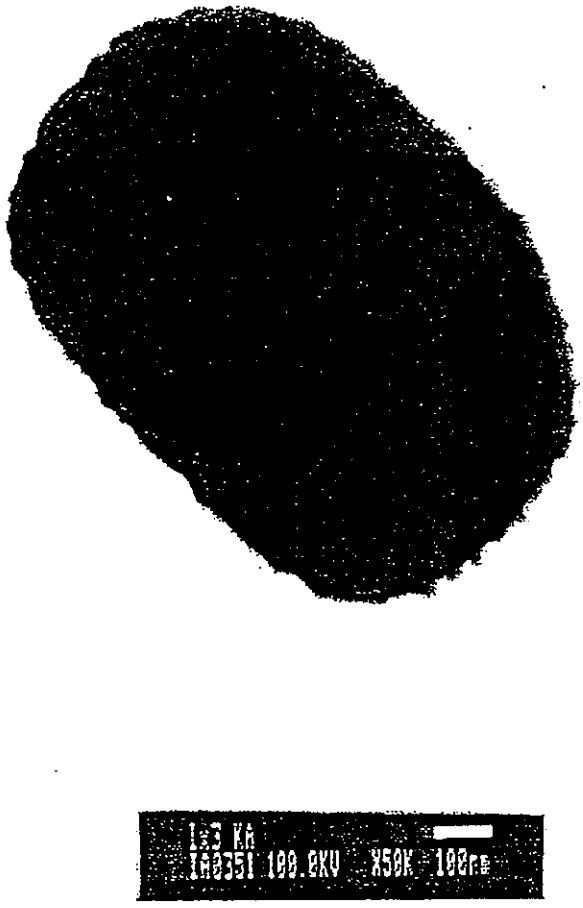


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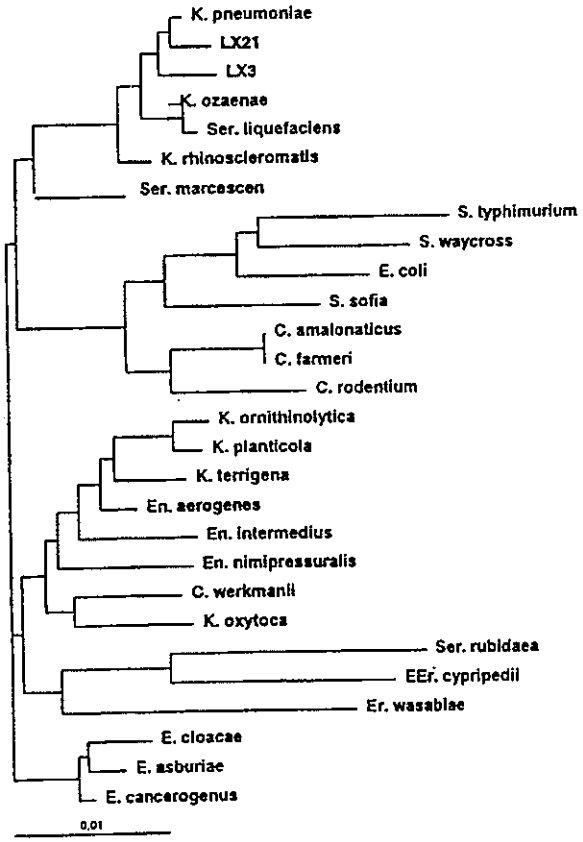

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LX3
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Ser. liquefaciens
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Ser. marcescen
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S. waycross
E. coli
S. sofia
C. amalonaticus
C. farmeri
C. rodentium
K. ornithinolytica
K. planticola
K. terrigena
En. aerogenes
En. intermedius
En. nimipressuralis
C. werkmanii
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E. cloacae
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0,01

Figure 2.

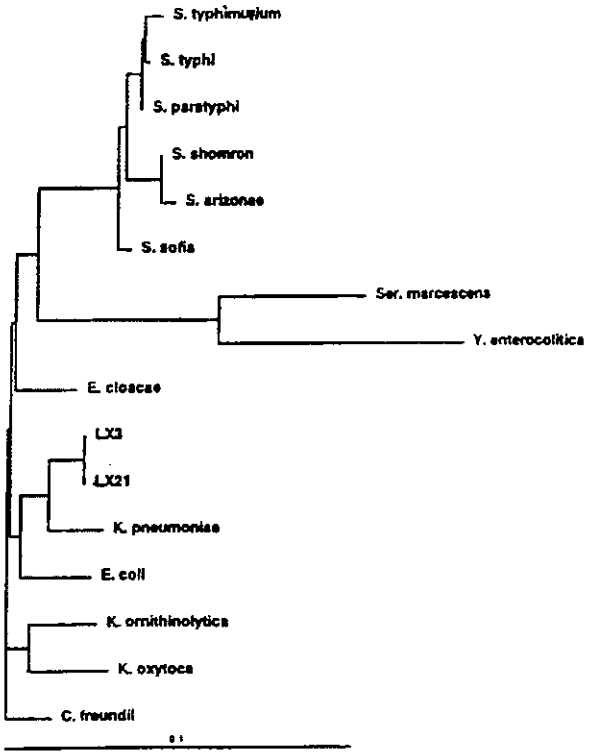

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S. typhi
S. paratyphi
S. shomron
S. arizonae
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Ser. marcescens
Y. enterocolitica
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LX21
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E. coli
K. ornithinolytica
K. oxytoca
C. freundii

Figure 3.

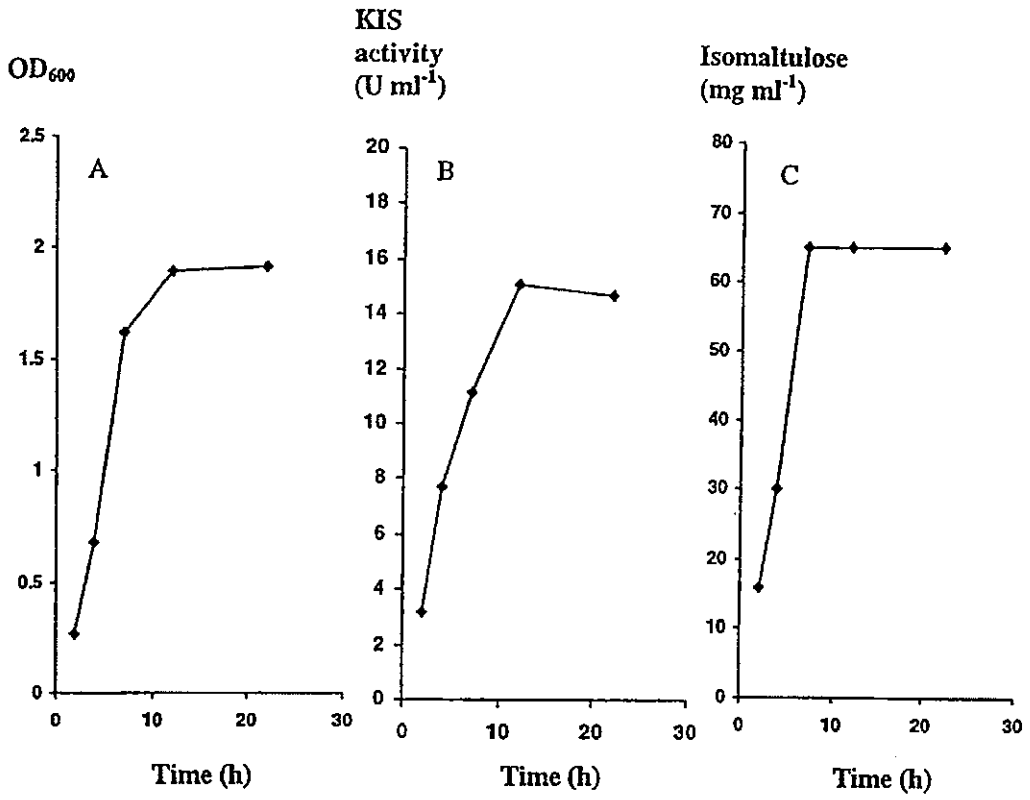

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2
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20
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Time (h)
KIS activity (U ml-1)
B
20
18
16
14
12
10
8
6
4
2
0
0
10
20
30
Time (h)
Isomaltulose (mg ml-1)
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60
50
40
30
20
10
0
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10
20
30
Time (h)

Figure 4.

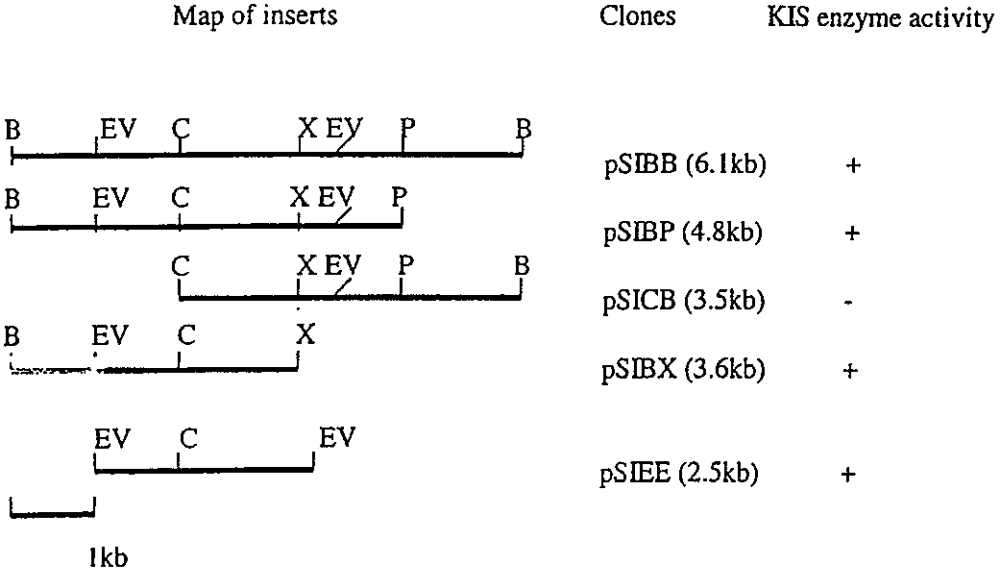

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KIS enzyme activity
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B EV C X EV P
C X EV P B
B EV C X
EV C EV
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pSIBP (4.8kb) +
pSICB (3.5kb) -
pSIBX (3.6kb) +
pSIEE (2.5kb) +

Figure 5.

Figure 6A

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Fig.6 B

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Figure 6.

Gene	Putative sucrose inducible promoter	
KIS	$^{-55}$TTTTCTTTAATAACAATT^{-37}	SEQIDNO3
RolC	$^{-113}$ATTAATTAATAAATTTGT^{-96}	SEQIDNO29
PI-II	$^{-867}$ATTAATTATTATTTTTCC^{-850}	SEQIDNO30
StPS20	$^{-183}$ATTATATAATACTAATAA^{-166}	SEQIDNO31
CHSA	$^{-351}$ATTATGTCATAAATTCTA^{-334}	SEQIDNO32
gSPOA1	$^{-970}$CTTAATTTACTAATTTGG^{-953}	SEQIDNO33

Figure 7.

Enzyme	Putative sucrose binding site	
SIM1	^{193} V-D-G-W-**R**-M-**D**-V-I-G-S-I ^{204}	SEQIDNO34
SIM2	^{192} V-D-G-W-**R**-M-**D**-V-I-G-S-I ^{203}	SEQIDNO41
TPH	^{196} I-D-G-F-**R**-L-**D**-V-I-N-L-I ^{206}	SEQIDNO35
GG	^{188} I-G-G-F-**R**-M-**D**-V-I-D-L-I ^{199}	SEQIDNO36
DSRS	^{545} F-D-G-I-**R**-V-**D**-A-V-D-N-V ^{556}	SEQIDNO37
DSRA	^{284} F-D-G-Y-**R**-V-**D**-A-V-D-N-V ^{291}	SEQIDNO38
GTFB	^{445} F-D-S-I-**R**-V-**D**-A-V-D-N-V ^{456}	SEQIDNO39
GTFC	^{471} F-D-S-I-**R**-V-**D**-A-V-D-N-V ^{482}	SEQIDNO39
GTFD	^{463} F-D-G-V-**R**-V-**D**-A-V-D-N-V ^{474}	SEQIDNO40
GTFJ	^{472} F-D-G-I-**R**-V-**D**-A-V-D-N-V ^{483}	SEQIDNO42
KIS	^{321} F-D-L-I-**R**-L-**D**-R-D-S-N-E ^{332}	SEQIDNO4

Figure 8.

SEQUENCE LISTING

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Li, Xianzhen
Zhang, Daohai

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ctcattcaca actgactttg caaggaaatt att atg tct ttt gtt acg cta cgt 234
Met Ser Phe Val Thr Leu Arg
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Thr Gly Val Ala Val Ala Leu Ser Ser Leu Ile Ile Ser Leu Ala Cys
10 15 20

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Pro Ala Val Ser Ala Ala Pro Ser Leu Asn Gln Asp Ile His Val Gln
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Gly Tyr Asp Ile Ser Asn Tyr Arg Gln Ile Met Lys Glu Tyr Gly Thr
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Met Glu Asp Phe Asp Ser Leu Val Ala Glu Met Lys Lys Arg Asn Met
120                 125                 130                 135

cgc tta atg atc gac gtg gtc att aac cat acc agt gat caa cac ccg      666
Arg Leu Met Ile Asp Val Val Ile Asn His Thr Ser Asp Gln His Pro
                140                 145                 150

tgg ttt att cag agt aaa agc gat aaa aac aac cct tat cgt gac tat      714
Trp Phe Ile Gln Ser Lys Ser Asp Lys Asn Asn Pro Tyr Arg Asp Tyr
            155                 160                 165

tat ttc tgg cgt gac gga aaa gat aat cag cca cct aat aat tac ccc      762
Tyr Phe Trp Arg Asp Gly Lys Asp Asn Gln Pro Pro Asn Asn Tyr Pro
        170                 175                 180

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Ser Phe Phe Gly Gly Ser Ala Trp Gln Lys Asp Ala Lys Ser Gly Gln
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tac tat tta cac tat ttt gcc aga cag caa cct gat ctc aac tgg gat      858
Tyr Tyr Leu His Tyr Phe Ala Arg Gln Gln Pro Asp Leu Asn Trp Asp
200                 205                 210                 215

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Asn Pro Lys Val Arg Glu Asp Leu Tyr Ala Met Leu Arg Phe Trp Leu
                220                 225                 230

gat aaa ggc gtt tca ggc atg cga ttt gat acg gtg gca act tat tcc      954
Asp Lys Gly Val Ser Gly Met Arg Phe Asp Thr Val Ala Thr Tyr Ser
            235                 240                 245

aaa atc ccg gga ttt ccc aat ctg aca cct gaa caa cag aaa aat ttt     1002
Lys Ile Pro Gly Phe Pro Asn Leu Thr Pro Glu Gln Gln Lys Asn Phe
        250                 255                 260

gct gaa caa tac acc atg ggg cct aat att cat cga tac att cag gaa     1050
Ala Glu Gln Tyr Thr Met Gly Pro Asn Ile His Arg Tyr Ile Gln Glu
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Met Asn Arg Lys Val Leu Ser Arg Tyr Asp Val Ala Thr Ala Gly Glu
280                 285                 290                 295

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Ile Phe Gly Val Pro Leu Asp Arg Ser Ser Gln Phe Phe Asp Arg Arg
                300                 305                 310

cga cat gag ctg aat atg gcg ttt atg ttt gac ctc att cgt ctc gat     1194
Arg His Glu Leu Asn Met Ala Phe Met Phe Asp Leu Ile Arg Leu Asp
            315                 320                 325

cgc gac agc aat gaa cgc tgg cgt cac aag tcg tgg tcg ctc tct cag     1242
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tgg aac acg ttc ttc tta gat aac cat gac aac ccc cgt gcg gta tct      1338
Trp Asn Thr Phe Phe Leu Asp Asn His Asp Asn Pro Arg Ala Val Ser
360                 365                 370                 375

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His Phe Gly Asp Asp Arg Pro Gln Trp Arg Glu Ala Ser Ala Lys Ala
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Tyr Leu Lys Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr
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Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln
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His Thr Ser Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys
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<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer sequences used for sequencing of the kis gene

<400> 7
tgacgagtgg cggacgggtg 20

<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer sequences used for sequencing of the kis gene

<400> 8
ccatggtgtg acgggcggtg tg 22

<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer sequences used for sequencing of the kis gene

<400> 9
tacgggaggc agcagtgggg aata 24

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer sequences used for sequencing of the kis gene

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atgcagttcc caggttgagc 20

<210> 11
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<220>
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<400> 11
gaaatccccg ggctcaacct g 21

<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 12
acatcgttta cggcgtggac tacc 24

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer sequences used for sequencing of the kis gene

<400> 13
ggccgcaagg ttaaaactca aatg 24

<210> 14
<211> 20
<212> DNA
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<223> Description of Artificial Sequence: primer sequences used for sequencing of the kis gene

<400> 14
ccggaccgct ggcaacaaag 20

<210> 15
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<212> DNA
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<220>
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<400> 15
cagttccgcg ttggcctg 18

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<400> 16
cggttggcgt catcgtgttc 20

<210> 17
<211> 22
<212> DNA
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<220>
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<400> 17
cccgctggca atatttctga ct 22

<210> 18
<211> 24
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<220>
<223> Description of Artificial Sequence: primer sequences used for sequencing of the kis gene

<400> 18
cacgaccact acccttctc ctga 24

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer sequences used for sequencing of the kis gene

<400> 19
cctcgcctca tttaaagaca ccaa 24

<210> 20
<211> 22
<212> DNA
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<400> 20
taggcgccat ataccagagc ag 22

<210> 21
<211> 24
<212> DNA
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<400> 21
cgtgactatt atttctggcg tgac 24

<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer sequences used for sequencing of the kis gene

<400> 22
cgtcgcccgc tgagtgaggt aa
22

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer sequences used for sequencing of the kis gene

<400> 23
tagataacca tgacaacc
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<210> 24
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer sequences used for sequencing of the kis gene

<400> 24
gcggtggcca catcatacc
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<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer sequences used for sequencing of the kis gene

<400> 25
cgccgtttat ttatcaaggt tcag
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<210> 26
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
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<400> 26
ggagcattgc cgtaaagat
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<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 27
ctatactctc ccggctaatg atgc 24

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<400> 28
ccaccatgca ggatattcac ttt 23

<210> 29
<211> 18
<212> DNA
<213> Agrobacterium rhizogenes

<400> 29
attaattaat aaatttgt 18

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

<400> 30
attaattatt atttttcc 18

<210> 31
<211> 18
<212> DNA
<213> Potato

<400> 31
attatataat actaataa 18

<210> 32
<211> 18
<212> DNA
<213> Petunia sp.

<400> 32
attatgtcat aaattcta 18

<210> 33
<211> 18
<212> DNA
<213> Sweet potato

<400> 33
cttaatttac taatttgg 18

<210> 34
<211> 12
<212> PRT

<213> Bacillus coagulans

<400> 34
Val Asp Gly Trp Arg Met Asp Val Ile Gly Ser Ile
1 5 10

<210> 35
<211> 12
<212> PRT
<213> Bacillus subtilis

<400> 35
Ile Asp Gly Phe Arg Leu Asp Val Ile Asn Leu Ile
1 5 10

<210> 36
<211> 12
<212> PRT
<213> Streptococcus equisimilis

<400> 36
Ile Gly Gly Phe Arg Met Asp Val Ile Asp Leu Ile
1 5 10

<210> 37
<211> 12
<212> PRT
<213> L. mesenteroides NRRL B-512F

<400> 37
Phe Asp Gly Ile Arg Val Asp Ala Val Asp Asn Val
1 5 10

<210> 38
<211> 12
<212> PRT
<213> L. mesenteroides NRRL B-1299

<400> 38
Phe Asp Gly Tyr Arg Val Asp Ala Val Asp Asn Val
1 5 10

<210> 39
<211> 12
<212> PRT
<213> S. mutans GS5

<400> 39
Phe Asp Ser Ile Arg Val Asp Ala Val Asp Asn Val
1 5 10

<210> 40
<211> 12
<212> PRT
<213> S. mutans GS5

<400> 40

Phe Asp Gly Val Arg Val Asp Ala Val Asp Asn Val
1 5 10

<210> 41
<211> 12
<212> PRT
<213> Bacillus sp.

<400> 41
Val Asp Gly Trp Arg Met Asp Val Ile Gly Ser Ile
1 5 10

<210> 42
<211> 12
<212> PRT
<213> S. salivarius ATCC25975

<400> 42
Phe Asp Gly Ile Arg Val Asp Ala Val Asp Asn Val
1 5 10