Fig 1 :

Pea Chalcone reductase DNA sequence (SEQ ID No. 1)

```
1     ATGGGTAGTG TTGAAATCCC AACAAAGGTG CTTACCAACA CATCTGCTCA AATTAAGATG
61    CCTGTTGTTG GAATGGGATC AGCACCTGAC TTCACATGCA AGAAAGACAC TAAAGAAGCA
121   ATCATCGAAG CCATCAAACA AGGTTACAGA CACTTTGATA CTGCTGCTGC TTATGGATCC
181   GAACAAGCTC TTGGTGAGGC TTTGAATGAG GCTATTCAAC TTGGTCTTGT CACTAGAGAA
241   CAGCTTTTTG TTACTTCTAA ACTTTGGGTT ACTGAAAATC ATCCTCACCT TGTTCTTCCT
301   GCTCTACAAA AATCTCTCAA GACTCTTCAG TTGGATTACT TGGATTTGTA TTTGATTCAT
361   TGGCCACTTA GTTCTCAGCC CGGAAAGTTT TCATTTCCAA TTGATGTGGC TGATCTATTG
421   CCATTTGATG TAAAAGGTGT GTGGGAATCC ATGGAAGAGG CTTTGAGACT TGGACTCACG
481   AAAGCTATTG GTGTCAGTAA CTTCTCTGTC AAGAAACTTC AAAAGCTACT ATCTGTTGCC
541   ACTGTTCTTC CTGCTGTTAA TCAAGTAGAG ATGAACCTTG CATGGCAACA AAAGAAGCTA
601   AGAGAATTTT GCAATGAAAA TGGAATAGTG TTGACTGCAT TTTCACCGTT GAGGAAAGGC
661   GCCAGCCGAG GAGCAAATGA GGTTATGGAG AATGATATGC TTAAACAGAT TGCAGATGCT
721   CATGGAAAGT CTATTGCACA AATTTCTCTG AGATGGTTAT ATGAACAAGG AATCACTTTT
781   GTTCCAAAGA GCTATGATAA GGAGAGAATG AGTCAAAATT TGAGAATCTT TGATTGGACA
841   CTGACAAAGG AGGATCATGA GAAAATTGAT CAAATTAAGC AGAATCGTTT GATCCCTGGA
901   CCAACCAAGC CAAGTCTCAA TGATCTTTGG GATGATGAAA TATAAG
```

Pea Chalcone reductase protein sequence (SEQ ID No. 2)

```
Met Gly Ser Val Glu Ile Pro Thr Lys Val Leu Thr Asn Thr Ser Ala Gln Ile Lys Met
Pro Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr Cys Lys Lys Asp Thr Lys Glu Ala
Ile Ile Glu Ala Ile Lys Gln Gly Tyr Arg His Phe Asp Thr Ala Ala Ala Tyr Gly Ser
Glu Gln Ala Leu Gly Glu Ala Leu Asn Glu Ala Ile Gln Leu Gly Leu Val Thr Arg Glu
Gln Leu Phe Val Thr Ser Lys Leu Trp Val Thr Glu Asn His Pro His Leu Val Leu Pro
Ala Leu Gln Lys Ser Leu Lys Thr Leu Gln Leu Asp Tyr Leu Asp Leu Tyr Leu Ile His
Trp Pro Leu Ser Ser Gln Pro Gly Lys Phe Ser Phe Pro Ile Asp Val Ala Asp Leu Leu
Pro Phe Asp Val Lys Gly Val Trp Glu Ser Met Glu Glu Ala Leu Arg Leu Gly Leu Thr
Lys Ala Ile Gly Val Ser Asn Phe Ser Val Lys Lys Leu Gln Lys Leu Leu Ser Val Ala
Thr Val Leu Pro Ala Val Asn Gln Val Glu Met Asn Leu Ala Trp Gln Gln Lys Lys Leu
Arg Glu Phe Cys Asn Glu Asn Gly Ile Val Leu Thr Ala Phe Ser Pro Leu Arg Lys Gly
Ala Ser Arg Gly Ala Asn Glu Val Met Glu Asn Asp Met Leu Lys Gln Ile Ala Asp Ala
His Gly Lys Ser Ile Ala Gln Ile Ser Leu Arg Trp Leu Tyr Glu Gln Gly Ile Thr Phe
Val Pro Lys Ser Tyr Asp Lys Glu Arg Met Ser Gln Asn Leu Arg Ile Phe Asp Trp Thr
Leu Thr Lys Glu Asp His Glu Lys Ile Asp Gln Ile Lys Gln Asn Arg Leu Ile Pro Gly
Pro Thr Lys Pro Ser Leu Asn Asp Leu Trp Asp Asp Glu Ile
```

Fig 2 : Soy isoflavone synthase DNA sequence (SEQ ID No. 3)

```
1     ATGGTGCTTG AACTTGCACT TGGTTTATTG GTTTTGGCTC TGTTTCTGCA CTTGCGTCCC
61    ACACCCACTG CAAAATCAAA AGCACTTCGC CATCTCCCAA ACCCACCAAG CCCAAAGCCT
121   CGTCTTCCCT TCATAGGACA CCTTCATCTC TTAAAAGACA AACTTCTCCA CTACGCACTC
181   ATCGACCTCT CCAAAAAACA TGGTCCCTTA TTCTCTCTCT ACTTTGGCTC CATGCCAACC
241   GTTGTTGCCT CCACACCAGA ATTGTTCAAG CTCTTCCTCC AAACGCACGA GGCAACTTCC
301   TTCAACACAA GGTTCCAAAC CTCAGCCATA AGACGCCTCA CCTATGATAG CTCAGTGGCA
361   ATGGTTCCCT TCGGGCCCTA CTGGAAGTTC GTGAGGAAGC TCATCATGAA CGACCTTCTC
421   AACGCCACCA CTGTAAACAA GTTGAGGCCT TTGAGGACCC AACAGACGCG TAAGTTCCTT
481   AGGGTTATGG CCCAAGGCGC AGAGGCACAG AAGCCCCTTG ACTTGACCGA GGAGCTTCTG
541   AAATGGACCA ACAGCACCAT CTCCATGATG ATGCTCGGCG AGGCTGAGGA GATCAGAGAC
601   ATCGCTCGCG AGGTTCTTAA GATCTTTGGC GAATACAGCC TCACTGACTT CATCTGGCCA
661   TTGAAGCATC TCAAGGTTGG AAAGTATGAG AAGAGGATCG ACGACATCTT GAACAAGTTC
721   GACCCTGTCG TTGAAAGGGT CATCAAGAAG CGCCGTGAGA TCGTGAGGAG GAGAAAGAAC
781   GGAGAGGTTG TTGAGGGTGA GGTCAGCGGG GTTTTCCTTG ACACTTTGCT CGAGTTCGCT
841   GAGGATGAGA CTATGGAGAT CAAAATCACC AAGGACCACA TCAAGGGTCT TGTTGTAGAC
901   TTTTTCTCGG CAGGAACAGA CTCAACAGCG GTGGCAACAG AGTGGGCATT GGCAGAACTC
961   ATCAACAATC CTAAGGTGTT GGAAAAGGCT CGTGAGGAGG TCTACAGTGT TGTGGGAAAG
1021  GACAGACTTG TGGACGAAGT TGACACTCAA AACCTTCCTT ACATTAGAGC AATCGTGAAG
1081  GAGACATTCC GCATGCACCC GCCACTCCCA GTGGTCAAAA GAAAGTGCAC AGAAGAGTGT
1141  GAGATTAATG GATATGTGAT CCCAGAGGGA GCATTGATTC TCTTCAATGT ATGGCAAGTA
1201  GGAAGAGACC CCAAATACTG GGACAGACCA TCGGAGTTCC GTCCTGAGAG GTTCCTAGAG
1261  ACAGGGGCTG AAGGGGAAGC AGGGCCTCTT GATCTTAGGG GACAACATTT TCAACTTCTC
1321  CCATTTGGGT CTGGGAGGAG AATGTGCCCT GGAGTCAATC TGGCTACTTC GGGAATGGCA
1381  ACACTTCTTG CATCTCTTAT TCAGTGCTTC GACTTGCAAG TGCTGGGTCC ACAAGGACAG
1441  ATATTGAAGG GTGGTGACGC CAAAGTTAGC ATGGAAGAGA GAGCCGGCCT CACTGTTCCA
1501  AGGGCACATA GTCTTGTCTG TGTTCCACTT GCAAGGATCG GCGTTGCATC TAAACTCCTT
1561  TCTTAAG
```

Soy isoflavone synthase protein sequence (SEQ ID No. 4)

```
Met Val Leu Glu Leu Ala Leu Gly Leu Leu Val Leu Ala Leu Phe Leu His Leu
Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu Pro Asn Pro Pro
Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu His Leu Leu Lys Asp Lys
Leu Leu His Tyr Ala Leu Ile Asp Leu Ser Lys Lys His Gly Pro Leu Phe Ser
Leu Tyr Phe Gly Ser Met Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys
Leu Phe Leu Gln Thr His Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser
Ala Ile Arg Arg Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro
Tyr Trp Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Thr Arg Lys Phe Leu Arg Val
Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr Glu Glu Leu Leu
Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu Gly Glu Ala Glu Glu Ile
Arg Asp Ile Ala Arg Glu Val Leu Lys Ile Phe Gly Glu Tyr Ser Leu Thr Asp
Phe Ile Trp Pro Leu Lys His Leu Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp
Asp Ile Leu Asn Lys Phe Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg
Glu Ile Val Arg Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly
Val Phe Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala Gly Thr
Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu Ile Asn Asn Pro
Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser Val Val Gly Lys Asp Arg
Leu Val Asp Glu Val Asp Thr Gln Asn Leu Pro Tyr Ile Arg Ala Ile Val Lys
Glu Thr Phe Arg Met His Pro Pro Leu Pro Val Val Lys Arg Lys Cys Thr Glu
Glu Cys Glu Ile Asn Gly Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn
Val Trp Gln Val Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg
Pro Glu Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met Cys Pro
Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala Ser Leu Ile Gln
```

Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln Ile Leu Lys Gly Gly Asp
Ala Lys Val Ser Met Glu Glu Arg Ala Gly Leu Thr Val Pro Arg Ala His Ser
Leu Val Cys Val Pro Leu Ala Arg Ile Gly Val Ala Ser Lys Leu Leu Ser

Fig 3:

Lotus corniculatus chalcone isomerase DNA sequence (SEQ ID No. 5)

```
1     ATGGCTGCAT CCCTCACCCC AATCCAGGTC GAGAACCTTC AATTTCCTGC GTCTGTCACC
61    TCTCCAGCCA CCGCCAAGTC TTATTTCCTC GGTGGTGCAG GGGAGAGAGG GTTGACGATT
121   GAGGGGAAGT TCATAAAATT CACTGGCATA GGAGTGTATT TGGAAGATAC AGCAGTGGAT
181   TCACTCGCCA CCAAGTGGAA GGGTAAGAGT TCACAAGAGC TGCAGGACTC CCTTGACTTC
241   TTCAGAGACA TCATTTCAAG TCCCTCTGAG AAGTTAATTC GAGGGTCCAA GCTGAGGCCA
301   TTGAGTGGCG TGGAGTATTC AAGAAAGGTG ATGGAGAATT GTGTGGCACA CATGAAGTCT
361   GCTGGAACTT ATGGTGAAGC AGAGGCCACA GCCATTGAAA AATTTGCAGA AGCCTTCAGG
421   AAGGTGGATT TTCCACCAGG TTCCTCTGTT TTCTACCGAC AATCAACAGA TGGAAAATTA
481   GGGCTTAGTT TCTCTTTGGA TGACACGATA CCAGAAGAAG AGGCTGTAGT TATAGAGAAC
541   AAGGCACTCT CAGAGGCAGT GTTAGAGACC ATGATTGGCG AGCATGCTGT TTCCCCTGAT
601   TTGAAGCGTT GTTTGGCTGA AAGGTTGCCT ATTGTGATGA ACCAGGGTCT TCTCCTCACT
661   GGAAACTGAT
```

Lotus corniculatus chalcone isomerase protein (SEQ ID No. 6)

Met Ala Ala Ser Leu Thr Pro Ile Gln Val Glu Asn Leu Gln Phe Pro Ala Ser
Val Thr Ser Pro Ala Thr Ala Lys Ser Tyr Phe Leu Gly Gly Ala Gly Glu Arg
Gly Leu Thr Ile Glu Gly Lys Phe Ile Lys Phe Thr Gly Ile Gly Val Tyr Leu
Glu Asp Thr Ala Val Asp Ser Leu Ala Thr Lys Trp Lys Gly Lys Ser Ser Gln
Glu Leu Gln Asp Ser Leu Asp Phe Phe Arg Asp Ile Ile Ser Ser Pro Ser Glu
Lys Leu Ile Arg Gly Ser Lys Leu Arg Pro Leu Ser Gly Val Glu Tyr Ser Arg
Lys Val Met Glu Asn Cys Val Ala His Met Lys Ser Ala Gly Thr Tyr Gly Glu
Ala Glu Ala Thr Ala Ile Glu Lys Phe Ala Glu Ala Phe Arg Lys Val Asp Phe
Pro Pro Gly Ser Ser Val Phe Tyr Arg Gln Ser Thr Asp Gly Lys Leu Gly Leu
Ser Phe Ser Leu Asp Asp Thr Ile Pro Glu Glu Glu Ala Val Val Ile Glu Asn
Lys Ala Leu Ser Glu Ala Val Leu Glu Thr Met Ile Gly Glu His Ala Val Ser
Pro Asp Leu Lys Arg Cys Leu Ala Glu Arg Leu Pro Ile Val Met Asn Gln Gly
Leu Leu Leu Thr Gly Asn

Fig 4:

ID No.	Primer	Primer Sequence (5' to 3')
13	GPTV1	Ttgtccagatagcccagtagctg
14	GPTV2	Cgacaatctgatcatgagcggag
15	30035S	Cgcaagacccttcctctatataag
16	Gus2	Gcatcacgcagttcaacgctg
17	152	Ggaaacagctatgaccatgattac
18	160	Aaggatccgtcgacatc
19	167	Agtcccccatggtacgtcctgtagaaacc
20	168	Cgttttcgtcggtaatcaccattcc
21	191	Tttcccagtcacgacgttgt
22	198	Gacatcgataatacgac
23	248	Tgctacctctagagaatttccccg
24	321	ctaagcccc/taag/tattccatcaggtgatt
25	322	ccaggtggaaaatta/cacat/gt/gcttgaaa/gagc
26	323	tttgaaaagt/ctaat/aa/cgagggtca/gaag
27	324	tactcaaggaaggtt/gatggag/aactgt/cgtgg
28	329	cgcgagctcatgtaccccgggatttccactagtttaagggttaactacatggtcgacgta cata
29	330	agcttatgtacgtcgaccatgtagttaacccttaaactagtggaaatcccggggtacatg agctcgcgat
30	331	aattcgagctcatgtaccccgggatttccactagtttaagggttaactacatggtcgacg
31	332	ctagcgtcgaccatgtagttaacccttaaactagtggaaatcccggggtacatgagctcg
32	333	catggatgcgtagttaagcct
33	334	ctagaggcttacatacgcatc
34	337	Aattcatgtacgagctcaattcccccgggataggcactagtgctgctgttaactacatgg tcgacttattaa
35	338	Aggtttaataagtcgaccatgtagttaacagcagcactagtgcctatcccgggggaattg agctcgtacatg
36	339	Gaacaccatggtgcttgaacttgc
37	340	Tccagtagggcccgaagggaaccattgccac
38	341	Ccttcgggccctactggaag
39	342	Cagcgaactcgagcaaagtg
40	343	Cactttgctcgagttcgctgaggatgagactatggagatcaaaatcaccaaggaccacat caagggtcttgttgtagac
41	344	atgacgagctagcttattaagaaaggag
42	362	ggtgtgtggggatccatggaagaggctttg
43	363	cctcggctcgcgcctttcctcaacggtgaaaatgcagtcaacac
44	384	caacaacccatgggtagtgttgaaatcccaacaaaggtgcttacc
45	385	agcaactgctagcttatatttcatcatcccaaagatc
46	386	tagattgccatggctgcatccctcaccccaatccaggtcgag
47	387	aaactttgctagcttatcagtttccagtgaggagaagac
48	398	gcttgttcggatccataagcagc
49	399	tgcttatggatccgaacaagctcttggtgaggctttgaatg
50	400	cagccacatcaattggaaatg
51	401	tcatttccaattgatgtggctgatctattgccatttgatgtaaaaggtgtgtgggaatcc atggaagaggctttgaga
52	402	cacaagagctgcaggactcccttga
53	403	gggagtcctgcagctcttgtgaac
54	624	agctgcgatcgcaagcttggtaccgggaattctctaga
55	625	aatttctagagaattcccggtaccaagcttgcttgcgatcgc
56	626	tcgacccatggcccgctagccaattggagct
57	627	ccaattggctagcgggccatggg
58	640	ccacccacgagggaacatcgtg
59	641	gaattcccatggtttacactcgaggtcctctccaaatga

Fig.5.

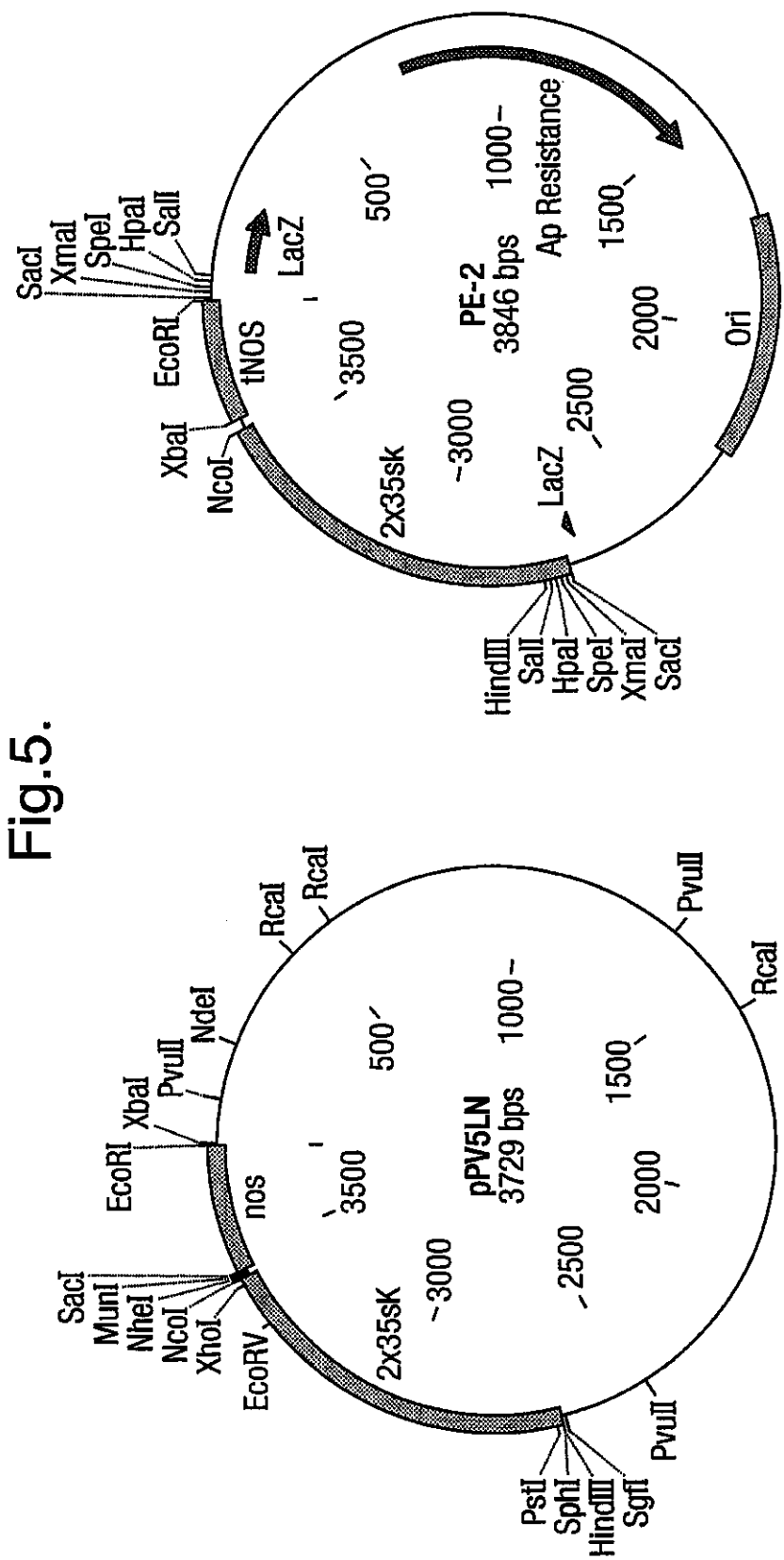

SacI
XmaI
SpeI
HpaI
SalI
EcoRI
XbaI
NcoI
tNOS
LacZ
500
1000
1500
2000
Ori
Ap Resistance
PE-2
3846 bps
3500
-3000
2500
2x35sk
LacZ
HindIII
SalI
HpaI
SpeI
XmaI
SacI
RcaI
RcaI
PvuII
NdeI
PvuII
XbaI
EcoRI
SacI
MunI
NheI
NcoI
XhoI
EcoRV
nos
pPV5LN
3729 bps
2x35sK
PstI
SphI
HindIII
SgfI
PvuII
PvuII
RcaI

Fig.5 (Cont I).

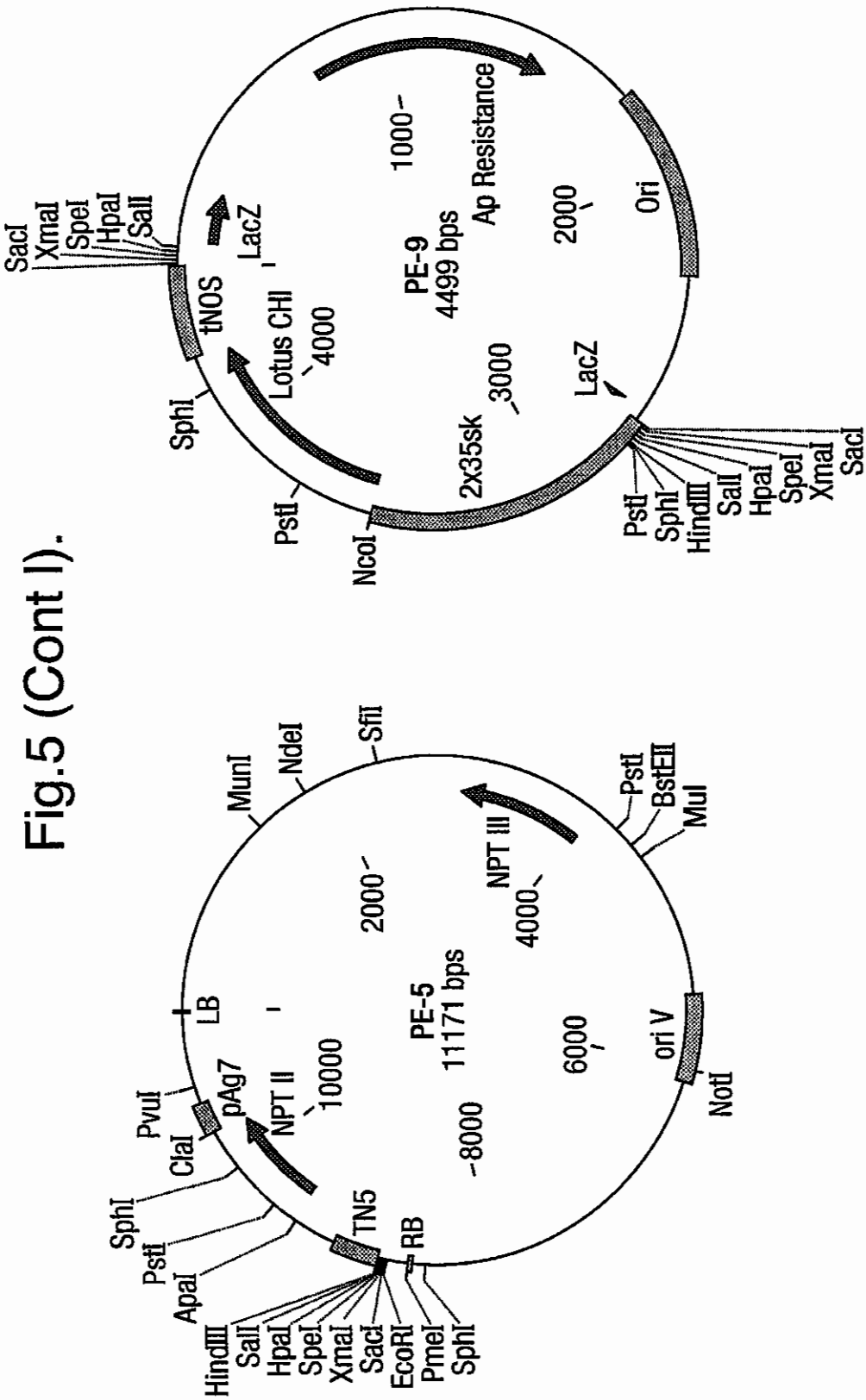

PE-9
4499 bps
1000
2000
3000
4000
Ap Resistance
Ori
LacZ
Lotus CHI
tNOS
2x35sk
SacI
XmaI
SpeI
HpaI
SalI
SphI
PstI
NcoI
HindIII
PE-5
11171 bps
2000
4000
6000
8000
10000
NPT III
NPT II
ori V
LB
RB
TN5
pAg7
MunI
NdeI
SfiI
PstI
BstEII
MuI
NotI
PvuI
ClaI
ApaI
EcoRI
PmeI

Fig.5 (Cont II).

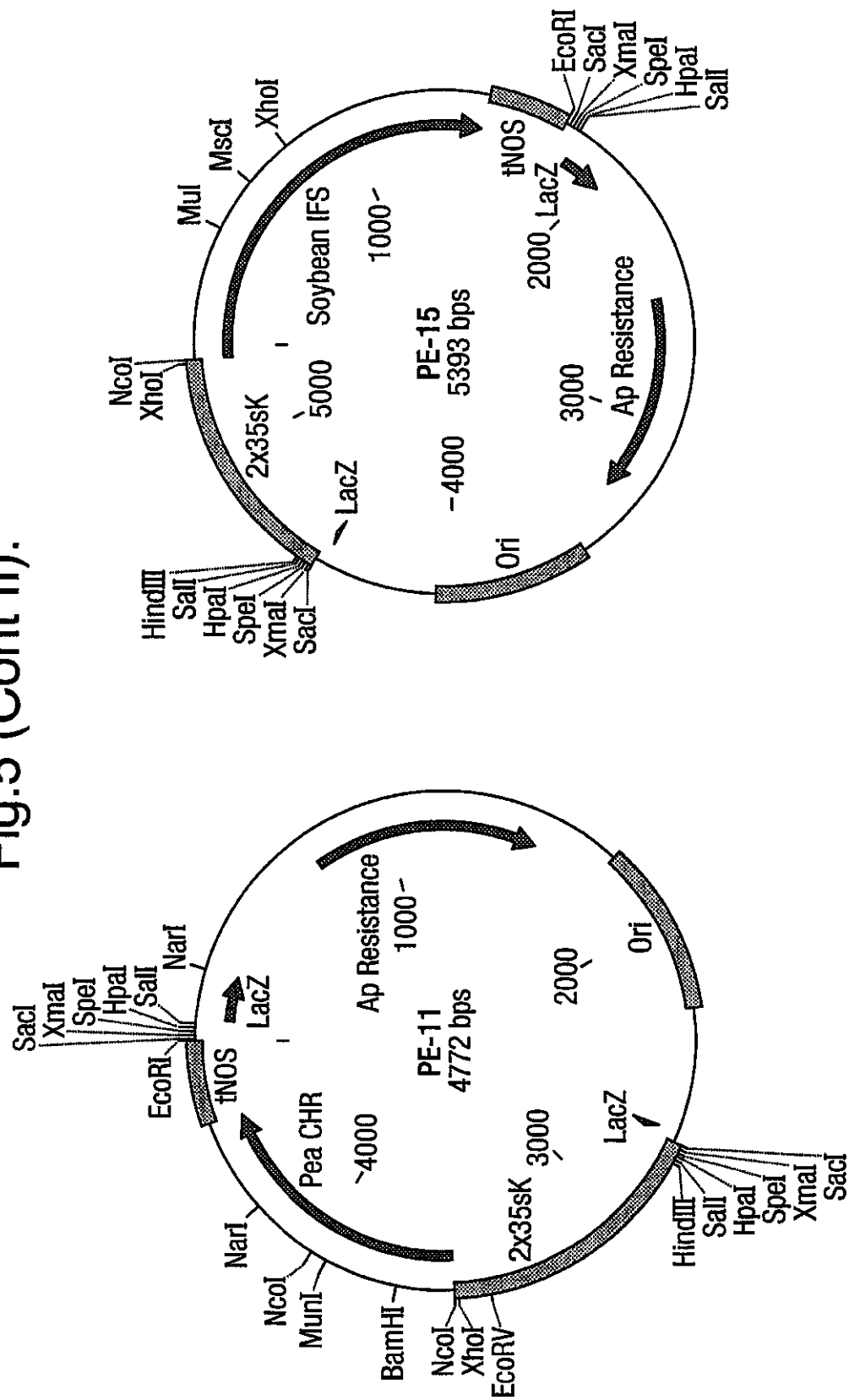

PE-15
5393 bps
Soybean IFS
1000
2000
LacZ
tNOS
EcoRI
SacI
XmaI
SpeI
HpaI
SalI
3000
Ap Resistance
Ori
4000
LacZ
2x35sK
5000
NcoI
XhoI
MscI
MluI
HindIII
SalI
HpaI
SpeI
XmaI
SacI
PE-11
4772 bps
Ap Resistance
1000
2000
Ori
LacZ
3000
2x35sK
4000
Pea CHR
tNOS
EcoRI
SacI
XmaI
SpeI
HpaI
SalI
NarI
NcoI
MunI
BamHI
NcoI
XhoI
EcoRV
HindIII
SalI
HpaI
SpeI
XmaI
SacI

Fig.5 (Cont III).

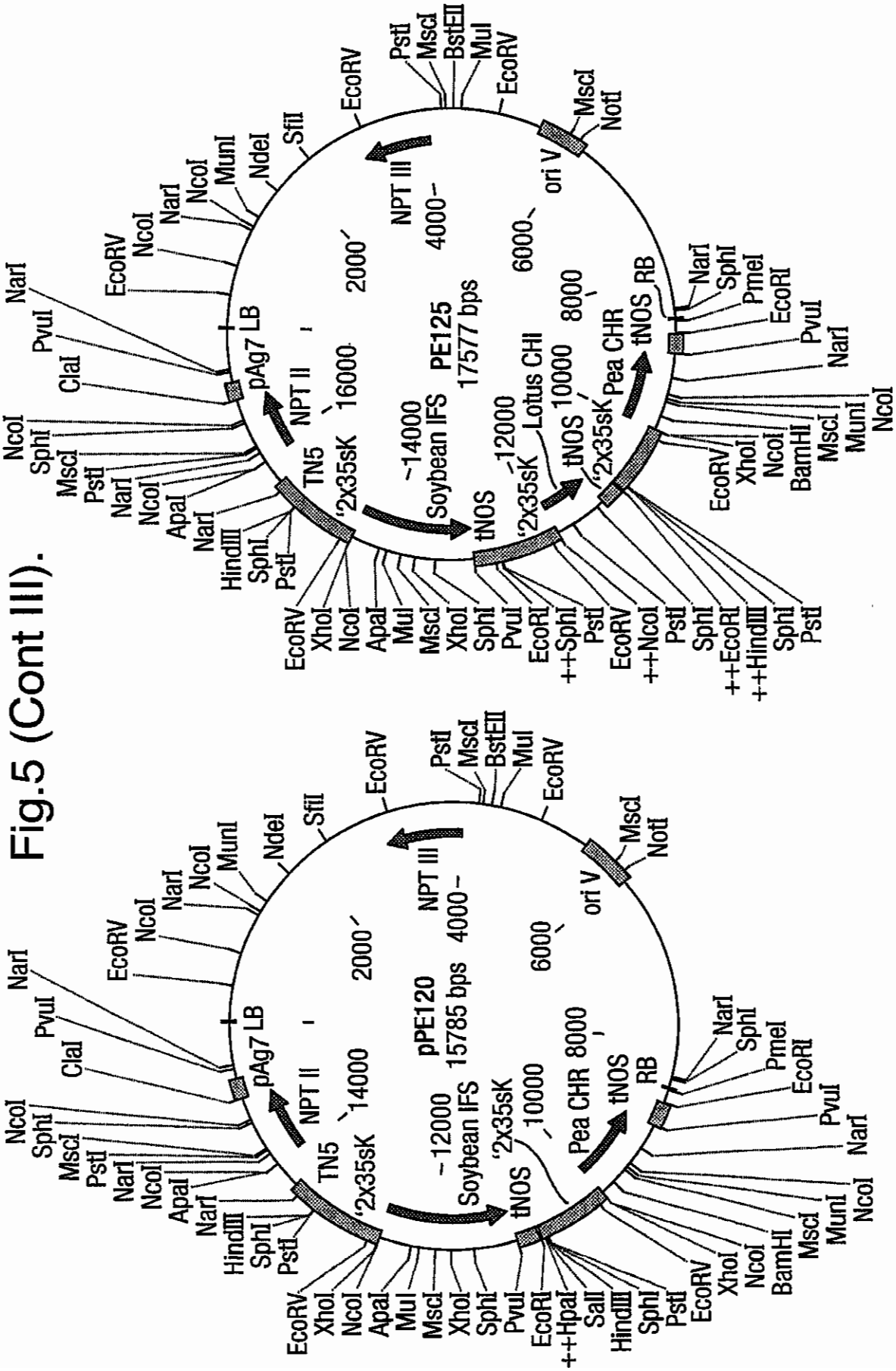


Fig.5 (Cont IIII).

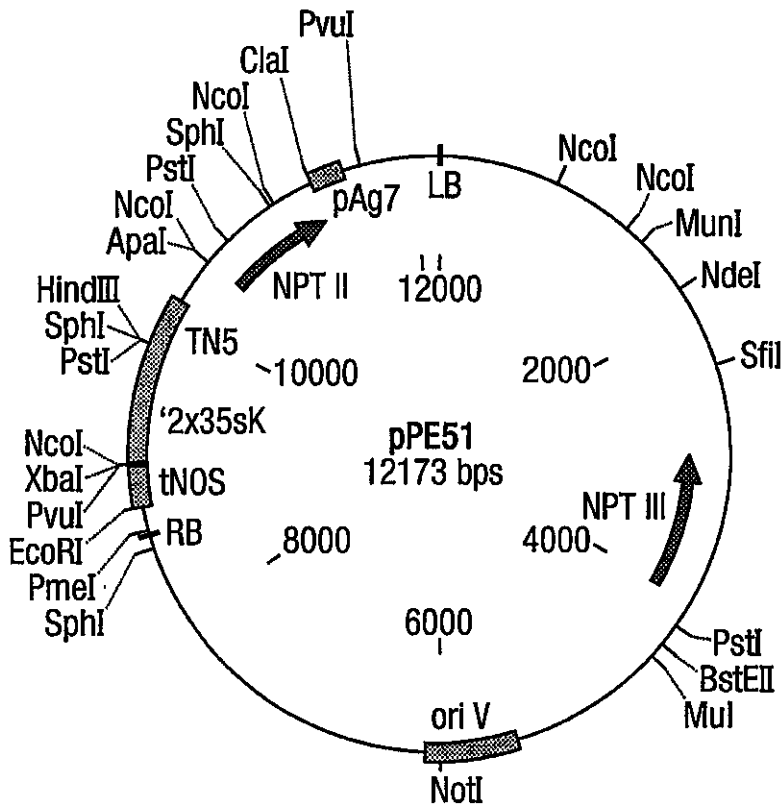


Fig.6a.

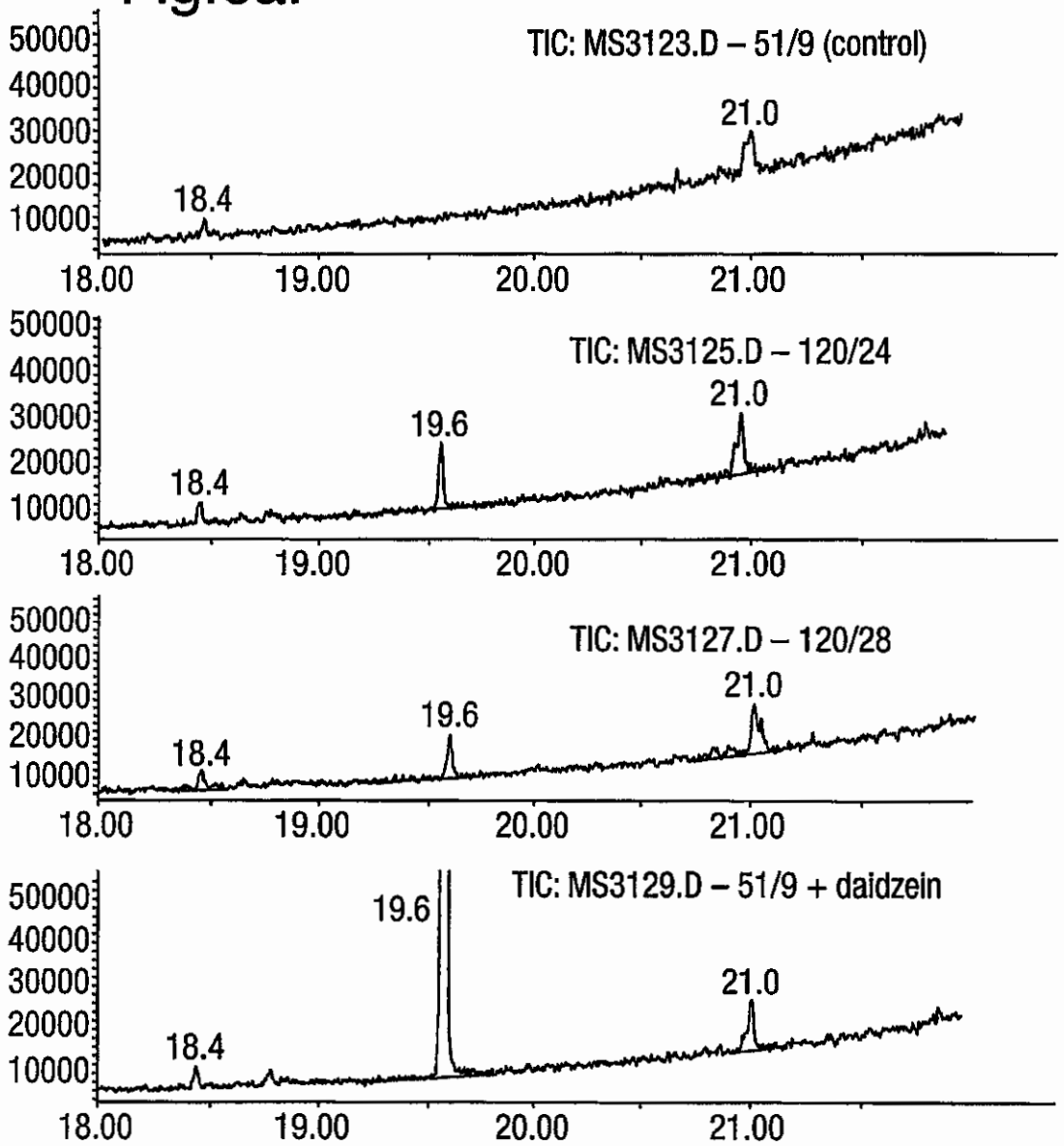

TIC: MS3123.D – 51/9 (control)
TIC: MS3125.D – 120/24
TIC: MS3127.D – 120/28
TIC: MS3129.D – 51/9 + daidzein
50000
40000
30000
20000
10000
18.4
19.6
21.0
18.00
19.00
20.00
21.00

Fig.6b.

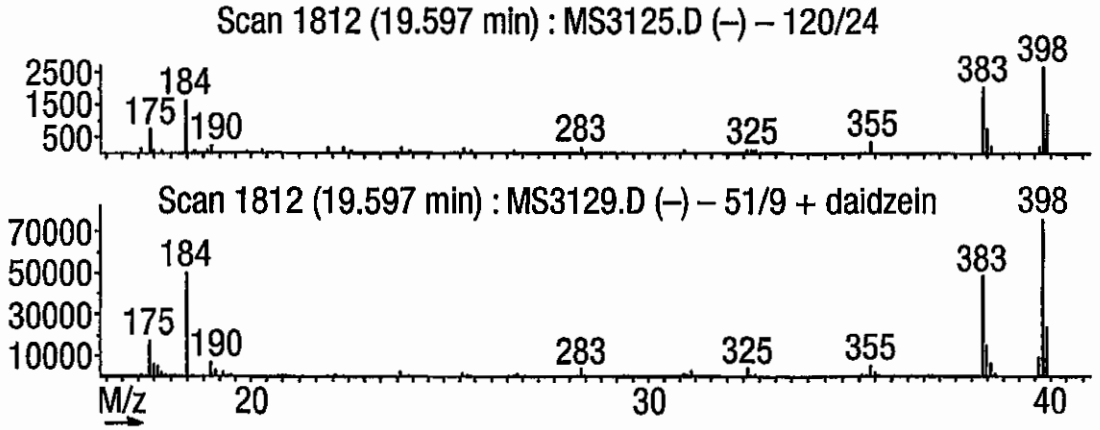

Scan 1812 (19.597 min) : MS3125.D (–) – 120/24
Scan 1812 (19.597 min) : MS3129.D (–) – 51/9 + daidzein
2500
1500
500
70000
50000
30000
10000
184
175
190
283
325
355
383
398
M/z
20
30
40

Fig.7.

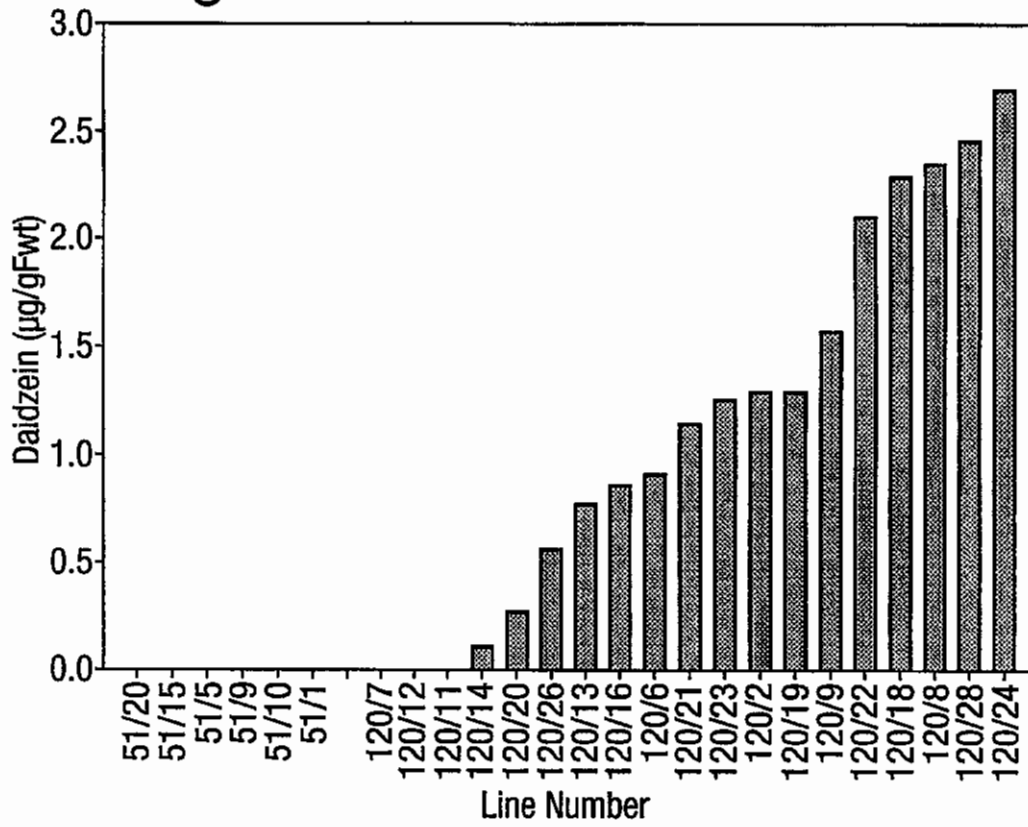
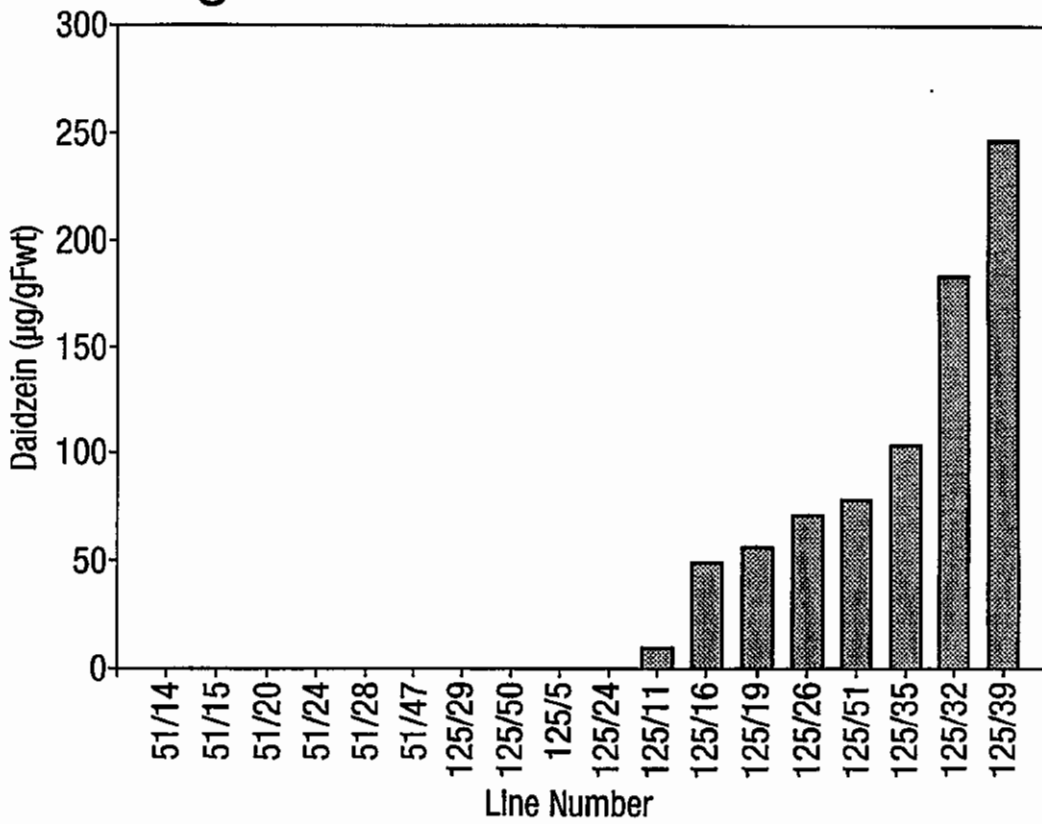

Daidzein (µg/gFwt)
3.0
2.5
2.0
1.5
1.0
0.5
0.0
51/20
51/15
51/5
51/9
51/10
51/1
120/7
120/12
120/11
120/14
120/20
120/26
120/13
120/16
120/6
120/21
120/23
120/2
120/19
120/9
120/22
120/18
120/8
120/28
120/24
Line Number

Fig.8.


Daidzein (µg/gFwt)
300
250
200
150
100
50
0
51/14
51/15
51/20
51/24
51/28
51/47
125/29
125/50
125/5
125/24
125/11
125/16
125/19
125/26
125/51
125/35
125/32
125/39
Line Number

SEQUENCE LISTING

<110> Unilever Plc

<120> Nutritionally Enhanced Plants

<130> T3087(C)

<160> 53

<170> PatentIn version 3.1

<210> 1
<211> 946
<212> DNA
<213> pea

<220>
<221> misc_feature
<223> Pea Chalcone reductase DNA sequence

<400> 1
atgggtagtg ttgaaatccc aacaaaggtg cttaccaaca catctgctca aattaagatg 60

cctgttgttg gaatgggatc agcacctgac ttcacatgca agaaagacac taaagaagca 120

atcatcgaag ccatcaaaca aggttacaga cactttgata ctgctgctgc ttatggatcc 180

gaacaagctc ttggtgaggc tttgaatgag gctattcaac ttggtcttgt cactagagaa 240

cagctttttg ttacttctaa actttgggtt actgaaaatc atcctcacct tgttcttcct 300

gctctacaaa aatctctcaa gactcttcag ttggattact tggatttgta tttgattcat 360

tggccactta gttctcagcc cggaaagttt tcatttccaa ttgatgtggc tgatctattg 420

ccatttgatg taaaaggtgt gtgggaatcc atggaagagg ctttgagact tggactcacg 480

aaagctattg gtgtcagtaa cttctctgtc aagaaacttc aaaagctact atctgttgcc 540

actgttcttc ctgctgttaa tcaagtagag atgaaccttg catggcaaca aaagaagcta 600

agagaatttt gcaatgaaaa tggaatagtg ttgactgcat tttcaccgtt gaggaaaggc 660

gccagccgag gagcaaatga ggttatggag aatgatatgc ttaaacagat tgcagatgct 720

catggaaagt ctattgcaca aatttctctg agatggttat atgaacaagg aatcactttt 780

gttccaaaga gctatgataa ggagagaatg agtcaaaatt tgagaatctt tgattggaca 840

ctgacaaagg aggatcatga gaaaattgat caaattaagc agaatcgttt gatccctgga 900

ccaaccaagc caagtctcaa tgatctttgg gatgatgaaa tataag 946

<210> 2
<211> 314
<212> PRT
<213> pea

<220>
<221> MISC_FEATURE
<223> Pea Chalcone reductase protein sequence

<400> 2

Met Gly Ser Val Glu Ile Pro Thr Lys Val Leu Thr Asn Thr Ser Ala
1 5 10 15

Gln Ile Lys Met Pro Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr
20 25 30

Cys Lys Lys Asp Thr Lys Glu Ala Ile Ile Glu Ala Ile Lys Gln Gly
35 40 45

Tyr Arg His Phe Asp Thr Ala Ala Ala Tyr Gly Ser Glu Gln Ala Leu
50 55 60

Gly Glu Ala Leu Asn Glu Ala Ile Gln Leu Gly Leu Val Thr Arg Glu
65 70 75 80

Gln Leu Phe Val Thr Ser Lys Leu Trp Val Thr Glu Asn His Pro His
85 90 95

Leu Val Leu Pro Ala Leu Gln Lys Ser Leu Lys Thr Leu Gln Leu Asp
100 105 110

Tyr Leu Asp Leu Tyr Leu Ile His Trp Pro Leu Ser Ser Gln Pro Gly
115 120 125

Lys Phe Ser Phe Pro Ile Asp Val Ala Asp Leu Leu Pro Phe Asp Val
130 135 140

Lys Gly Val Trp Glu Ser Met Glu Glu Ala Leu Arg Leu Gly Leu Thr
145 150 155 160

Lys Ala Ile Gly Val Ser Asn Phe Ser Val Lys Lys Leu Gln Lys Leu
165 170 175

Leu Ser Val Ala Thr Val Leu Pro Ala Val Asn Gln Val Glu Met Asn
180 185 190

Leu Ala Trp Gln Gln Lys Lys Leu Arg Glu Phe Cys Asn Glu Asn Gly
195 200 205

Ile Val Leu Thr Ala Phe Ser Pro Leu Arg Lys Gly Ala Ser Arg Gly
210 215 220

```
Ala Asn Glu Val Met Glu Asn Asp Met Leu Lys Gln Ile Ala Asp Ala
225                 230                 235                 240

His Gly Lys Ser Ile Ala Gln Ile Ser Leu Arg Trp Leu Tyr Glu Gln
                245                 250                 255

Gly Ile Thr Phe Val Pro Lys Ser Tyr Asp Lys Glu Arg Met Ser Gln
            260                 265                 270

Asn Leu Arg Ile Phe Asp Trp Thr Leu Thr Lys Glu Asp His Glu Lys
        275                 280                 285

Ile Asp Gln Ile Lys Gln Asn Arg Leu Ile Pro Gly Pro Thr Lys Pro
    290                 295                 300

Ser Leu Asn Asp Leu Trp Asp Asp Glu Ile
305                 310
```

<210> 3
<211> 1567
<212> DNA
<213> soy

<220>
<221> misc_feature
<223> Soy isoflavone synthase DNA sequence

<400> 3

```
atggtgcttg aacttgcact tggtttattg gttttggctc tgtttctgca cttgcgtccc     60

acacccactg caaaatcaaa agcacttcgc catctcccaa acccaccaag cccaaagcct    120

cgtcttccct tcataggaca ccttcatctc ttaaaagaca aacttctcca ctacgcactc    180

atcgacctct ccaaaaaaca tggtcccttа ttctctctct actttggctc catgccaacc    240

gttgttgcct ccacaccaga attgttcaag ctcttcctcc aaacgcacga ggcaacttcc    300

ttcaacacaa ggttccaaac ctcagccata agacgcctca cctatgatag ctcagtggca    360

atggttccct tcgggcccta ctggaagttc gtgaggaagc tcatcatgaa cgaccttctc    420

aacgccacca ctgtaaacaa gttgaggcct ttgaggaccc aacagacgcg taagttcctt    480

agggttatgg cccaaggcgc agaggcacag aagcccctg acttgaccga ggagcttctg    540

aaatggacca acagcaccat ctccatgatg atgctcggcg aggctgagga gatcagagac    600

atcgctcgcg aggttcttaa gatctttggc gaatacagcc tcactgactt catctggcca    660

ttgaagcatc tcaaggttgg aaagtatgag aagaggatcg acgacatctt gaacaagttc    720
```

gaccctgtcg ttgaaagggt catcaagaag cgccgtgaga tcgtgaggag gagaaagaac 780

ggagaggttg ttgagggtga ggtcagcggg gttttccttg acactttgct cgagttcgct 840

gaggatgaga ctatggagat caaaatcacc aaggaccaca tcaagggtct tgttgtagac 900

tttttctcgg caggaacaga ctcaacagcg gtggcaacag agtgggcatt ggcagaactc 960

atcaacaatc ctaaggtgtt ggaaaaggct cgtgaggagg tctacagtgt tgtgggaaag 1020

gacagacttg tggacgaagt tgacactcaa aaccttcctt acattagagc aatcgtgaag 1080

gagacattcc gcatgcaccc gccactccca gtggtcaaaa gaaagtgcac agaagagtgt 1140

gagattaatg gatatgtgat cccagaggga gcattgattc tcttcaatgt atggcaagta 1200

ggaagagacc ccaaatactg ggacagacca tcggagttcc gtcctgagag gttcctagag 1260

acaggggctg aaggggaagc agggcctctt gatcttaggg gacaacattt tcaacttctc 1320

ccatttgggt ctgggaggag aatgtgccct ggagtcaatc tggctacttc gggaatggca 1380

acacttcttg catctcttat tcagtgcttc gacttgcaag tgctgggtcc acaaggacag 1440

atattgaagg gtggtgacgc caaagttagc atggaagaga gagccggcct cactgttcca 1500

agggcacata gtcttgtctg tgttccactt gcaaggatcg gcgttgcatc taaactcctt 1560

tcttaag 1567

<210> 4
<211> 521
<212> PRT
<213> soy

<220>
<221> MISC_FEATURE
<223> Soy isoflavone synthase protein sequence

<400> 4

Met Val Leu Glu Leu Ala Leu Gly Leu Leu Val Leu Ala Leu Phe Leu
1 5 10 15

His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu
20 25 30

Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
35 40 45

His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
50 55 60

Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
65 70 75 80

```
Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
                85                  90                  95

Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
            100                 105                 110

Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
        115                 120                 125

Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
    130                 135                 140

Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Thr Arg Lys Phe Leu
145                 150                 155                 160

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

Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
            180                 185                 190

Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
        195                 200                 205

Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
    210                 215                 220

Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
225                 230                 235                 240

Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
                245                 250                 255

Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
            260                 265                 270

Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
        275                 280                 285

Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
    290                 295                 300

Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
305                 310                 315                 320
```

```
Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
                325                 330                 335

Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
            340                 345                 350

Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
        355                 360                 365

Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
    370                 375                 380

Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
385                 390                 395                 400

Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
                405                 410                 415

Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
            420                 425                 430

Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
        435                 440                 445

Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
    450                 455                 460

Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
465                 470                 475                 480

Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
                485                 490                 495

Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
            500                 505                 510

Ile Gly Val Ala Ser Lys Leu Leu Ser
        515                 520
```

<210> 5
<211> 670
<212> DNA
<213> Lotus corniculatus

<220>
<221> misc_feature
<223> Lotus corniculatus chalcone isomerase DNA sequence

<400> 5
atggctgcat ccctcacccc aatccaggtc gagaaccttc aatttcctgc gtctgtcacc 60

tctccagcca ccgccaagtc ttatttcctc ggtggtgcag gggagagagg gttgacgatt 120

gaggggaagt tcataaaatt cactggcata ggagtgtatt tggaagatac agcagtggat 180

tcactcgcca ccaagtggaa gggtaagagt tcacaagagc tgcaggactc ccttgacttc 240

ttcagagaca tcatttcaag tccctctgag aagttaattc gagggtccaa gctgaggcca 300

ttgagtggcg tggagtattc aagaaaggtg atggagaatt gtgtggcaca catgaagtct 360

gctggaactt atggtgaagc agaggccaca gccattgaaa aatttgcaga agccttcagg 420

aaggtggatt ttccaccagg ttcctctgtt ttctaccgac aatcaacaga tggaaaatta 480

gggcttagtt tctctttgga tgacacgata ccagaagaag aggctgtagt tatagagaac 540

aaggcactct cagaggcagt gttagagacc atgattggcg agcatgctgt ttcccctgat 600

ttgaagcgtt gtttggctga aaggttgcct attgtgatga accagggtct tctcctcact 660

ggaaactgat 670

<210> 6
<211> 222
<212> PRT
<213> lotus corniculatus

<220>
<221> MISC_FEATURE
<223> Lotus corniculatus chalcone isomerase protein

<400> 6

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

Ala Ser Val Thr Ser Pro Ala Thr Ala Lys Ser Tyr Phe Leu Gly Gly
20 25 30

Ala Gly Glu Arg Gly Leu Thr Ile Glu Gly Lys Phe Ile Lys Phe Thr
35 40 45

Gly Ile Gly Val Tyr Leu Glu Asp Thr Ala Val Asp Ser Leu Ala Thr
50 55 60

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

Phe Arg Asp Ile Ile Ser Ser Pro Ser Glu Lys Leu Ile Arg Gly Ser

85 90 95

Lys Leu Arg Pro Leu Ser Gly Val Glu Tyr Ser Arg Lys Val Met Glu
100 105 110

Asn Cys Val Ala His Met Lys Ser Ala Gly Thr Tyr Gly Glu Ala Glu
115 120 125

Ala Thr Ala Ile Glu Lys Phe Ala Glu Ala Phe Arg Lys Val Asp Phe
130 135 140

Pro Pro Gly Ser Ser Val Phe Tyr Arg Gln Ser Thr Asp Gly Lys Leu
145 150 155 160

Gly Leu Ser Phe Ser Leu Asp Asp Thr Ile Pro Glu Glu Glu Ala Val
165 170 175

Val Ile Glu Asn Lys Ala Leu Ser Glu Ala Val Leu Glu Thr Met Ile
180 185 190

Gly Glu His Ala Val Ser Pro Asp Leu Lys Arg Cys Leu Ala Glu Arg
195 200 205

Leu Pro Ile Val Met Asn Gln Gly Leu Leu Leu Thr Gly Asn
210 215 220

<210> 7
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Primer Sequence GPTV1

<400> 7
ttgtccagat agcccagtag ctg 23

<210> 8
<211> 23
<212> DNA
<213> artificial

<220>
<223> Primer sequence GPTV2

<400> 8
cgacaatctg atcatgagcg gag 23

<210> 9
<211> 24

<212> DNA
<213> artificial

<220>
<223> primer sequence 300 35S

<400> 9
cgcaagaccc ttcctctata taag 24

<210> 10
<211> 21
<212> DNA
<213> artificial

<220>
<223> primer sequence Gus2

<400> 10
gcatcacgca gttcaacgct g 21

<210> 11
<211> 24
<212> DNA
<213> artificial

<220>
<223> primer sequence 152

<400> 11
ggaaacagct atgaccatga ttac 24

<210> 12
<211> 17
<212> DNA
<213> artificial

<220>
<223> primer sequence 160

<400> 12
aaggatccgt cgacatc 17

<210> 13
<211> 29
<212> DNA
<213> artificial

<220>
<223> primer sequence 167

<400> 13
agtcccccat ggtacgtcct gtagaaacc 29

<210> 14
<211> 25
<212> DNA

<213> artificial

<220>
<223> primer sequence 168

<400> 14
cgttttcgtc ggtaatcacc attcc 25

<210> 15
<211> 20
<212> DNA
<213> artificial

<220>
<223> primer sequence 191

<400> 15
tttcccagtc acgacgttgt 20

<210> 16
<211> 17
<212> DNA
<213> artificial

<220>
<223> primer sequence 198

<400> 16
gacatcgata atacgac 17

<210> 17
<211> 24
<212> DNA
<213> artificial

<220>
<223> primer sequence 248

<400> 17
tgctacctct agagaatttc cccg 24

<210> 18
<211> 30
<212> DNA
<213> artificial

<220>
<223> primer sequence 321

<400> 18
ctaagcccct aagtattcca tcaggtgatt 30

<210> 19
<211> 34
<212> DNA
<213> artificial

<220>
<223> primer sequence 322

<400> 19
ccaggtggaa aattacacat gtgcttgaaa gagc 34

<210> 20
<211> 30
<212> DNA
<213> artificial

<220>
<223> primer sequence 323

<400> 20
tttgaaaagt ctaataacga gggtcagaag 30

<210> 21
<211> 33
<212> DNA
<213> artificial

<220>
<223> primer sequence 324

<400> 21
tactcaagga aggttgatgg agaactgtcg tgg 33

<210> 22
<211> 64
<212> DNA
<213> artificial

<220>
<223> primer sequence 329

<400> 22
cgcgagctca tgtaccccgg gatttccact agtttaaggg ttaactacat ggtcgacgta 60

cata 64

<210> 23
<211> 70
<212> DNA
<213> artificial

<220>
<223> primer sequence 330

<400> 23
agcttatgta cgtcgaccat gtagttaacc cttaaactag tggaaatccc ggggtacatg 60

agctcgcgat 70

<210> 24

<211> 60
<212> DNA
<213> artificial

<220>
<223> primer sequence 331

<400> 24
aattcgagct catgtacccc gggatttcca ctagtttaag ggttaactac atggtcgacg 60

<210> 25
<211> 60
<212> DNA
<213> artificial

<220>
<223> primer sequence 332

<400> 25
ctagcgtcga ccatgtagtt aacccttaaa ctagtggaaa tcccggggta catgagctcg 60

<210> 26
<211> 21
<212> DNA
<213> artificial

<220>
<223> primer sequence 333

<400> 26
catggatgcg tagttaagcc t 21

<210> 27
<211> 21
<212> DNA
<213> artificial

<220>
<223> primer sequence 334

<400> 27
ctagaggctt acatacgcat c 21

<210> 28
<211> 72
<212> DNA
<213> artificial

<220>
<223> primer sequence 337

<400> 28
aattcatgta cgagctcaat tcccccggga taggcactag tgctgctgtt aactacatgg 60

tcgacttatt aa 72

<210> 29
<211> 72
<212> DNA
<213> artificial

<220>
<223> primer sequence 338

<400> 29
aggtttaata agtcgaccat gtagttaaca gcagcactag tgcctatccc gggggaattg 60

agctcgtaca tg 72

<210> 30
<211> 24
<212> DNA
<213> artificial

<220>
<223> primer sequence 339

<400> 30
gaacaccatg gtgcttgaac ttgc 24

<210> 31
<211> 31
<212> DNA
<213> artificial

<220>
<223> primer sequence 340

<400> 31
tccagtaggg cccgaaggga accattgcca c 31

<210> 32
<211> 20
<212> DNA
<213> artificial

<220>
<223> primer sequence 341

<400> 32
ccttcgggcc ctactggaag 20

<210> 33
<211> 20
<212> DNA
<213> artificial

<220>
<223> primer sequence 342

<400> 33
cagcgaactc gagcaaagtg 20

<210> 34
<211> 79
<212> DNA
<213> artificial

<220>
<223> primer sequence 343

<400> 34
cactttgctc gagttcgctg aggatgagac tatggagatc aaaatcacca aggaccacat 60

caagggtctt gttgtagac 79

<210> 35
<211> 28
<212> DNA
<213> artificial

<220>
<223> primer sequence 344

<400> 35
atgacgagct agcttattaa gaaaggag 28

<210> 36
<211> 30
<212> DNA
<213> artificial

<220>
<223> primer sequence 362

<400> 36
ggtgtgtggg gatccatgga agaggctttg 30

<210> 37
<211> 44
<212> DNA
<213> artificial

<220>
<223> primer sequence 363

<400> 37
cctcggctcg cgcctttcct caacggtgaa aatgcagtca acac 44

<210> 38
<211> 45
<212> DNA
<213> artificial

<220>
<223> primer sequence 384

<400> 38
caacaaccca tgggtagtgt tgaaatccca acaaaggtgc ttacc 45

<210> 39
<211> 37
<212> DNA
<213> artificial

<220>
<223> primer sequence 385

<400> 39
agcaactgct agcttatatt tcatcatccc aaagatc 37

<210> 40
<211> 42
<212> DNA
<213> artificial

<220>
<223> primer sequence 386

<400> 40
tagattgcca tggctgcatc cctcacccca atccaggtcg ag 42

<210> 41
<211> 39
<212> DNA
<213> artificial

<220>
<223> primer sequence 387

<400> 41
aaactttgct agcttatcag tttccagtga ggagaagac 39

<210> 42
<211> 23
<212> DNA
<213> artificial

<220>
<223> primer sequence 398

<400> 42
gcttgttcgg atccataagc agc 23

<210> 43
<211> 41
<212> DNA
<213> artificial

<220>
<223> primer sequence 399

<400> 43
tgcttatgga tccgaacaag ctcttggtga ggctttgaat g 41

<210> 44
<211> 21
<212> DNA
<213> artificial

<220>
<223> primer sequence 400

<400> 44
cagccacatc aattggaaat g 21

<210> 45
<211> 78
<212> DNA
<213> artificial

<220>
<223> primer sequence 401

<400> 45
tcatttccaa ttgatgtggc tgatctattg ccatttgatg taaaaggtgt gtgggaatcc 60

atggaagagg ctttgaga 78

<210> 46
<211> 25
<212> DNA
<213> artificial

<220>
<223> primer sequence 402

<400> 46
cacaagagct gcaggactcc cttga 25

<210> 47
<211> 24
<212> DNA
<213> artificial

<220>
<223> primer sequence 403

<400> 47
gggagtcctg cagctcttgt gaac 24

<210> 48
<211> 38
<212> DNA
<213> artificial

<220>
<223> primer sequence 624

<400> 48
agctgcgatc gcaagcttgg taccgggaat tctctaga 38

<210> 49
<211> 42
<212> DNA
<213> artificial

<220>
<223> primer sequence 625

<400> 49
aatttctaga gaattcccgg taccaagctt gcttgcgatc gc 42

<210> 50
<211> 31
<212> DNA
<213> artificial

<220>
<223> primer sequence 626

<400> 50
tcgacccatg gcccgctagc caattggagc t 31

<210> 51
<211> 23
<212> DNA
<213> artificial

<220>
<223> primer sequence 627

<400> 51
ccaattggct agcgggccat ggg 23

<210> 52
<211> 22
<212> DNA
<213> artificial

<220>
<223> primer sequence 640

<400> 52
ccacccacga gggaacatcg tg 22

<210> 53
<211> 39
<212> DNA
<213> artificial

<220>
<223> primer sequence 641

<400> 53
gaattcccat ggtttacact cgaggtcctc tccaaatga 39