
145                 150                 155                 160

Thr Pro Ser Trp Ala Arg Glu Pro Leu Phe Glu Lys Ala Val Thr Pro
                165                 170                 175

Ser Asp Val Gly Lys Leu Asn Arg Leu Val Val Pro Lys Gln His Ala
            180                 185                 190

Glu Lys His Phe Pro Leu Lys Arg Thr Pro Glu Arg Thr Thr Thr Thr
        195                 200                 205

Gly Asn Gly Val Leu Leu Asn Phe Glu Asp Gly Glu Gly Lys Val Trp
    210                 215                 220

Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr
225                 230                 235                 240

Lys Gly Trp Ser Arg Phe Val Arg Glu Lys Gly Leu Ala Ala Gly Asp
                245                 250                 255

Ser Ile Ile Phe Ser Cys Ser Ala Tyr Gly Gln Glu Lys Gln Leu Phe
            260                 265                 270

Ile Asp Cys Lys Lys Asn Thr Thr Val Asn Ser Gly Lys Ser Ala Ser
        275                 280                 285

Pro Leu Pro Val Val Glu Thr Ala Lys Gly Glu Gln Val Arg Val Val
    290                 295                 300

Arg Leu Phe Gly Val Asp Ile Ala Gly Val Lys Arg Gly Arg Ala Ala
305                 310                 315                 320

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

Leu Pro His Gly Gln Arg Ser Pro Ala Leu Gly Ala Phe Val Leu
            340                 345                 350
```

<210> SEQ ID NO 249
<211> LENGTH: 348
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 249

```
Met Gly Val Glu Ile Leu Ser Ser Met Val Glu His Ser Phe Gln Tyr
1               5                   10                  15

Ser Ser Gly Ala Ser Ser Ala Thr Ala Glu Ser Gly Ala Val Gly Thr
            20                  25                  30

Pro Pro Arg His Leu Ser Leu Pro Val Ala Ile Ala Asp Glu Ser Leu
        35                  40                  45
```

-continued

Thr Ser Arg Ser Ala Ser Ser Arg Phe Lys Gly Val Val Pro Gln Pro
50 55 60

Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Arg His Ala Arg Val Trp
65 70 75 80

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

Ala Ser Leu Arg Tyr Arg Gly Gly Asp Ala Ala Phe Asn Phe Pro Cys
100 105 110

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

Glu Ile Val Asp Met Leu Arg Lys Gln Thr Tyr Ala Asp Glu Leu Arg
130 135 140

Gln Gly Leu Arg Arg Gly Arg Gly Met Gly Val Arg Ala Gln Pro Met
145 150 155 160

Pro Ser Trp Ala Arg Val Pro Leu Phe Glu Lys Ala Val Thr Pro Ser
165 170 175

Asp Val Gly Lys Leu Asn Arg Leu Val Val Pro Lys Gln His Ala Glu
180 185 190

Lys His Phe Pro Leu Lys Arg Ser Pro Glu Thr Thr Thr Thr Thr Gly
195 200 205

Asn Gly Val Leu Leu Asn Phe Glu Asp Gly Gln Gly Lys Val Trp Arg
210 215 220

Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys
225 230 235 240

Gly Trp Ser Arg Phe Val Arg Glu Lys Gly Leu Gly Ala Gly Asp Ser
245 250 255

Ile Met Phe Ser Cys Ser Ala Tyr Gly Gln Glu Lys Gln Phe Phe Ile
260 265 270

Asp Cys Lys Lys Asn Thr Thr Val Asn Gly Gly Lys Ser Ala Ser Pro
275 280 285

Leu Gln Val Met Glu Ile Ala Lys Ala Glu Gln Val Arg Val Val Arg
290 295 300

Leu Phe Gly Val Asp Ile Ala Gly Val Lys Arg Glu Arg Ala Ala Thr
305 310 315 320

Ala Glu Gln Gly Pro Gln Gly Trp Phe Lys Arg Gln Cys Met Ala His
325 330 335

Gly Gln His Ser Pro Ala Leu Gly Asp Phe Ala Leu
340 345

<210> SEQ ID NO 250
<211> LENGTH: 350
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 250

Met Gly Val Glu Ile Leu Ser Ser Met Val Glu His Ser Phe Gln Tyr
1 5 10 15

Ser Ser Gly Val Ser Thr Ala Thr Thr Glu Ser Gly Thr Ala Gly Thr
20 25 30

Pro Pro Arg Pro Leu Ser Leu Pro Val Ala Ile Ala Asp Glu Ser Val
35 40 45

-continued

```
Thr Ser Arg Ser Ala Ser Ser Arg Phe Lys Gly Val Val Pro Gln Pro
    50                  55                  60

Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Arg His Ala Arg Val Trp
65                  70                  75                  80

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

Ala Ser Leu Arg Tyr Arg Gly Arg Asp Val Ala Phe Asn Phe Pro Cys
            100                 105                 110

Ala Ala Val Glu Gly Glu Leu Ala Phe Leu Ala Ala His Ser Lys Ala
        115                 120                 125

Glu Ile Val Asp Met Leu Arg Lys Gln Thr Tyr Ala Asp Glu Leu Arg
    130                 135                 140

Gln Gly Leu Arg Arg Gly Arg Gly Met Gly Ala Arg Ala Gln Pro Thr
145                 150                 155                 160

Pro Ser Trp Ala Arg Glu Pro Leu Phe Glu Lys Ala Val Thr Pro Ser
                165                 170                 175

Asp Val Gly Lys Leu Asn Arg Leu Val Val Pro Lys Gln His Ala Glu
            180                 185                 190

Lys His Phe Pro Leu Lys Arg Thr Pro Glu Thr Pro Thr Thr Thr Gly
        195                 200                 205

Lys Gly Val Leu Leu Asn Phe Glu Asp Gly Glu Gly Lys Val Trp Arg
    210                 215                 220

Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys
225                 230                 235                 240

Gly Trp Ser Arg Phe Val Arg Glu Lys Gly Leu Gly Ala Gly Asp Ser
                245                 250                 255

Ile Leu Phe Ser Cys Ser Leu Tyr Glu Gln Glu Lys Gln Phe Phe Ile
            260                 265                 270

Asp Cys Lys Lys Asn Thr Ser Met Asn Gly Gly Lys Ser Ala Ser Pro
        275                 280                 285

Leu Pro Val Gly Val Thr Thr Lys Gly Glu Gln Val Arg Val Val Arg
    290                 295                 300

Leu Phe Gly Val Asp Ile Ser Gly Val Lys Arg Gly Arg Ala Ala Thr
305                 310                 315                 320

Ala Thr Ala Glu Gln Gly Leu Gln Glu Leu Phe Lys Arg Gln Cys Val
                325                 330                 335

Ala Pro Gly Gln His Ser Pro Ala Leu Gly Ala Phe Ala Leu
            340                 345                 350


<210> SEQ ID NO 251
<211> LENGTH: 308
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 251

Met Ala Ser Ser Lys Pro Thr Asn Pro Glu Val Asp Asn Asp Met Glu
1               5                   10                  15

Cys Ser Ser Pro Glu Ser Gly Ala Glu Asp Ala Val Glu Ser Ser Ser
            20                  25                  30

Pro Val Ala Ala Pro Ser Ser Arg Phe Lys Gly Val Val Pro Gln Pro
        35                  40                  45
```

-continued

```
Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Ser Arg Val Trp
    50                  55                  60

Leu Gly Thr Phe Gly Asp Glu Glu Ala Ala Ala Cys Ala Tyr Asp Val
65                  70                  75                  80

Ala Ala Leu Arg Phe Arg Gly Arg Asp Ala Val Thr Asn His Gln Arg
                85                  90                  95

Leu Pro Ala Ala Glu Gly Ala Gly Trp Ser Ser Thr Ser Glu Leu Ala
            100                 105                 110

Phe Leu Ala Asp His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys
        115                 120                 125

His Thr Tyr Asp Asp Glu Leu Arg Gln Gly Leu Arg Arg Gly His Gly
    130                 135                 140

Arg Ala Gln Pro Thr Pro Ala Trp Ala Arg Glu Phe Leu Phe Glu Lys
145                 150                 155                 160

Ala Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Val Pro
                165                 170                 175

Lys Gln His Ala Glu Lys His Phe Pro Pro Thr Thr Ala Ala Ala Ala
            180                 185                 190

Gly Ser Asp Gly Lys Gly Leu Leu Leu Asn Phe Glu Asp Gly Gln Gly
        195                 200                 205

Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr
    210                 215                 220

Val Leu Thr Lys Gly Trp Ser Arg Phe Val Gln Glu Lys Gly Leu Cys
225                 230                 235                 240

Ala Gly Asp Thr Val Thr Phe Ser Arg Ser Ala Tyr Val Met Asn Asp
                245                 250                 255

Thr Asp Glu Gln Leu Phe Ile Asp Tyr Lys Gln Ser Ser Lys Asn Asp
            260                 265                 270

Glu Ala Ala Asp Val Ala Thr Ala Asp Glu Asn Glu Ala Gly His Val
        275                 280                 285

Ala Val Lys Leu Phe Gly Val Asp Ile Gly Trp Ala Gly Met Ala Gly
    290                 295                 300

Ser Ser Gly Gly
305


<210> SEQ ID NO 252
<211> LENGTH: 293
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 252

Met Ala Ser Gly Lys Pro Thr Asn His Gly Met Glu Asp Asp Asn Asp
1               5                   10                  15

Met Glu Tyr Ser Ser Ala Glu Ser Gly Ala Glu Asp Ala Ala Glu Pro
            20                  25                  30

Ser Ser Ser Pro Val Leu Ala Pro Pro Arg Ala Ala Pro Ser Ser Arg
        35                  40                  45

Phe Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile
    50                  55                  60

Tyr Glu Lys His Ser Arg Val Trp Leu Gly Thr Phe Pro Asp Glu Asp
65                  70                  75                  80
```

-continued

```
Ala Ala Val Arg Ala Tyr Asp Val Ala Ala Leu Arg Phe Arg Gly Pro
                85                  90                  95

Asp Ala Val Ile Asn His Gln Arg Pro Thr Ala Ala Glu Glu Ala Gly
            100                 105                 110

Ser Ser Ser Ser Arg Ser Glu Leu Asp Pro Glu Leu Gly Phe Leu Ala
        115                 120                 125

Asp His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
    130                 135                 140

Asp Asp Glu Leu Arg Gln Gly Leu Arg Arg Gly Arg Gly Arg Ala Gln
145                 150                 155                 160

Pro Thr Pro Ala Trp Ala Arg Glu Leu Leu Phe Glu Lys Ala Val Thr
                165                 170                 175

Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Val Pro Lys Gln Gln
            180                 185                 190

Ala Glu Lys His Phe Pro Pro Thr Thr Ala Ala Ala Thr Gly Ser Asn
        195                 200                 205

Gly Lys Gly Val Leu Leu Asn Phe Glu Asp Gly Glu Gly Lys Val Trp
    210                 215                 220

Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr
225                 230                 235                 240

Lys Gly Trp Ser Arg Phe Val Lys Glu Thr Gly Leu Arg Ala Gly Asp
                245                 250                 255

Thr Val Ala Phe Tyr Arg Ser Ala Ser Asp Glu Asn Glu Thr Gly His
            260                 265                 270

Val Ala Val Lys Leu Phe Gly Val Asp Ile Ala Gly Gly Gly Met Ala
        275                 280                 285

Gly Ser Ser Gly Gly
    290


<210> SEQ ID NO 253
<211> LENGTH: 320
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 253

Met Ala Ser Gly Lys Pro Thr Asn His Gly Met Glu Asp Asp Asn Asp
1               5                   10                  15

Met Glu Tyr Ser Ser Ala Glu Ser Gly Ala Glu Asp Ala Ala Glu Pro
            20                  25                  30

Ser Ser Ser Pro Val Leu Ala Pro Pro Arg Ala Ala Pro Ser Ser Arg
        35                  40                  45

Phe Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile
    50                  55                  60

Tyr Glu Lys His Ser Arg Val Trp Leu Gly Thr Phe Pro Asp Glu Asp
65                  70                  75                  80

Ala Ala Ala Arg Ala Tyr Asp Val Ala Ala Leu Arg Phe Arg Gly Pro
                85                  90                  95

Asp Ala Val Ile Asn His Gln Arg Pro Thr Ala Ala Glu Glu Ala Gly
            100                 105                 110

Ser Ser Ser Ser Arg Ser Glu Leu Asp Pro Glu Leu Gly Phe Leu Ala
        115                 120                 125
```

-continued

```
Asp His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
    130                 135                 140

Asp Asp Glu Leu Arg Gln Gly Leu Arg Arg Gly Arg Gly Arg Ala Gln
145                 150                 155                 160

Pro Thr Pro Ala Trp Ala Arg Glu Leu Leu Phe Glu Lys Ala Val Thr
                165                 170                 175

Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Val Pro Lys Gln Gln
            180                 185                 190

Ala Glu Lys His Phe Pro Pro Thr Thr Ala Ala Ala Thr Gly Ser Asn
        195                 200                 205

Gly Lys Gly Val Leu Leu Asn Phe Glu Asp Gly Glu Gly Lys Val Trp
    210                 215                 220

Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr
225                 230                 235                 240

Lys Gly Trp Ser Arg Phe Val Lys Glu Thr Gly Leu Arg Ala Gly Asp
                245                 250                 255

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

Leu Phe Ile Asp Tyr Lys Lys Met Asn Lys Asn Asp Asp Ala Ala Asp
        275                 280                 285

Ala Ala Ile Ser Asp Glu Asn Glu Thr Gly His Val Ala Val Lys Leu
    290                 295                 300

Phe Gly Val Asp Ile Ala Gly Gly Gly Met Ala Gly Ser Ser Gly Gly
305                 310                 315                 320


<210> SEQ ID NO 254
<211> LENGTH: 350
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 254

Met Val Phe Ser Cys Ile Asp Glu Ser Ser Ser Thr Ser Glu Ser Phe
1               5                   10                  15

Ser Pro Ala Thr Ala Thr Ala Thr Ala Thr Ala Thr Lys Phe Ser Ala
            20                  25                  30

Pro Pro Leu Pro Pro Leu Arg Leu Asn Arg Met Arg Ser Gly Gly Ser
        35                  40                  45

Asn Val Val Leu Asp Ser Lys Asn Gly Val Asp Ile Asp Ser Arg Lys
    50                  55                  60

Leu Ser Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg
65                  70                  75                  80

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

Phe Cys Asp Glu Glu Glu Ala Ala His Ser Tyr Asp Ile Ala Ala Arg
            100                 105                 110

Lys Phe Arg Gly Arg Asp Ala Val Val Asn Phe Lys Thr Phe Leu Ala
        115                 120                 125

Ser Glu Asp Asp Asn Gly Glu Leu Cys Phe Leu Glu Ala His Ser Lys
    130                 135                 140

Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Leu
145                 150                 155                 160
```

-continued

Ala Gln Ser Asn Lys Arg Ser Gly Ala Asn Thr Asn Thr Asn Thr Thr
165 170 175

Gln Ser His Thr Val Ser Arg Thr Arg Glu Val Leu Phe Glu Lys Val
180 185 190

Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys
195 200 205

Gln His Ala Glu Lys Tyr Phe Pro Leu Pro Ser Leu Ser Val Thr Lys
210 215 220

Gly Val Leu Ile Asn Phe Glu Asp Val Thr Gly Lys Val Trp Arg Phe
225 230 235 240

Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly
245 250 255

Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val
260 265 270

Thr Phe Glu Arg Ser Thr Gly Ser Asp Arg Gln Leu Tyr Ile Asp Trp
275 280 285

Lys Ile Arg Ser Gly Pro Ser Lys Asn Pro Val Gln Val Val Val Arg
290 295 300

Leu Phe Gly Val Asp Ile Phe Asn Val Thr Ser Ala Lys Pro Ser Asn
305 310 315 320

Val Val Asp Ala Cys Gly Gly Lys Arg Ser Arg Asp Val Asp Met Phe
325 330 335

Ala Leu Arg Cys Ser Lys Lys His Ala Ile Ile Asn Ala Leu
340 345 350

<210> SEQ ID NO 255
<211> LENGTH: 351
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 255

Met Asp Gly Gly Cys Val Thr Asp Glu Thr Thr Thr Ser Ser Asp Ser
1 5 10 15

Leu Ser Val Pro Pro Pro Ser Arg Val Gly Ser Val Ala Ser Ala Val
20 25 30

Val Asp Pro Asp Gly Cys Cys Val Ser Gly Glu Ala Glu Ser Arg Lys
35 40 45

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

Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr
65 70 75 80

Phe Asn Glu Glu Asp Glu Ala Ala Arg Ala Tyr Asp Ile Ala Ala Leu
85 90 95

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

Ser Asp Asp Ala Glu Ser Glu Phe Leu Asn Ser His Ser Lys Phe Glu
115 120 125

Ile Val Asp Met Leu Arg Lys His Thr Tyr Asp Asp Glu Leu Gln Gln
130 135 140

Ser Thr Arg Gly Gly Arg Arg Arg Leu Asp Ala Asp Thr Ala Ser Ser
145 150 155 160

-continued

Gly Val Phe Asp Ala Lys Ala Arg Glu Gln Leu Phe Glu Lys Thr Val
165 170 175

Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln
180 185 190

His Ala Glu Lys His Phe Pro Leu Ser Gly Ser Gly Asp Glu Ser Ser
195 200 205

Pro Cys Val Ala Gly Ala Ser Ala Ala Lys Gly Met Leu Leu Asn Phe
210 215 220

Glu Asp Val Gly Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn
225 230 235 240

Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys
245 250 255

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

Gly Pro Asp Arg Gln Leu Tyr Ile Asp Cys Lys Ala Arg Ser Gly Glu
275 280 285

Val Asn Asn Asn Ala Gly Gly Leu Phe Val Pro Ile Gly Pro Val Val
290 295 300

Glu Pro Val Gln Met Val Arg Leu Phe Gly Val Asn Leu Leu Lys Leu
305 310 315 320

Pro Val Pro Gly Ser Asp Gly Val Gly Lys Arg Lys Glu Met Glu Leu
325 330 335

Phe Ala Phe Glu Cys Cys Lys Lys Leu Lys Val Ile Gly Ala Leu
340 345 350

<210> SEQ ID NO 256
<211> LENGTH: 362
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 256

Met Asp Gly Gly Ser Val Thr Asp Glu Thr Thr Thr Thr Ser Asn Ser
1 5 10 15

Leu Ser Val Pro Ala Asn Leu Ser Pro Pro Pro Leu Ser Leu Val Gly
20 25 30

Ser Gly Ala Thr Ala Val Val Tyr Pro Asp Gly Cys Cys Val Ser Gly
35 40 45

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

Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln
65 70 75 80

Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala Arg Ala
85 90 95

Tyr Asp Ile Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val Thr Asn
100 105 110

Phe Lys Pro Leu Ala Gly Ala Asp Asp Ala Glu Ala Glu Phe Leu Ser
115 120 125

Thr His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
130 135 140

Asp Asn Glu Leu Gln Gln Ser Thr Arg Gly Gly Arg Arg Arg Arg Asp
145 150 155 160

-continued

Ala Glu Thr Ala Ser Ser Gly Ala Phe Asp Ala Lys Ala Arg Glu Gln
165 170 175

Leu Phe Glu Lys Thr Val Thr Gln Ser Asp Val Gly Lys Leu Asn Arg
180 185 190

Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Ser Gly
195 200 205

Ser Gly Gly Gly Ala Leu Pro Cys Met Ala Ala Ala Ala Gly Ala Lys
210 215 220

Gly Met Leu Leu Asn Phe Glu Asp Val Gly Gly Lys Val Trp Arg Phe
225 230 235 240

Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly
245 250 255

Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Ala Val
260 265 270

Gln Phe Phe Lys Ser Thr Gly Leu Asp Arg Gln Leu Tyr Ile Asp Cys
275 280 285

Lys Ala Arg Ser Gly Lys Val Asn Asn Asn Ala Ala Gly Leu Phe Ile
290 295 300

Pro Val Gly Pro Val Val Glu Pro Val Gln Met Val Arg Leu Phe Gly
305 310 315 320

Val Asp Leu Leu Lys Leu Pro Val Pro Gly Ser Asp Gly Ile Gly Val
325 330 335

Gly Cys Asp Gly Lys Arg Lys Glu Met Glu Leu Phe Ala Phe Glu Cys
340 345 350

Ser Lys Lys Leu Lys Val Ile Gly Ala Leu
355 360

<210> SEQ ID NO 257
<211> LENGTH: 384
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 257

Met Asp Ala Ile Ser Cys Leu Asp Glu Ser Thr Thr Thr Glu Ser Leu
1 5 10 15

Ser Ile Ser Gln Ala Lys Pro Ser Ser Thr Ile Met Ser Ser Glu Lys
20 25 30

Ala Ser Pro Ser Pro Pro Pro Pro Asn Arg Leu Cys Arg Val Gly Ser
35 40 45

Gly Ala Ser Ala Val Val Asp Ser Asp Gly Gly Gly Gly Gly Gly Ser
50 55 60

Thr Glu Val Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val
65 70 75 80

Val Pro Gln Pro Asn Gly Arg Trp Gly Ser Gln Ile Tyr Glu Lys His
85 90 95

Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala Arg
100 105 110

Ala Tyr Asp Val Ala Val Gln Arg Phe Arg Gly Lys Asp Ala Val Thr
115 120 125

Asn Phe Lys Pro Leu Ser Gly Thr Asp Asp Asp Asp Gly Glu Ser Glu
130 135 140

-continued

```
Phe Leu Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys
145                 150                 155                 160

His Thr Tyr Asn Asp Glu Leu Glu Gln Ser Lys Arg Ser Arg Gly Phe
                165                 170                 175

Val Arg Arg Arg Gly Ser Ala Ala Gly Ala Gly Asn Gly Asn Ser Ile
            180                 185                 190

Ser Gly Ala Cys Val Met Lys Ala Arg Glu Gln Leu Phe Gln Lys Ala
        195                 200                 205

Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys
    210                 215                 220

Gln His Ala Glu Lys His Phe Pro Leu Gln Ser Ala Ala Asn Gly Val
225                 230                 235                 240

Ser Ala Thr Ala Thr Ala Ala Lys Gly Val Leu Leu Asn Phe Glu Asp
                245                 250                 255

Val Gly Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser
            260                 265                 270

Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys
        275                 280                 285

Asn Leu Lys Ala Gly Asp Thr Val Cys Phe Gln Arg Ser Thr Gly Pro
    290                 295                 300

Asp Arg Gln Leu Tyr Ile Asp Trp Lys Thr Arg Asn Val Val Asn Glu
305                 310                 315                 320

Val Ala Leu Phe Gly Pro Val Val Glu Pro Ile Gln Met Val Arg Leu
                325                 330                 335

Phe Gly Val Asn Ile Leu Lys Leu Pro Gly Ser Asp Ser Ile Ala Asn
            340                 345                 350

Asn Asn Asn Ala Ser Gly Cys Cys Asn Gly Lys Arg Arg Glu Met Glu
        355                 360                 365

Leu Phe Ser Leu Glu Cys Ser Lys Lys Pro Lys Ile Ile Gly Ala Leu
    370                 375                 380


<210> SEQ ID NO 258
<211> LENGTH: 401
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 258

Met Asp Ala Ile Ser Cys Met Asp Glu Ser Thr Thr Thr Glu Ser Leu
1                   5                   10                  15

Ser Ile Ser Leu Ser Pro Thr Ser Ser Ser Glu Lys Ala Lys Pro Ser
            20                  25                  30

Ser Met Ile Thr Ser Ser Glu Lys Val Ser Leu Ser Pro Pro Pro Ser
        35                  40                  45

Asn Arg Leu Cys Arg Val Gly Ser Gly Ala Ser Ala Val Val Asp Pro
    50                  55                  60

Asp Gly Gly Gly Ser Gly Ala Glu Val Glu Ser Arg Lys Leu Pro Ser
65                  70                  75                  80

Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala
                85                  90                  95

Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu
            100                 105                 110
```

-continued

```
Glu Asp Glu Ala Ala Arg Ala Tyr Asp Ile Ala Ala Gln Arg Phe Arg
        115                 120                 125

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

Asp Asp Gly Glu Ser Glu Phe Leu Asn Ser His Ser Lys Pro Glu Ile
145                 150                 155                 160

Val Asp Met Leu Arg Lys His Thr Tyr Asn Asp Glu Leu Glu Gln Ser
                165                 170                 175

Lys Arg Ser Arg Gly Val Val Arg Arg Arg Gly Ser Ala Ala Ala Gly
            180                 185                 190

Thr Ala Asn Ser Ile Ser Gly Ala Cys Phe Thr Lys Ala Arg Glu Gln
        195                 200                 205

Leu Phe Glu Lys Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg
    210                 215                 220

Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Gln Ser
225                 230                 235                 240

Ser Asn Gly Val Ser Ala Thr Thr Ile Ala Ala Val Thr Ala Thr Pro
                245                 250                 255

Thr Ala Ala Lys Gly Val Leu Leu Asn Phe Glu Asp Val Gly Gly Lys
            260                 265                 270

Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val
        275                 280                 285

Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Lys Ala
    290                 295                 300

Gly Asp Thr Val Cys Phe His Arg Ser Thr Gly Pro Asp Lys Gln Leu
305                 310                 315                 320

Tyr Ile Asp Trp Lys Thr Arg Asn Val Val Asn Asn Glu Val Ala Leu
                325                 330                 335

Phe Gly Pro Val Gly Pro Val Val Glu Pro Ile Gln Met Val Arg Leu
            340                 345                 350

Phe Gly Val Asn Ile Leu Lys Leu Pro Gly Ser Asp Thr Ile Val Gly
        355                 360                 365

Asn Asn Asn Asn Ala Ser Gly Cys Cys Asn Gly Lys Arg Arg Glu Met
    370                 375                 380

Glu Leu Phe Ser Leu Glu Cys Ser Lys Lys Pro Lys Ile Ile Gly Ala
385                 390                 395                 400

Leu


<210> SEQ ID NO 259
<211> LENGTH: 192
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 259

Met Ala Met His Ala Gly His Ala Trp Trp Gly Val Ala Met Tyr Thr
1               5                   10                  15

Asn His Tyr His His His Tyr Arg His Lys Thr Ser Asp Val Gly Lys
            20                  25                  30

Asn Arg Val Lys His Ala Arg Tyr Gly Gly Gly Asp Ser Gly Lys Gly
        35                  40                  45

Ser Asp Ser Gly Lys Trp Arg Arg Tyr Ser Tyr Trp Thr Ser Ser Ser
```

-continued

```
    50                  55                  60

Tyr Val Thr Lys Gly Trp Ser Arg Tyr Val Lys Lys Arg Asp Ala Gly
65                  70                  75                  80

Asp Val Val His Arg Val Arg Gly Gly Ala Ala Asp Arg Gly Cys Arg
                85                  90                  95

Arg Arg Gly Ser Ala Ala Ala Val Arg Val Thr Ala Asn Gly Gly Trp
            100                 105                 110

Ser Met Cys Tyr Ser Thr Ser Gly Ser Ser Tyr Asp Thr Ser Ala Asn
        115                 120                 125

Ser Tyr Ala Tyr His Arg Ser Val Asp Asp His Ser Asp His Ala Gly
    130                 135                 140

Ser Arg Ala Asp Ala Lys Ser Ser Ser Ala Ala Ser Ala Ser Arg Arg
145                 150                 155                 160

Arg Gly Val Asn Asp Cys Gly Ala Asp Ala Thr Ala Met Tyr Gly Tyr
                165                 170                 175

Met His His Ser Tyr Ala Ala Val Ser Thr Val Asn Tyr Trp Ser Val
            180                 185                 190


<210> SEQ ID NO 260
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 260

Phe Glu Lys Ser Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
1               5                   10                  15

Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asn Asn Asn
            20                  25                  30

Asn Asn Asn Gly Gly Ser Gly Asp Asp Val Ala Thr Thr Glu Lys Gly
        35                  40                  45

Met Leu Leu Ser Phe Glu Asp Glu Ser Gly Lys Cys Trp Lys Phe Arg
    50                  55                  60

Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp
65                  70                  75                  80

Ser Arg Tyr Val Lys Asp Lys His Leu Asp Ala Gly Asp Val Val Phe
                85                  90                  95

Phe Gln Arg His Arg Phe Asp Leu His Arg Leu Phe Ile Gly Trp Arg
            100                 105                 110

Arg Arg Gly Glu
        115


<210> SEQ ID NO 261
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 261

Phe Glu Lys Ser Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
1               5                   10                  15

Val Ile Pro Lys Gln His Ala Glu Arg Tyr Leu Pro Leu Asn Asn Cys
            20                  25                  30
```

-continued

```
Gly Gly Gly Gly Asp Val Thr Ala Glu Ser Thr Glu Lys Gly Val Leu
        35                  40                  45

Leu Ser Phe Glu Asp Glu Ser Gly Lys Ser Trp Lys Phe Arg Tyr Ser
    50                  55                  60

Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg
65                  70                  75                  80

Tyr Val Lys Asp Lys His Leu Asn Ala Gly Asp Val Val Leu Phe Gln
                85                  90                  95

Arg His Arg Phe Asp Ile His Arg Leu Phe Ile Gly Trp Arg Arg Arg
            100                 105                 110

Gly Glu


<210> SEQ ID NO 262
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 262

Phe Glu Lys Pro Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
1               5                   10                  15

Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Ser Gly Asp
            20                  25                  30

Ser Gly Gly Ser Glu Cys Lys Gly Leu Leu Leu Ser Phe Glu Asp Glu
        35                  40                  45

Ser Gly Lys Cys Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln
    50                  55                  60

Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys Asp Lys Arg
65                  70                  75                  80

Leu Asp Ala Gly Asp Val Val Leu Phe Glu Arg His Arg Val Asp Ala
                85                  90                  95

Gln Arg Leu Phe Ile Gly Trp Arg Arg Arg
            100                 105


<210> SEQ ID NO 263
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 263

Phe Glu Lys Pro Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
1               5                   10                  15

Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Ser Gly Gly
            20                  25                  30

Asp Ser Gly Ser Ser Glu Cys Lys Gly Leu Leu Leu Ser Phe Glu Asp
        35                  40                  45

Glu Ser Gly Lys Cys Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser
    50                  55                  60

Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys Asp Lys
65                  70                  75                  80

Arg Leu Asp Ala Gly Asp Val Val Leu Phe Gln Arg His Arg Ala Asp
                85                  90                  95
```

-continued

```
Ala Gln Arg Leu Phe Ile Gly Trp Arg Arg Arg
            100                 105


<210> SEQ ID NO 264
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 264

Phe Glu Lys Pro Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
1               5                   10                  15

Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asp Ser Ser
            20                  25                  30

Gly Gly Asp Ser Ala Ala Ala Lys Gly Leu Leu Leu Ser Phe Glu Asp
        35                  40                  45

Glu Ser Gly Lys Cys Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser
    50                  55                  60

Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys Asp Lys
65                  70                  75                  80

Arg Leu His Ala Gly Asp Val Val Leu Phe His Arg His Arg Ala His
                85                  90                  95

Pro Gln Arg Phe Phe Ile Ser Cys Thr Arg His
            100                 105


<210> SEQ ID NO 265
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 265

Phe Glu Lys Pro Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
1               5                   10                  15

Val Ile Pro Lys Gln His Ala Glu Arg Tyr Phe Pro Leu Gly Gly Gly
            20                  25                  30

Asp Ser Gly Glu Lys Gly Leu Leu Leu Ser Phe Glu Asp Glu Ser Gly
        35                  40                  45

Lys Pro Trp Arg Phe Arg Tyr Ser Tyr Trp Thr Ser Ser Gln Ser Tyr
    50                  55                  60

Val Leu Thr Lys Gly Trp Ser Arg Tyr Val Lys Glu Lys Arg Leu Asp
65                  70                  75                  80

Ala Gly Asp Val Val His Phe Glu Arg Val Arg Gly Leu Gly Ala Ala
                85                  90                  95

Asp Arg Leu Phe Ile Gly Cys Arg Arg Arg Gly Glu
            100                 105


<210> SEQ ID NO 266
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 266

Phe Glu Lys Ser Leu Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
```

-continued

1 5 10 15

Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asn Ala Val
20 25 30

Leu Val Ser Ser Ala Ala Ala Asp Thr Ser Ser Ser Glu Lys Gly Met
35 40 45

Leu Leu Ser Phe Glu Asp Glu Ser Gly Lys Ser Trp Arg Phe Arg Tyr
50 55 60

Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
65 70 75 80

Arg Phe Val Lys Asp Lys Gln Leu Asp Pro Gly Asp Val Val Phe Phe
85 90 95

Gln Arg His Arg Ser Asp Ser Arg Arg Leu Phe Ile Gly Trp Arg Arg
100 105 110

Arg Gly Gln
115

<210> SEQ ID NO 267
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 267

Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
1 5 10 15

Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asp Ala Ala
20 25 30

Ala Asn Glu Lys Gly Leu Leu Leu Ser Phe Glu Asp Arg Gly Gly Lys
35 40 45

Leu Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val
50 55 60

Met Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Asp Ala
65 70 75 80

Gly Asp Thr Val Ser Phe Cys Arg Gly Ala Ala Asp Ala Thr Arg Asp
85 90 95

Arg Leu Phe Ile Asp Trp Lys Arg Arg Val Glu
100 105

<210> SEQ ID NO 268
<211> LENGTH: 105
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 268

Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
1 5 10 15

Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asp Ala Ala
20 25 30

Ala Asn Glu Lys Gly Leu Leu Leu Ser Phe Glu Asp Arg Ala Gly Lys
35 40 45

Leu Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val
50 55 60

-continued

```
Met Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Asp Ala
65                  70                  75                  80

Gly Asp Thr Val Ser Phe Cys Arg Gly Ala Ala Asp Ala Ala Arg Asp
                85                  90                  95

Arg Leu Phe Ile Asp Trp Arg Lys Arg
            100                 105


<210> SEQ ID NO 269
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 269

Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
1               5                   10                  15

Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asp Ala Ala
            20                  25                  30

Ala Asn Glu Lys Gly Gln Leu Leu Ser Phe Glu Asp Arg Ala Gly Lys
        35                  40                  45

Leu Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val
    50                  55                  60

Met Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Asp Ala
65                  70                  75                  80

Gly Asp Thr Val Ser Phe Cys Arg Gly Ala Gly Asp Thr Ala Arg Asp
                85                  90                  95

Arg Leu Phe Ile Asp Trp Lys Arg Arg Ala Asp
            100                 105


<210> SEQ ID NO 270
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 270

Phe Asp Lys Val Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
1               5                   10                  15

Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Asp Ala Ser
            20                  25                  30

Ser Thr Asp Lys Gly Leu Leu Leu Ser Phe Glu Asp Arg Ala Gly Lys
        35                  40                  45

Pro Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val
    50                  55                  60

Met Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Asp Ala
65                  70                  75                  80

Gly Asp Thr Val Ser Phe Gly Arg Gly Val Gly Glu Ala Ala Arg Gly
                85                  90                  95

Arg Leu Phe Ile Asp Trp Arg Arg Arg Pro Asp
            100                 105


<210> SEQ ID NO 271
<211> LENGTH: 104
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
```

-continued

```
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 271

Phe Glu Lys Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
1               5                   10                  15

Val Ile Pro Lys Gln His Ala Glu Lys Tyr Phe Pro Leu Gln Ser Gly
            20                  25                  30

Ser Ala Ser Ser Lys Gly Val Leu Leu Asn Phe Glu Asp Val Thr Gly
        35                  40                  45

Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr
    50                  55                  60

Val Leu Ile Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Lys
65                  70                  75                  80

Ala Gly Asp Ile Val Ser Phe Gln Arg Ser Thr Gly Thr Glu Lys Gln
                85                  90                  95

Leu Tyr Ile Asp Trp Lys Ala Arg
            100


<210> SEQ ID NO 272
<211> LENGTH: 102
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: alignment

<400> SEQUENCE: 272

Phe Glu Lys Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
1               5                   10                  15

Val Val Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Lys Arg Thr
            20                  25                  30

Pro Glu Thr Pro Thr Thr Thr Gly Lys Gly Val Leu Leu Asn Phe Glu
        35                  40                  45

Asp Gly Glu Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser
    50                  55                  60

Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Arg Glu
65                  70                  75                  80

Lys Gly Leu Gly Ala Gly Asp Ser Ile Leu Phe Ser Cys Ser Leu Tyr
                85                  90                  95

Glu Gln Glu Lys Gln Phe
            100
```

1.-**16**. (canceled)

17. A method for altering a plant phenotype comprising reducing or abolishing the expression of a nucleic acid sequence encoding a NGAL2 polypeptide or reducing or abolishing the activity of a NGAL2 polypeptide, or reducing or abolishing the expression of a nucleic acid sequences encoding a NGAL3 polypeptide, or reducing or abolishing the activity of a NGAL3 polypeptide, or reducing or abolishing the expression of nucleic acid sequences encoding NGAL2 and NGAL3 polypeptides or reducing or abolishing the activity of a NGAL2 and NGAL3 polypeptide, relative to a control plant.

18.-**22**. (canceled)

23. The method according to claim **17**, wherein the NGAL2 polypeptide comprises SEQ D NO: 3, a functional variant or homologue thereof.

24. The method according to claim **17**, wherein the nucleic acid sequence encoding a NGAL2 polypeptide comprises SEQ ID NO: 1 or 2, a functional variant or homologue thereof.

25. The method according to claim **24** wherein the functional variant or homologue comprises a nucleic acid sequence as shown in SEQ ID NO: 49-145.

26. The method according to claim **17**, wherein the NGAL3 polypeptide comprises SEQ ID NO: 5, a functional variant or homologue thereof.

27. The method according to claim **17** wherein the NGAL3 nucleic acid sequence encoding a NGAL3 polypeptide comprises SEQ ID NO: 4, a functional variant or homologue thereof.

28. The method according to claim **27** wherein the functional variant or homologue comprises SEQ ID NOs:49-145.

29.-**33**. (canceled)

34. The method according to claim **17**, wherein said phenotype is characterised by increased seed size relative to a control plant.

35.-**36**. (canceled)

37. A vector comprising SEQ ID NO: 1, 2 or 3 or a functional variant or homolog thereof.

38. (canceled)

* * * * *