

Figure 1

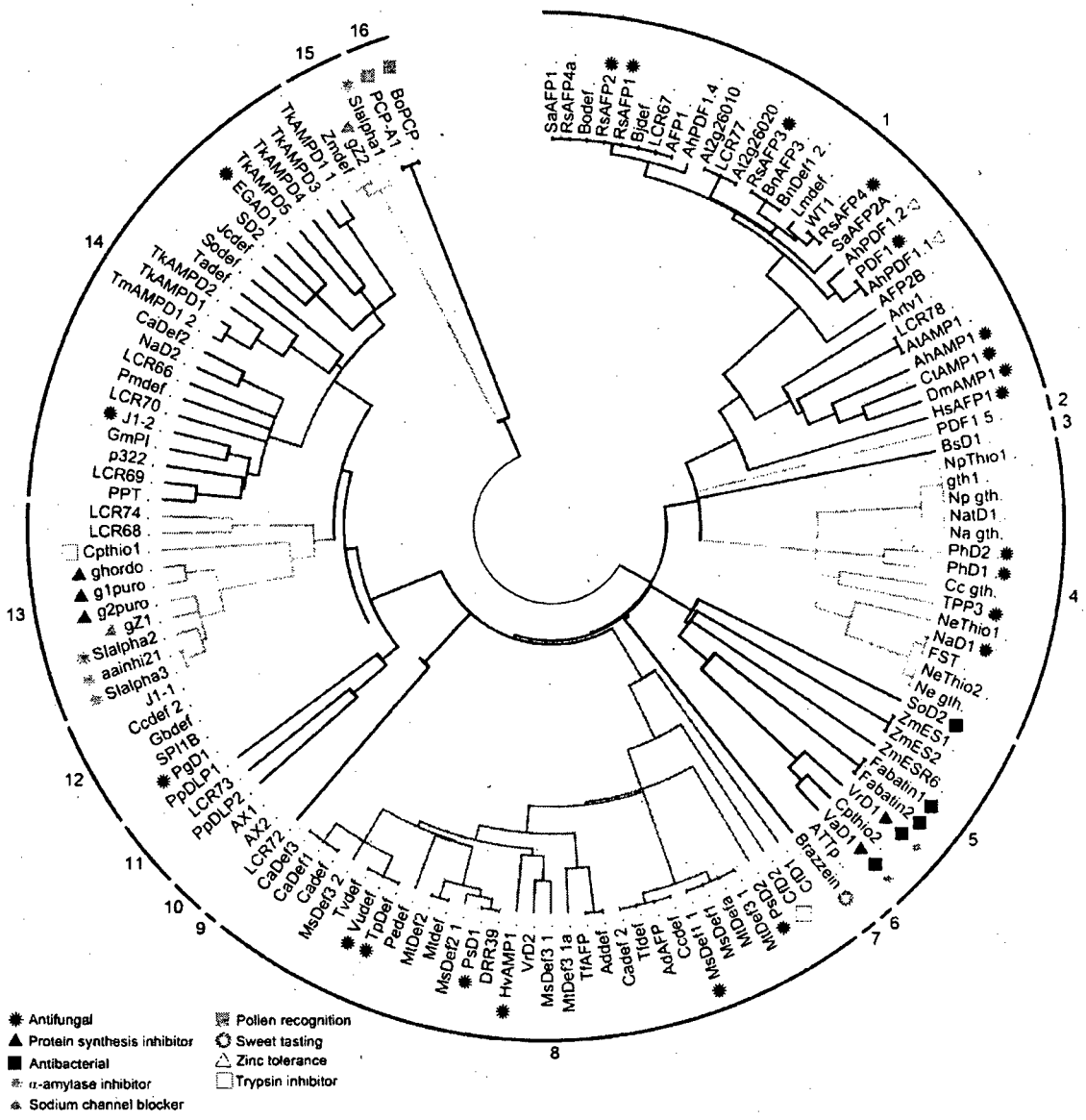

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
SaAFP1
RsAFP4a
Bodef
RsAFP2
RsAFP1
Bjdef
LCR67
AFP1
AhPDF1.4
At2g26010
LCR77
At2g26020
RsAFP3
BnAFP3
BnDef1.2
Lmdef
WT1
RsAFP4
SaAFP2A
AhPDF1.2
PDF1
AhPDF1.1
AFP2B
Arfv1
LCR78
AtAMP1
AhAMP1
ClAMP1
DmAMP1
HsAFP1
PDF1.5
BsD1
NpThio1
gth1
Np gth
NatD1
Na gth
PhD2
PhD1
Cc gth
TPP3
NeThio1
NaD1
FST
NeThio2
Ne gth
SoD2
ZmES1
ZmES2
ZmESR6
Fabalin1
Fabalin2
VrD1
Cpthio2
VaD1
ATTp
Brazzein
CJD1
PsDC2
MtDef3 1
MtDef1a
MsDef1 1
CcDef1
AdAFP
TlDef
Cadef2
AdDef
TfAFP
MsDef3 1a
VrD2
HvAMP1
DRR39
PsD1
MsDef2 1
MtDef
MtDef2
PeDef
TpDef
VuDef
TvDef
MsDef3 2
CaDef
CaDef1
CaDef3
LCR72
AX2
AX1
PpDLP2
LCR73
PpDLP1
PgD1
SPI1B
Gbdef
Ccdef 2
J1-1
Slalpha3
aainhi21
Slalpha2
gZ1
g2puro
g1puro
ghordo
Cpthio1
LCR68
LCR74
PPT
LCR69
p322
GmPI
J1-2
LCR70
Pmdef
LCR66
NaD2
CaDef2
TmAMPD1.2
TkAMPD1
TkAMPD2
Tadef
SOdef
Jcdef
SD2
EGAD1
TkAMPD5
TkAMPD4
TkAMPD3
TkAMPD1.1
Zmdef
gZ2
Slalpha1
PCP-A1
BoPCP
Antifungal
Protein synthesis inhibitor
Antibacterial
α-amylase inhibitor
Sodium channel blocker
Pollen recognition
Sweet tasting
Zinc tolerance
Trypsin inhibitor

Figure 2

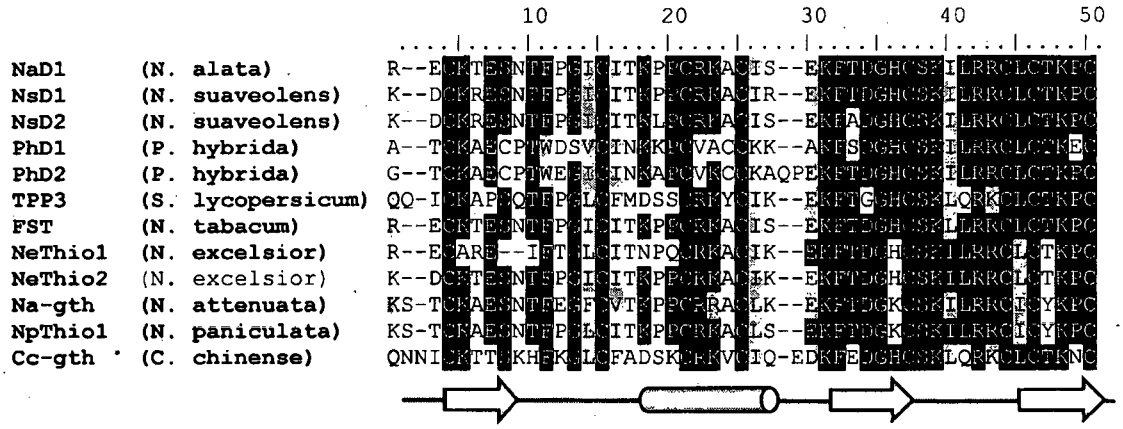

10
20
30
40
50
NaD1 (N. alata)
NsD1 (N. suaveolens)
NsD2 (N. suaveolens)
PhD1 (P. hybrida)
PhD2 (P. hybrida)
TPP3 (S. lycopersicum)
FST (N. tabacum)
NeThio1 (N. excelsior)
NeThio2 (N. excelsior)
Na-gth (N. attenuata)
NpThio1 (N. paniculata)
Cc-gth (C. chinense)

Figure 3A

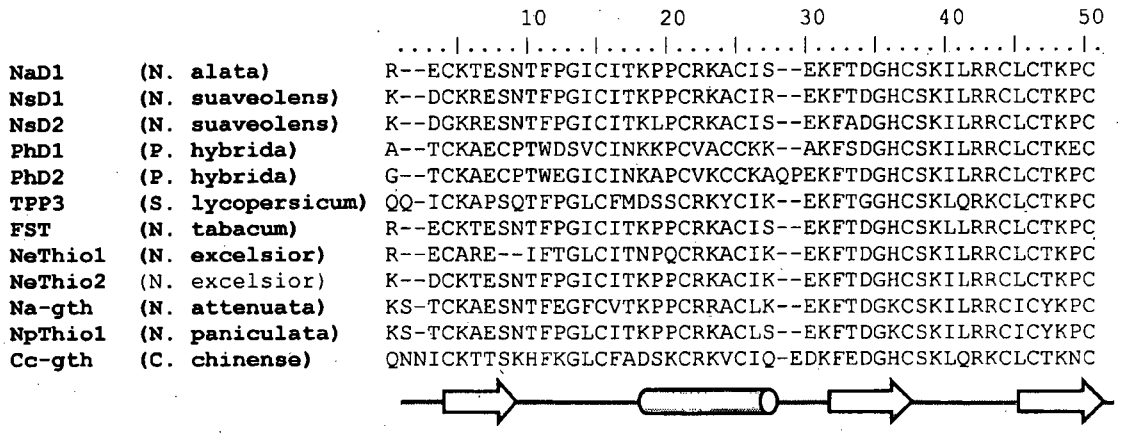

10
20
30
40
50
NaD1 (N. alata) R--ECKTESNTFPGICITKPPCRKACIS--EKFTDGHCSKILRRCLCTKPC
NsD1 (N. suaveolens) K--DCKRESNTFPGICITKPPCRKACIR--EKFTDGHCSKILRRCLCTKPC
NsD2 (N. suaveolens) K--DGKRESNTFPGICITKLPCRKACIS--EKFADGHCSKILRRCLCTKPC
PhD1 (P. hybrida) A--TCKAECPTWDSVCINKKPCVACCKK--AKFSDGHCSKILRRCLCTKEC
PhD2 (P. hybrida) G--TCKAECPTWEGICINKAPCVKCCKAQPEKFTDGHCSKILRRCLCTKPC
TPP3 (S. lycopersicum) QQ-ICKAPSQTFPGLCFMDSSCRKYCIK--EKFTGGHCSKLQRKCLCTKPC
FST (N. tabacum) R--ECKTESNTFPGICITKPPCRKACIS--EKFTDGHCSKLLRRCLCTKPC
NeThio1 (N. excelsior) R--ECARE--IFTGLCITNPQCRKACIK--EKFTDGHCSKILRRCLCTKPC
NeThio2 (N. excelsior) K--DCKTESNTFPGICITKPPCRKACIK--EKFTDGHCSKILRRCLCTKPC
Na-gth (N. attenuata) KS-TCKAESNTFEGFCVTKPPCRRACLK--EKFTDGKCSKILRRCICYKPC
NpThio1 (N. paniculata) KS-TCKAESNTFPGLCITKPPCRKACLS--EKFTDGKCSKILRRCICYKPC
Cc-gth (C. chinense) QNNICKTTSKHFKGLCFADSKCRKVCIQ-EDKFEDGHCSKLQRKCLCTKNC

Figure 3B

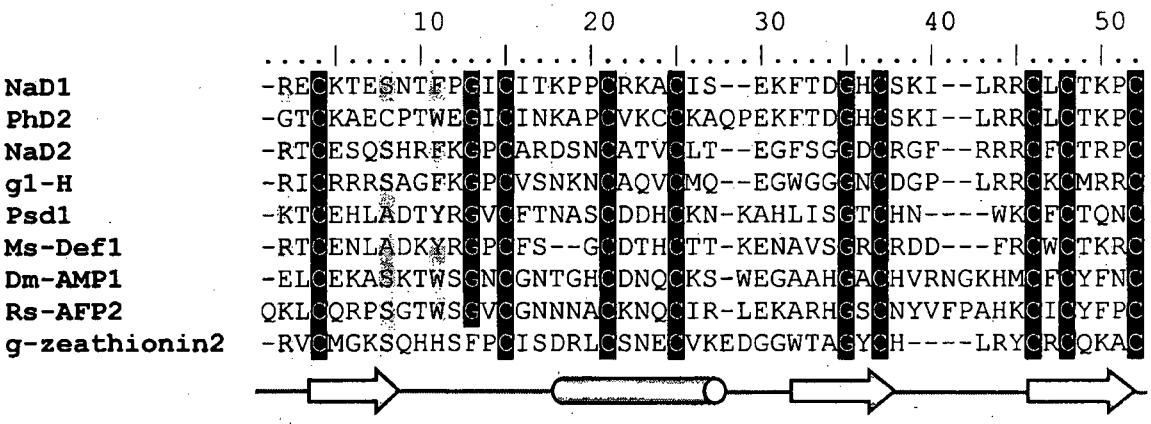

10
20
30
40
50
NaD1 -RECKTESNTFPGICITKPPCRKACIS--EKFTDGHCSKI--LRRCLCTKPC
PhD2 -GTCKAECPTWEGICINKAPCVKCCKAQPEKFTDGHCSKI--LRRCLCTKPC
NaD2 -RTCESQSHRFKGPCARDSNCATVCLT--EGFSGGDCRGF--RRRCFCTRPC
g1-H -RICRRRSAGFKGPCVSNKNCAQVCMQ--EGWGGGNCDGP--LRRCKCMRRC
Psd1 -KTCEHLADTYRGVCFTNASCDDHCKN-KAHLISGTCHN----WKCFCTQNC
Ms-Def1 -RTCENLADKYRGPCFS--GCDTHCTT-KENAVSGRCRDD---FRCWCTKRC
Dm-AMP1 -ELCEKASKTWSGNCGNTGHCDNQCKS-WEGAAHGACHVRNGKHMCFCYFNC
Rs-AFP2 QKLCQRPSGTWSGVCGNNNACKNQCIR-LEKARHGSCNYVFPAHKCICYFPC
g-zeathionin2 -RVCMGKSQHHSFPCISDRLCSNECVKEDGGWTAGYCH----LRYCRCQKAC

Figure 4

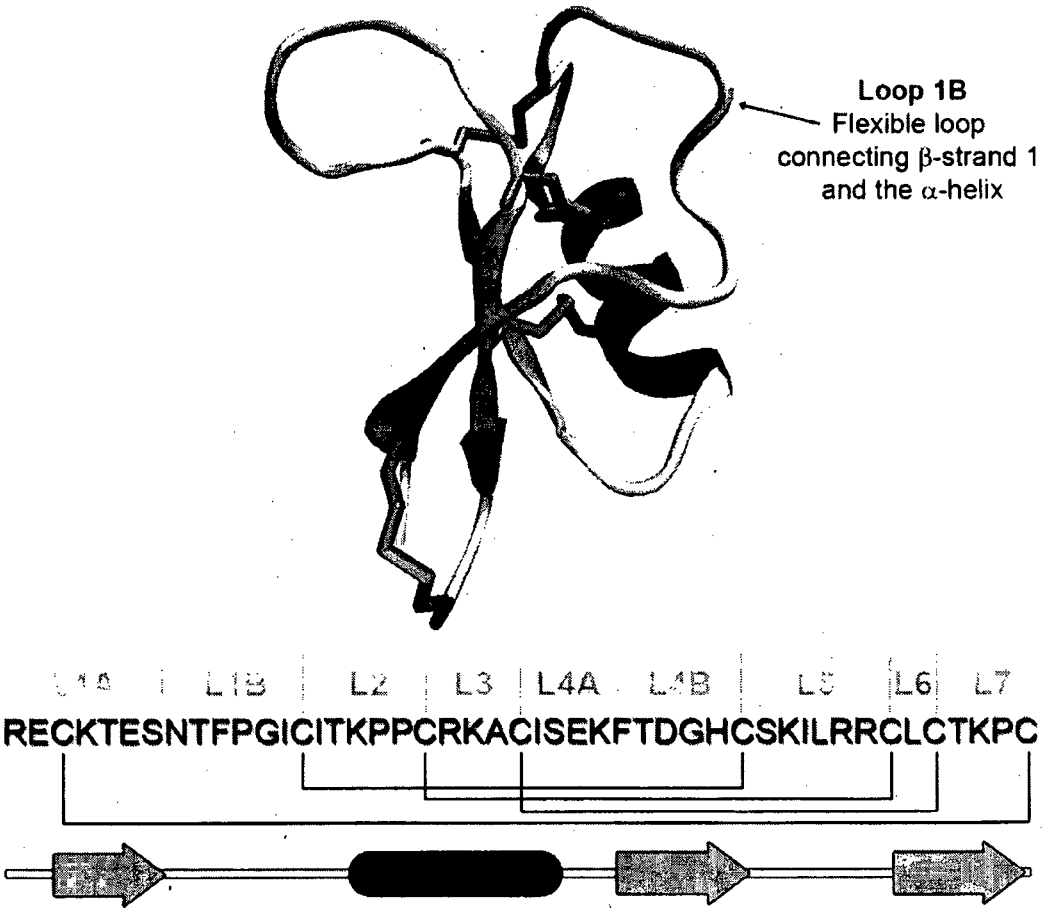

Loop 1B
Flexible loop
connecting β-strand 1
and the α-helix
L1B
L2
L3
L4A
L6
L7
RECKTESNTFPGICITKPPCRKACISEKFTDGHCSKILRRCLCTKPC

Figure 5

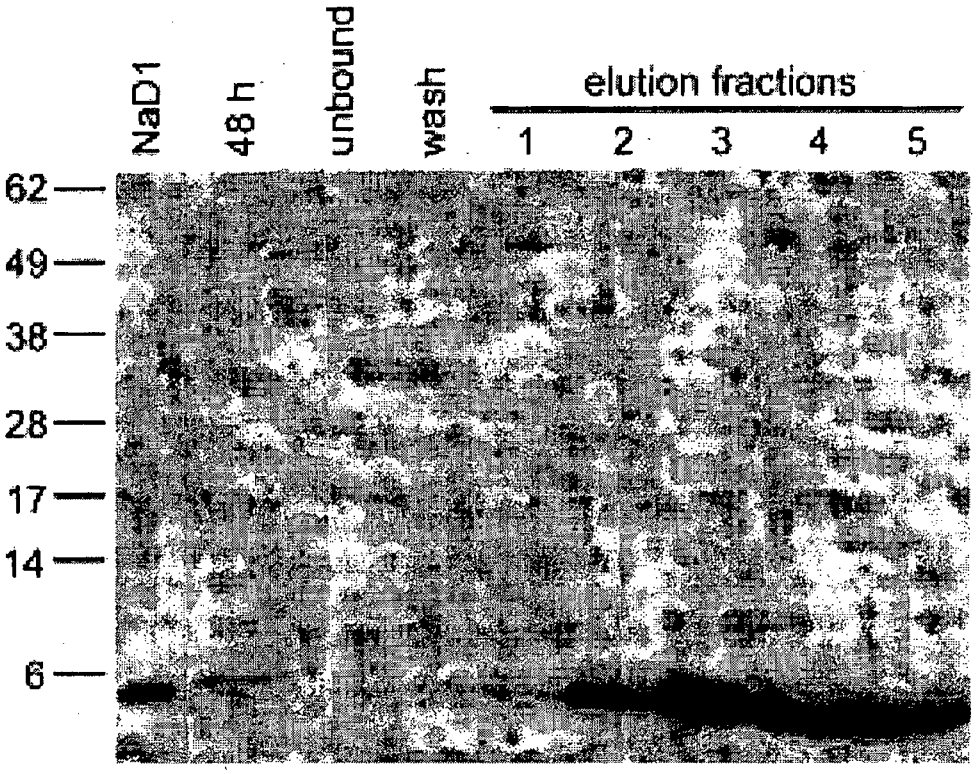

NaD1
48 h
unbound
wash
elution fractions
1
2
3
4
5
62
49
38
28
17
14
6

Figure 6A

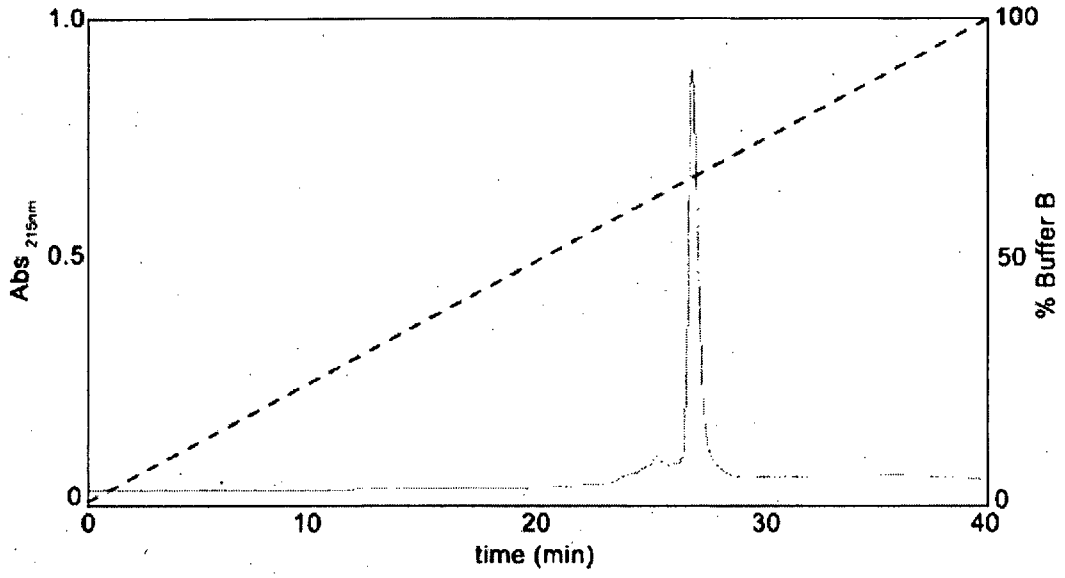


Figure 6B

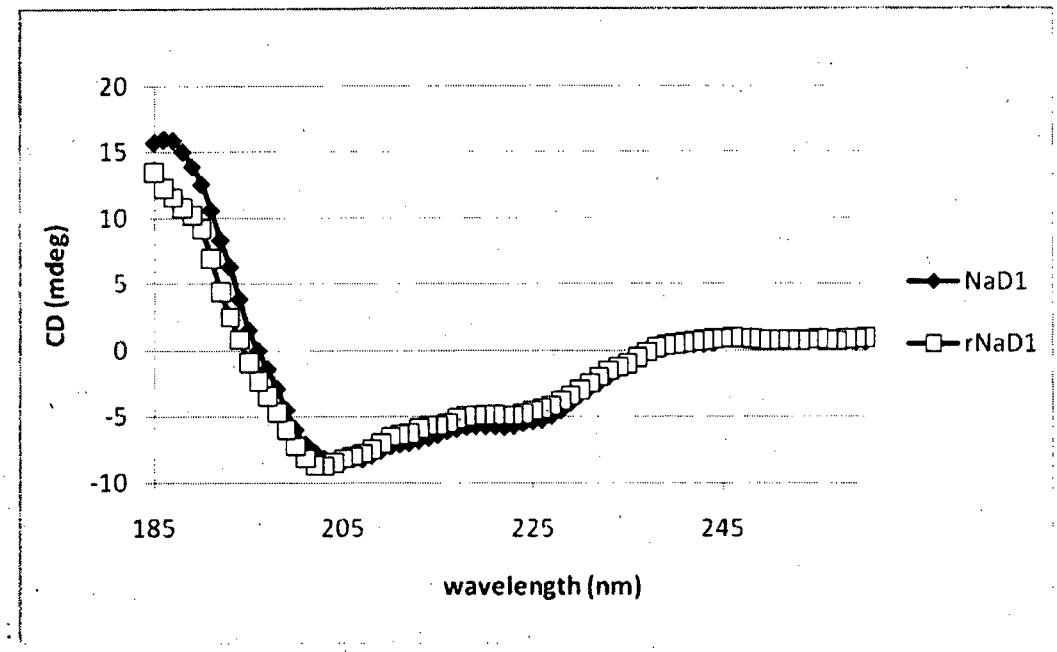

20
15
10
5
0
-5
-10
CD (mdeg)
185
205
225
245
wavelength (nm)
NaD1
rNaD1

Figure 6C

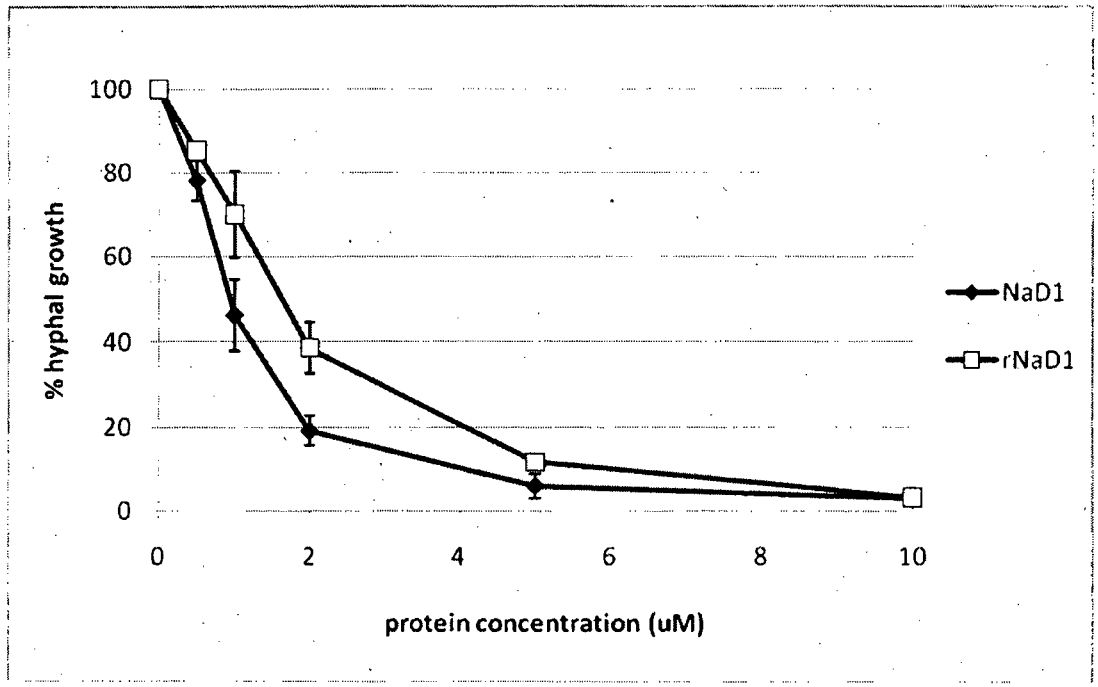

100
80
60
40
20
0
% hyphal growth
0
2
4
6
8
10
protein concentration (uM)
NaD1
rNaD1

Figure 6D

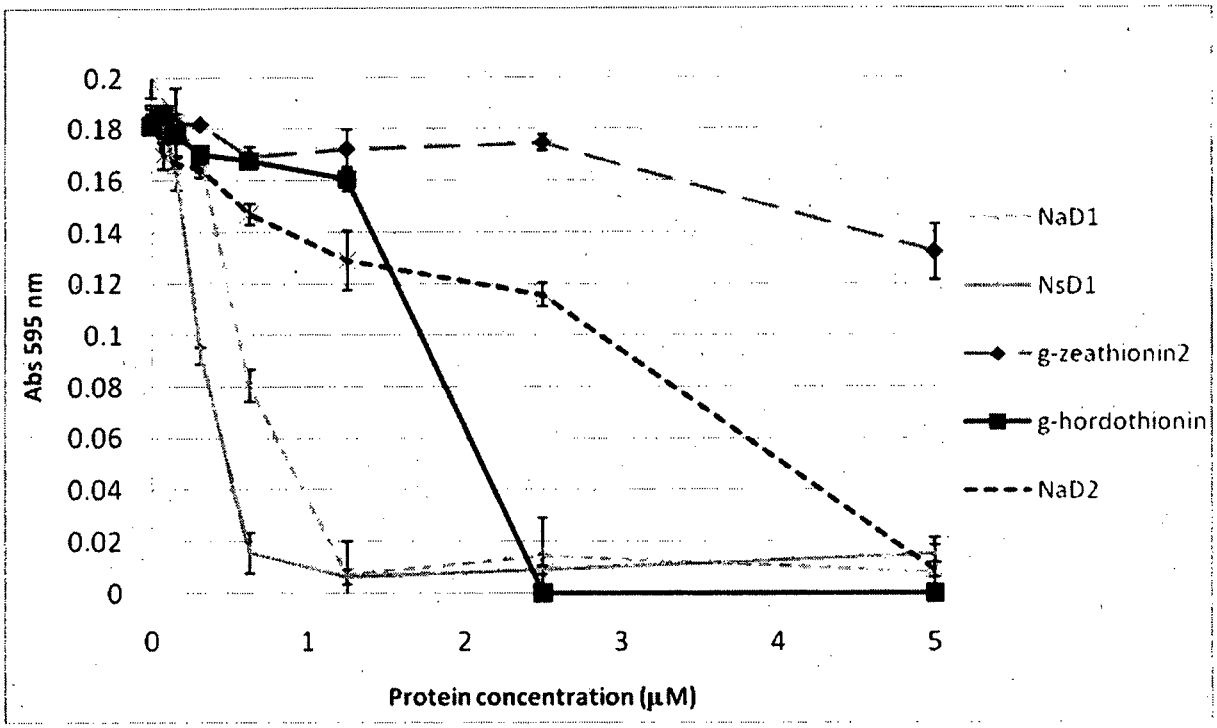
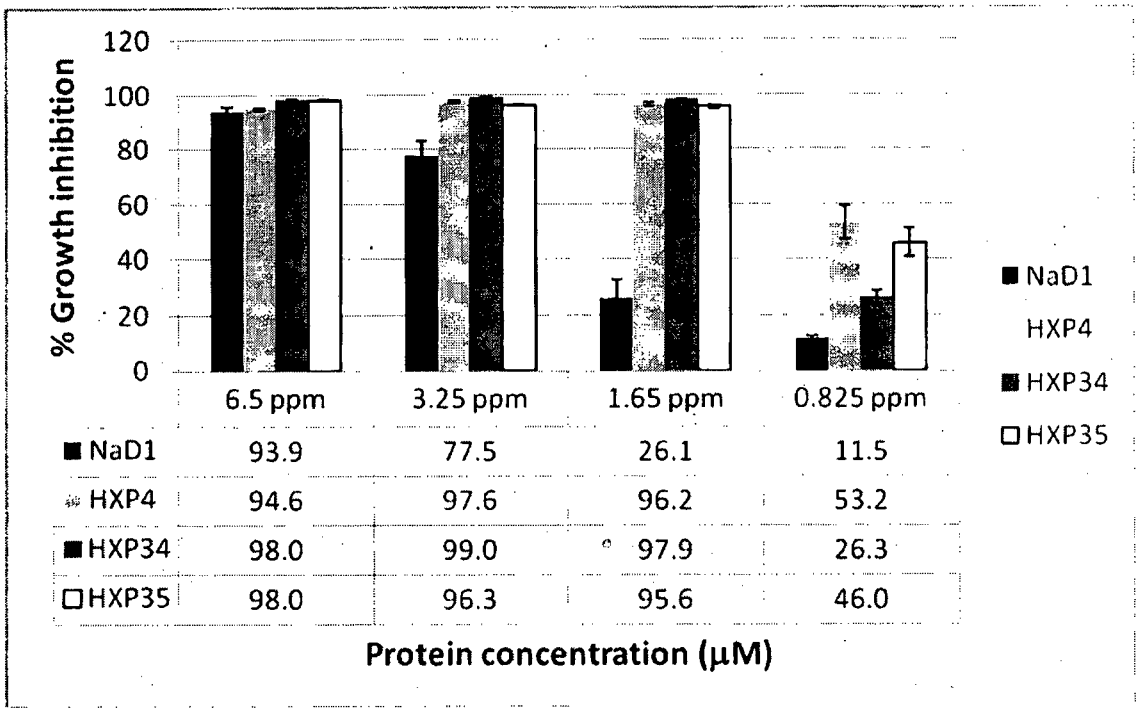
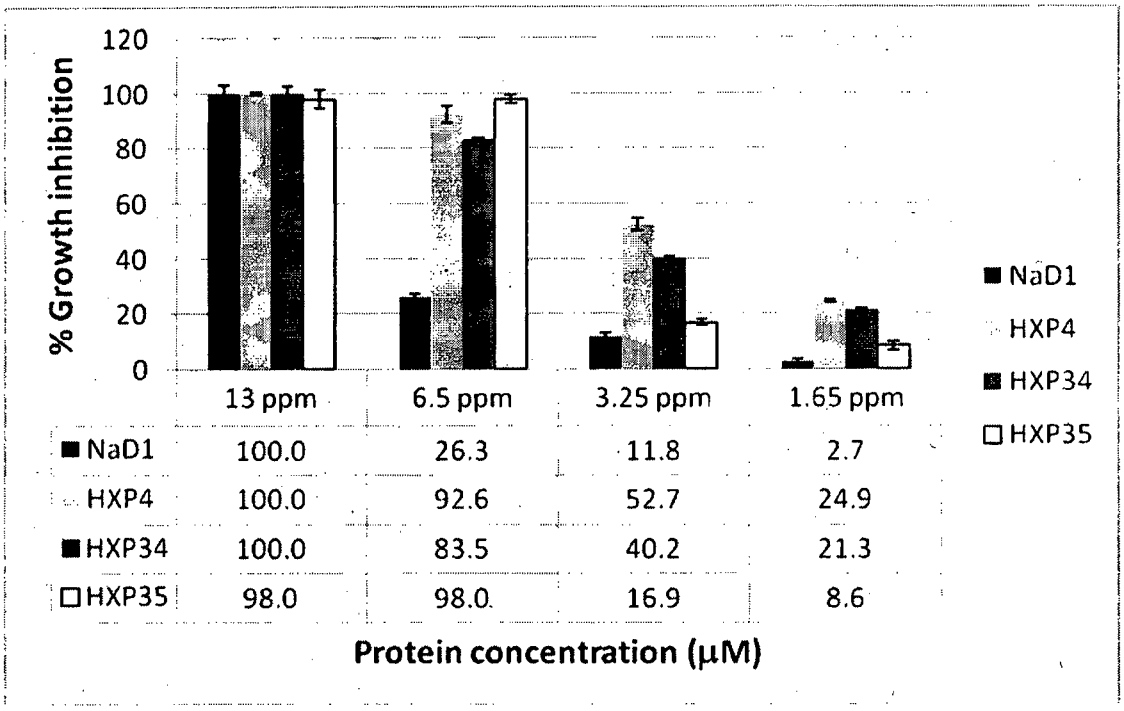

0.2
0.18
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
Abs 595 nm
0
1
2
3
4
5
Protein concentration (µM)
NaD1
NsD1
g-zeathionin2
g-hordothionin
NaD2

Figure 7



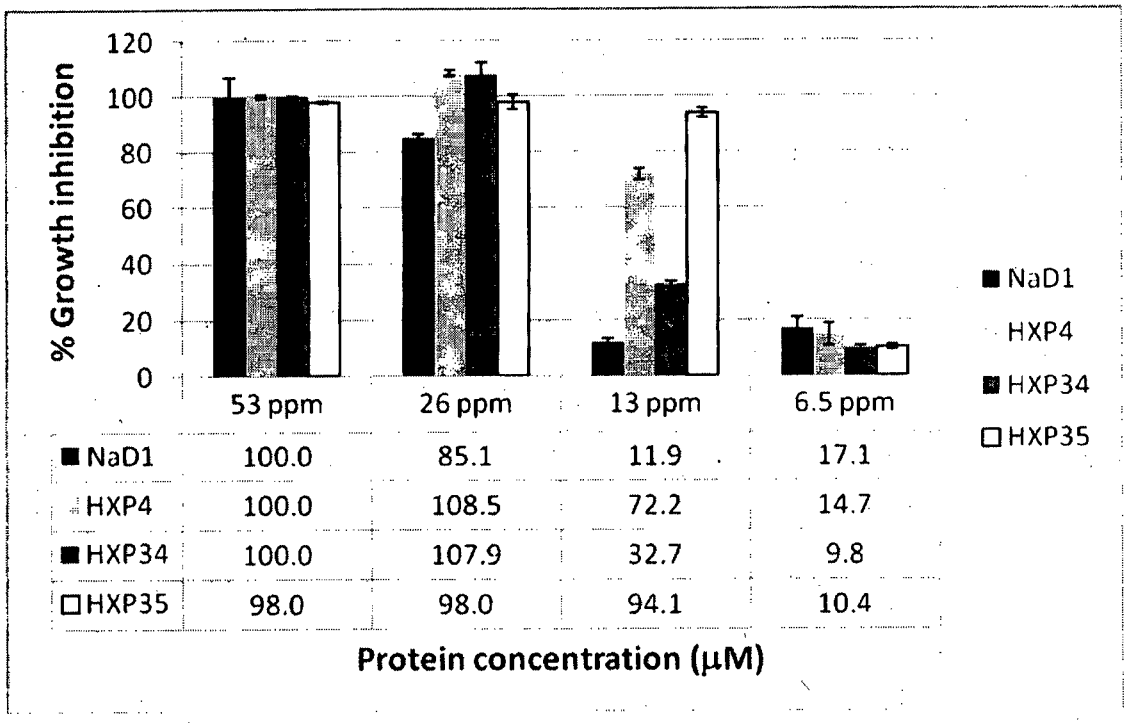
	6.5 ppm	3.25 ppm	1.65 ppm	0.825 ppm
NaD1	93.9	77.5	26.1	11.5
HXP4	94.6	97.6	96.2	53.2
HXP34	98.0	99.0	97.9	26.3
HXP35	98.0	96.3	95.6	46.0

Figure 8



	13 ppm	6.5 ppm	3.25 ppm	1.65 ppm
NaD1	100.0	26.3	11.8	2.7
HXP4	100.0	92.6	52.7	24.9
HXP34	100.0	83.5	40.2	21.3
HXP35	98.0	98.0	16.9	8.6

Figure 9



	53 ppm	26 ppm	13 ppm	6.5 ppm
NaD1	100.0	85.1	11.9	17.1
HXP4	100.0	108.5	72.2	14.7
HXP34	100.0	107.9	32.7	9.8
HXP35	98.0	98.0	94.1	10.4

Figure 10

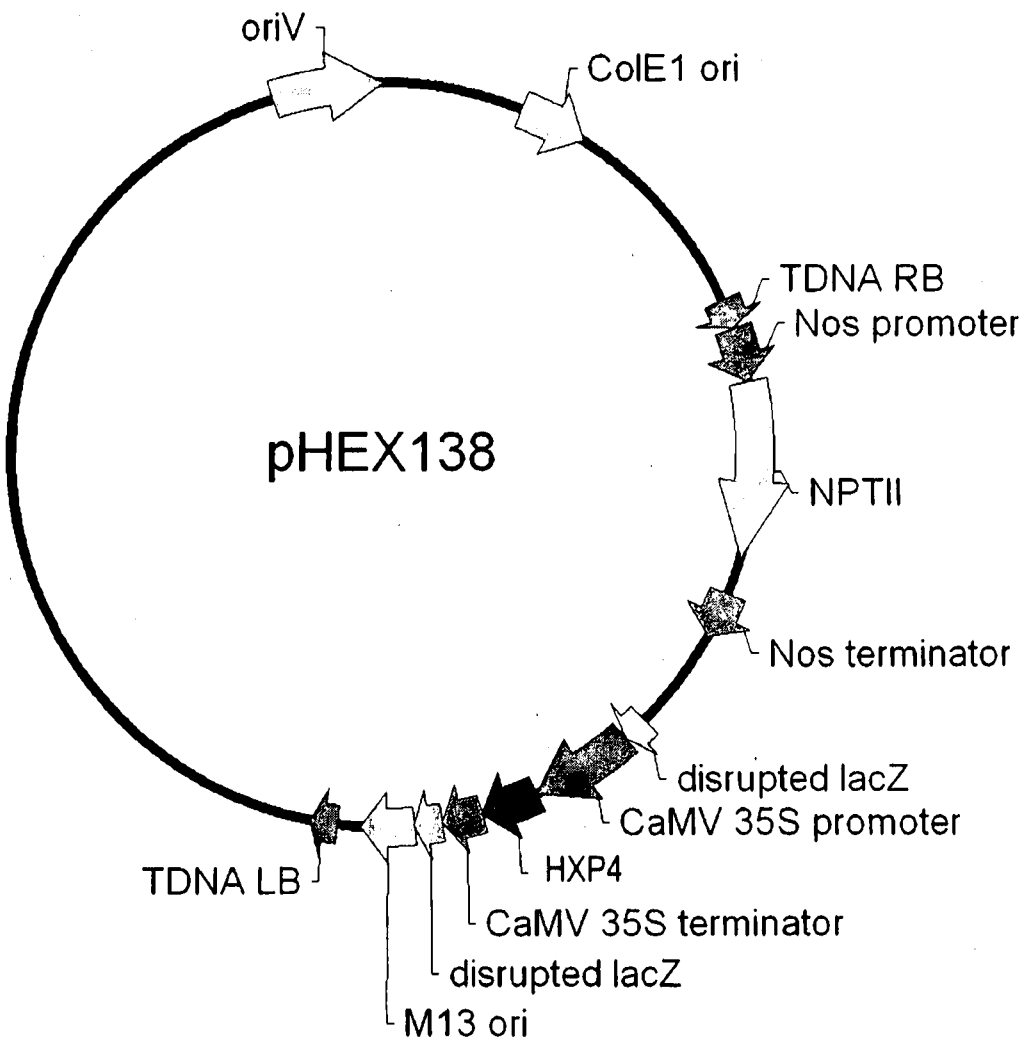

oriV
ColE1 ori
TDNA RB
Nos promoter
pHEX138
NPTII
Nos terminator
disrupted lacZ
CaMV 35S promoter
HXP4
TDNA LB
CaMV 35S terminator
disrupted lacZ
M13 ori

Figure 11

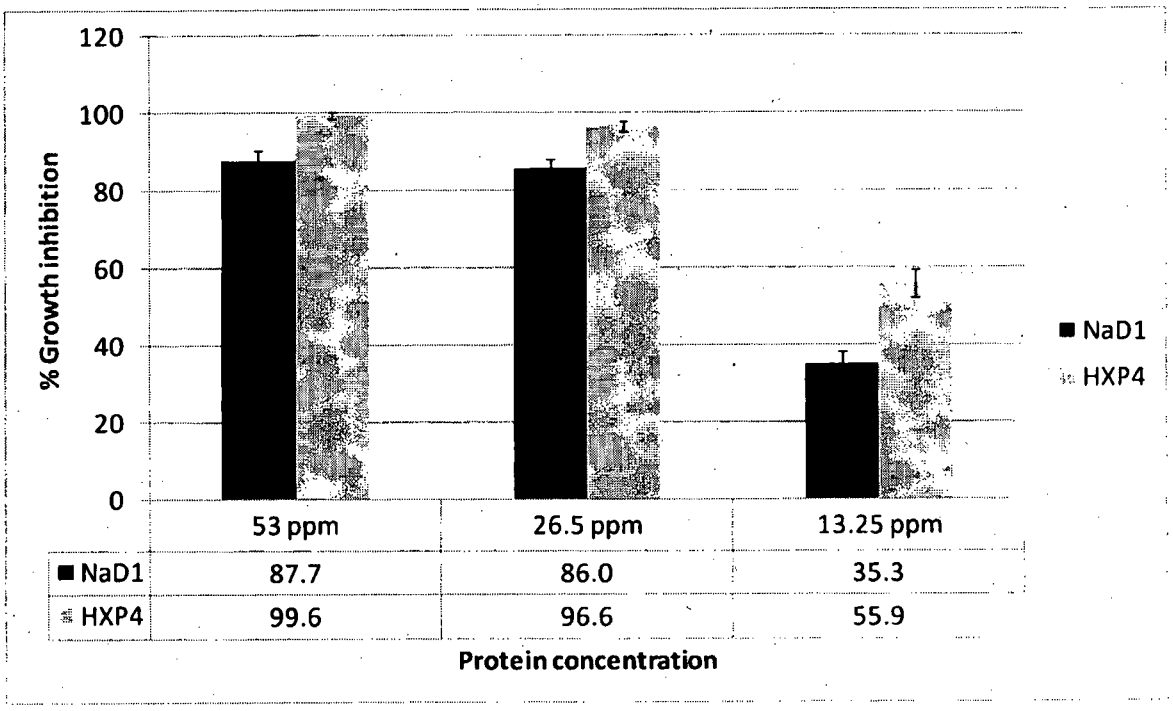

120
100
80
60
40
20
0
% Growth inhibition
NaD1
HXP4
53 ppm
26.5 ppm
13.25 ppm
NaD1 87.7 86.0 35.3
HXP4 99.6 96.6 55.9
Protein concentration

Figure 12

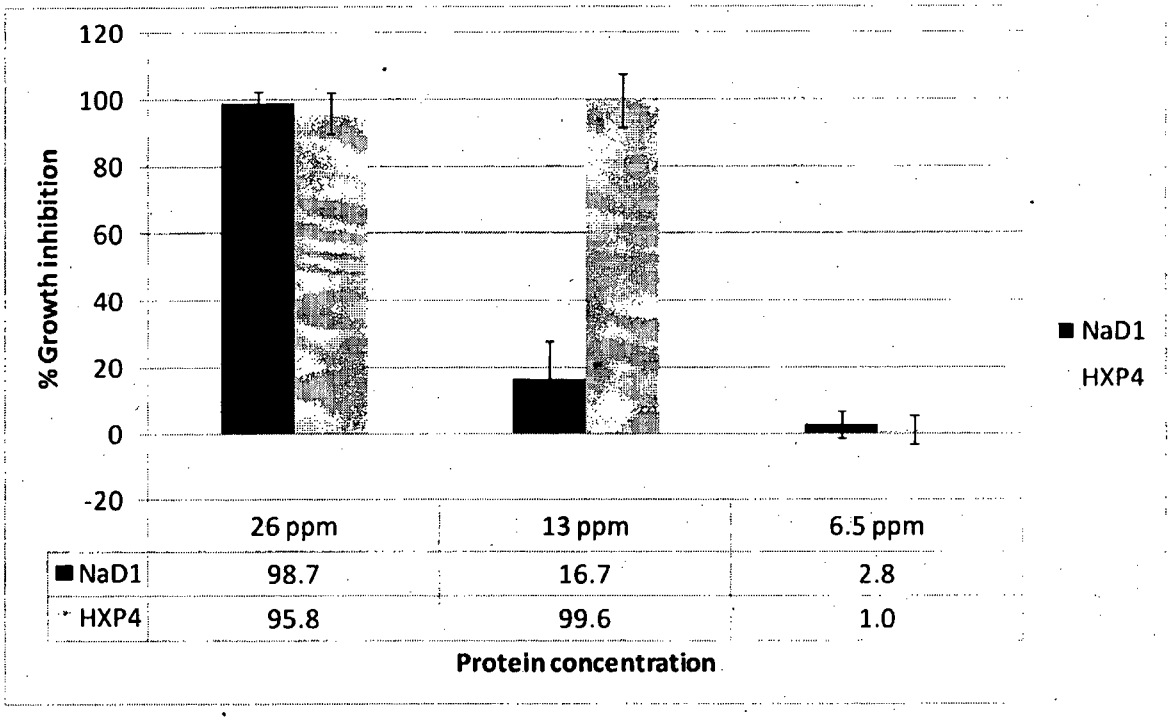

120
100
80
60
40
20
0
-20
% Growth inhibition
26 ppm
13 ppm
6.5 ppm
NaD1 98.7 16.7 2.8
HXP4 95.8 99.6 1.0
Protein concentration
NaD1
HXP4

Figure 13A

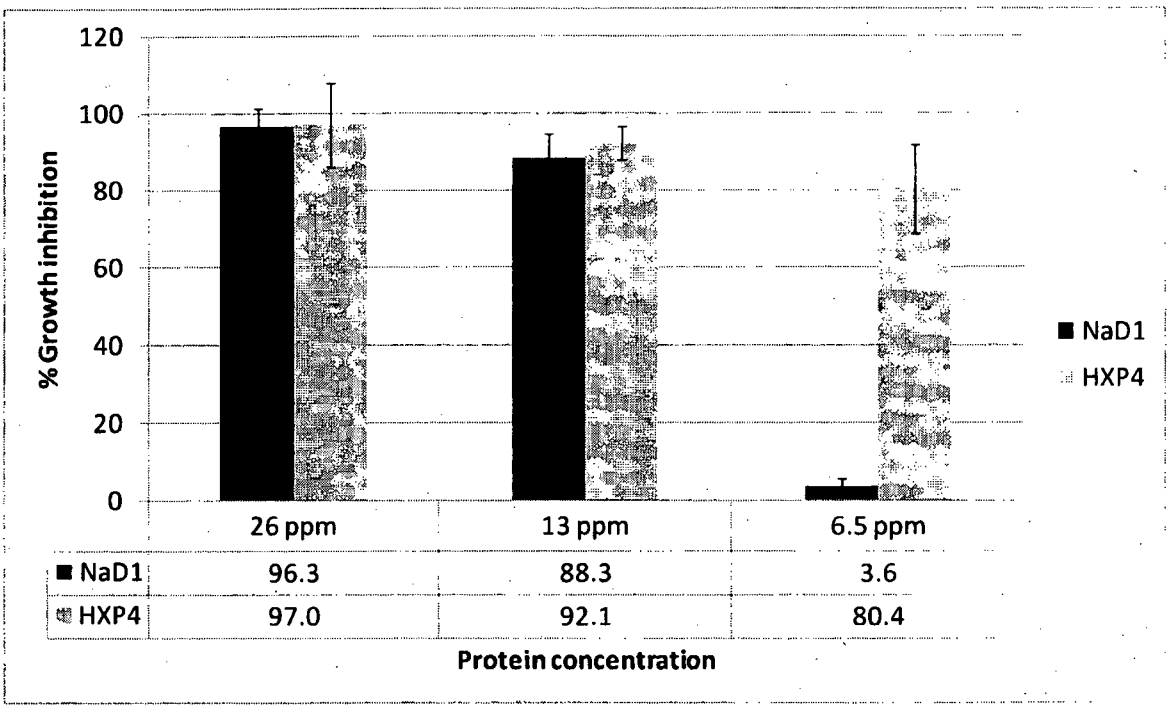

120
100
80
60
40
20
0
% Growth inhibition
26 ppm
13 ppm
6.5 ppm
NaD1
HXP4
NaD1 96.3 88.3 3.6
HXP4 97.0 92.1 80.4
Protein concentration

Figure 13B

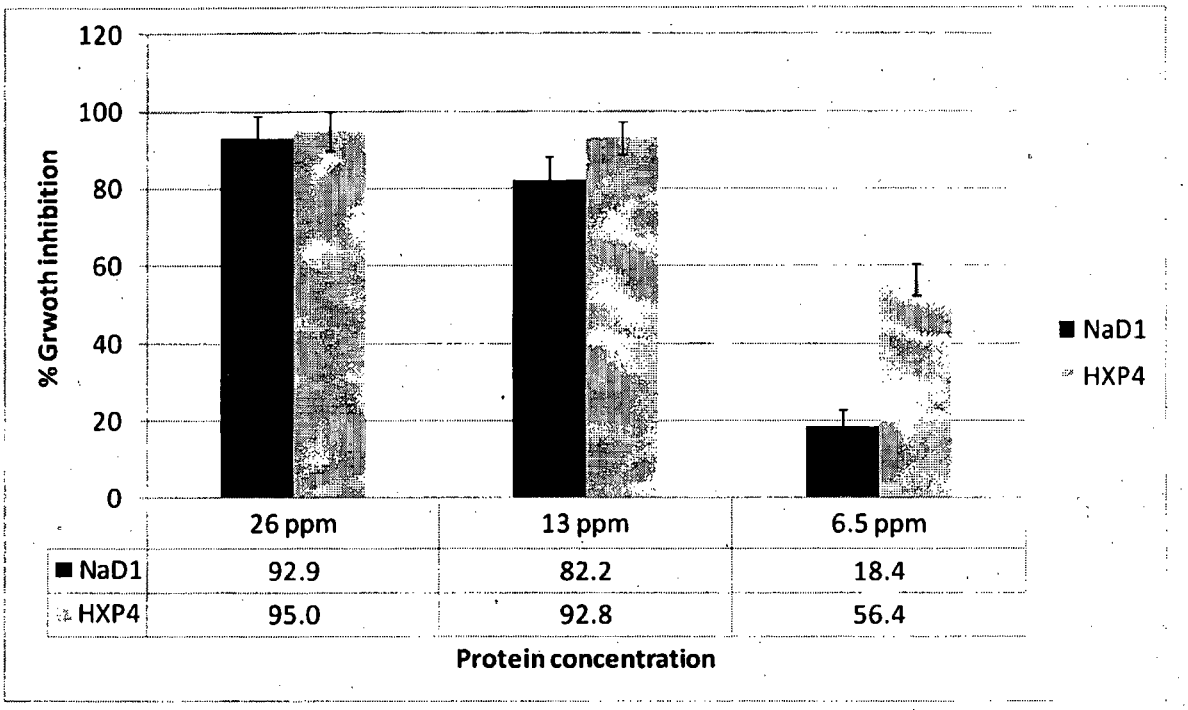

120
100
80
60
40
20
0
% Grwoth inhibition
NaD1
HXP4
26 ppm
13 ppm
6.5 ppm
NaD1 92.9 82.2 18.4
HXP4 95.0 92.8 56.4
Protein concentration

Figure 13C

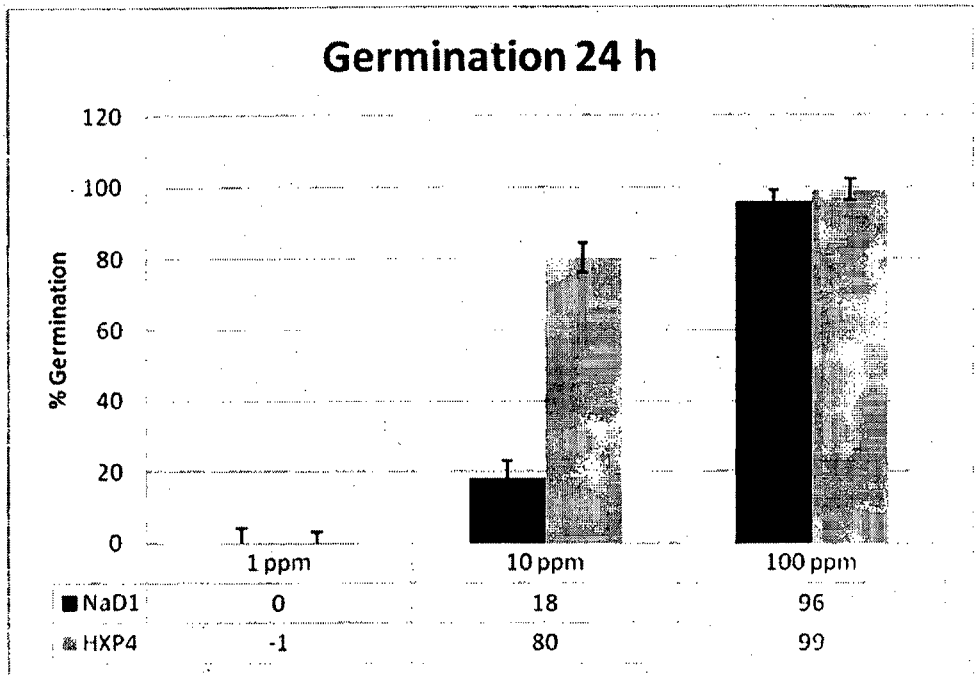

Germination 24 h
% Germination
120
100
80
60
40
20
0
1 ppm
10 ppm
100 ppm
NaD1 0 18 96
HXP4 -1 80 99

Figure 14A

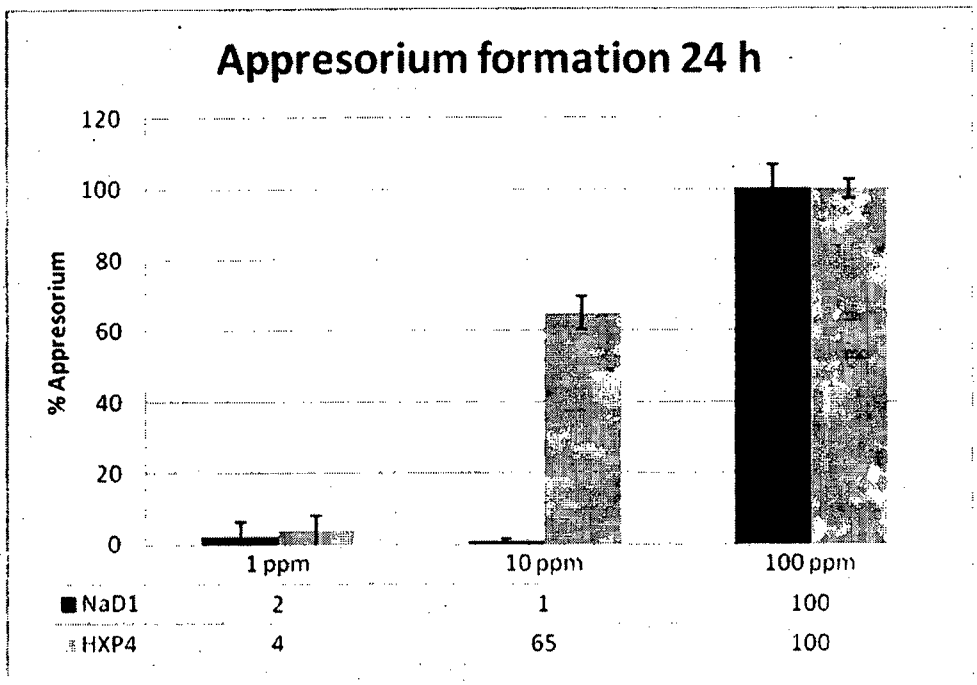

Appresorium formation 24 h
% Appresorium
120
100
80
60
40
20
0
1 ppm
10 ppm
100 ppm
NaD1
2
1
100
HXP4
4
65
100

Figure 14B

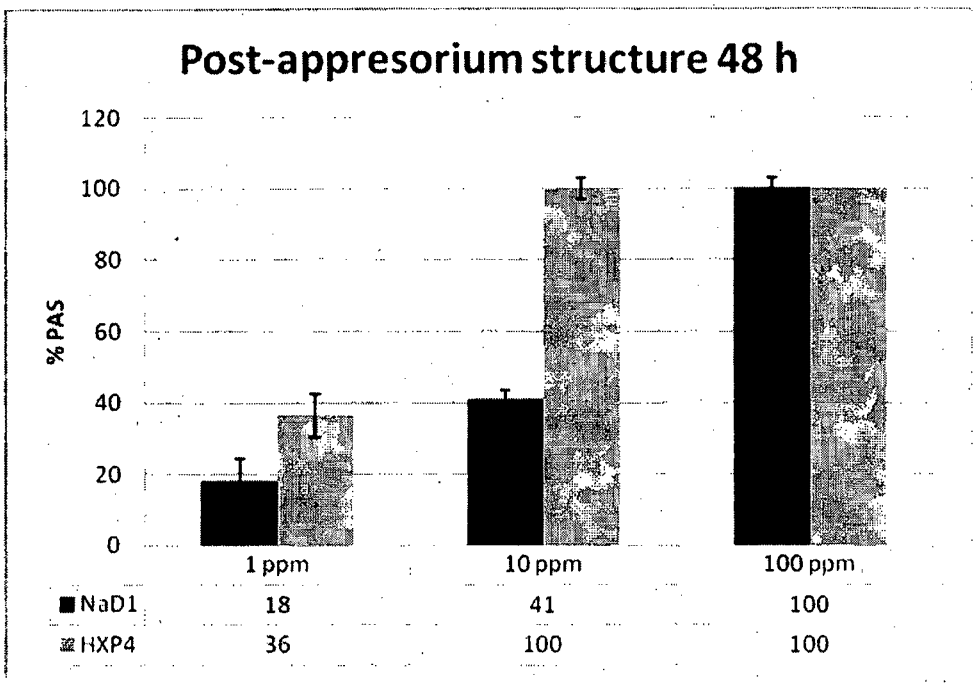

Post-appresorium structure 48 h
120
100
80
60
40
20
0
% PAS
1 ppm
10 ppm
100 ppm
NaD1 18 41 100
HXP4 36 100 100

Figure 14C

>SS_{BAA}-HvCPI6 for expression in corn

```
         10        20        30        40        50        60        70
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
atggccaacaagcacctgtccctctccctcttcctcgtgctcctcggcctctccgcctccctcgcctccg
 M  A  N  K  H  L  S  L  S  L  F  L  V  L  L  G  L  S  A  S  L  A  S

         80        90       100       110       120       130       140
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
gagccacctcggccctcggccgccgcggcgtgcttctgggcgggtggagccccgtcaaggacgtgaacga
G  A  T  S  A  L  G  R  R  G  V  L  L  G  G  W  S  P  V  K  D  V  N  D

        150       160       170       180       190       200       210
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
cccgcacgtccaggagctaggcgggtgggcggtggcccagcacgccagcctagccaaggacgggctgctc
  P  H  V  Q  E  L  G  G  W  A  V  A  Q  H  A  S  L  A  K  D  G  L  L

        220       230       240       250       260       270       280
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
ttccgccgggtgacgcgcggcgagcagcaggtggtgtccgggatgaactaccgcctcttcgtggtcgcgg
 F  R  R  V  T  R  G  E  Q  Q  V  V  S  G  M  N  Y  R  L  F  V  V  A

        290       300       310       320       330       340       350
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
cggacggctccggcaagagggtgacctatctcgcgcagatctacgagcactggagcaggacccgcaagct
A  D  G  S  G  K  R  V  T  Y  L  A  Q  I  Y  E  H  W  S  R  T  R  K  L

        360       370
....|....|....|....|....|....|.
cacgtccttcaagccggctgccggcggctga
  T  S  F  K  P  A  A  G  G  *
```

Figure 15

>SS_{BAA}-HvCPI6-L-HXP4-$CTPP_{NaD1}$

```
         10        20        30        40        50        60        70
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
atggccaacaagcacctgtccctctccctcttcctcgtgctcctcggcctctccgcctccctcgcctccg
 M  A  N  K  H  L  S  L  S  L  F  L  V  L  L  G  L  S  A  S  L  A  S

         80        90       100       110       120       130       140
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
gagccacctcggccctcggccgccgcggcgtgcttctgggcgggtggagccccgtcaaggacgtgaacga
G  A  T  S  A  L  G  R  R  G  V  L  L  G  G  W  S  P  V  K  D  V  N  D

       150       160       170       180       190       200       210
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
cccgcacgtccaggagctaggcgggtgggcggtggcccagcacgccagcctagccaaggacgggctgctc
  P  H  V  Q  E  L  G  G  W  A  V  A  Q  H  A  S  L  A  K  D  G  L  L

       220       230       240       250       260       270       280
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
ttccgccgggtgacgcgcggcgagcagcaggtggtgtccgggatgaactaccgcctcttcgtggtcgcgg
 F  R  R  V  T  R  G  E  Q  Q  V  V  S  G  M  N  Y  R  L  F  V  V  A

       290       300       310       320       330       340       350
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
cggacggctccggcaagagggtgacctatctcgcgcagatctacgagcactggagcaggacccgcaagct
A  D  G  S  G  K  R  V  T  Y  L  A  Q  I  Y  E  H  W  S  R  T  R  K  L

       360       370       380       390       400       410       420
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
cacgtccttcaagccggctgccggcggcgaggagaagaagaacagggagtgcaaaacagagagcaacacg
  T  S  F  K  P  A  A  G  GE  E  K  K  N  R  E  C  K  T  E  S  N  T

       430       440       450       460       470       480       490
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
ttccctggcatctgcattactaagccaccgtgccgcaaggcctgcatctccgaaaagtttacagacgggc
 F  P  G  I  C  I  T  K  P  P  C  R  K  A  C  I  S  E  K  F  T  D  G

       500       510       520       530       540       550       560
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
actgttccaaaatcctccgcaggtgcctctgcacgaagccgtgcgttttcgacgagaagatgacgaagac
H  C  S  K  I  L  R  R  C  L  C  T  K  P  C  V  F  D  E  K  M  T  K  T

       570       580       590       600       610       620       630
....|....|....|....|....|....|....|....|....|....|....|....|....|....|
tggggcggagattctcgctgaggaggccaagactctggcggctgccctgctggaagaggaaattatggac
  G  A  E  I  L  A  E  E  A  K  T  L  A  AA  L  L  E  EE  I  M  D

....|.
aattga
N  *
```

Figure 16