

SeqLst

SEQUENCE LISTING

<110> Evolva SA

<120> Recombinant Production of Steviol
Glycosides

<130> 30998-0010w01

<150> 61/521,084

<151> 2011-08-08

<150> 61/521,203

<151> 2011-08-08

<150> 61/521,051

<151> 2011-08-08

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<151> 2011-08-15

<150> 61/567,929

<151> 2011-12-07

<150> 61/603,639

<151> 2012-02-27

<160> 203

<170> FastSEQ for windows Version 4.0

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<211> 460

<212> PRT

<213> Stevia rebaudiana

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Pro Phe Pro Leu Gln Gly His Ile Asn Pro Phe Ile Gln Phe Gly Lys
20 25 30

Arg Leu Ile Ser Lys Gly Val Lys Thr Thr Leu Val Thr Thr Ile His
35 40 45

Thr Leu Asn Ser Thr Leu Asn His Ser Asn Thr Thr Thr Thr Ser Ile
50 55 60

Glu Ile Gln Ala Ile Ser Asp Gly Cys Asp Glu Gly Gly Phe Met Ser
65 70 75 80

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

SeqLst

Leu Ala Asp Leu Ile Lys Lys Leu Gln Ser Glu Gly Thr Thr Ile Asp
100 105 110

Ala Ile Ile Tyr Asp Ser Met Thr Glu Trp Val Leu Asp Val Ala Ile
115 120 125

Glu Phe Gly Ile Asp Gly Gly Ser Phe Phe Thr Gln Ala Cys Val Val
130 135 140

Asn Ser Leu Tyr Tyr His Val His Lys Gly Leu Ile Ser Leu Pro Leu
145 150 155 160

Gly Glu Thr Val Ser Val Pro Gly Phe Pro Val Leu Gln Arg Trp Glu
165 170 175

Thr Pro Leu Ile Leu Gln Asn His Glu Gln Ile Gln Ser Pro Trp Ser
180 185 190

Gln Met Leu Phe Gly Gln Phe Ala Asn Ile Asp Gln Ala Arg Trp Val
195 200 205

Phe Thr Asn Ser Phe Tyr Lys Leu Glu Glu Glu Val Ile Glu Trp Thr
210 215 220

Arg Lys Ile Trp Asn Leu Lys Val Ile Gly Pro Thr Leu Pro Ser Met
225 230 235 240

Tyr Leu Asp Lys Arg Leu Asp Asp Asp Lys Asp Asn Gly Phe Asn Leu
245 250 255

Tyr Lys Ala Asn His His Glu Cys Met Asn Trp Leu Asp Asp Lys Pro
260 265 270

Lys Glu Ser Val Val Tyr Val Ala Phe Gly Ser Leu Val Lys His Gly
275 280 285

Pro Glu Gln Val Glu Glu Ile Thr Arg Ala Leu Ile Asp Ser Asp Val
290 295 300

Asn Phe Leu Trp Val Ile Lys His Lys Glu Glu Gly Lys Leu Pro Glu
305 310 315 320

Asn Leu Ser Glu Val Ile Lys Thr Gly Lys Gly Leu Ile Val Ala Trp
325 330 335

Cys Lys Gln Leu Asp Val Leu Ala His Glu Ser Val Gly Cys Phe Val
340 345 350

SeqLst

Thr His Cys Gly Phe Asn Ser Thr Leu Glu Ala Ile Ser Leu Gly Val
355 360 365

Pro Val Val Ala Met Pro Gln Phe Ser Asp Gln Thr Thr Asn Ala Lys
370 375 380

Leu Leu Asp Glu Ile Leu Gly Val Gly Val Arg Val Lys Ala Asp Glu
385 390 395 400

Asn Gly Ile Val Arg Arg Gly Asn Leu Ala Ser Cys Ile Lys Met Ile
405 410 415

Met Glu Glu Glu Arg Gly Val Ile Ile Arg Lys Asn Ala Val Lys Trp
420 425 430

Lys Asp Leu Ala Lys Val Ala Val His Glu Gly Gly Ser Ser Asp Asn
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Asp Ile Val Glu Phe Val Ser Glu Leu Ile Lys Ala
450 455 460

<210> 2

<211> 1383

<212> DNA

<213> Stevia rebaudiana

<400> 2

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acaacactgg taaccactat ccacactttg aattctactc tgaaccactc aaatactact	180
actacaagta tagaaattca agctatatca gacggatgcg atgaggggtg ctttatgtct	240
gccggtgaat cttacttggg aacattcaag caagtgggat ccaagtctct ggccgatcta	300
atcaaaaagt tacagagtga aggcaccaca attgacgcca taatctacga ttctatgaca	360
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attgaatgga ctaggaagat ctggaatttg aaagtcattg gtccaacatt gccatcaatg	720
tatttgga caaagacttga tgatgataaa gataatggtt tcaatttgta caaggcta	780
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SeqLst

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aacctttctg aagtgataaa gaccggaaaa ggtctaatacg ttgcttggtg taaacaattg	1020
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agaggagtta tcataaggaa aaacgcagtt aagtggaagg atcttgcaaa ggttgccgtc	1320
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taa	1383

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 <212> PRT
 <213> Stevia rebaudiana

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Leu Leu His His Lys Gly Leu Gln Ile Thr Phe Val Asn Thr Asp Phe
 35 40 45

Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His Cys Leu Asp Gly
 50 55 60

Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly Val Ser His Ser
 65 70 75 80

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

Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr Lys Leu Pro Asp
 100 105 110

Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser Val Phe Thr Ile
 115 120 125

Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met Tyr Trp Thr Leu
 130 135 140

SeqLst

Ala	Ala	Cys	Gly	Phe	Met	Gly	Phe	Tyr	His	Ile	His	Ser	Leu	Ile	Glu
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Lys	Gly	Phe	Ala	Pro	Leu	Lys	Asp	Ala	Ser	Tyr	Leu	Thr	Asn	Gly	Tyr
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Leu	Asp	Thr	Val	Ile	Asp	Trp	Val	Pro	Gly	Met	Glu	Gly	Ile	Arg	Leu
			180					185					190		
Lys	Asp	Phe	Pro	Leu	Asp	Trp	Ser	Thr	Asp	Leu	Asn	Asp	Lys	Val	Leu
		195					200					205			
Met	Phe	Thr	Thr	Glu	Ala	Pro	Gln	Arg	Ser	His	Lys	Val	Ser	His	His
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Ile	Phe	His	Thr	Phe	Asp	Glu	Leu	Glu	Pro	Ser	Ile	Ile	Lys	Thr	Leu
225					230					235					240
Ser	Leu	Arg	Tyr	Asn	His	Ile	Tyr	Thr	Ile	Gly	Pro	Leu	Gln	Leu	Leu
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Leu	Asp	Gln	Ile	Pro	Glu	Glu	Lys	Lys	Gln	Thr	Gly	Ile	Thr	Ser	Leu
			260					265					270		
His	Gly	Tyr	Ser	Leu	Val	Lys	Glu	Glu	Pro	Glu	Cys	Phe	Gln	Trp	Leu
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Thr	Val	Met	Ser	Leu	Glu	Asp	Met	Thr	Glu	Phe	Gly	Trp	Gly	Leu	Ala
305					310					315					320
Asn	Ser	Asn	His	Tyr	Phe	Leu	Trp	Ile	Ile	Arg	Ser	Asn	Leu	Val	Ile
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Gly	Glu	Asn	Ala	Val	Leu	Pro	Pro	Glu	Leu	Glu	Glu	His	Ile	Lys	Lys
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Arg	Gly	Phe	Ile	Ala	Ser	Trp	Cys	Ser	Gln	Glu	Lys	Val	Leu	Lys	His
		355					360					365			
Pro	Ser	Val	Gly	Gly	Phe	Leu	Thr	His	Cys	Gly	Trp	Gly	Ser	Thr	Ile
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385					390					395					400

SeqLst

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
 405 410 415

Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val Lys Arg Leu Val
 420 425 430

Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg Asn Lys Ala Lys
 435 440 445

Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro Asn Gly Ser Ser
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Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
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Asn

<210> 4

<211> 1446

<212> DNA

<213> Stevia rebaudiana

<400> 4

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ataactttcg tgaataccga cttcatccat aatcaatttc tggaatctag tggccctcat	180
tgtttggacg gagccccagg gtttagattc gaaacaattc ctgacggtgt ttcacattcc	240
ccagaggcct ccatcccaat aagagagagt ttactgaggt caatagaaac caactttttg	300
gatcgtttca ttgacttggt cacaaaactt ccagaccac caacttgc atctctgat	360
ggctttctgt cagtgtttac tatcgacgct gccaaaaagt tgggtatccc agttatgatg	420
tactggactc ttgctgcatg cggtttcatg ggtttctatc acatccattc tcttatcgaa	480
aagggttttg ctccactgaa agatgcatca tacttaacca acggctacct ggatactggt	540
attgactggg taccaggtat ggaagggtata agacttaaag attttccttt ggattgggtct	600
acagacctta atgataaagt attgatgttt actacagaag ctccacaaag atctcataag	660
gtttcacatc atatctttca cacctttgat gaattggaac catcaatcat caaaaccttg	720
tctctaagat acaatcatat ctacactatt ggtccattac aattacttct agatcaaatt	780
cctgaagaga aaaagcaaac tgggtattaca tccttacacg gctactcttt agtgaaagag	840
gaaccagaat gttttcaatg gctacaaagt aaagagccta attctgtggt ctacgtcaac	900
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SeqLst

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tctcaggaaa aggtattgaa acatccttct gttggtggtt tccttactca ttgcggttgg	1140
ggctctacaa tcgaatcact aagtgcagga gttccaatga tttgttggcc atattcatgg	1200
gaccaactta caaattgtag gtatatctgt aaagagtggg aagttggatt agaaatggga	1260
acaaaggtta aacgtgatga agtgaaaaga ttggttcagg agttgatggg ggaagggtggc	1320
cacaagatga gaaacaaggc caaagattgg aaggaaaaag ccagaattgc tattgctcct	1380
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<210> 5
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 <212> PRT
 <213> Stevia rebaudiana

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Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
 35 40 45

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
 50 55 60

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
 65 70 75 80

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
 85 90 95

Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
 100 105 110

His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
 115 120 125

Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
 130 135 140

Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
 145 150 155 160

SeqLst

Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
 165 170 175
 Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
 180 185 190
 Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg
 195 200 205
 Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
 210 215 220
 His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
 225 230 235 240
 Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
 245 250 255
 Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
 260 265 270
 Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
 275 280 285
 Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
 290 295 300
 Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
 305 310 315 320
 Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
 325 330 335
 Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
 340 345 350
 Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
 355 360 365
 Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
 370 375 380
 Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
 385 390 395 400
 Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val

SeqLst

405	410	415
Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr		
420	425	430
Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val		
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Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala		
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Arg Ala Val Ala Ile Asp His Glu Ser		
465	470	

<210> 6
 <211> 1422
 <212> DNA
 <213> Stevia rebaudiana

<400> 6

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tcaccattga ttaacgtcgt tcaattgaca cttccaagag tacaggaatt accagaagat	240
gctgaagcta caacagatgt gcatcctgaa gatataccctt acttgaaaaa ggcattccgat	300
ggattacagc ctgaggtcac tagattcctt gagcaacaca gtccagattg gatcatatac	360
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aacggcagtg atggtagaac taccgttgaa gatttgacaa cccacacaaa gtggtttcca	540
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ccaggaatct cagacggcta tagaatgggt ttagtcctta aagggtctga ctgcctattg	660
tctaagtgtt accatgagtt tgggacacaa tggctaccac ttttggaac attacaccaa	720
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gaactatctg gattgccatt tgtctgggcc tacagaaaac caaaaggccc tgcaaagtcc	960
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acttcatggg ctccacaatt gagaatcctg agtcacgaat ctgtgtgcgg tttcctaaca	1080
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cgttccgttg tcgttgaaaa ggaaggcgaa atctacaagg ccaatgcccg tgaactttca	1320
aagatctaca atgacacaaa agtagagaag gaatatgttt ctcaatttgt agattaccta	1380
gagaaaaacg ctagagccgt agctattgat catgaatcct aa	1422

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 <211> 458
 <212> PRT
 <213> Stevia rebaudiana

<400> 7
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Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
 35 40 45

Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
 50 55 60

Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
 65 70 75 80

Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
 85 90 95

Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser
 100 105 110

Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
 115 120 125

Phe Ala Gln Ser Val Ala Asp Ser Leu Asn Leu Arg Arg Leu Val Leu
 130 135 140

Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
 145 150 155 160

Phe Asp Glu Leu Gly Tyr Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu
 165 170 175

Glu Gln Ala Ser Gly Phe Pro Met Leu Lys Val Lys Asp Ile Lys Ser
 180 185 190

SeqLst

Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
 195 200 205
 Lys Gln Thr Lys Ala Ser Ser Gly Val Ile Trp Asn Ser Phe Lys Glu
 210 215 220
 Leu Glu Glu Ser Glu Leu Glu Thr Val Ile Arg Glu Ile Pro Ala Pro
 225 230 235 240
 Ser Phe Leu Ile Pro Leu Pro Lys His Leu Thr Ala Ser Ser Ser Ser
 245 250 255
 Leu Leu Asp His Asp Arg Thr Val Phe Gln Trp Leu Asp Gln Gln Pro
 260 265 270
 Pro Ser Ser Val Leu Tyr Val Ser Phe Gly Ser Thr Ser Glu Val Asp
 275 280 285
 Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
 290 295 300
 Ser Phe Leu Trp Val Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
 305 310 315 320
 Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
 325 330 335
 Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
 340 345 350
 Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu
 355 360 365
 Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
 370 375 380
 Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
 385 390 395 400
 Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
 405 410 415
 Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
 420 425 430
 Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu

SeqLst

450

$\langle 210 \rangle$ 8

<211> 1377

<212> DNA

<213> Stevia rebaudiana

$\langle 400 \rangle$ 8

$\langle 210 \rangle$ 9

$\langle 211 \rangle$ 1422

<212> DNA

SeqLst

<213> Stevia rebaudiana

<400> 9

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ggtcacaaag tctcgtttct ttctaccacc agaaacattc aacgtctctc ttctcatatc    180
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gagctttctg ggttgccatt tgtttgggct tatagaaaac caaaagggtcc cgcaagtca    960
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acgagttggg cacctcagtt acgaatactg agccatgagt cggtttgtgg tttcttgact   1080
cattgtgggt ctggatcaat tgtggaaggg ctaatgtttg gtcaccctct aatcatgcta   1140
ccgatttttg gggaccaacc tctgaatgct cgattactgg aggacaaaca ggtgggaatc   1200
gagataccaa gaaatgagga agatggttgc ttgaccaagg agtcggttgc tagatcactg   1260
aggtccggtt ttgtggaaaa agaaggggag atctacaagg cgaacgcgag ggagctgagt   1320
aaaatctata acgacactaa ggttgaaaaa gaatatgtaa gccaatcgt agactatttg   1380
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<210> 10

<211> 473

<212> PRT

<213> Stevia rebaudiana

<400> 10

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20					25					30														
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Thr	Thr ₅₀	Arg	Asn	Ile	Gln	Arg ₅₅	Leu	Ser	Ser	His	Ile ₆₀	Ser	Pro	Leu	Ile									
Asn	Val	Val	Gln	Leu	Thr ₇₀	Leu	Pro	Arg	Val	Gln ₇₅	Glu	Leu	Pro	Glu	Asp ₈₀									
Ala	Glu	Ala	Thr	Thr ₈₅	Asp	Val	His	Pro	Glu ₉₀	Asp	Ile	Pro	Tyr	Leu ₉₅	Lys									
Lys	Ala	Ser	Asp ₁₀₀	Gly	Leu	Gln	Pro	Glu ₁₀₅	Val	Thr	Arg	Phe	Leu ₁₁₀	Glu	Gln									
His	Ser	Pro ₁₁₅	Asp	Trp	Ile	Ile	Tyr ₁₂₀	Asp	Tyr	Thr	His	Tyr ₁₂₅	Trp	Leu	Pro									
Ser	Ile ₁₃₀	Ala	Ala	Ser	Leu	Gly ₁₃₅	Ile	Ser	Arg	Ala	His ₁₄₀	Phe	Ser	Val	Thr									
Thr	Pro	Trp	Ala	Ile	Ala ₁₅₀	Tyr	Met	Gly	Pro	Ser ₁₅₅	Ala	Asp	Ala	Met	Ile ₁₆₀									
Asn	Gly	Ser	Asp	Gly ₁₆₅	Arg	Thr	Thr	Val	Glu ₁₇₀	Asp	Leu	Thr	Thr	Pro ₁₇₅	Pro									
Lys	Trp	Phe	Pro ₁₈₀	Phe	Pro	Thr	Lys	Val ₁₈₅	Cys	Trp	Arg	Lys	His ₁₉₀	Asp	Leu									
Ala	Arg	Leu	Val ₁₉₅	Pro	Tyr	Lys	Ala ₂₀₀	Pro	Gly	Ile	Ser	Asp ₂₀₅	Gly	Tyr	Arg									
Met	Gly ₂₁₀	Leu	Val	Leu	Lys	Gly ₂₁₅	Ser	Asp	Cys	Leu	Leu ₂₂₀	Ser	Lys	Cys	Tyr									
His	Glu	Phe	Gly	Thr	Gln ₂₃₀	Trp	Leu	Pro	Leu	Leu ₂₃₅	Glu	Thr	Leu	His	Gln ₂₄₀									
Val	Pro	Val	Val	Pro ₂₄₅	Val	Gly	Leu	Leu	Pro ₂₅₀	Pro	Glu	Val	Pro	Gly ₂₅₅	Asp									
Glu	Lys	Asp	Glu ₂₆₀	Thr	Trp	Val	Ser	Ile ₂₆₅	Lys	Lys	Trp	Leu	Asp ₂₇₀	Gly	Lys									

SeqLst

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
275 280 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
290 295 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305 310 315 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
325 330 335

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

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
355 360 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
370 375 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385 390 395 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
405 410 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
420 425 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
435 440 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Thr
450 455 460

Arg Ala Val Ala Ile Asp His Glu Ser
465 470

<210> 11

<211> 1422

<212> DNA

<213> Stevia rebaudiana

<400> 11

atggctacca gtgactccat agttgacgac cgtaagcagc ttcattgttgac gacgttccca 60

tggcttgctt tcggtcacat cctcccttac cttcagcttt cgaaattgat agctgaaaag 120

ggtcacaaag tctcgtttct ttctaccacc agaaacattc aacgtctctc ttctcatatc 180

SeqLst

```

tcgccactca taaatgttgt tcaactcaca cttccacgtg tccaagagct gccggaggat 240
gcagaggcga ccactgacgt ccaccctgaa gatattccat atctcaagaa ggcttctgat 300
ggctttcaac cggagggtcac ccggtttcta gaacaacact ctccggactg gattatttat 360
gattatactc actactgggt gccatccatc gcggctagcc tcggtatctc acgagcccac 420
ttctccgtca ccactccatg ggccattgct tatatgggac cctcagctga cgccatgata 480
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ccggggatat ctgatggata ccgtatgggg ctggttctta agggatctga ttgtttgctt 660
tccaaatggt accatgagtt tggaactcaa tggctacctc ttttggagac actacaccaa 720
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acatgggtgt caatcaagaa atggctcgat ggtaaacaaa aaggcagtgt ggtgtacggt 840
gcattaggaa gcgaggtttt ggtgagccaa accgaggttg ttgagttagc attgggtctc 900
gagctttctg gggtgccatt tggttgggct tatagaaaac caaaagggtcc cgcgaagtca 960
gactcggtagg agttgccaga cgggttcgtg gaacgaactc gtgaccgtgg gttggtctgg 1020
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cattgtgggt ctggatcaat tgtggaaggg ctaatgtttg gtcaccctct aatcatgcta 1140
ccgatttttg gggaccaacc tctgaatgct cgattactgg aggacaaaca ggtgggaatc 1200
gagataccaa gaaatgagga agatggttgc ttgaccaagg agtcggttgc tagatcactg 1260
agggtccgtt ttgtggaaaa agaaggggag atctacaagg cgaacgcgag ggagctgagt 1320
aaaatctata acgacactaa ggttgaaaaa gaatatgtaa gccaatcgt agactatttg 1380
gaaaagaata cgcgtgcggt tgccatcgat catgagagtt aa 1422

```

<210> 12

<211> 473

<212> PRT

<213> Stevia rebaudiana

<400> 12

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Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1           5           10           15

```

```

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Phe Leu Gln
          20          25          30

```

```

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
      35          40          45

```

```

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile

```

50		55		SeqLst		60									
Asn	Val	Val	Gln	Leu	Thr	Leu	Pro	Arg	Val	Gln	Glu	Leu	Pro	Glu	Asp
65					70					75					80
Ala	Glu	Ala	Thr	Thr	Asp	Val	His	Pro	Glu	Asp	Ile	Gln	Tyr	Leu	Lys
				85					90					95	
Lys	Ala	Val	Asp	Gly	Leu	Gln	Pro	Glu	Val	Thr	Arg	Phe	Leu	Glu	Gln
			100					105					110		
His	Ser	Pro	Asp	Trp	Ile	Ile	Tyr	Asp	Phe	Thr	His	Tyr	Trp	Leu	Pro
		115					120					125			
Ser	Ile	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Arg	Ala	Tyr	Phe	Cys	Val	Ile
	130					135					140				
Thr	Pro	Trp	Thr	Ile	Ala	Tyr	Leu	Ala	Pro	Ser	Ser	Asp	Ala	Met	Ile
145					150					155					160
Asn	Asp	Ser	Asp	Gly	Arg	Thr	Thr	Val	Glu	Asp	Leu	Thr	Thr	Pro	Pro
				165					170					175	
Lys	Trp	Phe	Pro	Phe	Pro	Thr	Lys	Val	Cys	Trp	Arg	Lys	His	Asp	Leu
			180					185					190		
Ala	Arg	Met	Glu	Pro	Tyr	Glu	Ala	Pro	Gly	Ile	Ser	Asp	Gly	Tyr	Arg
		195					200					205			
Met	Gly	Met	Val	Phe	Lys	Gly	Ser	Asp	Cys	Leu	Leu	Phe	Lys	Cys	Tyr
	210					215					220				
His	Glu	Phe	Gly	Thr	Gln	Trp	Leu	Pro	Leu	Leu	Glu	Thr	Leu	His	Gln
225					230					235					240
Val	Pro	Val	Val	Pro	Val	Gly	Leu	Leu	Pro	Pro	Glu	Ile	Pro	Gly	Asp
				245					250					255	
Glu	Lys	Asp	Glu	Thr	Trp	Val	Ser	Ile	Lys	Lys	Trp	Leu	Asp	Gly	Lys
			260					265					270		
Gln	Lys	Gly	Ser	Val	Val	Tyr	Val	Ala	Leu	Gly	Ser	Glu	Ala	Leu	Val
		275					280					285			
Ser	Gln	Thr	Glu	Val	Val	Glu	Leu	Ala	Leu	Gly	Leu	Glu	Leu	Ser	Gly
	290					295					300				

SeqLst

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
305 310 315 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
325 330 335

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

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
355 360 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Leu Phe Gly
370 375 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
385 390 395 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
405 410 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Asn Glu Gly Glu Ile Tyr
420 425 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
435 440 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
450 455 460

Arg Ala Val Ala Ile Asp His Glu Ser
465 470

<210> 13
<211> 1422
<212> DNA
<213> Stevia rebaudiana

<400> 13
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tggtttgctt tcggtcacat cctccctttc cttcagcttt cgaaattgat agctgaaaag 120
ggtcacaaag tctcgtttct ttctaccacc agaaacattc aacgtctctc ttctcatatc 180
tcgccactca taaatgttgt tcaactcaca cttccacgtg tccaagagct gccggaggat 240
gcagaggcga ccactgacgt ccaccctgaa gatattcaat atctcaagaa ggctgttgat 300
ggctttcaac cggagggtcac ccggtttcta gaacaacact ctccggactg gattatttat 360
gattttactc actactgggt gccatccatc gcggctagcc tcggtatctc acgagcctac 420

SeqLst

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ttctgcggtca tcaactccatg gaccattgct tatttggcac cctcatctga cgccatgata 480
aatgattcag atggtcgaac cacggttgag gatctcacga caccgcccac gtgggtttccc 540
tttccgacca aagtatgctg gcggaagcat gatcttgccc gaatggagcc ttacgaagct 600
ccagggatat ctgatggata ccgtatgggg atgggttttta agggatctga ttgtttgctt 660
ttcaaagtgt accatgagtt tggaaactcaa tggctacctc ttttggagac actacaccaa 720
gtaccggtgg ttccggtggg attactgccg ccggaataac ccggagacga gaaagatgaa 780
acatgggtgt caatcaagaa atggctcgat ggtaaacaaa aaggcagtggt ggtgtacggt 840
gcattaggaa gcgaggcttt ggtgagccaa accgaggttg ttgagttagc attgggtctc 900
gagctttctg ggttgccatt tgtttgggct tatagaaaac caaaagggtcc cgcaagtca 960
gactcgggtg agttgccaga cgggttcgtg gaacgaactc gtgaccgtgg gttgggtctgg 1020
acgagttggg cacctcagtt acgaatactg agccatgagt cggtttggtg tttcttgact 1080
cattgtgggt ctggatcaat tgtggaaggg ctaatgtttg gtcaccctct aatcatgcta 1140
ccgctttttg gggaccaacc tctgaatgct cgattactgg aggacaaaca ggtgggaatc 1200
gagataccaa gaaatgagga agatggttgc ttgaccaagg agtcggttgc tagatcactg 1260
agggccgttg ttgtggaaaa cgaaggggag atctacaagg cgaacgcgag ggagctgagt 1320
aaaatctata acgacactaa ggtggaaaaa gaatatgtaa gccaatcgt agactatttg 1380
gaaaagaatg cgcgtgcggt tgccatcgat catgagagtt aa 1422

```

<210> 14

<211> 485

<212> PRT

<213> Stevia rebaudiana

<400> 14

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Met Tyr Asn Val Thr Tyr His Gln Asn Ser Lys Ala Met Ala Thr Ser
1           5           10          15

```

```

Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val Ala Thr Phe Pro
          20          25          30

```

```

Trp Leu Ala Phe Gly His Ile Leu Pro Phe Leu Gln Leu Ser Lys Leu
          35          40          45

```

```

Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser Thr Thr Arg Asn
          50          55          60

```

```

Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile Asn Val Val Gln
65          70          75          80

```

```

Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp Ala Glu Ala Thr

```

SeqLst															
85								90				95			
Thr	Asp	Val	His 100	Pro	Glu	Asp	Ile	Gln 105	Tyr	Leu	Lys	Lys	Ala 110	Val	Asp
Gly	Leu	Gln 115	Pro	Glu	Val	Thr	Arg 120	Phe	Leu	Glu	Gln	His 125	Ser	Pro	Asp
Trp	Ile 130	Ile	Tyr	Asp	Phe	Thr 135	His	Tyr	Trp	Leu	Pro 140	Ser	Ile	Ala	Ala
Ser 145	Leu	Gly	Ile	Ser	Arg 150	Ala	Tyr	Phe	Cys	Val 155	Ile	Thr	Pro	Trp	Thr 160
Ile	Ala	Tyr	Leu	Ala 165	Pro	Ser	Ser	Asp	Ala 170	Met	Ile	Asn	Asp	Ser 175	Asp
Gly	Arg	Thr	Thr 180	Val	Glu	Asp	Leu	Thr 185	Thr	Pro	Pro	Lys	Trp 190	Phe	Pro
Phe	Pro	Thr 195	Lys	Val	Cys	Trp	Arg 200	Lys	His	Asp	Leu	Ala 205	Arg	Met	Glu
Pro	Tyr 210	Glu	Ala	Pro	Gly	Ile 215	Ser	Asp	Gly	Tyr	Arg 220	Met	Gly	Met	Val
Phe 225	Lys	Gly	Ser	Asp	Cys 230	Leu	Leu	Phe	Lys	Cys 235	Tyr	His	Glu	Phe	Gly 240
Thr	Gln	Trp	Leu	Pro 245	Leu	Leu	Glu	Thr	Leu 250	His	Gln	Val	Pro	Val 255	Val
Pro	Val	Gly	Leu 260	Leu	Pro	Pro	Glu	Ile 265	Pro	Gly	Asp	Glu	Lys 270	Asp	Glu
Thr	Trp	Val 275	Ser	Ile	Lys	Lys	Trp 280	Leu	Asp	Gly	Lys	Gln 285	Lys	Gly	Ser
Val	Val 290	Tyr	Val	Ala	Leu	Gly 295	Ser	Glu	Ala	Leu	Val 300	Ser	Gln	Thr	Glu
Val 305	Val	Glu	Leu	Ala	Leu 310	Gly	Leu	Glu	Leu	Ser 315	Gly	Leu	Pro	Phe	Val 320
Trp	Ala	Tyr	Arg	Lys 325	Pro	Lys	Gly	Pro	Ala 330	Lys	Ser	Asp	Ser	Val 335	Glu

SeqLst

Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg Gly Leu Val Trp
340 345 350

Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His Glu Ser Val Cys
355 360 365

Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val Glu Gly Leu Met
370 375 380

Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Cys Asp Gln Pro Leu
385 390 395 400

Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile Glu Ile Pro Arg
405 410 415

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

Arg Ser Val Val Val Glu Asn Glu Gly Glu Ile Tyr Lys Ala Asn Ala
435 440 445

Arg Ala Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val Glu Lys Glu Tyr
450 455 460

Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala Arg Ala Val Ala
465 470 475 480

Ile Asp His Glu Ser
485

<210> 15
<211> 1458
<212> DNA
<213> Stevia rebaudiana

<400> 15
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cctttccttc agctttcgaa attgatagct gaaaagggtc acaaagtctc gtttctttct 180
accaccagaa acattcaacg tctctcttct catatctcgc cactcataaa tgttgttcaa 240
ctcacacttc cacgtgtcca agagctgccg gaggatgcag aggcgaccac tgacgtccac 300
cctgaagata ttcaatatct caagaaggct gttgatggc ttcaaccgga ggtcaccggg 360
tttctagaac aacactctcc ggactggatt atttatgatt ttactcacta ctggttgcc 420
tccatcgcg ctagcctcgg tatctcacga gcctacttct gcgtcatcac tccatggacc 480
attgcttatt tggcaccctc atctgacgcc atgataaatg attcagatgg tcgaaccacg 540

SeqLst

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gttgaggatc tcacgacacc gcccgaagtgg tttccctttc cgaccaaagt atgctggcgg      600
aagcatgatc ttgcccgaat ggagccttac gaagctccgg ggatatctga tggataccgt      660
atgggggatgg tttttaaggg atctgattgt ttgcttttca aatgttacca tgagtttgga      720
actcaatggc tacctctttt ggagacacta caccaagtac cggtgggttcc ggtgggatta      780
ctgccgccgg aaatacccgg agacgagaaa gatgaaacat ggggtgtcaat caagaaatgg      840
ctcgatggta aacaaaaagg cagtgtggtg tacgttgcac taggaagcga ggctttggtg      900
agccaaaccg aggttggtga gttagcattg ggtctcgagc tttctgggtt gccatttggt      960
tgggcttata gaaaaccaa aggtcccgcg aagtcagact cggtggagtt gccagacggg     1020
ttcgtggaac gaactcgtga ccgtgggttg gtctggacga gttgggcacc tcagttacga     1080
atactgagcc acgagtcagt ttgtggtttc ttgactcatt gtggttcttg atcaattgtg     1140
gaagggctaa tgtttggtca ccctctaata atgctaccga ttttttgatga ccaacctctg     1200
aatgctcgat tactggagga caaacaggtg ggaatcgaga taccaagaaa tgaggaagat     1260
ggttgcttga ccaaggagtc ggttgctaga tcttgaggtt ccgttggtgt ggaaaacgaa     1320
ggggagatct acaaggcgaa cgcgagggcg ctgagtaaaa tctataacga cactaaggtg     1380
gaaaaagaat atgtaagcca attcgtagac tatttggaag agaatgcgcg tgcggttgcc     1440
atcgatcatg agagttaa                                     1458

```

<210> 16

<211> 473

<212> PRT

<213> Stevia rebaudiana

<400> 16

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Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
1          5          10         15

```

```

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Phe Leu Gln
20          25          30

```

```

Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
35          40          45

```

```

Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
50          55          60

```

```

Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
65          70          75          80

```

```

Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Gln Tyr Leu Lys
85          90          95

```

SeqLst

Lys Ala Val Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
 100 105 110
 His Ser Pro Asp Trp Ile Ile Tyr Asp Phe Thr His Tyr Trp Leu Pro
 115 120 125
 Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala Tyr Phe Cys Val Ile
 130 135 140
 Thr Pro Trp Thr Ile Ala Tyr Leu Ala Pro Ser Ser Asp Ala Met Ile
 145 150 155 160
 Asn Asp Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
 165 170 175
 Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
 180 185 190
 Ala Arg Met Glu Pro Tyr Glu Ala Pro Gly Ile Ser Asp Gly Tyr Arg
 195 200 205
 Met Gly Met Val Phe Lys Gly Ser Asp Cys Leu Leu Phe Lys Cys Tyr
 210 215 220
 His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
 225 230 235 240
 Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
 245 250 255
 Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
 260 265 270
 Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Ala Leu Val
 275 280 285
 Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
 290 295 300
 Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
 305 310 315 320
 Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
 325 330 335
 Gly Leu Val Trp Thr Ser Trp Ala Pro Gln Leu Arg Ile Leu Ser His
 340 345 350

SeqLst

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
 355 360 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Cys
 370 375 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
 385 390 395 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
 405 410 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Asn Glu Gly Glu Ile Tyr
 420 425 430

Lys Ala Asn Ala Arg Ala Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
 435 440 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
 450 455 460

Arg Ala Val Ala Ile Asp His Glu Ser
 465 470

<210> 17

<211> 1422

<212> DNA

<213> Stevia rebaudiana

<400> 17

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ggtcacaaag tctcgtttct ttctaccacc agaaacattc aacgtctctc ttctcatatc	180
tcgccactca taaatgttgt tcaactcaca cttccacgtg tccaagagct gccggaggat	240
gcagaggcga ccactgacgt ccaccctgaa gatattcaat atctcaagaa ggctgttgat	300
ggctcttaac cggagggtcac ccggtttcta gaacaacact ctccggactg gattatttat	360
gattttactc actactggtt gccatccatc gcggctagcc tcggtatctc acgagcctac	420
ttctgcgtca tcaactccatg gaccattgct tatttggcac cctcatctga cgccatgata	480
aatgattcag atggtcgaac cacggttgag gatctcacga caccgcccac gtgggtttccc	540
tttccgacca aagtatgctg gcggaagcat gatcttgccc gaatggagcc ttacgaagct	600
ccggggatat ctgatggata ccgtatgggg atggttttta agggatctga ttgtttgctt	660
ttcaaagtgt accatgagtt tggaactcaa tggctacctc ttttgagac actacaccaa	720

SeqLst

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gcattaggaa	gcgaggcttt	ggtgagccaa	accgaggttg	ttgagttagc	attgggtctc	900
gagctttctg	ggttgccatt	tgtttgggct	tatagaaaac	caaaagggtcc	cgcgaaagtca	960
gactcgggtg	agttgccaga	cgggttcgtg	gaacgaactc	gtgaccgtgg	gttgggtctgg	1020
acgagttggg	cacctcagtt	acgaatactg	agccacgagt	cagtttgtgg	tttcttgact	1080
cattgtgggt	ctggatcaat	tgtggaagg	ctaattgttg	gtcacctctt	aatcatgcta	1140
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gagataccaa	gaaatgagga	agatggttgc	ttgaccaagg	agtcggttgc	tagatcactg	1260
agggtccgtt	ttgtggaaaa	cgaaggggag	atctacaagg	cgaacgcgag	ggcgctgagt	1320
aaaatctata	acgacactaa	ggtggaaaaa	gaatatgtaa	gccaatcgt	agactatttg	1380
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<210> 18

<211> 1086

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 18

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aacttactaa	atccaactca	aaagctaaga	ccagtttcat	catcttcctt	accttctttc	120
tcatcagtta	gtgcgattct	tactgaaaaa	catcaatcta	atccttctga	gaacaacaat	180
ttgcaaactc	atctagaaac	tcctttcaac	tttgatagtt	atatgttgga	aaaagtcaac	240
atggttaacg	aggcgcttga	tgcattctgtc	ccactaaaag	acccaatcaa	aatccatgaa	300
tccatgagat	actctttatt	ggcaggcggt	aagagaatca	gaccaatgat	gtgtattgca	360
gcctgcgaaa	tagtcggagg	taatatcctt	aacgccatgc	cagccgcatg	tgccgtggaa	420
atgattcata	ctatgtcttt	ggtgcatgac	gatcttccat	gtatggataa	tgatgacttc	480
agaagaggta	aacctatttc	acacaagggtc	tacggggagg	aaatggcagt	attgaccggc	540
gatgctttac	taagtattatc	tttcgaacat	atagctactg	ctacaaagg	tgatcaaaag	600
gatagaatcg	tcagagctat	aggggagttg	gcccgttcag	ttggctccga	aggttttagtg	660
gctggacaag	ttgtagatat	cttgtcagag	ggtgctgatg	ttggattaga	tcacctagaa	720
tacattcaca	tccacaaaac	agcaatgttg	cttgagtcct	cagtagttat	tggcgctatc	780
atgggaggag	gatctgatca	gcagatcgaa	aagttgagaa	aattcgctag	atctattgggt	840

SeqLst

ctactattcc aagttgtgga tgacattttg gatgttaca aatctaccga agagttgggg	900
aaaacagctg gtaaggattt gttgacagat aagacaactt acccaaagtt gttaggtata	960
gaaaagtcca gagaatttgc cgaaaaactt aacaaggaag cacaagagca attaagtggc	1020
tttgatagac gtaaggcagc tcctttgatc gcgttagcca actacaatgc gtaccgtcaa	1080
aattga	1086

<210> 19

<211> 1029

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 19

atggctgagc aacaaatata taacttgctg tctatgtttg atgcttcaca tgctagtcag	60
aaattagaaa ttactgtcca aatgatggac acataccatt acagagaaac gcctccagat	120
tcctcatctt ctgaaggcgg ttcatgtct agatacgacg agagaagagt ctctttgcct	180
ctcagtcata atgctgcctc tccagatatt gtatcacaaac tatgtttttc cactgcaatg	240
tcttcagagt tgaatcacag atggaaatct caaagattaa aggtggccga ttctccttac	300
aactatatcc taacattacc atcaaaagga attagagggtg cctttatcga ttccctgaac	360
gtatggttgg aggttccaga ggatgaaaca tcagtcatca aggaagttat tggatatgctc	420
cacaactctt cattaatcat tgatgacttc caagataatt ctccacttag aagaggaaag	480
ccatctaccc atacagtctt cggccctgcc caggctatca atactgctac ttacgttata	540
gttaaagcaa tcgaaaagat acaagacata gtgggacacg atgcattggc agatgttacg	600
ggtactatta caactatfff ccaagggtcag gccatggact tgtggtggac agcaaatgca	660
atcgttccat caatacagga atacttactt atggtaaacg ataaaaccgg tgctctcttt	720
agactgagtt tggagttggt agctctgaat tccgaagcca gtatttctga ctctgcttta	780
gaaagtttat ctagtgtgtg ttctttgcta ggtcaatact tccaaatcag agacgactat	840
atgaacttga tcgataacaa gtatacagat cagaaaggct tctgcgaaga tcttgatgaa	900
ggcaagtact cactaacact tattcatgcc ctccaaactg attcatccga tctactgacc	960
aacatccttt caatgagaag agtgcaagga aagttaacgg cacaaaagag atgttggttc	1020
tggaatatga	1029

<210> 20

<211> 903

<212> DNA

<213> Artificial Sequence

SeqLst

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 20

atggaaaaga ctaaggagaa agcagaacgt atcttgctgg agccatacag atacttatta	60
caactaccag gaaagcaagt ccgttctaaa ctatcacaaag cggttcaatca ctgggttaaaa	120
gttcctgaag ataagttaca aatcattatt gaagtcacag aaatgctaca caatgcttct	180
ttactgatcg atgatataga ggattcttcc aaactgagaa gaggttttcc tgtcgctcat	240
tccatatacg ggggtaccaag tgtaatcaac tcagctaatt acgtctactt cttgggattg	300
gaaaaagtat tgacattaga tcatccagac gctgtaaagc tattcaccag acaacttctt	360
gaattgcatc aagggtcaagg tttggatatac tattggagag acacttatac ttgccaaca	420
gaagaggagt acaaagcaat gggttctaaa aagactggcg gtttggtcgg acttgccggt	480
ggctctgatgc aacttttctc tgattacaag gaggacttaa agcctctggt ggataccttg	540
ggcttggtttt tccagattag agatgactac gctaacttac attcaaagga atattcagaa	600
aacaaatcat tctgtgaaga tttgactgaa ggggaagtta gttttccaac aatccacgcc	660
at ttgggtcaa gaccagaatc tactcaagtg caaaacattc tgcgtcagag aacagagaat	720
attgacatca aaaagtattg tgttcagtac ttggaagatg ttgggttcttt tgcttacaca	780
agacatacac ttagagaatt agaggcaaaa gcatacaagc aaatagaagc ctgtggaggc	840
aatccttctc tagtggcatt gggttaaaca ttgtccaaaa tgttcaccga ggaaaacaag	900
taa	903

<210> 21

<211> 1020

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 21

atggcaagat tctatcttct taacgcacta ttgatgggta tctcattaca atcaactaca	60
gccttcactc cagctaaact tgcttatcca acaacaacaa cagctctaaa tgtcgcttcc	120
gccgaaactt ctttcagtct agatgaatac ttggcctcta agataggacc tatagagtct	180
gccttggaag catcagtcaa atccagaatt ccacagaccg ataagatctg cgaatctatg	240
gcctactctt tgatggcagg aggcaagaga attagaccag tggtgtgtat cgctgcatgt	300
gagatgttcg gtggatccca agatgtcgct atgcctactg ctgtggcatt agaaatgata	360
cacacaatgt ctttgattca tgatgatttg ccatccatgg ataacgatga cttgagaaga	420

					SeqLst		
ggtaaacc	caaaccat	gtcg	gttttc	ggcga	agatgtag	ctattcttgc aggtgactct	480
ttattgtc	aa	cttccttc	gagc	gtcgct	agagaa	caa aaggagtgtc agcagaaaag	540
atcgtggat	gt	ttatcgct	ag	attagg	caaa	tctgttggtg ccgagggcct tgctggcggt	600
caagttat	gg	acttagaat	gt	tgaagc	taaa	ccaggtacca cattagacga cttgaaatgg	660
attcatat	cc	ataaaacc	gc	tacatt	gtta	caagttgctg tagcttctgg tgcagttcta	720
ggtggtg	caa	ctcctga	aga	ggttgct	gca	tgcgagttgt ttgctatgaa tataggctct	780
gcctttc	aag	ttgccg	acga	tatcctt	gat	gtaaccgctt catcagaaga tttgggtaaa	840
actgcagg	ca	aagatga	agc	tactgata	ag	acaacttacc caaagttatt aggattagaa	900
gagagta	agg	catacg	caag	acaacta	atc	gatgaagcca aggaaagttt ggctcctttt	960
ggagata	gag	ctgcccc	ttt	attggcc	att	gcagatttca ttattgatag aaagaattga	1020

<210> 22

<211> 1068

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 22

atgcacttag	caccacgtag	agtc	cctaga	ggtaga	aagat	caccac	ctga	cagagttc	ct	60
gaaagaca	aag	gtgc	cttggg	taga	agacgt	ggag	ctggct	ctactgg	ctg	120
gctgctgg	tg	ttcacc	gtag	aagagg	agga	ggcg	aggctg	atccat	cagc	180
agaggctgg	c	aagccg	ggtg	tggc	accggt	ttgc	ctgatg	aggtgg	gtg	240
gccttagaa	a	tg	tttcat	gc	ttttg	cttta	atccat	gatg	atata	300
actaga	aagag	gctcccc	aac	tg	ttcac	aga	gccctag	ctg	atcg	360
gaccagat	c	aggccg	gttca	actagg	agtt	tctact	gcta	tcttgg	ttgg	420
ttgacat	ggt	ccgat	gaatt	gttata	cgt	ct	cattgact	c	acata	480
ctaccatt	gg	taacag	ctat	gagag	ctgaa	accgtt	catg	gccaat	atct	540
agtgctag	aa	gacctg	gggac	cgata	cttct	cttg	cattga	gaatag	ccag	600
gcagctta	ca	aatgga	acg	tccact	gcac	attgg	tgag	ccctg	gctg	660
gaactatta	g	cagggc	tttc	agcata	cgc	ttgcc	agctg	gagaag	cctt	720
gatgacct	gc	taggcg	tctt	cggtg	atcca	agacg	tacag	ggaaac	ctga	780
cttagagg	tg	gaaag	catac	tgtctt	agtc	gcctt	ggcaa	gagaac	atgc	840
cagagaca	ca	cattg	gatac	attatt	gggt	acacc	aggtc	ttgata	gaca	900
agacta	agat	gcgtatt	ggt	agcaact	ggt	gcaag	agccg	aagccg	aaag	960

	SeqLst	
gagagaagag atcaagcatt aactgcattg aacgcattaa cactgccacc tccttttagct		1020
gaggcattag caagattgac attaggggtct acagctcatc ctgcctaa		1068

<210> 23
 <211> 993
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 23	
atgtcatatt tcgataacta cttcaatgag atagttaatt ccgtgaacga catcattaag	60
tccttacatct ctggcgacgt accaaaacta tacgaagcct cctaccattt gtttacatca	120
ggaggaaaga gactaagacc attgatcctt acaattttctt ctgatctttt cggtggacag	180
agagaaagag catactatgc tggcgacgca atcgaagttt tgcacacatt cactttgggt	240
cacgatgata tcatggatca agataacatt cgtagagggtc ttcctactgt acatgtcaag	300
tatggcctac ctttggccat tttagctggg gacttattgc atgcaaaagc ctttcaattg	360
ttgactcagg cattgagagg tctaccatct gaaactatca tcaaggcggt tgatatcttt	420
acaagatcta tcattatcat atcagaagggt caagctgtcg atatggaatt cgaagataga	480
attgatatca aggaacaaga gtatttggat atgatatctc gtaaaaccgc tgccttattc	540
tcagcttctt cttccattgg ggcgttgata gctggagcta atgataacga tgtgagatta	600
atgtccgatt tcggtacaaa tcttggggtc gcatttcaaa ttgtagatga tatacttggt	660
ttaacagctg atgaaaaaga gctaggaaaa cctgttttca gtgatatcag agaaggtaaa	720
aagaccatat tagtcattaa gacttttagaa ttgtgtaagg aagacgagaa aaagattgtg	780
ttaaaagcgc taggcaacaa gtcagcatca aaggaagagt tgatgagttc tgctgacata	840
atcaaaaagt actcattgga ttacgcctac aacttagctg agaaatacta caaaaacgcc	900
atcgattctc taaatcaagt ttcaagtaaa agtgatattc caggggaaggc attgaaatat	960
cttgctgaat tcaccatcag aagacgtaag taa	993

<210> 24
 <211> 894
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 24	
atgggtcgac aaactttcaa cctggatacc tacttatccc aaagacaaca acaagttgaa	60
gaggccctaa gtgctgctct tgtgccagct taccctgaga gaataacga agctatgaga	120

SeqLst

tactccctcc	tggcaggtgg	caaaagatta	agacctatct	tatgttttagc	tgcttgcgaa	180
ttggcaggtg	gttctgttga	acaagccatg	ccaactgcgt	gtgcacttga	aatgatccat	240
acaatgtcac	taattcatga	tgacctgcca	gccatggata	acgatgattt	cagaagagga	300
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gtcgtagacc	ttgaatctga	aggtaaagct	atttccttag	aaacattgga	gtatatccac	540
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agacagaaag	cggaagagtt	gattcaatct	gctaaggaag	ccttaagacc	ttacggttca	840
caagcagagc	cactcctagc	gctggcagac	ttcatcacac	gtcgtcagca	ttaa	894

<210> 25

<211> 1116

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 25

atggcctctg	ttactttggg	ttcctggatc	gtcgtccacc	accataacca	tcaccatcca	60
tcatttatcc	taactaaatc	tcgttcaaga	tcctgtccta	ttactaac	caaaccaatc	120
tcttttcgtt	caaagagaac	agtttctct	agtagttcta	tcgtgtcctc	tagtgtcgtc	180
actaaggaag	acaatctgag	acagtctgaa	ccttcttcct	ttgatttcat	gtcatatatc	240
attactaagg	cagaactagt	gaataaggct	cttgattcag	cagttccatt	aagagagcca	300
ttgaaaatcc	atgaagcaat	gagatactct	cttctagctg	gcgggaagag	agtcagacct	360
gtactctgca	tagcagcgtg	cgaattagtt	ggtaggcgag	aatcaaccgc	tatgcctgcc	420
gcttgctgctg	tagaaatgat	tcatacaatg	tcactgatac	acgatgattt	gccatgtatg	480
gataacgatg	atctgagaag	gggtaagcca	actaaccata	aggttttcgg	cgaagatggt	540
gccgtcttag	ctggtgatgc	tttgttatct	ttcgcgttcg	aacatttggc	atccgcaaca	600
tcaagtgatg	ttgtgtcacc	agtaagagta	gtagagcag	ttggagaact	ggctaaagct	660
attggaactg	agggtttagt	tgcagggtcaa	gtcgtcgata	tctcttccga	aggtcttgat	720
ttgaatgatg	taggtcttga	acatctcgaa	ttcatccatc	ttcacaagac	agctgcactt	780

SeqLst

ttagaagcca gtgcggttct cggcgcaatt gttggcggag ggagtgatga cgaaattgag	840
agattgagga agtttgctag atgtatagga ttactgttcc aagtagtaga cgatatacta	900
gatgtgacaa agtcttccaa agagttggga aaaacagctg gtaaagattt gattgccgac	960
aaattgacct accctaagat tatggggcta gaaaaatcaa gagaatttgc cgagaaactc	1020
aatagagagg cgcgtgatca actgttgggt ttcgattctg ataaagttgc accactctta	1080
gccttagcca actacatcgc ttacagacaa aactaa	1116

<210> 26

<211> 1086

<212> DNA

<213> Stevia rebaudiana

<400> 26

atggctcttg taaatcccac agctttgttc tatggaacct ccataagaac cagacccaca	60
aacttgctca acccgaccca aaaacttcga cccgtttcct cgtcttcttt gccttccttc	120
tcttcagttt ctgcaatctt gacggaaaaa caccaatcaa acccatcaga aaacaataac	180
ttgcaaacc atctcgaaac accattcaat ttcgactctt acatgctgga gaaagtaaac	240
atggtgaatg aagctctgga cgcttcgggt ccaactcaaag acccgataaa gatccatgaa	300
tccatgcggt actcccttct agctggcggg aaacgcatcc gaccgatgat gtgcatcgcc	360
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atgattcaca ccatgtcact agttcatgac gaccttccat gcatggataa cgacgacttc	480
cgacgtggaa aaccaataag ccacaagggtg tacgggtgaag aaatggcgggt tctaaccggg	540
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gacaggatcg tccgagccat tgggtgaactc gcaagggtccg ttggctcgga gggtttggtc	660
gccggtcagg tgggtgatat ttatccgaa ggggctgatg ttgggttaga ccacttgag	720
tatattcata tacacaagac tgcaatgttg cttgagagct cggtcgtgat cggcgcgatc	780
atgggcgggtg ggtctgacca acagatcgaa aagttgcgaa agtttgcgag atcgattggt	840
ttgttgtttc aggtggtaga tgatattctt gatgtcacia agtcgactga ggaattgggg	900
aaaacggcgg gaaaagattt gctgacggac aagacaacgt atccgaagtt gttggggatc	960
gaaaaatcga gagaatttgc ggagaaatta aacaaggaag cgcaagaaca attgtcgggg	1020
tttgatcgcc gcaaggcggc tccgttaatt gcccttgcta attacaatgc ttataggcaa	1080
aactga	1086

<210> 27

<211> 1029

<212> DNA

<213> Gibberella fujikuroi

SeqLst

<400> 27
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aagttggaga ttacggttca gatgatggat acctaccatt acagagaaac tcctccagac 120
tcttcctctt cagaaggcgg ttccttatct cgctatgatg agcgacgggt ctcccttccg 180
ctctctcaca atgcagcctc cccagacata gtctcccagt tatgcttctc aacagctatg 240
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aactacatcc tgactcttcc atctaaagggt attcgtgggg ctttcattga ctactgaat 360
gtctggctcg aggtccccga agacgagacc tcggtgatca aagaggatgat tggcatgctc 420
cacaactcgt ctctcataat cgatgacttc caagacaact cccacttcg gcggggcaag 480
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aggttatcgc ttgaactact ggcgtgaac tctgaagcat ccatcagtga cagcgcgctt 780
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tggaagtga 1029

<210> 28
<211> 903
<212> DNA
<213> Mus musculus

<400> 28
atggagaaaa ctaaagagaa agctgagagg attcttctag agccctatag gtacttactt 60
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gttcagaag acaagctaca gattatcatt gaagtgactg aaatgttgca taatgccagt 180
ttactcattg atgatattga agacagttca aagctccgac gtgggtttccc agtggctcac 240
agcatctatg gtgtcccac tgcattaat tctgccatt acgtctactt ccttggactg 300
gaaaaagtct taaccttga tccccggat gcggtgaagc ttttcacacg ccagcttctg 360
gaacttcac agggacaagg cctcgatatt tactggaggg acacctacac ttgtccaact 420
gaagaagaat ataaagccat ggtgttgacg aagacagggt gtttgtttg attagcagta 480
ggtcttatgc agctgttctc tgattacaaa gaagatctaa agccactgct tgacacactt 540

	SeqLst	
gggctctttt tccagattag agatgattat gccaatctac actccaaaga atacagtgaa		600
aacaaaagtt tctgtgaaga cttgacagaa gggaagttct cattccccac tatccatgcc		660
atttgggtcaa ggccagaaag caccaggtta cagaacatcc tgcgccagag aacagagaat		720
atagatatta aaaagtattg tgtgcagtac ctggaggatg taggttcttt tgcatacact		780
cgacacactc ttagagagct tgaagctaaa gcctacaaac aaattgaggc ctgtggtggg		840
aacccttcac tagtggcttt agtcaagcac ttaagtaaga tgttcacaga agaaaataaa		900
taa		903

<210> 29
 <211> 1020
 <212> DNA
 <213> *Thalassiosira pseudonana*

<400> 29		
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gcattcacc cggcaaaact cgcctaccca acaaccacca ctgcattaaa cgttgcctct		120
gccgaaacat catttagcct cgatgaatac ctagcctcca aaatcggacc cattgaatca		180
gctctcgagg catctgtcaa atctcgcat cctcaaactg acaagatatg cgagtctatg		240
gcatactcac tcatggctgg aggaaagcgt atccgtccc ttttgatcat tgctgcttgt		300
gaaatgtttg ggggaagtca agatgtggct atgccgacgg ctgtggcttt ggagatgatt		360
catactatga gtcttattca tgacgatttg ccttcaatgg acaacgatga tctccgacga		420
ggaaagccaa ctaatcatgt tgtctttgga gaggatgttg ctattcttgc tggggattct		480
cttctcagta cgtcttttga acatgttgcc cgtgaaacca aaggagtgtc agctgaaaag		540
attgtagatg ttatcgctcg cctcgggaag tctgtgggtg cagaggggtct tgctggtgga		600
caggttatgg atcttgagtg tgaggcgaag ccaggaacta ccctcgacga tctcaagtgg		660
attcacattc acaaaactgc cactcttctt caagtggcag tggcatcagg tgctgttctt		720
ggagggggcca caccagagga gggtgctgct tgtgaactgt tcgcaatgaa tattggactt		780
gccttccagg tcgctgatga tattttggac gtgacggcat cgagtgagga tcttggtgaaa		840
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gagagtaagg catacgctcg acaactcata gacgaagcaa aggaatcttt ggctcctttc		960
ggtgatcgtg ctgctccatt gttggcaatt gccgacttta tcattgatcg aaagaactag		1020

<210> 30
 <211> 1068
 <212> DNA
 <213> *Streptomyces clavuligerus*

<400> 30		
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SeqLst

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gcgctggaga	tgttccacgc	gttcgcgctg	atccacgacg	acatcatgga	tgactccgcg	300
accaggcgcg	gcagcccgac	ggtgcaccgg	gcactcgccg	accggctcgg	cgccgctctc	360
gaccccgacc	aagccggaca	actgggggtg	agcacggcga	tcctcgtcgg	ggacctcgcc	420
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ctgcccctgg	tcacggccat	gcgcgcggaa	acggtccacg	gccagtacct	ggacatcacc	540
tccgcccgcc	ggcccggcac	ggacacctca	ctggcgctgc	gaatcgcgcg	ctacaaaacc	600
gctgcttaca	ccatggaacg	ccccctgcac	atcggaagcag	cgctcgccgg	cgcacgaccg	660
gaactcctgg	cagggtctag	cgcctacgcg	ctgccggcgg	gcgaggcatt	ccagctcgcc	720
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cggctgcgct	gcgtcctcgt	cgccaccggg	gcccgggcgg	aagccgaacg	cctgatcacc	960
gaacggcgcg	accaggccct	caccgcgctc	aacgccctga	cactgcccc	accgctcgcc	1020
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<210> 31

<211> 993

<212> DNA

<213> *Sulfolobus acidicaldarius*

<400> 31

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ggaggtaaga	ggttaagacc	attaatctta	actatatcat	cagatttatt	cggaggacag	180
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tacggcttac	ccttagcaat	attagctggg	gattttactac	atgcaaaggc	ttttcagctc	360
ttaaccagg	ctcttagagg	tttgccaagt	gaaaccataa	ttaaggcttt	cgatattttc	420
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attgatataa	aggagcagga	ataccttgac	atgatctcac	gtaagacagc	tgcatatttc	540
tcggcatcct	caagtatagg	cgcaacttatt	gctgggtgcta	atgataatga	tgtaagactg	600
atgtctgatt	tcggtacgaa	tctaggtatt	gcatttcaga	ttgttgacga	tatcttaggt	660

SeqLst

ctaacagcag	acgaaaagga	acttggaag	cctgttttta	gtgatattag	ggagggtaaa	720
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ctaaaggcgt	taggtaataa	gtcagcctca	aaagaagaat	taatgagctc	agcagatata	840
attaagaaat	actctttaga	ttatgcatac	aatttagcag	agaaatatta	taaaaatgct	900
atagactctt	taaatcaagt	ctcctctaag	agtgatatac	ctggaaaggc	tttaaaatat	960
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<210> 32
 <211> 894
 <212> DNA
 <213> *Synechococcus* sp.

<400> 32						
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tacagcctgc	tggcgggggg	gaaacgcctg	aggccgatcc	tctgtctggc	ggcctgtgag	180
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cggcagaaag	ctgaggaact	gatccaatcg	gccaaggagg	cgttgcgccc	ctacggatcc	840
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<210> 33
 <211> 1116
 <212> DNA
 <213> *Arabidopsis thaliana*

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	SeqLst	
acaaaagaag acaatctacg ccaatctgaa ccacccctctt tcgatttcat gtcgtacatc		240
atcaccaaag ccgaattagt caacaaagct ttagattcag ctgttcctct ccgtgagcca		300
ctcaagatcc acgaagcgat gcgttactct cttctcgccg gtggcaaaag agttagacca		360
gttctctgca tcgctgcttg tgaactcgtc ggagggtgaag aatcaaccgc tatgccagca		420
gcttgcgccg tcgagatgat tcacaccatg tcgttgatcc acgacgatct cccttgatg		480
gataacgacg atctccgccc tggaaaaccg accaaccaca aagtgtttgg tgaagacgtc		540
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agttctgatg ttgtttctcc ggtgagagtg gttcgagccg ttggagaatt ggctaaagcg		660
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aggttaagaa agtttgcgag atgtattggt ttgttgtttc aggtggttga tgatatcttg		900
gatgtgacga aatcgtcgaa agagttaggg aaaactgctg ggaaagattt gattgctgat		960
aagttgacgt atcctaagat tatgggtttg gagaaatcga gagagtttgc tgagaaattg		1020
aatagagagg ctcgtgatca gcttttaggg ttgattctg ataaggttgc tcctttgttg		1080
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<210> 34

<211> 2364

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 34

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gacatcaact tcagatgtaa agcagtttct aaagagtact ctgatctggt gcagaaagat		180
gaggcttctt tcacaaaatg ggacgatgac aagggtgaaag atcatcttga taccaacaaa		240
aacttatacc caaatgatga gattaaggaa tttgttgaat cagtaaaggc tatgttcggt		300
agtatgaatg acggggagat aaacgtctct gcatacgata ctgcatgggt tgctttgggt		360
caagatgtcg atggatcagg tagtcctcag ttcccttctt ctttagaatg gattgccaac		420
aatcaattgt cagatggatc atggggagat catttgctgt tctcagctca cgatagaatc		480
atcaacacat tagcatgcgt tattgcactt acaagttgga atgttcatcc ttctaagtgt		540
gaaaaagggt tgaattttct gagagaaaac atttgcaa atagaagatga aaacgcagaa		600

SeqLst						
catatgccaa	ttggttttga	agtaacattc	ccatcactaa	ttgatatcgc	gaaaaagttg	660
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ccacaatatc	aaagattgtc	tactgtgaca	aattctgtgt	gtcacgatat	taccaaactt	2160
cacaatttca	aggagaattc	caccacagtg	gattcaaagg	ttcaggaact	agtccagttg	2220
gttttttagtg	acacaccaga	tgatttggat	caagatatga	aacaaacatt	cctgacagtg	2280
atgaagacat	tctactacaa	ggcgtgggtg	gatccaaaca	ctataaacga	tcatatatct	2340
aaagttttcg	aaatcgtaat	ttga				2364

<210> 35
<211> 1584

SeqLst

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 35

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tacgaaacag caaggctagt tgcccatgct acatggttag gtggacacgc cacaagagt	180
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ttagtcccta cattatctgc tggtcacgca ttattgacat gtcttgctc tcctgctcag	300
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gttccttgctg aggtccagc tgctttgttg gattccttag aagcagcact tacaccacaa	900
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agaggcagag caagattgtg tggagccttg ccactgactc ctttatggca tgataaggat	1500
ttgtatactc cagtaagagt agtcagagct gccagagctg ctgctctgta cactaccaga	1560
gatctattgt taccaccatt gtaa	1584

SeqLst

<210> 36
 <211> 1551
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 36
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 gaattgtact gtcctactag agtcgtaaga gtagctgagc tagctggcct gtgggttagca 1500
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SeqLst

<210> 37

<211> 2364

<212> DNA

<213> Stevia rebaudiana

<400> 37

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gacatcaact tccggtgtaa agcggtatcc aaagagtact ctgatttact acaaaaagat	180
gaggcttcat ttaccaagtg ggacgatgac aaagtgaagg accatttgga cacaaataag	240
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catatgccaa ttggttttga agtcacgttc ccgtcgctaa tagatatcgc aaagaagcta	660
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aaactcacia agataccaat ggaagtattg cacaaagtgc ccacaacttt acttcatagt	780
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gccaaattgg actacaataa ctatgtggcc gtgcttcaac tcgaatggta cactatccag	1620
caatggatatg ttgatatcgg tatcgaaaag tttgaaagtg acaatatcaa aagcgtatta	1680
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SeqLst

gcgtgggcta aaaccacccat attagttgac aagatcacct caatTTTTga ttcatacaca	1800
tcctcaaaag aggacataac agcctttata gacaaattta ggaacaaatc gtcttctaag	1860
aagcattcaa taaatggaga accatggcac gaggtgatgg ttgcactgaa aaagacccta	1920
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caagcttggg agatgtggtt gacgaaattg caagatggag tagatgtgac agcgggaatta	2040
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aaggtgttcg agattgtaat atga	2364

<210> 38

<211> 1584

<212> DNA

<213> Streptomyces clavuligerus

<400> 38

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gaccacggag tgcctcatga ccggctcctg cgcgcagttg acgcgggcct gacggcactg	360
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gacagcgac ggcgctacct ggaagaactc cagcaccgat acagcggccc ggtgccctcc	780
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ggcgctccag cgggtgcggg actgccgccg gacgcggatg acaccgccgc cgttctgctg	960
gcgcttgcca cgcacggccg cgggcgccgt cccgagggtcc tcatggacta ccgcacggac	1020

SeqLst

ggctactttcc agtgcttcat cggcgaacgc acccctttcca tcagcaccaa tgcccatgtc	1080
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gccatggaca ccgcatcagc gtggctcctc gcggctcaga agcaggatgg cagctggctc	1200
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agggggcgcg cccgcctctg cggcgctttg ccgctgactc ccctatggca tgacaaggac	1500
ctgtacacgc cgggtacgtgt cgtccgcgcc gcccggtgcc cgcacctgta caccacccgt	1560
gacctgttc tgccgcccct gtga	1584

<210> 39

<211> 1551

<212> DNA

<213> Bradyrhizobium japonicum

<400> 39

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gatggcggca gcgtcgggtcc gtccgtctac gacacggcgc aggcgctgcg cttccacggc	120
aacgtcaccg gtcggcagga cgcatacgcg tggctcatcg cgcagcaaca ggccgacggc	180
ggatggggaa gcgcggactt cccgctgttc cgccatgcgc ccacgtgggc ggcgttactg	240
gcattgcagc gtgccgatcc tcttcccggg gctgcggacg cagtccagac tgcaacgagg	300
ttcctccagc gccagcccga tccctacgca catgcgggtg cagaagacgc gccgatcggc	360
gcggagctga tcctgccgca gttttgcggg gaggccgcat gggtgctggg tggcgtagcg	420
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ccgaccaccg catgcccgga tgacgacggc agcatcggca tcagtccggc ggccaccgcc	600
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gttgcgttgt gcgtcctgca ccttgaggc cgtgacccgg cggtcgatgc gttgcgcat	960
ttcgaaatcg gcgagctgtt cgtcaccttc cccggcgaac gcaatgcctc ggtgtcgacc	1020
aacattcatg ccctgcatgc gttgcgactg ttgggaaagc ccgccgcggg cgccagcgcg	1080

SeqLst

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gatgagcgcg cgctggcggc gctgctgcag gcgcagcgcg acgacggtgg ctggggcgcg	1260
ggtcgcgggt ccacgttcga ggaaaccgcc tatgcgctgt ttgctgtgca cgtgatggat	1320
gggagcgaag aggcgacagg gcgccggcgc atcgcgcagg tggaggcgcg tgcgctggag	1380
tggatgctcg cccgccatgc ggcgcatgga ttgccgcaga cgccgctgtg gatcggcaag	1440
gaactgtatt gcccactcg ggctgtgcgc gtggccgaac tcgccgggtt gtggctggcg	1500
cttcgttggg ggcggcgcg cctggccgag ggggcaggag cgccgccatg a	1551

<210> 40

<211> 2355

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 40

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ataatcgata cgaccaagga gagaatacaa aaacaattca aaaatgttga aatttcagtt	180
tcttcttatg atactgcgtg ggttgccatg gttccatcac ctaattctcc aaagtctcca	240
tgtttcccag aatgtttgaa ttggctgatt aacaaccagt tgaatgatgg atcttgggggt	300
ttagtcaatc acacgcacaa tcacaacat ccacttttga aagattcttt atcctcaact	360
ttggcttgca tcgtggccct aaagagatgg aacgtaggtg aggatcagat taacaagggg	420
cttagtttca ttgaatctaa cttggcttcc gcgactgaaa aatctcaacc atctccaata	480
ggattcgata tcatctttcc aggtctgtta gagtacgcca aaaatctaga tatcaactta	540
ctgtctaagc aaactgattt ctactaatg ttacacaaga gagaattaga acaaaagaga	600
tgtcattcaa acgaaatgga tggttacctt gcttatatct ctgaagggtt tggtaatctt	660
tacgattgga atatggtgaa aaagtaccag atgaaaaatg gctcagtttt caattcccct	720
tctgcaactg cggcagcatt cattaacat caaaatccag gatgcctgaa ctatttgaat	780
tcactactag acaaattcgg caacgcagtt ccaactgtat accctcacga tttgtttatc	840
agattgagta tgggtggatac aattgaaaga cttggtatat cccaccactt tagagtcgag	900
atcaaaaatg ttttgatga gacataccgt tgttgggtgg agagagatga acaaatcttt	960
atggatgttg tgacgtgcgc gttggccttt agattgttgc gtattaacgg ttacgaagtt	1020
agtccagatc cacttgccga aattacaaac gaattagctt taaaggatga atacgccgct	1080

SeqLst

cttgaaacat atcatgcgtc acatatcctt taccaagagg acttatcatc tggaaaacaa	1140
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aaactgatcc ataaagaggt tgaaaatgca ctttaagttcc ctattaacac cggcttagaa	1260
cgtattaaca caagacgtaa catccagctt tacaacgtag acaatactag aatcttgaaa	1320
accacttacc attcttccaa catatcaaac actgattacc taagattagc tgttgaagat	1380
ttctacacat gtcagtctat ctatagagaa gagctgaaag gattagagag atgggtcggt	1440
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gttgccgcca ctttatcaag tccagaattg tcagatgcac gtatttcttg ggctaaaaac	1560
ggaattttga caactgttgt tgatgatttc tttgatattg gcgggacaat cgacgaattg	1620
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gaacatgtta gaatactgtt cttggctctg aaagatgcta tctgttggat cggggatgag	1740
gctttcaa at ggcaagctag agatgtgacg tctcacgtca ttcaaacctg gctagaactg	1800
atgaactcta tgttgagaga agcaatttgg actagagatg catacgttcc tacattaac	1860
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tactttgtag gaccaaagct atccgaggaa atcgtcgaat catcagaata ccataacttg	1980
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gtcgaagagg aagtagttga ggaaatgatg atgatgatca aaaacaagag aaaggagttg	2160
atgaaactaa tcttcgaaga gaacggttca attgttccta gagcatgtaa ggatgcattt	2220
tggaacatgt gtcagtgtgct aaactttttc tacgcaaacg acgatgggtt tactgggaac	2280
acaatactag atacagtaaa agacatcata tacaaccctt tggctttagt aaacgaaaac	2340
gaggagcaaa gataa	2355

<210> 41

<211> 2355

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 41

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ctttctgcaa ttcatactgc cagtactagt catggagggtc aaacaaaccc aacaaatttg	120
ataatcgata ctactaagga gagaatccaa aagctattca aaaatgttga aatctcagta	180
tcattcttatg acaccgcatg gggtgcaatg gtgccatcac ctaattcccc aaaaagtcca	240

SeqLst

tgttttccag	agtgccttgaa	ttgggttaatc	aataatcagt	taaacgatgg	ttcttggggt	300
ttagtcaacc	acactcataa	ccacaatcat	ccattattga	aggactcttt	atcatcaaca	360
ttagcctgta	ttgttgcaat	gaaaagatgg	aatgtaggtg	aagatcaaata	caacaagggt	420
ttatcattca	tagaatccaa	tctagcttct	gctaccgaca	aatcacaacc	atctccaatc	480
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gtggaagagg aagtcgttga ggaaatgatg atgatgatca aaaacaagag aaaggaattg		2160
atgaaattga ttttcgagga aaatggttca atcgtaacct gagcttgtaa agatgctttt		2220
tggaatatgt gccatgttct taacttcttt tacgctaattg atgatggctt cactggaaat		2280
acaatattgg atacagttaa agatatcatc tacaaccac ttgttttggt caatgagaac		2340
gaggaacaaa gataa		2355

<210> 42

<211> 1773

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 42

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ttctcatccg gtggccatgc tttgagattc gggagtagtc tgccatgttg gagaaggacc	120
cctacccaaa gatctacttc ttctctact actagaccag ctgccgaagt gtcatacagg	180
aagagtaaac aacatgatca ggaagctagt gaagcgacta tcagacaaca attacaactt	240
gtggatgtcc tggagaatat ggaatatcc agacattttg ctgcagagat aaagtgcata	300
ctagacagaa cttacagatc ttggttaca agacacgagg aaatcatgct ggacactatg	360
acatgtgcta tggcttttag aatcctaaga ttgaacggat acaacgtttc atcagatgaa	420
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accagaacac tacttgaatt acacaaggct tcaacagtta gtatctctga ggatgaatct	540
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ggcgactga gaaagccttc ttatttcaa gaggttgaac atgacttga tggacctttt	660
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tctagtcaag tcgaaagagc aaaagaggtg gacgctgtca taaatgagcc actgaagttg		1740
caaggttctc atacactggg atctgatggt taa		1773

<210> 43

<211> 2232

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 43

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acaccttggt ttccagaatg tactaaatgg atcctagaaa atcagttggg tgatggtagt	180
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gacattatct ttccaggtat gattgaatac gctatagact tagacctgaa tctaccacta	420
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				SeqLst	
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<210> 44
 <211> 2355
 <212> DNA
 <213> Stevia rebaudiana

<400> 44	atgaatcttt	cactatgcat	cgcgtcccct	ttgttaacca	aatcaaactg	acccgcggct	60
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	atcattgata	caaccaaaga	acggatccaa	aaacagttta	aaaatgtaga	aatttctggt	180
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	cttggttaatc	acactcataa	tcataatcac	ccgttgctta	aagattctct	atcttcaaca	360
	ttagcatgta	ttgttgcatt	aaaaagatgg	aatgttgggg	aagatcaaat	aaataaaggt	420

SeqLst						
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2355

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<211> 2355

<212> DNA

<213> Stevia rebaudiana

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<211> 1773

<212> DNA

<213> Zea mays

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SeqLst

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<211> 2232

<212> DNA

<213> Populus trichocarpa

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<210> 48

<211> 2952

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 48

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<211> 2646

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

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SeqLst

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aagagaatcc acttgaatat ggctaaaatc atgcatgcct tctacaagga tactgatgga	2580
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<210> 50

<211> 2952

<212> DNA

<213> *Phomopsis amygdali*

<400> 50

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<210> 51

<211> 2646

<212> DNA

<213> *Physcomitrella patens*

<400> 51

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SeqLst

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gcgcgagt	cagcgctg	tggtcacat	ggccctcag	tccatcggt	tttgtagtg	540
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<210> 52

<211> 1542

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 52

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agatcccaat caaatcatct tccaagagtg cctgaagtcc cagggtgtcc attgttagga	180
aatctgttac aattgaagga gaaaaagcca tacatgactt ttacgagatg ggcagcgaca	240
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aagcatagaa ttacagaga tatcatgatg gataacatat ctactcaact tcatgaattc	540
gtgaaaaaca acccagaaca ggaagaggta gaccttagaa aaatctttca atctgagtta	600
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ggagcaatcg atgttgattg gagagacttc tttccatacc taaagtgggt cccaaacaaa	780

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<210> 53

<211> 1530

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 53

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ttgccaagtg ttccagtagt gcctggtttt ccagttattg ggaatttggt gcaactaaag		180
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gagccagtta actttagagc aattttcgaa cacgaattgt ttggtgtagc attaaagcaa		600
gccttcggta aagacgtaga atccatatac gtcaaggagt taggcgtaac attatcaaaa		660
gatgaaatct ttaagggtgct tgtacatgat atgatggagg gtgcaattga tgtagattgg		720
agagatttct tcccatattt gaaatggatc cctaataagt cttttgaagc taggatacaa		780

SeqLst						
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gatggtgaag	aggaaaatgt	cgatacttat	gggttaacat	ctcaaaagtt	ataccacta	1500
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<210> 54

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 54

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gcatggttat	gttcttatgt	gatacatgtt	ttatcatctt	cctctacagt	aaaagtgcca	180
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caggaatggg	tgactactac	agcagaatat	tcagaatcac	ttttcattac	agggtttatc	720
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atcactatcg attctgatat gattccagac ccaagagcta gactttgcgt cagaaaaaga		1560
tcacttagag atgaatga		1578

<210> 55

<211> 1500

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 55

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ctatcttaca tcggcgact aagatggaca agacgtggca gagagatact tcaagaggga	180
tatgatggct acagaggatc tacattcaaa atcgcgatgt tagaccgttg gatcgtgatc	240
gcaaatgggtc ctaaactagc tgatgaagtc agacgtagac cagatgaaga gttaaacttt	300
atggacggat taggagcatt cgtccaaact aagtacacct taggtgaagc tattcataac	360
gatccatacc atgtcgatat cataagagaa aaactaaca gaggccttcc agccgtgctt	420
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SeqLst						
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agagaagaga	tcgaaccatt	agtcaaagag	gagggctgga	ccaaggctgc	tatgggaaaa	1020
atgtggtggt	tagattcatt	tctaagagaa	tctcaaagat	acaatggcat	taacatcgta	1080
tctttaacta	gaatggctga	caaagatatt	acattgagtg	atggcacatt	tttgccaaaa	1140
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aactatgatg	taaagttgcc	tggtgacggg	aaacgtccat	tgaacatgta	ttgggggtcca	1440
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<210> 56
 <211> 1542
 <212> DNA
 <213> Stevia rebaudiana

<400> 56		
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aggagccaat	caaaccatct ccctcgggtt cccgaggtac ctggtgtgcc attattgggg	180
aattttattgc	agttgaagga gaagaaacct tacatgactt ttacaagatg ggcggcaact	240
tatggtccga	tttattcgat taaaaccgga gcaacttcta tggtagctgt cagttcaa	300
gaaattgcaa	aggaggcatt gggtaccaga tttcaatcta tctcaaccag aaacctatca	360
aaggcattaa	aggttctcac agcagataaa accatggtgg cgatgagtga ttatgatgat	420
tatcataaga	ctgtcaaacg ccatatactg accgctgttt tgggaccaa tgctcagaag	480
aaacaccgca	tccataggga catcatgatg gataatatat caaccaact tcatgaattt	540
gttaaaaata	atcctgaaca agaggaagtg gatctaagga aaatattcca atccgaactt	600
tttggttag	ctatgagaca agcattggga aaggatgtgg agagcttata tgttgaggat	660
cttaaaatca	ccatgaaccg agacgagata tttcaggtat tggttgttga cccgatgatg	720
ggtgcaattg	acgtcgactg gagagatttc ttcccgtatc taaagtgggt cccgaataaa	780
aagtttgaaa	acacgatcca acaaatgtat atccggagag aagctgtgat gaagtctctt	840
attaaagaac	ataaaaaacg tattgcatcc ggagagaaat taaacagcta cattgattac	900

SeqLst						
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attattgaat	catcagacac	cactatgggt	acaactgaat	gggctatgta	tgaacttgca	1020
aaaaacccca	aacttcagga	tcgtttgtat	cgggatatca	aaagtgtttg	cgggtcagag	1080
aagattacag	aagaacactt	gtctcaactg	ccatacataa	ctgccatttt	tcatgaaacc	1140
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aatgaaacga	tagattttcca	gaaaacaatg	gcgtttggag	gtggaaagcg	cgtatgtgct	1380
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gagtggaaac	tgaaagayat	gacccaagaa	gaagttaata	cgattgggct	tacgaccag	1500
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<210> 57
 <211> 1530
 <212> DNA
 <213> Arabidopsis thaliana

<400> 57	atggccttct	tctccatgat	ctccattctc	cttggttttg	ttatctcctc	cttcatcttc	60
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	gagaagaaac	ctcacaagac	tttcactaga	tggtcagaga	tttatgggtcc	tatttactct	240
	ataaagatgg	gttcttcttc	tcttattgtc	ctcaattcta	ctgagactgc	caaagaggcc	300
	atgggtgacgc	ggtttttcgtc	tatctcaacg	aggaagtgtg	caaatgcgtt	gacagtcctt	360
	acttgtgaca	aatctatggg	tgctactagt	gattatgatg	atttccacaa	gttgggtgaaa	420
	cgggtgtctct	tgaacgggtct	tttgggtgct	aatgcacaga	aacgaaaaag	acattacaga	480
	gatgcactca	ttgaaaatgt	gtcttccaag	ttgcatgccc	atgctaggga	ccatccacaa	540
	gaacctgtaa	acttcagagc	tatatattgag	catgagcttt	tcgggtgtagc	attgaagcaa	600
	gcttttggga	aagatgtgga	atccatttat	gttaaagaac	tcgggtgtgac	ttgtcgaaa	660
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	caaaagcata	aacgtagact	cgcgggtgatg	aatgctctga	ttcaagatcg	actgaagcag	840
	aatggttcag	aatcggatga	tgattgctat	ctcaacttct	tgatgtcgga	agcgaaaaca	900
	ctaaccaagg	agcaaattgc	tatcttgggt	tgggagacga	ttatcgagac	agctgacact	960
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SeqLst						
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tctcaagttc	cttatctcaa	tggagtattc	catgaaacgc	ttaggaaata	cagtcctgct	1140
cctctagtcc	ccattcgcta	tgcccacgaa	gatacgcaaa	tcggagggcta	tcatgtccct	1200
gcaggaagtg	agattgcaat	aaacatctat	ggatgcaaca	tggataagaa	gcgttgggag	1260
agaccagagg	actggtggcc	ggagcggttt	cttgatgatg	gcaaatacga	aacgtcggat	1320
cttcacaaga	caatggcggt	tggagcggga	aagaggggtt	gtgctgggtg	tcttcaagca	1380
tctctcatgg	caggcattgc	cattgggagg	ttagtgcaag	aattcgagtg	gaagcttaga	1440
gacggtgaag	aagagaatgt	ggatacatat	ggcttgacct	ctcagaagct	ttatcctctt	1500
atggctatta	tcaatccaag	gcgttcttaa				1530

<210> 58

<211> 1578

<212> DNA

<213> *Gibberella fujikoro*

<400> 58

atgagtaagt	ccaacagcat	gaacagtacc	agccatgaaa	cgttattcca	gcagctcgtc	60
ttaggtcttg	acagaatgcc	gctaattggac	gttacttggc	tgatctacgt	ggcctttggc	120
gcttggttat	gctcttatgt	catccatgtc	ctatcgctct	cttctacagt	caaagtgtcc	180
gtcgtaggct	accgcagcgt	ctttgagcct	acatggcttc	tccgtttgcg	ctttgtttgg	240
gaagggggat	ctatcatcgg	ccaaggctac	aacaaattta	aagactctat	cttccagggtg	300
cgaaagcttg	gtaccgatat	cgatcatcat	ccgccaaact	acatcgatga	ggtcagaaaag	360
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caagaatggg	tgacgaccac	tgcagagtac	agcgagagcc	tgttcataac	tggctttatt	720
ctccgcgttg	tccccatat	tctaagacca	ttcatagccc	cgctgctacc	ctcctacaga	780
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caaggtgatg	gcaacgagga	catcctgtca	tggatgaggg	atgctgcgac	aggggaagaa	900
aagcaaattg	acaacattgc	ccagcggatg	cttatcctga	gtctcgcgtc	tattcacact	960
acggcaatga	cgatgacgca	tgctatgtat	gacttatgtg	cttgccctga	gtacatagag	1020
cctcttagag	atgagggtcaa	aagtgtcggt	ggcgctagtg	gttgggacaa	gacggcggtg	1080
aatcgattcc	acaaactcga	cagctttctc	aaagagtcac	aacgcttcaa	ccccgtgttc	1140

	SeqLst	
ctcttaacgt tcaatcgc	ttatcaccaa tccatgacac tctcagatgg caccaacatc	1200
ccatcaggca ctcgcatcgc	ggttccctct caccgcatgc ttcaggactc agcgcgatgc	1260
ccaggccccga cgccaccaac	cgagtttgat ggatttagat actcaaagat tcgctcagac	1320
tcaaactatg cacagaaata	tctcttctcc atgactgatt ctagtaacat ggcgtttggg	1380
tatgggaaat acgcctgccc	agggcggttc tatgcatcta atgagatgaa gctgactttg	1440
gcgatactcc ttttacaatt	tgagttcaag ttgccagatg ggaaaggaag accacgaaat	1500
atcactattg atagtgcac	gatacctgat ccgagagcta ggctgtgcgt taggaagcga	1560
tcactgagag atgaatga		1578

<210> 59

<211> 1500

<212> DNA

<213> *Trametes versicolor*

<400> 59

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agatggtaca gagacccgct	tcggtccatt cctacggttg ggggctctga ccttcccatc	120
ctctcataca tcggggcgct	caggtggacc cgccgcggaa gagagatact gcaagaaggt	180
tatgatgggt atcgcgatc	cacgttcaag atcgcgatgc tcgaccggtg gatcgatc	240
gccaacggcc caaagctcgc	cgacgaggtg aggaggcgtc ctgacgaaga gctaaacttc	300
atggacggac tgggagcggt	cgtgcagacg aagtataccc ttggggaagc aatccacaat	360
gacccgtacc acgtggacat	tattcgtgag aagctgacgc gaggcctccc ggcagtcctg	420
ccggacgtca tcgaggaact	cacgctagcc gttcgccagt acatcccgcg ggaaggagat	480
gaatgggtca gcgtgaactg	ctccaaagca gcgcgggaca tcgtcgcccg ggcaagcaac	540
cgcgctctttg tcgggttgcc	cgcttgccgc aaccagggtt atctcgacct cgccattgac	600
ttcacctga gcgttgtaa	agacagggcg atcatcaata tggtcccgga gttgctgaaa	660
cctatcgtcg gacgcgtggt	tggaaatgcc actaggaacg tgcgccgcgc ggtcccattc	720
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gagaaaccga acgacatgct	ccagtggatc atggacgagg cagcctcgcg ggactcctcc	840
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aacaccatca cccacgctct	ttaccacctc gccgagatgc cggagaccct acagccgctg	960
cggaagaga tcgagccgct	cgtcaaggaa gaaggctgga cgaaggccgc catgggcaag	1020
atgtggtggc tcgacagctt	cctgcgggag tcacagcgct acaatggcat caacatcgtc	1080
tccctgacgc gcatggccga	caaggacata acgctcagcg acggcacggt cctcccgaag	1140
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	SeqLst	
gcgctgggtct tcgacccggtt ccgcttctcc cgcatgcgcg cccgcgaggg cgagggcacg		1260
aagcaccagt tcgtcaacac ctccgtggag tacgtgccct tcggccacgg gaagcacgcc		1320
tgccccgggc ggttcttcgc ggccaacgag ctgaaggcga tgctcgcgta catcgtgctc		1380
aactacgacg tgaagctgcc cggcgatggc aagcgcccc tgaacatgta ctggggcccg		1440
acggctcttg ctcgtccggc tgggcagggt ctcttccgca agaggcagg gtcgctgtag		1500

<210> 60

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 60

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ctggctttgt actatctact gtccttcac taaaaacat ctaaaaagac atgtacacct	120
cctaaagcat ctggtgaaat cattccaatt acaggaatca tattgaatct gctatctggc	180
tcaagtggtc tacctattat cttagcactt gcctcttttag cagacagatg tggtcctatt	240
ttcaccatta ggctgggtat taggagagt ctagtagtat caaattggga aatcgctaag	300
gagattttca ctaccacga tttgatagtt tctaatagac caaaatactt agccgctaag	360
attcttgggt tcaattatgt ttcatctct ttcgctccat acggcccata ttgggtcgga	420
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gtaagagttt ttgaactaga aaactctatg aaatctatca gagaatcatg gaaggagaaa	540
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caagctaacg atgacaaaaa ggaggatatg gatttcatgg atatcatgat ctccatgaca	900
gaagcaaatt caccacttga aggatacggc actgatacta ttatcaagac cacatgtatg	960
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gattgtactg ttgctgggta tagaattcca aagggcacct gcttggtgat taacatgtgg	1260

	SeqLst	
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ttgacaccta atcaaaagga tgttgatgtg atcgggtatgg atttcgaatt gataccattt		1380
ggtgccggca gaagatattg tccaggtact agattggctt tacagatggt gcatatcgta		1440
ttagcgacat tgctgcaaaa cttcgaaatg tcaacaccaa acgatgcgcc agtcgatatg		1500
actgcttctg ttggcatgac aaatgccaaa gcatcacctt tagaagtctt gctatcacct		1560
cgtgttaa at ggctcctaa		1578

<210> 61
 <211> 1431
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 61		
atgatacaag ttttaactcc aattctactc ttcctcatct tcttcgtttt ctggaaagtc		60
tacaaacatc aaaagactaa aatcaatcta ccaccagggt ccttcggctg gccatttttg		120
ggtgaaacct tagccttact tagagcaggc tgggattctg agccagaaag attcgtaaga		180
gagcgtatca aaaagcatgg atctccactt gttttcaaga catcactatt tggagacaga		240
ttcgtgttc tttgcggtcc agctggtaat aagtttttgt tctgcaacga aaacaaatta		300
gtggcatctt ggtggccagt ccctgtaagg aagtgttcg gtaaaagttt actcacaata		360
agaggagatg aagcaaaatg gatgagaaaa atgctattgt cttacttggg tccagatgca		420
tttgccacac attatgccgt tactatggat gttgtaacac gtagacatat tgatgtccat		480
tggaggggca aggaggaagt taatgtattt caaacagtta agttgtacgc attcgaatta		540
gctttagat tattcatgaa cctagatgac ccaaaccaca tcgcaaaact cggtagtctt		600
ttcaacattt tcctcaaagg gatcatcgag cttcctatag acgttcctgg aactagattt		660
tactccagta aaaaggccgc agctgccatt agaattgaat tgaaaaagct cattaaagct		720
agaaaactcg aattgaagga gggtaaggcg tcttcttcac aggacttgct ttctcatcta		780
ttaacatcac ctgatgagaa tgggatgttc ttgacagaag aggaaatagt cgataacatt		840
ctacttttgt tattcgctgg tcacgatacc tctgcactat caataacact tttgatgaaa		900
accttaggtg aacacagtga tgtgtacgac aaggttttga aggaacaatt agaaatttcc		960
aaaacaaagg aggcttgga atcactaaag tgggaagata tccagaagat gaagtactca		1020
tggtcagtaa tctgtgaagt catgagattg aatcctcctg tcatagggac atacagagag		1080
gcgttggttg atatcgacta tgctggttac actatcccaa aaggatggaa gttgcattgg		1140
tcagctgttt ctactcaaag agacgaagcc aatttcgaag atgtaactag attcgatcca		1200

	SeqLst	
tccagatttg aaggggcagg ccctactcca ttcacatttg tgcctttcgg tggaggtcct		1260
agaatgtgtt taggcaaaga gtttgccagg ttagaagtgt tagcatttct ccacaacatt		1320
gttaccaact ttaagtggga tcttctaadc cctgatgaga agatcgaata tgatccaatg		1380
gctactccag ctaagggtct gcccaattaga cttcatccac accaagtcta a		1431

<210> 62

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 62

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ttctcagttg gttatcacgt ttacggtaga gctgtgggtc aacaatggag aatgagaaga	120
tcactgaagc tacaagggtg taaaggccca ccaccatcca tcttcaatgg taacgtctca	180
gaaatgcaac gtatccaatc cgaagctaaa cactgctctg gcgataacat tatctcacat	240
gattattctt cttcattatt cccacacttc gatcactgga gaaaacagta cggcagaatc	300
tacacatact ctactggatt aaagcaacac ttgtacatca atcatccaga aatggtgaag	360
gagctatctc agactaacac attgaacttg ggtagaatca cccatataac caaaagattg	420
aatcctatct taggtaacgg aatcataacc tctaattggc ctcatggggc ccatcagcgt	480
agaattatcg cctacgagtt tactcatgat aagatcaagg gtatgggttg tttgatggtt	540
gagtctgcta tgcctatgtt gaataagtgg gaggagatgg taaagagagg cggagaaatg	600
ggatgcgaca taagagttga tgaggacttg aaagatgttt cagcagatgt gattgcaaaa	660
gcctgtttcg gatcctcatt ttctaaagggt aaggctatct tctctatgat aagagatttg	720
cttacagcta tcacaaagag aagtgttcta ttcagattca acggattcac tgatatggtc	780
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ctgatgcaat tgatttttga aggggcaatg cgttcatgtg acggtaacct ttgggataaa	960
tcagcatata gaagatttgt tgtagataat tgtaaatcta tctacttcgc agggcatgat	1020
agtacagctg tctcagtgtc atgggtgtttg atgttactgg ccctaaaccc atcatggcaa	1080
gttaagatcc gtgatgaaat tctgtcttct tgcaaaaatg gtattccaga tgccgaaagt	1140
atcccaaacc ttaaaacagt gactatgggtt attcaagaga caatgagatt ataccctcca	1200
gcaccaatcg tcgggagaga agcctctaaa gatatcagat tgggcatct agttgttcct	1260
aaaggcgtct gtatatggac actaatacca gctttacaca gagatcctga gatttgggga	1320

	SeqLst	
ccagatgcaa acgattttcaa accagaaaga ttttctgaag gaattttcaaa ggcttgtaag		1380
tatcctcaaa gttacattcc atttgggtctg ggtcctagaa catgcgttgg taaaaacttt		1440
ggcatgatgg aagtaaaggt tcttgtttcc ctgattgtct ccaagttctc tttcactcta		1500
tctcctacct accaacatag tcctagtcac aaacttttag tagaaccaca acatgggggtg		1560
gtaattagag tggtttaa		1578

<210> 63

<211> 1590

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 63

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ctctcttatt gtttacttct ctggagaagt agagcgggta acaaaaagat tgccccagaa	120
gctgccgctg catggcctat tatcggccac ctccacttac ttgcagggtg atcccatcaa	180
ctaccacata ttacattggg taacatggca gataagtacg gtcctgtatt cacaatcaga	240
ataggcttgc atagagctgt agttgtctca tcttgggaaa tggcaaagga atgttcaaca	300
gctaattgatc aagtgtcttc ttcaagacct gaactattag cttctaagtt gttgggttat	360
aactacgcca tgtttggttt ttcaccatac ggttcatact ggagagaaat gagaaagatc	420
atctctctcg aattactatc taattccaga ttggaactat tgaaagatgt tagagcctca	480
gaagttgtca catctattaa ggaactatac aaattgtggg cggaagaa gaatgagtca	540
ggattggttt ctgtcgagat gaaacaatgg ttcggagatt tgactttaaa cgtgatcttg	600
agaatggtgg ctggtaaaag atacttctcc gcgagtgcg cttcagaaaa caaacaggcc	660
cagcgttgta gaagagtctt cagagaattc ttccatctct ccggcttggt tgtggttgct	720
gatgctatac cttttcttgg atggctcgat tggggaagac acgagaagac cttgaaaaag	780
accgccatag aaatggattc catcgcccag gagtggcttg aggaacatag acgtagaaaa	840
gattctggag atgataattc taccacagat ttcatggacg ttatgcaatc tgtgctagat	900
ggcaaaaatc taggcggata cgatgctgat acgattaaca aggctacatg ctttaactctt	960
atatcagggtg gcagtgatac tactgtagtt tctttgacat gggctcttag tcttgtgtta	1020
aacaatagag atactttgaa aaaggcacag gaagagttag acatccaagt cggtaaggaa	1080
agattgggta acgagcaaga catcagtaag ttagtttact tgcaagcaat agtaaaagag	1140
acactcagac tttatccacc aggtcctttg ggtgggttga gacaattcac tgaagattgt	1200
acactagggtg gctatcacgt ttcaaaagga actagattaa tcatgaactt atccaagatt	1260

	SeqLst	
caaaaagatc cacgtatttg gtctgaccc actgaattcc aaccagagag attccttacg		1320
actcataaag atgtcgatcc acgtggtaaa cactttgaat tcattccatt cggcgcagga		1380
agacgtgcat gtcctgggtat cacattcgga ttacaagtac tacatctaac attggcatct		1440
ttcttgcatg cgtttgaatt ttcaacacca tcaaatgagc aggttaacat gagagaatca		1500
ttaggtctta cgaatatgaa atctacccca ttagaagttt tgattttctcc aagactatcc		1560
cttaattgct tcaaccttat gaaaatttga		1590

<210> 64

<211> 1440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 64

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taccctatca taggtgaaag tttagaattc ctatccacag gctggaaggg acatcctgaa	180
aagttcatat ttgatagaat gcgtaagtac agtagtgagt tattcaagac ttctattgta	240
ggcgaatcca cagttgtttg ctgtggggca gctagtaaca aattcctatt ctctaacgaa	300
aacaaactgg taactgcctg gtggccagat tctgttaaca aaatcttccc aacaacttca	360
ctggattcta atttgaagga ggaatctata aagatgagaa agttgctgcc acagttcttc	420
aaaccagaag cacttcaaag atacgtcggc gttatggatg taatcgaca aagacatfff	480
gtcactcact gggacaacaa aaatgagatc acagtttatc cacttgctaa aagatacact	540
ttcttgcttg cgtgtagact gttcatgtct gttgaggatg aaaatcatgt ggcgaaattc	600
tcagacctat tccaactaat cgctgcaggc atcatttcac ttcttatcga tcttctgggt	660
actccattca acaaggccat aaaggcttca aatttcatta gaaaagagct gataaagatt	720
atcaaacaaa gacgtgttga tctggcagag ggtacagcat ctccaacca ggatatcttg	780
tcacatatgc tattaacatc tgatgaaaac ggtaaatcta tgaacgagtt gaacattgcc	840
gacaagattc ttggactatt gataggaggc cacgatacag cttcagtagc ttgcacattt	900
ctagtgaagt acttaggaga attaccacat atctacgata aagtctacca agagcaaagt	960
gaaattgcca agtccaaacc tgctggggaa ttgttgaatt gggatgactt gaaaaagatg	1020
aagtattcat ggaatgtggc atgtgaggta atgagattgt caccaccttt acaagggtgg	1080
tttagagagg ctataactga ctttatgttt aacggtttct ctattccaaa agggtggaag	1140
ttatactggc ccgccaactc tacacacaaa aatgcagaat gtttcccaat gcctgagaaa	1200

	SeqLst	
ttcgatccta ccagatttga aggtaatggt ccagcgcctt atacatttgt accatttcggt		1260
ggaggcccta gaatgtgtcc tggaaaggaa tacgctagat tagaaatctt ggttttcatg		1320
cataatctgg tcaaacgttt taagtgggaa aagggtattc cagacgaaaa gattattgtc		1380
gatccattcc caatcccagc taaagatctt ccaatccggt tgtatcctca caaagcttaa		1440

<210> 65
 <211> 1572
 <212> DNA
 <213> Stevia rebaudiana

<400> 65		
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ccacctaaag caagcgggtga gcaccctata acaggccact taaaccttct tagtggttca		180
tccggtcttc cccatctagc cttagcatct ttggctgacc gatgtgggccc catattcacc		240
atccgacttg gcatacgtag agttttggtg gttagtaatt gggaaattgc taaggagatc		300
ttcactaccc atgatttgat tgtttcaaac cgtcccaa atctcgtgc aaagattttg		360
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gttttcgaac tagaaaactc catgaaaagc atacgcgagt cttggaaaga gaaaaaagac		540
gaagaaggta aagtgttggt ggagatgaaa aaatgggttt gggaaattgaa tatgaatata		600
gttcttagaa ctgttgctgg taaacagtac actggaactg ttgatgatgc ggatgcgaag		660
aggattagtg aattgtttag agaatgggtt cattacacag gaaggtttgt tgtgggagat		720
gcttttcctt ttcttgggtg gttggatttg ggtggatata agaagaccat ggaactagt		780
gcttccagac tagattccat ggtctcaaaa tgggttagacg agcatcgcaa aaagcaggct		840
aacgacgaca aaaaagagga catggatttc atggacatca tgatatcgat gactgaagcc		900
aattccccct tggaggggtta tgggtacggat acaataatta aaaccacttg catgactctt		960
attgtcagtg gtgtagatac aacctccatc gtgctaactt gggcactctc gttactactg		1020
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cgacaagtaa acgaatcaga tctagtaaac ctaatctacc ttgaagccgt attaaaagaa		1140
gcattgacgac tatacccagc agcattcctt ggaggtccta gagccttttt agaagactgc		1200
accgtggcag ggtaccgtat cccaaaaggc acatgtctac ttattaacat gtggaaactt		1260
catcgtgatc caaacatatg gtcagaccca tgtgagttta aaccagagag gttcttaacc		1320
ccaaacaaaa aggacgtaga tgttattgga atggattttg agttaatccc atttggtgcg		1380
ggaagaagggt attgtccagg gacacgtttg gcattacaaa tgttacacat agttctggcc		1440

	SeqLst	
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agtgttgga tgacaaatgc gaaggcaagt ccacttgaag ttctactttc gccacgtggt		1560
aagtgggtcat ag		1572

<210> 66
 <211> 1431
 <212> DNA
 <213> Stevia rebaudiana

<400> 66		
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tacaagcacc agaaaaccaa aatcaatctt ccaccgggaa gcttcggatg gccatttctg		120
ggcgaaactc tggcactcct acgtgcagggt tgggactcag agccggagag atttgttcgt		180
gaacggatca agaaacacgg aagtcctcta gtgtttaaga cgtcgttggt tggcgaccgt		240
tttgcggtgt tgtgtggacc tgccggaaac aagttcctgt tctgcaacga gaacaagctg		300
gtggcgctgt ggtggccggt tccggtgagg aagcttttcg gcaagtctct gctcacgatt		360
cgtggtgatg aagctaagt gatgaggaag atgttggtat cgtatctcg tcctgatgct		420
ttcgcaactc attatgccgt caccatggac gtcgtcacc gtcggcatat cgacgttcat		480
tggcgaggga aggaagagg gaacgtattc caaacgtta agttatatgc ctttgagctt		540
gcatgtcgtt tattcatgaa cctagacgac ccaaaccaca ttgcaaaact cggttccttg		600
ttcaacattt tcttgaaagg catcattgag cttccaatcg acgtcccagg gacacgattt		660
tatagctcca aaaaagcagc agcagctatc aggattgaac taaaaaaatt gattaaagca		720
agaaaactgg aactgaaaga aggggaaggca tcatcttcac aagacctct atcacatttg		780
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tggagtgtta tatgtgaagt catgagacta aatccacctg ttataggaac ctatagagag		1080
gcccttgtgg atattgatta tgcgggttat accatcccca aaggatggaa gctgcactgg		1140
agtgctgtat cgacacaaag ggacgaggct aactttgaag acgtaacacg ttttgacca		1200
tcacggtttg aaggcgcagg accgactcca ttcaccttg ttccgtttg aggggggcct		1260
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gtcaccaatt tcaaatggga cctgttgata cctgatgaga aaatagaata tgatcccatg		1380
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<210> 67

SeqLst

<211> 1578

<212> DNA

<213> *Arabidopsis thaliana*

<400> 67

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agtttaaagt tgcaaggcgt gaagggtcct ccaccgtcga tctttaacgg caatgtgtcg	180
gagatgcaac ggattcagtc ggaggctaaa cactgttccg gcgataacat catttctcat	240
gactattctt cttctctatt tcctcatttc gatcactggc gaaaacaata cggaaggatt	300
tacacatact caacgggggt aaagcagcac ctttacataa accacccgga aatggtgaag	360
gagcttagcc aaaccaacac acttaacctt ggtagaatca ctcacatcac caaacgcctt	420
aaccccatc tcggcaatgg catcatcacc tctaattggc ctcatgggc ccatcaacgt	480
cgtatcattg cctatgagtt taccacgac aaaatcaagg gaatggttg tttaatggtg	540
gaatctgcca tgccaatgtt gaacaaatgg gaagagatgg tgaaaagagg aggagaaatg	600
ggttgtagaca taagagtgga cgaagacctt aaggatgtct cagctgatgt catcgctaag	660
gcttgctttg ggagctcttt ttcaaaaggc aaagcaatat tctctatgat tagggatctt	720
ttaaccgcca ttactaaacg aagcgtcctc ttcagattca atggcttcac tgatatggtg	780
tttgaagta agaagcatgg tgatgtggat attgatgcgc ttgagatgga attagaatct	840
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ggtatgatgg aagtgaaagt gcttgtttca cttattgtct caaagttcag ttttactctt	1500
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gtcattaggg ttgtttga	1578

<210> 68

<211> 1590

<212> DNA

SeqLst

<213> vitis vinifera

<400> 68

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gctgctgctg catggcccat aatcgggtcac ctacacctgt tagctgggtgg ttctcatcag	180
cttccccaca taaccttggg aaacatggcc gacaaatatg gaccgggtctt cacaattcgg	240
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aactacgcca tgtttggttt ctctccatac ggttcttact ggcgtgaaat gcgcaagata	420
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aggatgggtgg caggggaagcg ttatttcagt gcttcagatg caagtgaaaa taaacaggcg	660
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ttcttacatg cgtttgaatt ttcaactcca tcaaatgaac aggtcaatat gcgcgagagc	1500
cttggactta caaatatgaa atctacccca cttgaagttc tcatttctcc acgcttatca	1560
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<210> 69

<211> 1440

<212> DNA

<213> Medicago trunculata

SeqLst

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<400> 69
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tacccaatca taggtgaaag ccttgagttc ttatcaacag gatggaaagg acatcctgaa      180
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ggagaatcta cggtggtttg ttgcgagca gcaagtaaca agtttttggt ttcaaacgag      300
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cacaatttgg tgaaaagggt taagtgggaa aagggtgattc cagatgagaa gattattggt     1380
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<210> 70

<211> 2133

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 70

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atgcaatcag attcagtcaa agtctctcca tttgatttgg tttccgctgc tatgaatggc      60
aaggcaatgg aaaagttgaa cgctagtgaa tctgaagatc caacaacatt gcctgcacta     120

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SeqLst

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ccagttccac	aagttatcgt	tgtaaagaag	aaagagaagg	agtcagaggt	tgatgacggg	300
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gatgactacg	ctgcagatga	tgatgaatat	gaggaaaaac	tgaaaaagga	atccttagcc	480
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gcattgtcag	aattgatcgt	cgcattttca	agagaaggga	ctgccaaaga	gtacgttcag	1920
cacaagatga	gtcaaaaagc	ctccgatata	tggaaaacttc	taagtgaagg	tgccatatctt	1980

	SeqLst	
tatgtctgtg gcgatgcaaa gggcatggcc aaggatgtcc atagaactct gcatacaatt		2040
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atgtctggaa gatacttaag agatgtttgg taa		2133

<210> 71
 <211> 2079
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

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ggtttcgttg tcttattgtg gaaaaagacc acggcagatc gttccggcga gctaaagcca		180
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actatagtcc aggaacagga aggcgttagt tcttctgaag cggaagcaat tgtgaaaaag		2040
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<210> 72

<211> 2142

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 72

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gctgcagggtg gtgcttccaa gcctggcaga actagaaaca tcgtcgaagc tatggaggaa	180
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gagagagatg atttgacccc tgaagcgaat gaggtatact tgggagaacc taataagcta	780
cacttggaag gtacagcgaa aggtccattc aactcccaca acccatatat cgcaccaatt	840

SeqLst						
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<210> 73

<211> 2133

<212> DNA

<213> Stevia rebaudiana

<400> 73

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ccggtgccgc	aggtaatcgt	tgtaagaag	aaagagaagg	agtctgaggt	tgatgatggc	300
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SeqLst							
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<210> 74
<211> 2079

SeqLst

<212> DNA

<213> *Arabidopsis thaliana*

<400> 74

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SeqLst

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accattgttc aggagcagga aggtgtgagt tcgtcagagg cagaggctat agttaagaaa	2040
cttcaaaccg aaggaagata cctcagagat gtctggtga	2079

<210> 75

<211> 2142

<212> DNA

<213> Giberella fujikuroi

<400> 75

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SeqLst

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<210> 76

<211> 459

<212> PRT

<213> Ipomoea purpurea

<400> 76

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Met Gly Ser Gln Ala Thr Thr Tyr His Met Ala Met Tyr Pro Trp Phe
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Gly Val Gly His Leu Thr Gly Phe Phe Arg Leu Ala Asn Lys Leu Ala
20          25          30

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

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Lys Leu Glu Ser Phe Asn Leu His Pro His Leu Ile Ser Phe Val Pro
50          55          60

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Ile Val Val Pro Ser Ile Pro Gly Leu Pro Pro Gly Ala Glu Thr Thr
65          70          75          80

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

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Lys Thr Gln Asn Asp Ile Glu Ile Ile Leu Lys Asp Leu Lys Val Asp
100         105         110

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Val Val Phe Tyr Asp Phe Thr His Trp Leu Pro Ser Leu Ala Arg Lys

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SeqLst															
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Glu	Ala	Asp	Met	Met	Lys	Ala	Pro	Ala	Ser	Phe	Pro	Asp	Pro	Ser	Ile
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Lys	Leu	His	Ala	His	Glu	Ala	Arg	Gly	Phe	Thr	Ala	Arg	Thr	Val	Met
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Lys	Phe	Gly	Gly	Asp	Ile	Thr	Phe	Phe	Asp	Arg	Ile	Phe	Thr	Ala	Val
		195					200					205			
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Lys	Glu	Lys	Ile	Gln	Gly	Arg	Gly	Ile	Val	His	Gly	Glu	Trp	Val	Gln
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Cys	Gly	Trp	Ala	Ser	Leu	Ser	Glu	Ala	Leu	Val	Asn	Asp	Cys	Gln	Ile
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SeqLst

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Ser Val Ser Leu Lys Val Gly Val Glu Val Glu Lys Gly Glu Glu Asp
 385 390 395 400

Gly Val Phe Ser Arg Glu Ser Val Cys Lys Ala Val Lys Ala Val Met
 405 410 415

Asp Glu Lys Ser Glu Ile Gly Arg Glu Val Arg Gly Asn His Asp Lys
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 450 455

<210> 77
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 <212> DNA
 <213> Ipomoea purpurea

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<212> PRT

<213> Bellis perennis

<400> 78

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Met Gln Tyr Leu Lys Asn Asn Leu Thr Ser Gln Tyr Ser Lys Ser Ile
50 55 60

Gln Leu Ile Glu Leu Asn Leu Pro Ser Ser Ser Glu Leu Pro Leu Gln
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Tyr His Thr Thr His Gly Leu Pro Pro His Leu Thr Lys Thr Leu Ser
85 90 95

Asp Asp Tyr Gln Lys Ser Gly Pro Asp Phe Glu Thr Ile Leu Ile Lys
100 105 110

Leu Asn Pro His Leu Val Ile Tyr Asp Phe Asn Gln Leu Trp Ala Pro
115 120 125

Glu Val Ala Ser Thr Leu His Ile Pro Ser Ile Gln Leu Leu Ser Gly
130 135 140

Cys Val Ala Leu Tyr Ala Leu Asp Ala His Leu Tyr Thr Lys Pro Leu
145 150 155 160

Asp Glu Asn Leu Ala Lys Phe Pro Phe Pro Glu Ile Tyr Pro Lys Asn
165 170 175

SeqLst

Arg Asp Ile Pro Lys Gly Gly Ser Lys Tyr Ile Glu Arg Phe Val Asp
 180 185 190
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 Leu Glu Gly Lys Tyr Ile Asp Tyr Leu Ser Lys Thr Leu Gly Lys Lys
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 Val Leu Pro Val Gly Pro Leu Val Gln Glu Ala Ser Leu Leu Gln Asp
 225 230 235 240
 Asp His Ile Trp Ile Met Lys Trp Leu Asp Lys Lys Glu Glu Ser Ser
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 Val Val Phe Val Cys Phe Gly Ser Glu Tyr Ile Leu Ser Asp Asn Glu
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 Ile Glu Asp Ile Ala Tyr Gly Leu Glu Leu Ser Gln Val Ser Phe Val
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 Val Gly Asp Lys Gly Leu Val Ile Asp Lys Trp Val Pro Gln Ala Asn
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SeqLst

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<212> DNA
<213> *Bellis perennis*

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<212> DNA
<213> *Zea mays*

<400> 80

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SeqLst

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<210> 81
 <211> 827
 <212> PRT
 <213> Zea mays

<400> 81
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Ala Arg Ala Gln His Thr Ser Glu Ser Ala Ala Val Ala Lys Gly Ser
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Ser Leu Thr Pro Ile Val Arg Thr Asp Ala Glu Ser Arg Arg Thr Arg
 65 70 75 80

Trp Pro Thr Asp Asp Asp Asp Ala Glu Pro Leu Val Asp Glu Ile Arg
 85 90 95

Ala Met Leu Thr Ser Met Ser Asp Gly Asp Ile Ser Val Ser Ala Tyr
 100 105 110

Asp Thr Ala Trp Val Gly Leu Val Pro Arg Leu Asp Gly Gly Glu Gly
 115 120 125

Pro Gln Phe Pro Ala Ala Val Arg Trp Ile Arg Asn Asn Gln Leu Pro
 130 135 140

SeqLst

Asp Gly Ser Trp Gly Asp Ala Ala Leu Phe Ser Ala Tyr Asp Arg Leu
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 165 170 175
 Pro Glu Met Arg Gly Arg Gly Leu Ser Phe Leu Gly Arg Asn Met Trp
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 Lys Leu Ala Thr Glu Asp Glu Glu Ser Met Pro Ile Gly Phe Glu Leu
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 Ala Phe Pro Ser Leu Ile Glu Leu Ala Lys Ser Leu Gly Val His Asp
 210 215 220
 Phe Pro Tyr Asp His Gln Ala Leu Gln Gly Ile Tyr Ser Ser Arg Glu
 225 230 235 240
 Ile Lys Met Lys Arg Ile Pro Lys Glu Val Met His Thr Val Pro Thr
 245 250 255
 Ser Ile Leu His Ser Leu Glu Gly Met Pro Gly Leu Asp Trp Ala Lys
 260 265 270
 Leu Leu Lys Leu Gln Ser Ser Asp Gly Ser Phe Leu Phe Ser Pro Ala
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 Ala Thr Ala Tyr Ala Leu Met Asn Thr Gly Asp Asp Arg Cys Phe Ser
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 Tyr Ile Asp Arg Thr Val Lys Lys Phe Asn Gly Gly Val Pro Asn Val
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 Tyr Pro Val Asp Leu Phe Glu His Ile Trp Ala Val Asp Arg Leu Glu
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 340 345 350
 Asp Tyr Val Asn Arg His Trp Thr Glu Asp Gly Ile Cys Trp Ala Arg
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 Asn Ser Asp Val Lys Glu Val Asp Asp Thr Ala Met Ala Phe Arg Leu
 370 375 380
 Leu Arg Leu His Gly Tyr Ser Val Ser Pro Asp Val Phe Lys Asn Phe
 385 390 395 400

SeqLst

Glu Lys Asp Gly Glu Phe Phe Ala Phe Val Gly Gln Ser Asn Gln Ala
 405 410 415
 Val Thr Gly Met Tyr Asn Leu Asn Arg Ala Ser Gln Ile Ser Phe Pro
 420 425 430
 Gly Glu Asp Val Leu His Arg Ala Gly Ala Phe Ser Tyr Glu Phe Leu
 435 440 445
 Arg Arg Lys Glu Ala Glu Gly Ala Leu Arg Asp Lys Trp Ile Ile Ser
 450 455 460
 Lys Asp Leu Pro Gly Glu Val Val Tyr Thr Leu Asp Phe Pro Trp Tyr
 465 470 475 480
 Gly Asn Leu Pro Arg Val Glu Ala Arg Asp Tyr Leu Glu Gln Tyr Gly
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 Gly Gly Asp Asp Val Trp Ile Gly Lys Thr Leu Tyr Arg Met Pro Leu
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 Val Asn Asn Asp Val Tyr Leu Glu Leu Ala Arg Met Asp Phe Asn His
 515 520 525
 Cys Gln Ala Leu His Gln Leu Glu Trp Gln Gly Leu Lys Arg Trp Tyr
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 Thr Glu Asn Arg Leu Met Asp Phe Gly Val Ala Gln Glu Asp Ala Leu
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 Thr Asp Ser Leu Ala Arg Glu Ala Gln Pro Ile His Gly Gly Asp Pro

SeqLst															
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Val	Glu 690	Gln	Glu	Gly	Ser	Arg 695	Met	Val	His	Asp	Lys 700	Gln	Thr	Cys	Leu
Leu 705	Leu	Ala	Arg	Met	Ile 710	Glu	Ile	Ser	Ala	Gly 715	Arg	Ala	Ala	Gly	Glu 720
Ala	Ala	Ser	Glu	Asp 725	Gly	Asp	Arg	Arg	Ile 730	Ile	Gln	Leu	Thr	Gly 735	Ser
Ile	Cys	Asp	Ser 740	Leu	Lys	Gln	Lys	Met 745	Leu	Val	Ser	Gln	Asp 750	Pro	Glu
Lys	Asn	Glu 755	Glu	Met	Met	Ser	His 760	Val	Asp	Asp	Glu	Leu 765	Lys	Leu	Arg
Ile	Arg 770	Glu	Phe	Val	Gln	Tyr 775	Leu	Leu	Arg	Leu	Gly 780	Glu	Lys	Lys	Thr
Gly 785	Ser	Ser	Glu	Thr	Arg 790	Gln	Thr	Phe	Leu	Ser 795	Ile	Val	Lys	Ser	Cys 800
Tyr	Tyr	Ala	Ala	His 805	Cys	Pro	Pro	His	Val 810	Val	Asp	Arg	His	Ile 815	Ser
Arg	Val	Ile	Phe 820	Glu	Pro	Val	Ser	Ala 825	Ala	Lys					

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<211> 1398

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

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ggtgtaaaga caaactgggt aaccactatc cacactttga attctactct gaaccactca		180
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	SeqLst	
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 <211> 1437
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

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gctgaaaaag gacataaagt gtcattcctt tcaacaacta gaaacattca aagattatct		180
ttccacatat caccattgat taacgtcggt caattgacac ttccaagagt acaggaatta		240
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SeqLst						
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gttggaaattg	aaatcccacg	taatgaggaa	gatggatgtt	taaccaagga	gtctgtggcc	1260
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gaactttcaa	agatctacaa	tgacacaaaa	gtagagaagg	aatatgtttc	tcaatttgta	1380
gattacctag	agaaaaacgc	tagagccgta	gctattgatc	atgaatccta	agtcgac	1437

<210> 85

<211> 1392

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 85

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tctaaagggt	tttctattac	aatctttcac	accaattttca	acaaacaaaa	aacatccaat	180
taccacacatt	tcacattcag	attcatactt	gataatgatc	cacaagatga	acgtattttca	240
aacttaccta	cccacgggtc	tttagctgga	atgagaattc	caatcatcaa	tgaacatggg	300
gccgatgagc	ttagaagaga	attagagtta	cttatgttgg	catccgaaga	ggacgaggaa	360
gtctcttgtc	tgattactga	cgctctatgg	tactttgccc	aatctgtggc	tgatagtttg	420
aatttgagga	gattgggtact	aatgacatcc	agtctgttta	actttcacgc	tcatgttagt	480

				SeqLst	
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aagtttagcac	aactattaca	ccataaggg	ga	ttacagataa	ctttcgtgaa taccgacttc 300
atccataatc	aatttctgga	atctagtgg	c	cctcattggt	tggacggagc cccaggggtt 360
agattcgaaa	caattcctga	cggtgtttca	cattccccag	aggcctccat	cccaataaga 420
gagagtttac	tgagggtcaat	agaaaccaac	tttttggatc	gtttcattga	cttggtcaca 480
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ttcatgggtt	tctatcacat	ccattctctt	atcgaaaagg	gttttgctcc	actgaaagat 660
gcatcatact	taaccaacgg	ctacctggat	actggttattg	actgggtacc	aggtatggaa 720
gggtataagac	ttaaagattt	tcctttggat	tgggtctacag	accttaatga	taaagtattg 780
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gcaggagttc	caatgatattg	ttggccatat	tcatgggacc	aacttacaaa	ttgtaggtat 1380
atctgtaaag	agtgggaagt	tggattagaa	atgggaacaa	aggttaaacg	tgatgaagtg 1440
aaaagattgg	ttcaggagtt	gatgggggaa	gggtggccaca	agatgagaaa	caaggccaaa 1500
gattggaagg	aaaaagccag	aattgctatt	gctcctaacg	ggtcatcctc	tctaaacatt 1560
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<210> 88

<211> 533

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 88

Met	Thr	Ser	Phe	Ala	Glu	Tyr	Trp	Asn	Leu	Leu	Ser	Pro	Thr	Ser	Phe
1				5					10					15	

SeqLst

Ala Glu Tyr Trp Asn Leu Leu Ser Pro Thr Ser Phe Ala Glu Tyr Trp
20 25 30

Asn Leu Phe Ser Pro Thr Ser Phe Ala Glu Tyr Trp Asn Leu Leu Ser
35 40 45

Pro Ala Ser Lys Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His
50 55 60

Val Ile Phe Ile Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu
65 70 75 80

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

Asn Thr Asp Phe Ile His Asn Gln Phe Leu Glu Ser Ser Gly Pro His
100 105 110

Cys Leu Asp Gly Ala Pro Gly Phe Arg Phe Glu Thr Ile Pro Asp Gly
115 120 125

Val Ser His Ser Pro Glu Ala Ser Ile Pro Ile Arg Glu Ser Leu Leu
130 135 140

Arg Ser Ile Glu Thr Asn Phe Leu Asp Arg Phe Ile Asp Leu Val Thr
145 150 155 160

Lys Leu Pro Asp Pro Pro Thr Cys Ile Ile Ser Asp Gly Phe Leu Ser
165 170 175

Val Phe Thr Ile Asp Ala Ala Lys Lys Leu Gly Ile Pro Val Met Met
180 185 190

Tyr Trp Thr Leu Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His
195 200 205

Ser Leu Ile Glu Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu
210 215 220

Thr Asn Gly Tyr Leu Asp Thr Val Ile Asp Trp Val Pro Gly Met Glu
225 230 235 240

Gly Ile Arg Leu Lys Asp Phe Pro Leu Asp Trp Ser Thr Asp Leu Asn
245 250 255

Asp Lys Val Leu Met Phe Thr Thr Glu Ala Pro Gln Arg Ser His Lys
260 265 270

SeqLst

Val Ser His His Ile Phe His Thr Phe Asp Glu Leu Glu Pro Ser Ile
 275 280 285
 Ile Lys Thr Leu Ser Leu Arg Tyr Asn His Ile Tyr Thr Ile Gly Pro
 290 295 300
 Leu Gln Leu Leu Leu Asp Gln Ile Pro Glu Glu Lys Lys Gln Thr Gly
 305 310 315 320
 Ile Thr Ser Leu His Gly Tyr Ser Leu Val Lys Glu Glu Pro Glu Cys
 325 330 335
 Phe Gln Trp Leu Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn
 340 345 350
 Phe Gly Ser Thr Thr Val Met Ser Leu Glu Asp Met Thr Glu Phe Gly
 355 360 365
 Trp Gly Leu Ala Asn Ser Asn His Tyr Phe Leu Trp Ile Ile Arg Ser
 370 375 380
 Asn Leu Val Ile Gly Glu Asn Ala Val Leu Pro Pro Glu Leu Glu Glu
 385 390 395 400
 His Ile Lys Lys Arg Gly Phe Ile Ala Ser Trp Cys Ser Gln Glu Lys
 405 410 415
 Val Leu Lys His Pro Ser Val Gly Gly Phe Leu Thr His Cys Gly Trp
 420 425 430
 Gly Ser Thr Ile Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp
 435 440 445
 Pro Tyr Ser Trp Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu
 450 455 460
 Trp Glu Val Gly Leu Glu Met Gly Thr Lys Val Lys Arg Asp Glu Val
 465 470 475 480
 Lys Arg Leu Val Gln Glu Leu Met Gly Glu Gly Gly His Lys Met Arg
 485 490 495
 Asn Lys Ala Lys Asp Trp Lys Glu Lys Ala Arg Ile Ala Ile Ala Pro
 500 505 510
 Asn Gly Ser Ser Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr
 515 520 525

SeqLst

Val Leu Ala Arg Asn
530

<210> 89
<211> 1893
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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<400> 89
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gttggtgcac aaaaagacac ttatactatg aaagaggttc ttttttatct tggccagtat      180
attatgacta aacgattata tgatgagaag caacaacata ttgtatattg ttcaaattgat      240
cttctaggag atttgtttgg cgtgccaaagc ttctctgtga aagagcacag gaaaatatat      300
accatgatct acaggaactt ggtagtagtc aatcagcagg aatcatcgga cttaggtaca      360
tctgtgagtg agaacagggtg tcaccttgaa ggtgggagtg atcaaaagga ccttgtacaa      420
gagcttcagg aagagaaacc ttcattctca catttggttt ctagaccatc taccggtggt      480
agcggatcct ctggaggcag tgctagtaaa atggcagagc aacaaaagat caaaaagtca      540
cctcacgtct tacttattcc atttcctctg caaggacata tcaaccatt catacaattt      600
gggaaaagat tgattagtaa ggggtgtaaag acaacactgg taaccactat ccacactttg      660
aattctactc tgaaccactc aaatactact actacaagta tagaaattca agctatatca      720
gacggatgcg atgaggggtg ctttatgtct gccggtgaat ctacttgga aacattcaag      780
caagtgggat ccaagtctct ggccgatcta atcaaaaagt tacagagtga aggcaccaca      840
attgacgcca taatctacga ttctatgaca gagtgggttt tagacgttgc tatcgaattt      900
ggtattgatg gaggttcctt tttcacacaa gcatgtgttg tgaattctct atactaccat      960
gtgcataaag ggttaatctc ttaccattg ggtgaaactg tttcagttcc aggttttcca     1020
gtgttacaac gttgggaaac cccattgatc ttacaaaatc atgaacaaat acaatcacct     1080
tggtcccaga tgttgtttgg tcaattcgct aacatcgatc aagcaagatg ggtctttact     1140
aattcattct ataagttaga ggaagaggta attgaatgga ctaggaagat ctggaatttg     1200
aaagtcattg gtccaacatt gccatcaatg tatttggaac aaagacttga tgatgataaa     1260
gataatgggt tcaatttgta caaggcta atcatcgaat gtatgaattg gctggatgac     1320
aaaccaaagg aatcagttgt atatgttgct ttcggctctc ttgttaaaca tgggtccagaa     1380
caagttgagg agattacaag agcacttata gactctgacg taaacttttt gtgggtcatt     1440

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SeqLst

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aagcacaag aggaggggaa actgccagaa aacctttctg aagtgataaa gaccggaaaa 1500
ggctctaatcg ttgcttggtg taaacaattg gatgttttag ctcatgaatc tgtaggctgt 1560
tttgtaacac attgcggatt caactctaca ctagaagcca tttccttagg cgtacctgtc 1620
gttgcaatgc ctcatgtctc cgatcagaca accaacgcta aacttttgga cgaaatacta 1680
ggggtgggtg tcagagttaa agcagacgag aatggtatcg tcagaagagg gaacctagct 1740
tcattgtatca aaatgatcat ggaagaggaa agaggagtta tcataaggaa aaacgcagtt 1800
aagtggaagg atcttgcaaa ggttgccgtc catgaaggcg gctcttcaga taatgatatt 1860
gttgaatttg tgtccgaact aatcaaagcc taa 1893

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<210> 90

<211> 630

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 90

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Met Cys Asn Thr Asn Met Ser Val Pro Thr Asp Gly Ala Val Thr Thr
1           5           10           15

```

```

Ser Gln Ile Pro Ala Ser Glu Gln Glu Thr Leu Val Arg Pro Lys Pro
                20           25           30

```

```

Leu Leu Leu Lys Leu Leu Lys Ser Val Gly Ala Gln Lys Asp Thr Tyr
35           40           45

```

```

Thr Met Lys Glu Val Leu Phe Tyr Leu Gly Gln Tyr Ile Met Thr Lys
50           55           60

```

```

Arg Leu Tyr Asp Glu Lys Gln Gln His Ile Val Tyr Cys Ser Asn Asp
65           70           75           80

```

```

Leu Leu Gly Asp Leu Phe Gly Val Pro Ser Phe Ser Val Lys Glu His
85           90           95

```

```

Arg Lys Ile Tyr Thr Met Ile Tyr Arg Asn Leu Val Val Val Asn Gln
100           105           110

```

```

Gln Glu Ser Ser Asp Ser Gly Thr Ser Val Ser Glu Asn Arg Cys His
115           120           125

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```

Leu Glu Gly Gly Ser Asp Gln Lys Asp Leu Val Gln Glu Leu Gln Glu
130           135           140

```

SeqLst

Glu Lys Pro Ser Ser Ser His Leu Val Ser Arg Pro Ser Thr Gly Gly
 145 150 155 160
 Ser Gly Ser Ser Gly Gly Ser Ala Ser Lys Met Ala Glu Gln Gln Lys
 165 170 175
 Ile Lys Lys Ser Pro His Val Leu Leu Ile Pro Phe Pro Leu Gln Gly
 180 185 190
 His Ile Asn Pro Phe Ile Gln Phe Gly Lys Arg Leu Ile Ser Lys Gly
 195 200 205
 Val Lys Thr Thr Leu Val Thr Thr Ile His Thr Leu Asn Ser Thr Leu
 210 215 220
 Asn His Ser Asn Thr Thr Thr Thr Ser Ile Glu Ile Gln Ala Ile Ser
 225 230 235 240
 Asp Gly Cys Asp Glu Gly Gly Phe Met Ser Ala Gly Glu Ser Tyr Leu
 245 250 255
 Glu Thr Phe Lys Gln Val Gly Ser Lys Ser Leu Ala Asp Leu Ile Lys
 260 265 270
 Lys Leu Gln Ser Glu Gly Thr Thr Ile Asp Ala Ile Ile Tyr Asp Ser
 275 280 285
 Met Thr Glu Trp Val Leu Asp Val Ala Ile Glu Phe Gly Ile Asp Gly
 290 295 300
 Gly Ser Phe Phe Thr Gln Ala Cys Val Val Asn Ser Leu Tyr Tyr His
 305 310 315 320
 Val His Lys Gly Leu Ile Ser Leu Pro Leu Gly Glu Thr Val Ser Val
 325 330 335
 Pro Gly Phe Pro Val Leu Gln Arg Trp Glu Thr Pro Leu Ile Leu Gln
 340 345 350
 Asn His Glu Gln Ile Gln Ser Pro Trp Ser Gln Met Leu Phe Gly Gln
 355 360 365
 Phe Ala Asn Ile Asp Gln Ala Arg Trp Val Phe Thr Asn Ser Phe Tyr
 370 375 380
 Lys Leu Glu Glu Glu Val Ile Glu Trp Thr Arg Lys Ile Trp Asn Leu
 385 390 395 400

SeqLst

Lys Val Ile Gly Pro Thr Leu Pro Ser Met Tyr Leu Asp Lys Arg Leu
 405 410 415
 Asp Asp Asp Lys Asp Asn Gly Phe Asn Leu Tyr Lys Ala Asn His His
 420 425 430
 Glu Cys Met Asn Trp Leu Asp Asp Lys Pro Lys Glu Ser Val Val Tyr
 435 440 445
 Val Ala Phe Gly Ser Leu Val Lys His Gly Pro Glu Gln Val Glu Glu
 450 455 460
 Ile Thr Arg Ala Leu Ile Asp Ser Asp Val Asn Phe Leu Trp Val Ile
 465 470 475 480
 Lys His Lys Glu Glu Gly Lys Leu Pro Glu Asn Leu Ser Glu Val Ile
 485 490 495
 Lys Thr Gly Lys Gly Leu Ile Val Ala Trp Cys Lys Gln Leu Asp Val
 500 505 510
 Leu Ala His Glu Ser Val Gly Cys Phe Val Thr His Cys Gly Phe Asn
 515 520 525
 Ser Thr Leu Glu Ala Ile Ser Leu Gly Val Pro Val Val Ala Met Pro
 530 535 540
 Gln Phe Ser Asp Gln Thr Thr Asn Ala Lys Leu Leu Asp Glu Ile Leu
 545 550 555 560
 Gly Val Gly Val Arg Val Lys Ala Asp Glu Asn Gly Ile Val Arg Arg
 565 570 575
 Gly Asn Leu Ala Ser Cys Ile Lys Met Ile Met Glu Glu Glu Arg Gly
 580 585 590
 Val Ile Ile Arg Lys Asn Ala Val Lys Trp Lys Asp Leu Ala Lys Val
 595 600 605
 Ala Val His Glu Gly Gly Ser Ser Asp Asn Asp Ile Val Glu Phe Val
 610 615 620
 Ser Glu Leu Ile Lys Ala
 625 630

<210> 91

SeqLst

<211> 1932

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 91

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gttggtgcac aaaaagacac ttatactatg aaagagggtc ttttttatct tggccagtat	180
attatgacta aacgattata tgatgagaag caacaacata ttgtatattg ttcaaagtat	240
cttctaggag atttggttg cgtgccaagc ttctctgtga aagagcacag gaaaatatat	300
accatgatct acaggaactt ggtagtagtc aatcagcagg aatcatcgga cttaggtaca	360
tctgtgagtg agaacagggtg tcaccttgaa ggtgggagtg atcaaaagga ccttgtacaa	420
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agcggatcct ctggaggcag tgctagtaaa atggctacat ctgattctat tgttgatgac	540
aggaagcagt tgcattgtgg tactttccct tggcttgctt tcggtcatat actgccttac	600
ctacaactat caaaactgat agctgaaaaa ggacataaag tgtcattcct ttcaacaact	660
agaaacattc aaagattatc ttccacata tcaccattga ttaacgtcgt tcaattgaca	720
cttccaagag tacaggaatt accagaagat gctgaagcta caacagatgt gcatcctgaa	780
gatatccctt acttgaaaaa ggcattccgat ggattacagc ctgaggtcac tagattcctt	840
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tacatgggtc catccgctga tgctatgatt aacggcagtg atggtagaac taccgttgaa	1020
gatttgacaa cccaccaa gtggtttcca tttccaacta aagtctgttg gagaaaacac	1080
gacttagcaa gactggttcc atacaaggca ccaggaatct cagacggcta tagaatgggt	1140
ttagtcctta aagggtctga ctgcctattg tctaagtgtt accatgagtt tgggacacaa	1200
tggctaccac ttttggaac attacaccaa gttcctgtcg taccagttgg tctattacct	1260
ccagaaatcc ctggtgatga gaaggacgag acttgggttt caatcaaaaa gtgggttagac	1320
gggaagcaaa aaggctcagt ggtatatgtg gcaactgggt ccgaagtgtt agtatctcaa	1380
acagaagttg tggaacttgc cttaggtttg gaactatctg gattgccatt tgtctgggcc	1440
tacagaaaac caaaaggccc tgcaaagtcc gattcagttg aattgccaga cggctttgtc	1500
gagagaacta gagatagagg gttggtatgg acttcatggg ctccacaatt gagaatcctg	1560
agtcacgaat ctgtgtgcgg tttcctaaca cattgtggtt ctggttctat agttgaagga	1620

SeqLst

ctgatgtttg gtcattccact tatcatgttg ccaatctttg gtgaccagcc tttgaatgca	1680
cgtctgttag aagataaaca agttggaatt gaaatccac gtaatgagga agatggatgt	1740
ttaaccaagg agtctgtggc cagatcatta cgttccgttg tcgttgaaaa ggaaggcgaa	1800
atctacaagg ccaatgcccg tgaactttca aagatctaca atgacacaaa agtagagaag	1860
gaatatgttt ctcaatttgt agattaccta gagaaaaacg ctagagccgt agctattgat	1920
catgaatcct aa	1932

<210> 92
 <211> 643
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 92
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 20 25 30

Leu Leu Leu Lys Leu Leu Lys Ser Val Gly Ala Gln Lys Asp Thr Tyr
 35 40 45

Thr Met Lys Glu Val Leu Phe Tyr Leu Gly Gln Tyr Ile Met Thr Lys
 50 55 60

Arg Leu Tyr Asp Glu Lys Gln Gln His Ile Val Tyr Cys Ser Asn Asp
 65 70 75 80

Leu Leu Gly Asp Leu Phe Gly Val Pro Ser Phe Ser Val Lys Glu His
 85 90 95

Arg Lys Ile Tyr Thr Met Ile Tyr Arg Asn Leu Val Val Val Asn Gln
 100 105 110

Gln Glu Ser Ser Asp Ser Gly Thr Ser Val Ser Glu Asn Arg Cys His
 115 120 125

Leu Glu Gly Gly Ser Asp Gln Lys Asp Leu Val Gln Glu Leu Gln Glu
 130 135 140

Glu Lys Pro Ser Ser Ser His Leu Val Ser Arg Pro Ser Thr Gly Gly
 145 150 155 160

SeqLst

Ser Gly Ser Ser Gly Gly Ser Ala Ser Lys Met Ala Thr Ser Asp Ser
165 170 175

Ile Val Asp Asp Arg Lys Gln Leu His Val Ala Thr Phe Pro Trp Leu
180 185 190

Ala Phe Gly His Ile Leu Pro Tyr Leu Gln Leu Ser Lys Leu Ile Ala
195 200 205

Glu Lys Gly His Lys Val Ser Phe Leu Ser Thr Thr Arg Asn Ile Gln
210 215 220

Arg Leu Ser Ser His Ile Ser Pro Leu Ile Asn Val Val Gln Leu Thr
225 230 235 240

Leu Pro Arg Val Gln Glu Leu Pro Glu Asp Ala Glu Ala Thr Thr Asp
245 250 255

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

Gln Pro Glu Val Thr Arg Phe Leu Glu Gln His Ser Pro Asp Trp Ile
275 280 285

Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro Ser Ile Ala Ala Ser Leu
290 295 300

Gly Ile Ser Arg Ala His Phe Ser Val Thr Thr Pro Trp Ala Ile Ala
305 310 315 320

Tyr Met Gly Pro Ser Ala Asp Ala Met Ile Asn Gly Ser Asp Gly Arg
325 330 335

Thr Thr Val Glu Asp Leu Thr Thr Pro Pro Lys Trp Phe Pro Phe Pro
340 345 350

Thr Lys Val Cys Trp Arg Lys His Asp Leu Ala Arg Leu Val Pro Tyr
355 360 365

Lys Ala Pro Gly Ile Ser Asp Gly Tyr Arg Met Gly Leu Val Leu Lys
370 375 380

Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr His Glu Phe Gly Thr Gln
385 390 395 400

Trp Leu Pro Leu Leu Glu Thr Leu His Gln Val Pro Val Val Pro Val
405 410 415

SeqLst

Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp Glu Lys Asp Glu Thr Trp
 420 425 430

Val Ser Ile Lys Lys Trp Leu Asp Gly Lys Gln Lys Gly Ser Val Val
 435 440 445

Tyr Val Ala Leu Gly Ser Glu Val Leu Val Ser Gln Thr Glu Val Val
 450 455 460

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

Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser Asp Ser Val Glu Leu Pro
 485 490 495

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

Trp Ala Pro Gln Leu Arg Ile Leu Ser His Glu Ser Val Cys Gly Phe
 515 520 525

Leu Thr His Cys Gly Ser Gly Ser Ile Val Glu Gly Leu Met Phe Gly
 530 535 540

His Pro Leu Ile Met Leu Pro Ile Phe Gly Asp Gln Pro Leu Asn Ala
 545 550 555 560

Arg Leu Leu Glu Asp Lys Gln Val Gly Ile Glu Ile Pro Arg Asn Glu
 565 570 575

Glu Asp Gly Cys Leu Thr Lys Glu Ser Val Ala Arg Ser Leu Arg Ser
 580 585 590

Val Val Val Glu Lys Glu Gly Glu Ile Tyr Lys Ala Asn Ala Arg Glu
 595 600 605

Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val Glu Lys Glu Tyr Val Ser
 610 615 620

Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala Arg Ala Val Ala Ile Asp
 625 630 635 640

His Glu Ser

<210> 93
 <211> 1887

SeqLst

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 93

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gttggtgcac aaaaagacac ttatactatg aaagagggtc ttttttatct tggccagtat	180
attatgacta aacgattata tgatgagaag caacaacata ttgtatattg ttcaaattgat	240
cttctaggag atttgtttgg cgtgccaaagc ttctctgtga aagagcacag gaaaatatat	300
accatgatct acaggaactt ggtagtagtc aatcagcagg aatcatcgga cttaggtaca	360
tctgtgagtg agaacagggtg tcaccttgaa ggtgggagtg atcaaaagga ccttgtacaa	420
gagcttcagg aagagaaacc ttcattctca catttggttt ctagaccatc taccggtggt	480
agcggatcct ctggaggcag tgctagtaaa atggaaaaca agaccgaaac aacagttaga	540
cgtaggcgta gaatcattct gtttccagta ctttttcaag ggcacatcaa tccaatacta	600
caactagcca acgttttgta ctctaaaggc ttttctatta caatctttca caccaatttc	660
aacaaaccaa aaacatccaa ttaccacat ttcacattca gattcatact tgataatgat	720
ccacaagatg aacgtatttc aaacttacct acccacggtc ctttagctgg aatgagaatt	780
ccaatcatca atgaacatgg tgccgatgag cttagaagag aattagagtt acttatgttg	840
gcatccgaag aggacgagga agtctcttgt ctgattactg acgctctatg gtactttgcc	900
caatctgtgg ctgatagttt gaatttgagg agattggtac taatgacatc cagtctgttt	960
aactttcacg ctcatgttag ttaccacaa ttgacgaat tgggatactt ggaccctgat	1020
gacaagacta ggtagagga acaggcctct ggttttccta tgttgaaagt caaagatatc	1080
aagtctgcct attctaattg gcaaatcttg aaagagatct taggaaagat gatcaaacag	1140
acaaaggctt catctggagt gatttggaa agtttcaaag agttagaaga gtctgaattg	1200
gagactgtaa tcagagaaat tccagcacct tcattcctga taccattacc aaaacatttg	1260
actgcttcct cttcctcttt gttggatcat gacagaacag tttttcaatg gttggaccaa	1320
caaccaccta gttctgtttt gtacgtgtca tttggtagta cttctgaagt cgatgaaaag	1380
gacttccttg aaatcgcaag aggcttagtc gatagtaagc agtcattcct ttgggtcgtg	1440
cgtccagggt tcgtgaaagg ctcaacatgg gtcgaaccac ttccagatgg ttttctaggc	1500
gaaagaggta gaatagtcaa atgggttcct caacaggaag ttttagctca tggcgctatt	1560
ggggcattct ggactcattc cggatggaat tcaactttag aatcagtatg cgaaggggta	1620
cctatgatct tttcagattt tggctttgat caaccactga acgcaagata catgtctgat	1680

SeqLst

gttttgaaag tgggtgtata tctagaaaat ggctgggaaa ggggtgaaat agctaatagca 1740
 ataagacgtg ttatggttga tgaagagggg gagtatatca gacaaaacgc aagagtgtctg 1800
 aagcaaaagg ccgacgtttc tctaatagaag ggaggctctt catacgaatc cttagaatct 1860
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<210> 94

<211> 628

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 94

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Ser Gln Ile Pro Ala Ser Glu Gln Glu Thr Leu Val Arg Pro Lys Pro
 20 25 30

Leu Leu Leu Lys Leu Leu Lys Ser Val Gly Ala Gln Lys Asp Thr Tyr
 35 40 45

Thr Met Lys Glu Val Leu Phe Tyr Leu Gly Gln Tyr Ile Met Thr Lys
 50 55 60

Arg Leu Tyr Asp Glu Lys Gln Gln His Ile Val Tyr Cys Ser Asn Asp
 65 70 75 80

Leu Leu Gly Asp Leu Phe Gly Val Pro Ser Phe Ser Val Lys Glu His
 85 90 95

Arg Lys Ile Tyr Thr Met Ile Tyr Arg Asn Leu Val Val Val Asn Gln
 100 105 110

Gln Glu Ser Ser Asp Ser Gly Thr Ser Val Ser Glu Asn Arg Cys His
 115 120 125

Leu Glu Gly Gly Ser Asp Gln Lys Asp Leu Val Gln Glu Leu Gln Glu
 130 135 140

Glu Lys Pro Ser Ser Ser His Leu Val Ser Arg Pro Ser Thr Gly Gly
 145 150 155 160

Ser Gly Ser Ser Gly Gly Ser Ala Ser Lys Met Glu Asn Lys Thr Glu
 165 170 175

SeqLst

Thr Thr Val Arg Arg Arg Arg Arg Ile Ile Leu Phe Pro Val Pro Phe
 180 185 190
 Gln Gly His Ile Asn Pro Ile Leu Gln Leu Ala Asn Val Leu Tyr Ser
 195 200 205
 Lys Gly Phe Ser Ile Thr Ile Phe His Thr Asn Phe Asn Lys Pro Lys
 210 215 220
 Thr Ser Asn Tyr Pro His Phe Thr Phe Arg Phe Ile Leu Asp Asn Asp
 225 230 235 240
 Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro Thr His Gly Pro Leu Ala
 245 250 255
 Gly Met Arg Ile Pro Ile Ile Asn Glu His Gly Ala Asp Glu Leu Arg
 260 265 270
 Arg Glu Leu Glu Leu Leu Met Leu Ala Ser Glu Glu Asp Glu Glu Val
 275 280 285
 Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr Phe Ala Gln Ser Val Ala
 290 295 300
 Asp Ser Leu Asn Leu Arg Arg Leu Val Leu Met Thr Ser Ser Leu Phe
 305 310 315 320
 Asn Phe His Ala His Val Ser Leu Pro Gln Phe Asp Glu Leu Gly Tyr
 325 330 335
 Leu Asp Pro Asp Asp Lys Thr Arg Leu Glu Glu Gln Ala Ser Gly Phe
 340 345 350
 Pro Met Leu Lys Val Lys Asp Ile Lys Ser Ala Tyr Ser Asn Trp Gln
 355 360 365
 Ile Leu Lys Glu Ile Leu Gly Lys Met Ile Lys Gln Thr Lys Ala Ser
 370 375 380
 Ser Gly Val Ile Trp Asn Ser Phe Lys Glu Leu Glu Glu Ser Glu Leu
 385 390 395 400
 Glu Thr Val Ile Arg Glu Ile Pro Ala Pro Ser Phe Leu Ile Pro Leu
 405 410 415
 Pro Lys His Leu Thr Ala Ser Ser Ser Ser Leu Leu Asp His Asp Arg
 420 425 430

SeqLst

Thr Val Phe Gln Trp Leu Asp Gln Gln Pro Pro Ser Ser Val Leu Tyr
 435 440 445

Val Ser Phe Gly Ser Thr Ser Glu Val Asp Glu Lys Asp Phe Leu Glu
 450 455 460

Ile Ala Arg Gly Leu Val Asp Ser Lys Gln Ser Phe Leu Trp Val Val
 465 470 475 480

Arg Pro Gly Phe Val Lys Gly Ser Thr Trp Val Glu Pro Leu Pro Asp
 485 490 495

Gly Phe Leu Gly Glu Arg Gly Arg Ile Val Lys Trp Val Pro Gln Gln
 500 505 510

Glu Val Leu Ala His Gly Ala Ile Gly Ala Phe Trp Thr His Ser Gly
 515 520 525

Trp Asn Ser Thr Leu Glu Ser Val Cys Glu Gly Val Pro Met Ile Phe
 530 535 540

Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn Ala Arg Tyr Met Ser Asp
 545 550 555 560

Val Leu Lys Val Gly Val Tyr Leu Glu Asn Gly Trp Glu Arg Gly Glu
 565 570 575

Ile Ala Asn Ala Ile Arg Arg Val Met Val Asp Glu Glu Gly Glu Tyr
 580 585 590

Ile Arg Gln Asn Ala Arg Val Leu Lys Gln Lys Ala Asp Val Ser Leu
 595 600 605

Met Lys Gly Gly Ser Ser Tyr Glu Ser Leu Glu Ser Leu Val Ser Tyr
 610 615 620

Ile Ser Ser Leu
 625

<210> 95

<211> 473

<212> PRT

<213> Stevia rebaudiana

<400> 95

Met Ala Thr Ser Asp Ser Ile Val Asp Asp Arg Lys Gln Leu His Val
 1 5 10 15

SeqLst

Ala Thr Phe Pro Trp Leu Ala Phe Gly His Ile Leu Pro Tyr Leu Gln
 20 25 30
 Leu Ser Lys Leu Ile Ala Glu Lys Gly His Lys Val Ser Phe Leu Ser
 35 40 45
 Thr Thr Arg Asn Ile Gln Arg Leu Ser Ser His Ile Ser Pro Leu Ile
 50 55 60
 Asn Val Val Gln Leu Thr Leu Pro Arg Val Gln Glu Leu Pro Glu Asp
 65 70 75 80
 Ala Glu Ala Thr Thr Asp Val His Pro Glu Asp Ile Pro Tyr Leu Lys
 85 90 95
 Lys Ala Ser Asp Gly Leu Gln Pro Glu Val Thr Arg Phe Leu Glu Gln
 100 105 110
 His Ser Pro Asp Trp Ile Ile Tyr Asp Tyr Thr His Tyr Trp Leu Pro
 115 120 125
 Ser Ile Ala Ala Ser Leu Gly Ile Ser Arg Ala His Phe Ser Val Thr
 130 135 140
 Thr Pro Trp Ala Ile Ala Tyr Met Gly Pro Ser Ala Asp Ala Met Ile
 145 150 155 160
 Asn Gly Ser Asp Gly Arg Thr Thr Val Glu Asp Leu Thr Thr Pro Pro
 165 170 175
 Lys Trp Phe Pro Phe Pro Thr Lys Val Cys Trp Arg Lys His Asp Leu
 180 185 190
 Ala Arg Leu Val Pro Tyr Lys Ala Pro Gly Ile Ser Asp Arg Cys Arg
 195 200 205
 Met Gly Leu Val Leu Lys Gly Ser Asp Cys Leu Leu Ser Lys Cys Tyr
 210 215 220
 His Glu Phe Gly Thr Gln Trp Leu Pro Leu Leu Glu Thr Leu His Gln
 225 230 235 240
 Val Pro Val Val Pro Val Gly Leu Leu Pro Pro Glu Ile Pro Gly Asp
 245 250 255
 Glu Lys Asp Glu Thr Trp Val Ser Ile Lys Lys Trp Leu Asp Gly Lys
 260 265 270

SeqLst

Gln Lys Gly Ser Val Val Tyr Val Ala Leu Gly Ser Glu Val Leu Val
 275 280 285

Ser Gln Thr Glu Val Val Glu Leu Ala Leu Gly Leu Glu Leu Ser Gly
 290 295 300

Leu Pro Phe Val Trp Ala Tyr Arg Lys Pro Lys Gly Pro Ala Lys Ser
 305 310 315 320

Asp Ser Val Glu Leu Pro Asp Gly Phe Val Glu Arg Thr Arg Asp Arg
 325 330 335

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

Glu Ser Val Cys Gly Phe Leu Thr His Cys Gly Ser Gly Ser Ile Val
 355 360 365

Glu Gly Leu Met Phe Gly His Pro Leu Ile Met Leu Pro Ile Phe Gly
 370 375 380

Asp Gln Pro Leu Asn Ala Arg Leu Leu Glu Asp Lys Gln Val Gly Ile
 385 390 395 400

Glu Ile Pro Arg Asn Glu Glu Asp Gly Cys Leu Thr Lys Glu Ser Val
 405 410 415

Ala Arg Ser Leu Arg Ser Val Val Val Glu Lys Glu Gly Glu Ile Tyr
 420 425 430

Lys Ala Asn Ala Arg Glu Leu Ser Lys Ile Tyr Asn Asp Thr Lys Val
 435 440 445

Glu Lys Glu Tyr Val Ser Gln Phe Val Asp Tyr Leu Glu Lys Asn Ala
 450 455 460

Arg Ala Val Ala Ile Asp His Glu Ser
 465 470

<210> 96

<211> 1422

<212> DNA

<213> Stevia rebaudiana

<400> 96

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tggcttgctt tcggtcacat cctcccttac cttcagcttt cgaaattgat agctgaaaag 120

SeqLst

ggtcacaaag tctcgtttct ttctaccacc agaaacattc aacgtctctc ttctcatatc	180
tcgccactca taaatgttgt tcaactcaca cttccacgtg tccaagagct gccggaggat	240
gcagaggcga cactgacgt ccaccctgaa gatattccat atctcaagaa ggcttctgat	300
ggctttcaac cggagggtcac ccggtttcta gaacaacact ctccggactg gattatttat	360
gattatactc actactgggt gccatccatc gcggctagcc tcggtatctc acgagcccac	420
ttctccgtca cactccatg ggccattgct tatatgggac cctcagctga cgccatgata	480
aatggttcag atggtcgaac cacggttgag gatctcacga caccgcccac gtggttttccc	540
tttccgacca aagtatgctg gcggaagcat gatcttgccc gactgggtgcc ttacaaagct	600
ccggggatat ctgatcgatg ccgtatgggg ctggttctta agggatctga ttgtttgctc	660
tccaaagtgt accatgagtt tggaactcaa tggtactctc ttttgagac actacaccaa	720
gtaccgggtg ttccgggtgg attactgcca ccggaatac ccggagacga gaaagatgaa	780
acatgggtgt caatcaagaa atggctcgat ggtaaacaaa aaggcagtggt ggtgtacgtt	840
gcattaggaa gcgaggtttt ggtgagccaa accgaggttg ttgagttagc attgggtctc	900
gagctttctg ggttgccatt tggttgggct tatagaaaac caaaagggtcc cgcaagtca	960
gactcgggtg agttgccaga cgggttcgtg gaacgaactc gtgaccgtgg gttggtctgg	1020
acgagtcggg cacctcagtt acgaatactg agccatgagt cggtttgtgg gttcttgacg	1080
cattgtgggt ctggatcaat tgtggaagg ctaatgtttg gtcaccctct aatcatgcta	1140
ccgatttttg gggaccaacc tctgaatgct cgattactgg aggacaaaca ggtgggaatc	1200
gagataccaa gaaatgagga agatggttgc ttgaccaagg agtcggttgc tagatcactg	1260
aggtccgttg ttgtggaaaa agaaggggag atctacaagg cgaacgcgag ggagctgagt	1320
aaaatctata acgacactaa ggttgaaaaa gaatatgtaa gccaatcgt agactatttg	1380
gaaaagaatg cgctgctggg tgccatcgat catgagagtt aa	1422

<210> 97

<211> 1380

<212> DNA

<213> Stevia rebaudiana

<400> 97

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ttcagtatca catcttttca caccaacttc aacaaaccca aaacatctaa ttaccctcac	180
ttcactttca gattcatcct cgacaacgac ccacaagacg aacgcatttc caatctaccg	240
actcatgggtc cgctcgctgg tatgcggatt ccgattatca acgaacacgg agctgacgaa	300
ttacgacgcg aactggaact gttgatgtta gcttctgaag aagatgaaga ggtatcgtgt	360

SeqLst

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cggcttgttt tgatgacaag cagcttgttt aattttcatg cacatgtttc acttcctcag      480
tttgatgagc ttggttacct cgatcctgat gacaaaaccc gtttggaaga acaagcgagt      540
gggtttccta tgctaaaagt gaaagacatc aagtctgctg attcgaactg gcaaatactc      600
aaagagatat tagggaagat gataaaacaa acaaaagcat cttcaggagt catctggaac      660
tcatttaagg aactcgaaga gtctgagctc gaaactgtta tccgtgagat cccggctcca      720
agtttcttga taccactccc caagcatttg acagcctctt ccagcagctt actagaccac      780
gatcgaaccg tttttccatg gttagaccaa caaccgtcac gttcgggtact gtatgttagt      840
tttggttagtg gtactgaagt actggatgag aaagatttct tggaaatagc tcgtggggtg      900
gttgatagca agcagtcggt tttatgggtg gttcgacctg ggtttgtcaa gggttcgacg      960
tgggtcgaac cgttgccaga tgggttcttg ggtgaaagag gacgtattgt gaaatggggt      1020
ccacagcaag aagtgctagc tcatggagca ataggcgcat tctggactca tagcggatgg      1080
aactctacgt tggaagcgt ttgtgaaggt gttcctatga ttttctcgga ttttgggctc      1140
gatcaaccgt tgaatgctag atacatgagt gatgttttga aggtaggggt gtatttgga      1200
aatgggtggg aaagaggaga gatagcaaat gcaataagaa gagttatggt ggatgaagaa      1260
ggagaataca ttagacagaa tgcaagagtt ttgaaacaaa aggcagatgt ttctttgatg      1320
aagggtgggt cgtcttacga atcattagag tctctagttt cttacatttc atcgttgtaa      1380

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<210> 98

<211> 459

<212> PRT

<213> Stevia rebaudiana

<400> 98

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          20          25          30

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Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
          35          40          45

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Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
          50          55          60

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Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65          70          75          80

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Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His

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SeqLst															
85								90				95			
Gly	Ala	Asp	Glu 100	Leu	Arg	Arg	Glu	Leu 105	Glu	Leu	Leu	Met	Leu 110	Ala	Ser
Glu	Glu	Asp 115	Glu	Glu	Val	Ser	Cys 120	Leu	Ile	Thr	Asp	Ala 125	Leu	Trp	Tyr
Phe	Ala 130	Gln	Ser	Val	Ala	Asp 135	Ser	Leu	Asn	Leu	Arg 140	Arg	Leu	Val	Leu
Met 145	Thr	Ser	Ser	Leu	Phe 150	Asn	Phe	His	Ala	His 155	Val	Ser	Leu	Pro	Gln 160
Phe	Asp	Glu	Leu	Gly 165	Tyr	Leu	Asp	Pro	Asp 170	Asp	Lys	Thr	Arg	Leu 175	Glu
Glu	Gln	Ala	Ser 180	Gly	Phe	Pro	Met	Leu 185	Lys	Val	Lys	Asp	Ile 190	Lys	Ser
Ala	Tyr	Ser 195	Asn	Trp	Gln	Ile	Leu 200	Lys	Glu	Ile	Leu	Gly 205	Lys	Met	Ile
Lys	Gln 210	Thr	Lys	Ala	Ser	Ser 215	Gly	Val	Ile	Trp	Asn 220	Ser	Phe	Lys	Glu
Leu 225	Glu	Glu	Ser	Glu	Leu 230	Glu	Thr	Val	Ile	Arg 235	Glu	Ile	Pro	Ala	Pro 240
Ser	Phe	Leu	Ile	Pro 245	Leu	Pro	Lys	His	Leu 250	Thr	Ala	Ser	Ser	Ser 255	Ser
Leu	Leu	Asp	His 260	Asp	Arg	Thr	Val	Phe 265	Pro	Trp	Leu	Asp	Gln 270	Gln	Pro
Ser	Arg	Ser 275	Val	Leu	Tyr	Val	Ser 280	Phe	Gly	Ser	Gly	Thr 285	Glu	Val	Leu
Asp	Glu 290	Lys	Asp	Phe	Leu	Glu 295	Ile	Ala	Arg	Gly	Leu 300	Val	Asp	Ser	Lys
Gln 305	Ser	Phe	Leu	Trp	Val 310	Val	Arg	Pro	Gly	Phe 315	Val	Lys	Gly	Ser	Thr 320
Trp	Val	Glu	Pro	Leu 325	Pro	Asp	Gly	Phe	Leu 330	Gly	Glu	Arg	Gly	Arg 335	Ile

SeqLst

Val Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly
340 345 350

Ala Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys
355 360 365

Glu Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu
370 375 380

Asn Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu
385 390 395 400

Asn Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met
405 410 415

Val Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys
420 425 430

Gln Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser
435 440 445

Leu Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 99
<211> 1380
<212> DNA
<213> Stevia rebaudiana

<220>
<221> modified_base
<222> (861)..(863)
<223> a, c, t, g, unknown or other

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ttcagtatca ccatctttca caccaacttc aacaaaccca aaacatctaa ttaccctcac 180
ttcactttca gattcatcct cgacaacgac ccacaagacg aacgcatttc caatctaccg 240
actcatggtc cgctcgctgg tatgcggatt ccgattatca acgaacacgg agctgacgaa 300
ttacgacgcg aactggaact gttgatgtta gcttctgaag aagatgaaga ggtatcgtgt 360
ttaatcacgg atgctctttg gtacttcgcg caatctgttg ctgacagtct taacctccga 420
cggcttgttt tgatgacaag cagcttgttt aattttcatg cacatgtttc acttcctcag 480
tttgatgagc ttggttacct cgatcctgat gacaaaaccc gtttggaaga acaagcgagt 540
gggtttccta tgctaaaagt gaaagacatc aagtctgcgt attcgaactg gcaaatactc 600

SeqLst

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aaagagatat tagggaagat gataaaacaa acaaaagcat cttcaggagt catctggaac      660
tcatttaagg aactcgaaga gtctgagctc gaaactgtta tccgtgagat cccggctcca      720
agtttcttga taccactccc caagcatttg acagcctctt ccagcagctt actagaccac      780
gatcgaaccg tttttcaatg gttagaccaa caaccgcaa gttcgggtact gtatgttagt      840
tttggtagta ctagtgaagt nnnngatgag aaagatttct tggaaatagc tcgtggggtg      900
gttgatagca agcagtcgtt tttatgggtg gttcgacctg ggtttgtcaa gggttcgacg      960
tgggtcgaac cgttgccaga tgggttcgtg gccgaaagag ggcgtattgt gaaatgggtt     1020
ccgcaacagg aagtgatagc tcatggagca atcgggtgcat tctggactca tagcggatgg     1080
aactctacat tggaaagcgt ttgtgaagggt gttcctatga ttttctcgga ttttgggctc     1140
gatcaaccgt tgaatgctag atacatgagt gatgttttga aggtaggggt gtatttggaa     1200
aatgggtggg aaagaggaga gatagcaaat gcaatacgaa gagttatggg ggatgaagaa     1260
ggagaataca ttagacagaa tgcaagagtt ttgaaacaaa aggcagatgt ttctttgatg     1320
aagggtgggt catcttacga atcattagag tctctagttt cttacatttc atcgttgtaa     1380

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<210> 100
<211> 459
<212> PRT
<213> Stevia rebaudiana

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<220>
<221> MOD_RES
<222> (288)..(288)
<223> Any amino acid

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<400> 100
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1          5          10          15

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Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20          25          30

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Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35          40          45

```

```

Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50          55          60

```

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Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65          70          75          80

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```

Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85          90          95

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SeqLst

Gly Ala Asp Glu₁₀₀ Leu Arg Arg Glu₁₀₅ Leu Glu Leu Leu Met₁₁₀ Leu Ala Ser
 Glu Glu Asp₁₁₅ Glu Glu Val Ser Cys₁₂₀ Leu Ile Thr Asp₁₂₅ Ala Leu Trp Tyr
 Phe Ala Gln Ser Val Ala Asp₁₃₅ Ser Leu Asn Leu Arg₁₄₀ Arg Leu Val Leu
 Met₁₄₅ Thr Ser Ser Leu Phe₁₅₀ Asn Phe His Ala His₁₅₅ Val Ser Leu Pro Gln₁₆₀
 Phe Asp Glu Leu Gly₁₆₅ Tyr Leu Asp Pro Asp₁₇₀ Asp Lys Thr Arg Leu₁₇₅ Glu
 Glu Gln Ala Ser₁₈₀ Gly Phe Pro Met₁₈₅ Leu Lys Val Lys Asp Ile₁₉₀ Lys Ser
 Ala Tyr Ser₁₉₅ Asn Trp Gln Ile Leu₂₀₀ Lys Glu Ile Leu Gly₂₀₅ Lys Met Ile
 Lys Gln Thr Lys Ala Ser Ser₂₁₅ Gly Val Ile Trp Asn₂₂₀ Ser Phe Lys Glu
 Leu₂₂₅ Glu Glu Ser Glu Leu₂₃₀ Glu Thr Val Ile Arg₂₃₅ Glu Ile Pro Ala Pro₂₄₀
 Ser Phe Leu Ile Pro₂₄₅ Leu Pro Lys His Leu₂₅₀ Thr Ala Ser Ser Ser₂₅₅ Ser
 Leu Leu Asp His₂₆₀ Asp Arg Thr Val Phe₂₆₅ Gln Trp Leu Asp Gln₂₇₀ Gln Pro
 Pro Ser Ser₂₇₅ Val Leu Tyr Val Ser₂₈₀ Phe Gly Ser Thr Ser₂₈₅ Glu Val Xaa
 Asp Glu₂₉₀ Lys Asp Phe Leu Glu₂₉₅ Ile Ala Arg Gly Leu₃₀₀ Val Asp Ser Lys
 Gln₃₀₅ Ser Phe Leu Trp Val₃₁₀ Val Arg Pro Gly Phe₃₁₅ Val Lys Gly Ser Thr₃₂₀
 Trp Val Glu Pro Leu₃₂₅ Pro Asp Gly Phe Val₃₃₀ Ala Glu Arg Gly Arg₃₃₅ Ile
 Val Lys Trp Val₃₄₀ Pro Gln Gln Glu Val₃₄₅ Ile Ala His Gly Ala₃₅₀ Ile Gly

SeqLst

Ala Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys
 355 360 365

Glu Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu
 370 375 380

Asn Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu
 385 390 395 400

Asn Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met
 405 410 415

Val Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys
 420 425 430

Gln Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser
 435 440 445

Leu Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
 450 455

<210> 101
 <211> 1380
 <212> DNA
 <213> Stevia rebaudiana

<220>
 <221> modified_base
 <222> (861)..(863)
 <223> a, c, t, g, unknown or other

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 ttcagtatca ccatctttca caccaacttc aacaaacca aaacatctaa ttaccctcac 180
 ttcactttca gattcatcct cgacaacgac ccacaagacg aacgcatttc caatctaccg 240
 actcatgggtc cgctcgctgg tatgcggatt ccgattatca acgaacacgg agctgacgaa 300
 ttacgacgcg aactggaact gttgatgtta gcttctgaag aagatgaaga ggtatcgtgt 360
 ttaatcacgg atgctctttg gtacttcgcg caatctgttg ctgacagtct taacctccga 420
 cggcttgttt tgatgacaag cagcttgttt aattttcatg cacatgtttc acttcctcag 480
 tttgatgagc ttggttacct cgatcctgat gacaaaaccc gtttggaaga acaagcgagt 540
 gggtttccta tgctaaaagt gaaagacatc aagtctgcgt attcgaactg gcaaatactc 600
 aaagagatat tagggaagat gataaaacaa acaaagcat cttcaggagt catctggaac 660

SeqLst

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tcatttaagg aactcgaaga gtctgagctc gaaactgtta tccgtgagat cccggctcca      720
agtttcttga taccactccc caagcatttg acagcctctt ccagcagctt actagaccac      780
gatcgaaccg tttttcaatg gtttagacca caaccgcca gttcgggtact gtatgttagt      840
tttggtagta ctagtgaagt nnnnggatgag aaagatttct tggaaatagc tcgtggggtg      900
gttgatagca agcagtcggt tttatgggtg gttcgacctg ggtttgtcaa gggttcgacg      960
tgggtcgaac cgttgccaga tgggttcttg ggtgaaagag gacgtattgt gaaatggggt    1020
ccacagcaag aagtgctagc tcatggagca ataggcgcat tctggactca tagcggatgg    1080
aactctacgt tggaaagcgt ttgtgaaggt gttcctatga ttttctcgga ttttgggctc    1140
gatcaaccgt tgaatgctag atacatgagt gatgttttga aggtaggggt gtatttggaa    1200
aatgggtggg aaagaggaga gatagcaaat gcaataagaa gagttatggt ggatgaagaa    1260
ggagaataca ttagacagaa tgcaagagtt ttgaaacaaa aggcatgtgt ttctttgatg    1320
aagggtgggt cgtcttacga atcattagag tctctagttt cttacatttc atcgttgtaa    1380

```

```

<210> 102
<211> 459
<212> PRT
<213> Stevia rebaudiana

```

```

<220>
<221> MOD_RES
<222> (288)..(288)
<223> Any amino acid

```

```

<400> 102
Met Glu Asn Lys Thr Glu Thr Thr Val Arg Arg Arg Arg Arg Ile Ile
1          5          10          15

```

```

Leu Phe Pro Val Pro Phe Gln Gly His Ile Asn Pro Ile Leu Gln Leu
20          25          30

```

```

Ala Asn Val Leu Tyr Ser Lys Gly Phe Ser Ile Thr Ile Phe His Thr
35          40          45

```

```

Asn Phe Asn Lys Pro Lys Thr Ser Asn Tyr Pro His Phe Thr Phe Arg
50          55          60

```

```

Phe Ile Leu Asp Asn Asp Pro Gln Asp Glu Arg Ile Ser Asn Leu Pro
65          70          75          80

```

```

Thr His Gly Pro Leu Ala Gly Met Arg Ile Pro Ile Ile Asn Glu His
85          90          95

```

```

Gly Ala Asp Glu Leu Arg Arg Glu Leu Glu Leu Leu Met Leu Ala Ser

```

															SeqLst															
100										105										110										
Glu	Glu	Asp	Glu	Glu	Val	Ser	Cys	Leu	Ile	Thr	Asp	Ala	Leu	Trp	Tyr															
		115					120					125																		
Phe	Ala	Gln	Ser	Val	Ala	Asp	Ser	Leu	Asn	Leu	Arg	Arg	Leu	Val	Leu															
	130					135					140																			
Met	Thr	Ser	Ser	Leu	Phe	Asn	Phe	His	Ala	His	Val	Ser	Leu	Pro	Gln															
145					150					155					160															
Phe	Asp	Glu	Leu	Gly	Tyr	Leu	Asp	Pro	Asp	Asp	Lys	Thr	Arg	Leu	Glu															
				165					170					175																
Glu	Gln	Ala	Ser	Gly	Phe	Pro	Met	Leu	Lys	Val	Lys	Asp	Ile	Lys	Ser															
			180					185					190																	
Ala	Tyr	Ser	Asn	Trp	Gln	Ile	Leu	Lys	Glu	Ile	Leu	Gly	Lys	Met	Ile															
		195					200					205																		
Lys	Gln	Thr	Lys	Ala	Ser	Ser	Gly	Val	Ile	Trp	Asn	Ser	Phe	Lys	Glu															
	210					215					220																			
Leu	Glu	Glu	Ser	Glu	Leu	Glu	Thr	Val	Ile	Arg	Glu	Ile	Pro	Ala	Pro															
225					230					235					240															
Ser	Phe	Leu	Ile	Pro	Leu	Pro	Lys	His	Leu	Thr	Ala	Ser	Ser	Ser	Ser															
				245					250					255																
Leu	Leu	Asp	His	Asp	Arg	Thr	Val	Phe	Gln	Trp	Leu	Asp	Gln	Gln	Pro															
			260					265					270																	
Pro	Ser	Ser	Val	Leu	Tyr	Val	Ser	Phe	Gly	Ser	Thr	Ser	Glu	Val	Xaa															
		275					280					285																		
Asp	Glu	Lys	Asp	Phe	Leu	Glu	Ile	Ala	Arg	Gly	Leu	Val	Asp	Ser	Lys															
	290					295					300																			
Gln	Ser	Phe	Leu	Trp	Val	Val	Arg	Pro	Gly	Phe	Val	Lys	Gly	Ser	Thr															
305					310					315					320															
Trp	Val	Glu	Pro	Leu	Pro	Asp	Gly	Phe	Leu	Gly	Glu	Arg	Gly	Arg	Ile															
				325					330					335																
Val	Lys	Trp	Val	Pro	Gln	Gln	Glu	Val	Leu	Ala	His	Gly	Ala	Ile	Gly															
			340					345					350																	

SeqLst

Ala Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys
355 360 365

Glu Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu
370 375 380

Asn Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu
385 390 395 400

Asn Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met
405 410 415

Val Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys
420 425 430

Gln Lys Ala Asp Val Ser Leu Met Lys Gly Gly Ser Ser Tyr Glu Ser
435 440 445

Leu Glu Ser Leu Val Ser Tyr Ile Ser Ser Leu
450 455

<210> 103
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 103
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ccattcgtga aatcatttgg ggctcttatg aaagcagata ccttggaatt ggcatcagca 120
tcagtcgctg ggttgctgaa caagacctca ctggacccta gagatatcga tcatatcggt 180
tggggtaatg ttgtacttca aggatcagct cataactgcg ccagagaaat agttatcgac 240
cttaacatgc ctaaaaagat catcggtaat ttgacatcta tggcctgtgc ttcaggctta 300
tcttctttgt cacaagcctg tatgctaata gaggggtggtc atgccgatgt cgtcattgct 360
ggcggttctg attcagtctc caacactgaa gtgcctttgc caagatccgt cacttacggt 420
ctaattgatgg cccaaaggaa ggggtgttatg ggcttcttta aggaagcagg atacaacca 480
ttcaaattgg ttccaggcgg tattgcttta accgaacgta gtacaggaaa aactatgggt 540
tggcatggag acttaattgc tgagttaaac tctatatcta gagatgacca ggaagccctg 600
gctgtggctt ctcatgcaaa tgctgctaga gcagaaaaag ctgggtactt taaggaggaa 660
attgtacctg tgacaatcga caaaaagggc aaaaagactg aagtaacatg tgatgatggt 720
atgcaaagag atacagaaaa gatgaaggcc aagatgccat cattgaagcc tgttttcaga 780

SeqLst

```

aaagagggag gtacaataac agcagccact tccagtactc tgactgatgg tggctctgca      840
atgttggtta tgtcagagga aaaggccaaa aagttggggt atccaactga tgtctgcgtg      900
aagtcttggg atttcagtgg tatcgatcct tacccacaac ttttgttagc accagttcta      960
ggttgggggtc cagctttgaa aaaggccgga ttaacccta aagatatcga tttgtacgaa     1020
attcacgaag catttgctgc acaagttcta gccacaatta agtgtttgaa gtctcaggaa     1080
ttcttcgata ggtacgctaa cggtgcaaag ccagtattaa ctgaggatat tgatctttct     1140
aaactaaatg ttaatggcgg ttccttagca cttggccacc cattcgccgc tacaggaggt     1200
agaatcgtaa tctctctagc aaatgagttg agaagatccg gaaagagaca cgggctggtc     1260
agtatttgtg cagctggagg gttaggcgga gtagctatac ttgagcatac agcaagtaag     1320
taa                                                                    1323

```

```

<210> 104
<211> 440
<212> PRT
<213> Leishmania infantum

```

```

<400> 104
Met His Ser Thr Arg His Ile Leu Arg Gln Arg Ala Val Leu Val Thr
1          5          10          15

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

Asp Thr Leu Glu Leu Ala Ser Ala Ser Val Ala Gly Leu Leu Asn Lys
35          40          45

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

Val Leu Gln Gly Ser Ala His Asn Cys Ala Arg Glu Ile Val Ile Asp
65          70          75          80

Leu Asn Met Pro Lys Lys Ile Ile Gly Asn Leu Thr Ser Met Ala Cys
85          90          95

Ala Ser Gly Leu Ser Ser Leu Ser Gln Ala Cys Met Leu Ile Glu Gly
100         105         110

Gly His Ala Asp Val Val Ile Ala Gly Gly Ser Asp Ser Val Ser Asn
115         120         125

Thr Glu Val Pro Leu Pro Arg Ser Val Thr Tyr Gly Leu Met Met Ala
130         135         140

```

SeqLst

Gln Arg Lys Gly Val Met Gly Phe Phe Lys Glu Ala Gly Tyr Asn Pro
 145 150 155 160
 Phe Lys Trp Phe Pro Gly Gly Ile Ala Leu Thr Glu Arg Ser Thr Gly
 165 170 175
 Lys Thr Met Gly Trp His Gly Asp Leu Ile Ala Glu Leu Asn Ser Ile
 180 185 190
 Ser Arg Asp Asp Gln Glu Ala Leu Ala Val Ala Ser His Ala Asn Ala
 195 200 205
 Ala Arg Ala Glu Lys Ala Gly Tyr Phe Lys Glu Glu Ile Val Pro Val
 210 215 220
 Thr Ile Asp Lys Lys Gly Lys Lys Thr Glu Val Thr Cys Asp Asp Val
 225 230 235 240
 Met Gln Arg Asp Thr Glu Lys Met Lys Ala Lys Met Pro Ser Leu Lys
 245 250 255
 Pro Val Phe Arg Lys Glu Gly Gly Thr Ile Thr Ala Ala Thr Ser Ser
 260 265 270
 Thr Leu Thr Asp Gly Gly Ser Ala Met Leu Val Met Ser Glu Glu Lys
 275 280 285
 Ala Lys Lys Leu Gly Tyr Pro Thr Asp Val Cys Val Lys Ser Trp Tyr
 290 295 300
 Phe Ser Gly Ile Asp Pro Tyr Pro Gln Leu Leu Leu Ala Pro Val Leu
 305 310 315 320
 Gly Trp Gly Pro Ala Leu Lys Lys Ala Gly Leu Thr Pro Lys Asp Ile
 325 330 335
 Asp Leu Tyr Glu Ile His Glu Ala Phe Ala Ala Gln Val Leu Ala Thr
 340 345 350
 Ile Lys Cys Leu Lys Ser Gln Glu Phe Phe Asp Arg Tyr Ala Asn Gly
 355 360 365
 Ala Lys Pro Val Leu Thr Glu Asp Ile Asp Leu Ser Lys Leu Asn Val
 370 375 380
 Asn Gly Gly Ser Leu Ala Leu Gly His Pro Phe Ala Ala Thr Gly Gly
 385 390 395 400

SeqLst

Arg Ile Val Ile Ser Leu Ala Asn Glu Leu Arg Arg Ser Gly Lys Arg
 405 410 415

His Gly Leu Val Ser Ile Cys Ala Ala Gly Gly Leu Gly Gly Val Ala
 420 425 430

Ile Leu Glu His Thr Ala Ser Lys
 435 440

<210> 105

<211> 1584

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 105

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caaaaggctt ctacaccagt tttaaccaat aaaacagtca tttctggatc gaaagtcaaa	120
agtttatcat ctgcgcaatc gagctcatca ggaccttcat catctagtga ggaagatgat	180
tcccgcgata ttgaaagctt ggataagaaa atacgtcctt tagaagaatt agaagcatta	240
ttaagtagtg gaaatacaaa acaattgaag aacaaagagg tcgctgcctt ggttattcac	300
ggtaagttac ctttgtacgc tttggagaaa aaattagggtg atactacgag agcggttgcg	360
gtacgtagga aggctctttc aattttggca gaagctcctg tatttagcatc tgatcgttta	420
ccatataaaa attatgacta cgaccgcgta tttggcgctt gttgtgaaaa tgttataggt	480
tacatgcctt tgcccgttgg tgttataggc cccttgggta tcgatggtag atcttatcat	540
ataccaatgg caactacaga gggttgtttg gtagcttctg ccatgcgtgg ctgtaaggca	600
atcaatgctg gcggtggtgc aacaactgtt ttaactaagg atggtatgac aagaggccca	660
gtagtccgtt tcccaacttt gaaaagatct ggtgcctgta agatatgggt agactcagaa	720
gagggacaaa acgcaattaa aaaagctttt aactctacat caagatttgc acgtctgcaa	780
catattcaaa cttgtctagc aggagattta ctcttcatga gatttagaac aactactggt	840
gacgcaatgg gtatgaatat gatttctaaa ggtgtcgaat actcattaaa gcaaattgta	900
gaagagtatg gctgggaaga tatggagggt gtctccgttt ctggtaacta ctgtaccgac	960
aaaaaaccag ctgccatcaa ctggatcgaa ggtcgtggta agagtgtcgt cgcagaagct	1020
actattcctg gtgatgttgt cagaaaagtg ttaaaaagtg atgtttccgc attggttgag	1080
ttgaacattg ctaagaattt gggttgatct gcaatggctg ggtctgttgg tggatttaac	1140
gcacatgcag ctaatttagt gacagctggt ttcttggcat taggacaaga tcctgcacaa	1200

SeqLst

```

aatgttgaaa gttccaactg tataacattg atgaaagaag tggacggtga tttgagaatt      1260
tccgtatcca tgccatccat cgaagtaggt accatcggtg gtggtactgt tctagaacca      1320
caaggtgcca tgttggactt attaggtgta agaggcccg c atgctaccgc tcctggtacc      1380
aacgcacgtc aattagcaag aatagttgcc tgtgccgtct tggcaggtga attatcctta      1440
tgtgctgccc tagcagccgg ccatttggtt caaagtcata tgaccacaa caggaaacct      1500
gctgaaccaa caaaacctaa caatttgac gccactgata taaatcgttt gaaagatggg      1560
tccgtcacct gcattaaatc ctaa                                             1584

```

<210> 106

<211> 527

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 106

```

Met Ala Ala Asp Gln Leu Val Lys Thr Glu Val Thr Lys Lys Ser Phe
1          5          10          15

```

```

Thr Ala Pro Val Gln Lys Ala Ser Thr Pro Val Leu Thr Asn Lys Thr
          20          25          30

```

```

Val Ile Ser Gly Ser Lys Val Lys Ser Leu Ser Ser Ala Gln Ser Ser
          35          40          45

```

```

Ser Ser Gly Pro Ser Ser Ser Ser Glu Glu Asp Asp Ser Arg Asp Ile
          50          55          60

```

```

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

```

```

Leu Ser Ser Gly Asn Thr Lys Gln Leu Lys Asn Lys Glu Val Ala Ala
          85          90          95

```

```

Leu Val Ile His Gly Lys Leu Pro Leu Tyr Ala Leu Glu Lys Lys Leu
          100          105          110

```

```

Gly Asp Thr Thr Arg Ala Val Ala Val Arg Arg Lys Ala Leu Ser Ile
          115          120          125

```

```

Leu Ala Glu Ala Pro Val Leu Ala Ser Asp Arg Leu Pro Tyr Lys Asn
          130          135          140

```

```

Tyr Asp Tyr Asp Arg Val Phe Gly Ala Cys Cys Glu Asn Val Ile Gly
145          150          155          160

```

```

Tyr Met Pro Leu Pro Val Gly Val Ile Gly Pro Leu Val Ile Asp Gly

```

SeqLst															
165								170				175			
Thr	Ser	Tyr	His 180	Ile	Pro	Met	Ala	Thr 185	Thr	Glu	Gly	Cys	Leu 190	Val	Ala
Ser	Ala	Met 195	Arg	Gly	Cys	Lys	Ala 200	Ile	Asn	Ala	Gly	Gly 205	Gly	Ala	Thr
Thr	Val 210	Leu	Thr	Lys	Asp	Gly 215	Met	Thr	Arg	Gly	Pro 220	Val	Val	Arg	Phe
Pro 225	Thr	Leu	Lys	Arg	Ser 230	Gly	Ala	Cys	Lys	Ile 235	Trp	Leu	Asp	Ser	Glu 240
Glu	Gly	Gln	Asn	Ala 245	Ile	Lys	Lys	Ala	Phe 250	Asn	Ser	Thr	Ser	Arg 255	Phe
Ala	Arg	Leu	Gln 260	His	Ile	Gln	Thr	Cys 265	Leu	Ala	Gly	Asp	Leu 270	Leu	Phe
Met	Arg	Phe 275	Arg	Thr	Thr	Thr	Gly 280	Asp	Ala	Met	Gly	Met 285	Asn	Met	Ile
Ser	Lys 290	Gly	Val	Glu	Tyr	Ser 295	Leu	Lys	Gln	Met	Val 300	Glu	Glu	Tyr	Gly
Trp 305	Glu	Asp	Met	Glu	Val 310	Val	Ser	Val	Ser	Gly 315	Asn	Tyr	Cys	Thr	Asp 320
Lys	Lys	Pro	Ala	Ala 325	Ile	Asn	Trp	Ile	Glu 330	Gly	Arg	Gly	Lys	Ser 335	Val
Val	Ala	Glu	Ala 340	Thr	Ile	Pro	Gly	Asp 345	Val	Val	Arg	Lys	Val 350	Leu	Lys
Ser	Asp	Val 355	Ser	Ala	Leu	Val	Glu 360	Leu	Asn	Ile	Ala	Lys 365	Asn	Leu	Val
Gly	Ser 370	Ala	Met	Ala	Gly	Ser 375	Val	Gly	Gly	Phe	Asn 380	Ala	His	Ala	Ala
Asn 385	Leu	Val	Thr	Ala	Val 390	Phe	Leu	Ala	Leu	Gly 395	Gln	Asp	Pro	Ala	Gln 400
Asn	Val	Glu	Ser	Ser 405	Asn	Cys	Ile	Thr	Leu 410	Met	Lys	Glu	Val	Asp 415	Gly

SeqLst

Asp Leu Arg Ile Ser Val Ser Met Pro Ser Ile Glu Val Gly Thr Ile
420 425 430

Gly Gly Gly Thr Val Leu Glu Pro Gln Gly Ala Met Leu Asp Leu Leu
435 440 445

Gly Val Arg Gly Pro His Ala Thr Ala Pro Gly Thr Asn Ala Arg Gln
450 455 460

Leu Ala Arg Ile Val Ala Cys Ala Val Leu Ala Gly Glu Leu Ser Leu
465 470 475 480

Cys Ala Ala Leu Ala Ala Gly His Leu Val Gln Ser His Met Thr His
485 490 495

Asn Arg Lys Pro Ala Glu Pro Thr Lys Pro Asn Asn Leu Asp Ala Thr
500 505 510

Asp Ile Asn Arg Leu Lys Asp Gly Ser Val Thr Cys Ile Lys Ser
515 520 525

<210> 107
<211> 3681
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 107
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gtatctgttt tcgtgtagc tacattagct tacttccaca tcttgccgg aatcaagcac 120
tcaagtttct ttgcatcttc tcacccctcct gctatcagac ctgcttttgc acatctgacc 180
aacggggaat ggggtgccgt ctcccaacat gattggactg aagcatggaa gcatcctggc 240
ggttcacttg atgcattaga acttcaacaa gtagttttca ctttagatga caagactcaa 300
ccatctgctg tgctagatgc atccgcaatt agtcagcact tagtttccaa tgttcctgca 360
ttatctggaa aagcctactc ttcatgtgc caccatccaa atgtatcagg cacctcctgt 420
tttacatcag tttctggtcc aggagcttca ccaatcttga cactgagttt taagcctgga 480
actagagacg attggtagg atcattaagg aaggagaaaa ctatcacact agatgggggt 540
aagtacgacg ttggagccgg aaaaagacaa gagtcaatcg gcgatatgga atcatctaag 600
tggttgctt atgcattatc agctttggta cttagatttt gggaattaac aaaggcagat 660
tccttagata tactagtggg tctaactggg tacatcctaa tgcacgtaac attcatgaga 720
ttgttcttgg catccagagc acttggcagt aacttttggg tatcagctgg catattctcc 780

SeqLst

tccgcaacaa	tttctttcct	attcacttta	ccaatgtgta	gatctatgga	tattccactt	840
gatccaattg	ccttgacaga	agccctgcca	ttcttggtgt	gtaccgtagg	ttttgacaaa	900
ccacttagat	tggcaagagc	tgtgatggct	catcctaata	tccttaaacc	tcaagatgat	960
ggtaggatga	aagctgccgg	agatgtcatt	cttgaggcac	tggacagagt	tggtaacatg	1020
atattgagag	attacgcttt	agagatcgca	gttctattcg	ttggcgtaa	ctccagagtt	1080
ggcggcttta	aggaattttg	tgctgtagct	gcagcattac	ttgctatgga	cagattaatg	1140
acattcacac	tttatacagc	agtgttaacc	atcatggttg	aggtaaggcg	tatcaaaaag	1200
gtcagagata	tgactaaggc	tagatctaga	agttcttcta	ttaccgccgt	tacagccaac	1260
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gagacaacta	aaaacctaa	acaaagagcc	actgattcag	ccatcggtgt	taagggttca	1380
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ccaattccta	gagttgacat	tactacccca	gccatagcca	atatcttggtc	tcatctagct	1620
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gtcgctgctc	cagtctacgt	ccatgctcta	ccattggccc	ctgctttaag	agcttcaaac	1740
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ccagttgtta	gtaagtggat	cgtagcattg	ctagctgtct	ctgttgcat	gaatggatac	1860
ttgttaaagg	gtatagccgc	aggttccggg	ttggctgcca	tgagagctgt	tagatctcaa	1920
gggtgttcgtt	tcagatctag	agctagaagt	atcgtaaaga	tatctgatga	acctgagcca	1980
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ccattgacta	ttttctcaag	accactgaac	ttagaaacag	tggacaaaaa	gttacaagat	2160
gctctgccaa	taagatcccc	accacctgtt	gaaccaatca	ctccagaatc	tagagaagtg	2220
gaaccaaccc	aagtagaagt	aagatctcta	gctgaatgtg	tggatgtggt	cgagaatggg	2280
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ctggttccta	tgaaagatta	tgattacgcc	agagtcatgg	gtgcctgttg	tgaaaacggt	2520
atcggataca	tgccattacc	actagggatt	gcagggtccat	tgaagattga	tggcttgatg	2580
tatcctatac	caatggcaac	cgcagaagg	accttggttg	catctacttc	taggggctgt	2640

SeqLst

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gggccagcta tagactttcc ttccatcgtc agagctgcag aggctaaggc cttcattgaa	2760
tcagaagatg gatacgctac aatcagggag gctttcgagt ctacttctag atttgccaag	2820
ttgcaaaaga tcaagtgtgc actagctggt cgtactcttt ttgtcagatt tgctactaga	2880
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aaaaagcctg cagctatttc atggatcgaa ggtaggggaa aatctattgt agcagaagca	3060
gttattcctg gtaaggctgt taagtcagtc ctgaaaacaa cagtcgagtc tctttgcaat	3120
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gctcatgccg ccaacatcct aacagctgtg ttcctagcca caggtcagga tcctgctcaa	3240
aatgtcgaat cttctaattg catgacttta atggaaccaa caaacggcgg tgaggatttg	3300
ctaattgacaa tttcaatgcc atgtatagag gtaggaaccg ttggtggagg gacaattctg	3360
gaaccacaag gtgcagtttt ggatttggtg ggcgttagag gggctcacc c tactaatcct	3420
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tctttgataa gtgccttagc cgcaggatcat ttggttagag ctcattctgc ccacaatcgt	3540
tctcaattga atacaccaat gccatccaga ccacatactc ctggccctga ggatgtctca	3600
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tacgttgctg aagcaaaata a	3681

<210> 108
 <211> 1226
 <212> PRT
 <213> Ganoderma lucidum

<400> 108
 Met Arg Ala Val Leu Arg Leu Leu Ser Thr His Thr Val Phe Ser Pro
 1 5 10 15

 Ile Glu Thr Ile Val Ser Val Phe Val Leu Ala Thr Leu Ala Tyr Phe
 20 25 30

 His Ile Leu Ser Gly Ile Lys His Ser Ser Phe Phe Ala Ser Ser His
 35 40 45

 Pro Pro Ala Ile Arg Pro Ala Phe Ala His Leu Thr Asn Gly Glu Trp
 50 55 60

 Val Ala Val Ser Gln His Asp Trp Thr Glu Ala Trp Lys His Pro Gly
 65 70 75 80

SeqLst

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

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

His Leu Val Ser Asn Val Pro Ala Leu Ser Gly Lys Ala Tyr Ser Ser
115 120 125

Leu Cys His His Pro Asn Val Ser Gly Thr Ser Cys Phe Thr Ser Val
130 135 140

Ser Gly Pro Gly Ala Ser Pro Ile Leu Thr Leu Ser Phe Lys Pro Gly
145 150 155 160

Thr Arg Asp Asp Trp Leu Gly Ser Leu Arg Lys Glu Lys Thr Ile Thr
165 170 175

Leu Asp Gly Val Lys Tyr Asp Val Gly Ala Gly Lys Arg Gln Glu Ser
180 185 190

Ile Gly Asp Met Glu Ser Ser Lys Trp Val Ala Tyr Ala Leu Ser Ala
195 200 205

Leu Val Leu Arg Phe Trp Glu Leu Thr Lys Ala Asp Ser Leu Asp Ile
210 215 220

Leu Val Val Leu Thr Gly Tyr Ile Leu Met His Val Thr Phe Met Arg
225 230 235 240

Leu Phe Leu Ala Ser Arg Ala Leu Gly Ser Asn Phe Trp Leu Ser Ala
245 250 255

Gly Ile Phe Ser Ser Ala Thr Ile Ser Phe Leu Phe Thr Leu Pro Met
260 265 270

Cys Arg Ser Met Asp Ile Pro Leu Asp Pro Ile Ala Leu Thr Glu Ala
275 280 285

Leu Pro Phe Leu Val Cys Thr Val Gly Phe Asp Lys Pro Leu Arg Leu
290 295 300

Ala Arg Ala Val Met Ala His Pro Asn Ile Leu Lys Pro Gln Asp Asp
305 310 315 320

Gly Arg Met Lys Ala Ala Gly Asp Val Ile Leu Glu Ala Leu Asp Arg
325 330 335

SeqLst

Val Gly Asn Met Ile Leu Arg Asp Tyr Ala Leu Glu Ile Ala Val Leu
 340 345 350
 Phe Val Gly Val Asn Ser Arg Val Gly Gly Leu Lys Glu Phe Cys Ala
 355 360 365
 Val Ala Ala Ala Leu Leu Ala Met Asp Arg Leu Met Thr Phe Thr Leu
 370 375 380
 Tyr Thr Ala Val Leu Thr Ile Met Val Glu Val Arg Arg Ile Lys Lys
 385 390 395 400
 Val Arg Asp Met Thr Lys Ala Arg Ser Arg Ser Ser Ser Ile Thr Ala
 405 410 415
 Val Thr Ala Asn Gly Thr Ala Ile Arg Gly Val Leu Ser Arg Lys Ser
 420 425 430
 Ser Lys Gln Ser Val Thr Glu Pro Glu Thr Thr Lys Asn Leu Arg Gln
 435 440 445
 Arg Ala Thr Asp Ser Ala Ile Gly Val Lys Gly Ser Leu Leu Lys Asp
 450 455 460
 Gly Gly Arg Leu Gln Glu Ala Glu Glu Asn Pro Met Ala Arg Leu Lys
 465 470 475 480
 Leu Leu Leu Ile Ala Ser Phe Leu Thr Leu His Ile Leu Asn Phe Cys
 485 490 495
 Thr Thr Leu Thr Ser Ala Thr Ala Asn Ala Arg His Gln Arg His Pro
 500 505 510
 Phe Arg Thr Val Gln Glu Val Val Pro Ile Pro Arg Val Asp Ile Thr
 515 520 525
 Thr Pro Ala Ile Ala Asn Ile Leu Ser His Leu Ala Val Ala Gln Glu
 530 535 540
 Pro Met Phe Thr Val Val Gly Ser Glu Pro Ile Glu Leu Leu Val Lys
 545 550 555 560
 Val Ala Ala Pro Val Tyr Val His Ala Leu Pro Leu Ala Pro Ala Leu
 565 570 575
 Arg Ala Ser Asn Thr Asn Thr Gly Glu Ala Ile Glu Asn Phe Met Ser
 580 585 590

SeqLst

Ser Trp Ser Ser Leu Val Gly Asp Pro Val Val Ser Lys Trp Ile Val
 595 600 605
 Ala Leu Leu Ala Val Ser Val Ala Leu Asn Gly Tyr Leu Leu Lys Gly
 610 615 620
 Ile Ala Ala Gly Ser Gly Leu Ala Ala Met Arg Ala Val Arg Ser Gln
 625 630 635 640
 Gly Val Arg Phe Arg Ser Arg Ala Arg Ser Ile Val Lys Ile Ser Asp
 645 650 655
 Glu Pro Glu Pro Glu Pro Glu His Ser Ile Asp Pro Ala Pro Val Val
 660 665 670
 Phe Phe Ala Ser Ala Ala Pro Ala Val Glu Ala Pro Ala Pro Ala Pro
 675 680 685
 Ala Pro Glu Pro Glu Pro Pro Val Asn Arg Pro Pro Pro Leu Thr Ile
 690 695 700
 Phe Ser Arg Pro Leu Asn Leu Glu Thr Val Asp Lys Lys Leu Gln Asp
 705 710 715 720
 Ala Leu Pro Ile Arg Ser Pro Pro Pro Val Glu Pro Ile Thr Pro Glu
 725 730 735
 Ser Arg Glu Val Glu Pro Thr Gln Val Glu Val Arg Ser Leu Ala Glu
 740 745 750
 Cys Val Asp Val Phe Glu Asn Gly Pro Arg Pro Val Ser Val Ala Leu
 755 760 765
 Lys Thr Leu Asn Asp Glu Glu Val Ile Leu Leu Cys Gln Thr Gly Lys
 770 775 780
 Ile Ala Pro Tyr Ala Leu Val Lys Met Leu Ala Asp Phe Asp Arg Ala
 785 790 795 800
 Val Arg Val Arg Arg Ala Leu Ile Ser Arg Ala Ser Arg Thr Lys Thr
 805 810 815
 Leu Glu Asn Ser Leu Val Pro Met Lys Asp Tyr Asp Tyr Ala Arg Val
 820 825 830
 Met Gly Ala Cys Cys Glu Asn Val Ile Gly Tyr Met Pro Leu Pro Leu

SeqLst															
835					840					845					
Gly	Ile	Ala	Gly	Pro	Leu	Lys	Ile	Asp	Gly	Leu	Met	Tyr	Pro	Ile	Pro
850						855					860				
Met	Ala	Thr	Ala	Glu	Gly	Thr	Leu	Val	Ala	Ser	Thr	Ser	Arg	Gly	Cys
865					870					875					880
Lys	Ala	Leu	Asn	Ala	Gly	Gly	Gly	Val	Thr	Thr	Val	Leu	Thr	Ala	Asp
				885					890					895	
Gly	Met	Thr	Arg	Gly	Pro	Ala	Ile	Asp	Phe	Pro	Ser	Ile	Val	Arg	Ala
			900					905					910		
Ala	Glu	Ala	Lys	Ala	Phe	Ile	Glu	Ser	Glu	Asp	Gly	Tyr	Ala	Thr	Ile
		915					920					925			
Arg	Glu	Ala	Phe	Glu	Ser	Thr	Ser	Arg	Phe	Ala	Lys	Leu	Gln	Lys	Ile
	930					935					940				
Lys	Cys	Ala	Leu	Ala	Gly	Arg	Thr	Leu	Phe	Val	Arg	Phe	Ala	Thr	Arg
945					950					955					960
Thr	Gly	Asp	Ala	Met	Gly	Met	Asn	Met	Ile	Ser	Lys	Ala	Thr	Glu	Lys
				965					970					975	
Ala	Leu	Asp	Val	Leu	Ser	His	Glu	Phe	Pro	Glu	Met	Val	Val	Leu	Ala
			980					985					990		
Leu	Ser	Gly	Asn	Tyr	Cys	Thr	Asp	Lys	Lys	Pro	Ala	Ala	Ile	Ser	Trp
		995					1000					1005			
Ile	Glu	Gly	Arg	Gly	Lys	Ser	Ile	Val	Ala	Glu	Ala	Val	Ile	Pro	
	1010					1015					1020				
Gly	Lys	Val	Val	Lys	Ser	Val	Leu	Lys	Thr	Thr	Val	Glu	Ser	Leu	
	1025					1030					1035				
Cys	Asn	Val	Asn	Thr	Lys	Lys	Asn	Leu	Ile	Gly	Ser	Ala	Met	Ala	
	1040					1045					1050				
Gly	Ser	Val	Gly	Gly	Phe	Asn	Ala	His	Ala	Ala	Asn	Ile	Leu	Thr	
	1055					1060					1065				
Ala	Val	Phe	Leu	Ala	Thr	Gly	Gln	Asp	Pro	Ala	Gln	Asn	Val	Glu	
	1070					1075					1080				

SeqLst

Ser Ser Asn Cys Met Thr Leu Met Glu Pro Thr Asn Gly Gly Glu
1085 1090 1095

Asp Leu Leu Met Thr Ile Ser Met Pro Cys Ile Glu Val Gly Thr
1100 1105 1110

Val Gly Gly Gly Thr Ile Leu Glu Pro Gln Gly Ala Val Leu Asp
1115 1120 1125

Leu Leu Gly Val Arg Gly Ala His Pro Thr Asn Pro Gly Gln Asn
1130 1135 1140

Ala Gln Gln Leu Ala Arg Ile Ile Ala Ser Ala Val Met Ala Gly
1145 1150 1155

Glu Leu Ser Leu Ile Ser Ala Leu Ala Ala Gly His Leu Val Arg
1160 1165 1170

Ala His Leu Ala His Asn Arg Ser Gln Leu Asn Thr Pro Met Pro
1175 1180 1185

Ser Arg Pro His Thr Pro Gly Pro Glu Asp Val Ser His Val Gln
1190 1195 1200

Gln Leu Pro Thr Pro Ser Ala Ser Asp Asp Lys Gly Val Thr Ala
1205 1210 1215

Gln Gly Tyr Val Val Glu Ala Lys
1220 1225

<210> 109

<211> 2667

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 109

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ttaccggaac aacaagattt gtggttgga ttatgagtggt cctaagctgg aagaggat	180
gtgtgagttca gacatcatca tacttactat aacaagatgc attgcaatat tgtatatcta	240
cttccaattt caaaacctta gacaattggg tagtaaatac atcctaggca tcgccggatt	300
gttcactatt ttctctagtt ttgttttctc aaccgtcggt attcactttt tggacaaaga	360
gttaactggt ttgaacgaag ctctaccatt cttcttgctg ctggtagatt tgtccagagc	420
ttccgcttta	

SeqLst

gctaaattcg	ctctgtcctc	taattctcaa	gatgaagtta	gagagaatat	agcaagggga	480
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gttggcacia	tgtccggcgt	tagacagtta	gaaatcatgt	gttgtttttg	ctgtatgagt	600
gtcttggcta	actactttgt	ctttatgaca	ttctttccag	cttgcgtttc	tttggtattg	660
gagctgtcaa	gagaatcaag	agaaggcaga	ccaatatggc	aactatcaca	tttcgccaga	720
gtgttagaag	aggaggaaaa	caaaccta	cctgtcacac	agagagtga	aatgatcatg	780
tctttgggtt	tagtcctagt	gcatgctcat	tctagatgga	tcgcagatcc	atccccctcag	840
aattctacag	ctgataactc	taaagttagt	ttaggttttag	atgaaaatgt	aagtaagagg	900
attgaacctt	ccgtgtcttt	gtggcaattc	tacttatcaa	aaatgatttc	catggatatt	960
gaacaagtga	taacgttgtc	tttggcttta	ttgttagccg	ttaagtacat	tttctttgag	1020
caagccgaaa	cggaatctac	attatcactg	aaaaacccaa	ttacatcccc	agtcgttacc	1080
cagaaaaaga	taactgatga	ttgctgtaga	agagatccag	tgttgggtcag	gaatgatcaa	1140
aagttccacg	ccatggagga	ggaaactagg	aaaaacagag	aaaggaaagt	tgaagttatc	1200
aagcctctat	tagcagaaaa	tgacacttca	catagggcca	ctttcgttgt	cggcaattca	1260
tctcttttag	gtacgtcatt	ggagctggaa	acacaggaac	cagaaatgga	actaccagtt	1320
gaaccaagac	caaatgagga	atgtttgcaa	atactagaga	acgctgaaaa	gggagccaag	1380
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gccggtccac	tatgtttgga	cggtaaggaa	tttcaagtac	ctatggcaac	gactgaaggc	1680
tgcttagttg	catctacaaa	cagaggttgt	agagccattg	gattaggtgg	cgggtgcttct	1740
tcaagagtct	tggctgacgg	tatgactaga	ggtcctgttg	tgagatttcc	tagggcctgt	1800
gactctgcag	aagttaaggc	ttggttgga	actccagaag	gtttcaccgt	aatcaaagag	1860
gcctttgatt	ccacatcaag	ggtggccaga	ttacaaaaac	tacacatgtc	tgtcgctggg	1920
agaaatctgt	atatcagatt	tcaatccaga	tccggcgacg	caatgggtat	gaatatgatt	1980
tcaaaagggg	cagaaaaggc	tttgtcaaag	ctgcaggagt	atttcccaga	gatgcaaatc	2040
ttggccgtat	ctggcaacta	ttgcacagac	aaaaagcctg	ccgccatcaa	ctggattgaa	2100
ggaagaggca	aatctgtggt	ttgtgaagct	gtaattccag	ccaaagtgtg	tagagaagtg	2160
ttaaagacca	caacagaagc	tatgattgaa	gtaaacataa	acaaaaactt	agtaggggtct	2220
gccatggctg	gttcaattgg	aggatacaac	gctcatgctg	ccaatattgt	aaccgctatc	2280

SeqLst

tacatcgcat gtggacaaga tgctgccc	aatgtcggtt cctcaaattg catcacattg	2340
atggaagcat ctggccctac aaacgaggat	ttgtatatca gttgcacaat gccatctata	2400
gaaatagggga ctgtggggagg aggaactaac	ttactttccac agcaagcctg cttacaaatg	2460
ctgggtgtac aaggagcctg tagagataat	ccaggggaga acgctagaca acttgccaga	2520
attgtttgtg ggacagttat ggctggtgaa	cttagtctaa tggcagcttt ggctgctggg	2580
cacctggtga gatctcatat gattcataat	agaagtaaga ttaaccttca agatttgcaa	2640
ggtacgtgta cgaaaaaggc tgcctaa		2667

<210> 110
 <211> 888
 <212> PRT
 <213> Bos taurus

<400> 110
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 20 25 30

Ser Met Asn Met Phe Thr Gly Asn Asn Lys Ile Cys Gly Trp Asn Tyr
 35 40 45

Glu Cys Pro Lys Leu Glu Glu Asp Val Leu Ser Ser Asp Ile Ile Ile
 50 55 60

Leu Thr Ile Thr Arg Cys Ile Ala Ile Leu Tyr Ile Tyr Phe Gln Phe
 65 70 75 80

Gln Asn Leu Arg Gln Leu Gly Ser Lys Tyr Ile Leu Gly Ile Ala Gly
 85 90 95

Leu Phe Thr Ile Phe Ser Ser Phe Val Phe Ser Thr Val Val Ile His
 100 105 110

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

Leu Leu Leu Val Asp Leu Ser Arg Ala Ser Ala Leu Ala Lys Phe Ala
 130 135 140

Leu Ser Ser Asn Ser Gln Asp Glu Val Arg Glu Asn Ile Ala Arg Gly
 145 150 155 160

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

SeqLst

Leu Val Ile Gly Val Gly Thr Met Ser Gly Val Arg Gln Leu Glu Ile
 180 185 190
 Met Cys Cys Phe Gly Cys Met Ser Val Leu Ala Asn Tyr Phe Val Phe
 195 200 205
 Met Thr Phe Phe Pro Ala Cys Val Ser Leu Val Leu Glu Leu Ser Arg
 210 215 220
 Glu Ser Arg Glu Gly Arg Pro Ile Trp Gln Leu Ser His Phe Ala Arg
 225 230 235 240
 Val Leu Glu Glu Glu Glu Asn Lys Pro Asn Pro Val Thr Gln Arg Val
 245 250 255
 Lys Met Ile Met Ser Leu Gly Leu Val Leu Val His Ala His Ser Arg
 260 265 270
 Trp Ile Ala Asp Pro Ser Pro Gln Asn Ser Thr Ala Asp Asn Ser Lys
 275 280 285
 Val Ser Leu Gly Leu Asp Glu Asn Val Ser Lys Arg Ile Glu Pro Ser
 290 295 300
 Val Ser Leu Trp Gln Phe Tyr Leu Ser Lys Met Ile Ser Met Asp Ile
 305 310 315 320
 Glu Gln Val Ile Thr Leu Ser Leu Ala Leu Leu Leu Ala Val Lys Tyr
 325 330 335
 Ile Phe Phe Glu Gln Ala Glu Thr Glu Ser Thr Leu Ser Leu Lys Asn
 340 345 350
 Pro Ile Thr Ser Pro Val Val Thr Gln Lys Lys Ile Thr Asp Asp Cys
 355 360 365
 Cys Arg Arg Asp Pro Val Leu Val Arg Asn Asp Gln Lys Phe His Ala
 370 375 380
 Met Glu Glu Glu Thr Arg Lys Asn Arg Glu Arg Lys Val Glu Val Ile
 385 390 395 400
 Lys Pro Leu Leu Ala Glu Asn Asp Thr Ser His Arg Ala Thr Phe Val
 405 410 415
 Val Gly Asn Ser Ser Leu Leu Gly Thr Ser Leu Glu Leu Glu Thr Gln

SeqLst															
420					425					430					
Glu	Pro	Glu	Met	Glu	Leu	Pro	Val	Glu	Pro	Arg	Pro	Asn	Glu	Glu	Cys
		435					440					445			
Leu	Gln	Ile	Leu	Glu	Asn	Ala	Glu	Lys	Gly	Ala	Lys	Phe	Leu	Ser	Asp
	450					455					460				
Ala	Glu	Ile	Ile	Gln	Leu	Val	Asn	Ala	Lys	His	Ile	Pro	Ala	Tyr	Lys
465					470					475					480
Leu	Glu	Thr	Leu	Met	Glu	Thr	His	Glu	Arg	Gly	Val	Ser	Ile	Arg	Arg
				485					490					495	
Gln	Leu	Leu	Ser	Lys	Lys	Leu	Pro	Glu	Pro	Ser	Ser	Leu	Gln	Tyr	Leu
			500					505					510		
Pro	Tyr	Arg	Asp	Tyr	Asn	Tyr	Ser	Leu	Val	Met	Gly	Ala	Cys	Cys	Glu
		515					520					525			
Asn	Val	Ile	Gly	Tyr	Met	Pro	Ile	Pro	Val	Gly	Val	Ala	Gly	Pro	Leu
	530					535					540				
Cys	Leu	Asp	Gly	Lys	Glu	Phe	Gln	Val	Pro	Met	Ala	Thr	Thr	Glu	Gly
545					550					555					560
Cys	Leu	Val	Ala	Ser	Thr	Asn	Arg	Gly	Cys	Arg	Ala	Ile	Gly	Leu	Gly
				565					570					575	
Gly	Gly	Ala	Ser	Ser	Arg	Val	Leu	Ala	Asp	Gly	Met	Thr	Arg	Gly	Pro
			580					585					590		
Val	Val	Arg	Phe	Pro	Arg	Ala	Cys	Asp	Ser	Ala	Glu	Val	Lys	Ala	Trp
		595					600					605			
Leu	Glu	Thr	Pro	Glu	Gly	Phe	Thr	Val	Ile	Lys	Glu	Ala	Phe	Asp	Ser
	610					615					620				
Thr	Ser	Arg	Val	Ala	Arg	Leu	Gln	Lys	Leu	His	Met	Ser	Val	Ala	Gly
625					630					635					640
Arg	Asn	Leu	Tyr	Ile	Arg	Phe	Gln	Ser	Arg	Ser	Gly	Asp	Ala	Met	Gly
				645					650					655	
Met	Asn	Met	Ile	Ser	Lys	Gly	Thr	Glu	Lys	Ala	Leu	Ser	Lys	Leu	Gln
			660					665					670		

SeqLst

Glu Tyr Phe Pro Glu Met Gln Ile Leu Ala Val Ser Gly Asn Tyr Cys
675 680 685

Thr Asp Lys Lys Pro Ala Ala Ile Asn Trp Ile Glu Gly Arg Gly Lys
690 695 700

Ser Val Val Cys Glu Ala Val Ile Pro Ala Lys Val Val Arg Glu Val
705 710 715 720

Leu Lys Thr Thr Thr Glu Ala Met Ile Glu Val Asn Ile Asn Lys Asn
725 730 735

Leu Val Gly Ser Ala Met Ala Gly Ser Ile Gly Gly Tyr Asn Ala His
740 745 750

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

Ala Gln Asn Val Gly Ser Ser Asn Cys Ile Thr Leu Met Glu Ala Ser
770 775 780

Gly Pro Thr Asn Glu Asp Leu Tyr Ile Ser Cys Thr Met Pro Ser Ile
785 790 795 800

Glu Ile Gly Thr Val Gly Gly Gly Thr Asn Leu Leu Pro Gln Gln Ala
805 810 815

Cys Leu Gln Met Leu Gly Val Gln Gly Ala Cys Arg Asp Asn Pro Gly
820 825 830

Glu Asn Ala Arg Gln Leu Ala Arg Ile Val Cys Gly Thr Val Met Ala
835 840 845

Gly Glu Leu Ser Leu Met Ala Ala Leu Ala Ala Gly His Leu Val Arg
850 855 860

Ser His Met Ile His Asn Arg Ser Lys Ile Asn Leu Gln Asp Leu Gln
865 870 875 880

Gly Thr Cys Thr Lys Lys Ala Ala
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<210> 111

<211> 1704

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial sequence: Synthetic

SeqLst

polynucleotide

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<400> 111
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ttgtacctga ccaatacggt tttcttcact cttttctttt ccgtagcata ttacctgttg      180
catagggtgga gagacaagat tagatccgga acacctttac acgttgtgac actgactgaa      240
ctatccgcaa ttgtactgct gattgcttcc ttcattctatc ttttaggctt tttcgggtatt      300
gattttgtgc aatctttcac atcaagagaa aatgagcaac taaacaacga tgatcacaaac      360
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tgctcaattg ccggtaaaaa cttgtacatt aggtttactt gctccacagg cgacgccatg     1020
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cctgatattg acgtaattgg gatctcttgg aagttctgct ctgacaaaaa gccaacagct     1140
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atgccatcta tagaagttgg cacggtggga ggtggcactc agctagcctc tcaatcagcc     1500
tgtttgaact tgcttggtgt aaagggtgcc tgtatagaat ccccaggatc aaacgcccag     1560
ttgttagcta gaatcgttgc tggttctggt ctggcaggcg aattaagttt gatgtcagct     1620
ataagtgtcg ggcaactagt taaatctcat atgaaataca ataggtctag tagagatatg     1680
tcagcaatag cttctaaggt ctaa                                           1704

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<210> 112

SeqLst

<211> 567

<212> PRT

<213> Artemisia annua

<400> 112

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Thr Lys Gln Pro Ser His Arg Ser His Ser Pro Thr Pro Ile Pro Lys
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Ala Ser Asp Ala Leu Pro Leu Pro Leu Tyr Leu Thr Asn Thr Phe Phe
 35 40 45

Phe Thr Leu Phe Phe Ser Val Ala Tyr Tyr Leu Leu His Arg Trp Arg
 50 55 60

Asp Lys Ile Arg Ser Gly Thr Pro Leu His Val Val Thr Leu Thr Glu
 65 70 75 80

Leu Ser Ala Ile Val Leu Leu Ile Ala Ser Phe Ile Tyr Leu Leu Gly
 85 90 95

Phe Phe Gly Ile Asp Phe Val Gln Ser Phe Thr Ser Arg Glu Asn Glu
 100 105 110

Gln Leu Asn Asn Asp Asp His Asn Val Val Ser Thr Asn Asn Val Leu
 115 120 125

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

Asn Asp Asn Asp Asn Asp Asp Val Ile Val Lys Ser Val Val Ser
 145 150 155 160

Gly Glu Val Asn Ser Tyr Ser Leu Glu Ala Ser Leu Gly Asp Cys Tyr
 165 170 175

Arg Ala Ala Lys Ile Arg Lys Arg Ala Val Glu Arg Ile Val Gly Arg
 180 185 190

Glu Val Leu Gly Leu Gly Phe Glu Gly Phe Asp Tyr Glu Ser Ile Leu
 195 200 205

Gly Gln Cys Cys Glu Met Pro Ile Gly Tyr Val Gln Val Pro Val Gly
 210 215 220

Val Ala Gly Pro Leu Leu Leu Asn Gly Gly Glu Phe Met Val Pro Met
 225 230 235 240

SeqLst

Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Thr Asn Arg Gly Cys Lys
 245 250 255
 Ala Ile Cys Leu Ser Gly Gly Ala Thr Ala Ile Leu Leu Lys Asp Gly
 260 265 270
 Met Thr Arg Ala Pro Val Val Arg Phe Ala Thr Ala Glu Arg Ala Ser
 275 280 285
 Gln Leu Lys Phe Tyr Leu Glu Asp Gly Val Asn Phe Asp Thr Leu Ser
 290 295 300
 Val Val Phe Asn Lys Ser Ser Arg Phe Ala Arg Leu Gln Asn Ile Gln
 305 310 315 320
 Cys Ser Ile Ala Gly Lys Asn Leu Tyr Ile Arg Phe Thr Cys Ser Thr
 325 330 335
 Gly Asp Ala Met Gly Met Asn Met Val Ser Lys Gly Val Gln Asn Val
 340 345 350
 Leu Asp Phe Leu Gln Asn Asp Phe Pro Asp Met Asp Val Ile Gly Ile
 355 360 365
 Ser Trp Lys Phe Cys Ser Asp Lys Lys Pro Thr Ala Val Asn Trp Ile
 370 375 380
 Glu Gly Arg Gly Lys Ser Val Val Phe Gln Ala Val Ile Thr Lys Lys
 385 390 395 400
 Val Val Arg Lys Ser Ala Leu Asn Pro Gln Thr Cys Thr Cys Arg Thr
 405 410 415
 Leu Thr Cys Leu Arg Pro Leu Leu Val Leu Leu Leu Leu Val Leu Leu
 420 425 430
 Val Asp Leu Met His Met Leu His Ile Val Ser Ala Val Phe Ile Ala
 435 440 445
 Thr Gly Gln Asp Pro Ala Gln Asn Ile Glu Ser Ser His Cys Ile Thr
 450 455 460
 Met Met Glu Ala Val Asn Asn Gly Lys Asp Leu His Val Asn Val Thr
 465 470 475 480
 Met Pro Ser Ile Glu Val Gly Thr Val Gly Gly Gly Thr Gln Leu Ala

SeqLst

485	490	495
Ser Gln Ser Ala Cys Leu Asn Leu Leu Gly Val Lys Gly Ala Cys Ile		
500	505	510
Glu Ser Pro Gly Ser Asn Ala Gln Leu Leu Ala Arg Ile Val Ala Gly		
515	520	525
Ser Val Leu Ala Gly Glu Leu Ser Leu Met Ser Ala Ile Ser Ala Gly		
530	535	540
Gln Leu Val Lys Ser His Met Lys Tyr Asn Arg Ser Ser Arg Asp Met		
545	550	555
Ser Ala Ile Ala Ser Lys Val		
565		

<210> 113
 <211> 1308
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 113 atgtttagaa gagctatact gttaggatgc tctgctgcc aagacaccatg gtctgagtgt	60
tctaacgctc aattagttga tgcagttaag tctagaaaga tctcattcta cggctcttgaa	120
caagccttgg aaccagatta tagaagggtc atcgaagtaa ggagagaggt tgtctctgaa	180
atcgccctcac aacagccaga agcaaaaaag aagcaatccg cattgcacac aataccattt	240
gagaattatg attggaataa ggtcgttggc caaaactgtg aaaacattat tggatacgtc	300
ccaataccac tgggcgttgc tggccctatt ttgattgatg gtaaagagta cccaatacca	360
atggctacaa cagaaggcgc tttggctcgt agtactcata gaggtgctag agctattaca	420
agatccggag gttgtaagac attgttatta ggtgaaggta tgacaagagc accagtgggt	480
gaattgcctt cattagagga agctgggcgt ttgcacaagt actgtaatga gaacttctta	540
tctttaaagg aagcatttga atcaactacc caatatggaa aacttaattc tttaaagtgc	600
gtactagctg gtagaaaagc atacccttaga ttcagagcca ctacaggcga tgctatgggc	660
atgaacatga taacaaaggg ttagacaaa gcaactgtctg ttctacagca acatttcctt	720
tcaatggaaa tcctagccct aagtggtaat tactgtaccg acaaaaagcc atctgctgta	780
aattggattg atggcagagg taaatcagtg gttgcagaag ccactttatt ggctgatggt	840
gtcgaagata ctctgaaatg tacagtcgat tctttggtat ccttgaatat cgacaaaaac	900

SeqLst

```

cttgttgggt cagctatggc tggttctggt ggaggtttta acgcccaggc tgcaaacgct      960
gtggcagcca ttttcattgc aaccgggtcaa gatcctgctc aagtggtaga aagttcaatg      1020
tgtatcacta caatgtccaa ggtaggtaac gatctattga tctctgtgac catgccttct      1080
atcgaggtcg gggtcgtggg aggagggact ggtcttgctg cccaaagagg atgcttagag      1140
ttaatagggg gcggaggccc atctaaggag tctcctggta ctaatgccc acttctaagt      1200
agagttgttg cagctggcgt tttatcagcc gaactttcct tgatgtccgg actggcagca      1260
ggtcacatctat tgtcagcaca tatgagattg aacagaaaga agaaataa      1308

```

```

<210> 114
<211> 435
<212> PRT
<213> Trypanosoma cruzi

```

```

<400> 114
Met Phe Arg Arg Ala Ile Leu Leu Gly Cys Ser Ala Ala Lys Thr Pro
1      5      10      15

```

```

Trp Ser Glu Cys Ser Asn Ala Gln Leu Val Asp Ala Val Lys Ser Arg
      20      25      30

```

```

Lys Ile Ser Phe Tyr Gly Leu Glu Gln Ala Leu Glu Pro Asp Tyr Arg
      35      40      45

```

```

Arg Ala Ile Glu Val Arg Arg Glu Val Val Ser Glu Ile Ala Ser Gln
      50      55      60

```

```

Gln Pro Glu Ala Lys Lys Lys Gln Ser Ala Leu His Thr Ile Pro Phe
      65      70      75      80

```

```

Glu Asn Tyr Asp Trp Asn Lys Val Val Gly Gln Asn Cys Glu Asn Ile
      85      90      95

```

```

Ile Gly Tyr Val Pro Ile Pro Leu Gly Val Ala Gly Pro Ile Leu Ile
      100      105      110

```

```

Asp Gly Lys Glu Tyr Pro Ile Pro Met Ala Thr Thr Glu Gly Ala Leu
      115      120      125

```

```

Val Ala Ser Thr His Arg Gly Ala Arg Ala Ile Thr Arg Ser Gly Gly
      130      135      140

```

```

Cys Lys Thr Leu Leu Leu Gly Glu Gly Met Thr Arg Ala Pro Val Val
      145      150      155      160

```

```

Glu Leu Pro Ser Leu Glu Glu Ala Gly Arg Leu His Lys Tyr Cys Asn
      165      170      175

```

SeqLst

Glu Asn Phe Leu Ser Leu Lys Glu Ala Phe Glu Ser Thr Thr Gln Tyr
 180 185 190
 Gly Lys Leu Asn Ser Leu Lys Cys Val Leu Ala Gly Arg Lys Ala Tyr
 195 200 205
 Leu Arg Phe Arg Ala Thr Thr Gly Asp Ala Met Gly Met Asn Met Ile
 210 215 220
 Thr Lys Gly Val Asp Lys Ala Leu Ser Val Leu Gln Gln His Phe Pro
 225 230 235 240
 Ser Met Glu Ile Leu Ala Leu Ser Gly Asn Tyr Cys Thr Asp Lys Lys
 245 250 255
 Pro Ser Ala Val Asn Trp Ile Asp Gly Arg Gly Lys Ser Val Val Ala
 260 265 270
 Glu Ala Thr Leu Leu Ala Asp Val Val Glu Asp Thr Leu Lys Cys Thr
 275 280 285
 Val Asp Ser Leu Val Ser Leu Asn Ile Asp Lys Asn Leu Val Gly Ser
 290 295 300
 Ala Met Ala Gly Ser Val Gly Gly Phe Asn Ala Gln Ala Ala Asn Ala
 305 310 315 320
 Val Ala Ala Ile Phe Ile Ala Thr Gly Gln Asp Pro Ala Gln Val Val
 325 330 335
 Glu Ser Ser Met Cys Ile Thr Thr Met Ser Lys Val Gly Asn Asp Leu
 340 345 350
 Leu Ile Ser Val Thr Met Pro Ser Ile Glu Val Gly Val Val Gly Gly
 355 360 365
 Gly Thr Gly Leu Ala Ala Gln Arg Gly Cys Leu Glu Leu Ile Gly Cys
 370 375 380
 Gly Gly Pro Ser Lys Glu Ser Pro Gly Thr Asn Ala Gln Leu Leu Ser
 385 390 395 400
 Arg Val Val Ala Ala Gly Val Leu Ser Ala Glu Leu Ser Leu Met Ser
 405 410 415
 Gly Leu Ala Ala Gly His Leu Leu Ser Ala His Met Arg Leu Asn Arg

Lys Lys Lys
435

<210> 115
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

```
<400> 115
atgcaatccc tggacaaaaa ctttagacac ttatcaagac aacagaagtt acaacagcta      60
gttgataaac aatggctatc agaggaacaa ttcaatattc tacttaacca cccacttatt      120
gatgaagagg tagcaaactc attgatagaa aatgtcatcg cacagggcgc actgcctggt      180
ggtttactac caaatatcat cgttgatgac aaagcatacg tcgtgcctat gatggtggaa      240
gagccatctg ttgttgccgc tgcttcatac ggcgctaaat tggngaacca aacaggtggt      300
ttcaaaaccg tgtcctcaga acgtatcatg ataggtcaaa tagtatttga tggagtcgat      360
gataccgaga aactgtctgc agatatcaag gctcttgaaa aacaaatcca tcagattgca      420
gatgaggctt acccttctat taaggccaga ggtggaggct atcaaaggat cgccatcgat      480
acattcccag aacaacagtt gctttcattg aagggttttcg ttgatactaa ggatgctatg      540
ggcgctaata tgtaaacac aatcctagaa gcaatcacag cttttttgaa aaacgaattc      600
ccacaatctg atatcttgat gtctatcctt tccaaccacg caacagccag tgttgtcaag      660
gtccaggggtg aaatagacgt taaggatttg gcaagaggag aacgtactgg agaagagggtc      720
gctaagagaa tggaaagagc atctgtgtta gctcaagtgg acattcatag agcagcaaca      780
cacaataagg gtgttatgaa tggcattcat gctgtagtct tggctacagg taatgatact      840
agagggtgcag aagcctctgc tcacgcttac gcttccaaag acggtcaata tagagggata      900
gctacatgga gatacgatca agagagacaa aggttaatag gaactataga agttccaatg      960
actctggcca ttgttggtgg cggtaccaag gtactgccta ttgctaaggc ctcttttagaa     1020
ctgttaaacg tagaaagtgc ccaagagttg ggacatgttg tcgctgccgt tggactagct     1080
caaaacttcg ctgcatgtag agctttgggt tccgaaggta ttcaacaagg gcatatgtct     1140
ttgcaataca agtcttttagc catcgtagtc ggggctaagg gcgatgaaat tgctcaggta     1200
gccgaagcac taaagcaaga gccaaagagca aacactcaag ttgcagagag aattttgcaa     1260
gatttgagaa gtcaacaata a                                     1281
```

<210> 116

SeqLst

<211> 426

<212> PRT

<213> Staphylococcus aureus

<400> 116

Met Gln Ser Leu Asp Lys Asn Phe Arg His Leu Ser Arg Gln Gln Lys
 1 5 10 15

Leu Gln Gln Leu Val Asp Lys Gln Trp Leu Ser Glu Glu Gln Phe Asn
 20 25 30

Ile Leu Leu Asn His Pro Leu Ile Asp Glu Glu Val Ala Asn Ser Leu
 35 40 45

Ile Glu Asn Val Ile Ala Gln Gly Ala Leu Pro Val Gly Leu Leu Pro
 50 55 60

Asn Ile Ile Val Asp Asp Lys Ala Tyr Val Val Pro Met Met Val Glu
 65 70 75 80

Glu Pro Ser Val Val Ala Ala Ala Ser Tyr Gly Ala Lys Leu Val Asn
 85 90 95

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

Gln Ile Val Phe Asp Gly Val Asp Asp Thr Glu Lys Leu Ser Ala Asp
 115 120 125

Ile Lys Ala Leu Glu Lys Gln Ile His Gln Ile Ala Asp Glu Ala Tyr
 130 135 140

Pro Ser Ile Lys Ala Arg Gly Gly Gly Tyr Gln Arg Ile Ala Ile Asp
 145 150 155 160

Thr Phe Pro Glu Gln Gln Leu Leu Ser Leu Lys Val Phe Val Asp Thr
 165 170 175

Lys Asp Ala Met Gly Ala Asn Met Leu Asn Thr Ile Leu Glu Ala Ile
 180 185 190

Thr Ala Phe Leu Lys Asn Glu Phe Pro Gln Ser Asp Ile Leu Met Ser
 195 200 205

Ile Leu Ser Asn His Ala Thr Ala Ser Val Val Lys Val Gln Gly Glu
 210 215 220

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

SeqLst

Ala Lys Arg Met Glu Arg Ala Ser Val Leu Ala Gln Val Asp Ile His
245 250 255

Arg Ala Ala Thr His Asn Lys Gly Val Met Asn Gly Ile His Ala Val
260 265 270

Val Leu Ala Thr Gly Asn Asp Thr Arg Gly Ala Glu Ala Ser Ala His
275 280 285

Ala Tyr Ala Ser Lys Asp Gly Gln Tyr Arg Gly Ile Ala Thr Trp Arg
290 295 300

Tyr Asp Gln Glu Arg Gln Arg Leu Ile Gly Thr Ile Glu Val Pro Met
305 310 315 320

Thr Leu Ala Ile Val Gly Gly Gly Thr Lys Val Leu Pro Ile Ala Lys
325 330 335

Ala Ser Leu Glu Leu Leu Asn Val Glu Ser Ala Gln Glu Leu Gly His
340 345 350

Val Val Ala Ala Val Gly Leu Ala Gln Asn Phe Ala Ala Cys Arg Ala
355 360 365

Leu Val Ser Glu Gly Ile Gln Gln Gly His Met Ser Leu Gln Tyr Lys
370 375 380

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

Ala Glu Ala Leu Lys Gln Glu Pro Arg Ala Asn Thr Gln Val Ala Glu
405 410 415

Arg Ile Leu Gln Asp Leu Arg Ser Gln Gln
420 425

<210> 117

<211> 1311

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 117

atgcaggctt taagattgga taggagacat tacaaaagtg gcaagattag aagagcaatg 60

agttctagaa ttcttggttt ctacaaattg tcagtcgagg aaagactgaa aaaggttgct 120

SeqLst

```

gaatttgtag gggtatctga tgaggaagtg aaagctgttt tgtcacaagg tttacctttg      180
gacgtagctg atagaatgat cgaaaatgtg atcggtacat ttgaattacc acttggtata      240
gcaaccaatt tccttattga tggcaaggat tatctaatacc ctatggctat agaggaacca      300
tcagtagttg cagctgcttc taacgcagct agaatggcca gagagtctgg cgggtttaca      360
actgattaca caggggtccct gatgattggg caaattcaag tcacaaaact gttgaatcca      420
aatgcagcta agttcgaagt tctacgtcaa aaagacgaaa tcatagaaag agcaaatagag      480
tgtgatccaa tgttggtgaa tttgggcggg ggatgtaaag atatagaagc aaggggtgatc      540
gatacaatca tgggtaagat gctaattggt catctgatcg ttgatgttaa agacgctatg      600
gggtgcaaag ctgtcaacac tatgtgtgaa aaagttgctc ctttcacgga acgtattact      660
gggggaaagg tctatcttag aatcatttcc aacttggtcg catatagact tgctagagca      720
aaggccggtt ttgacaaaga cggtattggc ggagaggagg ttgtagaagg gatcatgctt      780
gcatacgctt tcgctgccgc tgacccattt cgttgcgcca cccacaataa gggatatcatg      840
aatggcatat cagccttaat gatcgctaca ggaaacgact ttagagccat tgaagcagga      900
gctcattcct atgctgcaat aggtggatag aaaccactaa ctacctacga agttgataga      960
aaaggtaatc tagtaggcac aattgaaata cctatggcag taggcgtgat tgggtggtgca     1020
accaaagtca acccactagc caagatctct cttagatagc taggagtga cactgctgaa     1080
gagttagcca gagtcgcagc cgctctaggg ttggctcaaa actttgctgc cttagagacc     1140
ttggccacag aaggtatcca aagaggtcac atggaattac atgccaggaa cttagcaatc     1200
atggctggag ctactggaga tgaggttgac agagttgtag agattatggg gagagatggc     1260
aaaatcagat tggactacgc taaggaagta ttggagagac tgcgttccta a              1311

```

<210> 118

<211> 436

<212> PRT

<213> Archaeoglobus fulgidus

<400> 118

```

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

```

```

Arg Arg Ala Met Ser Ser Arg Ile Pro Gly Phe Tyr Lys Leu Ser Val
          20          25          30

```

```

Glu Glu Arg Leu Lys Lys Val Ala Glu Phe Ala Gly Leu Ser Asp Glu
          35          40          45

```

```

Glu Val Lys Ala Val Leu Ser Gln Gly Leu Pro Leu Asp Val Ala Asp
          50          55          60

```

SeqLst

Arg Met Ile Glu Asn Val Ile Gly Thr Phe Glu Leu Pro Leu Gly Ile
 65 70 75 80
 Ala Thr Asn Phe Leu Ile Asp Gly Lys Asp Tyr Leu Ile Pro Met Ala
 85 90 95
 Ile Glu Glu Pro Ser Val Val Ala Ala Ala Ser Asn Ala Ala Arg Met
 100 105 110
 Ala Arg Glu Ser Gly Gly Phe Thr Thr Asp Tyr Thr Gly Ser Leu Met
 115 120 125
 Ile Gly Gln Ile Gln Val Thr Lys Leu Leu Asn Pro Asn Ala Ala Lys
 130 135 140
 Phe Glu Val Leu Arg Gln Lys Asp Glu Ile Ile Glu Arg Ala Asn Glu
 145 150 155 160
 Cys Asp Pro Met Leu Val Asn Leu Gly Gly Gly Cys Lys Asp Ile Glu
 165 170 175
 Ala Arg Val Ile Asp Thr Ile Met Gly Lys Met Leu Ile Val His Leu
 180 185 190
 Ile Val Asp Val Lys Asp Ala Met Gly Ala Asn Ala Val Asn Thr Met
 195 200 205
 Cys Glu Lys Val Ala Pro Phe Ile Glu Arg Ile Thr Gly Gly Lys Val
 210 215 220
 Tyr Leu Arg Ile Ile Ser Asn Leu Ala Ala Tyr Arg Leu Ala Arg Ala
 225 230 235 240
 Lys Ala Val Phe Asp Lys Asp Val Ile Gly Gly Glu Glu Val Val Glu
 245 250 255
 Gly Ile Met Leu Ala Tyr Ala Phe Ala Ala Ala Asp Pro Phe Arg Cys
 260 265 270
 Ala Thr His Asn Lys Gly Ile Met Asn Gly Ile Ser Ala Leu Met Ile
 275 280 285
 Ala Thr Gly Asn Asp Phe Arg Ala Ile Glu Ala Gly Ala His Ser Tyr
 290 295 300
 Ala Ala Ile Gly Gly Tyr Lys Pro Leu Thr Thr Tyr Glu Val Asp Arg
 305 310 315 320

SeqLst

Lys Gly Asn Leu Val Gly Thr Ile Glu Ile Pro Met Ala Val Gly Val
325 330 335

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

Ile Leu Gly Val Asn Thr Ala Glu Glu Leu Ala Arg Val Ala Ala Ala
355 360 365

Leu Gly Leu Ala Gln Asn Phe Ala Ala Leu Arg Ala Leu Ala Thr Glu
370 375 380

Gly Ile Gln Arg Gly His Met Glu Leu His Ala Arg Asn Leu Ala Ile
385 390 395 400

Met Ala Gly Ala Thr Gly Asp Glu Val Asp Arg Val Val Glu Ile Met
405 410 415

Val Arg Asp Gly Lys Ile Arg Leu Asp Tyr Ala Lys Glu Val Leu Glu
420 425 430

Arg Leu Arg Ser
435

<210> 119

<211> 1287

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 119

atgtccttag attcaagact gccagctttc agaaatctgt ctccagctgc aagactagat	60
cacattggcc aacttttggg actaagtcac gacgacgttt ccttttttagc aaacgccggt	120
gctttaccaa tggatatcgc taatggtatg attgaaaatg taatcgggac ctttgaactg	180
ccatatgcag tggccagtaa ctttcagatc aatggccgtg acgtcttagt accattagtt	240
gtggaggaac ctagtatcgt tgctgcagcc tcttacatgg caaagtttagc tagagccaat	300
gggtgggttca ctacatcttc atctgctcca ctaatgcatg cacaagtaca aattgtcggc	360
attcaggatc cactaaacgc aagattgtct ttactgcgta gaaaggatga gatcatagaa	420
ttagccaata ggaaggacca acttctgaat tcattgggcg gtggttgag agacatagag	480
gtgcatacat ttgccgatac tccaagagga ccaatgcttg tagcacacct tattgtcgat	540
gtgcgtgatg ccatgggagc taatactgtt aacactatgg ctgaagcagt agcacctctg	600

SeqLst

```

atggaagcca taacaggtgg ccaggtaaga ttgagaatcc tttccaattt ggctgatctt      660
agattggcca gagcccaagt gagaatcact cctcagcaat tggaaactgc cgaattctca      720
ggtgaggcag taattgaggg tatcttggac gcatatgctt ttgccgctgt ggacccttac      780
agagccgcta cccacaacaa aggcataatg aacggtatcg atcctttgat cgtcgctaca      840
ggaaatgatt ggagagctgt tgaggcagga gctcatgcat acgctttag atccggacat      900
tacggttcat taacaacatg ggaaaaagat aacaatggac acttggtcgg gacattggaa      960
atgcctatgc cagttgggtt agttgggggt gctacaaaaa cccatcctct tgctcaattg     1020
tctttgagga tacttggtgt caaaactgct caagcactag ccgaaattgc cgttgctggt     1080
ggtttggcac aaaacttggg tgcaatgcgt gctttagcta cagaaggcat ccaaagagga     1140
catatggctc tacacgctag aaacattgca gttgttgtag gagccagagg tgatgaggtt     1200
gattgggtgg ctagacaact tgtcgaatat catgatgtca gagcagacag ggctgtggca     1260
ttactgaaac agaagagagg tcaataa                                     1287

```

<210> 120

<211> 428

<212> PRT

<213> Pseudomonas mevalonii

<400> 120

```

Met Ser Leu Asp Ser Arg Leu Pro Ala Phe Arg Asn Leu Ser Pro Ala
1           5           10           15

```

```

Ala Arg Leu Asp His Ile Gly Gln Leu Leu Gly Leu Ser His Asp Asp
          20           25           30

```

```

Val Ser Leu Leu Ala Asn Ala Gly Ala Leu Pro Met Asp Ile Ala Asn
          35           40           45

```

```

Gly Met Ile Glu Asn Val Ile Gly Thr Phe Glu Leu Pro Tyr Ala Val
50           55           60

```

```

Ala Ser Asn Phe Gln Ile Asn Gly Arg Asp Val Leu Val Pro Leu Val
65           70           75           80

```

```

Val Glu Glu Pro Ser Ile Val Ala Ala Ala Ser Tyr Met Ala Lys Leu
          85           90           95

```

```

Ala Arg Ala Asn Gly Gly Phe Thr Thr Ser Ser Ser Ala Pro Leu Met
100           105           110

```

```

His Ala Gln Val Gln Ile Val Gly Ile Gln Asp Pro Leu Asn Ala Arg
115           120           125

```

SeqLst

Leu Ser Leu Leu Arg Arg Lys Asp Glu Ile Ile Glu Leu Ala Asn Arg
 130 135 140
 Lys Asp Gln Leu Leu Asn Ser Leu Gly Gly Gly Cys Arg Asp Ile Glu
 145 150 155 160
 Val His Thr Phe Ala Asp Thr Pro Arg Gly Pro Met Leu Val Ala His
 165 170 175
 Leu Ile Val Asp Val Arg Asp Ala Met Gly Ala Asn Thr Val Asn Thr
 180 185 190
 Met Ala Glu Ala Val Ala Pro Leu Met Glu Ala Ile Thr Gly Gly Gln
 195 200 205
 Val Arg Leu Arg Ile Leu Ser Asn Leu Ala Asp Leu Arg Leu Ala Arg
 210 215 220
 Ala Gln Val Arg Ile Thr Pro Gln Gln Leu Glu Thr Ala Glu Phe Ser
 225 230 235 240
 Gly Glu Ala Val Ile Glu Gly Ile Leu Asp Ala Tyr Ala Phe Ala Ala
 245 250 255
 Val Asp Pro Tyr Arg Ala Ala Thr His Asn Lys Gly Ile Met Asn Gly
 260 265 270
 Ile Asp Pro Leu Ile Val Ala Thr Gly Asn Asp Trp Arg Ala Val Glu
 275 280 285
 Ala Gly Ala His Ala Tyr Ala Cys Arg Ser Gly His Tyr Gly Ser Leu
 290 295 300
 Thr Thr Trp Glu Lys Asp Asn Asn Gly His Leu Val Gly Thr Leu Glu
 305 310 315 320
 Met Pro Met Pro Val Gly Leu Val Gly Gly Ala Thr Lys Thr His Pro
 325 330 335
 Leu Ala Gln Leu Ser Leu Arg Ile Leu Gly Val Lys Thr Ala Gln Ala
 340 345 350
 Leu Ala Glu Ile Ala Val Ala Val Gly Leu Ala Gln Asn Leu Gly Ala
 355 360 365
 Met Arg Ala Leu Ala Thr Glu Gly Ile Gln Arg Gly His Met Ala Leu
 370 375 380

SeqLst

His Ala Arg Asn Ile Ala Val Val Ala Gly Ala Arg Gly Asp Glu Val
 385 390 395 400

Asp Trp Val Ala Arg Gln Leu Val Glu Tyr His Asp Val Arg Ala Asp
 405 410 415

Arg Ala Val Ala Leu Leu Lys Gln Lys Arg Gly Gln
 420 425

<210> 121

<211> 361

<212> PRT

<213> Stevia rebaudiana

<400> 121

Met Ala Leu Val Asn Pro Thr Ala Leu Phe Tyr Gly Thr Ser Ile Arg
 1 5 10 15

Thr Arg Pro Thr Asn Leu Leu Asn Pro Thr Gln Lys Leu Arg Pro Val
 20 25 30

Ser Ser Ser Ser Leu Pro Ser Phe Ser Ser Val Ser Ala Ile Leu Thr
 35 40 45

Glu Lys His Gln Ser Asn Pro Ser Glu Asn Asn Asn Leu Gln Thr His
 50 55 60

Leu Glu Thr Pro Phe Asn Phe Asp Ser Tyr Met Leu Glu Lys Val Asn
 65 70 75 80

Met Val Asn Glu Ala Leu Asp Ala Ser Val Pro Leu Lys Asp Pro Ile
 85 90 95

Lys Ile His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg
 100 105 110

Ile Arg Pro Met Met Cys Ile Ala Ala Cys Glu Ile Val Gly Gly Asn
 115 120 125

Ile Leu Asn Ala Met Pro Ala Ala Cys Ala Val Glu Met Ile His Thr
 130 135 140

Met Ser Leu Val His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe
 145 150 155 160

Arg Arg Gly Lys Pro Ile Ser His Lys Val Tyr Gly Glu Glu Met Ala
 165 170 175

SeqLst

Val Leu Thr Gly Asp Ala Leu Leu Ser Leu Ser Phe Glu His Ile Ala
 180 185 190
 Thr Ala Thr Lys Gly Val Ser Lys Asp Arg Ile Val Arg Ala Ile Gly
 195 200 205
 Glu Leu Ala Arg Ser Val Gly Ser Glu Gly Leu Val Ala Gly Gln Val
 210 215 220
 Val Asp Ile Leu Ser Glu Gly Ala Asp Val Gly Leu Asp His Leu Glu
 225 230 235 240
 Tyr Ile His Ile His Lys Thr Ala Met Leu Leu Glu Ser Ser Val Val
 245 250 255
 Ile Gly Ala Ile Met Gly Gly Gly Ser Asp Gln Gln Ile Glu Lys Leu
 260 265 270
 Arg Lys Phe Ala Arg Ser Ile Gly Leu Leu Phe Gln Val Val Asp Asp
 275 280 285
 Ile Leu Asp Val Thr Lys Ser Thr Glu Glu Leu Gly Lys Thr Ala Gly
 290 295 300
 Lys Asp Leu Leu Thr Asp Lys Thr Thr Tyr Pro Lys Leu Leu Gly Ile
 305 310 315 320
 Glu Lys Ser Arg Glu Phe Ala Glu Lys Leu Asn Lys Glu Ala Gln Glu
 325 330 335
 Gln Leu Ser Gly Phe Asp Arg Arg Lys Ala Ala Pro Leu Ile Ala Leu
 340 345 350
 Ala Asn Tyr Asn Ala Tyr Arg Gln Asn
 355 360
 <210> 122
 <211> 342
 <212> PRT
 <213> Gibberella fujikuroi
 <400> 122
 Met Ala Glu Gln Gln Ile Ser Asn Leu Leu Ser Met Phe Asp Ala Ser
 1 5 10 15
 His Ala Ser Gln Lys Leu Glu Ile Thr Val Gln Met Met Asp Thr Tyr
 20 25 30

SeqLst

His Tyr Arg Glu Thr Pro Pro Asp Ser Ser Ser Ser Glu Gly Gly Ser
35 40 45

Leu Ser Arg Tyr Asp Glu Arg Arg Val Ser Leu Pro Leu Ser His Asn
50 55 60

Ala Ala Ser Pro Asp Ile Val Ser Gln Leu Cys Phe Ser Thr Ala Met
65 70 75 80

Ser Ser Glu Leu Asn His Arg Trp Lys Ser Gln Arg Leu Lys Val Ala
85 90 95

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

Gly Ala Phe Ile Asp Ser Leu Asn Val Trp Leu Glu Val Pro Glu Asp
115 120 125

Glu Thr Ser Val Ile Lys Glu Val Ile Gly Met Leu His Asn Ser Ser
130 135 140

Leu Ile Ile Asp Asp Phe Gln Asp Asn Ser Pro Leu Arg Arg Gly Lys
145 150 155 160

Pro Ser Thr His Thr Val Phe Gly Pro Ala Gln Ala Ile Asn Thr Ala
165 170 175

Thr Tyr Val Ile Val Lys Ala Ile Glu Lys Ile Gln Asp Ile Val Gly
180 185 190

His Asp Ala Leu Ala Asp Val Thr Gly Thr Ile Thr Thr Ile Phe Gln
195 200 205

Gly Gln Ala Met Asp Leu Trp Trp Thr Ala Asn Ala Ile Val Pro Ser
210 215 220

Ile Gln Glu Tyr Leu Leu Met Val Asn Asp Lys Thr Gly Ala Leu Phe
225 230 235 240

Arg Leu Ser Leu Glu Leu Leu Ala Leu Asn Ser Glu Ala Ser Ile Ser
245 250 255

Asp Ser Ala Leu Glu Ser Leu Ser Ser Ala Val Ser Leu Leu Gly Gln
260 265 270

Tyr Phe Gln Ile Arg Asp Asp Tyr Met Asn Leu Ile Asp Asn Lys Tyr
275 280 285

SeqLst

Thr Asp Gln Lys Gly Phe Cys Glu Asp Leu Asp Glu Gly Lys Tyr Ser
 290 295 300

Leu Thr Leu Ile His Ala Leu Gln Thr Asp Ser Ser Asp Leu Leu Thr
 305 310 315 320

Asn Ile Leu Ser Met Arg Arg Val Gln Gly Lys Leu Thr Ala Gln Lys
 325 330 335

Arg Cys Trp Phe Trp Lys
 340

<210> 123

<211> 300

<212> PRT

<213> Mus musculus

<400> 123

Met Glu Lys Thr Lys Glu Lys Ala Glu Arg Ile Leu Leu Glu Pro Tyr
 1 5 10 15

Arg Tyr Leu Leu Gln Leu Pro Gly Lys Gln Val Arg Ser Lys Leu Ser
 20 25 30

Gln Ala Phe Asn His Trp Leu Lys Val Pro Glu Asp Lys Leu Gln Ile
 35 40 45

Ile Ile Glu Val Thr Glu Met Leu His Asn Ala Ser Leu Leu Ile Asp
 50 55 60

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

Ser Ile Tyr Gly Val Pro Ser Val Ile Asn Ser Ala Asn Tyr Val Tyr
 85 90 95

Phe Leu Gly Leu Glu Lys Val Leu Thr Leu Asp His Pro Asp Ala Val
 100 105 110

Lys Leu Phe Thr Arg Gln Leu Leu Glu Leu His Gln Gly Gln Gly Leu
 115 120 125

Asp Ile Tyr Trp Arg Asp Thr Tyr Thr Cys Pro Thr Glu Glu Glu Tyr
 130 135 140

Lys Ala Met Val Leu Gln Lys Thr Gly Gly Leu Phe Gly Leu Ala Val
 145 150 155 160

SeqLst

Gly Leu Met Gln Leu Phe Ser Asp Tyr Lys Glu Asp Leu Lys Pro Leu
165 170 175

Leu Asp Thr Leu Gly Leu Phe Phe Gln Ile Arg Asp Asp Tyr Ala Asn
180 185 190

Leu His Ser Lys Glu Tyr Ser Glu Asn Lys Ser Phe Cys Glu Asp Leu
195 200 205

Thr Glu Gly Lys Phe Ser Phe Pro Thr Ile His Ala Ile Trp Ser Arg
210 215 220

Pro Glu Ser Thr Gln Val Gln Asn Ile Leu Arg Gln Arg Thr Glu Asn
225 230 235 240

Ile Asp Ile Lys Lys Tyr Cys Val Gln Tyr Leu Glu Asp Val Gly Ser
245 250 255

Phe Ala Tyr Thr Arg His Thr Leu Arg Glu Leu Glu Ala Lys Ala Tyr
260 265 270

Lys Gln Ile Glu Ala Cys Gly Gly Asn Pro Ser Leu Val Ala Leu Val
275 280 285

Lys His Leu Ser Lys Met Phe Thr Glu Glu Asn Lys
290 295 300

<210> 124
<211> 339
<212> PRT
<213> Thalassiosira pseudonana

<400> 124
Met Ala Arg Phe Tyr Phe Leu Asn Ala Leu Leu Met Val Ile Ser Leu
1 5 10 15

Gln Ser Thr Thr Ala Phe Thr Pro Ala Lys Leu Ala Tyr Pro Thr Thr
20 25 30

Thr Thr Ala Leu Asn Val Ala Ser Ala Glu Thr Ser Phe Ser Leu Asp
35 40 45

Glu Tyr Leu Ala Ser Lys Ile Gly Pro Ile Glu Ser Ala Leu Glu Ala
50 55 60

Ser Val Lys Ser Arg Ile Pro Gln Thr Asp Lys Ile Cys Glu Ser Met
65 70 75 80

Ala Tyr Ser Leu Met Ala Gly Gly Lys Arg Ile Arg Pro Val Leu Cys

														SeqLst																
85														90		95														
Ile	Ala	Ala	Cys	Glu	Met	Phe	Gly	Gly	Ser	Gln	Asp	Val	Ala	Met	Pro															
			100					105					110																	
Thr	Ala	Val	Ala	Leu	Glu	Met	Ile	His	Thr	Met	Ser	Leu	Ile	His	Asp															
		115					120					125																		
Asp	Leu	Pro	Ser	Met	Asp	Asn	Asp	Asp	Leu	Arg	Arg	Gly	Lys	Pro	Thr															
	130					135					140																			
Asn	His	Val	Val	Phe	Gly	Glu	Asp	Val	Ala	Ile	Leu	Ala	Gly	Asp	Ser															
145					150					155					160															
Leu	Leu	Ser	Thr	Ser	Phe	Glu	His	Val	Ala	Arg	Glu	Thr	Lys	Gly	Val															
				165					170					175																
Ser	Ala	Glu	Lys	Ile	Val	Asp	Val	Ile	Ala	Arg	Leu	Gly	Lys	Ser	Val															
			180					185					190																	
Gly	Ala	Glu	Gly	Leu	Ala	Gly	Gly	Gln	Val	Met	Asp	Leu	Glu	Cys	Glu															
		195					200					205																		
Ala	Lys	Pro	Gly	Thr	Thr	Leu	Asp	Asp	Leu	Lys	Trp	Ile	His	Ile	His															
	210					215					220																			
Lys	Thr	Ala	Thr	Leu	Leu	Gln	Val	Ala	Val	Ala	Ser	Gly	Ala	Val	Leu															
225					230					235					240															
Gly	Gly	Ala	Thr	Pro	Glu	Glu	Val	Ala	Ala	Cys	Glu	Leu	Phe	Ala	Met															
				245					250					255																
Asn	Ile	Gly	Leu	Ala	Phe	Gln	Val	Ala	Asp	Asp	Ile	Leu	Asp	Val	Thr															
			260					265					270																	
Ala	Ser	Ser	Glu	Asp	Leu	Gly	Lys	Thr	Ala	Gly	Lys	Asp	Glu	Ala	Thr															
		275					280					285																		
Asp	Lys	Thr	Thr	Tyr	Pro	Lys	Leu	Leu	Gly	Leu	Glu	Glu	Ser	Lys	Ala															
	290					295					300																			
Tyr	Ala	Arg	Gln	Leu	Ile	Asp	Glu	Ala	Lys	Glu	Ser	Leu	Ala	Pro	Phe															
305					310					315					320															
Gly	Asp	Arg	Ala	Ala	Pro	Leu	Leu	Ala	Ile	Ala	Asp	Phe	Ile	Ile	Asp															
				325					330					335																

SeqLst

Arg Lys Asn

<210> 125

<211> 355

<212> PRT

<213> Streptomyces clavuligerus

<400> 125

Met His Leu Ala Pro Arg Arg Val Pro Arg Gly Arg Arg Ser Pro Pro
 1 5 10 15

Asp Arg Val Pro Glu Arg Gln Gly Ala Leu Gly Arg Arg Arg Gly Ala
 20 25 30

Gly Ser Thr Gly Cys Ala Arg Ala Ala Ala Gly Val His Arg Arg Arg
 35 40 45

Gly Gly Gly Glu Ala Asp Pro Ser Ala Ala Val His Arg Gly Trp Gln
 50 55 60

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

Ala Leu Glu Met Phe His Ala Phe Ala Leu Ile His Asp Asp Ile Met
 85 90 95

Asp Asp Ser Ala Thr Arg Arg Gly Ser Pro Thr Val His Arg Ala Leu
 100 105 110

Ala Asp Arg Leu Gly Ala Ala Leu Asp Pro Asp Gln Ala Gly Gln Leu
 115 120 125

Gly Val Ser Thr Ala Ile Leu Val Gly Asp Leu Ala Leu Thr Trp Ser
 130 135 140

Asp Glu Leu Leu Tyr Ala Pro Leu Thr Pro His Arg Leu Ala Ala Val
 145 150 155 160

Leu Pro Leu Val Thr Ala Met Arg Ala Glu Thr Val His Gly Gln Tyr
 165 170 175

Leu Asp Ile Thr Ser Ala Arg Arg Pro Gly Thr Asp Thr Ser Leu Ala
 180 185 190

Leu Arg Ile Ala Arg Tyr Lys Thr Ala Ala Tyr Thr Met Glu Arg Pro
 195 200 205

Leu His Ile Gly Ala Ala Leu Ala Gly Ala Arg Pro Glu Leu Leu Ala

															SeqLst	
210					215					220						
Gly	Leu	Ser	Ala	Tyr	Ala	Leu	Pro	Ala	Gly	Glu	Ala	Phe	Gln	Leu	Ala	
225					230					235					240	
Asp	Asp	Leu	Leu	Gly	Val	Phe	Gly	Asp	Pro	Arg	Arg	Thr	Gly	Lys	Pro	
				245					250					255		
Asp	Leu	Asp	Asp	Leu	Arg	Gly	Gly	Lys	His	Thr	Val	Leu	Val	Ala	Leu	
			260					265					270			
Ala	Arg	Glu	His	Ala	Thr	Pro	Glu	Gln	Arg	His	Thr	Leu	Asp	Thr	Leu	
		275					280					285				
Leu	Gly	Thr	Pro	Gly	Leu	Asp	Arg	Gln	Gly	Ala	Ser	Arg	Leu	Arg	Cys	
	290					295					300					
Val	Leu	Val	Ala	Thr	Gly	Ala	Arg	Ala	Glu	Ala	Glu	Arg	Leu	Ile	Thr	
305					310					315					320	
Glu	Arg	Arg	Asp	Gln	Ala	Leu	Thr	Ala	Leu	Asn	Ala	Leu	Thr	Leu	Pro	
				325					330					335		
Pro	Pro	Leu	Ala	Glu	Ala	Leu	Ala	Arg	Leu	Thr	Leu	Gly	Ser	Thr	Ala	
			340					345					350			
His	Pro	Ala														
		355														

<210> 126
 <211> 330
 <212> PRT
 <213> Sulfolobus acidicaldarius

<400> 126																
Met	Ser	Tyr	Phe	Asp	Asn	Tyr	Phe	Asn	Glu	Ile	Val	Asn	Ser	Val	Asn	
1				5					10					15		
Asp	Ile	Ile	Lys	Ser	Tyr	Ile	Ser	Gly	Asp	Val	Pro	Lys	Leu	Tyr	Glu	
			20					25					30			
Ala	Ser	Tyr	His	Leu	Phe	Thr	Ser	Gly	Gly	Lys	Arg	Leu	Arg	Pro	Leu	
		35					40					45				
Ile	Leu	Thr	Ile	Ser	Ser	Asp	Leu	Phe	Gly	Gly	Gln	Arg	Glu	Arg	Ala	
	50					55					60					
Tyr	Tyr	Ala	Gly	Ala	Ala	Ile	Glu	Val	Leu	His	Thr	Phe	Thr	Leu	Val	
65					70					75					80	

SeqLst

His Asp Asp Ile Met Asp Gln Asp Asn Ile Arg Arg Gly Leu Pro Thr
 85 90 95
 Val His Val Lys Tyr Gly Leu Pro Leu Ala Ile Leu Ala Gly Asp Leu
 100 105 110
 Leu His Ala Lys Ala Phe Gln Leu Leu Thr Gln Ala Leu Arg Gly Leu
 115 120 125
 Pro Ser Glu Thr Ile Ile Lys Ala Phe Asp Ile Phe Thr Arg Ser Ile
 130 135 140
 Ile Ile Ile Ser Glu Gly Gln Ala Val Asp Met Glu Phe Glu Asp Arg
 145 150 155 160
 Ile Asp Ile Lys Glu Gln Glu Tyr Leu Asp Met Ile Ser Arg Lys Thr
 165 170 175
 Ala Ala Leu Phe Ser Ala Ser Ser Ser Ile Gly Ala Leu Ile Ala Gly
 180 185 190
 Ala Asn Asp Asn Asp Val Arg Leu Met Ser Asp Phe Gly Thr Asn Leu
 195 200 205
 Gly Ile Ala Phe Gln Ile Val Asp Asp Ile Leu Gly Leu Thr Ala Asp
 210 215 220
 Glu Lys Glu Leu Gly Lys Pro Val Phe Ser Asp Ile Arg Glu Gly Lys
 225 230 235 240
 Lys Thr Ile Leu Val Ile Lys Thr Leu Glu Leu Cys Lys Glu Asp Glu
 245 250 255
 Lys Lys Ile Val Leu Lys Ala Leu Gly Asn Lys Ser Ala Ser Lys Glu
 260 265 270
 Glu Leu Met Ser Ser Ala Asp Ile Ile Lys Lys Tyr Ser Leu Asp Tyr
 275 280 285
 Ala Tyr Asn Leu Ala Glu Lys Tyr Tyr Lys Asn Ala Ile Asp Ser Leu
 290 295 300
 Asn Gln Val Ser Ser Lys Ser Asp Ile Pro Gly Lys Ala Leu Lys Tyr
 305 310 315 320
 Leu Ala Glu Phe Thr Ile Arg Arg Arg Lys

325

SeqLst
330

<210> 127

<211> 297

<212> PRT

<213> Synechococcus sp.

<400> 127

Met Val Ala Gln Thr Phe Asn Leu Asp Thr Tyr Leu Ser Gln Arg Gln
1 5 10 15Gln Gln Val Glu Glu Ala Leu Ser Ala Ala Leu Val Pro Ala Tyr Pro
20 25 30Glu Arg Ile Tyr Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys
35 40 45Arg Leu Arg Pro Ile Leu Cys Leu Ala Ala Cys Glu Leu Ala Gly Gly
50 55 60Ser Val Glu Gln Ala Met Pro Thr Ala Cys Ala Leu Glu Met Ile His
65 70 75 80Thr Met Ser Leu Ile His Asp Asp Leu Pro Ala Met Asp Asn Asp Asp
85 90 95Phe Arg Arg Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Ile
100 105 110Ala Ile Leu Ala Gly Asp Ala Leu Leu Ala Tyr Ala Phe Glu His Ile
115 120 125Ala Ser Gln Thr Arg Gly Val Pro Pro Gln Leu Val Leu Gln Val Ile
130 135 140Ala Arg Ile Gly His Ala Val Ala Ala Thr Gly Leu Val Gly Gly Gln
145 150 155 160Val Val Asp Leu Glu Ser Glu Gly Lys Ala Ile Ser Leu Glu Thr Leu
165 170 175Glu Tyr Ile His Ser His Lys Thr Gly Ala Leu Leu Glu Ala Ser Val
180 185 190Val Ser Gly Gly Ile Leu Ala Gly Ala Asp Glu Glu Leu Leu Ala Arg
195 200 205Leu Ser His Tyr Ala Arg Asp Ile Gly Leu Ala Phe Gln Ile Val Asp
210 215 220

SeqLst

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

Gly Lys Asp Gln Ala Ala Ala Lys Ala Thr Tyr Pro Ser Leu Leu Gly
 245 250 255

Leu Glu Ala Ser Arg Gln Lys Ala Glu Glu Leu Ile Gln Ser Ala Lys
 260 265 270

Glu Ala Leu Arg Pro Tyr Gly Ser Gln Ala Glu Pro Leu Leu Ala Leu
 275 280 285

Ala Asp Phe Ile Thr Arg Arg Gln His
 290 295

<210> 128

<211> 371

<212> PRT

<213> Arabidopsis thaliana

<400> 128

Met Ala Ser Val Thr Leu Gly Ser Trp Ile Val Val His His His Asn
 1 5 10 15

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

Pro Ile Thr Leu Thr Lys Pro Ile Ser Phe Arg Ser Lys Arg Thr Val
 35 40 45

Ser Ser Ser Ser Ser Ile Val Ser Ser Ser Val Val Thr Lys Glu Asp
 50 55 60

Asn Leu Arg Gln Ser Glu Pro Ser Ser Phe Asp Phe Met Ser Tyr Ile
 65 70 75 80

Ile Thr Lys Ala Glu Leu Val Asn Lys Ala Leu Asp Ser Ala Val Pro
 85 90 95

Leu Arg Glu Pro Leu Lys Ile His Glu Ala Met Arg Tyr Ser Leu Leu
 100 105 110

Ala Gly Gly Lys Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu
 115 120 125

Leu Val Gly Gly Glu Glu Ser Thr Ala Met Pro Ala Ala Cys Ala Val
 130 135 140

SeqLst

Glu Met Ile His Thr Met Ser Leu Ile His Asp Asp Leu Pro Cys Met
 145 150 155 160
 Asp Asn Asp Asp Leu Arg Arg Gly Lys Pro Thr Asn His Lys Val Phe
 165 170 175
 Gly Glu Asp Val Ala Val Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala
 180 185 190
 Phe Glu His Leu Ala Ser Ala Thr Ser Ser Asp Val Val Ser Pro Val
 195 200 205
 Arg Val Val Arg Ala Val Gly Glu Leu Ala Lys Ala Ile Gly Thr Glu
 210 215 220
 Gly Leu Val Ala Gly Gln Val Val Asp Ile Ser Ser Glu Gly Leu Asp
 225 230 235 240
 Leu Asn Asp Val Gly Leu Glu His Leu Glu Phe Ile His Leu His Lys
 245 250 255
 Thr Ala Ala Leu Leu Glu Ala Ser Ala Val Leu Gly Ala Ile Val Gly
 260 265 270
 Gly Gly Ser Asp Asp Glu Ile Glu Arg Leu Arg Lys Phe Ala Arg Cys
 275 280 285
 Ile Gly Leu Leu Phe Gln Val Val Asp Asp Ile Leu Asp Val Thr Lys
 290 295 300
 Ser Ser Lys Glu Leu Gly Lys Thr Ala Gly Lys Asp Leu Ile Ala Asp
 305 310 315 320
 Lys Leu Thr Tyr Pro Lys Ile Met Gly Leu Glu Lys Ser Arg Glu Phe
 325 330 335
 Ala Glu Lys Leu Asn Arg Glu Ala Arg Asp Gln Leu Leu Gly Phe Asp
 340 345 350
 Ser Asp Lys Val Ala Pro Leu Leu Ala Leu Ala Asn Tyr Ile Ala Tyr
 355 360 365
 Arg Gln Asn
 370

<210> 129

<211> 787

SeqLst

<212> PRT

<213> Stevia rebaudiana

<400> 129

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

Ser Pro Ala Thr Thr Phe Arg His His Leu Ser Pro Ala Thr Thr Asn
 20 25 30

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

Val Ser Lys Glu Tyr Ser Asp Leu Leu Gln Lys Asp Glu Ala Ser Phe
 50 55 60

Thr Lys Trp Asp Asp Asp Lys Val Lys Asp His Leu Asp Thr Asn Lys
 65 70 75 80

Asn Leu Tyr Pro Asn Asp Glu Ile Lys Glu Phe Val Glu Ser Val Lys
 85 90 95

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

Asp Thr Ala Trp Val Ala Leu Val Gln Asp Val Asp Gly Ser Gly Ser
 115 120 125

Pro Gln Phe Pro Ser Ser Leu Glu Trp Ile Ala Asn Asn Gln Leu Ser
 130 135 140

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

Ile Asn Thr Leu Ala Cys Val Ile Ala Leu Thr Ser Trp Asn Val His
 165 170 175

Pro Ser Lys Cys Glu Lys Gly Leu Asn Phe Leu Arg Glu Asn Ile Cys
 180 185 190

Lys Leu Glu Asp Glu Asn Ala Glu His Met Pro Ile Gly Phe Glu Val
 195 200 205

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

Pro Glu Asp Thr Pro Ala Leu Lys Glu Ile Tyr Ala Arg Arg Asp Ile
 225 230 235 240

SeqLst

Lys Leu Thr Lys Ile Pro Met Glu Val Leu His Lys Val Pro Thr Thr
 245 250 255
 Leu Leu His Ser Leu Glu Gly Met Pro Asp Leu Glu Trp Glu Lys Leu
 260 265 270
 Leu Lys Leu Gln Cys Lys Asp Gly Ser Phe Leu Phe Ser Pro Ser Ser
 275 280 285
 Thr Ala Phe Ala Leu Met Gln Thr Lys Asp Glu Lys Cys Leu Gln Tyr
 290 295 300
 Leu Thr Asn Ile Val Thr Lys Phe Asn Gly Gly Val Pro Asn Val Tyr
 305 310 315 320
 Pro Val Asp Leu Phe Glu His Ile Trp Val Val Asp Arg Leu Gln Arg
 325 330 335
 Leu Gly Ile Ala Arg Tyr Phe Lys Ser Glu Ile Lys Asp Cys Val Glu
 340 345 350
 Tyr Ile Asn Lys Tyr Trp Thr Lys Asn Gly Ile Cys Trp Ala Arg Asn
 355 360 365
 Thr His Val Gln Asp Ile Asp Asp Thr Ala Met Gly Phe Arg Val Leu
 370 375 380
 Arg Ala His Gly Tyr Asp Val Thr Pro Asp Val Phe Arg Gln Phe Glu
 385 390 395 400
 Lys Asp Gly Lys Phe Val Cys Phe Ala Gly Gln Ser Thr Gln Ala Val
 405 410 415
 Thr Gly Met Phe Asn Val Tyr Arg Ala Ser Gln Met Leu Phe Pro Gly
 420 425 430
 Glu Arg Ile Leu Glu Asp Ala Lys Lys Phe Ser Tyr Asn Tyr Leu Lys
 435 440 445
 Glu Lys Gln Ser Thr Asn Glu Leu Leu Asp Lys Trp Ile Ile Ala Lys
 450 455 460
 Asp Leu Pro Gly Glu Val Gly Tyr Ala Leu Asp Ile Pro Trp Tyr Ala
 465 470 475 480
 Ser Leu Pro Arg Leu Glu Thr Arg Tyr Tyr Leu Glu Gln Tyr Gly Gly
 485 490 495

SeqLst

Glu Asp Asp Val Trp Ile Gly Lys Thr Leu Tyr Arg Met Gly Tyr Val
 500 505 510
 Ser Asn Asn Thr Tyr Leu Glu Met Ala Lys Leu Asp Tyr Asn Asn Tyr
 515 520 525
 Val Ala Val Leu Gln Leu Glu Trp Tyr Thr Ile Gln Gln Trp Tyr Val
 530 535 540
 Asp Ile Gly Ile Glu Lys Phe Glu Ser Asp Asn Ile Lys Ser Val Leu
 545 550 555 560
 Val Ser Tyr Tyr Leu Ala Ala Ala Ser Ile Phe Glu Pro Glu Arg Ser
 565 570 575
 Lys Glu Arg Ile Ala Trp Ala Lys Thr Thr Ile Leu Val Asp Lys Ile
 580 585 590
 Thr Ser Ile Phe Asp Ser Ser Gln Ser Ser Lys Glu Asp Ile Thr Ala
 595 600 605
 Phe Ile Asp Lys Phe Arg Asn Lys Ser Ser Ser Lys Lys His Ser Ile
 610 615 620
 Asn Gly Glu Pro Trp His Glu Val Met Val Ala Leu Lys Lys Thr Leu
 625 630 635 640
 His Gly Phe Ala Leu Asp Ala Leu Met Thr His Ser Gln Asp Ile His
 645 650 655
 Pro Gln Leu His Gln Ala Trp Glu Met Trp Leu Thr Lys Leu Gln Asp
 660 665 670
 Gly Val Asp Val Thr Ala Glu Leu Met Val Gln Met Ile Asn Met Thr
 675 680 685
 Ala Gly Arg Trp Val Ser Lys Glu Leu Leu Thr His Pro Gln Tyr Gln
 690 695 700
 Arg Leu Ser Thr Val Thr Asn Ser Val Cys His Asp Ile Thr Lys Leu
 705 710 715 720
 His Asn Phe Lys Glu Asn Ser Thr Thr Val Asp Ser Lys Val Gln Glu
 725 730 735
 Leu Val Gln Leu Val Phe Ser Asp Thr Pro Asp Asp Leu Asp Gln Asp

SeqLst															
740								745				750			
Met	Lys	Gln	Thr	Phe	Leu	Thr	Val	Met	Lys	Thr	Phe	Tyr	Tyr	Lys	Ala
		755					760					765			
Trp	Cys	Asp	Pro	Asn	Thr	Ile	Asn	Asp	His	Ile	Ser	Lys	Val	Phe	Glu
	770					775					780				
Ile	Val	Ile													
785															
<210> 130															
<211> 527															
<212> PRT															
<213> Streptomyces clavuligerus															
<400> 130															
Met	Pro	Asp	Ala	His	Asp	Ala	Pro	Pro	Pro	Gln	Ile	Arg	Gln	Arg	Thr
1				5					10					15	
Leu	Val	Asp	Glu	Ala	Thr	Gln	Leu	Leu	Thr	Glu	Ser	Ala	Glu	Asp	Ala
			20					25					30		
Trp	Gly	Glu	Val	Ser	Val	Ser	Glu	Tyr	Glu	Thr	Ala	Arg	Leu	Val	Ala
		35					40					45			
His	Ala	Thr	Trp	Leu	Gly	Gly	His	Ala	Thr	Arg	Val	Ala	Phe	Leu	Leu
	50					55					60				
Glu	Arg	Gln	His	Glu	Asp	Gly	Ser	Trp	Gly	Pro	Pro	Gly	Gly	Tyr	Arg
65					70					75					80
Leu	Val	Pro	Thr	Leu	Ser	Ala	Val	His	Ala	Leu	Leu	Thr	Cys	Leu	Ala
				85					90					95	
Ser	Pro	Ala	Gln	Asp	His	Gly	Val	Pro	His	Asp	Arg	Leu	Leu	Arg	Ala
			100					105					110		
Val	Asp	Ala	Gly	Leu	Thr	Ala	Leu	Arg	Arg	Leu	Gly	Thr	Ser	Asp	Ser
		115					120					125			
Pro	Pro	Asp	Thr	Ile	Ala	Val	Glu	Leu	Val	Ile	Pro	Ser	Leu	Leu	Glu
	130					135					140				
Gly	Ile	Gln	His	Leu	Leu	Asp	Pro	Ala	His	Pro	His	Ser	Arg	Pro	Ala
145					150					155					160
Phe	Ser	Gln	His	Arg	Gly	Ser	Leu	Val	Cys	Pro	Gly	Gly	Leu	Asp	Gly
				165					170					175	

SeqLst

Arg Thr Leu Gly Ala Leu Arg Ser His Ala Ala Ala Gly Thr Pro Val
 180 185 190
 Pro Gly Lys Val Trp His Ala Ser Glu Thr Leu Gly Leu Ser Thr Glu
 195 200 205
 Ala Ala Ser His Leu Gln Pro Ala Gln Gly Ile Ile Gly Gly Ser Ala
 210 215 220
 Ala Ala Thr Ala Thr Trp Leu Thr Arg Val Ala Pro Ser Gln Gln Ser
 225 230 235 240
 Asp Ser Ala Arg Arg Tyr Leu Glu Glu Leu Gln His Arg Tyr Ser Gly
 245 250 255
 Pro Val Pro Ser Ile Thr Pro Ile Thr Tyr Phe Glu Arg Ala Trp Leu
 260 265 270
 Leu Asn Asn Phe Ala Ala Ala Gly Val Pro Cys Glu Ala Pro Ala Ala
 275 280 285
 Leu Leu Asp Ser Leu Glu Ala Ala Leu Thr Pro Gln Gly Ala Pro Ala
 290 295 300
 Gly Ala Gly Leu Pro Pro Asp Ala Asp Asp Thr Ala Ala Val Leu Leu
 305 310 315 320
 Ala Leu Ala Thr His Gly Arg Gly Arg Arg Pro Glu Val Leu Met Asp
 325 330 335
 Tyr Arg Thr Asp Gly Tyr Phe Gln Cys Phe Ile Gly Glu Arg Thr Pro
 340 345 350
 Ser Ile Ser Thr Asn Ala His Val Leu Glu Thr Leu Gly His His Val
 355 360 365
 Ala Gln His Pro Gln Asp Arg Ala Arg Tyr Gly Ser Ala Met Asp Thr
 370 375 380
 Ala Ser Ala Trp Leu Leu Ala Ala Gln Lys Gln Asp Gly Ser Trp Leu
 385 390 395 400
 Asp Lys Trp His Ala Ser Pro Tyr Tyr Ala Thr Val Cys Cys Thr Gln
 405 410 415
 Ala Leu Ala Ala His Ala Ser Pro Ala Thr Ala Pro Ala Arg Gln Arg

SeqLst

420

425

430

Ala Val Arg Trp Val Leu Ala Thr Gln Arg Ser Asp Gly Gly Trp Gly
 435 440 445

Leu Trp His Ser Thr Val Glu Glu Thr Ala Tyr Ala Leu Gln Ile Leu
 450 455 460

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

Arg Gly Arg Ala Arg Leu Cys Gly Ala Leu Pro Leu Thr Pro Leu Trp
 485 490 495

His Asp Lys Asp Leu Tyr Thr Pro Val Arg Val Val Arg Ala Ala Arg
 500 505 510

Ala Ala Ala Leu Tyr Thr Thr Arg Asp Leu Leu Leu Pro Pro Leu
 515 520 525

<210> 131

<211> 516

<212> PRT

<213> Bradyrhizobium japonicum

<400> 131

Met Asn Ala Leu Ser Glu His Ile Leu Ser Glu Leu Arg Arg Leu Leu
 1 5 10 15

Ser Glu Met Ser Asp Gly Gly Ser Val Gly Pro Ser Val Tyr Asp Thr
 20 25 30

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

Tyr Ala Trp Leu Ile Ala Gln Gln Gln Ala Asp Gly Gly Trp Gly Ser
 50 55 60

Ala Asp Phe Pro Leu Phe Arg His Ala Pro Thr Trp Ala Ala Leu Leu
 65 70 75 80

Ala Leu Gln Arg Ala Asp Pro Leu Pro Gly Ala Ala Asp Ala Val Gln
 85 90 95

Thr Ala Thr Arg Phe Leu Gln Arg Gln Pro Asp Pro Tyr Ala His Ala
 100 105 110

Val Pro Glu Asp Ala Pro Ile Gly Ala Glu Leu Ile Leu Pro Gln Phe
 115 120 125

SeqLst

Cys Gly Glu Ala Ala Trp Leu Leu Gly Gly Val Ala Phe Pro Arg His
 130 135 140
 Pro Ala Leu Leu Pro Leu Arg Gln Ala Cys Leu Val Lys Leu Gly Ala
 145 150 155 160
 Val Ala Met Leu Pro Ser Gly His Pro Leu Leu His Ser Trp Glu Ala
 165 170 175
 Trp Gly Thr Ser Pro Thr Thr Ala Cys Pro Asp Asp Asp Gly Ser Ile
 180 185 190
 Gly Ile Ser Pro Ala Ala Thr Ala Ala Trp Arg Ala Gln Ala Val Thr
 195 200 205
 Arg Gly Ser Thr Pro Gln Val Gly Arg Ala Asp Ala Tyr Leu Gln Met
 210 215 220
 Ala Ser Arg Ala Thr Arg Ser Gly Ile Glu Gly Val Phe Pro Asn Val
 225 230 235 240
 Trp Pro Ile Asn Val Phe Glu Pro Cys Trp Ser Leu Tyr Thr Leu His
 245 250 255
 Leu Ala Gly Leu Phe Ala His Pro Ala Leu Ala Glu Ala Val Arg Val
 260 265 270
 Ile Val Ala Gln Leu Glu Ala Arg Leu Gly Val His Gly Leu Gly Pro
 275 280 285
 Ala Leu His Phe Ala Ala Asp Ala Asp Asp Thr Ala Val Ala Leu Cys
 290 295 300
 Val Leu His Leu Ala Gly Arg Asp Pro Ala Val Asp Ala Leu Arg His
 305 310 315 320
 Phe Glu Ile Gly Glu Leu Phe Val Thr Phe Pro Gly Glu Arg Asn Ala
 325 330 335
 Ser Val Ser Thr Asn Ile His Ala Leu His Ala Leu Arg Leu Leu Gly
 340 345 350
 Lys Pro Ala Ala Gly Ala Ser Ala Tyr Val Glu Ala Asn Arg Asn Pro
 355 360 365
 His Gly Leu Trp Asp Asn Glu Lys Trp His Val Ser Trp Leu Tyr Pro

SeqLst
380

370

375

Thr Ala His Ala Val Ala Ala Leu Ala Gln Gly Lys Pro Gln Trp Arg
385 390 395 400

Asp Glu Arg Ala Leu Ala Ala Leu Leu Gln Ala Gln Arg Asp Asp Gly
405 410 415

Gly Trp Gly Ala Gly Arg Gly Ser Thr Phe Glu Glu Thr Ala Tyr Ala
420 425 430

Leu Phe Ala Leu His Val Met Asp Gly Ser Glu Glu Ala Thr Gly Arg
435 440 445

Arg Arg Ile Ala Gln Val Val Ala Arg Ala Leu Glu Trp Met Leu Ala
450 455 460

Arg His Ala Ala His Gly Leu Pro Gln Thr Pro Leu Trp Ile Gly Lys
465 470 475 480

Glu Leu Tyr Cys Pro Thr Arg Val Val Arg Val Ala Glu Leu Ala Gly
485 490 495

Leu Trp Leu Ala Leu Arg Trp Gly Arg Arg Val Leu Ala Glu Gly Ala
500 505 510

Gly Ala Ala Pro
515

<210> 132

<211> 784

<212> PRT

<213> Stevia rebaudiana

<400> 132

Met Asn Leu Ser Leu Cys Ile Ala Ser Pro Leu Leu Thr Lys Ser Asn
1 5 10 15

Arg Pro Ala Ala Leu Ser Ala Ile His Thr Ala Ser Thr Ser His Gly
20 25 30

Gly Gln Thr Asn Pro Thr Asn Leu Ile Ile Asp Thr Thr Lys Glu Arg
35 40 45

Ile Gln Lys Gln Phe Lys Asn Val Glu Ile Ser Val Ser Ser Tyr Asp
50 55 60

Thr Ala Trp Val Ala Met Val Pro Ser Pro Asn Ser Pro Lys Ser Pro
65 70 75 80

SeqLst

Cys Phe Pro Glu Cys Leu Asn Trp Leu Ile Asn Asn Gln Leu Asn Asp
 85 90 95
 Gly Ser Trp Gly Leu Val Asn His Thr His Asn His Asn His Pro Leu
 100 105 110
 Leu Lys Asp Ser Leu Ser Ser Thr Leu Ala Cys Ile Val Ala Leu Lys
 115 120 125
 Arg Trp Asn Val Gly Glu Asp Gln Ile Asn Lys Gly Leu Ser Phe Ile
 130 135 140
 Glu Ser Asn Leu Ala Ser Ala Thr Glu Lys Ser Gln Pro Ser Pro Ile
 145 150 155 160
 Gly Phe Asp Ile Ile Phe Pro Gly Leu Leu Glu Tyr Ala Lys Asn Leu
 165 170 175
 Asp Ile Asn Leu Leu Ser Lys Gln Thr Asp Phe Ser Leu Met Leu His
 180 185 190
 Lys Arg Glu Leu Glu Gln Lys Arg Cys His Ser Asn Glu Met Asp Gly
 195 200 205
 Tyr Leu Ala Tyr Ile Ser Glu Gly Leu Gly Asn Leu Tyr Asp Trp Asn
 210 215 220
 Met Val Lys Lys Tyr Gln Met Lys Asn Gly Ser Val Phe Asn Ser Pro
 225 230 235 240
 Ser Ala Thr Ala Ala Ala Phe Ile Asn His Gln Asn Pro Gly Cys Leu
 245 250 255
 Asn Tyr Leu Asn Ser Leu Leu Asp Lys Phe Gly Asn Ala Val Pro Thr
 260 265 270
 Val Tyr Pro His Asp Leu Phe Ile Arg Leu Ser Met Val Asp Thr Ile
 275 280 285
 Glu Arg Leu Gly Ile Ser His His Phe Arg Val Glu Ile Lys Asn Val
 290 295 300
 Leu Asp Glu Thr Tyr Arg Cys Trp Val Glu Arg Asp Glu Gln Ile Phe
 305 310 315 320
 Met Asp Val Val Thr Cys Ala Leu Ala Phe Arg Leu Leu Arg Ile Asn

															SeqLst															
325										330					335															
Gly	Tyr	Glu	Val	Ser	Pro	Asp	Pro	Leu	Ala	Glu	Ile	Thr	Asn	Glu	Leu															
			340					345					350																	
Ala	Leu	Lys	Asp	Glu	Tyr	Ala	Ala	Leu	Glu	Thr	Tyr	His	Ala	Ser	His															
		355					360					365																		
Ile	Leu	Tyr	Gln	Glu	Asp	Leu	Ser	Ser	Gly	Lys	Gln	Ile	Leu	Lys	Ser															
	370					375					380																			
Ala	Asp	Phe	Leu	Lys	Glu	Ile	Ile	Ser	Thr	Asp	Ser	Asn	Arg	Leu	Ser															
385					390					395				400																
Lys	Leu	Ile	His	Lys	Glu	Val	Glu	Asn	Ala	Leu	Lys	Phe	Pro	Ile	Asn															
				405					410					415																
Thr	Gly	Leu	Glu	Arg	Ile	Asn	Thr	Arg	Arg	Asn	Ile	Gln	Leu	Tyr	Asn															
			420					425					430																	
Val	Asp	Asn	Thr	Arg	Ile	Leu	Lys	Thr	Thr	Tyr	His	Ser	Ser	Asn	Ile															
		435					440					445																		
Ser	Asn	Thr	Asp	Tyr	Leu	Arg	Leu	Ala	Val	Glu	Asp	Phe	Tyr	Thr	Cys															
	450					455					460																			
Gln	Ser	Ile	Tyr	Arg	Glu	Glu	Leu	Lys	Gly	Leu	Glu	Arg	Trp	Val	Val															
465					470					475				480																
Glu	Asn	Lys	Leu	Asp	Gln	Leu	Lys	Phe	Ala	Arg	Gln	Lys	Thr	Ala	Tyr															
				485					490					495																
Cys	Tyr	Phe	Ser	Val	Ala	Ala	Thr	Leu	Ser	Ser	Pro	Glu	Leu	Ser	Asp															
			500					505					510																	
Ala	Arg	Ile	Ser	Trp	Ala	Lys	Asn	Gly	Ile	Leu	Thr	Thr	Val	Val	Asp															
		515					520					525																		
Asp	Phe	Phe	Asp	Ile	Gly	Gly	Thr	Ile	Asp	Glu	Leu	Thr	Asn	Leu	Ile															
	530					535					540																			
Gln	Cys	Val	Glu	Lys	Trp	Asn	Val	Asp	Val	Asp	Lys	Asp	Cys	Cys	Ser															
545					550					555				560																
Glu	His	Val	Arg	Ile	Leu	Phe	Leu	Ala	Leu	Lys	Asp	Ala	Ile	Cys	Trp															
				565					570					575																

SeqLst

Ile Gly Asp Glu Ala Phe Lys Trp Gln Ala Arg Asp Val Thr Ser His
580 585 590

Val Ile Gln Thr Trp Leu Glu Leu Met Asn Ser Met Leu Arg Glu Ala
595 600 605

Ile Trp Thr Arg Asp Ala Tyr Val Pro Thr Leu Asn Glu Tyr Met Glu
610 615 620

Asn Ala Tyr Val Ser Phe Ala Leu Gly Pro Ile Val Lys Pro Ala Ile
625 630 635 640

Tyr Phe Val Gly Pro Lys Leu Ser Glu Glu Ile Val Glu Ser Ser Glu
645 650 655

Tyr His Asn Leu Phe Lys Leu Met Ser Thr Gln Gly Arg Leu Leu Asn
660 665 670

Asp Ile His Ser Phe Lys Arg Glu Phe Lys Glu Gly Lys Leu Asn Ala
675 680 685

Val Ala Leu His Leu Ser Asn Gly Glu Ser Gly Lys Val Glu Glu Glu
690 695 700

Val Val Glu Glu Met Met Met Met Ile Lys Asn Lys Arg Lys Glu Leu
705 710 715 720

Met Lys Leu Ile Phe Glu Glu Asn Gly Ser Ile Val Pro Arg Ala Cys
725 730 735

Lys Asp Ala Phe Trp Asn Met Cys His Val Leu Asn Phe Phe Tyr Ala
740 745 750

Asn Asp Asp Gly Phe Thr Gly Asn Thr Ile Leu Asp Thr Val Lys Asp
755 760 765

Ile Ile Tyr Asn Pro Leu Val Leu Val Asn Glu Asn Glu Glu Gln Arg
770 775 780

<210> 133
<211> 784
<212> PRT
<213> Stevia rebaudiana

<400> 133
Met Asn Leu Ser Leu Cys Ile Ala Ser Pro Leu Leu Thr Lys Ser Ser
1 5 10 15

Arg Pro Thr Ala Leu Ser Ala Ile His Thr Ala Ser Thr Ser His Gly

															SeqLst															
20					25					30																				
Gly	Gln	Thr	Asn	Pro	Thr	Asn	Leu	Ile	Ile	Asp	Thr	Thr	Lys	Glu	Arg															
		35					40					45																		
Ile	Gln	Lys	Leu	Phe	Lys	Asn	Val	Glu	Ile	Ser	Val	Ser	Ser	Tyr	Asp															
	50					55					60																			
Thr	Ala	Trp	Val	Ala	Met	Val	Pro	Ser	Pro	Asn	Ser	Pro	Lys	Ser	Pro															
65					70					75					80															
Cys	Phe	Pro	Glu	Cys	Leu	Asn	Trp	Leu	Ile	Asn	Asn	Gln	Leu	Asn	Asp															
				85					90					95																
Gly	Ser	Trp	Gly	Leu	Val	Asn	His	Thr	His	Asn	His	Asn	His	Pro	Leu															
			100					105					110																	
Leu	Lys	Asp	Ser	Leu	Ser	Ser	Thr	Leu	Ala	Cys	Ile	Val	Ala	Leu	Lys															
		115					120					125																		
Arg	Trp	Asn	Val	Gly	Glu	Asp	Gln	Ile	Asn	Lys	Gly	Leu	Ser	Phe	Ile															
	130					135					140																			
Glu	Ser	Asn	Leu	Ala	Ser	Ala	Thr	Asp	Lys	Ser	Gln	Pro	Ser	Pro	Ile															
145					150					155					160															
Gly	Phe	Asp	Ile	Ile	Phe	Pro	Gly	Leu	Leu	Glu	Tyr	Ala	Lys	Asn	Leu															
				165					170					175																
Asp	Ile	Asn	Leu	Leu	Ser	Lys	Gln	Thr	Asp	Phe	Ser	Leu	Met	Leu	His															
			180					185					190																	
Lys	Arg	Glu	Leu	Glu	Gln	Lys	Arg	Cys	His	Ser	Asn	Glu	Ile	Asp	Gly															
		195					200					205																		
Tyr	Leu	Ala	Tyr	Ile	Ser	Glu	Gly	Leu	Gly	Asn	Leu	Tyr	Asp	Trp	Asn															
	210					215					220																			
Met	Val	Lys	Lys	Tyr	Gln	Met	Lys	Asn	Gly	Ser	Val	Phe	Asn	Ser	Pro															
225					230					235					240															
Ser	Ala	Thr	Ala	Ala	Ala	Phe	Ile	Asn	His	Gln	Asn	Pro	Gly	Cys	Leu															
				245					250					255																
Asn	Tyr	Leu	Asn	Ser	Leu	Leu	Asp	Lys	Phe	Gly	Asn	Ala	Val	Pro	Thr															
			260					265					270																	

SeqLst

Val Tyr Pro Leu Asp Leu Tyr Ile Arg Leu Ser Met Val Asp Thr Ile
275 280 285

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

Leu Asp Glu Thr Tyr Arg Cys Trp Val Glu Arg Asp Glu Gln Ile Phe
305 310 315 320

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

Gly Tyr Lys Val Ser Pro Asp Gln Leu Ala Glu Ile Thr Asn Glu Leu
340 345 350

Ala Phe Lys Asp Glu Tyr Ala Ala Leu Glu Thr Tyr His Ala Ser Gln
355 360 365

Ile Leu Tyr Gln Glu Asp Leu Ser Ser Gly Lys Gln Ile Leu Lys Ser
370 375 380

Ala Asp Phe Leu Lys Gly Ile Leu Ser Thr Asp Ser Asn Arg Leu Ser
385 390 395 400

Lys Leu Ile His Lys Glu Val Glu Asn Ala Leu Lys Phe Pro Ile Asn
405 410 415

Thr Gly Leu Glu Arg Ile Asn Thr Arg Arg Asn Ile Gln Leu Tyr Asn
420 425 430

Val Asp Asn Thr Arg Ile Leu Lys Thr Thr Tyr His Ser Ser Asn Ile
435 440 445

Ser Asn Thr Tyr Tyr Leu Arg Leu Ala Val Glu Asp Phe Tyr Thr Cys
450 455 460

Gln Ser Ile Tyr Arg Glu Glu Leu Lys Gly Leu Glu Arg Trp Val Val
465 470 475 480

Gln Asn Lys Leu Asp Gln Leu Lys Phe Ala Arg Gln Lys Thr Ala Tyr
485 490 495

Cys Tyr Phe Ser Val Ala Ala Thr Leu Ser Ser Pro Glu Leu Ser Asp
500 505 510

Ala Arg Ile Ser Trp Ala Lys Asn Gly Ile Leu Thr Thr Val Val Asp
515 520 525

SeqLst

Asp Phe Phe Asp Ile Gly Gly Thr Ile Asp Glu Leu Thr Asn Leu Ile
 530 535 540
 Gln Cys Val Glu Lys Trp Asn Val Asp Val Asp Lys Asp Cys Cys Ser
 545 550 555 560
 Glu His Val Arg Ile Leu Phe Leu Ala Leu Lys Asp Ala Ile Cys Trp
 565 570 575
 Ile Gly Asp Glu Ala Phe Lys Trp Gln Ala Arg Asp Val Thr Ser His
 580 585 590
 Val Ile Gln Thr Trp Leu Glu Leu Met Asn Ser Met Leu Arg Glu Ala
 595 600 605
 Ile Trp Thr Arg Asp Ala Tyr Val Pro Thr Leu Asn Glu Tyr Met Glu
 610 615 620
 Asn Ala Tyr Val Ser Phe Ala Leu Gly Pro Ile Val Lys Pro Ala Ile
 625 630 635 640
 Tyr Phe Val Gly Pro Lys Leu Ser Glu Glu Ile Val Glu Ser Ser Glu
 645 650 655
 Tyr His Asn Leu Phe Lys Leu Met Ser Thr Gln Gly Arg Leu Leu Asn
 660 665 670
 Asp Ile His Ser Phe Lys Arg Glu Phe Lys Glu Gly Lys Leu Asn Ala
 675 680 685
 Val Ala Leu His Leu Ser Asn Gly Glu Ser Gly Lys Val Glu Glu Glu
 690 695 700
 Val Val Glu Glu Met Met Met Met Ile Lys Asn Lys Arg Lys Glu Leu
 705 710 715 720
 Met Lys Leu Ile Phe Glu Glu Asn Gly Ser Ile Val Pro Arg Ala Cys
 725 730 735
 Lys Asp Ala Phe Trp Asn Met Cys His Val Leu Asn Phe Phe Tyr Ala
 740 745 750
 Asn Asp Asp Gly Phe Thr Gly Asn Thr Ile Leu Asp Thr Val Lys Asp
 755 760 765
 Ile Ile Tyr Asn Pro Leu Val Leu Val Asn Glu Asn Glu Glu Gln Arg
 770 775 780

SeqLst

<210> 134

<211> 590

<212> PRT

<213> Zea mays

<400> 134

Met Ala Met Pro Val Lys Leu Thr Pro Ala Ser Leu Ser Leu Lys Ala
1 5 10 15

Val Cys Cys Arg Phe Ser Ser Gly Gly His Ala Leu Arg Phe Gly Ser
20 25 30

Ser Leu Pro Cys Trp Arg Arg Thr Pro Thr Gln Arg Ser Thr Ser Ser
35 40 45

Ser Thr Thr Arg Pro Ala Ala Glu Val Ser Ser Gly Lys Ser Lys Gln
50 55 60

His Asp Gln Glu Ala Ser Glu Ala Thr Ile Arg Gln Gln Leu Gln Leu
65 70 75 80

Val Asp Val Leu Glu Asn Met Gly Ile Ser Arg His Phe Ala Ala Glu
85 90 95

Ile Lys Cys Ile Leu Asp Arg Thr Tyr Arg Ser Trp Leu Gln Arg His
100 105 110

Glu Glu Ile Met Leu Asp Thr Met Thr Cys Ala Met Ala Phe Arg Ile
115 120 125

Leu Arg Leu Asn Gly Tyr Asn Val Ser Ser Asp Glu Leu Tyr His Val
130 135 140

Val Glu Ala Ser Gly Leu His Asn Ser Leu Gly Gly Tyr Leu Asn Asp
145 150 155 160

Thr Arg Thr Leu Leu Glu Leu His Lys Ala Ser Thr Val Ser Ile Ser
165 170 175

Glu Asp Glu Ser Ile Leu Asp Ser Ile Gly Ser Arg Ser Arg Thr Leu
180 185 190

Leu Arg Glu Gln Leu Glu Ser Gly Gly Ala Leu Arg Lys Pro Ser Leu
195 200 205

Phe Lys Glu Val Glu His Ala Leu Asp Gly Pro Phe Tyr Thr Thr Leu
210 215 220

SeqLst

Asp Arg Leu His His Arg Trp Asn Ile Glu Asn Phe Asn Ile Ile Glu
 225 230 235 240
 Gln His Met Leu Glu Thr Pro Tyr Leu Ser Asn Gln His Thr Ser Arg
 245 250 255
 Asp Ile Leu Ala Leu Ser Ile Arg Asp Phe Ser Ser Ser Gln Phe Thr
 260 265 270
 Tyr Gln Gln Glu Leu Gln His Leu Glu Ser Trp Val Lys Glu Cys Arg
 275 280 285
 Leu Asp Gln Leu Gln Phe Ala Arg Gln Lys Leu Ala Tyr Phe Tyr Leu
 290 295 300
 Ser Ala Ala Gly Thr Met Phe Ser Pro Glu Leu Ser Asp Ala Arg Thr
 305 310 315 320
 Leu Trp Ala Lys Asn Gly Val Leu Thr Thr Ile Val Asp Asp Phe Phe
 325 330 335
 Asp Val Ala Gly Ser Lys Glu Glu Leu Glu Asn Leu Val Met Leu Val
 340 345 350
 Glu Met Trp Asp Glu His His Lys Val Glu Phe Tyr Ser Glu Gln Val
 355 360 365
 Glu Ile Ile Phe Ser Ser Ile Tyr Asp Ser Val Asn Gln Leu Gly Glu
 370 375 380
 Lys Ala Ser Leu Val Gln Asp Arg Ser Ile Thr Lys His Leu Val Glu
 385 390 395 400
 Ile Trp Leu Asp Leu Leu Lys Ser Met Met Thr Glu Val Glu Trp Arg
 405 410 415
 Leu Ser Lys Tyr Val Pro Thr Glu Lys Glu Tyr Met Ile Asn Ala Ser
 420 425 430
 Leu Ile Phe Gly Leu Gly Pro Ile Val Leu Pro Ala Leu Tyr Phe Val
 435 440 445
 Gly Pro Lys Ile Ser Glu Ser Ile Val Lys Asp Pro Glu Tyr Asp Glu
 450 455 460
 Leu Phe Lys Leu Met Ser Thr Cys Gly Arg Leu Leu Asn Asp Val Gln
 465 470 475 480

SeqLst

Thr Phe Glu Arg Glu Tyr Asn Glu Gly Lys Leu Asn Ser Val Ser Leu
 485 490 495

Leu Val Leu His Gly Gly Pro Met Ser Ile Ser Asp Ala Lys Arg Lys
 500 505 510

Leu Gln Lys Pro Ile Asp Thr Cys Arg Arg Asp Leu Leu Ser Leu Val
 515 520 525

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

Lys Met Cys Lys Val Cys Tyr Phe Phe Tyr Ser Thr Thr Asp Gly Phe
 545 550 555 560

Ser Ser Gln Val Glu Arg Ala Lys Glu Val Asp Ala Val Ile Asn Glu
 565 570 575

Pro Leu Lys Leu Gln Gly Ser His Thr Leu Val Ser Asp Val
 580 585 590

<210> 135

<211> 743

<212> PRT

<213> Populus trichocarpa

<400> 135

Met Gln Asn Phe His Gly Thr Lys Glu Arg Ile Lys Lys Met Phe Asp
 1 5 10 15

Lys Ile Glu Leu Ser Val Ser Ser Tyr Asp Thr Ala Trp Val Ala Met
 20 25 30

Val Pro Ser Pro Asp Cys Pro Glu Thr Pro Cys Phe Pro Glu Cys Thr
 35 40 45

Lys Trp Ile Leu Glu Asn Gln Leu Gly Asp Gly Ser Trp Ser Leu Pro
 50 55 60

His Gly Asn Pro Leu Leu Val Lys Asp Ala Leu Ser Ser Thr Leu Ala
 65 70 75 80

Cys Ile Leu Ala Leu Lys Arg Trp Gly Ile Gly Glu Glu Gln Ile Asn
 85 90 95

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

SeqLst

Glu Gln His Lys Pro Ile Gly Phe Asp Ile Ile Phe Pro Gly Met Ile
 115 120 125
 Glu Tyr Ala Ile Asp Leu Asp Leu Asn Leu Pro Leu Lys Pro Thr Asp
 130 135 140
 Ile Asn Ser Met Leu His Arg Arg Ala Leu Glu Leu Thr Ser Gly Gly
 145 150 155 160
 Gly Lys Asn Leu Glu Gly Arg Arg Ala Tyr Leu Ala Tyr Val Ser Glu
 165 170 175
 Gly Ile Gly Lys Leu Gln Asp Trp Glu Met Ala Met Lys Tyr Gln Arg
 180 185 190
 Lys Asn Gly Ser Leu Phe Asn Ser Pro Ser Thr Thr Ala Ala Ala Phe
 195 200 205
 Ile His Ile Gln Asp Ala Glu Cys Leu His Tyr Ile Arg Ser Leu Leu
 210 215 220
 Gln Lys Phe Gly Asn Ala Val Pro Thr Ile Tyr Pro Leu Asp Ile Tyr
 225 230 235 240
 Ala Arg Leu Ser Met Val Asp Ala Leu Glu Arg Leu Gly Ile Asp Arg
 245 250 255
 His Phe Arg Lys Glu Arg Lys Phe Val Leu Asp Glu Thr Tyr Arg Phe
 260 265 270
 Trp Leu Gln Gly Glu Glu Glu Ile Phe Ser Asp Asn Ala Thr Cys Ala
 275 280 285
 Leu Ala Phe Arg Ile Leu Arg Leu Asn Gly Tyr Asp Val Ser Leu Glu
 290 295 300
 Asp His Phe Ser Asn Ser Leu Gly Gly Tyr Leu Lys Asp Ser Gly Ala
 305 310 315 320
 Ala Leu Glu Leu Tyr Arg Ala Leu Gln Leu Ser Tyr Pro Asp Glu Ser
 325 330 335
 Leu Leu Glu Lys Gln Asn Ser Arg Thr Ser Tyr Phe Leu Lys Gln Gly
 340 345 350
 Leu Ser Asn Val Ser Leu Cys Gly Asp Arg Leu Arg Lys Asn Ile Ile
 355 360 365

SeqLst

Gly Glu Val His Asp Ala Leu Asn Phe Ser Asp His Ala Asn Leu Gln
 370 375 380
 Arg Leu Ala Ile Arg Arg Arg Ile Lys His Tyr Ala Thr Asp Asp Thr
 385 390 395 400
 Arg Ile Leu Lys Thr Ser Tyr Arg Cys Ser Thr Ile Gly Asn Gln Asp
 405 410 415
 Phe Leu Lys Leu Ala Val Glu Asp Phe Asn Ile Cys Gln Ser Ile Gln
 420 425 430
 Arg Glu Glu Phe Lys His Ile Glu Arg Trp Val Val Glu Arg Arg Leu
 435 440 445
 Asp Lys Leu Lys Phe Ala Arg Gln Lys Glu Ala Tyr Cys Tyr Phe Ser
 450 455 460
 Ala Ala Ala Thr Leu Phe Ala Pro Glu Leu Ser Asp Ala Arg Met Ser
 465 470 475 480
 Trp Ala Lys Asn Gly Val Leu Thr Thr Val Val Asp Asp Phe Phe Asp
 485 490 495
 Val Gly Gly Ser Glu Glu Glu Leu Val Asn Leu Ile Glu Leu Ile Glu
 500 505 510
 Arg Trp Asp Val Asn Gly Ser Ala Asp Phe Cys Ser Glu Glu Val Glu
 515 520 525
 Ile Ile Tyr Ser Ala Ile His Ser Thr Ile Ser Glu Ile Gly Asp Lys
 530 535 540
 Ser Phe Gly Trp Gln Gly Arg Asp Val Lys Ser Gln Val Ile Lys Ile
 545 550 555 560
 Trp Leu Asp Leu Leu Lys Ser Met Leu Thr Glu Ala Gln Trp Ser Ser
 565 570 575
 Asn Lys Ser Val Pro Thr Leu Asp Glu Tyr Met Thr Thr Ala His Val
 580 585 590
 Ser Phe Ala Leu Gly Pro Ile Val Leu Pro Ala Leu Tyr Phe Val Gly
 595 600 605
 Pro Lys Leu Ser Glu Glu Val Ala Gly His Pro Glu Leu Leu Asn Leu

SeqLst
620

610

615

Tyr Lys Val Thr Ser Thr Cys Gly Arg Leu Leu Asn Asp Trp Arg Ser
625 630 635 640

Phe Lys Arg Glu Ser Glu Glu Gly Lys Leu Asn Ala Ile Ser Leu Tyr
645 650 655

Met Ile His Ser Gly Gly Ala Ser Thr Glu Glu Glu Thr Ile Glu His
660 665 670

Phe Lys Gly Leu Ile Asp Ser Gln Arg Arg Gln Leu Leu Gln Leu Val
675 680 685

Leu Gln Glu Lys Asp Ser Ile Ile Pro Arg Pro Cys Lys Asp Leu Phe
690 695 700

Trp Asn Met Ile Lys Leu Leu His Thr Phe Tyr Met Lys Asp Asp Gly
705 710 715 720

Phe Thr Ser Asn Glu Met Arg Asn Val Val Lys Ala Ile Ile Asn Glu
725 730 735

Pro Ile Ser Leu Asp Glu Leu
740

<210> 136

<211> 983

<212> PRT

<213> Phomopsis amygdali

<400> 136

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

Arg Thr Leu Gln Asp Tyr Asp Asp Arg Tyr Gly Phe Gly Thr Met Ser
20 25 30

Cys Ala Ala Tyr Asp Thr Ala Trp Val Ser Leu Val Thr Lys Thr Val
35 40 45

Asp Gly Arg Lys Gln Trp Leu Phe Pro Glu Cys Phe Glu Phe Leu Leu
50 55 60

Glu Thr Gln Ser Asp Ala Gly Gly Trp Glu Ile Gly Asn Ser Ala Pro
65 70 75 80

Ile Asp Gly Ile Leu Asn Thr Ala Ala Ser Leu Leu Ala Leu Lys Arg
85 90 95

SeqLst

His Val Gln Thr Glu Gln Ile Ile Gln Pro Gln His Asp His Lys Asp
 100 105 110
 Leu Ala Gly Arg Ala Glu Arg Ala Ala Ala Ser Leu Arg Ala Gln Leu
 115 120 125
 Ala Ala Leu Asp Val Ser Thr Thr Glu His Val Gly Phe Glu Ile Ile
 130 135 140
 Val Pro Ala Met Leu Asp Pro Leu Glu Ala Glu Asp Pro Ser Leu Val
 145 150 155 160
 Phe Asp Phe Pro Ala Arg Lys Pro Leu Met Lys Ile His Asp Ala Lys
 165 170 175
 Met Ser Arg Phe Arg Pro Glu Tyr Leu Tyr Gly Lys Gln Pro Met Thr
 180 185 190
 Ala Leu His Ser Leu Glu Ala Phe Ile Gly Lys Ile Asp Phe Asp Lys
 195 200 205
 Val Arg His His Arg Thr His Gly Ser Met Met Gly Ser Pro Ser Ser
 210 215 220
 Thr Ala Ala Tyr Leu Met His Ala Ser Gln Trp Asp Gly Asp Ser Glu
 225 230 235 240
 Ala Tyr Leu Arg His Val Ile Lys His Ala Ala Gly Gln Gly Thr Gly
 245 250 255
 Ala Val Pro Ser Ala Phe Pro Ser Thr His Phe Glu Ser Ser Trp Ile
 260 265 270
 Leu Thr Thr Leu Phe Arg Ala Gly Phe Ser Ala Ser His Leu Ala Cys
 275 280 285
 Asp Glu Leu Asn Lys Leu Val Glu Ile Leu Glu Gly Ser Phe Glu Lys
 290 295 300
 Glu Gly Gly Ala Ile Gly Tyr Ala Pro Gly Phe Gln Ala Asp Val Asp
 305 310 315 320
 Asp Thr Ala Lys Thr Ile Ser Thr Leu Ala Val Leu Gly Arg Asp Ala
 325 330 335
 Thr Pro Arg Gln Met Ile Lys Val Phe Glu Ala Asn Thr His Phe Arg

SeqLst

340	345	350
Thr Tyr Pro Gly Glu Arg Asp	Pro Ser Leu Thr Ala	Asn Cys Asn Ala
355	360	365
Leu Ser Ala Leu Leu His Gln	Pro Asp Ala Ala Met	Tyr Gly Ser Gln
370	375	380
Ile Gln Lys Ile Thr Lys Phe Val Cys Asp	Tyr Trp Trp Lys Ser Asp	
385	390	400
Gly Lys Ile Lys Asp Lys Trp Asn Thr Cys Tyr Leu Tyr Pro Ser Val		
405	410	415
Leu Leu Val Glu Val Leu Val Asp Leu Val Ser Leu Leu Glu Gln Gly		
420	425	430
Lys Leu Pro Asp Val Leu Asp Gln Glu Leu Gln Tyr Arg Val Ala Ile		
435	440	445
Thr Leu Phe Gln Ala Cys Leu Arg Pro Leu Leu Asp Gln Asp Ala Glu		
450	455	460
Gly Ser Trp Asn Lys Ser Ile Glu Ala Thr Ala Tyr Gly Ile Leu Ile		
465	470	475
Leu Thr Glu Ala Arg Arg Val Cys Phe Phe Asp Arg Leu Ser Glu Pro		
485	490	495
Leu Asn Glu Ala Ile Arg Arg Gly Ile Ala Phe Ala Asp Ser Met Ser		
500	505	510
Gly Thr Glu Ala Gln Leu Asn Tyr Ile Trp Ile Glu Lys Val Ser Tyr		
515	520	525
Ala Pro Ala Leu Leu Thr Lys Ser Tyr Leu Leu Ala Ala Arg Trp Ala		
530	535	540
Ala Lys Ser Pro Leu Gly Ala Ser Val Gly Ser Ser Leu Trp Thr Pro		
545	550	555
Pro Arg Glu Gly Leu Asp Lys His Val Arg Leu Phe His Gln Ala Glu		
565	570	575
Leu Phe Arg Ser Leu Pro Glu Trp Glu Leu Arg Ala Ser Met Ile Glu		
580	585	590

SeqLst

Ala Ala Leu Phe Thr Pro Leu Leu Arg Ala His Arg Leu Asp Val Phe
595 600 605

Pro Arg Gln Asp Val Gly Glu Asp Lys Tyr Leu Asp Val Val Pro Phe
610 615 620

Phe Trp Thr Ala Ala Asn Asn Arg Asp Arg Thr Tyr Ala Ser Thr Leu
625 630 635 640

Phe Leu Tyr Asp Met Cys Phe Ile Ala Met Leu Asn Phe Gln Leu Asp
645 650 655

Glu Phe Met Glu Ala Thr Ala Gly Ile Leu Phe Arg Asp His Met Asp
660 665 670

Asp Leu Arg Gln Leu Ile His Asp Leu Leu Ala Glu Lys Thr Ser Pro
675 680 685

Lys Ser Ser Gly Arg Ser Ser Gln Gly Thr Lys Asp Ala Asp Ser Gly
690 695 700

Ile Glu Glu Asp Val Ser Met Ser Asp Ser Ala Ser Asp Ser Gln Asp
705 710 715 720

Arg Ser Pro Glu Tyr Asp Leu Val Phe Ser Ala Leu Ser Thr Phe Thr
725 730 735

Lys His Val Leu Gln His Pro Ser Ile Gln Ser Ala Ser Val Trp Asp
740 745 750

Arg Lys Leu Leu Ala Arg Glu Met Lys Ala Tyr Leu Leu Ala His Ile
755 760 765

Gln Gln Ala Glu Asp Ser Thr Pro Leu Ser Glu Leu Lys Asp Val Pro
770 775 780

Gln Lys Thr Asp Val Thr Arg Val Ser Thr Ser Thr Thr Thr Phe Phe
785 790 795 800

Asn Trp Val Arg Thr Thr Ser Ala Asp His Ile Ser Cys Pro Tyr Ser
805 810 815

Phe His Phe Val Ala Cys His Leu Gly Ala Ala Leu Ser Pro Lys Gly
820 825 830

Ser Asn Gly Asp Cys Tyr Pro Ser Ala Gly Glu Lys Phe Leu Ala Ala
835 840 845

SeqLst

Ala Val Cys Arg His Leu Ala Thr Met Cys Arg Met Tyr Asn Asp Leu
850 855 860

Gly Ser Ala Glu Arg Asp Ser Asp Glu Gly Asn Leu Asn Ser Leu Asp
865 870 875 880

Phe Pro Glu Phe Ala Asp Ser Ala Gly Asn Gly Gly Ile Glu Ile Gln
885 890 895

Lys Ala Ala Leu Leu Arg Leu Ala Glu Phe Glu Arg Asp Ser Tyr Leu
900 905 910

Glu Ala Phe Arg Arg Leu Gln Asp Glu Ser Asn Arg Val His Gly Pro
915 920 925

Ala Gly Gly Asp Glu Ala Arg Leu Ser Arg Arg Arg Met Ala Ile Leu
930 935 940

Glu Phe Phe Ala Gln Gln Val Asp Leu Tyr Gly Gln Val Tyr Val Ile
945 950 955 960

Arg Asp Ile Ser Ala Arg Ile Pro Lys Asn Glu Val Glu Lys Lys Arg
965 970 975

Lys Leu Asp Asp Ala Phe Asn
980

<210> 137

<211> 881

<212> PRT

<213> Physcomitrella patens

<400> 137

Met Ala Ser Ser Thr Leu Ile Gln Asn Arg Ser Cys Gly Val Thr Ser
1 5 10 15

Ser Met Ser Ser Phe Gln Ile Phe Arg Gly Gln Pro Leu Arg Phe Pro
20 25 30

Gly Thr Arg Thr Pro Ala Ala Val Gln Cys Leu Lys Lys Arg Arg Cys
35 40 45

Leu Arg Pro Thr Glu Ser Val Leu Glu Ser Ser Pro Gly Ser Gly Ser
50 55 60

Tyr Arg Ile Val Thr Gly Pro Ser Gly Ile Asn Pro Ser Ser Asn Gly
65 70 75 80

SeqLst

His Leu Gln Glu Gly Ser Leu Thr His Arg Leu Pro Ile Pro Met Glu
85 90 95

Lys Ser Ile Asp Asn Phe Gln Ser Thr Leu Tyr Val Ser Asp Ile Trp
100 105 110

Ser Glu Thr Leu Gln Arg Thr Glu Cys Leu Leu Gln Val Thr Glu Asn
115 120 125

Val Gln Met Asn Glu Trp Ile Glu Glu Ile Arg Met Tyr Phe Arg Asn
130 135 140

Met Thr Leu Gly Glu Ile Ser Met Ser Pro Tyr Asp Thr Ala Trp Val
145 150 155 160

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

Ser Leu Gln Trp Ile Ile Asp Asn Gln Leu Pro Asp Gly Asp Trp Gly
180 185 190

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

Cys Val Ile Ala Leu Lys Thr Trp Gly Val Gly Ala Gln Asn Val Glu
210 215 220

Arg Gly Ile Gln Phe Leu Gln Ser Asn Ile Tyr Lys Met Glu Glu Asp
225 230 235 240

Asp Ala Asn His Met Pro Ile Gly Phe Glu Ile Val Phe Pro Ala Met
245 250 255

Met Glu Asp Ala Lys Ala Leu Gly Leu Asp Leu Pro Tyr Asp Ala Thr
260 265 270

Ile Leu Gln Gln Ile Ser Ala Glu Arg Glu Lys Lys Met Lys Lys Ile
275 280 285

Pro Met Ala Met Val Tyr Lys Tyr Pro Thr Thr Leu Leu His Ser Leu
290 295 300

Glu Gly Leu His Arg Glu Val Asp Trp Asn Lys Leu Leu Gln Leu Gln
305 310 315 320

Ser Glu Asn Gly Ser Phe Leu Tyr Ser Pro Ala Ser Thr Ala Cys Ala
325 330 335

SeqLst

Leu Met Tyr Thr Lys Asp Val Lys Cys Phe Asp Tyr Leu Asn Gln Leu
 340 345 350
 Leu Ile Lys Phe Asp His Ala Cys Pro Asn Val Tyr Pro Val Asp Leu
 355 360 365
 Phe Glu Arg Leu Trp Met Val Asp Arg Leu Gln Arg Leu Gly Ile Ser
 370 375 380
 Arg Tyr Phe Glu Arg Glu Ile Arg Asp Cys Leu Gln Tyr Val Tyr Arg
 385 390 395 400
 Tyr Trp Lys Asp Cys Gly Ile Gly Trp Ala Ser Asn Ser Ser Val Gln
 405 410 415
 Asp Val Asp Asp Thr Ala Met Ala Phe Arg Leu Leu Arg Thr His Gly
 420 425 430
 Phe Asp Val Lys Glu Asp Cys Phe Arg Gln Phe Phe Lys Asp Gly Glu
 435 440 445
 Phe Phe Cys Phe Ala Gly Gln Ser Ser Gln Ala Val Thr Gly Met Phe
 450 455 460
 Asn Leu Ser Arg Ala Ser Gln Thr Leu Phe Pro Gly Glu Ser Leu Leu
 465 470 475 480
 Lys Lys Ala Arg Thr Phe Ser Arg Asn Phe Leu Arg Thr Lys His Glu
 485 490 495
 Asn Asn Glu Cys Phe Asp Lys Trp Ile Ile Thr Lys Asp Leu Ala Gly
 500 505 510
 Glu Val Glu Tyr Asn Leu Thr Phe Pro Trp Tyr Ala Ser Leu Pro Arg
 515 520 525
 Leu Glu His Arg Thr Tyr Leu Asp Gln Tyr Gly Ile Asp Asp Ile Trp
 530 535 540
 Ile Gly Lys Ser Leu Tyr Lys Met Pro Ala Val Thr Asn Glu Val Phe
 545 550 555 560
 Leu Lys Leu Ala Lys Ala Asp Phe Asn Met Cys Gln Ala Leu His Lys
 565 570 575
 Lys Glu Leu Glu Gln Val Ile Lys Trp Asn Ala Ser Cys Gln Phe Arg
 580 585 590

SeqLst

Asp Leu Glu Phe Ala Arg Gln Lys Ser Val Glu Cys Tyr Phe Ala Gly
 595 600 605
 Ala Ala Thr Met Phe Glu Pro Glu Met Val Gln Ala Arg Leu Val Trp
 610 615 620
 Ala Arg Cys Cys Val Leu Thr Thr Val Leu Asp Asp Tyr Phe Asp His
 625 630 635 640
 Gly Thr Pro Val Glu Glu Leu Arg Val Phe Val Gln Ala Val Arg Thr
 645 650 655
 Trp Asn Pro Glu Leu Ile Asn Gly Leu Pro Glu Gln Ala Lys Ile Leu
 660 665 670
 Phe Met Gly Leu Tyr Lys Thr Val Asn Thr Ile Ala Glu Glu Ala Phe
 675 680 685
 Met Ala Gln Lys Arg Asp Val His His His Leu Lys His Tyr Trp Asp
 690 695 700
 Lys Leu Ile Thr Ser Ala Leu Lys Glu Ala Glu Trp Ala Glu Ser Gly
 705 710 715 720
 Tyr Val Pro Thr Phe Asp Glu Tyr Met Glu Val Ala Glu Ile Ser Val
 725 730 735
 Ala Leu Glu Pro Ile Val Cys Ser Thr Leu Phe Phe Ala Gly His Arg
 740 745 750
 Leu Asp Glu Asp Val Leu Asp Ser Tyr Asp Tyr His Leu Val Met His
 755 760 765
 Leu Val Asn Arg Val Gly Arg Ile Leu Asn Asp Ile Gln Gly Met Lys
 770 775 780
 Arg Glu Ala Ser Gln Gly Lys Ile Ser Ser Val Gln Ile Tyr Met Glu
 785 790 795 800
 Glu His Pro Ser Val Pro Ser Glu Ala Met Ala Ile Ala His Leu Gln
 805 810 815
 Glu Leu Val Asp Asn Ser Met Gln Gln Leu Thr Tyr Glu Val Leu Arg
 820 825 830
 Phe Thr Ala Val Pro Lys Ser Cys Lys Arg Ile His Leu Asn Met Ala

SeqLst

835

840

845

Lys Ile Met His Ala Phe Tyr Lys Asp Thr Asp Gly Phe Ser Ser Leu
 850 855 860

Thr Ala Met Thr Gly Phe Val Lys Lys Val Leu Phe Glu Pro Val Pro
 865 870 875 880

Glu

<210> 138

<211> 513

<212> PRT

<213> Stevia rebaudiana

<400> 138

Met Asp Ala Val Thr Gly Leu Leu Thr Val Pro Ala Thr Ala Ile Thr
 1 5 10 15

Ile Gly Gly Thr Ala Val Ala Leu Ala Val Ala Leu Ile Phe Trp Tyr
 20 25 30

Leu Lys Ser Tyr Thr Ser Ala Arg Arg Ser Gln Ser Asn His Leu Pro
 35 40 45

Arg Val Pro Glu Val Pro Gly Val Pro Leu Leu Gly Asn Leu Leu Gln
 50 55 60

Leu Lys Glu Lys Lys Pro Tyr Met Thr Phe Thr Arg Trp Ala Ala Thr
 65 70 75 80

Tyr Gly Pro Ile Tyr Ser Ile Lys Thr Gly Ala Thr Ser Met Val Val
 85 90 95

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

Ser Ile Ser Thr Arg Asn Leu Ser Lys Ala Leu Lys Val Leu Thr Ala
 115 120 125

Asp Lys Thr Met Val Ala Met Ser Asp Tyr Asp Asp Tyr His Lys Thr
 130 135 140

Val Lys Arg His Ile Leu Thr Ala Val Leu Gly Pro Asn Ala Gln Lys
 145 150 155 160

Lys His Arg Ile His Arg Asp Ile Met Met Asp Asn Ile Ser Thr Gln
 165 170 175

SeqLst

Leu His Glu Phe Val Lys Asn Asn Pro Glu Gln Glu Glu Val Asp Leu
 180 185 190
 Arg Lys Ile Phe Gln Ser Glu Leu Phe Gly Leu Ala Met Arg Gln Ala
 195 200 205
 Leu Gly Lys Asp Val Glu Ser Leu Tyr Val Glu Asp Leu Lys Ile Thr
 210 215 220
 Met Asn Arg Asp Glu Ile Phe Gln Val Leu Val Val Asp Pro Met Met
 225 230 235 240
 Gly Ala Ile Asp Val Asp Trp Arg Asp Phe Phe Pro Tyr Leu Lys Trp
 245 250 255
 Val Pro Asn Lys Lys Phe Glu Asn Thr Ile Gln Gln Met Tyr Ile Arg
 260 265 270
 Arg Glu Ala Val Met Lys Ser Leu Ile Lys Glu His Lys Lys Arg Ile
 275 280 285
 Ala Ser Gly Glu Lys Leu Asn Ser Tyr Ile Asp Tyr Leu Leu Ser Glu
 290 295 300
 Ala Gln Thr Leu Thr Asp Gln Gln Leu Leu Met Ser Leu Trp Glu Pro
 305 310 315 320
 Ile Ile Glu Ser Ser Asp Thr Thr Met Val Thr Thr Glu Trp Ala Met
 325 330 335
 Tyr Glu Leu Ala Lys Asn Pro Lys Leu Gln Asp Arg Leu Tyr Arg Asp
 340 345 350
 Ile Lys Ser Val Cys Gly Ser Glu Lys Ile Thr Glu Glu His Leu Ser
 355 360 365
 Gln Leu Pro Tyr Ile Thr Ala Ile Phe His Glu Thr Leu Arg Arg His
 370 375 380
 Ser Pro Val Pro Ile Ile Pro Leu Arg His Val His Glu Asp Thr Val
 385 390 395 400
 Leu Gly Gly Tyr His Val Pro Ala Gly Thr Glu Leu Ala Val Asn Ile
 405 410 415
 Tyr Gly Cys Asn Met Asp Lys Asn Val Trp Glu Asn Pro Glu Glu Trp

SeqLst

420

425

430

Asn Pro Glu Arg Phe Met Lys Glu Asn Glu Thr Ile Asp Phe Gln Lys
 435 440 445

Thr Met Ala Phe Gly Gly Gly Lys Arg Val Cys Ala Gly Ser Leu Gln
 450 455 460

Ala Leu Leu Thr Ala Ser Ile Gly Ile Gly Arg Met Val Gln Glu Phe
 465 470 475 480

Glu Trp Lys Leu Lys Asp Met Thr Gln Glu Glu Val Asn Thr Ile Gly
 485 490 495

Leu Thr Thr Gln Met Leu Arg Pro Leu Arg Ala Ile Ile Lys Pro Arg
 500 505 510

Ile

<210> 139

<211> 509

<212> PRT

<213> Arabidopsis thaliana

<400> 139

Met Ala Phe Phe Ser Met Ile Ser Ile Leu Leu Gly Phe Val Ile Ser
 1 5 10 15

Ser Phe Ile Phe Ile Phe Phe Phe Lys Lys Leu Leu Ser Phe Ser Arg
 20 25 30

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

Gly Phe Pro Val Ile Gly Asn Leu Leu Gln Leu Lys Glu Lys Lys Pro
 50 55 60

His Lys Thr Phe Thr Arg Trp Ser Glu Ile Tyr Gly Pro Ile Tyr Ser
 65 70 75 80

Ile Lys Met Gly Ser Ser Ser Leu Ile Val Leu Asn Ser Thr Glu Thr
 85 90 95

Ala Lys Glu Ala Met Val Thr Arg Phe Ser Ser Ile Ser Thr Arg Lys
 100 105 110

Leu Ser Asn Ala Leu Thr Val Leu Thr Cys Asp Lys Ser Met Val Ala
 115 120 125

SeqLst

Thr Ser Asp Tyr Asp Asp Phe His Lys Leu Val Lys Arg Cys Leu Leu
 130 135 140
 Asn Gly Leu Leu Gly Ala Asn Ala Gln Lys Arg Lys Arg His Tyr Arg
 145 150 155 160
 Asp Ala Leu Ile Glu Asn Val Ser Ser Lys Leu His Ala His Ala Arg
 165 170 175
 Asp His Pro Gln Glu Pro Val Asn Phe Arg Ala Ile Phe Glu His Glu
 180 185 190
 Leu Phe Gly Val Ala Leu Lys Gln Ala Phe Gly Lys Asp Val Glu Ser
 195 200 205
 Ile Tyr Val Lys Glu Leu Gly Val Thr Leu Ser Lys Asp Glu Ile Phe
 210 215 220
 Lys Val Leu Val His Asp Met Met Glu Gly Ala Ile Asp Val Asp Trp
 225 230 235 240
 Arg Asp Phe Phe Pro Tyr Leu Lys Trp Ile Pro Asn Lys Ser Phe Glu
 245 250 255
 Ala Arg Ile Gln Gln Lys His Lys Arg Arg Leu Ala Val Met Asn Ala
 260 265 270
 Leu Ile Gln Asp Arg Leu Lys Gln Asn Gly Ser Glu Ser Asp Asp Asp
 275 280 285
 Cys Tyr Leu Asn Phe Leu Met Ser Glu Ala Lys Thr Leu Thr Lys Glu
 290 295 300
 Gln Ile Ala Ile Leu Val Trp Glu Thr Ile Ile Glu Thr Ala Asp Thr
 305 310 315 320
 Thr Leu Val Thr Thr Glu Trp Ala Ile Tyr Glu Leu Ala Lys His Pro
 325 330 335
 Ser Val Gln Asp Arg Leu Cys Lys Glu Ile Gln Asn Val Cys Gly Gly
 340 345 350
 Glu Lys Phe Lys Glu Glu Gln Leu Ser Gln Val Pro Tyr Leu Asn Gly
 355 360 365
 Val Phe His Glu Thr Leu Arg Lys Tyr Ser Pro Ala Pro Leu Val Pro

SeqLst

370 375 380

Ile Arg Tyr Ala His Glu Asp Thr Gln Ile Gly Gly Tyr His Val Pro
385 390 395 400

Ala Gly Ser Glu Ile Ala Ile Asn Ile Tyr Gly Cys Asn Met Asp Lys
 405 410 415

Lys Arg Trp Glu Arg Pro Glu Asp Trp Trp Pro Glu Arg Phe Leu Asp
 420 425 430

Asp Gly Lys Tyr Glu Thr Ser Asp Leu His Lys Thr Met Ala Phe Gly
 435 440 445

Ala Gly Lys Arg Val Cys Ala Gly Ala Leu Gln Ala Ser Leu Met Ala
 450 455 460

Gly Ile Ala Ile Gly Arg Leu Val Gln Glu Phe Glu Trp Lys Leu Arg
465 470 475 480

Asp Gly Glu Glu Glu Asn Val Asp Thr Tyr Gly Leu Thr Ser Gln Lys
 485 490 495

Leu Tyr Pro Leu Met Ala Ile Ile Asn Pro Arg Arg Ser
 500 505

<210> 140
<211> 525
<212> PRT
<213> Gibberella fujikoroii

<400> 140
Met Ser Lys Ser Asn Ser Met Asn Ser Thr Ser His Glu Thr Leu Phe
1 5 10 15

Gln Gln Leu Val Leu Gly Leu Asp Arg Met Pro Leu Met Asp Val His
 20 25 30

Trp Leu Ile Tyr Val Ala Phe Gly Ala Trp Leu Cys Ser Tyr Val Ile
 35 40 45

His Val Leu Ser Ser Ser Ser Thr Val Lys Val Pro Val Val Gly Tyr
50 55 60

Arg Ser Val Phe Glu Pro Thr Trp Leu Leu Arg Leu Arg Phe Val Trp
65 70 75 80

Glu Gly Gly Ser Ile Ile Gly Gln Gly Tyr Asn Lys Phe Lys Asp Ser
 85 90 95

SeqLst

Ile Phe Gln Val Arg Lys Leu Gly Thr Asp Ile Val Ile Ile Pro Pro
 100 105 110
 Asn Tyr Ile Asp Glu Val Arg Lys Leu Ser Gln Asp Lys Thr Arg Ser
 115 120 125
 Val Glu Pro Phe Ile Asn Asp Phe Ala Gly Gln Tyr Thr Arg Gly Met
 130 135 140
 Val Phe Leu Gln Ser Asp Leu Gln Asn Arg Val Ile Gln Gln Arg Leu
 145 150 155 160
 Thr Pro Lys Leu Val Ser Leu Thr Lys Val Met Lys Glu Glu Leu Asp
 165 170 175
 Tyr Ala Leu Thr Lys Glu Met Pro Asp Met Lys Asn Asp Glu Trp Val
 180 185 190
 Glu Val Asp Ile Ser Ser Ile Met Val Arg Leu Ile Ser Arg Ile Ser
 195 200 205
 Ala Arg Val Phe Leu Gly Pro Glu His Cys Arg Asn Gln Glu Trp Leu
 210 215 220
 Thr Thr Thr Ala Glu Tyr Ser Glu Ser Leu Phe Ile Thr Gly Phe Ile
 225 230 235 240
 Leu Arg Val Val Pro His Ile Leu Arg Pro Phe Ile Ala Pro Leu Leu
 245 250 255
 Pro Ser Tyr Arg Thr Leu Leu Arg Asn Val Ser Ser Gly Arg Arg Val
 260 265 270
 Ile Gly Asp Ile Ile Arg Ser Gln Gln Gly Asp Gly Asn Glu Asp Ile
 275 280 285
 Leu Ser Trp Met Arg Asp Ala Ala Thr Gly Glu Glu Lys Gln Ile Asp
 290 295 300
 Asn Ile Ala Gln Arg Met Leu Ile Leu Ser Leu Ala Ser Ile His Thr
 305 310 315 320
 Thr Ala Met Thr Met Thr His Ala Met Tyr Asp Leu Cys Ala Cys Pro
 325 330 335
 Glu Tyr Ile Glu Pro Leu Arg Asp Glu Val Lys Ser Val Val Gly Ala

SeqLst

340

345

350

Ser Gly Trp Asp Lys Thr Ala Leu Asn Arg Phe His Lys Leu Asp Ser
 355 360 365

Phe Leu Lys Glu Ser Gln Arg Phe Asn Pro Val Phe Leu Leu Thr Phe
 370 375 380

Asn Arg Ile Tyr His Gln Ser Met Thr Leu Ser Asp Gly Thr Asn Ile
 385 390 395 400

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

Ser Ala His Val Pro Gly Pro Thr Pro Pro Thr Glu Phe Asp Gly Phe
 420 425 430

Arg Tyr Ser Lys Ile Arg Ser Asp Ser Asn Tyr Ala Gln Lys Tyr Leu
 435 440 445

Phe Ser Met Thr Asp Ser Ser Asn Met Ala Phe Gly Tyr Gly Lys Tyr
 450 455 460

Ala Cys Pro Gly Arg Phe Tyr Ala Ser Asn Glu Met Lys Leu Thr Leu
 465 470 475 480

Ala Ile Leu Leu Leu Gln Phe Glu Phe Lys Leu Pro Asp Gly Lys Gly
 485 490 495

Arg Pro Arg Asn Ile Thr Ile Asp Ser Asp Met Ile Pro Asp Pro Arg
 500 505 510

Ala Arg Leu Cys Val Arg Lys Arg Ser Leu Arg Asp Glu
 515 520 525

<210> 141

<211> 499

<212> PRT

<213> Trametes versicolor

<400> 141

Met Glu Asp Pro Thr Val Leu Tyr Ala Cys Leu Ala Ile Ala Val Ala
 1 5 10 15

Thr Phe Val Val Arg Trp Tyr Arg Asp Pro Leu Arg Ser Ile Pro Thr
 20 25 30

Val Gly Gly Ser Asp Leu Pro Ile Leu Ser Tyr Ile Gly Ala Leu Arg
 35 40 45

SeqLst

Trp Thr Arg Arg Gly Arg Glu Ile Leu Gln Glu Gly Tyr Asp Gly Tyr
 50 55 60
 Arg Gly Ser Thr Phe Lys Ile Ala Met Leu Asp Arg Trp Ile Val Ile
 65 70 75 80
 Ala Asn Gly Pro Lys Leu Ala Asp Glu Val Arg Arg Arg Pro Asp Glu
 85 90 95
 Glu Leu Asn Phe Met Asp Gly Leu Gly Ala Phe Val Gln Thr Lys Tyr
 100 105 110
 Thr Leu Gly Glu Ala Ile His Asn Asp Pro Tyr His Val Asp Ile Ile
 115 120 125
 Arg Glu Lys Leu Thr Arg Gly Leu Pro Ala Val Leu Pro Asp Val Ile
 130 135 140
 Glu Glu Leu Thr Leu Ala Val Arg Gln Tyr Ile Pro Thr Glu Gly Asp
 145 150 155 160
 Glu Trp Val Ser Val Asn Cys Ser Lys Ala Ala Arg Asp Ile Val Ala
 165 170 175
 Arg Ala Ser Asn Arg Val Phe Val Gly Leu Pro Ala Cys Arg Asn Gln
 180 185 190
 Gly Tyr Leu Asp Leu Ala Ile Asp Phe Thr Leu Ser Val Val Lys Asp
 195 200 205
 Arg Ala Ile Ile Asn Met Phe Pro Glu Leu Leu Lys Pro Ile Val Gly
 210 215 220
 Arg Val Val Gly Asn Ala Thr Arg Asn Val Arg Arg Ala Val Pro Phe
 225 230 235 240
 Val Ala Pro Leu Val Glu Glu Arg Arg Arg Leu Met Glu Glu Tyr Gly
 245 250 255
 Glu Asp Trp Ser Glu Lys Pro Asn Asp Met Leu Gln Trp Ile Met Asp
 260 265 270
 Glu Ala Ala Ser Arg Asp Ser Ser Val Lys Ala Ile Ala Glu Arg Leu
 275 280 285
 Leu Met Val Asn Phe Ala Ala Ile His Thr Ser Ser Asn Thr Ile Thr

														SeqLst			
290				295				300									
His	Ala	Leu	Tyr	His	Leu	Ala	Glu	Met	Pro	Glu	Thr	Leu	Gln	Pro	Leu		
305					310					315					320		
Arg	Glu	Glu	Ile	Glu	Pro	Leu	Val	Lys	Glu	Glu	Gly	Trp	Thr	Lys	Ala		
				325					330					335			
Ala	Met	Gly	Lys	Met	Trp	Trp	Leu	Asp	Ser	Phe	Leu	Arg	Glu	Ser	Gln		
			340					345					350				
Arg	Tyr	Asn	Gly	Ile	Asn	Ile	Val	Ser	Leu	Thr	Arg	Met	Ala	Asp	Lys		
		355					360					365					
Asp	Ile	Thr	Leu	Ser	Asp	Gly	Thr	Phe	Leu	Pro	Lys	Gly	Thr	Leu	Val		
	370					375					380						
Ala	Val	Pro	Ala	Tyr	Ser	Thr	His	Arg	Asp	Asp	Ala	Val	Tyr	Ala	Asp		
385					390					395					400		
Ala	Leu	Val	Phe	Asp	Pro	Phe	Arg	Phe	Ser	Arg	Met	Arg	Ala	Arg	Glu		
				405					410					415			
Gly	Glu	Gly	Thr	Lys	His	Gln	Phe	Val	Asn	Thr	Ser	Val	Glu	Tyr	Val		
			420					425					430				
Pro	Phe	Gly	His	Gly	Lys	His	Ala	Cys	Pro	Gly	Arg	Phe	Phe	Ala	Ala		
		435					440					445					
Asn	Glu	Leu	Lys	Ala	Met	Leu	Ala	Tyr	Ile	Val	Leu	Asn	Tyr	Asp	Val		
	450					455					460						
Lys	Leu	Pro	Gly	Asp	Gly	Lys	Arg	Pro	Leu	Asn	Met	Tyr	Trp	Gly	Pro		
465					470					475					480		
Thr	Val	Leu	Pro	Ala	Pro	Ala	Gly	Gln	Val	Leu	Phe	Arg	Lys	Arg	Gln		
				485					490					495			
Val Ser Leu																	

<210> 142
 <211> 525
 <212> PRT
 <213> Stevia rebaudiana

<400> 142
 Met Gly Leu Phe Pro Leu Glu Asp Ser Tyr Ala Leu Val Phe Glu Gly
 1 5 10 15

SeqLst

Leu Ala Ile Thr Leu Ala Leu Tyr Tyr Leu Leu Ser Phe Ile Tyr Lys
 20 25 30

Thr Ser Lys Lys Thr Cys Thr Pro Pro Lys Ala Ser Gly Glu Ile Ile
 35 40 45

Pro Ile Thr Gly Ile Ile Leu Asn Leu Leu Ser Gly Ser Ser Gly Leu
 50 55 60

Pro Ile Ile Leu Ala Leu Ala Ser Leu Ala Asp Arg Cys Gly Pro Ile
 65 70 75 80

Phe Thr Ile Arg Leu Gly Ile Arg Arg Val Leu Val Val Ser Asn Trp
 85 90 95

Glu Ile Ala Lys Glu Ile Phe Thr Thr His Asp Leu Ile Val Ser Asn
 100 105 110

Arg Pro Lys Tyr Leu Ala Ala Lys Ile Leu Gly Phe Asn Tyr Val Ser
 115 120 125

Phe Ser Phe Ala Pro Tyr Gly Pro Tyr Trp Val Gly Ile Arg Lys Ile
 130 135 140

Ile Ala Thr Lys Leu Met Ser Ser Ser Arg Leu Gln Lys Leu Gln Phe
 145 150 155 160

Val Arg Val Phe Glu Leu Glu Asn Ser Met Lys Ser Ile Arg Glu Ser
 165 170 175

Trp Lys Glu Lys Lys Asp Glu Glu Gly Lys Val Leu Val Glu Met Lys
 180 185 190

Lys Trp Phe Trp Glu Leu Asn Met Asn Ile Val Leu Arg Thr Val Ala
 195 200 205

Gly Lys Gln Tyr Thr Gly Thr Val Asp Asp Ala Asp Ala Lys Arg Ile
 210 215 220

Ser Glu Leu Phe Arg Glu Trp Phe His Tyr Thr Gly Arg Phe Val Val
 225 230 235 240

Gly Asp Ala Phe Pro Phe Leu Gly Trp Leu Asp Leu Gly Gly Tyr Lys
 245 250 255

Lys Thr Met Glu Leu Val Ala Ser Arg Leu Asp Ser Met Val Ser Lys

SeqLst															
260				265				270							
Trp	Leu	Asp 275	Glu	His	Arg	Lys	Lys 280	Gln	Ala	Asn	Asp	Asp 285	Lys	Lys	Glu
Asp	Met 290	Asp	Phe	Met	Asp	Ile 295	Met	Ile	Ser	Met	Thr 300	Glu	Ala	Asn	Ser
Pro 305	Leu	Glu	Gly	Tyr	Gly 310	Thr	Asp	Thr	Ile	Ile 315	Lys	Thr	Thr	Cys	Met 320
Thr	Leu	Ile	Val	Ser 325	Gly	Val	Asp	Thr	Thr 330	Ser	Ile	Val	Leu	Thr 335	Trp
Ala	Leu	Ser	Leu 340	Leu	Leu	Asn	Asn	Arg 345	Asp	Thr	Leu	Lys	Lys 350	Ala	Gln
Glu	Glu	Leu 355	Asp	Met	Cys	Val	Gly 360	Lys	Gly	Arg	Gln	Val 365	Asn	Glu	Ser
Asp	Leu 370	Val	Asn	Leu	Ile	Tyr 375	Leu	Glu	Ala	Val	Leu 380	Lys	Glu	Ala	Leu
Arg 385	Leu	Tyr	Pro	Ala	Ala 390	Phe	Leu	Gly	Gly	Pro 395	Arg	Ala	Phe	Leu	Glu 400
Asp	Cys	Thr	Val	Ala 405	Gly	Tyr	Arg	Ile	Pro 410	Lys	Gly	Thr	Cys	Leu 415	Leu
Ile	Asn	Met	Trp 420	Lys	Leu	His	Arg	Asp 425	Pro	Asn	Ile	Trp	Ser 430	Asp	Pro
Cys	Glu	Phe 435	Lys	Pro	Glu	Arg	Phe 440	Leu	Thr	Pro	Asn	Gln 445	Lys	Asp	Val
Asp	Val 450	Ile	Gly	Met	Asp	Phe 455	Glu	Leu	Ile	Pro	Phe 460	Gly	Ala	Gly	Arg
Arg 465	Tyr	Cys	Pro	Gly	Thr 470	Arg	Leu	Ala	Leu	Gln 475	Met	Leu	His	Ile	Val 480
Leu	Ala	Thr	Leu	Leu 485	Gln	Asn	Phe	Glu	Met 490	Ser	Thr	Pro	Asn	Asp 495	Ala
Pro	Val	Asp	Met 500	Thr	Ala	Ser	Val	Gly 505	Met	Thr	Asn	Ala	Lys 510	Ala	Ser

SeqLst
 Pro Leu Glu Val Leu Leu Ser Pro Arg Val Lys Trp Ser
 515 520 525

<210> 143
 <211> 476
 <212> PRT
 <213> Stevia rebaudiana

<400> 143
 Met Ile Gln Val Leu Thr Pro Ile Leu Leu Phe Leu Ile Phe Phe Val
 1 5 10 15

Phe Trp Lys Val Tyr Lys His Gln Lys Thr Lys Ile Asn Leu Pro Pro
 20 25 30

Gly Ser Phe Gly Trp Pro Phe Leu Gly Glu Thr Leu Ala Leu Leu Arg
 35 40 45

Ala Gly Trp Asp Ser Glu Pro Glu Arg Phe Val Arg Glu Arg Ile Lys
 50 55 60

Lys His Gly Ser Pro Leu Val Phe Lys Thr Ser Leu Phe Gly Asp Arg
 65 70 75 80

Phe Ala Val Leu Cys Gly Pro Ala Gly Asn Lys Phe Leu Phe Cys Asn
 85 90 95

Glu Asn Lys Leu Val Ala Ser Trp Trp Pro Val Pro Val Arg Lys Leu
 100 105 110

Phe Gly Lys Ser Leu Leu Thr Ile Arg Gly Asp Glu Ala Lys Trp Met
 115 120 125

Arg Lys Met Leu Leu Ser Tyr Leu Gly Pro Asp Ala Phe Ala Thr His
 130 135 140

Tyr Ala Val Thr Met Asp Val Val Thr Arg Arg His Ile Asp Val His
 145 150 155 160

Trp Arg Gly Lys Glu Glu Val Asn Val Phe Gln Thr Val Lys Leu Tyr
 165 170 175

Ala Phe Glu Leu Ala Cys Arg Leu Phe Met Asn Leu Asp Asp Pro Asn
 180 185 190

His Ile Ala Lys Leu Gly Ser Leu Phe Asn Ile Phe Leu Lys Gly Ile
 195 200 205

Ile Glu Leu Pro Ile Asp Val Pro Gly Thr Arg Phe Tyr Ser Ser Lys

										SeqLst											
210					215					220											
Lys	Ala	Ala	Ala	Ala	Ile	Arg	Ile	Glu	Leu	Lys	Lys	Leu	Ile	Lys	Ala						
225					230					235					240						
Arg	Lys	Leu	Glu	Leu	Lys	Glu	Gly	Lys	Ala	Ser	Ser	Ser	Gln	Asp	Leu						
				245					250					255							
Leu	Ser	His	Leu	Leu	Thr	Ser	Pro	Asp	Glu	Asn	Gly	Met	Phe	Leu	Thr						
			260					265					270								
Glu	Glu	Glu	Ile	Val	Asp	Asn	Ile	Leu	Leu	Leu	Leu	Phe	Ala	Gly	His						
		275					280					285									
Asp	Thr	Ser	Ala	Leu	Ser	Ile	Thr	Leu	Leu	Met	Lys	Thr	Leu	Gly	Glu						
	290					295					300										
His	Ser	Asp	Val	Tyr	Asp	Lys	Val	Leu	Lys	Glu	Gln	Leu	Glu	Ile	Ser						
305					310					315					320						
Lys	Thr	Lys	Glu	Ala	Trp	Glu	Ser	Leu	Lys	Trp	Glu	Asp	Ile	Gln	Lys						
				325					330					335							
Met	Lys	Tyr	Ser	Trp	Ser	Val	Ile	Cys	Glu	Val	Met	Arg	Leu	Asn	Pro						
			340					345					350								
Pro	Val	Ile	Gly	Thr	Tyr	Arg	Glu	Ala	Leu	Val	Asp	Ile	Asp	Tyr	Ala						
		355					360					365									
Gly	Tyr	Thr	Ile	Pro	Lys	Gly	Trp	Lys	Leu	His	Trp	Ser	Ala	Val	Ser						
	370					375					380										
Thr	Gln	Arg	Asp	Glu	Ala	Asn	Phe	Glu	Asp	Val	Thr	Arg	Phe	Asp	Pro						
385					390					395					400						
Ser	Arg	Phe	Glu	Gly	Ala	Gly	Pro	Thr	Pro	Phe	Thr	Phe	Val	Pro	Phe						
				405					410					415							
Gly	Gly	Gly	Pro	Arg	Met	Cys	Leu	Gly	Lys	Glu	Phe	Ala	Arg	Leu	Glu						
			420					425					430								
Val	Leu	Ala	Phe	Leu	His	Asn	Ile	Val	Thr	Asn	Phe	Lys	Trp	Asp	Leu						
		435					440					445									
Leu	Ile	Pro	Asp	Glu	Lys	Ile	Glu	Tyr	Asp	Pro	Met	Ala	Thr	Pro	Ala						
	450					455					460										

SeqLst
 Lys Gly Leu Pro Ile Arg Leu His Pro His Gln Val
 465 470 475

<210> 144
 <211> 525
 <212> PRT
 <213> Arabidopsis thaliana

<400> 144
 Met Glu Ser Leu Val Val His Thr Val Asn Ala Ile Trp Cys Ile Val
 1 5 10 15

Ile Val Gly Ile Phe Ser Val Gly Tyr His Val Tyr Gly Arg Ala Val
 20 25 30

Val Glu Gln Trp Arg Met Arg Arg Ser Leu Lys Leu Gln Gly Val Lys
 35 40 45

Gly Pro Pro Pro Ser Ile Phe Asn Gly Asn Val Ser Glu Met Gln Arg
 50 55 60

Ile Gln Ser Glu Ala Lys His Cys Ser Gly Asp Asn Ile Ile Ser His
 65 70 75 80

Asp Tyr Ser Ser Ser Leu Phe Pro His Phe Asp His Trp Arg Lys Gln
 85 90 95

Tyr Gly Arg Ile Tyr Thr Tyr Ser Thr Gly Leu Lys Gln His Leu Tyr
 100 105 110

Ile Asn His Pro Glu Met Val Lys Glu Leu Ser Gln Thr Asn Thr Leu
 115 120 125

Asn Leu Gly Arg Ile Thr His Ile Thr Lys Arg Leu Asn Pro Ile Leu
 130 135 140

Gly Asn Gly Ile Ile Thr Ser Asn Gly Pro His Trp Ala His Gln Arg
 145 150 155 160

Arg Ile Ile Ala Tyr Glu Phe Thr His Asp Lys Ile Lys Gly Met Val
 165 170 175

Gly Leu Met Val Glu Ser Ala Met Pro Met Leu Asn Lys Trp Glu Glu
 180 185 190

Met Val Lys Arg Gly Gly Glu Met Gly Cys Asp Ile Arg Val Asp Glu
 195 200 205

Asp Leu Lys Asp Val Ser Ala Asp Val Ile Ala Lys Ala Cys Phe Gly

															SeqLst	
210					215					220						
Ser	Ser	Phe	Ser	Lys	Gly	Lys	Ala	Ile	Phe	Ser	Met	Ile	Arg	Asp	Leu	
225					230					235					240	
Leu	Thr	Ala	Ile	Thr	Lys	Arg	Ser	Val	Leu	Phe	Arg	Phe	Asn	Gly	Phe	
				245					250					255		
Thr	Asp	Met	Val	Phe	Gly	Ser	Lys	Lys	His	Gly	Asp	Val	Asp	Ile	Asp	
			260					265					270			
Ala	Leu	Glu	Met	Glu	Leu	Glu	Ser	Ser	Ile	Trp	Glu	Thr	Val	Lys	Glu	
		275					280					285				
Arg	Glu	Ile	Glu	Cys	Lys	Asp	Thr	His	Lys	Lys	Asp	Leu	Met	Gln	Leu	
	290					295					300					
Ile	Leu	Glu	Gly	Ala	Met	Arg	Ser	Cys	Asp	Gly	Asn	Leu	Trp	Asp	Lys	
305					310					315					320	
Ser	Ala	Tyr	Arg	Arg	Phe	Val	Val	Asp	Asn	Cys	Lys	Ser	Ile	Tyr	Phe	
				325					330					335		
Ala	Gly	His	Asp	Ser	Thr	Ala	Val	Ser	Val	Ser	Trp	Cys	Leu	Met	Leu	
			340					345					350			
Leu	Ala	Leu	Asn	Pro	Ser	Trp	Gln	Val	Lys	Ile	Arg	Asp	Glu	Ile	Leu	
		355					360					365				
Ser	Ser	Cys	Lys	Asn	Gly	Ile	Pro	Asp	Ala	Glu	Ser	Ile	Pro	Asn	Leu	
	370					375					380					
Lys	Thr	Val	Thr	Met	Val	Ile	Gln	Glu	Thr	Met	Arg	Leu	Tyr	Pro	Pro	
385					390					395					400	
Ala	Pro	Ile	Val	Gly	Arg	Glu	Ala	Ser	Lys	Asp	Ile	Arg	Leu	Gly	Asp	
				405					410					415		
Leu	Val	Val	Pro	Lys	Gly	Val	Cys	Ile	Trp	Thr	Leu	Ile	Pro	Ala	Leu	
			420					425					430			
His	Arg	Asp	Pro	Glu	Ile	Trp	Gly	Pro	Asp	Ala	Asn	Asp	Phe	Lys	Pro	
		435					440					445				
Glu	Arg	Phe	Ser	Glu	Gly	Ile	Ser	Lys	Ala	Cys	Lys	Tyr	Pro	Gln	Ser	
	450					455					460					

SeqLst

Tyr Ile Pro Phe Gly Leu Gly Pro Arg Thr Cys Val Gly Lys Asn Phe
 465 470 475 480

Gly Met Met Glu Val Lys Val Leu Val Ser Leu Ile Val Ser Lys Phe
 485 490 495

Ser Phe Thr Leu Ser Pro Thr Tyr Gln His Ser Pro Ser His Lys Leu
 500 505 510

Leu Val Glu Pro Gln His Gly Val Val Ile Arg Val Val
 515 520 525

<210> 145
 <211> 529
 <212> PRT
 <213> Vitis vinifera

<400> 145
 Met Tyr Phe Leu Leu Gln Tyr Leu Asn Ile Thr Thr Val Gly Val Phe
 1 5 10 15

Ala Thr Leu Phe Leu Ser Tyr Cys Leu Leu Leu Trp Arg Ser Arg Ala
 20 25 30

Gly Asn Lys Lys Ile Ala Pro Glu Ala Ala Ala Ala Trp Pro Ile Ile
 35 40 45

Gly His Leu His Leu Leu Ala Gly Gly Ser His Gln Leu Pro His Ile
 50 55 60

Thr Leu Gly Asn Met Ala Asp Lys Tyr Gly Pro Val Phe Thr Ile Arg
 65 70 75 80

Ile Gly Leu His Arg Ala Val Val Val Ser Ser Trp Glu Met Ala Lys
 85 90 95

Glu Cys Ser Thr Ala Asn Asp Gln Val Ser Ser Ser Arg Pro Glu Leu
 100 105 110

Leu Ala Ser Lys Leu Leu Gly Tyr Asn Tyr Ala Met Phe Gly Phe Ser
 115 120 125

Pro Tyr Gly Ser Tyr Trp Arg Glu Met Arg Lys Ile Ile Ser Leu Glu
 130 135 140

Leu Leu Ser Asn Ser Arg Leu Glu Leu Leu Lys Asp Val Arg Ala Ser
 145 150 155 160

Glu Val Val Thr Ser Ile Lys Glu Leu Tyr Lys Leu Trp Ala Glu Lys

SeqLst															
165								170				175			
Lys	Asn	Glu	Ser180	Gly	Leu	Val	Ser	Val185	Glu	Met	Lys	Gln	Trp190	Phe	Gly
Asp	Leu	Thr195	Leu	Asn	Val	Ile	Leu200	Arg	Met	Val	Ala	Gly205	Lys	Arg	Tyr
Phe	Ser210	Ala	Ser	Asp	Ala	Ser215	Glu	Asn	Lys	Gln	Ala220	Gln	Arg	Cys	Arg
Arg225	Val	Phe	Arg	Glu	Phe230	Phe	His	Leu	Ser	Gly235	Leu	Phe	Val	Val	Ala240
Asp	Ala	Ile	Pro	Phe245	Leu	Gly	Trp	Leu	Asp250	Trp	Gly	Arg	His	Glu255	Lys
Thr	Leu	Lys	Lys260	Thr	Ala	Ile	Glu	Met265	Asp	Ser	Ile	Ala	Gln270	Glu	Trp
Leu	Glu	Glu275	His	Arg	Arg	Arg	Lys280	Asp	Ser	Gly	Asp	Asp285	Asn	Ser	Thr
Gln	Asp290	Phe	Met	Asp	Val	Met295	Gln	Ser	Val	Leu	Asp300	Gly	Lys	Asn	Leu
Gly305	Gly	Tyr	Asp	Ala	Asp310	Thr	Ile	Asn	Lys	Ala315	Thr	Cys	Leu	Thr	Leu320
Ile	Ser	Gly	Gly	Ser325	Asp	Thr	Thr	Val	Val330	Ser	Leu	Thr	Trp	Ala335	Leu
Ser	Leu	Val	Leu340	Asn	Asn	Arg	Asp	Thr345	Leu	Lys	Lys	Ala	Gln350	Glu	Glu
Leu	Asp	Ile355	Gln	Val	Gly	Lys	Glu360	Arg	Leu	Val	Asn	Glu365	Gln	Asp	Ile
Ser	Lys370	Leu	Val	Tyr	Leu	Gln375	Ala	Ile	Val	Lys	Glu380	Thr	Leu	Arg	Leu
Tyr385	Pro	Pro	Gly	Pro	Leu390	Gly	Gly	Leu	Arg	Gln395	Phe	Thr	Glu	Asp	Cys400
Thr	Leu	Gly	Gly	Tyr405	His	Val	Ser	Lys	Gly410	Thr	Arg	Leu	Ile	Met415	Asn

SeqLst

Leu Ser Lys Ile Gln Lys Asp Pro Arg Ile Trp Ser Asp Pro Thr Glu
 420 425 430

Phe Gln Pro Glu Arg Phe Leu Thr Thr His Lys Asp Val Asp Pro Arg
 435 440 445

Gly Lys His Phe Glu Phe Ile Pro Phe Gly Ala Gly Arg Arg Ala Cys
 450 455 460

Pro Gly Ile Thr Phe Gly Leu Gln Val Leu His Leu Thr Leu Ala Ser
 465 470 475 480

Phe Leu His Ala Phe Glu Phe Ser Thr Pro Ser Asn Glu Gln Val Asn
 485 490 495

Met Arg Glu Ser Leu Gly Leu Thr Asn Met Lys Ser Thr Pro Leu Glu
 500 505 510

Val Leu Ile Ser Pro Arg Leu Ser Leu Asn Cys Phe Asn Leu Met Lys
 515 520 525

Ile

<210> 146

<211> 479

<212> PRT

<213> Medicago trunculata

<400> 146

Met Glu Pro Asn Phe Tyr Leu Ser Leu Leu Leu Leu Phe Val Thr Phe
 1 5 10 15

Ile Ser Leu Ser Leu Phe Phe Ile Phe Tyr Lys Gln Lys Ser Pro Leu
 20 25 30

Asn Leu Pro Pro Gly Lys Met Gly Tyr Pro Ile Ile Gly Glu Ser Leu
 35 40 45

Glu Phe Leu Ser Thr Gly Trp Lys Gly His Pro Glu Lys Phe Ile Phe
 50 55 60

Asp Arg Met Arg Lys Tyr Ser Ser Glu Leu Phe Lys Thr Ser Ile Val
 65 70 75 80

Gly Glu Ser Thr Val Val Cys Cys Gly Ala Ala Ser Asn Lys Phe Leu
 85 90 95

Phe Ser Asn Glu Asn Lys Leu Val Thr Ala Trp Trp Pro Asp Ser Val

SeqLst															
100				105				110							
Asn	Lys	Ile 115	Phe	Pro	Thr	Thr	Ser 120	Leu	Asp	Ser	Asn	Leu 125	Lys	Glu	Glu
Ser	Ile 130	Lys	Met	Arg	Lys	Leu 135	Leu	Pro	Gln	Phe	Phe 140	Lys	Pro	Glu	Ala
Leu 145	Gln	Arg	Tyr	Val	Gly 150	Val	Met	Asp	Val	Ile 155	Ala	Gln	Arg	His	Phe 160
Val	Thr	His	Trp	Asp 165	Asn	Lys	Asn	Glu	Ile 170	Thr	Val	Tyr	Pro	Leu 175	Ala
Lys	Arg	Tyr	Thr 180	Phe	Leu	Leu	Ala	Cys 185	Arg	Leu	Phe	Met	Ser 190	Val	Glu
Asp	Glu	Asn 195	His	Val	Ala	Lys	Phe 200	Ser	Asp	Pro	Phe	Gln 205	Leu	Ile	Ala
Ala	Gly 210	Ile	Ile	Ser	Leu	Pro 215	Ile	Asp	Leu	Pro	Gly 220	Thr	Pro	Phe	Asn
Lys 225	Ala	Ile	Lys	Ala	Ser 230	Asn	Phe	Ile	Arg	Lys 235	Glu	Leu	Ile	Lys	Ile 240
Ile	Lys	Gln	Arg	Arg 245	Val	Asp	Leu	Ala	Glu 250	Gly	Thr	Ala	Ser	Pro 255	Thr
Gln	Asp	Ile	Leu 260	Ser	His	Met	Leu	Leu 265	Thr	Ser	Asp	Glu	Asn 270	Gly	Lys
Ser	Met	Asn 275	Glu	Leu	Asn	Ile	Ala 280	Asp	Lys	Ile	Leu	Gly 285	Leu	Leu	Ile
Gly	Gly 290	His	Asp	Thr	Ala	Ser 295	Val	Ala	Cys	Thr	Phe 300	Leu	Val	Lys	Tyr
Leu 305	Gly	Glu	Leu	Pro	His 310	Ile	Tyr	Asp	Lys	Val 315	Tyr	Gln	Glu	Gln	Met 320
Glu	Ile	Ala	Lys	Ser 325	Lys	Pro	Ala	Gly	Glu 330	Leu	Leu	Asn	Trp	Asp 335	Asp
Leu	Lys	Lys	Met 340	Lys	Tyr	Ser	Trp	Asn 345	Val	Ala	Cys	Glu	Val 350	Met	Arg

SeqLst

Leu Ser Pro Pro Leu Gln Gly Gly Phe Arg Glu Ala Ile Thr Asp Phe
355 360 365

Met Phe Asn Gly Phe Ser Ile Pro Lys Gly Trp Lys Leu Tyr Trp Ser
370 375 380

Ala Asn Ser Thr His Lys Asn Ala Glu Cys Phe Pro Met Pro Glu Lys
385 390 395 400

Phe Asp Pro Thr Arg Phe Glu Gly Asn Gly Pro Ala Pro Tyr Thr Phe
405 410 415

Val Pro Phe Gly Gly Gly Pro Arg Met Cys Pro Gly Lys Glu Tyr Ala
420 425 430

Arg Leu Glu Ile Leu Val Phe Met His Asn Leu Val Lys Arg Phe Lys
435 440 445

Trp Glu Lys Val Ile Pro Asp Glu Lys Ile Ile Val Asp Pro Phe Pro
450 455 460

Ile Pro Ala Lys Asp Leu Pro Ile Arg Leu Tyr Pro His Lys Ala
465 470 475

<210> 147
<211> 710
<212> PRT
<213> Stevia rebaudiana

<400> 147
Met Gln Ser Asp Ser Val Lys Val Ser Pro Phe Asp Leu Val Ser Ala
1 5 10 15

Ala Met Asn Gly Lys Ala Met Glu Lys Leu Asn Ala Ser Glu Ser Glu
20 25 30

Asp Pro Thr Thr Leu Pro Ala Leu Lys Met Leu Val Glu Asn Arg Glu
35 40 45

Leu Leu Thr Leu Phe Thr Thr Ser Phe Ala Val Leu Ile Gly Cys Leu
50 55 60

Val Phe Leu Met Trp Arg Arg Ser Ser Ser Lys Lys Leu Val Gln Asp
65 70 75 80

Pro Val Pro Gln Val Ile Val Val Lys Lys Lys Glu Lys Glu Ser Glu
85 90 95

Val Asp Asp Gly Lys Lys Lys Val Ser Ile Phe Tyr Gly Thr Gln Thr

SeqLst

Tyr Ser Glu Asn Leu Ser Glu Val Val Asp Glu Ala Leu Lys Leu Leu
355 360 365

Gly Leu Ser Pro Asp Thr Tyr Phe Ser Val His Ala Asp Lys Glu Asp
370 375 380

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

Thr Leu Arg Asp Ala Leu Thr Arg Tyr Ala Asp Val Leu Ser Ser Pro
405 410 415

Lys Lys Val Ala Leu Leu Ala Leu Ala Ala His Ala Ser Asp Pro Ser
420 425 430

Glu Ala Asp Arg Leu Lys Phe Leu Ala Ser Pro Ala Gly Lys Asp Glu
435 440 445

Tyr Ala Gln Trp Ile Val Ala Asn Gln Arg Ser Leu Leu Glu Val Met
450 455 460

Gln Ser Phe Pro Ser Ala Lys Pro Pro Leu Gly Val Phe Phe Ala Ala
465 470 475 480

Val Ala Pro Arg Leu Gln Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Pro
485 490 495

Lys Met Ser Pro Asn Arg Ile His Val Thr Cys Ala Leu Val Tyr Glu
500 505 510

Thr Thr Pro Ala Gly Arg Ile His Arg Gly Leu Cys Ser Thr Trp Met
515 520 525

Lys Asn Ala Val Pro Leu Thr Glu Ser Pro Asp Cys Ser Gln Ala Ser
530 535 540

Ile Phe Val Arg Thr Ser Asn Phe Arg Leu Pro Val Asp Pro Lys Val
545 550 555 560

Pro Val Ile Met Ile Gly Pro Gly Thr Gly Leu Ala Pro Phe Arg Gly
565 570 575

Phe Leu Gln Glu Arg Leu Ala Leu Lys Glu Ser Gly Thr Glu Leu Gly
580 585 590

Ser Ser Ile Phe Phe Phe Gly Cys Arg Asn Arg Lys Val Asp Phe Ile
595 600 605

SeqLst

Tyr Glu Asp Glu Leu Asn Asn Phe Val Glu Thr Gly Ala Leu Ser Glu
610 615 620

Leu Ile Val Ala Phe Ser Arg Glu Gly Thr Ala Lys Glu Tyr Val Gln
625 630 635 640

His Lys Met Ser Gln Lys Ala Ser Asp Ile Trp Lys Leu Leu Ser Glu
645 650 655

Gly Ala Tyr Leu Tyr Val Cys Gly Asp Ala Lys Gly Met Ala Lys Asp
660 665 670

Val His Arg Thr Leu His Thr Ile Val Gln Glu Gln Gly Ser Leu Asp
675 680 685

Ser Ser Lys Ala Glu Leu Tyr Val Lys Asn Leu Gln Met Ser Gly Arg
690 695 700

Tyr Leu Arg Asp Val Trp
705 710

<210> 148

<211> 692

<212> PRT

<213> Arabidopsis thaliana

<400> 148

Met Thr Ser Ala Leu Tyr Ala Ser Asp Leu Phe Lys Gln Leu Lys Ser
1 5 10 15

Ile Met Gly Thr Asp Ser Leu Ser Asp Asp Val Val Leu Val Ile Ala
20 25 30

Thr Thr Ser Leu Ala Leu Val Ala Gly Phe Val Val Leu Leu Trp Lys
35 40 45

Lys Thr Thr Ala Asp Arg Ser Gly Glu Leu Lys Pro Leu Met Ile Pro
50 55 60

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

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

Glu Gly Phe Ala Lys Ala Leu Ser Glu Glu Ile Lys Ala Arg Tyr Glu
100 105 110

SeqLst

Lys Ala Ala Val Lys Val Ile Asp Leu Asp Asp Tyr Ala Ala Asp Asp
 115 120 125

Asp Gln Tyr Glu Glu Lys Leu Lys Lys Glu Thr Leu Ala Phe Phe Cys
 130 135 140

Val Ala Thr Tyr Gly Asp Gly Glu Pro Thr Asp Asn Ala Ala Arg Phe
 145 150 155 160

Tyr Lys Trp Phe Thr Glu Glu Asn Glu Arg Asp Ile Lys Leu Gln Gln
 165 170 175

Leu Ala Tyr Gly Val Phe Ala Leu Gly Asn Arg Gln Tyr Glu His Phe
 180 185 190

Asn Lys Ile Gly Ile Val Leu Asp Glu Glu Leu Cys Lys Lys Gly Ala
 195 200 205

Lys Arg Leu Ile Glu Val Gly Leu Gly Asp Asp Asp Gln Ser Ile Glu
 210 215 220

Asp Asp Phe Asn Ala Trp Lys Glu Ser Leu Trp Ser Glu Leu Asp Lys
 225 230 235 240

Leu Leu Lys Asp Glu Asp Asp Lys Ser Val Ala Thr Pro Tyr Thr Ala
 245 250 255

Val Ile Pro Glu Tyr Arg Val Val Thr His Asp Pro Arg Phe Thr Thr
 260 265 270

Gln Lys Ser Met Glu Ser Asn Val Ala Asn Gly Asn Thr Thr Ile Asp
 275 280 285

Ile His His Pro Cys Arg Val Asp Val Ala Val Gln Lys Glu Leu His
 290 295 300

Thr His Glu Ser Asp Arg Ser Cys Ile His Leu Glu Phe Asp Ile Ser
 305 310 315 320

Arg Thr Gly Ile Thr Tyr Glu Thr Gly Asp His Val Gly Val Tyr Ala
 325 330 335

Glu Asn His Val Glu Ile Val Glu Glu Ala Gly Lys Leu Leu Gly His
 340 345 350

Ser Leu Asp Leu Val Phe Ser Ile His Ala Asp Lys Glu Asp Gly Ser
 355 360 365

SeqLst

Pro Leu Glu Ser Ala Val Pro Pro Pro Phe Pro Gly Pro Cys Thr Leu
 370 375 380
 Gly Thr Gly Leu Ala Arg Tyr Ala Asp Leu Leu Asn Pro Pro Arg Lys
 385 390 395 400
 Ser Ala Leu Val Ala Leu Ala Ala Tyr Ala Thr Glu Pro Ser Glu Ala
 405 410 415
 Glu Lys Leu Lys His Leu Thr Ser Pro Asp Gly Lys Asp Glu Tyr Ser
 420 425 430
 Gln Trp Ile Val Ala Ser Gln Arg Ser Leu Leu Glu Val Met Ala Ala
 435 440 445
 Phe Pro Ser Ala Lys Pro Pro Leu Gly Val Phe Phe Ala Ala Ile Ala
 450 455 460
 Pro Arg Leu Gln Pro Arg Tyr Tyr Ser Ile Ser Ser Ser Pro Arg Leu
 465 470 475 480
 Ala Pro Ser Arg Val His Val Thr Ser Ala Leu Val Tyr Gly Pro Thr
 485 490 495
 Pro Thr Gly Arg Ile His Lys Gly Val Cys Ser Thr Trp Met Lys Asn
 500 505 510
 Ala Val Pro Ala Glu Lys Ser His Glu Cys Ser Gly Ala Pro Ile Phe
 515 520 525
 Ile Arg Ala Ser Asn Phe Lys Leu Pro Ser Asn Pro Ser Thr Pro Ile
 530 535 540
 Val Met Val Gly Pro Gly Thr Gly Leu Ala Pro Phe Arg Gly Phe Leu
 545 550 555 560
 Gln Glu Arg Met Ala Leu Lys Glu Asp Gly Glu Glu Leu Gly Ser Ser
 565 570 575
 Leu Leu Phe Phe Gly Cys Arg Asn Arg Gln Met Asp Phe Ile Tyr Glu
 580 585 590
 Asp Glu Leu Asn Asn Phe Val Asp Gln Gly Val Ile Ser Glu Leu Ile
 595 600 605
 Met Ala Phe Ser Arg Glu Gly Ala Gln Lys Glu Tyr Val Gln His Lys
 610 615 620

SeqLst

Met Met Glu Lys Ala Ala Gln Val Trp Asp Leu Ile Lys Glu Glu Gly
625 630 635 640

Tyr Leu Tyr Val Cys Gly Asp Ala Lys Gly Met Ala Arg Asp Val His
645 650 655

Arg Thr Leu His Thr Ile Val Gln Glu Gln Glu Gly Val Ser Ser Ser
660 665 670

Glu Ala Glu Ala Ile Val Lys Lys Leu Gln Thr Glu Gly Arg Tyr Leu
675 680 685

Arg Asp Val Trp
690

<210> 149

<211> 713

<212> PRT

<213> Gibberella fujikuroi

<400> 149

Met Ala Glu Leu Asp Thr Leu Asp Ile Val Val Leu Gly Val Ile Phe
1 5 10 15

Leu Gly Thr Val Ala Tyr Phe Thr Lys Gly Lys Leu Trp Gly Val Thr
20 25 30

Lys Asp Pro Tyr Ala Asn Gly Phe Ala Ala Gly Gly Ala Ser Lys Pro
35 40 45

Gly Arg Thr Arg Asn Ile Val Glu Ala Met Glu Glu Ser Gly Lys Asn
50 55 60

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

Ser Arg Leu Ala Lys Glu Gly Lys Ser Arg Phe Gly Leu Asn Thr Met
85 90 95

Ile Ala Asp Leu Glu Asp Tyr Asp Phe Asp Asn Leu Asp Thr Val Pro
100 105 110

Ser Asp Asn Ile Val Met Phe Val Leu Ala Thr Tyr Gly Glu Gly Glu
115 120 125

Pro Thr Asp Asn Ala Val Asp Phe Tyr Glu Phe Ile Thr Gly Glu Asp
130 135 140

SeqLst

Ala Ser Phe Asn Glu Gly Asn Asp Pro Pro Leu Gly Asn Leu Asn Tyr
 145 150 155 160
 Val Ala Phe Gly Leu Gly Asn Asn Thr Tyr Glu His Tyr Asn Ser Met
 165 170 175
 Val Arg Asn Val Asn Lys Ala Leu Glu Lys Leu Gly Ala His Arg Ile
 180 185 190
 Gly Glu Ala Gly Glu Gly Asp Asp Gly Ala Gly Thr Met Glu Glu Asp
 195 200 205
 Phe Leu Ala Trp Lys Asp Pro Met Trp Glu Ala Leu Ala Lys Lys Met
 210 215 220
 Gly Leu Glu Glu Arg Glu Ala Val Tyr Glu Pro Ile Phe Ala Ile Asn
 225 230 235 240
 Glu Arg Asp Asp Leu Thr Pro Glu Ala Asn Glu Val Tyr Leu Gly Glu
 245 250 255
 Pro Asn Lys Leu His Leu Glu Gly Thr Ala Lys Gly Pro Phe Asn Ser
 260 265 270
 His Asn Pro Tyr Ile Ala Pro Ile Ala Glu Ser Tyr Glu Leu Phe Ser
 275 280 285
 Ala Lys Asp Arg Asn Cys Leu His Met Glu Ile Asp Ile Ser Gly Ser
 290 295 300
 Asn Leu Lys Tyr Glu Thr Gly Asp His Ile Ala Ile Trp Pro Thr Asn
 305 310 315 320
 Pro Gly Glu Glu Val Asn Lys Phe Leu Asp Ile Leu Asp Leu Ser Gly
 325 330 335
 Lys Gln His Ser Val Val Thr Val Lys Ala Leu Glu Pro Thr Ala Lys
 340 345 350
 Val Pro Phe Pro Asn Pro Thr Thr Tyr Asp Ala Ile Leu Arg Tyr His
 355 360 365
 Leu Glu Ile Cys Ala Pro Val Ser Arg Gln Phe Val Ser Thr Leu Ala
 370 375 380
 Ala Phe Ala Pro Asn Asp Asp Ile Lys Ala Glu Met Asn Arg Leu Gly
 385 390 395 400

SeqLst

Ser Asp Lys Asp Tyr Phe His Glu Lys Thr Gly Pro His Tyr Tyr Asn
 405 410 415
 Ile Ala Arg Phe Leu Ala Ser Val Ser Lys Gly Glu Lys Trp Thr Lys
 420 425 430
 Ile Pro Phe Ser Ala Phe Ile Glu Gly Leu Thr Lys Leu Gln Pro Arg
 435 440 445
 Tyr Tyr Ser Ile Ser Ser Ser Ser Leu Val Gln Pro Lys Lys Ile Ser
 450 455 460
 Ile Thr Ala Val Val Glu Ser Gln Gln Ile Pro Gly Arg Asp Asp Pro
 465 470 475 480
 Phe Arg Gly Val Ala Thr Asn Tyr Leu Phe Ala Leu Lys Gln Lys Gln
 485 490 495
 Asn Gly Asp Pro Asn Pro Ala Pro Phe Gly Gln Ser Tyr Glu Leu Thr
 500 505 510
 Gly Pro Arg Asn Lys Tyr Asp Gly Ile His Val Pro Val His Val Arg
 515 520 525
 His Ser Asn Phe Lys Leu Pro Ser Asp Pro Gly Lys Pro Ile Ile Met
 530 535 540
 Ile Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly Phe Val Gln Glu
 545 550 555 560
 Arg Ala Lys Gln Ala Arg Asp Gly Val Glu Val Gly Lys Thr Leu Leu
 565 570 575
 Phe Phe Gly Cys Arg Lys Ser Thr Glu Asp Phe Met Tyr Gln Lys Glu
 580 585 590
 Trp Gln Glu Tyr Lys Glu Ala Leu Gly Asp Lys Phe Glu Met Ile Thr
 595 600 605
 Ala Phe Ser Arg Glu Gly Ser Lys Lys Val Tyr Val Gln His Arg Leu
 610 615 620
 Lys Glu Arg Ser Lys Glu Val Ser Asp Leu Leu Ser Gln Lys Ala Tyr
 625 630 635 640
 Phe Tyr Val Cys Gly Asp Ala Ala His Met Ala Arg Glu Val Asn Thr

SeqLst

645 650 655

Val Leu Ala Gln Ile Ile Ala Glu Gly Arg Gly Val Ser Glu Ala Lys
660 665 670

Gly Glu Glu Ile Val Lys Asn Met Arg Ser Ala Asn Gln Tyr Gln Val
675 680 685

Cys Ser Asp Phe Val Thr Leu His Cys Lys Glu Thr Thr Tyr Ala Asn
690 695 700

Ser Glu Leu Gln Glu Asp Val Trp Ser
705 710

<210> 150
<211> 453
<212> PRT
<213> Arabidopsis thaliana

<400> 150
Met Gly Gly Leu Lys Phe His Val Leu Met Tyr Pro Trp Phe Ala Thr
1 5 10 15

Gly His Met Thr Pro Phe Leu Phe Leu Ala Asn Lys Leu Ala Glu Lys
20 25 30

Gly His Thr Val Thr Phe Leu Leu Pro Lys Lys Ser Leu Lys Gln Leu
35 40 45

Glu His Phe Asn Leu Phe Pro His Asn Ile Val Phe Arg Ser Val Thr
50 55 60

Val Pro His Val Asp Gly Leu Pro Val Gly Thr Glu Thr Ala Ser Glu
65 70 75 80

Ile Pro Val Thr Ser Thr Asp Leu Leu Met Ser Ala Met Asp Leu Thr
85 90 95

Arg Asp Gln Val Glu Ala Val Val Arg Ala Val Glu Pro Asp Leu Ile
100 105 110

Phe Phe Asp Phe Ala His Trp Ile Pro Glu Val Ala Arg Asp Phe Gly
115 120 125

Leu Lys Thr Val Lys Tyr Val Val Val Ser Ala Ser Thr Ile Ala Ser
130 135 140

Met Leu Val Pro Gly Gly Glu Leu Gly Val Pro Pro Pro Gly Tyr Pro
145 150 155 160

SeqLst

Ser Ser Lys Val Leu Leu Arg Lys Gln Asp Ala Tyr Thr Met Lys Lys
 165 170 175
 Leu Glu Pro Thr Asn Thr Ile Asp Val Gly Pro Asn Leu Leu Glu Arg
 180 185 190
 Val Thr Thr Ser Leu Met Asn Ser Asp Val Ile Ala Ile Arg Thr Ala
 195 200 205
 Arg Glu Ile Glu Gly Asn Phe Cys Asp Tyr Ile Glu Lys His Cys Arg
 210 215 220
 Lys Lys Val Leu Leu Thr Gly Pro Val Phe Pro Glu Pro Asp Lys Thr
 225 230 235 240
 Arg Glu Leu Glu Glu Arg Trp Val Lys Trp Leu Ser Gly Tyr Glu Pro
 245 250 255
 Asp Ser Val Val Phe Cys Ala Leu Gly Ser Gln Val Ile Leu Glu Lys
 260 265 270
 Asp Gln Phe Gln Glu Leu Cys Leu Gly Met Glu Leu Thr Gly Ser Pro
 275 280 285
 Phe Leu Val Ala Val Lys Pro Pro Arg Gly Ser Ser Thr Ile Gln Glu
 290 295 300
 Ala Leu Pro Glu Gly Phe Glu Glu Arg Val Lys Gly Arg Gly Leu Val
 305 310 315 320
 Trp Gly Gly Trp Val Gln Gln Pro Leu Ile Leu Ser His Pro Ser Val
 325 330 335
 Gly Cys Phe Val Ser His Cys Gly Phe Gly Ser Met Trp Glu Ser Leu
 340 345 350
 Leu Ser Asp Cys Gln Ile Val Leu Val Pro Gln Leu Gly Asp Gln Val
 355 360 365
 Leu Asn Thr Arg Leu Leu Ser Asp Glu Leu Lys Val Ser Val Glu Val
 370 375 380
 Ala Arg Glu Glu Thr Gly Trp Phe Ser Lys Glu Ser Leu Cys Asp Ala
 385 390 395 400
 Val Asn Ser Val Met Lys Arg Asp Ser Glu Leu Gly Asn Leu Val Arg

SeqLst

405 410 415

Lys Asn His Thr 420 Lys Trp Arg Glu Thr 425 Val Ala Ser Pro Gly 430 Leu Met

Thr Gly Tyr Val 435 Asp Ala Phe Val 440 Glu Ser Leu Gln 445 Asp Leu Val Ser

Gly Thr Thr His Asp 450

SeqLst

aagtggaggg agacagtagc tagtcctgga ctaatgactg gttatgtcga tgcttttcgta	1320
gagtcattgc aggatcttgt ctctgggacc acccatgact ga	1362

<210> 152
 <211> 462
 <212> PRT
 <213> Oryza sativa

<400> 152

Met	Asp	Ser	Gly	Tyr	Ser	Ser	Ser	Tyr	Ala	Ala	Ala	Ala	Gly	Met	His
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Val	Val	Ile	Cys	Pro	Trp	Leu	Ala	Phe	Gly	His	Leu	Leu	Pro	Cys	Leu
			20					25					30		
Asp	Leu	Ala	Gln	Arg	Leu	Ala	Ser	Arg	Gly	His	Arg	Val	Ser	Phe	Val
		35					40					45			
Ser	Thr	Pro	Arg	Asn	Ile	Ser	Arg	Leu	Pro	Pro	Val	Arg	Pro	Ala	Leu
		50				55					60				
Ala	Pro	Leu	Val	Ala	Phe	Val	Ala	Leu	Pro	Leu	Pro	Arg	Val	Glu	Gly
65					70					75				80	
Leu	Pro	Asp	Gly	Ala	Glu	Ser	Thr	Asn	Asp	Val	Pro	His	Asp	Arg	Pro
				85					90					95	
Asp	Met	Val	Glu	Leu	His	Arg	Arg	Ala	Phe	Asp	Gly	Leu	Ala	Ala	Pro
			100					105					110		
Phe	Ser	Glu	Phe	Leu	Gly	Thr	Ala	Cys	Ala	Asp	Trp	Val	Ile	Val	Asp
			115				120					125			
Val	Phe	His	His	Trp	Ala	Ala	Ala	Ala	Ala	Leu	Glu	His	Lys	Val	Pro
			130			135					140				
Cys	Ala	Met	Met	Leu	Leu	Gly	Ser	Ala	His	Met	Ile	Ala	Ser	Ile	Ala
145					150					155					160
Asp	Arg	Arg	Leu	Glu	Arg	Ala	Glu	Thr	Glu	Ser	Pro	Ala	Ala	Ala	Gly
				165					170					175	
Gln	Gly	Arg	Pro	Ala	Ala	Ala	Pro	Thr	Phe	Glu	Val	Ala	Arg	Met	Lys
			180					185					190		
Leu	Ile	Arg	Thr	Lys	Gly	Ser	Ser	Gly	Met	Ser	Leu	Ala	Glu	Arg	Phe
		195					200					205			
Ser	Leu	Thr	Leu	Ser	Arg	Ser	Ser	Leu	Val	Val	Gly	Arg	Ser	Cys	Val
		210				215					220				
Glu	Phe	Glu	Pro	Glu	Thr	Val	Pro	Leu	Leu	Ser	Thr	Leu	Arg	Gly	Lys
225					230					235					240
Pro	Ile	Thr	Phe	Leu	Gly	Leu	Met	Pro	Pro	Leu	His	Glu	Gly	Arg	Arg
				245					250					255	
Glu	Asp	Gly	Glu	Asp	Ala	Thr	Val	Arg	Trp	Leu	Asp	Ala	Gln	Pro	Ala
			260					265					270		
Lys	Ser	Val	Val	Tyr	Val	Ala	Leu	Gly	Ser	Glu	Val	Pro	Leu	Gly	Val
		275					280					285			
Glu	Lys	Val	His	Glu	Leu	Ala	Leu	Gly	Leu	Glu	Leu	Ala	Gly	Thr	Arg
		290				295					300				
Phe	Leu	Trp	Ala	Leu	Arg	Lys	Pro	Thr	Gly	Val	Ser	Asp	Ala	Asp	Leu
305					310					315					320
Leu	Pro	Ala	Gly	Phe	Glu	Glu	Arg	Thr	Arg	Gly	Arg	Gly	Val	Val	Ala
				325					330					335	
Thr	Arg	Trp	Val	Pro	Gln	Met	Ser	Ile	Leu	Ala	His	Ala	Ala	Val	Gly
			340					345					350		
Ala	Phe	Leu	Thr	His	Cys	Gly	Trp	Asn	Ser	Thr	Ile	Glu	Gly	Leu	Met
			355				360					365			
Phe	Gly	His	Pro	Leu	Ile	Met	Leu	Pro	Ile	Phe	Gly	Asp	Gln	Gly	Pro
			370			375					380				
Asn	Ala	Arg	Leu	Ile	Glu	Ala	Lys	Asn	Ala	Gly	Leu	Gln	Val	Ala	Arg
385					390					395					400
Asn	Asp	Gly	Asp	Gly	Ser	Phe	Asp	Arg	Glu	Gly	Val	Ala	Ala	Ala	Ile
				405					410					415	

SeqLst

Arg	Ala	Val	Ala	Val	Glu	Glu	Glu	Ser	Ser	Lys	Val	Phe	Gln	Ala	Lys
			420					425					430		
Ala	Lys	Lys	Leu	Gln	Glu	Ile	Val	Ala	Asp	Met	Ala	Cys	His	Glu	Arg
		435					440					445			
Tyr	Ile	Asp	Gly	Phe	Ile	Gln	Gln	Leu	Arg	Ser	Tyr	Lys	Asp		
	450					455					460				

<210> 153
 <211> 1389
 <212> DNA
 <213> Oryza sativa

<400> 153

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cggggccacc	gcgtgtcggt	cgtctccacg	ccgcggaaca	tatccccgct	cccgcgggtg	180
cgccccgcgc	tcgcgccgct	cgtcgccttc	gtggcgctgc	cgctcccgcg	cgtcgagggg	240
ctccccgacg	gcgccgagtc	caccaacgac	gtccccacg	acaggccgga	catggctcgag	300
ctccaccgga	gggccttcga	cgggctcgcc	gcgcccttct	cggagttctt	gggcaccgcg	360
tgcgccgact	gggtcatcgt	cgacgtcttc	caccactggg	ccgcagccgc	cgctctcgag	420
cacaaggctg	catgtgcaat	gatgttggtg	ggctctgcac	atatgatcgc	ttccatagca	480
gacagacggc	tcgagcgcg	ggagacagag	tcgcctgcgg	ctgccgggca	gggacgcca	540
gcggcggcgc	caacgttcga	ggtggcgagg	atgaagtga	tacgaacca	aggctcatcg	600
ggaatgtccc	tcgccgagcg	cttctccttg	acgctctcga	ggagcagcct	cgtcgtcggg	660
cggagctgcg	tggagttcga	gccggagacc	gtcccgtctc	tgtcgacgct	ccgcggtaag	720
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gccgggacgc	gcttcctctg	ggctcttagg	aagcccactg	gcgtctccga	cgccgacctc	960
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aactcgacca	tcgaggggct	catgttcggc	cacccgctta	tcattgctgc	gatcttcggc	1140
gaccagggac	cgaacgcgcg	gctaatacga	gcgaagaacg	ccggattgca	ggtggcaaga	1200
aacgacggcg	atggatcggt	cgaccgagaa	ggcgctcgcg	cggcgattcg	tgcagtcgcg	1260
gtggaggaag	aaagcagcaa	agtgtttcaa	gccaaagcca	agaagctgca	ggagatcgct	1320
gcggacatgg	cctgccatga	gaggtacatc	gacggattca	ttcagcaatt	gagatcttac	1380
aaggattga						1389

<210> 154
 <211> 1389
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oryza sativa sequence that has been codon optimized for yeast

<400> 154

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agaggccata	gagtatcatt	tgtgtctact	cctagaaata	tctctcgttt	accaccagtc	180
agacctgctc	tagctcctct	agttgcattc	gttgctcttc	cacttccaag	agtagaagga	240
ttgccagacg	gcgctgaatc	tactaatgac	gtaccacatg	atagacctga	catggctcga	300
ttgcatagaa	gagcctttga	tggattggca	gtcccathtt	ctgagttcct	gggcacagca	360
tgtgcagact	gggttatagt	cgatgtattt	catcactggg	ctgctgcagc	cgcattggaa	420
cataaggctg	cttgtgctat	gatgttggtt	gggtcagcac	acatgatcgc	atccatagct	480
gatagaagat	tggaaagagc	tgaaacagaa	tccccagccg	cagcaggaca	aggtaggcca	540
gctgccgccc	caacctttga	agtggctaga	atgaaattga	ttcgtactaa	aggtagttca	600
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agatcctgcg	tcgagttcga	acctgaaaca	gtacctttac	tatctacttt	gagaggcaaa	720
cctattactt	tccttgggtc	aatgcctcca	ttacatgaag	gaaggagaga	agatggtgaa	780
gatgctactg	ttaggtgggt	agatgcccac	cctgctaagt	ctgttggtta	cgttgcattg	840

SeqLst

ggttctgagg	taccactagg	ggtggaaaag	gtgcatgaat	tagcattagg	acttgagctg	900
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aatgatgggtg	atgggttcctt	tgatagagaa	ggcgttgacg	ctgccatcag	agcagtcgcc	1260
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gctgacatgg	cttgtcacga	aagatacatc	gatggtttca	tccaacaatt	gagaagttat	1380
aaagactaa						1389

<210> 155

<211> 2506

<212> DNA

<213> Arabidopsis thaliana

<400> 155

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ggaacgagga	ttggactcag	aagtacagac	aagagctaac	aatgtgagct	ttgagcaaac	180
aaaggagaag	attaggaaga	tggtggagaa	agtggagctt	tctgtttcgg	cctacgatac	240
tagttgggta	gcaatgggtt	catcaccgag	ctcccaaaat	gctccacttt	tcccacagtg	300
tgtgaaatgg	ttattggata	atcaacatga	agatggatct	tggggacttg	ataaccatga	360
ccatcaatct	cttaagaagg	atgtgttatc	atctacactg	gctagtatcc	tcgctgtaaa	420
gaagtgggga	attggtgaaa	gacaaataaa	caagggtctc	cagtttattg	agctgaattc	480
tgcattagtc	actgatgaaa	ccatacagaa	accaacaggg	tttgatatta	tatttccttg	540
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aagagaagca	tatctggcct	atgttttaga	ggggacaaga	aacctaaaag	attgggattt	720
gatatgcaaa	tatcaaagga	aaaatgggtc	actgtttgat	tctccagcca	caacagcagc	780
tgcttttact	cagtttgggg	atgatgggtg	tctccgttat	ctctgttctc	tccttcagaa	840
attcgaggct	gcagtttcct	cagtttatcc	atttgatcaa	tatgcacgcc	ttagtataat	900
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tgatagggtg	attgtggaga	atagattgca	ggaactgaaa	tttgccagac	agaagctggc	1560
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tcctgagtac	agctcagaac	atgttgagat	catattctca	gttctaaggg	acaccattct	1800
cgaaacagga	gacaaagcat	tcacctatca	aggacgcaat	gtgacacacc	acattgtgaa	1860
aatttggttg	gatctgtcta	agtctatggt	gagagaagcc	gagtgggtcca	gtgacaagtc	1920
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ccaatataat	cagctctaca	agctcgtgag	cactatgggt	cgtcttctaa	atgacataca	2100
aggttttaag	agagaaagcg	cggaaaggga	gctgaatgag	gtttcattgc	acatgaaaca	2160
cgagagagac	aatcgcagca	aagaagtgat	atgaaaggtt	atgaaaggtt	tagcagagag	2220
aaagagggaa	gaattgcata	agctagtttt	ggaggagaaa	ggaagtgtgg	ttccaaggga	2280
atgcaaagaa	gcgttcttga	aaatgagcaa	agtgttgaa	ttattttaca	ggaaggacga	2340
tggaattcaca	tcaaattgatc	tgatgagtc	tgtaaatca	gtgatctacg	agcctgttag	2400
cttacagaaa	gaatctttta	cttgatccaa	gttgatctgg	caggtaaact	cagtaaatga	2460
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<210> 156

<211> 785

<212> PRT

SeqLst

<213> Arabidopsis thaliana

<400> 156

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Val Ser Phe Glu Gln Thr Lys Glu Lys Ile Arg Lys Met Leu Glu Lys
 35      40      45
Val Glu Leu Ser Val Ser Ala Tyr Asp Thr Ser Trp Val Ala Met Val
 50      55      60
Pro Ser Pro Ser Ser Gln Asn Ala Pro Leu Phe Pro Gln Cys Val Lys
 65      70      75      80
Trp Leu Leu Asp Asn Gln His Glu Asp Gly Ser Trp Gly Leu Asp Asn
 85      90      95
His Asp His Gln Ser Leu Lys Lys Asp Val Leu Ser Ser Thr Leu Ala
100      105      110
Ser Ile Leu Ala Leu Lys Lys Trp Gly Ile Gly Glu Arg Gln Ile Asn
115      120      125
Lys Gly Leu Gln Phe Ile Glu Leu Asn Ser Ala Leu Val Thr Asp Glu
130      135      140
Thr Ile Gln Lys Pro Thr Gly Phe Asp Ile Ile Phe Pro Gly Met Ile
145      150      155      160
Lys Tyr Ala Arg Asp Leu Asn Leu Thr Ile Pro Leu Gly Ser Glu Val
165      170      175
Val Asp Asp Met Ile Arg Lys Arg Asp Leu Asp Leu Lys Cys Asp Ser
180      185      190
Glu Lys Phe Ser Lys Gly Arg Glu Ala Tyr Leu Ala Tyr Val Leu Glu
195      200      205
Gly Thr Arg Asn Leu Lys Asp Trp Asp Leu Ile Val Lys Tyr Gln Arg
210      215      220
Lys Asn Gly Ser Leu Phe Asp Ser Pro Ala Thr Thr Ala Ala Ala Phe
225      230      235      240
Thr Gln Phe Gly Asn Asp Gly Cys Leu Arg Tyr Leu Cys Ser Leu Leu
245      250      255
Gln Lys Phe Glu Ala Ala Val Pro Ser Val Tyr Pro Phe Asp Gln Tyr
260      265      270
Ala Arg Leu Ser Ile Ile Val Thr Leu Glu Ser Leu Gly Ile Asp Arg
275      280      285
Asp Phe Lys Thr Glu Ile Lys Ser Ile Leu Asp Glu Thr Tyr Arg Tyr
290      295      300
Trp Leu Arg Gly Asp Glu Glu Ile Cys Leu Asp Leu Ala Thr Cys Ala
305      310      315
Leu Ala Phe Arg Leu Leu Leu Ala His Gly Tyr Asp Val Ser Tyr Asp
320      325      330      335
Pro Leu Lys Pro Phe Ala Glu Glu Ser Gly Phe Ser Asp Thr Leu Glu
340      345      350
Gly Tyr Val Lys Asn Thr Phe Ser Val Leu Glu Leu Phe Lys Ala Ala
355      360      365
Gln Ser Tyr Pro His Glu Ser Ala Leu Lys Lys Gln Cys Cys Trp Thr
370      375      380
Lys Gln Tyr Leu Glu Met Glu Leu Ser Ser Trp Val Lys Thr Ser Val
385      390      395      400
Arg Asp Lys Tyr Leu Lys Lys Glu Val Glu Asp Ala Leu Ala Phe Pro
405      410      415
Ser Tyr Ala Ser Leu Glu Arg Ser Asp His Arg Arg Lys Ile Leu Asn
420      425      430
Gly Ser Ala Val Glu Asn Thr Arg Val Thr Lys Thr Ser Tyr Arg Leu
435      440      445
His Asn Ile Cys Thr Ser Asp Ile Leu Lys Leu Ala Val Asp Asp Phe
450      455      460
Asn Phe Cys Gln Ser Ile His Arg Glu Glu Met Glu Arg Leu Asp Arg
465      470      475      480

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SeqLst

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			500					505					510			
Leu	Ser	Asp	Ala	Arg	Ile	Ser	Trp	Ala	Lys	Gly	Gly	Val	Leu	Thr	Thr	
		515					520					525				
Val	Val	Asp	Asp	Phe	Phe	Asp	Val	Gly	Gly	Ser	Lys	Glu	Glu	Leu	Glu	
	530					535					540					
Asn	Leu	Ile	His	Leu	Val	Glu	Lys	Trp	Asp	Leu	Asn	Gly	Val	Pro	Glu	
545				550					555					560		
Tyr	Ser	Ser	Glu	His	Val	Glu	Ile	Ile	Phe	Ser	Val	Leu	Arg	Asp	Thr	
				565					570					575		
Ile	Leu	Glu	Thr	Gly	Asp	Lys	Ala	Phe	Thr	Tyr	Gln	Gly	Arg	Asn	Val	
			580					585					590			
Thr	His	His	Ile	Val	Lys	Ile	Trp	Leu	Asp	Leu	Leu	Lys	Ser	Met	Leu	
	595						600					605				
Arg	Glu	Ala	Glu	Trp	Ser	Ser	Asp	Lys	Ser	Thr	Pro	Ser	Leu	Glu	Asp	
	610					615					620					
Tyr	Met	Glu	Asn	Ala	Tyr	Ile	Ser	Phe	Ala	Leu	Gly	Pro	Ile	Val	Leu	
625				630					635					640		
Pro	Ala	Thr	Tyr	Leu	Ile	Gly	Pro	Pro	Leu	Pro	Glu	Lys	Thr	Val	Asp	
			645					650						655		
Ser	His	Gln	Tyr	Asn	Gln	Leu	Tyr	Lys	Leu	Val	Ser	Thr	Met	Gly	Arg	
			660					665					670			
Leu	Leu	Asn	Asp	Ile	Gln	Gly	Phe	Lys	Arg	Glu	Ser	Ala	Glu	Gly	Lys	
		675					680					685				
Leu	Asn	Ala	Val	Ser	Leu	His	Met	Lys	His	Glu	Arg	Asp	Asn	Arg	Ser	
	690					695					700					
Lys	Glu	Val	Ile	Ile	Glu	Ser	Met	Lys	Gly	Leu	Ala	Glu	Arg	Lys	Arg	
705					710					715				720		
Glu	Glu	Leu	His	Lys	Leu	Val	Leu	Glu	Glu	Lys	Gly	Ser	Val	Val	Pro	
				725					730					735		
Arg	Glu	Cys	Lys	Glu	Ala	Phe	Leu	Lys	Met	Ser	Lys	Val	Leu	Asn	Leu	
			740					745					750			
Phe	Tyr	Arg	Lys	Asp	Asp	Gly	Phe	Thr	Ser	Asn	Asp	Leu	Met	Ser	Leu	
		755					760					765				
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Thr
785

<210> 157
 <211> 2490
 <212> DNA
 <213> Zea mays

<400> 157
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 ccaagattag acggcggtga aggtcctcaa ttccagcag ctgtgagatg gataagaaat 420
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 ggtgtccatg acttcccta tgatcaccag gccctacaag gaatctactc ttcaagagag 720
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SeqLst

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SeqLst

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SeqLst

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<210> 162

<211> 952

<212> PRT

<213> *Gibberella fujikuroi*

<400> 162

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35          40          45
Asp Thr Ala Trp Val Ala Met Ile Pro Lys Thr Arg Asp Asn Val Lys
50          55          60
Gln Trp Leu Phe Pro Glu Cys Phe His Tyr Leu Leu Lys Thr Gln Ala
65          70          75          80
Ala Asp Gly Ser Trp Gly Ser Leu Pro Thr Thr Gln Thr Ala Gly Ile
85          90          95
Leu Asp Thr Ala Ser Ala Val Leu Ala Leu Leu Cys His Ala Gln Glu
100         105         110
Pro Leu Gln Ile Leu Asp Val Ser Pro Asp Glu Met Gly Leu Arg Ile
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	SeqLst														
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Asp	Leu	Glu	Gln	Val	Tyr	Gly	Lys	Pro	Ser	Ser	Leu	Leu	His	Ser	Leu
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Phe	Pro	Thr	Thr	His	Phe	Glu	Cys	Ser	Trp	Ile	Ile	Ala	Thr	Leu	Leu
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Lys	Val	Phe	Glu	Gly	Lys	Asp	His	Phe	Thr	Thr	Phe	Gly	Ser	Glu	Arg
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Phe	Thr	Cys	Arg	Trp	Trp	Trp	Gly	Ser	Asp	His	Cys	Val	Lys	Asp	Lys
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Tyr	Lys	Leu	Ala	Ala	Leu	Gln	Ser	Ala	Ser	Leu	Glu	Val	Pro	Ala	Ala
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Thr	Ile	Gly	His	Ser	Val	Thr	Ser	Ala	Val	Pro	Ser	Ser	Asp	Leu	Glu
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Lys	Tyr	Met	Arg	Leu	Val	Arg	Lys	Thr	Ala	Leu	Phe	Ser	Pro	Leu	Asp
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Glu	Trp	Gly	Leu	Met	Ala	Ser	Ile	Ile	Glu	Ser	Ser	Phe	Phe	Val	Pro
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Leu	Leu	Gln	Ala	Gln	Arg	Val	Glu	Ile	Tyr	Pro	Arg	Asp	Asn	Ile	Lys
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Val	Asp	Glu	Asp	Lys	Tyr	Leu	Ser	Ile	Ile	Pro	Phe	Thr	Trp	Val	Gly
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SeqLst

Cys	Asn	Asn	Arg	Ser	Arg	Thr	Phe	Ala	Ser	Asn	Arg	Trp	Leu	Tyr	Asp
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Ala	Val	Ala	Gly	Pro	Val	Phe	Gly	Asp	Val	Ser	Leu	Leu	His	Gln	Thr
Ile	Asp	Lys	Val	Ile	Asp	Asn	Thr	Met	Gly	Asn	Leu	Ala	Arg	Ala	Asn
Gly	Thr	Val	His	Ser	Gly	Asn	Gly	His	Gln	His	Glu	Ser	Pro	Asn	Ile
Gly	Gln	Val	Glu	Asp	Thr	Leu	Thr	Arg	Phe	Thr	Asn	Ser	Val	Leu	Asn
His	Lys	Asp	Val	Leu	Asn	Ser	Ser	Ser	Ser	Asp	Gln	Asp	Thr	Leu	Arg
Arg	Glu	Phe	Arg	Thr	Phe	Met	His	Ala	His	Ile	Thr	Gln	Ile	Glu	Asp
Asn	Ser	Arg	Phe	Ser	Lys	Gln	Ala	Ser	Ser	Asp	Ala	Phe	Ser	Ser	Pro
Glu	Gln	Ser	Tyr	Phe	Gln	Trp	Val	Asn	Ser	Thr	Gly	Gly	Ser	His	Val
Ala	Cys	Ala	Tyr	Ser	Phe	Ala	Phe	Ser	Asn	Cys	Leu	Met	Ser	Ala	Asn
Leu	Leu	Gln	Gly	Lys	Asp	Ala	Phe	Pro	Ser	Gly	Thr	Gln	Lys	Tyr	Leu
Ile	Ser	Ser	Val	Met	Arg	His	Ala	Thr	Asn	Met	Cys	Arg	Met	Tyr	Asn
Asp	Phe	Gly	Ser	Ile	Ala	Arg	Asp	Asn	Ala	Glu	Arg	Asn	Val	Asn	Ser
Ile	His	Phe	Pro	Glu	Phe	Thr	Leu	Cys	Asn	Gly	Thr	Ser	Gln	Asn	Leu
Asp	Glu	Arg	Lys	Glu	Arg	Leu	Leu	Lys	Ile	Ala	Thr	Tyr	Glu	Gln	Gly
Tyr	Leu	Asp	Arg	Ala	Leu	Glu	Ala	Leu	Glu	Arg	Gln	Ser	Arg	Asp	Asp
Ala	Gly	Asp	Arg	Ala	Gly	Ser	Lys	Asp	Met	Arg	Lys	Leu	Lys	Ile	Val
Lys	Leu	Phe	Cys	Asp	Val	Thr	Asp	Leu	Tyr	Asp	Gln	Leu	Tyr	Val	Ile
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 <212> DNA
 <213> Stevia rebaudiana

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SeqLst

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<210> 164
 <211> 500
 <212> PRT
 <213> Stevia rebaudiana

<400> 164

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Thr Val Phe Pro Ser Ile Pro Ile Ile Gly His Leu Tyr Leu Leu Lys
      35      40      45
Lys Pro Leu Tyr Arg Thr Leu Ala Lys Ile Ala Ala Lys Tyr Gly Pro
      50      55      60
Ile Leu Gln Leu Gln Leu Gly Tyr Arg Arg Val Leu Val Ile Ser Ser
      65      70      75      80
Pro Ser Ala Ala Glu Cys Phe Thr Asn Asn Asp Val Ile Phe Ala
      85      90      95
Asn Arg Pro Lys Thr Leu Phe Gly Lys Ile Val Gly Gly Thr Ser Leu
      100      105      110
Gly Ser Leu Ser Tyr Gly Asp Gln Trp Arg Asn Leu Arg Arg Val Ala
      115      120      125
Ser Ile Glu Ile Leu Ser Val His Arg Leu Asn Glu Phe His Asp Ile
      130      135      140
Arg Val Asp Glu Asn Arg Leu Leu Ile Arg Lys Leu Arg Ser Ser Ser
      145      150      155      160
Ser Pro Val Thr Leu Ile Thr Val Phe Tyr Ala Leu Thr Leu Asn Val
      165      170      175
Ile Met Arg Met Ile Ser Gly Lys Arg Tyr Phe Asp Ser Gly Asp Arg
      180      185      190
Glu Leu Glu Glu Gly Lys Arg Phe Arg Glu Ile Leu Asp Glu Thr
      195      200      205
Leu Leu Leu Ala Gly Ala Ser Asn Val Gly Asp Tyr Leu Pro Ile Leu
      210      215      220
Asn Trp Leu Gly Val Lys Ser Leu Glu Lys Lys Leu Ile Ala Leu Gln
      225      230      235      240
Lys Lys Arg Asp Asp Phe Phe Gln Gly Leu Ile Glu Gln Val Arg Lys
      245      250      255
Ser Arg Gly Ala Lys Val Gly Lys Gly Arg Lys Thr Met Ile Glu Leu
      260      265      270
Leu Leu Ser Leu Gln Glu Ser Glu Pro Glu Tyr Tyr Thr Asp Ala Met
      275      280      285
Ile Arg Ser Phe Val Leu Gly Leu Leu Ala Ala Gly Ser Asp Thr Ser
      290      295      300
Ala Gly Thr Met Glu Trp Ala Met Ser Leu Leu Val Asn His Pro His
      305      310      315      320
Val Leu Lys Lys Ala Gln Ala Glu Ile Asp Arg Val Ile Gly Asn Asn
      325      330      335
Arg Leu Ile Asp Glu Ser Asp Ile Gly Asn Ile Pro Tyr Ile Gly Cys
      340      345      350
Ile Ile Asn Glu Thr Leu Arg Leu Tyr Pro Ala Gly Pro Leu Leu Phe

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SeqLst

Pro	His	355	Glu	Ser	Ser	Ala	Asp	360	Cys	Val	Ile	Ser	Gly	365	Tyr	Asn	Ile	Pro
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Lys	Val	Trp	Asp	Asp	Pro	Glu	Thr	Phe	Lys	Pro	Glu	Arg	Phe	Gln	Gly			
				405					410					415				
Leu	Glu	Gly	Thr	Arg	Asp	Gly	Phe	Lys	Leu	Met	Pro	Phe	Gly	Ser	Gly			
			420					425					430					
Arg	Arg	Gly	Cys	Pro	Gly	Glu	Gly	Leu	Ala	Ile	Arg	Leu	Leu	Gly	Met			
	435						440					445						
Thr	Leu	Gly	Ser	Val	Ile	Gln	Cys	Phe	Asp	Trp	Glu	Arg	Val	Gly	Asp			
	450					455					460							
Glu	Met	Val	Asp	Met	Thr	Glu	Gly	Leu	Gly	Val	Thr	Leu	Pro	Lys	Ala			
465					470				475						480			
Val	Pro	Leu	Val	Ala	Lys	Cys	Lys	Pro	Arg	Ser	Glu	Met	Thr	Asn	Leu			
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Leu	Ser	Glu	Leu															
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<210> 165
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<400> 165

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<400> 166

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SeqLst															
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Tyr	Ala	Ser	Gln	Thr	Gly	Thr	Ala	Glu	Asp	Tyr	Ala	Lys	Lys	Phe	Ser
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Lys	Glu	Leu	Val	Ala	Lys	Phe	Asn	Leu	Asn	Val	Met	Cys	Ala	Asp	Val
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Glu	Asn	Tyr	Asp	Phe	Glu	Ser	Leu	Asn	Asp	Val	Pro	Val	Ile	Val	Ser
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Ile	Phe	Ile	Ser	Thr	Tyr	Gly	Glu	Gly	Asp	Phe	Pro	Asp	Gly	Ala	Val
		115					120					125			
Asn	Phe	Glu	Asp	Phe	Ile	Cys	Asn	Ala	Glu	Ala	Gly	Ala	Leu	Ser	Asn
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Leu	Arg	Tyr	Asn	Met	Phe	Gly	Leu	Gly	Asn	Ser	Thr	Tyr	Glu	Phe	Phe
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Asn	Gly	Ala	Ala	Lys	Lys	Ala	Glu	Lys	His	Leu	Ser	Ala	Ala	Gly	Ala
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Asp	Glu	Leu	His	Leu	Asp	Glu	Gln	Glu	Ala	Lys	Phe	Thr	Ser	Gln	Phe
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Gln	Tyr	Thr	Val	Leu	Asn	Glu	Ile	Thr	Asp	Ser	Met	Ser	Leu	Gly	Glu
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Pro	Ser	Ala	His	Tyr	Leu	Pro	Ser	His	Gln	Leu	Asn	Arg	Asn	Ala	Asp
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Gly	Ile	Gln	Leu	Gly	Pro	Phe	Asp	Leu	Ser	Gln	Pro	Tyr	Ile	Ala	Pro
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Ile	Val	Lys	Ser	Arg	Glu	Leu	Phe	Ser	Ser	Asn	Asp	Arg	Asn	Cys	Ile
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His	Ser	Glu	Phe	Asp	Leu	Ser	Gly	Ser	Asn	Ile	Lys	Tyr	Ser	Thr	Gly
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Asp	His	Leu	Ala	Val	Trp	Pro	Ser	Asn	Pro	Leu	Glu	Lys	Val	Glu	Gln
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Phe	Leu	Ser	Ile	Phe	Asn	Leu	Asp	Pro	Glu	Thr	Ile	Phe	Asp	Leu	Lys
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Pro	Leu	Asp	Pro	Thr	Val	Lys	Val	Pro	Phe	Pro	Thr	Pro	Thr	Thr	Ile
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Asp	Gly	Ala	Lys	Trp	Asp	Thr	Val	Pro	Met	Gln	Phe	Leu	Val	Glu	Ser
			420					425					430		
Val	Pro	Gln	Met	Thr	Pro	Arg	Tyr	Tyr	Ser	Ile	Ser	Ser	Ser	Ser	Leu
		435					440					445			
Ser	Glu	Lys	Gln	Thr	Val	His	Val	Thr	Ser	Ile	Val	Glu	Asn	Phe	Pro
	450					455					460				
Asn	Pro	Glu	Leu	Pro	Asp	Ala	Pro	Pro	Val	Val	Gly	Val	Thr	Thr	Asn
	465				470					475				480	
Leu	Leu	Arg	Asn	Ile	Gln	Leu	Ala	Gln	Asn	Asn	Val	Asn	Ile	Ala	Glu
				485					490					495	
Thr	Asn	Leu	Pro	Val	His	Tyr	Asp	Leu	Asn	Gly	Pro	Arg	Lys	Leu	Phe
			500					505					510		
Ala	Asn	Tyr	Lys	Leu	Pro	Val	His	Val	Arg	Arg	Ser	Asn	Phe	Arg	Leu
		515					520					525			

SeqLst

Pro	Ser	Asn	Pro	Ser	Thr	Pro	Val	Ile	Met	Ile	Gly	Pro	Gly	Thr	Gly
	530					535					540				
Val	Ala	Pro	Phe	Arg	Gly	Phe	Ile	Arg	Glu	Arg	Val	Ala	Phe	Leu	Glu
545					550					555					560
Ser	Gln	Lys	Lys	Gly	Gly	Asn	Asn	Val	Ser	Leu	Gly	Lys	His	Ile	Leu
				565					570					575	
Phe	Tyr	Gly	Ser	Arg	Asn	Thr	Asp	Asp	Phe	Leu	Tyr	Gln	Asp	Glu	Trp
			580					585					590		
Pro	Glu	Tyr	Ala	Lys	Lys	Leu	Asp	Gly	Ser	Phe	Glu	Met	Val	Val	Ala
	595						600					605			
His	Ser	Arg	Leu	Pro	Asn	Thr	Lys	Lys	Val	Tyr	Val	Gln	Asp	Lys	Leu
	610					615					620				
Lys	Asp	Tyr	Glu	Asp	Gln	Val	Phe	Glu	Met	Ile	Asn	Asn	Gly	Ala	Phe
625					630					635					640
Ile	Tyr	Val	Cys	Gly	Asp	Ala	Lys	Gly	Met	Ala	Lys	Gly	Val	Ser	Thr
				645					650					655	
Ala	Leu	Val	Gly	Ile	Leu	Ser	Arg	Gly	Lys	Ser	Ile	Thr	Thr	Asp	Glu
			660					665					670		
Ala	Thr	Glu	Leu	Ile	Lys	Met	Leu	Lys	Thr	Ser	Gly	Arg	Tyr	Gln	Glu
		675					680					685			
Asp	Val	Trp													
	690														

<210> 167
 <211> 335
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 167

Met	Glu	Ala	Lys	Ile	Asp	Glu	Leu	Ile	Asn	Asn	Asp	Pro	Val	Trp	Ser
1				5					10					15	
Ser	Gln	Asn	Glu	Ser	Leu	Ile	Ser	Lys	Pro	Tyr	Asn	His	Ile	Leu	Leu
			20					25					30		
Lys	Pro	Gly	Lys	Asn	Phe	Arg	Leu	Asn	Leu	Ile	Val	Gln	Ile	Asn	Arg
		35					40					45			
Val	Met	Asn	Leu	Pro	Lys	Asp	Gln	Leu	Ala	Ile	Val	Ser	Gln	Ile	Val
	50					55					60				
Glu	Leu	Leu	His	Asn	Ser	Ser	Leu	Leu	Ile	Asp	Asp	Ile	Glu	Asp	Asn
65					70					75					80
Ala	Pro	Leu	Arg	Arg	Gly	Gln	Thr	Thr	Ser	His	Leu	Ile	Phe	Gly	Val
				85					90					95	
Pro	Ser	Thr	Ile	Asn	Thr	Ala	Asn	Tyr	Met	Tyr	Phe	Arg	Ala	Met	Gln
			100					105					110		
Leu	Val	Ser	Gln	Leu	Thr	Thr	Lys	Glu	Pro	Leu	Tyr	His	Asn	Leu	Ile
		115					120					125			
Thr	Ile	Phe	Asn	Glu	Glu	Leu	Ile	Asn	Leu	His	Arg	Gly	Gln	Gly	Leu
	130					135					140				
Asp	Ile	Tyr	Trp	Arg	Asp	Phe	Leu	Pro	Glu	Ile	Ile	Pro	Thr	Gln	Glu
145					150					155					160
Met	Tyr	Leu	Asn	Met	Val	Met	Asn	Lys	Thr	Gly	Gly	Leu	Phe	Arg	Leu
				165					170					175	
Thr	Leu	Arg	Leu	Met	Glu	Ala	Leu	Ser	Pro	Ser	Ser	His	His	Gly	His
			180					185					190		
Ser	Leu	Val	Pro	Phe	Ile	Asn	Leu	Leu	Gly	Ile	Ile	Tyr	Gln	Ile	Arg
		195					200					205			
Asp	Asp	Tyr	Leu	Asn	Leu	Lys	Asp	Phe	Gln	Met	Ser	Ser	Glu	Lys	Gly
	210					215					220				
Phe	Ala	Glu	Asp	Ile	Thr	Glu	Gly	Lys	Leu	Ser	Phe	Pro	Ile	Val	His
225					230					235					240
Ala	Leu	Asn	Phe	Thr	Lys	Thr	Lys	Gly	Gln	Thr	Glu	Gln	His	Asn	Glu
				245					250					255	
Ile	Leu	Arg	Ile	Leu	Leu	Leu	Arg	Thr	Ser	Asp	Lys	Asp	Ile	Lys	Leu

SeqLst

Lys	Leu	Ile	260	Gln	Ile	Leu	Glu	Phe	265	Asp	Thr	Asn	Ser	Leu	270	Ala	Tyr	Thr
		275						280						285				
Lys	Asn	Phe	Ile	Asn	Gln	Leu	Val	Asn	Met	Ile	Lys	Asn	Asp	Asn	Glu			
	290				295						300							
Asn	Lys	Tyr	Leu	Pro	Asp	Leu	Ala	Ser	His	Ser	Asp	Thr	Ala	Thr	Asn			
	305				310					315					320			
Leu	His	Asp	Glu	Leu	Leu	Tyr	Ile	Ile	Asp	His	Leu	Ser	Glu	Leu				
			325						330					335				

<210> 168
 <211> 712
 <212> PRT
 <213> Arabidopsis thaliana

<400> 168

Met	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Met	Ile	Asp	Leu	Met	Ala			
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Ala	Ile	Ile	Lys	Gly	Glu	Pro	Val	Ile	Val	Ser	Asp	Pro	Ala	Asn	Ala			
			20					25					30					
Ser	Ala	Tyr	Glu	Ser	Val	Ala	Ala	Glu	Leu	Ser	Ser	Met	Leu	Ile	Glu			
		35				40						45						
Asn	Arg	Gln	Phe	Ala	Met	Ile	Val	Thr	Thr	Ser	Ile	Ala	Val	Leu	Ile			
	50				55					60								
Gly	Cys	Ile	Val	Met	Leu	Val	Trp	Arg	Arg	Ser	Gly	Ser	Gly	Asn	Ser			
	65				70					75				80				
Lys	Arg	Val	Glu	Pro	Leu	Lys	Pro	Leu	Val	Ile	Lys	Pro	Arg	Glu	Glu			
			85					90					95					
Glu	Ile	Asp	Asp	Gly	Arg	Lys	Lys	Val	Thr	Ile	Phe	Phe	Gly	Thr	Gln			
			100					105					110					
Thr	Gly	Thr	Ala	Glu	Gly	Phe	Ala	Lys	Ala	Leu	Gly	Glu	Glu	Ala	Lys			
		115					120					125						
Ala	Arg	Tyr	Glu	Lys	Thr	Arg	Phe	Lys	Ile	Val	Asp	Leu	Asp	Asp	Tyr			
	130					135					140							
Ala	Ala	Asp	Asp	Asp	Glu	Tyr	Glu	Glu	Lys	Leu	Lys	Lys	Glu	Asp	Val			
	145				150					155				160				
Ala	Phe	Phe	Phe	Leu	Ala	Thr	Tyr	Gly	Asp	Gly	Glu	Pro	Thr	Asp	Asn			
			165					170					175					
Ala	Ala	Arg	Phe	Tyr	Lys	Trp	Phe	Thr	Glu	Gly	Asn	Asp	Arg	Gly	Glu			
		180						185					190					
Trp	Leu	Lys	Asn	Leu	Lys	Tyr	Gly	Val	Phe	Gly	Leu	Gly	Asn	Arg	Gln			
		195					200					205						
Tyr	Glu	His	Phe	Asn	Lys	Val	Ala	Lys	Val	Val	Asp	Asp	Ile	Leu	Val			
	210				215						220							
Glu	Gln	Gly	Ala	Gln	Arg	Leu	Val	Gln	Val	Gly	Leu	Gly	Asp	Asp	Asp			
	225				230					235				240				
Gln	Cys	Ile	Glu	Asp	Phe	Thr	Ala	Trp	Arg	Glu	Ala	Leu	Trp	Pro				
			245					250					255					
Glu	Leu	Asp	Thr	Ile	Leu	Arg	Glu	Glu	Gly	Asp	Thr	Ala	Val	Ala	Thr			
			260					265					270					
Pro	Tyr	Thr	Ala	Ala	Val	Leu	Glu	Tyr	Arg	Val	Ser	Ile	His	Asp	Ser			
		275					280					285						
Glu	Asp	Ala	Lys	Phe	Asn	Asp	Ile	Thr	Leu	Ala	Asn	Gly	Asn	Gly	Tyr			
	290				295						300							
Thr	Val	Phe	Asp	Ala	Gln	His	Pro	Tyr	Lys	Ala	Asn	Val	Ala	Val	Lys			
	305				310					315					320			
Arg	Glu	Leu	His	Thr	Pro	Glu	Ser	Asp	Arg	Ser	Cys	Ile	His	Leu	Glu			
			325					330					335					
Phe	Asp	Ile	Ala	Gly	Ser	Gly	Leu	Thr	Met	Lys	Leu	Gly	Asp	His	Val			
			340					345					350					
Gly	Val	Leu	Cys	Asp	Asn	Leu	Ser	Glu	Thr	Val	Asp	Glu	Ala	Leu	Arg			
		355					360					365						

SeqLst

Leu	Leu	Asp	Met	Ser	Pro	Asp	Thr	Tyr	Phe	Ser	Leu	His	Ala	Glu	Lys
370	370					375					380				
Glu	Asp	Gly	Thr	Pro	Ile	Ser	Ser	Ser	Leu	Pro	Pro	Pro	Phe	Pro	Pro
385					390					395					400
Cys	Asn	Leu	Arg	Thr	Ala	Leu	Thr	Arg	Tyr	Ala	Cys	Leu	Leu	Ser	Ser
				405					410					415	
Pro	Lys	Lys	Ser	Ala	Leu	Val	Ala	Leu	Ala	Ala	His	Ala	Ser	Asp	Pro
			420					425					430		
Thr	Glu	Ala	Glu	Arg	Leu	Lys	His	Leu	Ala	Ser	Pro	Ala	Gly	Lys	Asp
		435					440					445			
Glu	Tyr	Ser	Lys	Trp	Val	Val	Glu	Ser	Gln	Arg	Ser	Leu	Leu	Glu	Val
450					455						460				
Met	Ala	Glu	Phe	Pro	Ser	Ala	Lys	Pro	Pro	Leu	Gly	Val	Phe	Phe	Ala
465					470					475					480
Gly	Val	Ala	Pro	Arg	Leu	Gln	Pro	Arg	Phe	Tyr	Ser	Ile	Ser	Ser	Ser
				485					490					495	
Pro	Lys	Ile	Ala	Glu	Thr	Arg	Ile	His	Val	Thr	Cys	Ala	Leu	Val	Tyr
			500					505					510		
Glu	Lys	Met	Pro	Thr	Gly	Arg	Ile	His	Lys	Gly	Val	Cys	Ser	Thr	Trp
		515					520					525			
Met	Lys	Asn	Ala	Val	Pro	Tyr	Glu	Lys	Ser	Glu	Lys	Leu	Phe	Leu	Gly
530						535					540				
Arg	Pro	Ile	Phe	Val	Arg	Gln	Ser	Asn	Phe	Lys	Leu	Pro	Ser	Asp	Ser
545					550					555					560
Lys	Val	Pro	Ile	Ile	Met	Ile	Gly	Pro	Gly	Thr	Gly	Leu	Ala	Pro	Phe
			565						570					575	
Arg	Gly	Phe	Leu	Gln	Glu	Arg	Leu	Ala	Leu	Val	Glu	Ser	Gly	Val	Glu
			580					585					590		
Leu	Gly	Pro	Ser	Val	Leu	Phe	Phe	Gly	Cys	Arg	Asn	Arg	Arg	Met	Asp
		595					600					605			
Phe	Ile	Tyr	Glu	Glu	Glu	Leu	Gln	Arg	Phe	Val	Glu	Ser	Gly	Ala	Leu
610						615					620				
Ala	Glu	Leu	Ser	Val	Ala	Phe	Ser	Arg	Glu	Gly	Pro	Thr	Lys	Glu	Tyr
625					630					635					640
Val	Gln	His	Lys	Met	Met	Asp	Lys	Ala	Ser	Asp	Ile	Trp	Asn	Met	Ile
				645					650					655	
Ser	Gln	Gly	Ala	Tyr	Leu	Tyr	Val	Cys	Gly	Asp	Ala	Lys	Gly	Met	Ala
			660					665					670		
Arg	Asp	Val	His	Arg	Ser	Leu	His	Thr	Ile	Ala	Gln	Glu	Gln	Gly	Ser
		675					680					685			
Met	Asp	Ser	Thr	Lys	Ala	Glu	Gly	Phe	Val	Lys	Asn	Leu	Gln	Thr	Ser
690						695					700				
Gly	Arg	Tyr	Leu	Arg	Asp	Val	Trp								
705					710										

<210> 169
 <211> 709
 <212> PRT
 <213> Stevia rebaudiana

<400> 169

Met	Gln	Ser	Glu	Ser	Val	Glu	Ala	Ser	Thr	Ile	Asp	Leu	Met	Thr	Ala
1				5					10					15	
Val	Leu	Lys	Asp	Thr	Val	Ile	Asp	Thr	Ala	Asn	Ala	Ser	Asp	Asn	Gly
			20					25					30		
Asp	Ser	Lys	Met	Pro	Pro	Ala	Leu	Ala	Met	Met	Phe	Glu	Ile	Arg	Asp
		35					40					45			
Leu	Leu	Leu	Ile	Leu	Thr	Thr	Ser	Val	Ala	Val	Leu	Val	Gly	Cys	Phe
		50				55					60				
Val	Val	Leu	Val	Trp	Lys	Arg	Ser	Ser	Gly	Lys	Lys	Ser	Gly	Lys	Glu
65					70					75					80
Leu	Glu	Pro	Pro	Lys	Ile	Val	Val	Pro	Lys	Arg	Arg	Leu	Glu	Gln	Glu

SeqLst																		
				85					90					95				
Val	Asp	Asp	Gly	Lys	Lys	Lys	Val	Thr	Ile	Phe	Phe	Gly	Thr	Gln	Thr			
			100					105					110					
Gly	Thr	Ala	Glu	Gly	Phe	Ala	Lys	Ala	Leu	Phe	Glu	Glu	Ala	Lys	Ala			
		115					120					125						
Arg	Tyr	Glu	Lys	Ala	Ala	Phe	Lys	Val	Ile	Asp	Leu	Asp	Asp	Tyr	Ala			
		130				135					140							
Ala	Asp	Leu	Asp	Glu	Tyr	Ala	Glu	Lys	Leu	Lys	Lys	Glu	Thr	Tyr	Ala			
145					150					155					160			
Phe	Phe	Phe	Leu	Ala	Thr	Tyr	Gly	Asp	Gly	Glu	Pro	Thr	Asp	Asn	Ala			
				165					170					175				
Ala	Lys	Phe	Tyr	Lys	Trp	Phe	Thr	Glu	Gly	Asp	Glu	Lys	Gly	Val	Trp			
			180					185						190				
Leu	Gln	Lys	Leu	Gln	Tyr	Gly	Val	Phe	Gly	Leu	Gly	Asn	Arg	Gln	Tyr			
		195					200					205						
Glu	His	Phe	Asn	Lys	Ile	Gly	Ile	Val	Val	Asp	Asp	Gly	Leu	Thr	Glu			
	210					215					220							
Gln	Gly	Ala	Lys	Arg	Ile	Val	Pro	Val	Gly	Leu	Gly	Asp	Asp	Asp	Gln			
225					230					235					240			
Ser	Ile	Glu	Asp	Asp	Phe	Ser	Ala	Trp	Lys	Glu	Leu	Val	Trp	Pro	Glu			
				245					250					255				
Leu	Asp	Leu	Leu	Leu	Arg	Asp	Glu	Asp	Asp	Lys	Ala	Ala	Ala	Thr	Pro			
			260					265					270					
Tyr	Thr	Ala	Ala	Ile	Pro	Glu	Tyr	Arg	Val	Val	Phe	His	Asp	Lys	Pro			
		275					280					285						
Asp	Ala	Phe	Ser	Asp	Asp	His	Thr	Gln	Thr	Asn	Gly	His	Ala	Val	His			
	290					295					300							
Asp	Ala	Gln	His	Pro	Cys	Arg	Ser	Asn	Val	Ala	Val	Lys	Lys	Glu	Leu			
305					310					315				320				
His	Thr	Pro	Glu	Ser	Asp	Arg	Ser	Cys	Thr	His	Leu	Glu	Phe	Asp	Ile			
				325					330					335				
Ser	His	Thr	Gly	Leu	Ser	Tyr	Glu	Thr	Gly	Asp	His	Val	Gly	Val	Tyr			
			340					345					350					
Cys	Glu	Asn	Leu	Ile	Glu	Val	Val	Glu	Glu	Ala	Gly	Lys	Leu	Leu	Gly			
		355					360					365						
Leu	Ser	Thr	Asp	Thr	Tyr	Phe	Ser	Leu	His	Ile	Asp	Asn	Glu	Asp	Gly			
		370				375					380							
Ser	Pro	Leu	Gly	Gly	Pro	Ser	Leu	Gln	Pro	Pro	Phe	Pro	Pro	Cys	Thr			
385					390				395					400				
Leu	Arg	Lys	Ala	Leu	Thr	Asn	Tyr	Ala	Asp	Leu	Leu	Ser	Ser	Pro	Lys			
				405					410					415				
Lys	Ser	Thr	Leu	Leu	Ala	Leu	Ala	Ala	His	Ala	Ser	Asp	Pro	Thr	Glu			
			420					425					430					
Ala	Asp	Arg	Leu	Arg	Phe	Leu	Ala	Ser	Arg	Glu	Gly	Lys	Asp	Glu	Tyr			
		435					440					445						
Ala	Glu	Trp	Val	Val	Ala	Asn	Gln	Arg	Ser	Leu	Leu	Glu	Val	Met	Glu			
	450					455					460							
Ala	Phe	Pro	Ser	Ala	Arg	Pro	Pro	Leu	Gly	Val	Phe	Phe	Ala	Ala	Val			
465					470					475					480			
Ala	Pro	Arg	Leu	Gln	Pro	Arg	Tyr	Tyr	Ser	Ile	Ser	Ser	Ser	Pro	Lys			
				485					490					495				
Met	Glu	Pro	Asn	Arg	Ile	His	Val	Thr	Cys	Ala	Leu	Val	Tyr	Glu	Lys			
			500					505					510					
Thr	Pro	Ala	Gly	Arg	Ile	His	Lys	Gly	Ile	Cys	Ser	Thr	Trp	Met	Lys			
		515					520					525						
Asn	Ala	Val	Pro	Leu	Thr	Glu	Ser	Gln	Asp	Cys	Ser	Trp	Ala	Pro	Ile			
	530					535						540						
Phe	Val	Arg	Thr	Ser	Asn	Phe	Arg	Leu	Pro	Ile	Asp	Pro	Lys	Val	Pro			
545					550					555					560			
Val	Ile	Met	Ile	Gly	Pro	Gly	Thr	Gly	Leu	Ala	Pro	Phe	Arg	Gly	Phe			
				565					570					575				
Leu	Gln	Glu	Arg	Leu	Ala	Leu	Lys	Glu	Ser	Gly	Thr	Glu	Leu	Gly	Ser			
			580					585					590					

SeqLst

Ser	Ile	Leu	Phe	Phe	Gly	Cys	Arg	Asn	Arg	Lys	Val	Asp	Tyr	Ile	Tyr
		595					600					605			
Glu	Asn	Glu	Leu	Asn	Asn	Phe	Val	Glu	Asn	Gly	Ala	Leu	Ser	Glu	Leu
	610					615					620				
Asp	Val	Ala	Phe	Ser	Arg	Asp	Gly	Pro	Thr	Lys	Glu	Tyr	Val	Gln	His
625					630					635					640
Lys	Met	Thr	Gln	Lys	Ala	Ser	Glu	Ile	Trp	Asn	Met	Leu	Ser	Glu	Gly
				645					650					655	
Ala	Tyr	Leu	Tyr	Val	Cys	Gly	Asp	Ala	Lys	Gly	Met	Ala	Lys	Asp	Val
			660					665					670		
His	Arg	Thr	Leu	His	Thr	Ile	Val	Gln	Glu	Gln	Gly	Ser	Leu	Asp	Ser
		675					680					685			
Ser	Lys	Ala	Glu	Leu	Tyr	Val	Lys	Asn	Leu	Gln	Met	Ser	Gly	Arg	Tyr
	690					695					700				
Leu	Arg	Asp	Val	Trp											
705															

<210> 170
 <211> 660
 <212> PRT
 <213> Stevia rebaudiana

<400> 170

Met	Gln	Ser	Asn	Ser	Val	Lys	Ile	Ser	Pro	Leu	Asp	Leu	Val	Thr	Ala
1				5					10					15	
Leu	Phe	Ser	Gly	Lys	Val	Leu	Asp	Thr	Ser	Asn	Ala	Ser	Glu	Ser	Gly
			20					25					30		
Glu	Ser	Ala	Met	Leu	Pro	Thr	Ile	Ala	Met	Ile	Met	Glu	Asn	Arg	Glu
		35					40					45			
Leu	Leu	Met	Ile	Leu	Thr	Thr	Ser	Val	Ala	Val	Leu	Ile	Gly	Cys	Val
	50					55					60				
Val	Val	Leu	Val	Trp	Arg	Arg	Ser	Ser	Thr	Lys	Lys	Ser	Ala	Leu	Glu
65					70					75					80
Pro	Pro	Val	Ile	Val	Val	Pro	Lys	Arg	Val	Gln	Glu	Glu	Glu	Val	Asp
				85					90					95	
Asp	Gly	Lys	Lys	Lys	Val	Thr	Val	Phe	Phe	Gly	Thr	Gln	Thr	Gly	Thr
			100					105					110		
Ala	Glu	Gly	Phe	Ala	Lys	Ala	Leu	Val	Glu	Glu	Ala	Lys	Ala	Arg	Tyr
		115					120					125			
Glu	Lys	Ala	Val	Phe	Lys	Val	Ile	Asp	Leu	Asp	Asp	Tyr	Ala	Ala	Asp
	130					135					140				
Asp	Asp	Glu	Tyr	Glu	Glu	Lys	Leu	Lys	Lys	Glu	Ser	Leu	Ala	Phe	Phe
145				150						155					160
Phe	Leu	Ala	Thr	Tyr	Gly	Asp	Gly	Glu	Pro	Thr	Asp	Asn	Ala	Ala	Arg
			165						170					175	
Phe	Tyr	Lys	Trp	Phe	Thr	Glu	Gly	Asp	Ala	Lys	Gly	Glu	Trp	Leu	Asn
		180						185					190		
Lys	Leu	Gln	Tyr	Gly	Val	Phe	Gly	Leu	Gly	Asn	Arg	Gln	Tyr	Glu	His
		195					200					205			
Phe	Asn	Lys	Ile	Ala	Lys	Val	Val	Asp	Asp	Gly	Leu	Val	Glu	Gln	Gly
	210					215					220				
Ala	Lys	Arg	Leu	Val	Pro	Val	Gly	Leu	Gly	Asp	Asp	Asp	Gln	Cys	Ile
225					230					235					240
Glu	Asp	Asp	Phe	Thr	Ala	Trp	Lys	Glu	Leu	Val	Trp	Pro	Glu	Leu	Asp
				245					250					255	
Gln	Leu	Leu	Arg	Asp	Glu	Asp	Asp	Thr	Thr	Val	Ala	Thr	Pro	Tyr	Thr
			260					265					270		
Ala	Ala	Val	Ala	Glu	Tyr	Arg	Val	Phe	His	Glu	Lys	Pro	Asp	Ala	
		275					280				285				
Leu	Ser	Glu	Asp	Tyr	Ser	Tyr	Thr	Asn	Gly	His	Ala	Val	His	Asp	Ala
	290					295					300				
Gln	His	Pro	Cys	Arg	Ser	Asn	Val	Ala	Val	Lys	Lys	Glu	Leu	His	Ser

															SeqLst															
305	Pro	Glu	Ser	Asp	Arg	310	Ser	Cys	Thr	His	Leu	315	Glu	Phe	Asp	Ile	Ser	320	Asn											
					325						330						335													
	Thr	Gly	Leu	Ser	Tyr	Glu	Thr	Gly	Asp	His	Val	Gly	Val	Tyr	Cys	Glu														
				340					345						350															
	Asn	Leu	Ser	Glu	Val	Val	Asn	Asp	Ala	Glu	Arg	Leu	Val	Gly	Leu	Pro														
			355					360					365																	
	Pro	Asp	Thr	Tyr	Ser	Ser	Ile	His	Thr	Asp	Ser	Glu	Asp	Gly	Ser	Pro														
		370				375						380																		
	Leu	Gly	Gly	Ala	Ser	Leu	Pro	Pro	Pro	Phe	Pro	Pro	Cys	Thr	Leu	Arg														
	385				390					395						400														
	Lys	Ala	Leu	Thr	Cys	Tyr	Ala	Asp	Val	Leu	Ser	Ser	Pro	Lys	Lys	Ser														
				405					410						415															
	Ala	Leu	Leu	Ala	Leu	Ala	Ala	His	Ala	Thr	Asp	Pro	Ser	Glu	Ala	Asp														
				420				425						430																
	Arg	Leu	Lys	Phe	Leu	Ala	Ser	Pro	Ala	Gly	Lys	Asp	Glu	Tyr	Ser	Gln														
		435					440						445																	
	Trp	Ile	Val	Ala	Ser	Gln	Arg	Ser	Leu	Leu	Glu	Val	Met	Glu	Ala	Phe														
		450				455						460																		
	Pro	Ser	Ala	Lys	Pro	Ser	Leu	Gly	Val	Phe	Phe	Ala	Ser	Val	Ala	Pro														
	465				470					475						480														
	Arg	Leu	Gln	Pro	Arg	Tyr	Tyr	Ser	Ile	Ser	Ser	Ser	Pro	Lys	Met	Ala														
				485					490						495															
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			500					505					510																	
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		515				520						525																		
	Val	Pro	Met	Thr	Glu	Ser	Gln	Asp	Cys	Ser	Trp	Ala	Pro	Ile	Tyr	Val														
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	Arg	Thr	Ser	Asn	Phe	Arg	Leu	Pro	Ser	Asp	Pro	Lys	Val	Pro	Val	Ile														
	545			550						555						560														
	Met	Ile	Gly	Pro	Gly	Thr	Gly	Leu	Ala	Pro	Phe	Arg	Gly	Phe	Leu	Gln														
			565		570									575																
	Glu	Arg	Leu	Ala	Leu	Lys	Glu	Ala	Gly	Thr	Asp	Leu	Gly	Leu	Ser	Ile														
			580		585								590																	
	Leu	Phe	Phe	Gly	Cys	Arg	Asn	Arg	Lys	Val	Asp	Phe	Ile	Tyr	Glu	Asn														
		595			600							605																		
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	625			630						635					640															
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 <211> 2079
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Arabidopsis thaliana sequence that has been codon optimized for yeast

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 ggtttcgttg tcttattgtg gaaaaagacc acggcagatc gttccggcga gctaaagcca 180
 ctaatgatcc ctaagtctct gatggcgaaa gatgaggatg atgacttaga tctaggttct 240
 ggaaaaacga gagtctctat cttcttcggc acacaaaccg gaacagccga aggattcgct 300
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SeqLst

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tacaagtgg	ttactgaaga	gaacgaaaga	gatatcaagt	tgcagcaact	tgcttacggc	540
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gaagagttat	gcaaaaaggg	tgcgaaagaga	ttgattgaag	tcggttttagg	agatgatgat	660
caatctatcg	aggatgactt	taatgcatgg	aaggaatctt	tgtggtctga	attagataag	720
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<210> 172

<211> 2139

<212> DNA

<213> Artificial Sequence

<220>

<223> Arabidopsis thaliana sequence that has been codon optimized for yeast

<400> 172

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<210> 173

<211> 2130

<212> DNA

<213> Stevia rebaudiana

<400> 173

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<210> 174

<211> 2124

<212> DNA

<213> Stevia rebaudiana

<400> 174

SeqLst

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<210> 175

<211> 2427

<212> DNA

<213> Arabidopsis thaliana

<400> 175

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<400> 176

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<213> Arabidopsis thaliana

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 acagtattga aaccgaaaca ttttctaaag gcaacaagg tactccatat ttgctggacg 300
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 aaacatcccg ttttgtaaaa gagaaatcta ttccacatat ttcattcatt cggctaccat 420
 actaaggata aactaatccc gttgtttttt ggcctcgtca cataattata aactactaac 480

	SeqLst	
ccattatcag a		491
<210> 187		
<211> 28		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Hairpin loop forming sequence		
<400> 187		
cacaaataca cacactaaat taataatg		28
<210> 188		
<211> 47		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Hairpin loop forming sequence		
<400> 188		
cacaaataca cacactaaat taatatgaat tcgttaacga attcatg		47
<210> 189		
<211> 47		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Hairpin loop forming sequence		
<400> 189		
cacaaataca cacactaaat taatatgaat tcgttaacga actcatg		47
<210> 190		
<211> 47		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Hairpin loop forming sequence		
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<210> 191		
<211> 47		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Hairpin loop forming sequence		
<400> 191		
cacaaataca cacactaaat taatatgaat tcgttaacga aattatg		47
<210> 192		
<211> 444		
<212> PRT		
<213> Saccharomyces cerevisiae		
<400> 192		

SeqLst

Met	Gly	Lys	Leu	Leu	Gln	Leu	Ala	Leu	His	Pro	Val	Glu	Met	Lys	Ala
1				5					10					15	
Ala	Leu	Lys	Leu	Lys	Phe	Cys	Arg	Thr	Pro	Leu	Phe	Ser	Ile	Tyr	Asp
			20					25					30		
Gln	Ser	Thr	Ser	Pro	Tyr	Leu	Leu	His	Cys	Phe	Glu	Leu	Leu	Asn	Leu
		35					40					45			
Thr	Ser	Arg	Ser	Phe	Ala	Ala	Val	Ile	Arg	Glu	Leu	His	Pro	Glu	Leu
	50					55					60				
Arg	Asn	Cys	Val	Thr	Leu	Phe	Tyr	Leu	Ile	Leu	Arg	Ala	Leu	Asp	Thr
65					70					75				80	
Ile	Glu	Asp	Asp	Met	Ser	Ile	Glu	His	Asp	Leu	Lys	Ile	Asp	Leu	Leu
				85					90					95	
Arg	His	Phe	His	Glu	Lys	Leu	Leu	Leu	Thr	Lys	Trp	Ser	Phe	Asp	Gly
			100					105					110		
Asn	Ala	Pro	Asp	Val	Lys	Asp	Arg	Ala	Val	Leu	Thr	Asp	Phe	Glu	Ser
		115					120					125			
Ile	Leu	Ile	Glu	Phe	His	Lys	Leu	Lys	Pro	Glu	Tyr	Gln	Glu	Val	Ile
	130					135					140				
Lys	Glu	Ile	Thr	Glu	Lys	Met	Gly	Asn	Gly	Met	Ala	Asp	Tyr	Ile	Leu
145					150					155					160
Asp	Glu	Asn	Tyr	Asn	Leu	Asn	Gly	Leu	Gln	Thr	Val	His	Asp	Tyr	Asp
				165					170					175	
Val	Tyr	Cys	His	Tyr	Val	Ala	Gly	Leu	Val	Gly	Asp	Gly	Leu	Thr	Arg
			180					185					190		
Leu	Ile	Val	Ile	Ala	Lys	Phe	Ala	Asn	Glu	Ser	Leu	Tyr	Ser	Asn	Glu
		195					200					205			
Gln	Leu	Tyr	Glu	Ser	Met	Gly	Leu	Phe	Leu	Gln	Lys	Thr	Asn	Ile	Ile
	210					215					220				
Arg	Asp	Tyr	Asn	Glu	Asp	Leu	Val	Asp	Gly	Arg	Ser	Phe	Trp	Pro	Lys
225					230					235					240
Glu	Ile	Trp	Ser	Gln	Tyr	Ala	Pro	Gln	Leu	Lys	Asp	Phe	Met	Lys	Pro
				245					250					255	
Glu	Asn	Glu	Gln	Leu	Gly	Leu	Asp	Cys	Ile	Asn	His	Leu	Val	Leu	Asn
			260					265					270		
Ala	Leu	Ser	His	Val	Ile	Asp	Val	Leu	Thr	Tyr	Leu	Ala	Gly	Ile	His
		275					280					285			
Glu	Gln	Ser	Thr	Phe	Gln	Phe	Cys	Ala	Ile	Pro	Gln	Val	Met	Ala	Ile
	290					295					300				
Ala	Thr	Leu	Ala	Leu	Val	Phe	Asn	Asn	Arg	Glu	Val	Leu	His	Gly	Asn
305					310					315					320
Val	Lys	Ile	Arg	Lys	Gly	Thr	Thr	Cys	Tyr	Leu	Ile	Leu	Lys	Ser	Arg
				325					330					335	
Thr	Leu	Arg	Gly	Cys	Val	Glu	Ile	Phe	Asp	Tyr	Tyr	Leu	Arg	Asp	Ile
			340					345					350		
Lys	Ser	Lys	Leu	Ala	Val	Gln	Asp	Pro	Asn	Phe	Leu	Lys	Leu	Asn	Ile
		355					360					365			
Gln	Ile	Ser	Lys	Ile	Glu	Gln	Phe	Met	Glu	Glu	Met	Tyr	Gln	Asp	Lys
	370					375					380				
Leu	Pro	Pro	Asn	Val	Lys	Pro	Asn	Glu	Thr	Pro	Ile	Phe	Leu	Lys	Val
385					390					395					400
Lys	Glu	Arg	Ser	Arg	Tyr	Asp	Asp	Glu	Leu	Val	Pro	Thr	Gln	Gln	Glu
				405					410					415	
Glu	Glu	Tyr	Lys	Phe	Asn	Met	Val	Leu	Ser	Ile	Ile	Leu	Ser	Val	Leu
			420					425					430		
Leu	Gly	Phe	Tyr	Tyr	Ile	Tyr	Thr	Leu	His	Arg	Ala				
		435					440								

<210> 193
 <211> 460
 <212> PRT
 <213> Schizosaccharomyces pombe

SeqLst

<400> 193

```

Met Ser Leu Ala Asn Arg Ile Glu Glu Ile Arg Cys Leu Cys Gln Tyr
 1      5      10      15
Lys Leu Trp Asn Asp Leu Pro Ser Tyr Gly Glu Asp Glu Asn Val Pro
 20      25      30
Gln Asn Ile Arg Arg Cys Tyr Gln Leu Leu Asp Met Thr Ser Arg Ser
 35      40      45
Phe Ala Val Val Ile Lys Glu Leu Pro Asn Gly Ile Arg Glu Ala Val
 50      55      60
Met Ile Phe Tyr Leu Val Leu Arg Gly Leu Asp Thr Val Glu Asp Asp
 65      70      75      80
Met Thr Leu Pro Leu Asp Lys Lys Leu Pro Ile Leu Arg Asp Phe Tyr
 85      90      95
Lys Thr Ile Glu Val Glu Gly Trp Thr Phe Asn Glu Ser Gly Pro Asn
100      105      110
Glu Lys Asp Arg Gln Leu Leu Val Glu Phe Asp Val Val Ile Lys Glu
115      120      125
Tyr Leu Asn Leu Ser Glu Gly Tyr Arg Asn Val Ile Ser Asn Ile Thr
130      135      140
Lys Glu Met Gly Asp Gly Met Ala Tyr Tyr Ala Ser Leu Ala Glu Lys
145      150      155      160
Asn Asp Gly Phe Ser Val Glu Thr Ile Glu Asp Phe Asn Lys Tyr Cys
165      170      175
His Tyr Val Ala Gly Leu Val Gly Ile Gly Leu Ser Arg Leu Phe Ala
180      185      190
Gln Ser Lys Leu Glu Asp Pro Asp Leu Ala His Ser Gln Ala Ile Ser
195      200      205
Asn Ser Leu Gly Leu Phe Leu Gln Lys Val Asn Ile Ile Arg Asp Tyr
210      215      220
Arg Glu Asp Phe Asp Asp Asn Arg His Phe Trp Pro Arg Glu Ile Trp
225      230      235      240
Ser Lys Tyr Thr Ser Ser Phe Gly Asp Leu Cys Leu Pro Asp Asn Ser
245      250      255
Glu Lys Ala Leu Glu Cys Leu Ser Asp Met Thr Ala Asn Ala Leu Thr
260      265      270
His Ala Thr Asp Ala Leu Val Tyr Leu Ser Gln Leu Lys Thr Gln Glu
275      280      285
Ile Phe Asn Phe Cys Ala Ile Pro Gln Val Met Ala Ile Ala Thr Leu
290      295      300
Ala Ala Val Phe Arg Asn Pro Asp Val Phe Gln Thr Asn Val Lys Ile
305      310      315      320
Arg Lys Gly Gln Ala Val Gln Ile Ile Leu His Ser Val Asn Leu Lys
325      330      335
Asn Val Cys Asp Leu Phe Leu Arg Tyr Thr Arg Asp Ile His Tyr Lys
340      345      350
Asn Thr Pro Lys Asp Pro Asn Phe Leu Lys Ile Ser Ile Glu Cys Gly
355      360      365
Lys Ile Glu Gln Val Ser Glu Ser Leu Phe Pro Arg Arg Phe Arg Glu
370      375      380
Met Tyr Glu Lys Ala Tyr Val Ser Lys Leu Ser Glu Gln Lys Lys Gly
385      390      395      400
Asn Gly Thr Gln Lys Ala Ile Leu Asn Asp Glu Gln Lys Glu Leu Tyr
405      410      415
Arg Lys Asp Leu Gln Lys Leu Gly Ile Ser Ile Leu Phe Val Phe Phe
420      425      430
Ile Ile Leu Val Cys Leu Ala Val Ile Phe Tyr Val Phe Asn Ile Arg
435      440      445
Ile His Trp Ser Asp Phe Lys Glu Leu Asn Leu Phe
450      455      460

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<210> 194

<211> 445

SeqLst

<212> PRT

<213> Yarrowia lipolytica

<400> 194

```

Met Gly Lys Leu Ile Glu Leu Leu Leu His Pro Ser Glu Leu Ser Ala
 1      5      10      15
Ala Ile His Tyr Lys Leu Trp Arg Gln Pro Leu His Pro Arg Asp Leu
 20      25      30
Ser Lys Glu Ser Thr Glu Leu Arg Arg Cys Tyr Glu Leu Leu Asp Val
 35      40      45
Cys Ser Arg Ser Phe Ala Ala Val Ile Arg Glu Leu His Pro Glu Val
 50      55      60
Arg Asp Ala Val Met Leu Phe Tyr Leu Ile Leu Arg Ala Leu Asp Thr
 65      70      75      80
Ile Glu Asp Asp Met Thr Leu Ser Arg Asp Ile Lys Ile Pro Ile Leu
 85      90      95
Arg Asp Phe Thr Lys Cys Met Lys Thr Pro Gly Trp Lys Phe Thr Asp
100      105      110
Ser Asp Pro Asn Glu Arg Asp Arg Val Val Leu Gln Glu Phe Pro Val
115      120      125
Val Met Thr Glu Phe Asn Lys Leu Lys Pro Lys Tyr Gln Glu Val Ile
130      135      140
Tyr Asp Ile Thr Asp Arg Met Gly Asn Gly Met Ala Asp Tyr Val Ile
145      150      155      160
Asp Asp Asp Phe Asn Asn Gly Val Asp Thr Ile Ala Ala Tyr Asp
165      170      175
Leu Tyr Cys His His Val Ala Gly Ile Val Gly Glu Gly Leu Thr Arg
180      185      190
Ile Thr Ile Leu Ala Gly Phe Gly Thr Asp Val Leu His Glu Asn Pro
195      200      205
Arg Leu Gln Glu Ser Met Gly Leu Phe Leu Gln Lys Val Asn Ile Ile
210      215      220
Arg Asp Tyr Arg Glu Asp Ile Asp Val Asn Arg Ala Phe Trp Pro Arg
225      230      235      240
Glu Ile Trp His Lys Tyr Ala Glu Glu Met Arg Asp Phe Lys Asp Pro
245      250      255
Lys Tyr Ser Lys Lys Ala Leu His Cys Thr Ser Asp Leu Val Ala Asn
260      265      270
Ala Leu Gly His Ala Thr Asp Cys Leu Asp Tyr Leu Asp Asn Val Thr
275      280      285
Asp Pro Ser Thr Phe Thr Phe Cys Ala Ile Pro Gln Val Met Ala Ile
290      295      300
Ala Thr Leu Asp Leu Val Tyr Arg Asn Pro Asp Val Phe Gln Lys Asn
305      310      315      320
Val Lys Leu Arg Lys Gly Thr Thr Val Ser Leu Ile Leu Glu Ala Ser
325      330      335
Asn Val Ser Gly Val Cys Asp Ile Phe Thr Arg Tyr Ala Arg Lys Val
340      345      350
Tyr Lys Lys Ser Asp Pro Asn Asp Pro Asn Tyr Phe Arg Val Ser Val
355      360      365
Leu Cys Gly Lys Ile Glu Gln His Ala Ala Leu Ile Lys Arg Gln Arg
370      375      380
Gly Pro Pro Ala Lys Thr Ile Ala Gln Leu Glu Gly Glu Arg Lys Glu
385      390      395      400
Met Ala Leu Ser Leu Ile Val Cys Leu Ala Val Ile Phe Ser Met Ser
405      410      415
Gly Leu Met Ala Tyr Ile Ala Tyr Val Ser Gly Phe Arg Trp Ser Pro
420      425      430
Arg Glu Ile Phe Asp Ser Lys Met Phe Pro Leu Arg Asp
435      440      445

```

<210> 195

SeqLst

<211> 443

<212> PRT

<213> Candida glabrata

<400> 195

```

Met Gly Lys Val Leu Asp Leu Ala Leu His Pro Leu Glu Leu Arg Ala
1      5      10      15
Ala Leu Lys Leu Lys Phe Ile Arg Gln Pro Leu Phe Ser Thr Asn Asp
20      25      30
Thr Arg Ala Thr Pro Gln Leu Glu Arg Cys Tyr Glu Leu Leu Asn Leu
35      40      45
Thr Ser Arg Ser Phe Ala Ala Val Ile Met Glu Leu His Pro Glu Leu
50      55      60
Arg Asn Val Ile Met Val Phe Tyr Leu Ile Leu Arg Ala Leu Asp Thr
65      70      75      80
Val Glu Asp Asp Met Thr Ile Asp Pro Gln Leu Lys Val Lys Val Leu
85      90      95
Arg Glu Phe Asp Ser Lys Leu Asp Thr Asp Trp Ser Phe Asp Gly
100      105      110
Asn Asp Leu Lys Glu Lys Asp Arg Val Val Leu Thr Glu Phe Pro Cys
115      120      125
Ile Leu Gly Glu Tyr His Lys Leu Lys Pro Glu Tyr Gln Lys Val Ile
130      135      140
Lys Arg Ile Thr Gly Leu Met Gly Asn Gly Met Ala Asp Tyr Ile Leu
145      150      155      160
Asp Glu Asn Phe Asn Leu Asn Gly Val Gln Thr Val Lys Asp Tyr Asp
165      170      175
Lys Tyr Cys His Tyr Val Ala Gly Leu Val Gly Asp Gly Leu Thr Glu
180      185      190
Leu Ile Val Leu Ala Gly Phe Gly Ser Asp Asp Leu Tyr His Gly Lys
195      200      205
Asn Ser Phe Gln Leu Tyr Glu Ser Met Gly Leu Phe Leu Gln Lys Thr
210      215      220
Asn Ile Ile Arg Asp Tyr Ala Glu Asp Leu Asp Asp Gly Arg Ser Phe
225      230      235      240
Trp Pro Lys Glu Ile Trp Ser Glu Tyr Ala Thr Lys Leu Thr Asp Phe
245      250      255
Arg Asp Pro Lys Asn Thr Gln Lys Gly Val Asp Cys Ile Asn His Leu
260      265      270
Val Leu Asn Ala Leu Thr His Val Ile Asp Val Leu Thr Tyr Leu Ser
275      280      285
Ser Ile His Glu Gln Ser Ser Phe Gln Phe Cys Ala Ile Pro Gln Val
290      295      300
Met Ala Ile Ala Thr Leu Ala Lys Val Phe Asn Asn Pro Glu Val Leu
305      310      315      320
Arg Lys Asn Val Lys Ile Arg Lys Gly Thr Thr Cys Asp Leu Ile Leu
325      330      335
Asn Ser Arg Thr Leu Lys Gly Cys Val Asp Ile Phe Gln Tyr Tyr Leu
340      345      350
Arg Asp Met Lys Gln Arg Leu Pro Val Glu Asp Pro Asn Tyr Leu Lys
355      360      365
Phe Asn Ile Gln Val Ala Lys Ile Glu Gln Phe Ile Glu Glu Met Phe
370      375      380
Gln Asp Asn Leu Pro Ala Gly Val Glu Pro Arg Glu Thr Met Ile Tyr
385      390      395      400
Leu Lys Val Gln Glu Arg Leu Lys Trp Asp Thr Gln Val Ile Pro Arg
405      410      415
Val Gln Glu Glu Asp Tyr Lys Phe Asn Met Ala Leu Ser Val Val Phe
420      425      430
Cys Val Leu Ser Phe Tyr Phe Thr Lys
435      440

```

SeqLst

<210> 196

<211> 441

<212> PRT

<213> Ashbya gossypii

<400> 196

```

Met Gly Lys Val Val Gln Leu Phe Thr His Pro Leu Glu Leu Lys Ala
 1      5      10      15
Ala Leu Lys Leu Lys Phe Leu Arg Glu Pro Leu Tyr Pro Ala Asp Asp
 20      25      30
Thr Gln Gly Ser Ala Glu Leu Lys Arg Cys Tyr Gln Leu Gln Arg
 35      40      45
Thr Ser Arg Ser Phe Ala Ala Val Ile Met Glu Leu His Pro Glu Leu
 50      55      60
Arg Asn Ala Val Met Leu Phe Tyr Leu Ile Leu Arg Ala Leu Asp Thr
 65      70      75      80
Val Glu Asp Asp Met Thr Ile Ser Pro Lys Val Lys Val Pro Leu Leu
 85      90      95
Arg Glu Phe Asp Gln Lys Leu Lys Leu Asp Thr Trp Ser Phe Asp Gly
100      105      110
Asn Ala Lys Thr Glu Lys Asp Arg Asp Val Leu Val Glu Phe Ser Thr
115      120      125
Ile Leu Ala Glu Phe His Lys Leu Lys Pro Glu Tyr Gln Gln Val Ile
130      135      140
Ala Asp Ile Thr His Lys Met Gly Asn Gly Met Ala Asp Tyr Ile Leu
145      150      155      160
Asp Glu Lys Phe Asn Leu Ser Gly Leu Glu Thr Ile Gln Asp Tyr Asp
165      170      175
Arg Tyr Cys His Tyr Val Ala Gly Leu Val Gly Asp Gly Leu Thr His
180      185      190
Leu Ile Met Leu Ala Lys Phe Ser Ser Pro Gly Leu Tyr Tyr Asp Ser
195      200      205
Pro Asp Leu Tyr Glu Ser Met Gly Leu Phe Leu Gln Lys Thr Asn Ile
210      215      220
Ile Arg Asp Tyr Ala Glu Asp Leu Ala Asp Gly Arg Ser Phe Trp Pro
225      230      235      240
Lys Glu Ile Trp Ser His Tyr Ala Asp Asp Leu Ala Ser Phe Ser Lys
245      250      255
Pro Glu Asn Ala Thr Ala Gly Val Tyr Cys Ile Asn His Leu Val Leu
260      265      270
Asn Ala Leu Gly His Val Gln His Val Leu Thr Tyr Leu Ala Ser Leu
275      280      285
Arg Glu Gln Ser Ser Phe Gln Phe Cys Ala Ile Pro Gln Val Met Ala
290      295      300
Ile Ala Thr Leu Ala Leu Val Phe Gly Asn Glu Arg Val Leu Gln Thr
305      310      315      320
Ser Val Lys Ile Arg Lys Gly Thr Thr Cys Tyr Leu Ile Leu Lys Ser
325      330      335
Arg Thr Phe Gln Gly Cys Val Glu Ile Phe Glu His Tyr Leu Arg Asp
340      345      350
Ile Arg Lys Arg Leu Thr Val Ala Asp Pro Asn Tyr Leu Lys Leu Asn
355      360      365
Ile Glu Ile Ala Lys Leu Asp Lys Phe Ile Glu Glu Met Tyr Gln Asp
370      375      380
Lys Leu Pro Val Gly Ala Lys Pro Gln Glu Thr Glu Ile Tyr Lys Lys
385      390      395      400
Val Arg Glu Arg Ser Ala Tyr Asp Leu Glu Val Leu Pro Arg Glu Gln
405      410      415
Glu Glu Glu Phe Lys Phe Asn Val Leu Ser Ile Leu Phe Thr Val
420      425      430
Phe Gly Ala Leu Tyr Trp Tyr Ala Lys
435      440

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SeqLst

<210> 197
 <211> 443
 <212> PRT
 <213> Cyberlindnera jadinii

<400> 197
 Met Gly Lys Leu Leu Gln Leu Ala Leu His Pro Asp Glu Leu Ala Ser
 1 5 10 15
 Ile Val Gln Phe Lys Leu Phe Arg Lys Asn Glu Asn Ala Arg Asn Pro
 20 25 30
 Ala Thr Glu Ser Ala Glu Leu Ile Arg Cys Tyr Glu Leu Asn Leu
 35 40 45
 Thr Ser Arg Ser Phe Ala Ala Val Ile Glu Glu Leu His Pro Glu Leu
 50 55 60
 Arg Asn Val Ile Met Val Phe Tyr Leu Val Leu Arg Ala Leu Asp Thr
 65 70 75 80
 Val Glu Val Asp Met Ser Ile Glu Asn Ser Val Lys Leu Pro Val Leu
 85 90 95
 Arg Gln Phe His Glu Lys Leu Asp Thr Lys Asp Trp Thr Phe Asp Gly
 100 105 110
 Asn Ser Pro Asn Glu Lys Asp Arg Cys Val Leu Val Glu Phe Asp Arg
 115 120 125
 Ile Leu Gly Gln Tyr His Glu Leu Lys Pro Gln Tyr Gln Lys Val Ile
 130 135 140
 Lys Glu Ile Thr Glu Lys Met Gly Asn Gly Met Ala Asp Tyr Ile Glu
 145 150 155 160
 Asn Glu Asn Phe Asn Ser Asn Gly Leu Leu Thr Ile Glu Asp Tyr Asp
 165 170 175
 Leu Tyr Cys Tyr Tyr Val Ala Gly Leu Val Gly Asp Gly Leu Thr Gln
 180 185 190
 Leu Ile Val Leu Ala Lys Phe Gly Asn Ser Glu Leu Ser Val Asn Lys
 195 200 205
 Gln Leu Phe Lys Ser Met Gly Leu Phe Leu Gln Lys Thr Asn Ile Ile
 210 215 220
 Arg Asp Tyr Glu Glu Asp Gln Val Asp Gly Arg Ala Phe Trp Pro Lys
 225 230 235 240
 Glu Ile Trp Gly Lys Tyr Ala Asn Glu Leu Ser Asp Phe Met Lys Pro
 245 250 255
 Glu Asn Gln Ser Gln Gly Leu Trp Cys Ile Ser Glu Leu Val Cys Asn
 260 265 270
 Ala Leu Asp His Val Ile Asp Val Leu Gln Tyr Leu Ala Leu Val Glu
 275 280 285
 Glu Gln Thr Ser Phe Asn Phe Cys Ala Ile Pro Gln Val Met Ala Ile
 290 295 300
 Ala Thr Leu Glu Leu Val Phe Gln Asn Pro Gln Val Leu Thr Gln His
 305 310 315 320
 Val Lys Ile Arg Lys Gly Thr Thr Val Ser Leu Ile Leu Glu Ser Arg
 325 330 335
 Thr Leu Glu Gly Cys Ala Arg Ile Phe Arg Arg Tyr Leu Arg Lys Ile
 340 345 350
 His His Lys Ser His Pro Ser Asp Pro Asn Tyr Leu Arg Leu Gly Ile
 355 360 365
 Thr Ile Gly Lys Ile Glu Gln Phe Leu Asp Gly Met Tyr Pro His Tyr
 370 375 380
 Val Pro Lys Gly Ile Thr Pro Gln Thr Thr Ser Ile Arg Thr Gln Val
 385 390 395 400
 Val Lys Arg Leu Gln Leu Asp Glu Pro Met Lys Arg Asp Ile Asp Glu
 405 410 415
 Glu Ile Leu Lys Thr Arg Ile Leu Leu Ser Leu Gly Val Ala Val
 420 425 430
 Phe Gly Val Val Tyr Gly Val Val Arg Ile Ile
 435 440

SeqLst

<210> 198
 <211> 448
 <212> PRT
 <213> Candida albicans

<400> 198
 Met Gly Lys Phe Leu Gln Leu Leu Ser His Pro Thr Glu Leu Lys Ala
 1 5 10 15
 Val Ile Gln Leu Phe Gly Phe Arg Gln Pro Leu His Pro Gly Lys Arg
 20 25 30
 Asp Val Asn Asp Lys Glu Leu Gly Arg Cys Tyr Glu Leu Asn Leu
 35 40 45
 Thr Ser Arg Ser Phe Ala Ala Val Ile Glu Glu Leu His Pro Glu Leu
 50 55 60
 Arg Asp Ala Val Met Ile Phe Tyr Leu Val Leu Arg Ala Leu Asp Thr
 65 70 75 80
 Ile Glu Asp Asp Met Thr Ile Lys Ser Ser Ile Lys Ile Pro Leu Leu
 85 90 95
 Arg Glu Phe Asp Thr Lys Leu Asn Thr Lys Asn Trp Thr Phe Asp Gly
 100 105 110
 Tyr Gly Pro Asn Glu Lys Asp Arg Thr Val Leu Val Glu Phe Asp Lys
 115 120 125
 Ile Leu Asn Val Tyr His Arg Leu Lys Pro Gln Tyr Gln Asp Ile Ile
 130 135 140
 Lys Ser Ile Thr Phe Lys Met Gly Asn Gly Met Ala Asp Tyr Ile Leu
 145 150 155 160
 Asp Glu Glu Phe Asn Val Tyr Gly Val Ala Thr Val Glu Asp Tyr Asn
 165 170 175
 Leu Tyr Cys His Tyr Val Ala Gly Leu Val Gly Glu Gly Leu Thr Asn
 180 185 190
 Leu Phe Val Leu Ala Asn Phe Gly Asp Lys Thr Leu Thr Glu Asn Asn
 195 200 205
 Phe Ala Lys Ala Asp Ser Met Gly Leu Phe Leu Gln Lys Thr Asn Ile
 210 215 220
 Ile Arg Asp Tyr His Glu Asp Leu Gln Asp Gly Arg Ser Phe Trp Pro
 225 230 235 240
 Arg Glu Ile Trp Ser Lys Tyr Thr Glu Asn Leu Gln Asp Phe His Lys
 245 250 255
 Val Lys Thr Pro Ala Lys Glu Phe Ala Gly Val Ser Cys Ile Asn Glu
 260 265 270
 Leu Val Leu Asn Ala Leu Gly His Val Thr Asp Cys Leu Asp Tyr Leu
 275 280 285
 Ser Leu Val Lys Asp Pro Ser Ser Phe Ser Phe Cys Ala Ile Pro Gln
 290 295 300
 Val Met Ala Val Ala Thr Leu Ala Glu Val Tyr Asn Asn Pro Lys Val
 305 310 315 320
 Leu His Gly Val Val Lys Ile Arg Lys Gly Thr Thr Cys Arg Leu Ile
 325 330 335
 Leu Glu Ser Arg Thr Leu Pro Gly Val Val Lys Ile Phe Lys Glu Tyr
 340 345 350
 Ile Gln Val Ile Asn His Lys Ser Val Arg Asp Pro Asn Tyr Leu
 355 360 365
 Lys Ile Gly Ile Lys Cys Gly Glu Ile Glu Gln Tyr Cys Glu Met Ile
 370 375 380
 Tyr Pro Asn Lys Gln Ala Leu Pro Pro Ser Met Lys Ser Leu Pro Glu
 385 390 395 400
 Asn Lys Phe Thr Lys Ile Val Ala Ser Arg Glu Ser Ile Asp Leu Ser
 405 410 415
 Val Gln Arg Arg Ile Glu Pro Gly Asn Phe Asn Cys Asn Val Val Leu
 420 425 430
 Phe Gly Ile Gly Ala Leu Ile Leu Ser Leu Ile Tyr Phe Val Leu Tyr

435

440

SeqLst

445

<210> 199

<211> 731

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 199

Met	Thr	Glu	Phe	Tyr	Ser	Asp	Thr	Ile	Gly	Leu	Pro	Lys	Thr	Asp	Pro
1				5					10					15	
Arg	Leu	Trp	Arg	Leu	Arg	Thr	Asp	Glu	Leu	Gly	Arg	Glu	Ser	Trp	Glu
			20					25					30		
Tyr	Leu	Thr	Pro	Gln	Gln	Ala	Ala	Asn	Asp	Pro	Pro	Ser	Thr	Phe	Thr
		35				40						45			
Gln	Trp	Leu	Leu	Gln	Asp	Pro	Lys	Phe	Pro	Gln	Pro	His	Pro	Glu	Arg
	50					55					60				
Asn	Lys	His	Ser	Pro	Asp	Phe	Ser	Ala	Phe	Asp	Ala	Cys	His	Asn	Gly
65					70					75					80
Ala	Ser	Phe	Phe	Lys	Leu	Leu	Gln	Glu	Pro	Asp	Ser	Gly	Ile	Phe	Pro
				85					90					95	
Cys	Gln	Tyr	Lys	Gly	Pro	Met	Phe	Met	Thr	Ile	Gly	Tyr	Val	Ala	Val
			100					105					110		
Asn	Tyr	Ile	Ala	Gly	Ile	Glu	Ile	Pro	Glu	His	Glu	Arg	Ile	Glu	Leu
		115					120						125		
Ile	Arg	Tyr	Ile	Val	Asn	Thr	Ala	His	Pro	Val	Asp	Gly	Gly	Trp	Gly
	130					135					140				
Leu	His	Ser	Val	Asp	Lys	Ser	Thr	Val	Phe	Gly	Thr	Val	Leu	Asn	Tyr
145					150					155					160
Val	Ile	Leu	Arg	Leu	Gly	Leu	Pro	Lys	Asp	His	Pro	Val	Cys	Ala	
				165				170					175		
Lys	Ala	Arg	Ser	Thr	Leu	Leu	Arg	Leu	Gly	Gly	Ala	Ile	Gly	Ser	Pro
			180					185					190		
His	Trp	Gly	Lys	Ile	Trp	Leu	Ser	Ala	Leu	Asn	Leu	Tyr	Lys	Trp	Glu
		195					200					205			
Gly	Val	Asn	Pro	Ala	Pro	Pro	Glu	Thr	Trp	Leu	Leu	Pro	Tyr	Ser	Leu
	210					215					220				
Pro	Met	His	Pro	Gly	Arg	Trp	Trp	Val	His	Thr	Arg	Gly	Val	Tyr	Ile
225					230					235					240
Pro	Val	Ser	Tyr	Leu	Ser	Leu	Val	Lys	Phe	Ser	Cys	Pro	Met	Thr	Pro
				245					250					255	
Leu	Leu	Glu	Glu	Leu	Arg	Asn	Glu	Ile	Tyr	Thr	Lys	Pro	Phe	Asp	Lys
			260					265					270		
Ile	Asn	Phe	Ser	Lys	Asn	Arg	Asn	Thr	Val	Cys	Gly	Val	Asp	Leu	Tyr
		275					280					285			
Tyr	Pro	His	Ser	Thr	Thr	Leu	Asn	Ile	Ala	Asn	Ser	Leu	Val	Val	Phe
	290					295					300				
Tyr	Glu	Lys	Tyr	Leu	Arg	Asn	Arg	Phe	Ile	Tyr	Ser	Leu	Ser	Lys	Lys
305					310					315					320
Lys	Val	Tyr	Asp	Leu	Ile	Lys	Thr	Glu	Leu	Gln	Asn	Thr	Asp	Ser	Leu
				325					330					335	
Cys	Ile	Ala	Pro	Val	Asn	Gln	Ala	Phe	Cys	Ala	Leu	Val	Thr	Leu	Ile
			340					345					350		
Glu	Glu	Gly	Val	Asp	Ser	Glu	Ala	Phe	Gln	Arg	Leu	Gln	Tyr	Arg	Phe
		355					360					365			
Lys	Asp	Ala	Leu	Phe	His	Gly	Pro	Gln	Gly	Met	Thr	Ile	Met	Gly	Thr
	370					375					380				
Asn	Gly	Val	Gln	Thr	Trp	Asp	Cys	Ala	Phe	Ala	Ile	Gln	Tyr	Phe	Phe
385					390					395					400
Val	Ala	Gly	Leu	Ala	Glu	Arg	Pro	Glu	Phe	Tyr	Asn	Thr	Ile	Val	Ser
				405					410					415	
Ala	Tyr	Lys	Phe	Leu	Cys	His	Ala	Gln	Phe	Asp	Thr	Glu	Cys	Val	Pro
			420					425					430		

SeqLst

Gly	Ser	Tyr	Arg	Asp	Lys	Arg	Lys	Gly	Ala	Trp	Gly	Phe	Ser	Thr	Lys
		435					440					445			
Thr	Gln	Gly	Tyr	Thr	Val	Ala	Asp	Cys	Thr	Ala	Glu	Ala	Ile	Lys	Ala
	450					455					460				
Ile	Ile	Met	Val	Lys	Asn	Ser	Pro	Val	Phe	Ser	Glu	Val	His	His	Met
465				470					475						480
Ile	Ser	Ser	Glu	Arg	Leu	Phe	Glu	Gly	Ile	Asp	Val	Leu	Leu	Asn	Leu
				485					490					495	
Gln	Asn	Ile	Gly	Ser	Phe	Glu	Tyr	Gly	Ser	Phe	Ala	Thr	Tyr	Glu	Lys
			500					505					510		
Ile	Lys	Ala	Pro	Leu	Ala	Met	Glu	Thr	Leu	Asn	Pro	Ala	Glu	Val	Phe
		515					520					525			
Gly	Asn	Ile	Met	Val	Glu	Tyr	Pro	Tyr	Val	Glu	Cys	Thr	Asp	Ser	Ser
	530					535					540				
Val	Leu	Gly	Leu	Thr	Tyr	Phe	His	Lys	Tyr	Phe	Asp	Tyr	Arg	Lys	Glu
545					550					555					560
Glu	Ile	Arg	Thr	Arg	Ile	Arg	Ile	Ala	Ile	Glu	Phe	Ile	Lys	Lys	Ser
				565					570					575	
Gln	Leu	Pro	Asp	Gly	Ser	Trp	Tyr	Gly	Ser	Trp	Gly	Ile	Cys	Phe	Thr
			580					585					590		
Tyr	Ala	Gly	Met	Phe	Ala	Leu	Glu	Ala	Leu	His	Thr	Val	Gly	Glu	Thr
		595					600					605			
Tyr	Glu	Asn	Ser	Ser	Thr	Val	Arg	Lys	Gly	Cys	Asp	Phe	Leu	Val	Ser
	610					615					620				
Lys	Gln	Met	Lys	Asp	Gly	Gly	Trp	Gly	Glu	Ser	Met	Lys	Ser	Ser	Glu
625					630					635					640
Leu	His	Ser	Tyr	Val	Asp	Ser	Glu	Lys	Ser	Leu	Val	Val	Gln	Thr	Ala
				645					650					655	
Trp	Ala	Leu	Ile	Ala	Leu	Leu	Phe	Ala	Glu	Tyr	Pro	Asn	Lys	Glu	Val
			660					665					670		
Ile	Asp	Arg	Gly	Ile	Asp	Leu	Leu	Lys	Asn	Arg	Gln	Glu	Glu	Ser	Gly
		675					680					685			
Glu	Trp	Lys	Phe	Glu	Ser	Val	Glu	Gly	Val	Phe	Asn	His	Ser	Cys	Ala
	690					695				700					
Ile	Glu	Tyr	Pro	Ser	Tyr	Arg	Phe	Leu	Phe	Pro	Ile	Lys	Ala	Leu	Gly
705					710					715					720
Met	Tyr	Ser	Arg	Ala	Tyr	Glu	Thr	His	Thr	Leu					
				725					730						

<210> 200
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 200

Met	Glu	Phe	Val	Lys	Cys	Leu	Gly	His	Pro	Glu	Glu	Phe	Tyr	Asn	Leu
1				5					10					15	
Val	Arg	Phe	Arg	Ile	Gly	Gly	Lys	Arg	Lys	Val	Met	Pro	Lys	Met	Asp
			20					25					30		
Gln	Asp	Ser	Leu	Ser	Ser	Ser	Leu	Lys	Thr	Cys	Tyr	Lys	Tyr	Leu	Asn
		35					40					45			
Gln	Thr	Ser	Arg	Ser	Phe	Ala	Ala	Val	Ile	Gln	Ala	Leu	Asp	Gly	Glu
	50					55					60				
Met	Arg	Asn	Ala	Val	Cys	Ile	Phe	Tyr	Leu	Val	Leu	Arg	Ala	Leu	Asp
65					70					75					80
Thr	Leu	Glu	Asp	Asp	Met	Thr	Ile	Ser	Val	Glu	Lys	Lys	Val	Pro	Leu
				85					90					95	
Leu	His	Asn	Phe	His	Ser	Phe	Leu	Tyr	Gln	Pro	Asp	Trp	Arg	Phe	Met
			100					105					110		
Glu	Ser	Lys	Glu	Lys	Asp	Arg	Gln	Val	Leu	Glu	Asp	Phe	Pro	Thr	Ile
		115					120					125			
Ser	Leu	Glu	Phe	Arg	Asn	Leu	Ala	Glu	Lys	Tyr	Gln	Thr	Val	Ile	Ala

	SeqLst															
130	135	140														
Asp 145	Ile 130	Cys 145	Arg 145	Arg 145	Met 150	Gly 135	Ile 145	Gly 145	Met 155	Ala 140	Glu 140	Phe 140	Leu 140	Asp 140	Lys 160	
His 145	Val 145	Thr 145	Ser 165	Glu 165	Gln 150	Glu 135	Trp 145	Asp 170	Lys 155	Tyr 140	Cys 140	His 140	Tyr 140	Val 175	Ala 160	
Gly 145	Leu 145	Val 145	Gly 180	Ile 165	Gly 150	Leu 135	Ser 145	Arg 185	Leu 170	Phe 140	Ser 140	Ala 140	Ser 190	Glu 175	Phe 140	
Glu 145	Asp 145	Pro 195	Leu 180	Val 145	Gly 150	Glu 135	Asp 200	Thr 145	Glu 140	Arg 140	Ala 140	Asn 205	Ser 190	Met 140	Gly 140	
Leu 145	Phe 210	Leu 195	Gln 145	Lys 145	Thr 145	Asn 215	Ile 145	Ile 145	Arg 140	Asp 220	Tyr 140	Leu 140	Glu 140	Asp 140	Gln 140	
Gln 225	Gly 210	Gly 145	Arg 145	Glu 145	Phe 230	Trp 215	Pro 145	Gln 145	Glu 140	Val 235	Trp 220	Ser 140	Arg 140	Tyr 140	Val 240	
Lys 225	Lys 145	Leu 145	Gly 145	Asp 245	Phe 230	Ala 145	Lys 145	Pro 145	Glu 250	Asn 140	Ile 140	Asp 140	Leu 140	Ala 255	Val 240	
Gln 225	Cys 145	Leu 145	Asn 260	Glu 145	Leu 145	Ile 145	Thr 145	Asn 265	Ala 140	Leu 140	His 140	His 140	Ile 270	Pro 140	Asp 140	
Val 225	Ile 145	Thr 275	Tyr 145	Leu 145	Ser 145	Arg 145	Leu 280	Arg 145	Asn 140	Gln 140	Ser 140	Val 285	Phe 140	Asn 140	Phe 140	
Cys 225	Ala 290	Ile 145	Pro 145	Gln 145	Val 145	Met 295	Ala 145	Ile 145	Ala 140	Thr 140	Leu 300	Ala 140	Ala 140	Cys 140	Tyr 140	
Asn 305	Asn 145	Gln 145	Gln 145	Val 145	Phe 310	Lys 145	Gly 145	Ala 140	Val 140	Lys 315	Ile 140	Arg 140	Lys 140	Gly 140	Gln 320	
Ala 305	Val 145	Thr 145	Leu 145	Met 325	Met 145	Asp 145	Ala 140	Thr 140	Asn 330	Met 140	Pro 140	Ala 140	Val 140	Lys 335	Ala 140	
Ile 305	Ile 145	Tyr 145	Gln 145	Tyr 145	Met 145	Glu 145	Glu 145	Ile 145	Tyr 140	His 140	Arg 140	Ile 140	Pro 140	Asp 140	Ser 140	
Asp 305	Pro 145	Ser 355	Ser 145	Ser 145	Lys 145	Thr 145	Arg 145	Gln 145	Ile 140	Ile 140	Ser 140	Thr 140	Ile 140	Arg 140	Thr 140	
Gln 305	Asn 370	Leu 145	Pro 145	Asn 145	Cys 145	Gln 145	Leu 145	Ile 145	Ser 140	Arg 140	Ser 140	His 140	Tyr 140	Ser 140	Pro 140	
Ile 385	Tyr 145	Leu 145	Ser 145	Phe 145	Val 145	Met 145	Leu 145	Leu 145	Ala 140	Ala 140	Leu 140	Ser 140	Trp 140	Gln 140	Tyr 140	
Leu 385	Thr 145	Thr 145	Leu 145	Ser 405	Gln 145	Val 145	Thr 145	Glu 145	Asp 410	Tyr 140	Val 140	Gln 140	Thr 140	Gly 140	Glu 140	
His 385																

<210> 201
 <211> 416
 <212> PRT
 <213> Mus musculus

<400> 201																
Met 1	Glu 1	Phe 1	Val 1	Lys 5	Cys 1	Leu 1	Gly 1	His 1	Pro 10	Glu 1	Glu 1	Phe 1	Tyr 1	Asn 15	Leu 1	
Leu 1	Arg 1	Phe 1	Arg 20	Met 5	Gly 1	Gly 1	Arg 1	Arg 25	Asn 10	Phe 1	Ile 1	Pro 1	Lys 30	Met 15	Asp 1	
Gln 1	Asp 1	Ser 1	Leu 1	Ser 1	Ser 1	Ser 1	Leu 1	Lys 1	Thr 1	Cys 1	Tyr 1	Lys 1	Tyr 1	Leu 1	Asn 1	
Gln 1	Thr 1	Ser 1	Arg 1	Ser 1	Phe 1	Ala 1	Ala 1	Val 1	Ile 1	Gln 1	Ala 1	Leu 1	Asp 1	Gly 1	Asp 1	
Ile 1	Arg 1	His 1	Ala 1	Ile 1	Cys 1	Val 1	Phe 1	Tyr 1	Leu 1	Val 1	Leu 1	Arg 1	Ala 1	Leu 1	Asp 1	
Thr 1	Val 1	Glu 1	Asp 1	Asp 1	Met 1	Ser 1	Ile 1	Ser 1	Val 1	Glu 1	Lys 1	Lys 1	Ile 1	Pro 1	Leu 1	
Leu 1	Cys 1	Asn 1	Phe 1	His 1	Thr 1	Phe 1	Leu 1	Tyr 1	Asp 1	Pro 1	Glu 1	Trp 1	Arg 1	Phe 1	Thr 1	
Glu 1	Ser 1	Lys 1	Glu 1	Lys 1	Asp 1	Arg 1	Gln 1	Val 1	Leu 1	Glu 1	Asp 1	Phe 1	Pro 1	Thr 1	Ile 1	
Ser 1	Leu 1	Glu 1	Phe 1	Arg 1	Asn 1	Leu 1	Ala 1	Glu 1	Lys 1	Tyr 1	Gln 1	Thr 1	Val 1	Ile 1	Asp 1	
	130					135						140				

															SeqLst
Asp	Ile	Cys	His	Arg	Met	Gly	Cys	Gly	Met	Ala	Glu	Phe	Val	Asp	Lys
145					150					155					160
Asp	Val	Thr	Ser	Lys	Gln	Asp	Trp	Asp	Lys	Tyr	Cys	His	Tyr	Val	Ala
				165					170					175	
Gly	Leu	Val	Gly	Ile	Gly	Leu	Ser	Arg	Leu	Phe	Ser	Ala	Ser	Glu	Phe
			180					185					190		
Glu	Asp	Pro	Ile	Val	Gly	Glu	Asp	Ile	Glu	Cys	Ala	Asn	Ser	Met	Gly
		195					200					205			
Leu	Phe	Leu	Gln	Lys	Thr	Asn	Ile	Ile	Arg	Asp	Tyr	Leu	Glu	Asp	Gln
	210					215					220				
Gln	Glu	Gly	Arg	Lys	Phe	Trp	Pro	Gln	Glu	Val	Trp	Gly	Arg	Tyr	Ile
225					230					235					240
Lys	Lys	Leu	Glu	Asp	Phe	Ala	Lys	Pro	Glu	Asn	Val	Asp	Val	Ala	Val
				245					250					255	
Gln	Cys	Leu	Asn	Glu	Leu	Ile	Thr	Asn	Thr	Leu	Gln	His	Ile	Pro	Asp
			260					265					270		
Val	Leu	Thr	Tyr	Leu	Ser	Arg	Leu	Arg	Asn	Gln	Ser	Val	Phe	Asn	Phe
		275					280					285			
Cys	Ala	Ile	Pro	Gln	Val	Met	Ala	Ile	Ala	Thr	Leu	Ala	Ala	Cys	Tyr
	290					295					300				
Asn	Asn	Gln	Gln	Val	Phe	Lys	Gly	Val	Val	Lys	Ile	Arg	Lys	Gly	Gln
305					310					315					320
Ala	Val	Thr	Leu	Met	Met	Asp	Ala	Thr	Asn	Met	Pro	Ala	Val	Lys	Ala
				325					330					335	
Ile	Ile	Tyr	Gln	Tyr	Ile	Glu	Glu	Ile	Tyr	His	Arg	Ile	Pro	Asn	Ser
			340					345					350		
Asp	Pro	Ser	Ser	Ser	Lys	Thr	Lys	Gln	Val	Ile	Ser	Lys	Ile	Arg	Thr
		355					360					365			
Gln	Asn	Leu	Pro	Asn	Cys	Gln	Leu	Ile	Ser	Arg	Ser	His	Tyr	Ser	Pro
	370					375					380				
Ile	Tyr	Leu	Ser	Phe	Ile	Met	Leu	Leu	Ala	Ala	Leu	Ser	Trp	Gln	Tyr
385					390					395					400
Leu	Ser	Thr	Leu	Ser	Gln	Val	Thr	Glu	Asp	Tyr	Val	Gln	Arg	Glu	His
				405					410					415	

<210> 202
 <211> 416
 <212> PRT
 <213> Rattus norvegicus

<400> 202															
Met	Glu	Phe	Val	Lys	Cys	Leu	Gly	His	Pro	Glu	Glu	Phe	Tyr	Asn	Leu
1				5					10					15	
Leu	Arg	Phe	Arg	Met	Gly	Gly	Arg	Arg	Asn	Phe	Ile	Pro	Lys	Met	Asp
			20					25					30		
Arg	Asn	Ser	Leu	Ser	Asn	Ser	Leu	Lys	Thr	Cys	Tyr	Lys	Tyr	Leu	Asp
		35					40					45			
Gln	Thr	Ser	Arg	Ser	Phe	Ala	Ala	Val	Ile	Gln	Ala	Leu	Asp	Gly	Asp
	50					55					60				
Ile	Arg	His	Ala	Val	Cys	Val	Phe	Tyr	Leu	Ile	Leu	Arg	Ala	Met	Asp
65					70					75				80	
Thr	Val	Glu	Asp	Asp	Met	Ala	Ile	Ser	Val	Glu	Lys	Lys	Ile	Pro	Leu
				85					90					95	
Leu	Arg	Asn	Phe	His	Thr	Phe	Leu	Tyr	Glu	Pro	Glu	Trp	Arg	Phe	Thr
		100						105					110		
Glu	Ser	Lys	Glu	Lys	His	Arg	Val	Val	Leu	Glu	Asp	Phe	Pro	Thr	Ile
		115					120					125			
Ser	Leu	Glu	Phe	Arg	Asn	Leu	Ala	Glu	Lys	Tyr	Gln	Thr	Val	Ile	Ala
	130					135					140				
Asp	Ile	Cys	His	Arg	Met	Gly	Cys	Gly	Met	Ala	Glu	Phe	Leu	Asn	Lys
145					150					155					160
Asp	Val	Thr	Ser	Lys	Gln	Asp	Trp	Asp	Lys	Tyr	Cys	His	Tyr	Val	Ala

SeqLst

Gly	Leu	Val	Gly	165	Ile	Gly	Leu	Ser	Arg	170	Leu	Phe	Ser	Ala	Ser	175	Glu	Phe
Glu	Asp	Pro	180	Ile	Val	Gly	Glu	Asp	185	Thr	Glu	Cys	Ala	Asn	190	Ser	Met	Gly
Leu	Phe	195	Leu	Gln	Lys	Thr	Asn	200	Ile	Ile	Arg	Asp	Tyr	220	Leu	Glu	Asp	Gln
Gln	Glu	Gly	Arg	Gln	Phe	230	Trp	Pro	Gln	Glu	Val	Trp	Gly	Lys	Tyr	240	Val	
225	Lys	Lys	Leu	Glu	Asp	245	Phe	Val	Lys	Pro	Glu	Asn	Val	Asp	Val	255	Ala	Val
Lys	Cys	Leu	Asn	260	Glu	Leu	Ile	Thr	Asn	265	Ala	Leu	Gln	His	Ile	270	Pro	Asp
Val	Ile	Thr	Tyr	Leu	Ser	Arg	Leu	Arg	Asn	Gln	Ser	Val	Phe	Asn	Phe			
Cys	Ala	Ile	Pro	Gln	Val	Met	295	Ala	Ile	Ala	Thr	Leu	Ala	Ala	Cys	Tyr		
Asn	305	Asn	His	Gln	Val	Phe	310	Lys	Gly	Val	Val	Lys	Ile	Arg	Lys	Gly	Gln	
Ala	Val	Thr	Leu	Met	Met	Asp	Ala	Thr	Asn	Met	Pro	Ala	Val	Lys	Ala			
Ile	Ile	Tyr	Gln	Tyr	Ile	Glu	Glu	Ile	Tyr	His	Arg	Val	Pro	Asn	Ser			
Asp	Pro	Ser	Ala	Ser	Lys	Ala	Lys	360	Gln	Leu	Ile	Ser	Asn	Ile	Arg	Thr		
Gln	Ser	Leu	Pro	Asn	Cys	Gln	Leu	Ile	Ser	Arg	Ser	His	Tyr	Ser	Pro			
Ile	385	Tyr	Leu	Ser	Phe	Ile	Met	Leu	Leu	Ala	Ala	Leu	Ser	Trp	Gln	Tyr		
Leu	Ser	Thr	Leu	Ser	405	Gln	Val	Thr	Glu	Asp	410	Tyr	Val	Gln	Arg	Glu	His	

<210> 203
 <211> 396
 <212> PRT
 <213> Aspergillus nidulans

<400> 203

Met	Thr	Ser	Asp	Ser	His	Phe	His	Pro	Pro	His	Ala	Ile	Pro	Pro	Arg
1				5					10					15	
Ile	Ser	Ser	Asn	Arg	Met	Ser	Gly	Ala	25	Ser	Thr	Arg	Asp	Lys	Ala
Leu	Met	Gly	Asn	Phe	Glu	Lys	Asp	Trp	Leu	Ser	Lys	Gly	Asp	Lys	Leu
35							40					45			
Gln	Thr	Asn	Thr	Asp	Leu	Ser	Lys	Arg	His	Thr	Arg	Asn	Gln	Ser	Ser
50						55					60				
Leu	Asp	Gly	Thr	Lys	Tyr	Lys	Asp	Gly	Lys	Trp	75	Ser	Gln	Glu	Asn
65					70									80	
Glu	Val	Ile	Met	Gly	Pro	Tyr	Asp	Tyr	Met	Leu	Gln	His	Pro	Gly	Lys
85									90					95	
Asp	Leu	Arg	Arg	Gln	Met	Ile	Asn	Ala	Phe	Asn	Val	Trp	Leu	Lys	Val
100								105					110		
Pro	Ser	Glu	Ser	Leu	Ala	Ile	Ile	Thr	Lys	Val	Val	Ala	Met	Leu	His
115							120					125			
Thr	Ala	Ser	Leu	Leu	Ile	Asp	Asp	Val	Glu	Asp	Asn	Ser	Leu	Leu	Arg
130						135					140				
Arg	Gly	Ile	Pro	Val	Ala	His	Ser	Ile	Tyr	Gly	Thr	Ala	Gln	Thr	Ile
145					150					155				160	
Asn	Ser	Ala	Asn	Tyr	Val	Tyr	Phe	Leu	Ala	Leu	Gln	Glu	Val	Gln	Lys
165									170					175	
Leu	Lys	Ser	Pro	Ala	Ala	Ile	Asp	Ile	Tyr	Val	Gln	Glu	Leu	Leu	Asn
180								185					190		

SeqLst

Leu	His	Arg	Gly	Gln	Gly	Met	Asp	Leu	Phe	Trp	Arg	Asp	Thr	Leu	Thr
		195					200					205			
Cys	Pro	Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Met	Val	Gly	Asn	Lys	Thr	Gly
	210					215					220				
Gly	Leu	Phe	Arg	Leu	Ala	Val	Lys	Leu	Met	Gln	Ala	Glu	Ser	Ser	Thr
225					230					235					240
Gly	Lys	Asp	Cys	Val	Ala	Leu	Val	Asn	Val	Leu	Gly	Leu	Val	Phe	Gln
			245					250						255	
Ile	Cys	Asp	Asp	Tyr	Leu	Asn	Leu	Ser	Asp	Thr	Thr	Tyr	Thr	Gln	Asn
		260						265					270		
Lys	Gly	Leu	Cys	Glu	Asp	Leu	Thr	Glu	Gly	Lys	Phe	Ser	Phe	Pro	Ile
		275					280					285			
Ile	His	Ser	Ile	Arg	Ser	Asn	Pro	Gly	Asn	His	Gln	Leu	Ile	Asn	Ile
	290					295					300				
Leu	Arg	Gln	Arg	Thr	Lys	Asp	Glu	Glu	Val	Lys	Arg	Tyr	Ala	Leu	Gln
305					310					315					320
Tyr	Met	Glu	Ser	Thr	Gly	Ser	Phe	Lys	His	Thr	Gln	Asp	Val	Val	Arg
				325					330					335	
Gln	Leu	Arg	Ala	Arg	Ala	Leu	Gln	Leu	Ile	Glu	Glu	Ile	Glu	Asn	Ser
			340					345					350		
Glu	Asn	Gly	Glu	Gln	Pro	Glu	Glu	His	Asn	Asp	Gly	Thr	Met	Val	Arg
		355					360					365			
Ala	Ile	Leu	Asp	Lys	Ile	Thr	Glu	Ser	Thr	Leu	Ala	Asp	Thr	Asn	Thr
	370					375					380				
Thr	Thr	Arg	Asp	Ile	Asn	Gly	Asn	Cys	Ala	Thr	Arg				
385					390					395					