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<130> GHS/P544245WO

<140> PCT/EP2014/052363

<141> 2014-02-06

<150> US 61/761490

<151> 2013-02-06

<150> US 61/886442

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<170> PatentIn version 3.5

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Glu Glu Asp Glu Glu Val Ser Cys Leu Ile Thr Asp Ala Leu Trp Tyr
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Amended Sequence
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180 185 190

Ala Tyr Ser Asn Trp Gln Ile Leu Lys Glu Ile Leu Gly Lys Met Ile
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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
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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
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Ser Phe Leu Trp Val Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
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Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
325 330 335

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355 360 365

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Ala Arg Tyr Met Ser Asp Val Leu Lys Val Gly Val Tyr Leu Glu Asn
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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
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Glu Lys Ala Val Phe Lys Val Ile Asp Leu Asp Asp Tyr Ala Ala Asp
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Asp Asp Glu Tyr Glu Glu Lys Leu Lys Lys Glu Ser Leu Ala Phe Phe
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Phe Leu Ala Thr Tyr Gly Asp Gly Glu Pro Thr Asp Asn Ala Ala Arg
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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
Page 5

♀
Amended Sequence
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275 280 285

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290 295 300

Gln His Pro Cys Arg Ser Asn Val Ala Val Lys Lys Glu Leu His Ser
305 310 315 320

Pro Glu Ser Asp Arg Ser Cys Thr His Leu Glu Phe Asp Ile Ser 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
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Arg Leu Lys Phe Leu Ala Ser Pro Ala Gly Lys Asp Glu Tyr Ser Gln
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Amended Sequence
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Page 9

♀
Amended Sequence
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Pro Ser Pro Ser Ser Gln Asn Ala Pro Leu Phe Pro Gln Cys Val Lys
65 70 75 80
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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
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Page 10

♀
Amended Sequence

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

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225 230 235 240

Thr Gln Phe Gly Asn Asp Gly Cys Leu Arg Tyr Leu Cys Ser Leu Leu
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Gln Lys Phe Glu Ala Ala Val Pro Ser Val Tyr Pro Phe Asp Gln Tyr
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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
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Lys Gln Tyr Leu Glu Met Glu Leu Ser Ser Trp Val Lys Thr Ser Val
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Arg Asp Lys Tyr Leu Lys Lys Glu Val Glu Asp Ala Leu Ala Phe Pro
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420 425 430

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His Asn Ile Cys Thr Ser Asp Ile Leu Lys Leu Ala Val Asp Asp Phe
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♀
Amended Sequence

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515 520 525

Val Val Asp Asp Phe Phe Asp Val Gly Gly Ser Lys Glu Glu Leu Glu
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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
Page 12

♀
Amended Sequence

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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Page 13

♀
Amended Sequence

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Gly Cys Ile Val Met Leu Val Trp Arg Arg Ser Gly Ser Gly Asn Ser
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Thr Gly Thr Ala Glu Gly Phe Ala Lys Ala Leu Gly Glu Glu Ala Lys
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130 135 140
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145 150 155 160
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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
Page 14

♀
Amended Sequence
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 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

Leu Leu Asp Met Ser Pro Asp Thr Tyr Phe Ser Leu His Ala Glu Lys
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

♀
Amended Sequence

465 470 475 480

Gly Val Ala Pro Arg Leu Gln Pro Arg Phe Tyr Ser Ile Ser Ser Ser
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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
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♀
Amended Sequence
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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 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 Glu Gly Lys Arg Phe Arg Glu Ile Leu Asp Glu Thr
195 200 205

♀
Amended Sequence
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
355 360 365

Pro His Glu Ser Ser Ala Asp Cys Val Ile Ser Gly Tyr Asn Ile Pro
370 375 380

Arg Gly Thr Met Leu Ile Val Asn Gln Trp Ala Ile His His Asp Pro
385 390 395 400

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
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Amended Sequence
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Amended Sequence
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Ala Arg Ala Gln His Thr Ser Glu Ser Ala Ala Val Ala Lys Gly Ser
50 55 60

Ser Leu Thr Pro Ile Val Arg Thr Asp Ala Glu Ser Arg Arg Thr Arg
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Trp Pro Thr Asp Asp Asp Asp Ala Glu Pro Leu Val Asp Glu Ile Arg
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Ala Met Leu Thr Ser Met Ser Asp Gly Asp Ile Ser Val Ser Ala Tyr
100 105 110

♀
Amended Sequence

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

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

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

Pro Glu Met Arg Gly Arg Gly Leu Ser Phe Leu Gly Arg Asn Met Trp
180 185 190

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

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
275 280 285

Ala Thr Ala Tyr Ala Leu Met Asn Thr Gly Asp Asp Arg Cys Phe Ser
290 295 300

Tyr Ile Asp Arg Thr Val Lys Lys Phe Asn Gly Gly Val Pro Asn Val
305 310 315 320

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

Amended Sequence

Leu Arg Leu His Gly Tyr Ser Val Ser Pro Asp Val Phe Lys Asn Phe
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Glu Lys Asp Gly Glu Phe Phe Ala Phe Val Gly Gln Ser Asn Gln Ala
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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
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485 490 495

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595 600 605

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610 615 620

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♀
Amended Sequence
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725 730 735
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740 745 750
Lys Asn Glu Glu Met Met Ser His Val Asp Asp Glu Leu Lys Leu Arg
755 760 765
Ile Arg Glu Phe Val Gln Tyr Leu Leu Arg Leu Gly Glu Lys Lys Thr
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Page 24

♀
Amended Sequence
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<210> 15

<211> 473

<212> PRT

<213> Stevia rebaudiana

<400> 15

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 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

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♀
Amended Sequence
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 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

♀
Amended Sequence
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> 16
<211> 462
<212> PRT
<213> Oryza sativa

<400> 16

Met Asp Ser Gly Tyr Ser Ser Ser Tyr Ala Ala Ala Ala Gly Met His
1 5 10 15

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
Page 27

♀
Amended Sequence

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

Arg Ala Val Ala Val Glu Glu Glu Ser Ser Lys Val Phe Gln Ala Lys
Page 28

♀
Amended Sequence
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> 17

<211> 1389

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 17
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cggggccacc gcgtgtcgtt cgtctccacg ccgcggaaca tatcccgcct cccgccggtg 180
cgccccgcgc tcgcgccgct cgtcgccttc gtggcgctgc cgctcccgcg cgtcgagggg 240
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tgcgccgact gggtcatcgt ccacgtcttc caccactggg ccgcagccgc cgctctcgag 420
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gtggaggaag aaagcagcaa agtgtttcaa gccaaagcca agaagctgca ggagatcgtc 1320
gcggacatgg cctgccatga gaggtacatc gacggattca ttcagcaatt gagatcttac 1380
aaggattga 1389

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♀
Amended Sequence

<210> 18

<211> 1389

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 18
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agaggccata gagtatcatt tgtgtctact cctagaaata tctctcgttt acgaccagtc 180
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tgtgcagact gggttatagt cgatgtattt catcactggg ctgctgcacc cgcattggaa 420
cataaggtgc cttgtgctat gatgttgtta gggtcagcac acatgatggc atccatagct 480
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gctgacatgg cttgtcacga aagatacatc gatggtttca tccaacaatt gagaagttat 1380
aaagactaa 1389

<210> 19

<211> 460

<212> PRT

<213> Stevia rebaudiana

<400> 19

Met Ala Glu Gln Gln Lys Ile Lys Lys Ser Pro His Val Leu Leu Ile
1 5 10 15

♀
Amended Sequence

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

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

♀

Amended Sequence

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

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
435 440 445

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

<210> 20
<211> 481
<212> PRT
<213> Stevia rebaudiana
<400> 20
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1 5 10 15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
20 25 30

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

♀
Amended Sequence

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

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145 150 155 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
165 170 175

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
210 215 220

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
245 250 255

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
275 280 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
290 295 300

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
325 330 335

♀
Amended Sequence

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

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
370 375 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385 390 395 400

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
450 455 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465 470 475 480

Asn

<210> 21
<211> 785
<212> PRT
<213> Arabidopsis thaliana
<400> 21
Met Ser Ile Asn Leu Arg Ser Ser Gly Cys Ser Ser Pro Ile Ser Ala
1 5 10 15

Thr Leu Glu Arg Gly Leu Asp Ser Glu Val Gln Thr Arg Ala Asn Asn
20 25 30

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

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♀
Amended Sequence
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
305 310 315 320

Leu Ala Phe Arg Leu Leu Leu Ala His Gly Tyr Asp Val Ser Tyr Asp
325 330 335

Pro Leu Lys Pro Phe Ala Glu Glu Ser Gly Phe Ser Asp Thr Leu Glu
340 345 350

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♀
Amended Sequence
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

Trp Ile Val Glu Asn Arg Leu Gln Glu Leu Lys Phe Ala Arg Gln Lys
485 490 495

Leu Ala Tyr Cys Tyr Phe Ser Gly Ala Ala Thr Leu Phe Ser Pro Glu
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

♀

Amended Sequence

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 Asp 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

Val Lys Ser Val Ile Tyr Glu Pro Val Ser Leu Gln Lys Glu Ser Leu
770 775 780

Thr
785
<210>
<211>
<212>
<213>
22
894
DNA
Artificial Sequence
<220>
<223> Synthetic oligonucleotide
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aagccaacta atcacaaggt gttcggggaa gatatagcca tcttagcggg tgatgcgctt 360
ttagcttacg cttttgaaca tattgcttct caaacaagag gagtaccacc tcaattggtg 420
ctacaagtta ttgctagaat cggacacgcc gttgctgcaa caggcctcgt tggaggccaa

480

♀
Amended Sequence
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gcagatgaag agcttttggc cagattgtct cattacgcta gaatatagg cttggctttt 660
caaatcgtcg atgatatcct ggatgttact gctacatctg aacagttggg gaaaaccgct 720
ggtaaagacc aggcagccgc aaaggcaact tatccaagtc tattgggttt agaagcctct 780
agacagaaag cggaagagtt gattcaatct gctaaggaag ccttaagacc ttacggttca 840
caagcagagc cactcctagc gctggcagac ttcatcacac gtcgtcagca ttaa 894

<210> 23

<211> 1542

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 23
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agatcccaat caaatcatct tccaagagtg cctgaagtcc caggtgttcc attgttagga 180
aatctgttac aattgaagga gaaaaagcca tacatgactt ttacgagatg ggcagcgaca 240
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gagatagcca aggaggcatt ggtgaccaga ttccaatcca tatctacaag gaacttatct 360
aaagccctga aagtacttac agcagataag acaatggtcg caatgtcaga ttatgatgat 420
tatcataaaa cagttgagag acacatactg accgccgtct tgggtcctaa tgcacagaaa 480
aagcatagaa ttcaagaga tatcatgatg gataacatat ctactcaact tcatgaattc 540
gtgaaaaaca accaagaaca ggaagaggta gaccttagaa aaatctttca atctgagtta 600
ttcggcttag ctatgagaca agccttagga aaggatgttg aaagtttgta cgttgaagac 660
ctgaaaatca ccatgaatag agacgaaatc tttcaagtcc ttgttgttga tccaatgatg 720
ggagcaatcg atgttgattg gagagacttc tttccatacc taaagtgggt cccaaacaaa 780
aagttcgaaa atactattca acaaatgtac atcagaagag aagctgttat gaaatcttta 840
atcaaagagc acaaaaagag aatagcgtca ggcgaaaagc taaatagtta tatcgattac 900
cttttatttg aagctcaaac tttaaccgat cagcaactat tgatgtcctt gtgggaacca 960
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ctcagaagac actcaccagt tcctatcatt cctctaagac atgtacatga agataccgtt 1200
ctaggcggct accatgttcc tgctggcaca gaacttgccg ttaacatcta cggttgcaac 1260

atggacaaaa acgtttggga aaatccagag gaatggaacc cagaaagatt catgaaagag 1320
Page 38

♀
Amended Sequence

aatgagacaa ttgattttca aaagacgatg gccttcggtg gtggtaagag agtttgtgct
ggttccttgc aagccctttt aactgcatct attgggattg ggagaatggt tcaagagttc
gaatggaaac tgaaggatat gactcaagag gaagtgaaca cgataggcct aactacacaa
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PRT
Synechococcus sp.
24
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Gln Gln Val Glu Glu Ala Leu Ser Ala Ala Leu Val Pro Ala Tyr Pro
20 25 30
Glu Arg Ile Tyr Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys
35 40 45
Arg Leu Arg Pro Ile Leu Cys Leu Ala Ala Cys Glu Leu Ala Gly Gly
50 55 60
Ser Val Glu Gln Ala Met Pro Thr Ala Cys Ala Leu Glu Met Ile His
65 70 75 80
Thr Met Ser Leu Ile His Asp Asp Leu Pro Ala Met Asp Asn Asp Asp
85 90 95
Phe Arg Arg Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Ile
100 105 110
Ala Ile Leu Ala Gly Asp Ala Leu Leu Ala Tyr Ala Phe Glu His Ile
115 120 125
Ala Ser Gln Thr Arg Gly Val Pro Pro Gln Leu Val Leu Gln Val Ile
130 135 140
Ala Arg Ile Gly His Ala Val Ala Ala Thr Gly Leu Val Gly Gly Gln
145 150 155 160
Val Val Asp Leu Glu Ser Glu Gly Lys Ala Ile Ser Leu Glu Thr Leu
165 170 175
Glu Tyr Ile His Ser His Lys Thr Gly Ala Leu Leu Glu Ala Ser Val
180 185 190
Val Ser Gly Gly Ile Leu Ala Gly Ala Asp Glu Glu Leu Leu Ala Arg
195 200 205
Page 39

♀
Amended Sequence

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

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

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20 25 30

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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

♀
Amended Sequence
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

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

♀
Amended Sequence
Tyr Gly Cys Asn Met Asp Lys Asn Val Trp Glu Asn Pro Glu Glu Trp
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

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<213> Stevia rebaudiana
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20 25 30

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
Page 42

♀
Amended Sequence
130 135 140

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145 150 155 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
165 170 175

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
210 215 220

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
245 250 255

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
275 280 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
290 295 300

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
325 330 335

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

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
370 375 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385 390 395 400

Asp Gln Leu Thr Asn Cys Arg Tyr Ile Cys Lys Glu Trp Glu Val Gly
Page 43

♀
Amended Sequence
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
450 455 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465 470 475 480

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<400> 27
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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

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

♀
Amended Sequence

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
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

♀
Amended Sequence

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

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

♀
Amended Sequence

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

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<213> Stevia rebaudiana
<400> 28
Met Asn Leu Ser Leu Cys Ile Ala Ser Pro Leu Leu Thr Lys Ser Ser
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Arg Pro Thr 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 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

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♀

Amended Sequence

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 Glu 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 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 Glu 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

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♀
Amended Sequence

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

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

Page 49

♀
Amended Sequence

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

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<213> Zea mays
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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 Glu 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

♀
Amended Sequence
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

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

♀
Amended Sequence
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

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 Asn 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

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<212> PRT
<213> Populus trichocarpa

<400> 30
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Leu Thr Asp Pro Ala Ser Lys Leu Val Thr Gly Glu Phe Lys Thr Thr
20 25 30

Ser Leu Asn Phe His Gly Thr Lys Glu Arg Ile Lys Lys Met Phe Asp
35 40 45

Lys Ile Glu Leu Ser Val Ser Ser Tyr Asp Thr Ala Trp Val Ala Met
50 55 60

Val Pro Ser Pro Asp Cys Pro Glu Thr Pro Cys Phe Pro Glu Cys Thr
65 70 75 80

Lys Trp Ile Leu Glu Asn Gln Leu Gly Asp Gly Ser Trp Ser Leu Pro
85 90 95

His Gly Asn Pro Leu Leu Val Lys Asp Ala Leu Ser Ser Thr Leu Ala

♀
Amended Sequence
100 105 110

Cys Ile Leu Ala Leu Lys Arg Trp Gly Ile Gly Glu Glu Gln Ile Asn
115 120 125

Lys Gly Leu Arg Phe Ile Glu Leu Asn Ser Ala Ser Val Thr Asp Asn
130 135 140

Glu Gln His Lys Pro Ile Gly Phe Asp Ile Ile Phe Pro Gly Met Ile
145 150 155 160

Glu Tyr Ala Lys Asp Leu Asp Leu Asn Leu Pro Leu Lys Pro Thr Asp
165 170 175

Ile Asn Ser Met Leu His Arg Arg Ala Leu Glu Leu Thr Ser Gly Gly
180 185 190

Gly Lys Asn Leu Glu Gly Arg Arg Ala Tyr Leu Ala Tyr Val Ser Glu
195 200 205

Gly Ile Gly Lys Leu Gln Asp Trp Glu Met Ala Met Lys Tyr Gln Arg
210 215 220

Lys Asn Gly Ser Leu Phe Asn Ser Pro Ser Thr Thr Ala Ala Ala Phe
225 230 235 240

Ile His Ile Gln Asp Ala Glu Cys Leu His Tyr Ile Arg Ser Leu Leu
245 250 255

Gln Lys Phe Gly Asn Ala Val Pro Thr Ile Tyr Pro Leu Asp Ile Tyr
260 265 270

Ala Arg Leu Ser Met Val Asp Ala Leu Glu Arg Leu Gly Ile Asp Arg
275 280 285

His Phe Arg Lys Glu Arg Lys Phe Val Leu Asp Glu Thr Tyr Arg Phe
290 295 300

Trp Leu Gln Gly Glu Glu Glu Ile Phe Ser Asp Asn Ala Thr Cys Ala
305 310 315 320

Leu Ala Phe Arg Ile Leu Arg Leu Asn Gly Tyr Asp Val Ser Leu Glu
325 330 335

Asp His Phe Ser Asn Ser Leu Gly Gly Tyr Leu Lys Asp Ser Gly Ala
340 345 350

Ala Leu Glu Leu Tyr Arg Ala Leu Gln Leu Ser Tyr Pro Asp Glu Ser
355 360 365

Leu Leu Glu Lys Gln Asn Ser Arg Thr Ser Tyr Phe Leu Lys Gln Gly
Page 53

♀
Amended Sequence
370 375 380

Leu Ser Asn Val Ser Leu Cys Gly Asp Arg Leu Arg Lys Asn Ile Ile
385 390 395 400

Gly Glu Val His Asp Ala Leu Asn Phe Pro Asp His Ala Asn Leu Gln
405 410 415

Arg Leu Ala Ile Arg Arg Arg Ile Lys His Tyr Ala Thr Asp Asp Thr
420 425 430

Arg Ile Leu Lys Thr Ser Tyr Arg Cys Ser Thr Ile Gly Asn Gln Asp
435 440 445

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

Arg Glu Glu Phe Lys His Ile Glu Arg Trp Val Val Glu Arg Arg Leu
465 470 475 480

Asp Lys Leu Lys Phe Ala Arg Gln Lys Glu Ala Tyr Cys Tyr Phe Ser
485 490 495

Ala Ala Ala Thr Leu Phe Ala Pro Glu Leu Ser Asp Ala Arg Met Ser
500 505 510

Trp Ala Lys Asn Gly Val Leu Thr Thr Val Val Asp Asp Phe Phe Asp
515 520 525

Val Gly Gly Ser Glu Glu Glu Leu Val Asn Leu Ile Glu Leu Ile Glu
530 535 540

Arg Trp Asp Val Asn Gly Ser Ala Asp Phe Cys Ser Glu Glu Val Glu
545 550 555 560

Ile Ile Tyr Ser Ala Ile His Ser Thr Ile Ser Glu Ile Gly Asp Lys
565 570 575

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

Trp Leu Asp Leu Leu Lys Ser Met Leu Thr Glu Ala Gln Trp Ser Ser
595 600 605

Asn Lys Ser Val Pro Thr Leu Asp Glu Tyr Met Thr Thr Ala His Val
610 615 620

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

Pro Lys Leu Ser Glu Glu Val Ala Gly His Pro Glu Leu Leu Asn Leu
Page 54

♀
Amended Sequence
645 650 655

Tyr Lys Val Met Ser Thr Cys Gly Arg Leu Leu Asn Asp Trp Arg Ser
660 665 670

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

Met Ile His Ser Gly Gly Ala Ser Thr Glu Glu Glu Thr Ile Glu His
690 695 700

Phe Lys Gly Leu Ile Asp Ser Gln Arg Arg Gln Leu Leu Gln Leu Val
705 710 715 720

Leu Gln Glu Lys Asp Ser Ile Ile Pro Arg Pro Cys Lys Asp Leu Phe
725 730 735

Trp Asn Met Ile Lys Leu Leu His Thr Phe Tyr Met Lys Asp Asp Gly
740 745 750

Phe Thr Ser Asn Glu Met Arg Asn Val Val Lys Ala Ile Ile Asn Glu
755 760 765

Pro Ile Ser Leu Asp Glu Leu
770 775

<210> 31

<211> 2358

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 31
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ggattggact cagaagtaca gacaagagct aacaatgtga gctttgagca aacaaaggag 120

aagattagga agatgttgga gaaagtggag ctttctgttt cggcctacga tactagttgg 180

gtagcaatgg ttccatcacc gagctccaa aatgctccac ttttcccaca gtgtgtgaaa 240

tggttattgg ataatcaaca tgaagatgga tcttggggac ttgataacca tgaccatcaa 300

tctcttaaga aggatgtgtt atcatctaca ctggctagta tcctcgcgtt aaagaagtgg 360

ggaattggtg aaagacaaat aaacaagggt ctccagttta ttgagctgaa ttctgcatta 420

gtcactgatg aaaccataca gaaaccaaca gggtttgata ttatatttcc tgggatgatt 480

aaatatgcta gagatttgaa tctgacgatt ccattgggct cagaagtggt ggatgacatg 540

atacgaaaaa gagttctgga tcttaaatgt gatagtgaaa agttttcaaa gggaagagaa 600

gcatatctgg cctatgtttt agaggggaca agaaacctaa aagattggga tttgatagtc 660

aaatatcaaa ggaaaaatgg gtcactgttt gattctccag ccacaacagc agctgctttt 720

♀
Amended Sequence
acttcagtttg ggaatgatgg ttgtctccgt tatctctgtt ctctccttca gaaattcgag 780
gattgcagttc cttcagttta tccatttgat caatatgcac gccttagtat aattgtcact 840

cttgaaagct taggaattga tagagatttc aaaaccgaaa tcaaaagcat attggatgaa 900
acctatagat attggcttcg tggggatgaa gaaatatgtt tggacttggc cacttgtgct 960
ttggctttcc gattattgct tgctcatggc tatgatgtgt cttacgatcc gctaaaacca 1020
tttgcagaag aatctggttt ctctgatact ttggaaggat atgttaagaa tacgttttct 1080
gtgttagaat tatttaaggc tgctcaaagt tatccacatg aatcagcttt gaagaagcag 1140
tgttgttgga ctaaacaata tctggagatg gaattgtcca gctgggttaa gacctctgtt 1200
cgagataaat acctcaagaa agaggtcgag gatgctcttg cttttccctc ctatgcaagc 1260
ctagaaagat cagatcacag gagaaaaata ctcaatggtt ctgctgtgga aaacaccaga 1320
gttacaaaaa cctcatatcg tttgcacaat atttgcacct ctgatatcct gaagttagct 1380
gtggatgact tcaatttctg ccagtccata caccgtgaag aaatggaacg tcttgatagg 1440
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tatttctctg gggctgcaac tttattttct ccagaactat ctgatgctcg tatatcgtgg 1560
gccaaaggtg gagtacttac aacggttgta gacgacttct ttgatgttgg agggtccaaa 1620
gaagaactgg aaaacctcat acacttggtc gaaaagtggg atttgaacgg tgttcctgag 1680
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ttggatctgc tcaagtctat gttgagagaa gccgagtggt ccagtgacaa gtcaacacca 1860
agcttggagg attacatgga aaatgcgtac atatcatttg cattaggacc aattctcctc 1920
ccagctacct atctgatcgg acctccactt ccagagaaga cagtcgatag ccaacaatat 1980
aatcagctct acaagctcgt gagcactatg ggtcgtcttc taaatgacat acaaggtttt 2040
aagagagaaa gcgcggaagg gaagctgaat gcggtttcat tgcacatgaa aacacgagaga 2100
gacaatcgca gcaaagaagt gatcatagaa tcgatgaaag gtttagcaga gagaaagagg 2160
gaagaattgc ataagctagt tttggaggag aaaggaagtg tggttccaac ggaatgcaaa 2220
gaagcgttct tgaaaatgag caaagtgttg aacttatttt acaggaagca cgatggattc 2280
acatcaaatg atctgatgag tcttgttaaa tcagtgatct acgagccagt tagcttacag 2340
aaagaatctt taacttga 2358

<210> 32

<211> 785

<212> PRT

<213> Arabidopsis thaliana

<400> 32

Met Ser Ile Asn Leu Arg Ser Ser Gly Cys Ser Ser Pro Ile Ser Ala
1 5 10 15

♀
Amended Sequence
Thr Leu Glu Arg Gly Leu Asp Ser Glu Val Gln Thr Arg Ala Asn Asn
20 25 30

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

♀
Amended Sequence
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
305 310 315 320

Leu Ala Phe Arg Leu Leu Leu Ala His Gly Tyr Asp Val Ser Tyr Asp
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

Trp Ile Val Glu Asn Arg Leu Gln Glu Leu Lys Phe Ala Arg Gln Lys

485 490 495

Leu Ala Tyr Cys Tyr Phe Ser Gly Ala Ala Thr Leu Phe Ser Pro Glu
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

♀
Amended Sequence
Tyr Ser Ser Glu His Val Glu Ile Ile Phe Ser Val Leu Arg Asn 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

Val Lys Ser Val Ile Tyr Glu Pro Val Ser Leu Gln Lys Glu Ser Leu
770 775 780

Thr
785

<210> 33
<211> 513
<212> PRT
<213> Stevia rebaudiana
<400> 33

Met Asp Ala Val Thr Gly Leu Leu Thr Val Pro Ala Thr Ala Ile Thr
Page 59

♀
Amended Sequence

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

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
Page 60

♀
Amended Sequence
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
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 Glu 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> 34
<211> 509
<212> PRT
<213> Arabidopsis thaliana

♀
Amended Sequence

<400> 34
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

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

♀
Amended Sequence

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
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> 35
<211> 525
<212> PRT
<213> Fusarium fujikuroi
<400>
35
Page 63
♀
Amended Sequence

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

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

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♀
Amended Sequence

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
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> 36
<211> 499
<212>
PRT
Page 65
♀
Amended Sequence

<213> Trametes versicolor

<400> 36
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

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

♀
Amended Sequence
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
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> 37
<211> 1678
<212> DNA
<213> Artificial Sequence

♀
Amended Sequence

<220>

<223> Synthetic oligonucleotide

<400> 37
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tggaaggttt acaagcacca gaaaaccaaa atcaatcttc caccgggaag cttcggatgg 120
ccatttctgg gcgaaactct ggcactccta cgtgcaggtt gggactcaga gccggagaga 180
tttgttcgtg aacggatcaa gaaacacgga agtcctctag tgtttaagac gtcgttgttt 240
ggcgaccgtt ttgcggtgtt gtgtggacct gccggaaaca agttcctgtt ctgcaacgag 300
aacaagctgg tggcgtcgtg gtggccggtt ccggtgagga agcttttcgg caagtctctg 360
ctcacgattc gtggtgatga agctaagtgg atgaggaaga tgttgttatc gtatctcggt 420
cctgatgctt tcgcaagtca ttatgccgtc accatggacg tcgtcacccg tcggcatatc 480
gacgttcatt ggcgaaggaa ggaagaggtg aacgtattcc aaaccgttaa gttatatgcc 540
tttgagcttg catgtcgttt attcatgaac ctagacgacc caaaccacat tgcaaaactc 600
ggttccttgt tcatcatttt cttgaaaggc atcattgagc ttccaatcga cgtcccaggg 660
acacgatttt atagctccaa aaaagcagca gcagctatca ggattgaact aaaaaaattg 720
attaaagcaa gaaaactgga actgaaagaa gggaaggcat catcttcaca agacctctta 780
tcacatttgc ttacatctcc agatgaaaat ggtatgtttc taaccgaaga agagattgta 840
gacaacatct tgttactact ctttgcgggt catgatacct cggctctttc aatcactttg 900
ctcatgaaga ctcttggcga acattctgat gtttatgaca aggtgttaaa agagcaacta 960
gagatatgga agacgaaaga agcatgggag tccctgaaat gggaggacat acaaaagatg 1020
aaatacccct ggagtgttat atgtgaagtc atgagactaa atccacctgt tataggaacc 1080
tatagagagg cccttgtgga tattgattat gcgggttata ccatccccaa aggatggaag 1140
ctggactgga gtgctgtatc gacacaaagg gacgaggcta actttgaaga cgtaacacgt 1200
ttggacccat cacggtttga aggcgcagga ccgactccat tcacctttgt tccgtttgga 1260
gggggccta gaatgtgttt agggaaagaa tttgctcgat tggaagtact tgcgtttctt 1320

cacaatattg tcaccaattt caaatgggac ctgttgatac ctgatgagaa aatagaatat 1380
gatcccatgg ctaccccagc aaaggggctt ccaattcgtc ttcatcccca tcaagtttga 1440
ttacttcaag catgaatcag tgatgtgaag gtaaaccata atggatctta ttggtagtta 1500
cagattatgt gtttttatgg catgaagaag ttatgataaa taaaattgtg ttattctaca 1560
acttatgtaa tttgtgcctg taagtaactg aatctattaa tgttttatgt gacatgaaac 1620
ataaatgtat aattagtaaa ttttctgctc aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1678

<210> 38

<211> 476

<212> PRT

<213> Stevia rebaudiana

<400>
38
Page 68

♀
Amended Sequence

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 Asn 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
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

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♀
Amended Sequence

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

Lys Gly Leu Pro Ile Arg Leu His Pro His Gln Val
465 470 475

<210> 39
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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

Page 70

♀
Amended Sequence
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
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

♀

Amended Sequence

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

Lys Gly Leu Pro Ile Arg Leu His Pro His Gln Val
465 470 475

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<213> Arabidopsis thaliana
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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
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♀
Amended Sequence

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
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

♀
Amended Sequence
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

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

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<213> Vitis vinifera
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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
Page 74

♀
Amended Sequence

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
165 170 175

Lys Asn Glu Ser Gly Leu Val Ser Val Glu Met Lys Gln Trp Phe Gly
180 185 190

Asp Leu Thr Leu Asn Val Ile Leu Arg Met Val Ala Gly Lys Arg Tyr
195 200 205

Phe Ser Ala Ser Asp Ala Ser Glu Asn Lys Gln Ala Gln Arg Cys Arg
210 215 220

Arg Val Phe Arg Glu Phe Phe His Leu Ser Gly Leu Phe Val Val Ala
225 230 235 240

Asp Ala Ile Pro Phe Leu Gly Trp Leu Asp Trp Gly Arg His Glu Lys
245 250 255

Thr Leu Lys Lys Thr Ala Ile Glu Met Asp Ser Ile Ala Gln Glu Trp
260 265 270

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

Gln Asp Phe Met Asp Val Met Gln Ser Val Leu Asp Gly Lys Asn Leu
290 295 300

Gly Gly Tyr Asp Ala Asp Thr Ile Asn Lys Ala Thr Cys Leu Thr Leu
305 310 315 320

Ile Ser Gly Gly Ser Asp Thr Thr Val Val Ser Leu Thr Trp Ala Leu
325 330 335
Page 75

♀
Amended Sequence

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

Leu Asp Ile Gln Val Gly Lys Glu Arg Leu Val Asn Glu Gln Asp Ile
355 360 365

Ser Lys Leu Val Tyr Leu Gln Ala Ile Val Lys Glu Thr Leu Arg Leu
370 375 380

Tyr Pro Pro Gly Pro Leu Gly Gly Leu Arg Gln Phe Thr Glu Asp Cys
385 390 395 400

Thr Leu Gly Gly Tyr His Val Ser Lys Gly Thr Arg Leu Ile Met Asn
405 410 415

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 Ser Cys Ser Leu Tyr Asn
515 520 525

<210> 42
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<212> PRT
<213> Medicago truncatula
<400> 42
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

♀
Amended Sequence

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
100 105 110

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

Ser Ile Lys Met Arg Lys Leu Leu Pro Gln Phe Phe Lys Pro Glu Ala
130 135 140

Leu Gln Arg Tyr Val Gly Val Met Asp Val Ile Ala Gln Arg His Phe
145 150 155 160

Val Thr His Trp Asp Asn Lys Asn Glu Ile Thr Val Tyr Pro Leu Ala
165 170 175

Lys Arg Tyr Thr Phe Leu Leu Ala Cys Arg Leu Phe Met Ser Val Glu
180 185 190

Asp Glu Asn His Val Ala Lys Phe Ser Asp Pro Phe Gln Leu Ile Ala
195 200 205

Ala Gly Ile Ile Ser Leu Pro Ile Asp Leu Pro Gly Thr Pro Phe Asn
210 215 220

Lys Ala Ile Lys Ala Ser Asn Phe Ile Arg Lys Glu Leu Ile Lys Ile
225 230 235 240

Ile Lys Gln Arg Arg Val Asp Leu Ala Glu Gly Thr Ala Ser Pro Thr
245 250 255

Gln Asp Ile Leu Ser His Met Leu Leu Thr Ser Asp Glu Asn Gly Lys
260 265 270

Ser Met Asn Glu Leu Asn Ile Ala Asp Lys Ile Leu Gly Leu Leu Ile
275 280 285

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

Leu Gly Glu Leu Pro His Ile Tyr Asp Lys Val Tyr Gln Glu Gln Met
305 310 315 320

♀

Amended Sequence

Glu Ile Ala Lys Ser Lys Pro Ala Gly Glu Leu Leu Asn Trp Asp Asp
325 330 335

Leu Lys Lys Met Lys Tyr Ser Trp Asn Val Ala Cys Glu Val Met Arg
340 345 350

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> 43
<211> 522
<212> PRT
<213> Stevia rebaudiana
<400> 43
Met Gly Leu Phe Pro Leu Glu Asp Ser Tyr Ala Leu Val Phe Glu Gly
1 5 10 15

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 His Pro
35 40 45

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

Leu Ala Leu Ala Ser Leu Ala Asp Arg Cys Gly Pro Ile Phe Thr Ile
65 70 75 80

♀
Amended Sequence
Arg Leu Gly Ile Arg Arg Val Leu Val Val Ser Asn Trp Glu Ile Ala
85 90 95

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

Tyr Leu Ala Ala Lys Ile Leu Gly Phe Asn Tyr Val Ser Phe Ser Phe
115 120 125

Ala Pro Tyr Gly Pro Tyr Trp Val Gly Ile Arg Lys Ile Ile Ala Thr
130 135 140

Lys Leu Met Ser Ser Ser Arg Leu Gln Lys Leu Gln Phe Val Arg Val
145 150 155 160

Phe Glu Leu Glu Asn Ser Met Lys Ser Ile Arg Glu Ser Trp Lys Glu
165 170 175

Lys Lys Asp Glu Glu Gly Lys Val Leu Val Glu Met Lys Lys Trp Phe
180 185 190

Trp Glu Leu Asn Met Asn Ile Val Leu Arg Thr Val Ala Gly Lys Gln
195 200 205

Tyr Thr Gly Thr Val Asp Asp Ala Asp Ala Lys Arg Ile Ser Glu Leu
210 215 220

Phe Arg Glu Trp Phe His Tyr Thr Gly Arg Phe Val Val Gly Asp Ala
225 230 235 240

Phe Pro Phe Leu Gly Trp Leu Asp Leu Gly Gly Tyr Lys Lys Thr Met
245 250 255

Glu Leu Val Ala Ser Arg Leu Asp Ser Met Val Ser Lys Trp Leu Asp
260 265 270

Glu His Arg Lys Lys Gln Ala Asn Asp Asp Lys Lys Glu Asp Met Asp
275 280 285

Phe Met Asp Ile Met Ile Ser Met Thr Glu Ala Asn Ser Pro Leu Glu
290 295 300

Gly Tyr Gly Thr Asp Thr Ile Ile Lys Thr Thr Cys Met Thr Leu Ile
305 310 315 320

Val Ser Gly Val Asp Thr Thr Ser Ile Val Leu Thr Trp Ala Leu Ser
325 330 335

Leu Leu Leu Asn Asn Arg Asp Thr Leu Lys Lys Ala Gln Glu Glu Leu
340 345 350

♀
Amended Sequence
Asp Met Cys Val Gly Lys Gly Arg Gln Val Asn Glu Ser Asp Leu Val
355 360 365

Asn Leu Ile Tyr Leu Glu Ala Val Leu Lys Glu Ala Leu Arg Leu Tyr
370 375 380

Pro Ala Ala Phe Leu Gly Gly Pro Arg Ala Phe Leu Glu Asp Cys Thr
385 390 395 400

Val Ala Gly Tyr Arg Ile Pro Lys Gly Thr Cys Leu Leu Ile Asn Met
405 410 415

Trp Lys Leu His Arg Asp Pro Asn Ile Trp Ser Asp Pro Cys Glu Phe
420 425 430

Lys Pro Glu Arg Phe Leu Thr Pro Asn Gln Lys Asp Val Asp Val Ile
435 440 445

Gly Met Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Tyr Cys
450 455 460

Pro Gly Thr Arg Leu Ala Leu Gln Met Leu His Ile Val Leu Ala Thr
465 470 475 480

Leu Leu Gln Asn Phe Glu Met Ser Thr Pro Asn Asp Ala Pro Val Asp
485 490 495

Met Thr Ala Ser Val Gly Met Thr Asn Ala Lys Ala Ser Pro Leu Glu
500 505 510

Val Leu Leu Ser Pro Arg Val Lys Trp Ser
515 520

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<212> PRT
<213> Stevia rebaudiana
<400> 44
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

♀
Amended Sequence

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
100 105 110

Gly Thr Ala Glu Gly Phe Ala Lys Ala Leu Val Glu Glu Ala Lys Val
115 120 125

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

Ala Asp Asp Asp Glu Tyr Glu Glu Lys Leu Lys Lys Glu Ser Leu 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 Asn Phe Tyr Lys Trp Phe Thr Glu Gly Asp Asp Lys Gly Glu Trp
180 185 190

Leu Lys Lys Leu Gln Tyr Gly Val Phe Gly Leu Gly Asn Arg Gln Tyr
195 200 205

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

Met Gly Ala Lys Arg Leu Val Pro Val Gly Leu Gly Asp Asp Asp Gln
225 230 235 240

Cys Ile Glu Asp Asp Phe Thr Ala Trp Lys Glu Leu Val Trp Pro Glu
245 250 255

Leu Asp Gln Leu Leu Arg Asp Glu Asp Asp Thr Ser Val Thr Thr Pro
260 265 270

Tyr Thr Ala Ala Val Leu Glu Tyr Arg Val Val Tyr His Asp Lys Pro
275 280 285

Ala Asp Ser Tyr Ala Glu Asp Gln Thr His Thr Asn Gly His Val Val
290 295 300

His Asp Ala Gln His Pro Ser Arg Ser Asn Val Ala Phe Lys Lys Glu
305 310 315 320

Leu His Thr Ser Gln Ser Asp Arg Ser Cys Thr His Leu Glu Phe Asp
325 330 335

Ile Ser His Thr Gly Leu Ser Tyr Glu Thr Gly Asp His Val Gly Val
Page 81

♀
Amended Sequence
340 345 350

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

Tyr Glu Asp Glu Leu Asn Asn Phe Val Glu Thr Gly Ala Leu Ser Glu
Page 82

♀
Amended Sequence
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

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<212> PRT
<213> Arabidopsis thaliana
<400> 45
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

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
Page 83

♀
Amended Sequence

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

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
Page 84

♀
Amended Sequence

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

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
Page 85

♀
Amended Sequence

Arg Asp Val Trp
690

<210> 46
<211> 713
<212> PRT
<213> Fusarium fujikuroi
<400> 46
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

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

Page 86

♀
Amended Sequence

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

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

♀

Amended Sequence

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 Asp 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
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> 47
<211> 480
<212> PRT
<213> Stevia rebaudiana
<400> 47
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1 5 10 15

♀
Amended Sequence
Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
20 25 30

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

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145 150 155 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
165 170 175

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
210 215 220

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
245 250 255

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
275 280 285

♀
Amended Sequence
Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
290 295 300

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
325 330 335

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

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
370 375 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385 390 395 400

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
450 455 460

Ser Leu Asp Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465 470 475 480

<210> 48
<211> 787
<212> PRT
<213> Stevia rebaudiana
<400> 48
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
Page 90

♀
Amended Sequence
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 Glu 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

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
Page 91

♀

Amended Sequence
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

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
Page 92

♀
Amended Sequence
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
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> 49
<211> 527
<212> PRT
<213> Streptomyces clavuligerus
<400> 49
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

♀
Amended Sequence

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

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

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♀
Amended Sequence

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
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 Gly 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> 50
<211> 516
<212> PRT
<213> Bradyrhizobium diazoefficiens
<400> 50
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

♀
Amended Sequence

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

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

Page 96

♀
Amended Sequence

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
370 375 380

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> 51
<211> 2490
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide
<400> 51
atggttttgt cttcttcttg tactacagta ccacacttat cttcattagc tgtcgtgcaa 60
Page 97

♀
Amended Sequence
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gcaggaaggt ggagaagggc cttggctaga gcacagcaca catcagaatc cgcagctgtc 180
gcaaagggca gcagtttgac ccctatagtg agaactgacg ctgagtcaag gagaacaaga 240
tggccaaccg atgacgatga cgccgaacct ttagtggatg agatcagggc aatgcttact 300
tccatgtctg atggtgacat ttccgtgagc gcatacgata cagcctgggt cggattggtt 360
ccagagattag acggcggtga aggtcctcaa tttccagcag ctgtgagatg gataagaaat 420
atccagttgc ctgacggaag ttggggcgat gccgcattat tctctgccta tgacaggctt 480

atcaataccc ttgcctgcgt tgtaactttg acaaggtggt ccctagaacc agagatgaga 540
ggtagaggac tatctttttt gggtaggaac atgtggaaat tagcaactga agatgaagag 600
tcaatgccta ttggcttcga attagcattt ccatctttga tagagcttgc taagagccta 660
ggtgtccatg acttccctta tgatcaccag gccctacaag gaatctactc ttcaagagag 720
atcaaaatga agaggattcc aaaagaagtg atgcataccg ttccaacatc aatattgcac 780
agtttggagg gtatgcctgg cctagattgg gctaaactac ttaaactaca gagcagcgac 840
ggaagttttt tgttctcacc agctgccact gcatatgctt taatgaatac cggagatgac 900
aggtgtttta gctacatcga tagaacagta aagaaattca acggcggcgt ccctaatgtt 960
tatccagtgg atctatttga acatatttgg gccgttgata gacttgaaag attaggaatc 1020
tccaggtact tccaaaagga gatcgaacaa tgcatggatt atgtaaacag gcattggact 1080
gaggacggta tttgttgggc aaggaactct gatgtcaaag aggtggacga cacagctatg 1140
gcctttagac ttcttaggtt gcacggctac agcgtcagtc ctgatgtgtt taaaaacttc 1200
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ggtgccttct catatgagtt cttgaggaga aaagaagcag agggagcttt gagggacaag 1380
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gtttggattg gcaagacatt gtataggatg ccacttgtaa acaatgatgt atatttggaa 1560
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gcatgggcta gagccgcaat actagctaac gccgtgagca cccacttaag gaatagccca 1800
tcattcagag aaaggttaga gcattctctt aggtgtagac ctagtgaaga gacagatggc 1860
tcctggttta actcctcaag tggctctgat gcagttttag taaaggctct cttaagactt 1920
actgattcat tagccaggga agcacagcca atccatggag gtgacccaga agatattata 1980
cacaagttgt taagatctgc ttgggccgag tgggttaggg aaaaggaaga cgctgccgat 2040
agcgtgtgca atggtagttc tgcagtagaa caagagggat caagaatggt ccatgataaa 2100

♀
Amended Sequence
cagacctgtc tattattggc tagaatgatc gaaatttctg ccggtagggc agctggtgaa 2160
gcagccagtg aggacggcga tagaagaata attcaattta caggctccat ctgcgacagt 2220
cttaagcaaa aaatgctagt ttcacaggac cctgaaaaaa atgaagagat gatgtctcac 2280
gtggatgacg aattgaagtt gaggattaga gagttcgttc aatatttgct tagactaggt 2340
gaaaaaaaga ctggatctag cgaaaccagg caaaaatttt taagtatagt gaaatcatgt 2400
tactatgctg ctcattgccc acctcatgtc gttgatagac acattagtag agtgattttc 2460
gagccagtaa gtgccgcaaa gtaaccgcgg 2490
<210>
<211>
<212>
<213>
52
827
PRT
Zea mays
<400> 52
Met Val Leu Ser Ser Ser Cys Thr Thr Val Pro His Leu Ser Ser Leu
1 5 10 15
Ala Val Val Gln Leu Gly Pro Trp Ser Ser Arg Ile Lys Lys Lys Thr
20 25 30
Asp Thr Val Ala Val Pro Ala Ala Ala Gly Arg Trp Arg Arg Ala Leu
35 40 45
Ala Arg Ala Gln His Thr Ser Glu Ser Ala Ala Val Ala Lys Gly Ser
50 55 60
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
Asp Gly Ser Trp Gly Asp Ala Ala Leu Phe Ser Ala Tyr Asp Arg Leu
145 150 155 160

Ile Asn Thr Leu Ala Cys Val Val Thr Leu Thr Arg Trp Ser Leu Glu
165 170 175
Pro Glu Met Arg Gly Arg Gly Leu Ser Phe Leu Gly Arg Asn Met Trp
180 185 190
Page 99

♀
Amended Sequence

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

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
275 280 285

Ala Thr Ala Tyr Ala Leu Met Asn Thr Gly Asp Asp Arg Cys Phe Ser
290 295 300

Tyr Ile Asp Arg Thr Val Lys Lys Phe Asn Gly Gly Val Pro Asn Val
305 310 315 320

Tyr Pro Val Asp Leu Phe Glu His Ile Trp Ala Val Asp Arg Leu Glu
325 330 335

Arg Leu Gly Ile Ser Arg Tyr Phe Gln Lys Glu Ile Glu Gln Cys Met
340 345 350

Asp Tyr Val Asn Arg His Trp Thr Glu Asp Gly Ile Cys Trp Ala Arg
355 360 365

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

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
Page 100

♀
Amended Sequence

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

485 490 495

Gly Gly Asp Asp Val Trp Ile Gly Lys Thr Leu Tyr Arg Met Pro Leu
500 505 510

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
530 535 540

Thr Glu Asn Arg Leu Met Asp Phe Gly Val Ala Gln Glu Asp Ala Leu
545 550 555 560

Arg Ala Tyr Phe Leu Ala Ala Ala Ser Val Tyr Glu Pro Cys Arg Ala
565 570 575

Ala Glu Arg Leu Ala Trp Ala Arg Ala Ala Ile Leu Ala Asn Ala Val
580 585 590

Ser Thr His Leu Arg Asn Ser Pro Ser Phe Arg Glu Arg Leu Glu His
595 600 605

Ser Leu Arg Cys Arg Pro Ser Glu Glu Thr Asp Gly Ser Trp Phe Asn
610 615 620

Ser Ser Ser Gly Ser Asp Ala Val Leu Val Lys Ala Val Leu Arg Leu
625 630 635 640

Thr Asp Ser Leu Ala Arg Glu Ala Gln Pro Ile His Gly Gly Asp Pro
645 650 655

Glu Asp Ile Ile His Lys Leu Leu Arg Ser Ala Trp Ala Glu Trp Val
660 665 670

Arg Glu Lys Ala Asp Ala Ala Asp Ser Val Cys Asn Gly Ser Ser Ala
675 680 685

Val Glu Gln Glu Gly Ser Arg Met Val His Asp Lys Gln Thr Cys Leu
690 695 700

Leu Leu Ala Arg Met Ile Glu Ile Ser Ala Gly Arg Ala Ala Gly Glu
705 710 715 720

Ala Ala Ser Glu Asp Gly Asp Arg Arg Ile Ile Gln Leu Thr Gly Ser
725 730 735
Page 101

♀
Amended Sequence

Ile Cys Asp Ser Leu Lys Gln Lys Met Leu Val Ser Gln Asp Pro Glu
740 745 750

Lys Asn Glu Glu Met Met Ser His Val Asp Asp Glu Leu Lys Leu Arg
755 760 765

Ile Arg Glu Phe Val Gln Tyr Leu Leu Arg Leu Gly Glu Lys Lys Thr
770 775 780

Gly Ser Ser Glu Thr Arg Gln Thr Phe Leu Ser Ile Val Lys Ser Cys
785 790 795 800

Tyr Tyr Ala Ala His Cys Pro Pro His Val Val Asp Arg His Ile Ser
805 810 815

Arg Val Ile Phe Glu Pro Val Ser Ala Ala Lys
820 825

<210> 53

<211> 2570

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 53
cttcttcact aaatacttag acagagaaaa cagagctttt taaagccatg tctcttcagt 60
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cttcttcttt ccttaccatc tcaggatctc ctctcaatgt cgctagagac aaatccagaa 180
gcggttccat acattgttca aagcttcgaa ctcaagaata cattaattct caagaggttc 240
aacatgattt gcctctaata catgagtggc aacagcttca aggagaagat gctcctcaga 300
ttagtgttgg aagtaatagt aatgcattca aagaagcagt gaagagtgtg aaaacgatct 360
tgagaaacct aacggacggg gaaattacga tatcggctta cgatacagct tgggttgcat 420
tgatcgatgc cggagataaa actccggcgt ttccctccgc cgtgaaatgg atcgccgaga 480
accaactttc cgatggttct tggggagatg cgtatctctt ctcttatcat gatcgtctca 540
tcaataccct tgcatgcgtc gttgctctaa gatcatggaa tctctttcgt catcaatgca 600
acaaaggaat cacgtttttc cgggaaaata ttgggaagct agaagacgaa aatgatgagc 660
atatgccaat cggattcgaa gtagcattcc catcgttgct tgagatagct cgaggaataa 720
acattgatgt accgtacgat tctccggtct taaaagatat atacgtcaag aaagagctaa 780
agcttacaag gataccaaaa gagataatgc acaagatacc aacaacattg ttgcatagtt 840
tggaggggat gcgtgattta gattgggaaa agctcttgaa acttcaatct caagacggat 900
ctttcctctt ctctccttcc tctaccgctt ttgcattcat ggagacccga gacagtaact 960
gcctcgagta tttgcgaaat gccgtcaaac gtttcaatgg aggagttccc aatgtctttc 1020

♀
Amended Sequence
ccgtggatct tttcgagcac atatggatag tggatcggtt acaacgttta gggatatcga 1080
gatactttga agaagagatt aaagagtgtc ttgaatatgt ccacagatat tggaccgaca 1140
atggcatatg ttgggctaga tgttcccatg tccaagacat cgatgataca gccatggcat 1200
ttaggctctt aagacaacat ggataccaag tgtccgcaga tgtattcaag aactttgaga 1260
aagagggaga gtttttctgc tttgtggggc aatcaaacca agcagtaacc ggtatgttca 1320
acctataccg ggcatcacaa ttggcgtttc caagggaaga gatattgaaa aacgccaaag 1380
agttttctta taattatctg ctagaaaaag gggagagaga ggagttgatt gataagtgga 1440
ttataatgaa agacttacct ggcgagattg ggtttgcgtt agagattcca tggtacgcaa 1500
gcttgcctcg agtagagacg agattcttta ttgatcaata tggtggagaa aacgacgttt 1560
ggattggcaa gactctttat aggatgccat acgtgaacaa taatggatat ctggaattag 1620
caaaacaaga ttacaacaat tgccaagctc agcatcagct cgaatgggac atattccaaa 1680
agtggtatga agaaaatagg ttaagtgagt ggggtgtgcg cagaagtgag cttctcgagt 1740
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gggctaagtc aagtgtattg gttaaagcca tttcttcttc ttttggggaa tcctctgact 1860
ccagaagaag cttctccgat cagtttcatg aatacattgc caatgctcga cgaagtgatc 1920
atcactttaa tgacaggaac atgagattgg accgaccagg atcggttcag gccagtcggc 1980
ttgccggagt gttaatcggg actttgaatc aaatgtcttt tgacctttc atgtctcatg 2040
gccgtgacgt taacaatccc ctctatctat cgtggggaga ttggatggaa aaatggaaac 2100
tatatggaga tgaaggagaa ggagagctca tggtgaagat gataattcta atgaagaaca 2160
atgacctaac taacttcttc acccacactc acttcgttcg tctcgcggaa atcatcaatc 2220
gaatctgtct tcctggccaa tacttaaagg caaggagaaa cgatgagaag gagaagacaa 2280
taaagagtat ggaggaaggag atggggaaaa tggttgagtt agcattgtcg gagagtgaca 2340
catttcgtga cgccagcatc acgtttcttg atgtagcaaa agcattttac tactttgctt 2400
tatgtggcga tcatctccaa actcacatct ccaaagtctt gtttcaaaaa gtctagtaac 2460
ctcatcatca tcatcgatcc attaacaatc agtggatcga tgtatccata gatgcgtgaa 2520
taatatttca tgtagagaag gagaacaaat tagatcatgt agggttatca 2570

<210> 54

<211> 802

<212> PRT

<213> Arabidopsis thaliana

<400> 54

Met Ser Leu Gln Tyr His Val Leu Asn Ser Ile Pro Ser Thr Thr Phe
1 5 10 15

Leu Ser Ser Thr Lys Thr Thr Ile Ser Ser Ser Phe Leu Thr Ile Ser
20 25 30

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♀
Amended Sequence

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

His Cys Ser Lys Leu Arg Thr Gln Glu Tyr Ile Asn Ser Gln Glu Val
50 55 60

Gln His Asp Leu Pro Leu Ile His Glu Trp Gln Gln Leu Gln Gly Glu
65 70 75 80

Asp Ala Pro Gln Ile Ser Val Gly Ser Asn Ser Asn Ala Phe Lys Glu
85 90 95

Ala Val Lys Ser Val Lys Thr Ile Leu Arg Asn Leu Thr Asp Gly Glu
100 105 110

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

Gly Asp Lys Thr Pro Ala Phe Pro Ser Ala Val Lys Trp Ile Ala Glu
130 135 140

Asn Gln Leu Ser Asp Gly Ser Trp Gly Asp Ala Tyr Leu Phe Ser Tyr
145 150 155 160

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

Trp Asn Leu Phe Pro His Gln Cys Asn Lys Gly Ile Thr Phe Phe Arg
180 185 190

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

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

Asn Ile Asp Val Pro Tyr Asp Ser Pro Val Leu Lys Asp Ile Tyr Ala
225 230 235 240

Lys Lys Glu Leu Lys Leu Thr Arg Ile Pro Lys Glu Ile Met His Lys
245 250 255

Ile Pro Thr Thr Leu Leu His Ser Leu Glu Gly Met Arg Asp Leu Asp
260 265 270

Trp Glu Lys Leu Leu Lys Leu Gln Ser Gln Asp Gly Ser Phe Leu Phe
275 280 285

Ser Pro Ser Ser Thr Ala Phe Ala Phe Met Gln Thr Arg Asp Ser Asn
290 295 300

Page 104

♀
Amended Sequence

Cys Leu Glu Tyr Leu Arg Asn Ala Val Lys Arg Phe Asn Gly Gly Val
305 310 315 320

Pro Asn Val Phe Pro Val Asp Leu Phe Glu His Ile Trp Ile Val Asp
325 330 335

Arg Leu Gln Arg Leu Gly Ile Ser Arg Tyr Phe Glu Glu Glu Ile Lys
340 345 350

Glu Cys Leu Asp Tyr Val His Arg Tyr Trp Thr Asp Asn Gly Ile Cys
355 360 365

Trp Ala Arg Cys Ser His Val Gln Asp Ile Asp Asp Thr Ala Met Ala
370 375 380

Phe Arg Leu Leu Arg Gln His Gly Tyr Gln Val Ser Ala Asp Val Phe
385 390 395 400

Lys Asn Phe Glu Lys Glu Gly Glu Phe Phe Cys Phe Val Gly Gln Ser
405 410 415

Asn Gln Ala Val Thr Gly Met Phe Asn Leu Tyr Arg Ala Ser Gln Leu
420 425 430

Ala Phe Pro Arg Glu Glu Ile Leu Lys Asn Ala Lys Glu Phe Ser Tyr
435 440 445

Asn Tyr Leu Leu Glu Lys Arg Glu Arg Glu Glu Leu Ile Asp Lys Trp
450 455 460

Ile Ile Met Lys Asp Leu Pro Gly Glu Ile Gly Phe Ala Leu Glu Ile
465 470 475 480

Pro Trp Tyr Ala Ser Leu Pro Arg Val Glu Thr Arg Phe Tyr Ile Asp
485 490 495

Gln Tyr Gly Gly Glu Asn Asp Val Trp Ile Gly Lys Thr Leu Tyr Arg
500 505 510

Met Pro Tyr Val Asn Asn Asn Gly Tyr Leu Glu Leu Ala Lys Gln Asp
515 520 525

Tyr Asn Asn Cys Gln Ala Gln His Gln Leu Glu Trp Asp Ile Phe Gln
530 535 540

Lys Trp Tyr Glu Glu Asn Arg Leu Ser Glu Trp Gly Val Arg Arg Ser
545 550 555 560

Glu Leu Leu Glu Cys Tyr Tyr Leu Ala Ala Ala Thr Ile Phe Glu Ser
565 570 575

♀
Amended Sequence

Glu Arg Ser His Glu Arg Met Val Trp Ala Lys Ser Ser Val Leu Val
580 585 590

Lys Ala Ile Ser Ser Ser Phe Gly Glu Ser Ser Asp Ser Arg Arg Ser
595 600 605

Phe Ser Asp Gln Phe His Glu Tyr Ile Ala Asn Ala Arg Arg Ser Asp
610 615 620

His His Phe Asn Asp Arg Asn Met Arg Leu Asp Arg Pro Gly Ser Val
625 630 635 640

Gln Ala Ser Arg Leu Ala Gly Val Leu Ile Gly Thr Leu Asn Gln Met
645 650 655

Ser Phe Asp Leu Phe Met Ser His Gly Arg Asp Val Asn Asn Leu Leu
660 665 670

Tyr Leu Ser Trp Gly Asp Trp Met Glu Lys Trp Lys Leu Tyr Gly Asp
675 680 685

Glu Gly Glu Gly Glu Leu Met Val Lys Met Ile Ile Leu Met Lys Asn
690 695 700

Asn Asp Leu Thr Asn Phe Phe Thr His Thr His Phe Val Arg Leu Ala
705 710 715 720

Glu Ile Ile Asn Arg Ile Cys Leu Pro Arg Gln Tyr Leu Lys Ala Arg
725 730 735

Arg Asn Asp Glu Lys Glu Lys Thr Ile Lys Ser Met Glu Lys Glu Met
740 745 750

Gly Lys Met Val Glu Leu Ala Leu Ser Glu Ser Asp Thr Phe Arg Asp
755 760 765

Val Ser Ile Thr Phe Leu Asp Val Ala Lys Ala Phe Tyr Tyr Phe Ala
770 775 780

Leu Cys Gly Asp His Leu Gln Thr His Ile Ser Lys Val Leu Phe Gln
785 790 795 800

Lys Val

<210> 55
<211> 983
<212> PRT
<213> Diaporthe amygdali
<400> 55
Page 106

♀
Amended Sequence
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

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

♀
Amended Sequence
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
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
385 390 395 400

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

465 470 475 480

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

♀
Amended Sequence
Ala Lys Ser Pro Leu Gly Ala Ser Val Gly Ser Ser Leu Trp Thr Pro
545 550 555 560

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

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 Asn 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

Asp Trp Val Arg Thr Thr Ser Ala Asp His Ile Ser Cys Pro Tyr Ser
805 810 815

♀
Amended Sequence
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

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> 56
<211> 881
<212> PRT
<213> Physcomitrella patens
<400> 56
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

♀
Amended Sequence

65 70 75 80

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

Leu Met Tyr Thr Lys Asp Val Lys Cys Phe Asp Tyr Leu Asn Gln Leu

♀
Amended Sequence
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

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
Page 112

♀
Amended Sequence
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
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
Page 113

♀
Amended Sequence

<210> 57
<211> 952
<212> PRT
<213> Gibberella fujikuroi
<400> 57
Met Pro Gly Lys Ile Glu Asn Gly Thr Pro Lys Asp Leu Lys Thr Gly
1 5 10 15

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

Ser His His Ser Tyr Tyr Gly Leu Cys Ser Thr Ser Cys Gln Val Tyr
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
115 120 125

Glu His Gly Val Thr Ser Leu Lys Arg Gln Leu Ala Val Trp Asn Asp
130 135 140

Val Glu Asp Thr Asn His Ile Gly Val Glu Phe Ile Ile Pro Ala Leu
145 150 155 160

Leu Ser Met Leu Glu Lys Glu Leu Asp Val Pro Ser Phe Glu Phe Pro
165 170 175

Cys Arg Ser Ile Leu Glu Arg Met His Gly Glu Lys Leu Gly His Phe
180 185 190

Asp Leu Glu Gln Val Tyr Gly Lys Pro Ser Ser Leu Leu His Ser Leu
195 200 205

Glu Ala Phe Leu Gly Lys Leu Asp Phe Asp Arg Leu Ser His His Leu
210 215 220

Tyr His Gly Ser Met Met Ala Ser Pro Ser Ser Thr Ala Ala Tyr Leu
225 230 235 240
Page 114

♀
Amended Sequence

Ile Gly Ala Thr Lys Trp Asp Asp Glu Ala Glu Asp Tyr Leu Arg His
245 250 255

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

Phe Pro Thr Thr His Phe Glu Cys Ser Trp Ile Ile Ala Thr Leu Leu
275 280 285

Lys Val Gly Phe Thr Leu Lys Gln Ile Asp Gly Asp Gly Leu Arg Gly
290 295 300

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

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

Leu Ala Leu Ser Leu Val Asn Gln Pro Val Ser Pro Asp Ile Met Ile
340 345 350

Lys Val Phe Glu Gly Lys Asp His Phe Thr Thr Phe Gly Ser Glu Arg
355 360 365

Asp Pro Ser Leu Thr Ser Asn Leu His Val Leu Leu Ser Leu Leu Lys
370 375 380

Gln Ser Asn Leu Ser Gln Tyr His Pro Gln Ile Leu Lys Thr Thr Leu
385 390 395 400

Phe Thr Cys Arg Trp Trp Trp Gly Ser Asp His Cys Val Lys Asp Lys
405 410 415

Trp Asn Leu Ser His Leu Tyr Pro Thr Met Leu Leu Val Glu Ala Phe
420 425 430

Thr Glu Val Leu His Leu Ile Asp Gly Gly Glu Leu Ser Ser Leu Phe
435 440 445

Asp Glu Ser Phe Lys Cys Lys Ile Gly Leu Ser Ile Phe Gln Ala Val
450 455 460

Leu Arg Ile Ile Leu Thr Gln Asp Asn Asp Gly Ser Trp Arg Gly Tyr
465 470 475 480

Arg Glu Gln Thr Cys Tyr Ala Ile Leu Ala Leu Val Gln Ala Arg His
485 490 495

Val Cys Phe Phe Thr His Met Val Asp Arg Leu Gln Ser Cys Val Asp
500 505 510
Page 115

♀
Amended Sequence

Arg Gly Phe Ser Trp Leu Lys Ser Cys Ser Phe His Ser Gln Asp Leu
515 520 525

Thr Trp Thr Ser Lys Thr Ala Tyr Glu Val Gly Phe Val Ala Glu Ala
530 535 540

Tyr Lys Leu Ala Ala Leu Gln Ser Ala Ser Leu Glu Val Pro Ala Ala
545 550 555 560

Thr Ile Gly His Ser Val Thr Ser Ala Val Pro Ser Ser Asp Leu Glu
565 570 575

Lys Tyr Met Arg Leu Val Arg Lys Thr Ala Leu Phe Ser Pro Leu Asp
580 585 590

Glu Trp Gly Leu Met Ala Ser Ile Ile Glu Ser Ser Phe Phe Val Pro
595 600 605

Leu Leu Gln Ala Gln Arg Val Glu Ile Tyr Pro Arg Asp Asn Ile Lys
610 615 620

Val Asp Glu Asp Lys Tyr Leu Ser Ile Ile Pro Phe Thr Trp Val Gly
625 630 635 640

Cys Asn Asn Arg Ser Arg Thr Phe Ala Ser Asn Arg Trp Leu Tyr Asp
645 650 655

Met Met Tyr Leu Ser Leu Leu Gly Tyr Gln Thr Asp Glu Tyr Met Glu
660 665 670

Ala Val Ala Gly Pro Val Phe Gly Asp Val Ser Leu Leu His Gln Thr
675 680 685

Ile Asp Lys Val Ile Asp Asn Thr Met Gly Asn Leu Ala Arg Ala Asn
690 695 700

Gly Thr Val His Ser Gly Asn Gly His Gln His Glu Ser Pro Asn Ile
705 710 715 720

Gly Gln Val Glu Asp Thr Leu Thr Arg Phe Thr Asn Ser Val Leu Asn
725 730 735

His Lys Asp Val Leu Asn Ser Ser Ser Ser Asp Gln Asp Thr Leu Arg
740 745 750

Arg Glu Phe Arg Thr Phe Met His Ala His Ile Thr Gln Ile Glu Asp
755 760 765

Asn Ser Arg Phe Ser Lys Gln Ala Ser Ser Asp Ala Phe Ser Ser Pro
770 775 780

♀
Amended Sequence

Glu Gln Ser Tyr Phe Gln Trp Val Asn Ser Thr Gly Gly Ser His Val
785 790 795 800

Ala Cys Ala Tyr Ser Phe Ala Phe Ser Asn Cys Leu Met Ser Ala Asn
805 810 815

Leu Leu Gln Gly Lys Asp Ala Phe Pro Ser Gly Thr Gln Lys Tyr Leu
820 825 830

Ile Ser Ser Val Met Arg His Ala Thr Asn Met Cys Arg Met Tyr Asn
835 840 845

Asp Phe Gly Ser Ile Ala Arg Asp Asn Ala Glu Arg Asn Val Asn Ser
850 855 860

Ile His Phe Pro Glu Phe Thr Leu Cys Asn Gly Thr Ser Gln Asn Leu

865 870 875 880

Asp Glu Arg Lys Glu Arg Leu Leu Lys Ile Ala Thr Tyr Glu Gln Gly
885 890 895

Tyr Leu Asp Arg Ala Leu Glu Ala Leu Glu Arg Gln Ser Arg Asp Asp
900 905 910

Ala Gly Asp Arg Ala Gly Ser Lys Asp Met Arg Lys Leu Lys Ile Val
915 920 925

Lys Leu Phe Cys Asp Val Thr Asp Leu Tyr Asp Gln Leu Tyr Val Ile
930 935 940

Lys Asp Leu Ser Ser Ser Met Lys
945 950

<210> 58
<211> 361
<212> PRT
<213> Stevia rebaudiana
<400> 58
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

♀
Amended Sequence

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

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

♀
Amended Sequence

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> 59
<211> 342
<212> PRT
<213> Fusarium fujikuroi
<400> 59
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

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

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♀
Amended Sequence
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 Asn Asn Lys Tyr
275 280 285

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> 60
<211> 300
<212> PRT
<213> Mus musculus
<400> 60
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
Page 120

♀
Amended Sequence

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

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> 61
<211> 339
<212> PRT
<213> Thalassiosira pseudonana
<400> 61
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
Page 121

♀
Amended Sequence

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
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

♀
Amended Sequence

Gly Asp Arg Ala Ala Pro Leu Leu Ala Ile Ala Asp Phe Ile Ile Asp
325 330 335

Arg Lys Asn

<210> 62
<211> 355
<212> PRT
<213> Streptomyces clavuligerus
<400> 62
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

♀
Amended Sequence

Leu His Ile Gly Ala Ala Leu Ala Gly Ala Arg Pro Glu Leu Leu Ala
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> 63
<211> 330
<212> PRT
<213> Sulfolobus acidocaldarius
<400> 63
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

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♀
Amended Sequence
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
325 330

<210> 64
<211> 297
<212> PRT
<213>

Synechococcus sp.
Page 125
♀
Amended Sequence

<400> 64
Met Val Ala Gln Thr Phe Asn Leu Asp Thr Tyr Leu Ser Gln Arg Gln
1 5 10 15

Gln Gln Val Glu Glu Ala Leu Ser Ala Ala Leu Val Pro Ala Tyr Pro
20 25 30

Glu Arg Ile Tyr Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys
35 40 45

Arg Leu Arg Pro Ile Leu Cys Leu Ala Ala Cys Glu Leu Ala Gly Gly
50 55 60

Ser Val Glu Gln Ala Met Pro Thr Ala Cys Ala Leu Glu Met Ile His
65 70 75 80

Thr Met Ser Leu Ile His Asp Asp Leu Pro Ala Met Asp Asn Asp Asp
85 90 95

Phe Arg Arg Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Ile
100 105 110

Ala Ile Leu Ala Gly Asp Ala Leu Leu Ala Tyr Ala Phe Glu His Ile
115 120 125

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

Ala Arg Ile Gly His Ala Val Ala Ala Thr Gly Leu Val Gly Gly Gln
145 150 155 160

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

Glu Tyr Ile His Ser His Lys Thr Gly Ala Leu Leu Glu Ala Ser Val
180 185 190

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

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

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
Page 126

♀
Amended Sequence
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> 65

<211> 371
<212> PRT
<213> Arabidopsis thaliana
<400> 65
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

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

♀
Amended Sequence

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> 66
<211> 473
<212> PRT
<213> Stevia rebaudiana
<400> 66
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 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

♀
Amended Sequence

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 Gly Tyr Arg
195 200 205

Met Gly Met 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 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

♀
Amended Sequence

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 Ala
450 455 460

Arg Ala Val Ala Ile Asp His Glu Ser
465 470

<210> 67
<211> 459
<212> PRT
<213> Ipomoea purpurea
<400> 67
Met Gly Ser Gln Ala Thr Thr Tyr His Met Ala Met Tyr Pro Trp Phe
1 5 10 15

Gly Val Gly His Leu Thr Gly Phe Phe Arg Leu Ala Asn Lys Leu Ala
20 25 30

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

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

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

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

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

Val Val Phe Tyr Asp Phe Thr His Trp Leu Pro Ser Leu Ala Arg Lys
115 120 125

Ile Gly Ile Lys Ser Val Phe Tyr Ser Thr Ile Ser Pro Leu Met His
130 135 140

Gly Tyr Ala Leu Ser Pro Glu Arg Arg Val Val Gly Lys Gln Leu Thr
145 150 155 160

Glu Ala Asp Met Met Lys Ala Pro Ala Ser Phe Pro Asp Pro Ser Ile
165 170 175

Lys Leu His Ala His Glu Ala Arg Gly Phe Thr Ala Arg Thr Val Met
180 185 190

Lys Phe Gly Gly Asp Ile Thr Phe Phe Asp Arg Ile Phe Thr Ala Val
195 200 205

Ser Glu Ser Asp Gly Leu Ala Tyr Ser Thr Cys Arg Glu Ile Glu Gly
210 215 220

Gln Phe Cys Asp Tyr Ile Glu Thr Gln Phe Gln Lys Pro Val Leu Leu
225 230 235 240

Ala Gly Pro Ala Leu Pro Val Pro Ser Lys Ser Thr Met Glu Gln Lys
245 250 255

Trp Ser Asp Trp Leu Gly Lys Phe Lys Glu Gly Ser Val Ile Tyr Cys
260 265 270

Ala Phe Gly Ser Glu Cys Thr Leu Arg Lys Asp Lys Phe Gln Glu Leu
275 280 285

Leu Trp Gly Leu Glu Leu Thr Gly Met Pro Phe Phe Ala Ala Leu Lys
290 295 300

Pro Pro Phe Glu Thr Glu Ser Val Glu Ala Ala Ile Pro Glu Glu Leu
305 310 315 320

Lys Glu Lys Ile Gln Gly Arg Gly Ile Val His Gly Glu Trp Val Gln
325 330 335

Gln Gln Leu Phe Leu Gln His Pro Ser Val Gly Cys Phe Val Ser His
340 345 350

Cys Gly Trp Ala Ser Leu Ser Glu Ala Leu Val Asn Asp Cys Gln Ile
355 360 365

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♀
Amended Sequence
Val Leu Leu Pro Gln Val Gly Asp Gln Ile Ile Asn Ala Arg Ile Met
370 375 380

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
420 425 430

Leu Arg Gly Phe Leu Met Asn Ala Asp Leu Asp Ser Lys Tyr Met Asp
435 440 445

Ser Phe Asn Gln Lys Leu Gln Asp Leu Leu Gly
450 455

<210> 68

<211> 1380

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 68
atgggttctc aagctacaac ttaccatatg gccatgtatc catggcttgg ggttggacat 60
ttgactggtt tcttccgttt ggcaaacaaa ttagctggca aaggacatag aatctcattt 120
ctaattccta aaaacactca atctaagtta gaatctttca acgctcatcc acacttaatc 180
tcttttgtgc ctatcgttgt cccaagtata ccaggcctgc cacctggtgc agagactaca 240
tcagatgttc ctttcccaag tacacatttg ctaatggaag caatggacaa gactcaaaac 300
gatatagaga ttatcctgaa ggatcttaaa gtagatgttg ttttctatga ttttactcac 360
tggttgcctt ctctggccag aaagattggc attaagagtg tcttttactc caccatttct 420
cctttaatgc atggatatgc tttatcacca gaaagacgtg tagttggtaa gcaattgaca 480
gaggcagata tgatgaaggc cccagcttct ttcccagacc catccattaa gctacatgca 540
catgaagcta ggggttttac agccagaacc gttatgaaat tcggtggtga catcaccttt 600
ttcgatagaa tattcacagc agtttccgaa agtgatggcc tggcctactc tacttgtaga 660
gagatcgagg gacaattctg tgattacatt gaatcacaat tccagaagcc agtcttgtta 720
gccggtccag ctttgccagt cccatccaaa tctactatgg aacaaaagtg gtcagattgg 780
ttggggaaat tcaaggaagg ctccgtcatc tactgtgctt tcgggtctga atgtacattg 840
agaaaggaca aatttcagga acttttatgg ggtttggaat tgacaggaat gcctttcttc 900
gctgctctga agccaccttt tgagactgac tctgttgagg ctgctatccc tgaggaacta 960
aaggaaaaga ttcagggaag aggtatagta catggagaat gggtacaaca acaattgttt 1020
cttcaacacc catctgtcgg gtgcttcgtt tctcactgcg gctgggcaag tttatctgaa 1080

♀
Amended Sequence

gcccttgtta atgattgtca tatcgtgtta cttccacaag ttggcgatca gattatcaac
gccagaataa tgtcagtatc acttaaagtg ggcgtggaag ttgaaaaggg tgaggaggac
ggtgtctttt caagagaatc tgtgtgcaag gctgttaaag cagtaatgga tgaaaaatct
gaaatcggta gagaagtcag aggtaatcat gataaactga ggggtttctt gatgaatgca
gacttagatt caaagtacat ggattcattc aatcaaaagc tacaagattt gctaggttaa
1140
1200
1260
1320
1380
<210>
<211>
<212>
<213>
<400>
69
438
PRT
Bellis perennis

69
Met Asp Ser Lys Ile Asp Ser Lys Thr Phe Arg Val Val Met Leu Pro
1 5 10 15
Trp Leu Ala Tyr Ser His Ile Ser Ser Phe Leu Val Phe Ala Lys Arg
20 25 30
Leu Thr Asn His Asn Phe His Ile Tyr Ile Cys Ser Ser Gln Thr Asn
35 40 45
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
65 70 75 80
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
Arg Asp Ile Pro Lys Gly Gly Ser Lys Tyr Ile Glu Arg Phe Val Asp
180 185 190
Cys Met Arg Arg Ser Cys Glu Ile Ile Leu Val Arg Ser Thr Met Glu
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♀
Amended Sequence
195 200 205

Leu Glu Gly Lys Tyr Ile Asp Tyr Leu Ser Lys Thr Leu Gly Lys Lys
210 215 220

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
245 250 255

Val Val Phe Val Cys Phe Gly Ser Glu Tyr Ile Leu Ser Asp Asn Glu
260 265 270

Ile Glu Asp Ile Ala Tyr Gly Leu Glu Leu Ser Gln Val Ser Phe Val
275 280 285

Trp Ala Ile Arg Ala Lys Thr Ser Ala Leu Asn Gly Phe Ile Asp Arg
290 295 300

Val Gly Asp Lys Gly Leu Val Ile Asp Lys Trp Val Pro Gln Ala Asn
305 310 315 320

Ile Leu Ser His Ser Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp
325 330 335

Ser Ser Thr Met Glu Ser Ile Arg Tyr Gly Val Pro Ile Ile Ala Met
340 345 350

Pro Met Gln Phe Asp Gln Pro Tyr Asn Ala Arg Leu Met Glu Thr Val
355 360 365

Gly Ala Gly Ile Glu Val Gly Arg Asp Gly Glu Gly Arg Leu Lys Arg
370 375 380

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

Glu Ser Ile Arg Glu Lys Ala Lys Glu Leu Gly Glu Ile Met Lys Lys
405 410 415

Asn Met Glu Ala Glu Val Asp Gly Ile Val Ile Glu Asn Leu Val Lys
420 425 430

Leu Cys Glu Met Asn Asn
435

<210> 70
<211> 1317
<212> DNA
<213> Artificial Sequence
Page 134

♀
Amended Sequence

<220>

<223> Synthetic oligonucleotide

<400> 70
atggattcta aaatcgattc aaagacattc agagtcgtta tgttgccttg gcttgcatac 60
tcacacattt catcattcct agtgtttgcc aagagactaa caaatcaaaa cttccacatc 120
tacatttgtt cctctcaaac aaatatgcaa tacctgaaaa acaacttgac gtctcagtat 180
tcaaaatcta tacaactgat tgagttgaat cttccatcta gttccgaatt gcctctgcag 240
tatcatacta ctcacggact accaccacac cttacgaaaa cattgtctga tgattatcaa 300
aagtccggac ctgactttga aaccattttg atcaaattga acgcacatct ggtaatctac 360
gactttaatc aactttgggc tccagaggtt gctagtacac ttcatattcc atccatacag 420
ttactgtctg gttgcgtcgc cttatatgcc ttagacgccc atctgtacac aaagccacta 480
gacgaaaact tggctaagtt tcctttccca gaaatctatc ctaaaaacag agatattcct 540
aagggaggta gtaaatacat cgaaaggttc gtagactgta tgagaagatc ttgtgaaatc 600
atattagtca gaagtaccat ggaacttgaa ggaaaatatc ttgattactt gtctaagaca 660
ttagggaaaa aggtgttgcc agtagggcct ctggtgcaag aggcttcttt gttgcaagat 720
gatcatatat ggattatgaa gtggttagac aaaaacgagg agtcatccgt cgtgtttgtt 780
tgttttggtt ctgagtacat cttatcagac aacgaaatag aagatattgc ttatggccta 840
gagttgtccc aagtaagttt cgtttgggca ataagagcta agacttctgc cttaaatggc 900
ttcattgata gagtgggtga taaaggctta gtcatcgata aatgggttcc acaggctaac 960
atcttatctc actcttctac tggtggattc actagtcatt gcggttggtc atcaacaatg 1020
gaatctatta gatatggggt tcctattatc gccatgccaa tgcaattcga tcaaccttac 1080
aatgctaggt tgatggaaac tgttggtgca ggtatcgaag ttggcagaga tggcgaaggt 1140
agattgaaaa gagaagagat tgctgccgtg gttagaaagg tcgttgttga agattctggg 1200
gaatccataa gggagaaggc aaaggaattg ggagaaatca tgaaaaaaaa catggaggcc 1260
gaagtagatg gtatagtgat tgaaaaatta gttaagctat gtgagatgaa caattaa 1317

<210> 71

<211> 477

<212> PRT

<213> Arabidopsis thaliana

<400> 71

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

Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly
20 25 30

Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val
35 40 45

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♀

Amended Sequence
Lys Cys Ser Val Lys Val Gln Gln Gln Gln Gln Pro Pro Pro Ala Trp
50 55 60

Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro
65 70 75 80

Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr
85 90 95

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

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

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

Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly
145 150 155 160

Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val
165 170 175

Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala
180 185 190

Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile
195 200 205

Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys
210 215 220

Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln
225 230 235 240

Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly
245 250 255

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

Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr
275 280 285

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

His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His
305 310 315 320

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♀
Amended Sequence
Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val
325 330 335

Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr
340 345 350

Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg
355 360 365

Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn
370 375 380

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

Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu
405 410 415

Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val
420 425 430

Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser
435 440 445

Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala
450 455 460

Asn Val Gln Leu Ser Ser Gly Ala Arg Pro Val His Ala
465 470 475

<210> 72
<211> 440
<212> PRT
<213> Leishmania infantum
<400> 72
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
Page 137

♀
Amended Sequence
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

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
Page 138

♀
Amended Sequence
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

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> 73
<211> 527
<212> PRT
<213> Saccharomyces cerevisiae
<400> 73
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

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♀

Amended Sequence

Tyr Met Pro Leu Pro Val Gly Val Ile Gly Pro Leu Val Ile Asp Gly
165 170 175

Thr Ser Tyr His Ile Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala
180 185 190

Ser Ala Met Arg Gly Cys Lys Ala Ile Asn Ala Gly Gly Gly Ala Thr
195 200 205

Thr Val Leu Thr Lys Asp Gly Met Thr Arg Gly Pro Val Val Arg Phe
210 215 220

Pro Thr Leu Lys Arg Ser Gly Ala Cys Lys Ile Trp Leu Asp Ser Glu
225 230 235 240

Glu Gly Gln Asn Ala Ile Lys Lys Ala Phe Asn Ser Thr Ser Arg Phe
245 250 255

Ala Arg Leu Gln His Ile Gln Thr Cys Leu Ala Gly Asp Leu Leu Phe
260 265 270

Met Arg Phe Arg Thr Thr Thr Gly Asp Ala Met Gly Met Asn Met Ile
275 280 285

Ser Lys Gly Val Glu Tyr Ser Leu Lys Gln Met Val Glu Glu Tyr Gly
290 295 300

Trp Glu Asp Met Glu Val Val Ser Val Ser Gly Asn Tyr Cys Thr Asp
305 310 315 320

Lys Lys Pro Ala Ala Ile Asn Trp Ile Glu Gly Arg Gly Lys Ser Val
325 330 335

Val Ala Glu Ala Thr Ile Pro Gly Asp Val Val Arg Lys Val Leu Lys
340 345 350

Ser Asp Val Ser Ala Leu Val Glu Leu Asn Ile Ala Lys Asn Leu Val
355 360 365

Gly Ser Ala Met Ala Gly Ser Val Gly Gly Phe Asn Ala His Ala Ala
370 375 380

Asn Leu Val Thr Ala Val Phe Leu Ala Leu Gly Gln Asp Pro Ala Gln
385 390 395 400

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

Asp Leu Arg Ile Ser Val Ser Met Pro Ser Ile Glu Val Gly Thr Ile

420 425 430
Page 140

♀
Amended Sequence

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> 74
<211> 1226
<212> PRT
<213> Ganoderma lucidum
<400> 74
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

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

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♀
Amended Sequence

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

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

♀

Amended Sequence

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

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

♀
Amended Sequence

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
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

♀
Amended Sequence

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

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

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♀
Amended Sequence

Gln Gly Tyr Val Val Glu Ala Lys
1220 1225

<210> 75
<211> 888
<212> PRT
<213> Bos taurus
<400> 75
Met Leu Ser Arg Leu Phe Arg Met His Gly Leu Phe Val Ala Ser His
1 5 10 15

Pro Trp Glu Val Ile Val Gly Thr Val Thr Leu Thr Ile Cys Met Met
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

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

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♀
Amended Sequence
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
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

♀
Amended Sequence
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

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

♀
Amended Sequence
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
885

<210> 76
<211> 567
<212> PRT

<213> Artemisia annua
<400> 76
Met Asp Leu Arg Arg Lys Leu Pro Pro Lys Pro Pro Ser Ser Thr Thr
1 5 10 15

Thr Lys Gln Pro Ser His Arg Ser His Ser Pro Thr Pro Ile Pro Lys
20 25 30

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

♀
Amended Sequence
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 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

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
Page 150

♀
Amended Sequence

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
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
545 550 555 560

Ser Ala Ile Ala Ser Lys Val
565

<210> 77
<211> 435
<212> PRT
<213> Trypanosoma cruzi
<400> 77
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
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♀
Amended Sequence

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

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

♀
Amended Sequence

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
420 425 430

Lys Lys Lys
435

<210> 78
<211> 426
<212> PRT
<213> Staphylococcus aureus
<400> 78
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

♀
Amended Sequence

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

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

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♀
Amended Sequence

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> 79
<211> 481
<212> PRT
<213> Arabidopsis thaliana
<400> 79
Met His Ile Thr Lys Pro His Ala Ala Met Phe Ser Ser Pro Gly Met
1 5 10 15

Gly His Val Ile Pro Val Ile Glu Leu Gly Lys Arg Leu Ser Ala Asn
20 25 30

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

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

Pro Ser Pro Asp Ile Tyr Gly Leu Val Asp Pro Asp Asp His Val Val
65 70 75 80

Thr Lys Ile Gly Val Ile Met Arg Ala Ala Val Pro Ala Leu Arg Ser
85 90 95

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

Phe Gly Thr Asp Ala Leu Cys Leu Ala Lys Glu Phe Asn Met Leu Ser
115 120 125

Tyr Val Phe Ile Pro Thr Asn Ala Arg Phe Leu Gly Val Ser Ile Tyr
130 135 140

Tyr Pro Asn Leu Asp Lys Asp Ile Lys Glu Glu His Thr Val Gln Arg
145 150 155 160

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

Leu Asp Ala Tyr Leu Val Pro Asp Glu Pro Val Tyr Arg Asp Phe Val
180 185 190

Arg His Gly Leu Ala Tyr Pro Lys Ala Asp Gly Ile Leu Val Asn Thr
195 200 205

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♀
Amended Sequence
Trp Glu Glu Met Glu Pro Lys Ser Leu Lys Ser Leu Leu Asn Pro Lys
210 215 220

Leu Leu Gly Arg Val Ala Arg Val Pro Val Tyr Pro Ile Gly Pro Leu
225 230 235 240

Cys Arg Pro Ile Gln Ser Ser Glu Thr Asp His Pro Val Leu Asp Trp
245 250 255

Leu Asn Glu Gln Pro Asn Glu Ser Val Leu Tyr Ile Ser Phe Gly Ser
260 265 270

Gly Gly Cys Leu Ser Ala Lys Gln Leu Thr Glu Leu Ala Trp Gly Leu
275 280 285

Glu Gln Ser Gln Gln Arg Phe Val Trp Val Val Arg Pro Pro Val Asp
290 295 300

Gly Ser Cys Cys Ser Glu Tyr Val Ser Ala Asn Gly Gly Gly Thr Glu
305 310 315 320

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

Asp Arg Gly Phe Val Val Pro Ser Trp Ala Pro Gln Ala Glu Ile Leu
340 345 350

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

Thr Leu Glu Ser Val Val Gly Gly Val Pro Met Ile Ala Trp Pro Leu
370 375 380

Phe Ala Glu Gln Asn Met Asn Ala Ala Leu Leu Ser Asp Glu Leu Gly
385 390 395 400

Ile Ala Val Arg Leu Asp Asp Pro Lys Glu Asp Ile Ser Arg Trp Lys
405 410 415

Ile Glu Ala Leu Val Arg Lys Val Met Thr Glu Lys Glu Gly Glu Ala
420 425 430

Met Arg Arg Lys Val Lys Lys Leu Arg Asp Ser Ala Glu Met Ser Leu
435 440 445

Ser Ile Asp Gly Gly Gly Leu Ala His Glu Ser Leu Cys Arg Val Thr
450 455 460

Lys Glu Cys Gln Arg Phe Leu Glu Arg Val Val Asp Leu Ser Arg Gly
465 470 475 480

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♀
Amended Sequence

Ala

<210> 80
<211> 513
<212> PRT
<213> Arabidopsis thaliana
<400> 80
Met Gly Ala Tyr Glu Thr Glu Lys Pro Thr Lys Asp Ala Ala Ala Leu
1 5 10 15

Glu Thr Gln Ser Pro Glu Asp Phe Asp Gln Pro Ser Pro Leu Arg Lys
20 25 30

Ile Ile Ser Val Ala Ser Ile Ala Ala Gly Val Gln Phe Gly Trp Ala
35 40 45

Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln Leu Leu Gly Ile Pro
50 55 60

His Lys Trp Ser Ser Leu Ile Trp Leu Cys Gly Pro Val Ser Gly Met
65 70 75 80

Ile Val Gln Pro Ile Val Gly Phe His Ser Asp Arg Cys Arg Ser Lys
85 90 95

Phe Gly Arg Arg Arg Pro Phe Ile Ala Thr Gly Ala Ala Leu Val Ala
100 105 110

Val Ala Val Phe Leu Ile Gly Tyr Ala Ala Asp Phe Gly Tyr Lys Met
115 120 125

Gly Asp Lys Leu Glu Glu Lys Val Lys Val Arg Ala Ile Gly Ile Phe
130 135 140

Ala Leu Gly Phe Trp Ile Leu Asp Val Ala Asn Asn Thr Leu Gln Gly
145 150 155 160

Pro Cys Arg Ala Phe Leu Ala Asp Leu Ala Ala Gly Asp Ala Lys Arg
165 170 175

Thr Arg Val Ala Asn Ala Phe Phe Ser Phe Phe Met Ala Val Gly Asn
180 185 190

Val Leu Gly Tyr Ala Ala Gly Ser Tyr Thr Asn Leu His Lys Met Phe
195 200 205

Pro Phe Thr Met Thr Lys Ala Cys Asp Ile Tyr Cys Ala Asn Leu Lys
210 215 220

Thr Cys Phe Phe Leu Ser Ile Thr Leu Leu Leu Ile Val Thr Val Thr
Page 157

♀
Amended Sequence

225 230 235 240

Ser Leu Trp Tyr Val Asn Asp Lys Gln Trp Ser Pro Pro Pro Arg Asn
245 250 255

Ala Asp Asp Asp Glu Lys Thr Ser Ser Val Pro Leu Phe Gly Glu Ile
260 265 270

Phe Gly Ala Phe Lys Val Met Lys Arg Pro Met Trp Met Leu Leu Ile
275 280 285

Val Thr Ala Leu Asn Trp Ile Ala Trp Phe Pro Phe Leu Leu Phe Asp
290 295 300

Thr Asp Trp Met Gly Arg Glu Val Phe Gly Gly Asp Ser Asp Gly Asn
305 310 315 320

Glu Arg Ser Lys Lys Leu Tyr Ser Leu Gly Val Gln Ser Gly Ala Met
325 330 335

Gly Leu Met Phe Asn Ser Ile Val Leu Gly Phe Met Ser Leu Gly Val
340 345 350

Glu Trp Ile Gly Arg Lys Leu Gly Gly Ala Lys Arg Leu Trp Gly Ile
355 360 365

Val Asn Phe Ile Leu Ala Ala Gly Leu Ala Met Thr Val Leu Val Thr
370 375 380

Lys Phe Ala Glu Asp His Arg Lys Thr Ala Gly Asp Leu Ala Gly Pro
385 390 395 400

Ser Ala Ser Val Lys Ala Gly Ala Leu Ser Leu Phe Ala Val Leu Gly
405 410 415

Ile Pro Leu Ala Ile Thr Phe Ser Thr Pro Phe Ala Leu Ala Ser Ile
420 425 430

Phe Ser Ser Cys Ser Gly Ala Gly Gln Gly Leu Ser Leu Gly Val Leu
435 440 445

Asn Leu Ala Ile Val Ile Pro Gln Met Ile Val Ser Leu Gly Gly Gly
450 455 460

Pro Phe Asp Ala Leu Phe Gly Gly Gly Asn Leu Pro Ala Phe Ile Val
465 470 475 480

Ala Ala Ile Ala Ala Ala Ile Ser Gly Val Leu Ala Leu Thr Val Leu
485 490 495

Pro Ser Pro Pro Pro Asp Ala Pro Lys Ala Thr Thr Met Gly Gly Phe

♀
Amended Sequence

500 505

510

His

<210> 81
<211> 806
<212> PRT
<213> Coffea arabica
<400> 81
Met Ala Glu Arg Val Leu Thr Arg Val His Ser Leu Arg Glu Arg Leu
1 5 10 15

Asp Ala Thr Leu Ala Ala His Arg Asn Asp Val Leu Leu Phe Met Ser
20 25 30

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

Ala Glu Phe Glu Glu Ile Asn Lys Asp Gly Lys Gln Lys Ile His Asp
50 55 60

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

Pro Pro Trp Val Ala Leu Ala Ile Arg Leu Arg Pro Gly Val Trp Glu
85 90 95

Tyr Val Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val
100 105 110

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

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

Pro Lys Pro Thr Leu Thr Lys Tyr Ile Gly Asp Gly Val Glu Phe Leu
145 150 155 160

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

Pro Leu Leu Asp Phe Leu Arg Val His Gln Tyr Lys Gly Lys Thr Met
180 185 190

Met Leu Asn Asp Arg Ile Lys Asp Leu Asn Thr Leu Gln Ala Val Leu
195 200 205

Arg Lys Ala Glu Glu Tyr Leu Thr Thr Leu Ser Ala Asp Thr Pro Tyr
210 215 220

♀
Amended Sequence

Ser Glu Phe Glu His Lys Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp
225 230 235 240

Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Cys Met Leu Leu Asp
245 250 255

Leu Leu Gly Ala Pro Asp Ser Cys Thr Leu Glu Lys Phe Leu Gly Arg
260 265 270

Ile Pro Met Val Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe
275 280 285

Ala Gln Glu Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val
290 295 300

Tyr Ile Leu Asp Gln Val Pro Ala Leu Glu Arg Glu Met Leu Lys Arg
305 310 315 320

Ile Lys Glu Gln Gly Leu Asp Val Lys Pro Arg Ile Leu Ile Ile Thr
325 330 335

Arg Leu Leu Pro Asp Ala Pro Gly Thr Thr Cys Gly Gln Arg Leu Glu
340 345 350

Lys Val Tyr Gly Ser Glu Tyr Ser His Ile Leu Arg Val Pro Phe Arg
355 360 365

Thr Glu Lys Gly Val Val Arg Lys Trp Ile Ser Arg Phe Glu Val Trp

370 375 380

Pro Tyr Met Glu Thr Phe Thr Glu Asp Val Ala Lys Glu Val Thr Ala
385 390 395 400

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

Asn Leu Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys
420 425 430

Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp Ile
435 440 445

Tyr Leu Ser Lys Phe Asp Glu Lys Tyr His Phe Ser Cys Gln Phe Thr
450 455 460

Ala Asp Leu Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr
465 470 475 480

Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu Ser
485 490 495
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♀
Amended Sequence

His Met Ala Phe Thr Met Pro Gly Leu Tyr Arg Val Val His Gly Ile
500 505 510

Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Thr
515 520 525

Asn Leu Tyr Phe Pro His Thr Glu Lys Glu Lys Arg Leu Thr Ser Phe
530 535 540

His Pro Glu Ile Glu Glu Leu Leu Phe Ser Asp Val Glu Asn Glu Glu
545 550 555 560

His Leu Cys Val Leu Lys Asp Lys Lys Lys Pro Ile Leu Phe Thr Met
565 570 575

Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val Glu Leu Tyr
580 585 590

Ala Lys Asn Pro Lys Leu Arg Glu Leu Val Asn Leu Val Val Val Gly
595 600 605

Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu Gln Ala Glu Met
610 615 620

Lys Lys Met Tyr Ser Leu Ile Glu Thr Tyr Asn Leu Asn Gly Gln Phe
625 630 635 640

Arg Trp Ile Ser Ser Gln Met Asn Arg Val Arg Asn Gly Glu Leu Tyr
645 650 655

Arg Tyr Ile Ala Asp Thr Arg Gly Ala Phe Val Gln Pro Ala Phe Tyr
660 665 670

Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu Pro
675 680 685

Thr Phe Ala Thr Asn His Gly Gly Pro Ala Glu Ile Ile Ile His Gly
690 695 700

Lys Ser Gly Phe His Ile Asp Pro Tyr His Gly Glu Gln Val Ser Glu
705 710 715 720

Leu Leu Ala Asn Phe Phe Glu Arg Cys Lys Lys Glu Pro Ser Tyr Trp
725 730 735

Asp Thr Ile Ser Ala Gly Gly Leu Lys Arg Ile Gln Glu Lys Tyr Thr
740 745 750

Trp Gln Ile Tyr Ser Asp Arg Leu Leu Thr Leu Ala Gly Val Tyr Gly
755 760 765
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♀
Amended Sequence
Phe Trp Lys Cys Val Ser Lys Leu Asp Arg Gln Glu Ile Arg Arg Tyr
770 775 780
Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Leu Ala Glu Ala Val
785 790 795 800
Pro Leu Ala Val Asp Gln
805
<210>
<211>
<212>
<213>
82
19
DNA
Artificial sequence
<220>
<223> Synthetic oligonucleotide
<400> 82
tgaattcgtt aacgaattc 19
<210>
<211>
<212>
<213>
83
19
DNA
Artificial sequence
<220>
<223> Synthetic oligonucleotide
<400> 83
tgaattcgtt aacgaactc 19
<210>
<211>
<212>
<213>
84
19
DNA
Artificial sequence
<220>
<223> Synthetic oligonucleotide
<400> 84
tgaattcgtt aacgaagtc 19
<210>
<211>
<212>
<213>
85
19
DNA
Artificial sequence
<220>
<223> Synthetic oligonucleotide
<400> 85
tgaattcgtt aacgaaatt 19
<210>

<211>
<212>
<213>
86
473
PRT
Stevia rebaudiana
<400> 86
Page 162

♀
Amended Sequence

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 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 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 Val 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

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♀
Amended Sequence

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> 87
<211> 21
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic oligonucleotide
<400> 87
cggtaggtat tgattgtaat t 21
<210> 88
<211> 21
<212>
DNA
Page 164
♀
Amended Sequence

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 88
cttttcggtt agagcggatg t 21

<210> 89

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 89
atggctacat ctgattctat tgttgatgac aggaagcagt tgcatgtggc tactttccct 60
tggcttgctt tcggtcatat actgccttac ctacaactat caaaactgat agctgaaaaa 120
ggacataaag tgtcattcct ttcaacaact agaaacattc aaagattatc ttcccacata 180
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♀
Amended Sequence

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide

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<210> 91

<211> 1503

<212> DNA

<213> Stevia rebaudiana

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♀
Amended Sequence
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<211> 436

<212> PRT

<213> Archaeoglobus fulgidus

<400> 92

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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
Page 167

♀
Amended Sequence
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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

Lys Gly Asn Leu Val Gly Thr Ile Glu Ile Pro Met Ala Val Gly Val
Page 168

♀
Amended Sequence
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
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<210> 93
<211> 428
<212> PRT
<213> Pseudomonas mevalonii
<400> 93
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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

♀
Amended Sequence

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

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

Page 170

♀
Amended Sequence

Asp Trp Val Ala Arg Gln Leu Val Glu Tyr His Asp Val Arg Ala Asp
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Arg Ala Val Ala Leu Leu Lys Gln Lys Arg Gly Gln
420 425

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<211> 1323

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

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tggggtaatg ttgtacttca aggatcagct cataactgcg ccagagaaat agttatcgac 240
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<210> 95

<211>
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♀
Amended Sequence

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

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<210> 96

<211> 3681

<212> DNA

<213> Artificial Sequence

<220>
Page 172

♀
Amended Sequence

<223> Synthetic oligonucleotide

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Page 173

♀
Amended Sequence
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tctcaattga atacaccaat gccatccaga ccacatactc ctggccctga ggatgtctca 3600
catgtgcagc agctacctac accatctgca tctgatgata aaggtgttac agctcaaggt 3660
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<210> 97

<211> 2667

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

♀
Amended Sequence

<400> 97
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gacatcatca tacttactat aacaagatgc attgcaatat tgtatatcta cttccaattt 240
caaaacctta gacaattggg tagtaaatac atcctaggca tcgccggatt gttcactatt 300
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ttgaacgaag ctctaccatt cttcttgctg ctggtagatt tgtccagagc ttccgcttta 420
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♀
Amended Sequence
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ttaaagacca caacagaagc tatgattgaa gtaaacataa acaaaaactt agtagggtct 2220
gccatggctg gttcaattgg aggatacaac gctcatgctg ccaatattgt aaccgctatc 2280
tacatcgcat gtggacaaga tgctgcccaa aatgtcggtt cctcaaattg catcacattg 2340
atggaagcat ctggccctac aaacgaggat ttgtatatca gttgcacaat gccatctata 2400
gaaataggga ctgtgggagg aggaactaac ttacttccac agcaagcctg cttacaaatg 2460
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cacctggtga gatctcatat gattcataat agaagtaaga ttaaccttca agatttgcaa 2640
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<210> 98

<211> 1704

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 98
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ctatccgcaa ttgtactgct gattgcttcc ttcatctatc ttttaggctt tttcggtatt 300
gattttgtgc aatctttcac atcaagagaa aatgagcaac taaacaacga tgatcacaac 360
gtcgtgtcaa caaacaatgt tttatctgat agaaggttag tttacgacta tggattcgat 420
gtgacaggag acaacgataa cgataatgat gacgatgtta ttgtgaaaag tgtcgtttct 480
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gatacattgt ctgttgtctt taacaaaagt tctagatttg ccagattgca aaacatccaa 960
tgctcaattg ccggtaaaaa cttgtacatt aggtttactt gctccacagg cgacgccatg 1020
ggtatgaaca tggtttcaaa aggagtacaa aatgtattag acttttaca aaatgatttt 1080

♀
Amended Sequence
cctgatatgg acgtaattgg gatctcttgg aagttctgct ctgacaaaaa gccaacagct 1140
gtcaactgga ttgagggcag aggaaagtct gtcgttttcc aggccgtaat taccaaaaag 1200
gtggttagaa agtctgcact gaaccctcaa acttgcacat gtagaacttt gacctgttta 1260
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ataagtgctg ggcaagtagt taaatctcat atgaaataca ataggtctag tagagatatg 1680
tcagcaatag cttctaaggt ctaa 1704

<210> 99

<211> 1308

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 99
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ccaataccac tgggcgttgc tggccctatt ttgattgatg gtaaagagta cccaatacca 360
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tgtatcacta caatgtccaa ggtaggtaac gatctattga tctctgtgac cattgccttct 1080

♀
Amended Sequence
atcgaggtcg gggtcgtggg aggagggact ggtcttgctg cccaaaggtgg atgcttagag 1140
ttaatagggt gcggaggccc atctaaggag tctcctggta ctaatgccca acttctaagt 1200
agagttgttg cagctggcgt tttatcagcc gaactttcct tgatgtccgg actggcagca 1260
ggtcatctat tgtcagcaca tatgagattg aacagaaaga agaaataa 1308

<210> 100

<211> 1281

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

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gatgaagagg tagcaaactc attgatagaa aatgtcatcg cacagggcgc actgcctgtt 180
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gataccgaga aactgtctgc agatatcaag gctcttgaaa aacaaatcca tcagattgca 420
gatgaggctt acccttctat taaggccaga ggtggaggct atcaaaggat cgccatcgat 480
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gccgaagtac taaagcaaga gccaagagca aacactcaag ttgcagagag aattttgcaa 1260
gatttggaa gtcaacaata a 1281

<210> 101

<211> 1311

<212> DNA

<213>
Artificial Sequence
Page 178

♀
Amended Sequence

<220>

<223> Synthetic oligonucleotide

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atggctggag ctactggaga tgaggttgac agagttgtag agattatggt gagagatggc 1260
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<210> 102

<211> 1287

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

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ccatatgcag tggccagtaa ctttcagatc aatggccgtg acgtcttagt accattagtt 240
gtggaggaac ctagtatcgt tgctgcagcc tcttacatgg caaagttagc tagagccaat 300
Page 179

♀
Amended Sequence
ggtgggttca ctacatcttc atctgctcca ctaatgcatg cacaagtaca aattgtcggc 360
attcaggatc cactaaacgc aagattgtct ttactgcgta gaaaggatga gatcatagaa 420
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ttactgaaac agaagagagg tcaataa 1287

<210> 103

<211> 2355

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 103
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ataatcgata cgaccaagga gagaatacaa aaacaattca aaaatgttga aatttcagtt 180
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tgtcattcaa acgaaatgga tggttaccta gcttatattt ctgaaggtct tggtaatctt 660
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♀
Amended Sequence
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gaggagcaaa gataa 2355

<210> 104

<211> 2355

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 104
atgaatctgt ccctttgtat agctagtcca ctgttgacaa aatcttctag accaactgct 60
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♀
Amended Sequence

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ataatcgata ctactaagga gagaatccaa aagctattca aaaatgttga aattctcagta 180
tcatcttatg acaccgcatg ggttgcaatg gtgccatcac ctaattcccc taaaagtcca 240
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tactttgttg ggccaaagtt atccgaagag attgttgagt cttccgaata tcataaccta 1980
ttcaagttaa tgtcaacacc aggcagactt ctgaacgata tccactcctt caaaagagaa 2040
ttcaaggaag gtaagctaaa cgctgttgct ttgcacttgt ctaatggtga atctggcaaa 2100

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♀
Amended Sequence
gtggaagagg aagtcgttga ggaaatgatg atgatgatca aaaacaagag aaaggaattg 2160
atgaaattga ttttcgagga aaatggttca atcgtaccta gagcttgtaa agatgctttt 2220
tggaatatgt gccatgttct taacttcttt tacgctaatg atgatggctt cactggaaat 2280
acaatattgg atacagttaa agatatcatc tacaacccac ttgttttggt caatgagaac 2340
gaggaactaa gataa 2355

<210> 105

<211> 1773

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 105
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ttctcatccg gtggccatgc tttgagattc gggagtagtc tgccatgttg gagaaggacc 120
cctacccaaa gatctacttc ttcctctact actagaccag ctgccgaagt gtcatcaggt 180
aagagtaaac aacatgatca ggaagctagt gaagcgacta tcagacaaca attacaactt 240
gtggatgtcc tggagaatat gggaatatcc agacattttg ctgcagagat aaagtgcatt 300
ctagacagaa cttacagatc ttggttacaa agacacgagg aaatcatgct ggacactatg 360
acatgtgcta tggcttttag aatcctaaga ttgaacggat acaacgtttc atcagatgaa 420
ctataccacg ttgtagaggc atctggtctg cataattctt tgggtgggta tcttaacgat 480
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ggcgcactga gaaagccttc tttattcaaa gaggttgaac atgcactgga tggaccttt 660
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caacacatgt tggagactcc atacttatct aaccagcata catcaaggga tatcctagca 780
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gttttaccag ctttgtattt cgttggtcca aagatttcag aaagtatagt aaaggaccca 1380
gaatatgatg aattgttcaa actaatgtca acatgtggta gattgttgaa tgacgtgcaa 1440

♀
Amended Sequence
acgttcgaaa gagaatacaa tgagggtaaa ctgaattctg tcagtctatt ggttcttcac 1500
ggaggcccaa tgtctatttc agacgcaaag aggaaattac aaaagcctat tgatacgtgt 1560
agaagagatc ttctttcttt ggtccttaga gaagagtctg tagtaccaag accatgtaag 1620
gaactattct ggaaaatgtg taaagtgtgc catttctttt actcaacaac tgatgggttt 1680
tctagtcaag tcgaaagagc aaaagaggta gacgctgtca taaatgagcc actgaagttg 1740
caaggttctc atacactggt atctgatgat taa 1773

<210> 106

<211> 2232

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 106
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acaccttgtt ttccagaatg tactaaatgg atcctagaaa atcagttggg tgatggtagt 180
tggtcacttg ctcatggcaa tccacttcta gttaaagatg cattatcttc cactcttgct 240
tgtattctgg ctcttaaaag atggggaatc ggtgaggaac agattaacaa aggactgaga 300
ttcatagaac tcaactctgc tagtgtaacc gataacgaac aacacaaacc aattggattt 360
gacatttctt ttccaggtat gattgaatac gctatagact tagacctgaa tctaccacta 420
aaacgactg acattaactc catgttgcat cgtagagccc ttgaattgac atcaggtgga 480
ggcaaaaatc tagaaggtag aagagcttac ttggcctacg tctctgaagg aatcggtaag 540
ctgcaagatt gggaaatggc tatgaaatac caacgtaaaa acggatctct gttcaatagt 600
ccatcaacaa ctgcagctgc attcatccat atacaagatg ctgaatgcct ccactatatt 660

cgttctcttc tccagaaatt tggaaacgca gtccctacaa tataccctct cgatatctat 720
gccagacttt caatggtaga tgccctggaa cgtcttggta ttgatagaca tttcagaaag 780
gagagaaagt tcgttctgga tgaaacatac agattttggt tgcaaggaga agaggagatt 840
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gctaacttac aaagattagc tattcgtaga aggattaagc attacgctac tgacgataca 1200
aggattctaa aaacttccta cagatgctca acaatcggta accaagattt tctaaaactt 1260
gcagtggaag atttcaatat ctgtcaatca atacaaagag aggaattcaa gcatattgaa 1320
agatgggtcg ttgaaagacg tctagacaag ttaaagttcg ctagacaaaa agaggcctat 1380

♀
Amended Sequence
tgctatttct cagccgcagc aacattgttt gcccctgaat tgtctgatgc tagaatgtct 1440
tgggccaaaa atggtgtatt gacaactgtg gttgatgatt tcttcgatgt cggacgctct 1500
gaagaggaat tagttaactt gatagaattg atcgagcgtt gggatgtgaa tgggagtgca 1560
gatttttgta gtgaggaagt tgagattatc tattctgcta tccactcaac tatctctgaa 1620
ataggtgata agtcatttgg ctggcaaggt agagatgtaa agtctcaagt tatcaagatc 1680
tggctggact tattgaaatc aatgttaact gaagctcaat ggtcttcaaa taagtctgtt 1740
cctaccctag atgagtatat gacaaccgcc catgtttcat tcgcacttgc tccaattgta 1800
cttccagcct tatacttcgt tggcccaaag ttgtcagaag aggttgcagg tcatcctgaa 1860
ctactaaacc tctacaaagt cacatctact tgtggcagac tactgaagga ttggagaagt 1920
tttaagagag aatccgagga aggtaagctc aacgctatta gtttatccat gatccactcc 1980
ggtggtgctt ctacagaaga ggaaacaatc gaacatttca aaggttgat tgattctcag 2040
agaaggcaac tgttacaatt ggtgttgcaa gagaaggata gtatcatacc tagaccatgt 2100
aaagatctat tttggaatat gattaagtta ttacacactt tcttcatgaa agatgatggc 2160
ttcacctcaa atgagatgag gaatgtagtt aaggcaatca ttaacgaacc aatctcactg 2220
gatgaattat ga 2232

<210> 107

<211> 1542

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 107
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gctgtagcat tggcggtagc gctaatcttt tggtacctga aatcctacac atcagctaga 120
agatcccaat caaatcatct tcaaagagtg cctgaagtcc caggtgttcc attgttagga 180
aatctgttac aattgaagga gaaaaagcca tacatgactt ttacgagatg ggcagcgaca 240
tatggaccta tctatagtat caaaactggg gctacaagta tggttgtggt atcatctaat 300
gagatagcca aggaggcatt ggtgaccaga ttccaatcca tatctacaag gaacttatct 360
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tatcataaaa cagttaacag acacatactg accgccgtct tgggtcctaa tgcacagaaa 480
aagcatagaa ttcacagaga tatcatgatg gataacatat ctactcaact tcatgaattc 540
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ttcggcttag ctatgagaca agccttagga aaggatgttg aaagtttgta cgttgaagac 660
ctgaaaatca ctatgaatag agacgaaatc tttcaagtcc ttgttgttga tccaatgatg 720
ggagcaatcg atgttgattg gagagacttc tttccatacc taaagtgggt cccaaacaaa 780
aagttcgaaa atactattca acaaatgtac atcagaagag aagctgttat gaaatcttta 840

♀
Amended Sequence
atcaaagagc acaaaaagag aatagcgtca ggcgaaaagc taaatagtta tatcgattac 900
cttttatctg aagctcaaac tttaaccgat cagcaactat tgatgtcctt gtgggaacca 960
atcattgaat cttcagatac aacaatggtc acaacagaat gggcaatgta cgaattagct 1020
aaaaacccta aattgcaaga taggttgtac agagacatta agtccgtctg tggatctgaa 1080
aagataaccg aagagcatct atcacagctg ccttacatta cagctatttt ccacgaaaca 1140

ctgagaagac actcaccagt tcctatcatt cctctaagac atgtacatga agataccgtt 1200
ctaggcggct accatgttcc tgctggcaca gaacttgccg ttaacatcta cggttgcaac 1260
atggacaaaa acgtttggga aaatccagag gaatggaacc cagaaagatt catgaaagag 1320
aatgagacaa ttgattttca aaagacgatg gccttcggtg gtggtaagag agtttgtgct 1380
ggttccttgc aagccctttt aactgcatct attgggattg ggagaatggt tcaagagttc 1440
gaatggaaac tgaaggatat gactcaagag gaagtgaaca cgataggcct aactacacaa 1500
atgttaagac cattgagagc tattatcaaa cctaggatct aa 1542

<210> 108

<211> 1530

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 108
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ttgccaagtg ttccagtagt gcctggtttt ccagttattg ggaatttgtt gcaactaaag 180
gagaaaaagc ctcataaaac tttcactaga tggtcagaga tatatggtcc tatctactct 240
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acctgcgata agtctatggt cgccacttct gattatgatg acttccacaa attagttaag 420
agatgtttgc taaatggact tcttggtgct aatgctcaaa agaggaaaaag acactacaga 480
gatgctttga ttgaaaatgt gagttccaag ctacatgcac aggctagaga tcatccacaa 540
gagccagtta actttagagc aattttcgaa cacgaattgt ttggtgtagc attaaagcaa 600
gccttcggta aagacgtaga atccatatac gtcaaggagt taggcgtaac attatcaaaa 660
gatgaaatct ttaaggtgct tgtacatgat atgatggagg gtgcaattga tgtagattgg 720
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ttgactaagg aacagatcgc aatccttgtc tgggaaacaa tcattgaaac agcagatact 960
accttagtca caactgaatg ggccatatac gaggtagcca aacatccatc tgtgcaagat 1020

♀
Amended Sequence
aggttgtgta aggagatcca gaacgtgtgt ggtggagaga aattcaagga agagcagttg 1080
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gctgggtccg aaattgctat aaacacctac gggtgcaaca tggacaaaaa gagatgggaa 1260
agaccagaag attggtggcc agaaagattc ttagatgatg gcaaatatga aacatctgat 1320
ttgcataaaa caatggcttt cggagctggc aaaagagtgt gtgccggtgc tctacaagcc 1380
tccctaatgg ctggtatcgc tattggtaga ttggtccaag agttcgaatg gaaacttaga 1440
gatggtgaag aggaaaatgt cgatacttat gggttaacat ctcaaaagtt atacccacta 1500
atggcaatca tcaatcctag aagatcctaa 1530

<210> 109

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 109
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ttaggtttgg accgtatgcc attgatggat gttcactggt tgatctacgt tgctttcggc 120
gaatggttat gttcttatgt gatacatgtt ttatcatctt cctctacagt aaaagtgcca 180

gttgttggat acaggtctgt attcgaacct acatggttgc ttagacttag attcgtctgg 240
gaaggtggct ctatcatagg tcaagggtac aataagttta aagactctat tttccaagtt 300
aggaaattgg gaactgatat tgtcattata ccacctaact atattgatga agtgagaaaa 360
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gtgagattga tttccaggat ctccgccaga gtctttctag ggcctgaaca ctgtcgtaac 660
caggaatggt tgactactac agcagaatat tcagaatcac ttttcattac agggtttatc 720
ttaagagttg tacctcatat cttaagacca ttcatcgccc ctctattacc ttcatacagg 780
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aacagatttc ataagttgga ctccttccta aaagagtcac aaagattcaa cccagtactc 1140
ttattgacat tcaatagaat ctaccatcaa tctatgacct tatcagatgg cactaacatt 1200

♀
Amended Sequence
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ccaggtccaa ccccacctac tgaatttgat ggattcagat atagtaagat acgttctgat 1320
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gccatttttgt tgctacaatt tgagttcaaa ctaccagatg gtaaaggtcg tcctagaaat 1500
atcactatcg attctgatat gattccagac ccaagagcta gacttgcgct cagaaaaaga 1560
tcacttagag atgaatga 1578

<210> 110

<211> 1500

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 110
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ctatcttaca tcggcgcact aagatggaca agacgtggca gagagatact tcaagaggga 180
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atggacggat taggagcatt cgttccaaact aagtacacct taggtgaagc tattcataac 360
gatccatacc atgtcgatat cataagagaa aaactaacaa gaggccttcc agccgtgctt 420
cctgatgtca ttgaagagtt gacacttgcg gttagacagt acattccaac agaaggtgat 480
gaatgggtgt ccgtaaactg ttcaaaggcc gcaagagata ttgttgctag agcttctaat 540
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gttgctccat tggtggagga aagacgtaga cttatggaag agtacggtga agactggtct 780
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gccttagtat tcgatccttt cagattctca cgtatgagag cgagagaagg tgaaggtaca 1260
aagcactagt tcgttaatac ttcagtcgag tacgttccat ttggtcacgg aaagcatgct 1320

♀
Amended Sequence

tgtccaggaa gattcttcgc cgcaaacgaa ttgaaagcaa tgttggctta cattgttcta 1380
aactatgatg taaagttgcc tggtgacggt aaacgtccat tgaacatgta ttggggtcca 1440
acagttttgc ctgcaccagc aggccaagta ttgttcagaa agagacaagt tagtctataa 1500

<210> 111

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 111
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cctaaagcat ctggtgaaat cattccaatt acaggaatca tattgaatct gcatatctggc 180
tcaagtggtc tacctattat cttagcactt gcctctttag cagacagatg tggtcctatt 240
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gtaagagttt ttgaactaga aaactctatg aaatctatca gagaatcatg gaaggagaaa 540
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actgcttctg ttggcatgac aaatgccaaa gcatcacctt tagaagtctt gctatcacct 1560

♀
Amended Sequence
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<210> 112

<211> 1431

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 112
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ggtgaaacct tagccttact tagagcaggc tgggattctg agccagaaag attcgtaaga 180
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gttaccaact ttaagtggga tcttctaatc cctgatgaga agatcgaata tgatccaatg 1380
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<210> 113

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

♀
Amended Sequence

<223> Synthetic oligonucleotide

<400> 113
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tcactgaagc tacaaggtgt 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 aatcatatcc tctaatggtc ctcattgggc ccatcagcgt 480
agaattatcg cctacgagtt tactcatgat aagatcaagg gtatggttgg tttgatggtt 540
gagtctgcta tgcctatgtt gaatatgtgg gaggagatgg taaagagagg cggagaaatg 600
ggatgcgaca taagagttga tgaggacttg aaagatgttt cagcagatgt gattgcaaaa 660
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tctcctactt accaacatag tcctagtcac aaacttttag tagaaccaca acatggggtg 1560
gtaattagag tggtttaa 1578

<210> 114

<211> 1590

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 114
atgtacttcc tactacaata cctcaacatc acaaccgttg gtgtctttgc cacattgttt 60
Page 191

♀
Amended Sequence
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gctgccgctg catggcctat tatcggccac ctccacttac ttgcaggtgg atcccatcaa 180
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cagcgttgta gaagagtctt cagagaattc ttccatctct ccggcttctt tgtggttgct 720
gatgctatac cttttcttgg atggctcgat tggggaagac acgagaagac cttgaaaaag 780
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ttaggtctta cgaatatgaa atctacccca ttagaagttt tgatttctcc aagactatcc 1560
cttaattgct tcaaccttat gaaaatttga 1590

<210> 115

<211> 1440

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 115
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ctgtttttca tctttacaa acaaaagtcc ccattgaatt tgccaccagg gaaaatgggt 120

taccctatca taggtgaaag tttagaattc ctatccacag gctggaaggg acatcctgaa
180
Page 192

♀
Amended Sequence
aagttcatat ttgatagaat gcgtaagtac agtagtgagt tattcaagac ttctattgta 240
ggccaatcca cagttgtttg ctgtggggca gctagtaaca aattcctatt ctctaacgaa 300
aacaaactgg taactgcctg gtggccagat tctgttaaca aaatcttccc aacaacttca 360
ctggattcta atttgaagga ggaatctata aagatgagaa agttgctgcc acagttcttc 420

aaaccagaag cacttcaaag atacgtcggc gttatggatg taatcgcaca aagacatttt 480
gtcactcact gggacaacaa aaatgagatc acagtttatc cacttgctaa aagatacact 540
ttcttgcttg cgtgtagact gttcatgtct gttgaggatg aaaatcatgt ggcgaaattc 600
tcagacccat tccaactaat cgctgcaggc atcatttcac ttcctatcga tcttcctggt 660
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atcaaacaaa gacgtgttga tctggcagag ggtacagcat ctccaaccca ggatatcttg 780
tcacatatgc tattaacatc tgatgaaaac ggtaaatcta tgaacgagtt gaacattgcc 840
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cataatctgg tcaaacgttt taagtgggaa aaggttattc cagacgaaaa gattattgtc 1380
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<210> 116

<211> 2133

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 116
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aaggcaatgg aaaagttgaa cgctagtgaa tctgaagatt caacaacatt gcctgcacta 120
aagatgctag ttgaaaatag agaattgttg acactgttca caacttcctt cgcagttctt 180
attgggtgtc ttgtatttct aatgtggaga cgttcatcct ctaaaaagct ggtacaagat 240
ccagttccac aagttatcgt tgtaaagaag aaagaagaagg agtcagaggt tgatgacggg 300
aaaaagaaag tttctatttt ctacggcaca caaacaggaa ctgccgaagg ttttgctaaa 360
gcattagtcg aggaagcaaa agtgagatat gaaagagacct ctttcaaggt tatcgatcta 420
gatgactacg ctgcagatga tgatgaatat gaggaaaaac tgaaaaagga atccttagcc 480

♀
Amended Sequence
ttcttcttct tggccacata cggtgatggt gaacctactg ataatgctgc taacttctac 540
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tatgtctgtg gcgatgcaaa gggcatggcc aaggatgtcc atagaactct gcatacaatt 2040
gttcaggaac aagggagtct ggattcttcc aaggctgaat tgtacgtcaa aaacttacag 2100
atgtctggaa gatacttaag agatgtttgg taa 2133

<210> 117

<211> 2079

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 117
atgacttctg cactttatgc ctccgatctt ttcaaacaat tgaaaagtat catggaacg 60

♀
Amended Sequence

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ggtttcgttg tcttattgtg gaaaaagacc acggcagatc gttccgggga gctaaagcca 180
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ttacaaacag agggaagata cttgagagat gtgtggtaa 2079

♀
Amended Sequence

<210> 118

<211> 2142

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 118
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agggcaaaac aagccagaga tggtgtagaa gttggtaaaa cactgctgtt ctttggatgt 1740

♀
Amended Sequence
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<210> 119

<211> 2364

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 119
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aaagatggta aattcgtttg ctttgcaggg caatcaacac aagccgtgac aggaatgttt 1260
aacgtttaca gagcctctca aatgttgttc ccaggggaga gaattttgga agatgccaaa 1320

♀
Amended Sequence
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<210> 120

<211> 1584

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 120
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gccttccttc tggagagaca acacgaagac gggtcatggg gtccaccagg tggatatagg 240
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♀
Amended Sequence
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gatctattgt taccaccatt gtaa 1584

<210> 121

<211> 1551

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 121
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gctgaactga tcttgcctca gttttgtgga gaggctgctt ggttgttggg aggtgtggcc 420
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tggcctataa acgtattcga accatgctgg tcactgtaca ctctccatct tgccggtctg 780

♀
Amended Sequence
ttcgcccatc cagcactggc tgaggctgta agagttatcg ttgctcaact tgaagcaaga 840
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gaattgtact gtcctactag agtcgtaaga gtagctgagc tagctggcct gtggttagca 1500
ttaagatggg gcagaagagt attagctgaa ggtgctggtg ctgcacctta a 1551

<210> 122

<211> 2052

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 122
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aggccagaat acttgtatgg caaacaacca atgaccgcct tacattcatt agaggcttcc 600
ataggcaaaa tcgacttcga taaggtaaga caccaccgta cccatgggtc tatgatgggt 660
tctccttcat ctaccgcagc ctacttaatg cacgcttcac aatgggatgg tgactcagag 720
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gctttcccat caacacattt tgagtcatct tggattctta ccacattgtt tagagctgga 840
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tcattcgaga aggaaggtgg ggcaatcggt tacgctccag ggtttcaagc agatgttgat 960

♀
Amended Sequence

gatactgcta aaacaataag tacattagca gtccttggaa gagatgctac accaagacaa 1020
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tctttgacag ctaattgtaa tgctctatca gccttactac acgaaccaga tgcagcaatg 1140
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♀
Amended Sequence

<210> 123

<211> 2646

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 123
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♀
Amended Sequence
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gagtaa 2646

<210> 124

<211> 2859

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 124
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♀
Amended Sequence

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gatatgagaa agctgaaaat cgttaagtta ttctgtgatg ttacggactt atacgatcag 2820

♀
Amended Sequence
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<210> 125

<211> 1086

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 125
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gaaaagtcca gagaatttgc cgaaaaactt aacaaggaag cacaagagca attaagtggc 1020
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<210> 126

<211> 1029

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

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tcctcatctt ctgaaggcgg ttcatcgtct agatacgacg agagaagagt ctctttgcct 180
ctcagtcata atgctgcctc tccagatatt gtatcacaac tatgtttttc cactgcaatg 240

♀
Amended Sequence
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gtatggttgg aggttcgaga ggatgaaaca tcagtcatca aggaagttat tggtatgctc 420
cacaactctt cattagtcat tgatgacttc caagataatt ctccacttag aagaggaaag 480
ccatctaccc atacagtctt cggccctgcc caggctatca atactgctac ttacgttata 540
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atcgttccat caatacagga atacttactt atggtaaacg ataaaaccgg tgctctcttt 720
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ggcaagtact cactaacact tattcatgcc ctccaaactg attcatccga tctactgacc 960
aacatctttt caatgagaag agtgcaagga aagttaacgg cacaaaagag atgttggttc 1020
tggaaatga 1029

<210> 127

<211> 903

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

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gttcctgaag ataagttaca aatcattatt gaagtcacag aaatgctaca caatgcttct 180
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♀
Amended Sequence
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<210> 128

<211> 1020

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

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gccgaaactt ctttcagtct agatgaatac ttggcctcta agataggacc tatagagtct 180
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ttattgtcaa cttccttcga gcacgtcgct agagaaacaa aaggagtgtc agcagaaaag 540
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caagttatgg actttgaatg tgaagctaaa ccaggtacca cattagacga cttgaaatgg 660
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gagagtaagg catacgcaag acaactaatc gatgaagcca aggaaagttt ggctccttt 960
ggagatagtg ctgccccttt attggccatt gcagatttca ttattgatag aaagaattga 1020

<210> 129

<211> 1068

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 129
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actagaagag gctccccaac tgttcacaga gccctagctg atcgtttagg cgctgctctg 360

♀
Amended Sequence
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agactaagat gcgtattggt agcaactggt gcaagagccg aagccgaaag acttattaca 960
gagagaagag atcaagcatt aactgcattg aacgcattaa cactgccacc tcctttagct 1020
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<210> 130

<211> 993

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

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♀
Amended Sequence

<210> 131

<211> 894

<212> DNA

<213> Artificial Sequence

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<210> 132

<211> 1116

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

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gataacgatg atctgagaag gggtaagcca actaaccata aggttttcgg cgaagatgtt 540
Page 209

♀
Amended Sequence
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gccttagtca actacatcgc ttacagacaa aactaa 1116

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<211> 2340

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide

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♀
Amended Sequence
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<211> 777

<212> PRT

<213> Zea mays

<400> 134

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Thr Pro Ile Val Arg Thr Asp Ala Glu Ser Arg Arg Thr Arg Trp Pro
20 25 30

Thr Asp Asp Asp Asp Ala Glu Pro Leu Val Asp Glu Ile Arg Ala Met
35 40 45

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

Ala Trp Val Gly Leu Val Pro Arg Leu Asp Gly Gly Glu Gly Pro Gln
65 70 75 80

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♀
Amended Sequence

Phe Pro Ala Ala Val Arg Trp Ile Arg Asn Asn Gln Leu Pro Asp Gly
85 90 95

Ser Trp Gly Asp Ala Ala Leu Phe Ser Ala Tyr Asp Arg Leu Ile Asn
100 105 110

Thr Leu Ala Cys Val Val Thr Leu Thr Arg Trp Ser Leu Glu Pro Glu
115 120 125

Met Arg Gly Arg Gly Leu Ser Phe Leu Gly Arg Asn Met Trp Lys Leu
130 135 140

Ala Thr Glu Asp Glu Glu Ser Met Pro Ile Gly Phe Glu Leu Ala Phe
145 150 155 160

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

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

Met Lys Arg Ile Pro Lys Glu Val Met His Thr Val Pro Thr Ser Ile
195 200 205

Leu His Ser Leu Glu Gly Met Pro Gly Leu Asp Trp Ala Lys Leu Leu
210 215 220

Lys Leu Gln Ser Ser Asp Gly Ser Phe Leu Phe Ser Pro Ala Ala Thr
225 230 235 240

Ala Tyr Ala Leu Met Asn Thr Gly Asp Asp Arg Cys Phe Ser Tyr Ile
245 250 255

Asp Arg Thr Val Lys Lys Phe Asn Gly Gly Val Pro Asn Val Tyr Pro
260 265 270

Val Asp Leu Phe Glu His Ile Trp Ala Val Asp Arg Leu Glu Arg Leu
275 280 285

Gly Ile Ser Arg Tyr Phe Gln Lys Glu Ile Glu Gln Cys Met Asp Tyr
290 295 300

Val Asn Arg His Trp Thr Glu Asp Gly Ile Cys Trp Ala Arg Asn Ser
305 310 315 320

Asp Val Lys Glu Val Asp Asp Thr Ala Met Ala Phe Arg Leu Leu Arg
325 330 335

Leu His Gly Tyr Ser Val Ser Pro Asp Val Phe Lys Asn Phe Glu Lys
340 345 350

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♀
Amended Sequence

Asp Gly Glu Phe Phe Ala Phe Val Gly Gln Ser Asn Gln Ala Val Thr
355 360 365

Gly Met Tyr Asn Leu Asn Arg Ala Ser Gln Ile Ser Phe Pro Gly Glu
370 375 380

Asp Val Leu His Arg Ala Gly Ala Phe Ser Tyr Glu Phe Leu Arg Arg
385 390 395 400

Lys Glu Ala Glu Gly Ala Leu Arg Asp Lys Trp Ile Ile Ser Lys Asp
405 410 415

Leu Pro Gly Glu Val Val Tyr Thr Leu Asp Phe Pro Trp Tyr Gly Asn
420 425 430

Leu Pro Arg Val Glu Ala Arg Asp Tyr Leu Glu Gln Tyr Gly Gly Gly
435 440 445

Asp Asp Val Trp Ile Gly Lys Thr Leu Tyr Arg Met Pro Leu Val Asn
450 455 460

Asn Asp Val Tyr Leu Glu Leu Ala Arg Met Asp Phe Asn His Cys Gln
465 470 475 480

Ala Leu His Gln Leu Glu Trp Gln Gly Leu Lys Arg Trp Tyr Thr Glu
485 490 495

Asn Arg Leu Met Asp Phe Gly Val Ala Gln Glu Asp Ala Leu Arg Ala
500 505 510

Tyr Phe Leu Ala Ala Ala Ser Val Tyr Glu Pro Cys Arg Ala Ala Glu
515 520 525

Arg Leu Ala Trp Ala Arg Ala Ala Ile Leu Ala Asn Ala Val Ser Thr
530 535 540

His Leu Arg Asn Ser Pro Ser Phe Arg Glu Arg Leu Glu His Ser Leu
545 550 555 560

Arg Cys Arg Pro Ser Glu Glu Thr Asp Gly Ser Trp Phe Asn Ser Ser
565 570 575

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

Ser Leu Ala Arg Glu Ala Gln Pro Ile His Gly Gly Asp Pro Glu Asp
595 600 605

Ile Ile His Lys Leu Leu Arg Ser Ala Trp Ala Glu Trp Val Arg Glu
610 615 620

♀
Amended Sequence
Lys Ala Asp Ala Ala Asp Ser Val Cys Asn Gly Ser Ser Ala Val Glu
625 630 635 640
Gln Glu Gly Ser Arg Met Val His Asp Lys Gln Thr Cys Leu Leu Leu
645 650 655
Ala Arg Met Ile Glu Ile Ser Ala Gly Arg Ala Ala Gly Glu Ala Ala
660 665 670
Ser Glu Asp Gly Asp Arg Arg Ile Ile Gln Leu Thr Gly Ser Ile Cys
675 680 685
Asp Ser Leu Lys Gln Lys Met Leu Val Ser Gln Asp Pro Glu Lys Asn
690 695 700

Glu Glu Met Met Ser His Val Asp Asp Glu Leu Lys Leu Arg Ile Arg
705 710 715 720
Glu Phe Val Gln Tyr Leu Leu Arg Leu Gly Glu Lys Lys Thr Gly Ser
725 730 735
Ser Glu Thr Arg Gln Thr Phe Leu Ser Ile Val Lys Ser Cys Tyr Tyr
740 745 750
Ala Ala His Cys Pro Pro His Val Val Asp Arg His Ile Ser Arg Val
755 760 765
Ile Phe Glu Pro Val Ser Ala Ala Lys
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135
1555
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<223> Synthetic oligonucleotide
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♀
Amended Sequence
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♀
Amended Sequence

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<141> 2014-02-06

<150> US 61/761490
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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
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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
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Met Thr Ser Ser Leu Phe Asn Phe His Ala His Val Ser Leu Pro Gln
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Glu Lys Asp Phe Leu Glu Ile Ala Arg Gly Leu Val Asp Ser Lys Gln
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Ser Phe Leu Trp Val Val Arg Pro Gly Phe Val Lys Gly Ser Thr Trp
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Val Glu Pro Leu Pro Asp Gly Phe Leu Gly Glu Arg Gly Arg Ile Val
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Lys Trp Val Pro Gln Gln Glu Val Leu Ala His Gly Ala Ile Gly Ala
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Phe Trp Thr His Ser Gly Trp Asn Ser Thr Leu Glu Ser Val Cys Glu
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Gly Val Pro Met Ile Phe Ser Asp Phe Gly Leu Asp Gln Pro Leu Asn
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Gly Trp Glu Arg Gly Glu Ile Ala Asn Ala Ile Arg Arg Val Met Val
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Asp Glu Glu Gly Glu Tyr Ile Arg Gln Asn Ala Arg Val Leu Lys Gln
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Glu Ser Ala Met Leu Pro Thr Ile Ala Met Ile Met Glu Asn Arg Glu
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Leu Leu Met Ile Leu Thr Thr Ser Val Ala Val Leu Ile Gly Cys Val
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Val Val Leu Val Trp Arg Arg Ser Ser Thr Lys Lys Ser Ala Leu Glu
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Pro Pro Val Ile Val Val Pro Lys Arg Val Gln Glu Glu Glu Val Asp
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Asp Gly Lys Lys Lys Val Thr Val Phe Phe Gly Thr Gln Thr Gly Thr
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Glu Lys Ala Val Phe Lys Val Ile Asp Leu Asp Asp Tyr Ala Ala Asp
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Asp Asp Glu Tyr Glu Glu Lys Leu Lys Lys Glu Ser Leu Ala Phe Phe
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Phe Leu Ala Thr Tyr Gly Asp Gly Glu Pro Thr Asp Asn Ala Ala Arg
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Phe Tyr Lys Trp Phe Thr Glu Gly Asp Ala Lys Gly Glu Trp Leu Asn
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Lys Leu Gln Tyr Gly Val Phe Gly Leu Gly Asn Arg Gln Tyr Glu His
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Phe Asn Lys Ile Ala Lys Val Val Asp Asp Gly Leu Val Glu Gln Gly
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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
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370 375 380

Leu Gly Gly Ala Ser Leu Pro Pro Pro Phe Pro Pro Cys Thr Leu Arg
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Arg Leu Lys Phe Leu Ala Ser Pro Ala Gly Lys Asp Glu Tyr Ser Gln
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Glu Arg Leu Ala Leu Lys Glu Ala Gly Thr Asp Leu Gly Leu Ser Ile
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Ala Phe Ser Arg Glu Gly Pro Thr Lys Glu Tyr Val Gln His Lys Met
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Ser Glu Lys Ala Ser Asp Ile Trp Asn Leu Leu Ser Glu Gly Ala Tyr
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Leu Tyr Val Cys Gly Asp Ala Lys Gly Met Ala Lys Asp Val His Arg
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Thr Leu His Thr Ile Val Gln Glu Gln Gly Ser Leu Asp Ser Ser Lys
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gtattagagc ttttcaaggc tgcccaaagt taccctcatg agagtgcttt gaaaaagcag 1140

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agggacaagt acttgaaaaa ggaagtggag gatgctttgg catttccatc atatgcctct 1260

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tggatagtgg agaatagact acaggaatta aagttcgcca gacaaaaatt ggcttactgt 1500

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aatcaattat acaaattggt tagtaccatg ggtagactat taaacgatat ccagggcttt 2040

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gacaacagaa gcaaagaggt tattatagaa tccatgaaag gattggctga aaggaaaaga 2160

gaggaattac acaaacttgt actagaagag aaaggtagtg tcgttccaag agaatgcaag 2220

gaagccttct taaaaatgtc aaaagtgttg aacctttttt ataggaagga tgatggcttc 2280

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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

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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                 320

Leu Ala Phe Arg Leu Leu Leu Ala His Gly Tyr Asp Val Ser Tyr Asp
                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
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Asn Phe Cys Gln Ser Ile His Arg Glu Glu Met Glu Arg Leu Asp Arg
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Trp Ile Val Glu Asn Arg Leu Gln Glu Leu Lys Phe Ala Arg Gln Lys
                485                 490                 495

Leu Ala Tyr Cys Tyr Phe Ser Gly Ala Ala Thr Leu Phe Ser Pro Glu
            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
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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

Val Lys Ser Val Ile Tyr Glu Pro Val Ser Leu Gln Glu Glu Ser Leu
770 775 780

Thr
785

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attggacact tatacttact caaaaagcct ctttatagaa ctttagcaaa aattgccgct 180

aagtacggac caatactgca attacaactc ggctacagac gtgttctggt gatttcctca 240

ccatcagcag cagaagagtg ctttaccaat aacgatgtaa tcttcgcaaa tagacctaag 300

acattgtttg gcaaaatagt gggtggaaca tcccttggca gtttatccta cggcgatcaa 360

tggcgtaatc taaggagagt agcttctatc gaaatcctat cagttcatag gttgaacgaa 420

tttcatgata tcagagtgga tgagaacaga ttgttaatta gaaaacttag aagttcatct 480

tctcctgtta ctcttataac agtcttttat gctctaacat tgaacgtcat tatgagaatg 540

atctctggca aaagatattt cgacagtggg gatagagaat tggaggagga aggtaagaga 600

tttcgagaaa tcttagacga aacgttgctt ctagccggtg cttctaatgt tggcgactac 660

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aaagtaggca aaggtagaaa aacgatgatc gaactcttat tatctttgca agagtcagaa 840

cctgagtact atacagatgc tatgataaga tcttttgtcc taggtctgct ggctgcaggt 900

agtgatactt cagcgggcac tatggaatgg gccatgagct tactggtcaa tcacccacat 960

gtattgaaga aagctcaagc tgaaatcgat agagttatcg gtaataacag attgattgac 1020

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tatccagcag ggccattgtt gttcccacat gaaagttctg ccgactgcgt tatttccggt 1140

tacaatatac ctagaggtac aatgttaatc gtaaaccaat gggcgattca tcacgatcct 1200

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taa 1503

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<212> PRT
<213> Arabidopsis thaliana

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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 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

Leu Leu Asp Met Ser Pro Asp Thr Tyr Phe Ser Leu His Ala Glu Lys
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

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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
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<213> Artificial Sequence

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gaattgtctt caatgttgat cgaaaacaga caattcgcca tgatcgtaac tacatcaatc 180

gctgttttga tcggttgtat tgtcatgttg gtatggagaa gatccggtag tggtaattct 240

aaaagagtcg aacctttgaa accattagta attaagccaa gagaagaaga aatagatgac 300

ggtagaaaga aagttacaat atttttcggt acccaaactg gtacagctga aggttttgca 360

aaagccttag gtgaagaagc taaggcaaga tacgaaaaga ctagattcaa gatagtcgat 420

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gatattttgg tcgaacaagg tgctcaaaga ttagtccaag taggtttggg tgacgatgac 720

caatgtatag aagatgactt tactgcctgg agagaagctt tgtggcctga attagacaca 780

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tatttgtacg tttgcggtga cgcaaagggt atggccagag atgtccatag atctttgcac 2040

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<212> PRT
<213> Stevia rebaudiana

<400> 11

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

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 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 Glu Gly Lys Arg Phe Arg Glu Ile Leu Asp Glu Thr
        195                 200                 205
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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
        355                 360                 365

Pro His Glu Ser Ser Ala Asp Cys Val Ile Ser Gly Tyr Asn Ile Pro
    370                 375                 380

Arg Gly Thr Met Leu Ile Val Asn Gln Trp Ala Ile His His Asp Pro
385                 390                 395                 400

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
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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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<212> DNA
<213> Artificial Sequence

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gcaggaaggt ggagaagggc cttggctaga gcacagcaca catcagaatc cgcagctgtc 180

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actgattcat tagccaggga agcacagcca atccatggag gtgacccaga agatattata 1980

cacaagttgt taagatctgc ttgggccgag tgggttaggg aaaaggcaga cgctgccgat 2040

agcgtgtgca atggtagttc tgcagtagaa caagagggat caagaatggt ccatgataaa 2100

cagacctgtc tattattggc tagaatgatc gaaatttctg ccggtagggc agctggtgaa 2160

gcagccagtg aggacggcga tagaagaata attcaattaa caggctccat ctgcgacagt 2220

cttaagcaaa aaatgctagt ttcacaggac cctgaaaaaa atgaagagat gatgtctcac 2280

gtggatgacg aattgaagtt gaggattaga gagttcgttc aatatttgct tagactaggt 2340

gaaaaaaaga ctggatctag cgaaaccagg caaacatttt taagtatagt gaaatcatgt 2400

tactatgctg ctcattgccc acctcatgtc gttgatagac acattagtag agtgattttc 2460

gagccagtaa gtgccgcaaa gtaaccgcgg 2490

<210> 13
<211> 827
<212> PRT
<213> Zea mays

<400> 13

Met Val Leu Ser Ser Ser Cys Thr Thr Val Pro His Leu Ser Ser Leu
1 5 10 15

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

Asp Thr Val Ala Val Pro Ala Ala Ala Gly Arg Trp Arg Arg Ala Leu
35 40 45

Ala Arg Ala Gln His Thr Ser Glu Ser Ala Ala Val Ala Lys Gly Ser
50 55 60

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

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

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

Pro Glu Met Arg Gly Arg Gly Leu Ser Phe Leu Gly Arg Asn Met Trp
            180                 185                 190

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

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
        275                 280                 285

Ala Thr Ala Tyr Ala Leu Met Asn Thr Gly Asp Asp Arg Cys Phe Ser
    290                 295                 300

Tyr Ile Asp Arg Thr Val Lys Lys Phe Asn Gly Gly Val Pro Asn Val
305                 310                 315                 320

Tyr Pro Val Asp Leu Phe Glu His Ile Trp Ala Val Asp Arg Leu Glu
                325                 330                 335

Arg Leu Gly Ile Ser Arg Tyr Phe Gln Lys Glu Ile Glu Gln Cys Met
            340                 345                 350

Asp Tyr Val Asn Arg His Trp Thr Glu Asp Gly Ile Cys Trp Ala Arg
        355                 360                 365

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

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
                485                 490                 495

Gly Gly Asp Asp Val Trp Ile Gly Lys Thr Leu Tyr Arg Met Pro Leu
            500                 505                 510

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
    530                 535                 540

Thr Glu Asn Arg Leu Met Asp Phe Gly Val Ala Gln Glu Asp Ala Leu
545                 550                 555                 560

Arg Ala Tyr Phe Leu Ala Ala Ala Ser Val Tyr Glu Pro Cys Arg Ala
                565                 570                 575

Ala Glu Arg Leu Ala Trp Ala Arg Ala Ala Ile Leu Ala Asn Ala Val
            580                 585                 590

Ser Thr His Leu Arg Asn Ser Pro Ser Phe Arg Glu Arg Leu Glu His
        595                 600                 605

Ser Leu Arg Cys Arg Pro Ser Glu Glu Thr Asp Gly Ser Trp Phe Asn
    610                 615                 620

Ser Ser Ser Gly Ser Asp Ala Val Leu Val Lys Ala Val Leu Arg Leu
625                 630                 635                 640

Thr Asp Ser Leu Ala Arg Glu Ala Gln Pro Ile His Gly Gly Asp Pro
                645                 650                 655
```

```
Glu Asp Ile Ile His Lys Leu Leu Arg Ser Ala Trp Ala Glu Trp Val
            660                 665                 670

Arg Glu Lys Ala Asp Ala Ala Asp Ser Val Cys Asn Gly Ser Ser Ala
        675                 680                 685

Val Glu Gln Glu Gly Ser Arg Met Val His Asp Lys Gln Thr Cys Leu
    690                 695                 700

Leu Leu Ala Arg Met Ile Glu Ile Ser Ala Gly Arg Ala Ala Gly Glu
705                 710                 715                 720

Ala Ala Ser Glu Asp Gly Asp Arg Arg Ile Ile Gln Leu Thr Gly Ser
                725                 730                 735

Ile Cys Asp Ser Leu Lys Gln Lys Met Leu Val Ser Gln Asp Pro Glu
            740                 745                 750

Lys Asn Glu Glu Met Met Ser His Val Asp Asp Glu Leu Lys Leu Arg
        755                 760                 765

Ile Arg Glu Phe Val Gln Tyr Leu Leu Arg Leu Gly Glu Lys Lys Thr
    770                 775                 780

Gly Ser Ser Glu Thr Arg Gln Thr Phe Leu Ser Ile Val Lys Ser Cys
785                 790                 795                 800

Tyr Tyr Ala Ala His Cys Pro Pro His Val Val Asp Arg His Ile Ser
                805                 810                 815

Arg Val Ile Phe Glu Pro Val Ser Ala Ala Lys
            820                 825
```

<210> 14
<211> 1377
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 14

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atggaaaaca agaccgaaac aacagttaga cgtaggcgta gaatcattct gtttccagta       60

ccttttcaag ggcacatcaa tccaatacta caactagcca acgttttgta ctctaaaggt      120

ttttctatta caatctttca caccaatttc aacaaaccaa aaacatccaa ttacccacat      180

ttcacattca gattcatact tgataatgat ccacaagatg aacgtatttc aaacttacct      240

acccacggtc ctttagctgg aatgagaatt ccaatcatca atgaacatgg tgccgatgag      300

cttagaagag aattagagtt acttatgttg gcatccgaag aggacgagga agtctcttgt      360

ctgattactg acgctctatg gtactttgcc caatctgtgg ctgatagttt gaatttgagg      420
```

agattggtac taatgacatc cagtctgttt aactttcacg ctcatgttag tttaccacaa 480

tttgacgaat tgggatactt ggaccctgat gacaagacta ggttagagga acaggcctct 540

ggttttccta tgttgaaagt caaagatatc aagtctgcct attctaattg gcaaatcttg 600

aaagagatct taggaaagat gatcaaacag acaaaggctt catctggagt gatttggaac 660

agtttcaaag agttagaaga gtctgaattg gagactgtaa tcagagaaat tccagcacct 720

tcattcctga taccattacc aaaacatttg actgcttcct cttcctcttt gttggatcat 780

gacagaacag tttttcaatg gttggaccaa caaccaccta gttctgtttt gtacgtgtca 840

tttggtagta cttctgaagt cgatgaaaag gacttccttg aaatcgcaag aggcttagtc 900

gatagtaagc agtcattcct ttgggtcgtg cgtccaggtt tcgtgaaagg ctcaacatgg 960

gtcgaaccac ttccagatgg ttttctaggc gaaagaggta gaatagtcaa atgggttcct 1020

caacaggaag ttttagctca tggcgctatt ggggcattct ggactcattc cggatggaat 1080

tcaactttag aatcagtatg cgaaggggta cctatgatct tttcagattt tggtcttgat 1140

caaccactga acgcaagata catgtctgat gttttgaaag tgggtgtata tctagaaaat 1200

ggctgggaaa ggggtgaaat agctaatgca ataagacgtg ttatggttga tgaagagggg 1260

gagtatatca gacaaaacgc aagagtgctg aagcaaaagg ccgacgtttc tctaatgaag 1320

ggaggctctt catacgaatc cttagaatct cttgtttcct acatttcatc actgtaa 1377

<210> 15
<211> 473
<212> PRT
<213> Stevia rebaudiana

<400> 15

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 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 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
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> 16
<211> 462
<212> PRT
<213> Oryza sativa

<400> 16

Met Asp Ser Gly Tyr Ser Ser Ser Tyr Ala Ala Ala Ala Gly Met His
1 5 10 15

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

Arg Ala Val Ala Val Glu Glu Glu Ser Ser Lys Val Phe Gln Ala Lys
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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> 17
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 17
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ccgtggctcg ccttcggcca cctgctcccg tgcctcgacc tcgcccagcg cctcgcgtcg 120

cggggccacc gcgtgtcgtt cgtctccacg ccgcggaaca tatcccgcct cccgccggtg 180

cgccccgcgc tcgcgccgct cgtcgccttc gtggcgctgc cgctcccgcg cgtcgagggg 240

ctccccgacg gcgccgagtc caccaacgac gtcccccacg acaggccgga catggtcgag 300

ctccaccgga gggccttcga cgggctcgcc gcgcccttct cggagttctt gggcaccgcg 360

tgcgccgact gggtcatcgt cgacgtcttc caccactggg ccgcagccgc cgctctcgag 420

cacaaggtgc catgtgcaat gatgttgttg ggctctgcac atatgatcgc ttccatagca 480

gacagacggc tcgagcgcgc ggagacagag tcgcctgcgg ctgccgggca gggacgccca 540

gcggcggcgc caacgttcga ggtggcgagg atgaagttga tacgaaccaa aggctcatcg 600

ggaatgtccc tcgccgagcg cttctccttg acgctctcga ggagcagcct cgtcgtcggg 660

cggagctgcg tggagttcga gccggagacc gtcccgctcc tgtcgacgct ccgcggtaag 720

cctattacct tccttggcct tatgccgccg ttgcatgaag gccgccgcga ggacggcgag 780

gatgccaccg tccgctggct cgacgcgcag ccggccaagt ccgtcgtgta cgtcgcgcta 840

ggcagcgagg tgccactggg agtggagaag gtccacgagc tcgcgctcgg gctggagctc 900

gccgggacgc gcttcctctg ggctcttagg aagcccactg gcgtctccga cgccgacctc 960

ctccccgccg gcttcgagga gcgcacgcgc ggccgcggcg tcgtggcgac gagatgggtt 1020

cctcagatga gcatactggc gcacgccgcc gtgggcgcgt tcctgaccca ctgcggctgg 1080

aactcgacca tcgaggggct catgttcggc cacccgctta tcatgctgcc gatcttcggc 1140

gaccagggac cgaacgcgcg gctaatcgag gcgaagaacg ccggattgca ggtggcaaga 1200

aacgacggcg atggatcgtt cgaccgagaa ggcgtcgcgg cggcgattcg tgcagtcgcg 1260

gtggaggaag aaagcagcaa agtgtttcaa gccaaagcca agaagctgca ggagatcgtc 1320

gcggacatgg cctgccatga gaggtacatc gacggattca ttcagcaatt gagatcttac 1380

aaggattga 1389

<210> 18
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 18
atggatagtg gctactcctc atcttatgct gctgccgctg gtatgcacgt tgtgatctgc 60

ccttggttgg cctttggtca cctgttacca tgtctggatt tagcccaaag actggcctca 120

agaggccata gagtatcatt tgtgtctact cctagaaata tctctcgttt accaccagtc 180

agacctgctc tagctcctct agttgcattc gttgctcttc cacttccaag agtagaagga 240

ttgccagacg gcgctgaatc tactaatgac gtaccacatg atagacctga catggtcgaa 300

ttgcatagaa gagcctttga tggattggca gctccatttt ctgagttcct gggcacagca 360

tgtgcagact gggttatagt cgatgtattt catcactggg ctgctgcagc cgcattggaa 420

cataaggtgc cttgtgctat gatgttgtta gggtcagcac acatgatcgc atccatagct 480

gatagaagat tggaaagagc tgaaacagaa tccccagccg cagcaggaca aggtaggcca 540

gctgccgccc caacctttga agtggctaga atgaaattga ttcgtactaa aggtagttca 600

gggatgagtc ttgctgaaag gttttctctg acattatcta gatcatcatt agttgtaggt 660

agatcctgcg tcgagttcga acctgaaaca gtacctttac tatctacttt gagaggcaaa 720

cctattactt tccttggtct aatgcctcca ttacatgaag gaaggagaga agatggtgaa 780

gatgctactg ttaggtggtt agatgcccaa cctgctaagt ctgttgttta cgttgcattg 840

ggttctgagg taccactagg ggtggaaaag gtgcatgaat tagcattagg acttgagctg 900

gccggaacaa gattcctttg ggctttgaga aaaccaaccg gtgtttctga cgccgacttg 960

ctaccagctg ggttcgaaga gagaacaaga ggccgtggtg tcgttgctac tagatgggtc 1020

ccacaaatga gtattctagc tcatgcagct gtaggggcct ttctaaccca ttgcggttgg 1080

aactcaacaa tagaaggact gatgtttggt catccactta ttatgttacc aatctttggc 1140

gatcagggac ctaacgcaag attgattgag gcaaagaacg caggtctgca ggttgcacgt 1200

aatgatggtg atggttcctt tgatagagaa ggcgttgcag ctgccatcag agcagtcgcc 1260

gttgaggaag agtcatctaa agttttccaa gctaaggcca aaaaattaca agagattgtg 1320

gctgacatgg cttgtcacga aagatacatc gatggtttca tccaacaatt gagaagttat 1380

aaagactaa 1389

<210> 19
<211> 460
<212> PRT
<213> Stevia rebaudiana

<400> 19

Met Ala Glu Gln Gln Lys Ile Lys Lys Ser Pro His Val Leu Leu Ile
1 5 10 15

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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

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

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
        435                 440                 445

Asp Ile Val Glu Phe Val Ser Glu Leu Ile Lys Ala
    450                 455                 460
```

<210> 20
<211> 481
<212> PRT
<213> Stevia rebaudiana

<400> 20

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Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30

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

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

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
    210                 215                 220

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
                245                 250                 255

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
        275                 280                 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

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
                325                 330                 335
```

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

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
370 375 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385 390 395 400

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
450 455 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465 470 475 480

Asn

<210> 21
<211> 785
<212> PRT
<213> Arabidopsis thaliana

<400> 21

Met Ser Ile Asn Leu Arg Ser Ser Gly Cys Ser Ser Pro Ile Ser Ala
1 5 10 15

Thr Leu Glu Arg Gly Leu Asp Ser Glu Val Gln Thr Arg Ala Asn Asn
20 25 30

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

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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                 320

Leu Ala Phe Arg Leu Leu Leu Ala His Gly Tyr Asp Val Ser Tyr Asp
                325                 330                 335

Pro Leu Lys Pro Phe Ala Glu Glu Ser Gly Phe Ser Asp Thr Leu Glu
            340                 345                 350
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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

Trp Ile Val Glu Asn Arg Leu Gln Glu Leu Lys Phe Ala Arg Gln Lys
                485                 490                 495

Leu Ala Tyr Cys Tyr Phe Ser Gly Ala Ala Thr Leu Phe Ser Pro Glu
            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

Val Lys Ser Val Ile Tyr Glu Pro Val Ser Leu Gln Lys Glu Ser Leu
770 775 780

Thr
785

<210> 22
<211> 894
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 22
atggtcgcac aaactttcaa cctggatacc tacttatccc aaagacaaca acaagttgaa 60

gaggccctaa gtgctgctct tgtgccagct tatcctgaga gaatatacga agctatgaga 120

tactccctcc tggcaggtgg caaaagatta agacctatct tatgtttagc tgcttgcgaa 180

ttggcaggtg gttctgttga acaagccatg ccaactgcgt gtgcacttga aatgatccat 240

acaatgtcac taattcatga tgacctgcca gccatggata acgatgattt cagaagagga 300

aagccaacta atcacaaggt gttcggggaa gatatagcca tcttagcggg tgatgcgctt 360

ttagcttacg cttttgaaca tattgcttct caaacaagag gagtaccacc tcaattggtg 420

ctacaagtta ttgctagaat cggacacgcc gttgctgcaa caggcctcgt tggaggccaa 480

gtcgtagacc ttgaatctga aggtaaagct atttccttag aaacattgga gtatattcac 540

tcacataaga ctggagcctt gctggaagca tcagttgtct caggcggtat tctcgcaggg 600

gcagatgaag agcttttggc cagattgtct cattacgcta gagatatagg cttggctttt 660

caaatcgtcg atgatatcct ggatgttact gctacatctg aacagttggg gaaaaccgct 720

ggtaaagacc aggcagccgc aaaggcaact tatccaagtc tattgggttt agaagcctct 780

agacagaaag cggaagagtt gattcaatct gctaaggaag ccttaagacc ttacggttca 840

caagcagagc cactcctagc gctggcagac ttcatcacac gtcgtcagca ttaa 894

<210> 23
<211> 1542
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 23
atggatgctg tgacgggttt gttaactgtc ccagcaaccg ctataactat tggtggaact 60

gctgtagcat tggcggtagc gctaatcttt tggtacctga aatcctacac atcagctaga 120

agatcccaat caaatcatct tccaagagtg cctgaagtcc caggtgttcc attgttagga 180

aatctgttac aattgaagga gaaaaagcca tacatgactt ttacgagatg ggcagcgaca 240

tatggaccta tctatagtat caaaactggg gctacaagta tggttgtggt atcatctaat 300

gagatagcca aggaggcatt ggtgaccaga ttccaatcca tatctacaag gaacttatct 360

aaagccctga aagtacttac agcagataag acaatggtcg caatgtcaga ttatgatgat 420

tatcataaaa cagttaagag acacatactg accgccgtct tgggtcctaa tgcacagaaa 480

aagcatagaa ttcacagaga tatcatgatg gataacatat ctactcaact tcatgaattc 540

gtgaaaaaca acccagaaca ggaagaggta gaccttagaa aaatctttca atctgagtta 600

ttcggcttag ctatgagaca agccttagga aaggatgttg aaagtttgta cgttgaagac 660

ctgaaaatca ctatgaatag agacgaaatc tttcaagtcc ttgttgttga tccaatgatg 720

ggagcaatcg atgttgattg gagagacttc tttccatacc taaagtgggt cccaaacaaa 780

aagttcgaaa atactattca acaaatgtac atcagaagag aagctgttat gaaatcttta 840

atcaaagagc acaaaaagag aatagcgtca ggcgaaaagc taaatagtta tatcgattac 900

cttttatctg aagctcaaac tttaaccgat cagcaactat tgatgtcctt gtgggaacca 960

atcattgaat cttcagatac aacaatggtc acaacagaat gggcaatgta cgaattagct 1020

aaaaacccta aattgcaaga taggttgtac agagacatta agtccgtctg tggatctgaa 1080

aagataaccg aagagcatct atcacagctg ccttacatta cagctatttt ccacgaaaca 1140

ctgagaagac actcaccagt tcctatcatt cctctaagac atgtacatga agataccgtt 1200

ctaggcggct accatgttcc tgctggcaca gaacttgccg ttaacatcta cggttgcaac 1260

atggacaaaa acgtttggga aaatccagag gaatggaacc cagaaagatt catgaaagag 1320

aatgagacaa ttgattttca aaagacgatg gccttcggtg gtggtaagag agtttgtgct 1380

ggttccttgc aagccctttt aactgcatct attgggattg ggagaatggt tcaagagttc 1440

gaatggaaac tgaaggatat gactcaagag gaagtgaaca cgataggcct aactacacaa 1500

atgttaagac cattgagagc tattatcaaa cctaggatct aa 1542

<210> 24
<211> 297
<212> PRT
<213> Synechococcus sp.

<400> 24

Met Val Ala Gln Thr Phe Asn Leu Asp Thr Tyr Leu Ser Gln Arg Gln
1 5 10 15

Gln Gln Val Glu Glu Ala Leu Ser Ala Ala Leu Val Pro Ala Tyr Pro
20 25 30

Glu Arg Ile Tyr Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys
35 40 45

Arg Leu Arg Pro Ile Leu Cys Leu Ala Ala Cys Glu Leu Ala Gly Gly
50 55 60

Ser Val Glu Gln Ala Met Pro Thr Ala Cys Ala Leu Glu Met Ile His
65 70 75 80

Thr Met Ser Leu Ile His Asp Asp Leu Pro Ala Met Asp Asn Asp Asp
85 90 95

Phe Arg Arg Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Ile
100 105 110

Ala Ile Leu Ala Gly Asp Ala Leu Leu Ala Tyr Ala Phe Glu His Ile
115 120 125

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

Ala Arg Ile Gly His Ala Val Ala Ala Thr Gly Leu Val Gly Gly Gln
145 150 155 160

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

Glu Tyr Ile His Ser His Lys Thr Gly Ala Leu Leu Glu Ala Ser Val
180 185 190

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

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

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
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<210> 25
<211> 513
<212> PRT
<213> Stevia rebaudiana

<400> 25

```
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
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```
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

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
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> 26
<211> 480
<212> PRT
<213> Stevia rebaudiana

<400> 26

Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1 5 10 15

Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
20 25 30

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

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145 150 155 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
165 170 175

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
210 215 220

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
245 250 255

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
275 280 285

Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
290 295 300

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
325 330 335

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

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
370 375 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385 390 395 400

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
450 455 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465 470 475 480

<210> 27
<211> 784
<212> PRT
<213> Stevia rebaudiana

<400> 27

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

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

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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
                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

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> 28
<211> 784
<212> PRT
<213> Stevia rebaudiana

<400> 28

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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
            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

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

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
```

<210> 29
<211> 590
<212> PRT
<213> Zea mays

<400> 29

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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

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

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>  30
<211>  775
<212>  PRT
<213>  Populus trichocarpa

<400>  30

Met Ser Cys Ile Arg Pro Trp Phe Cys Pro Ser Ser Ile Ser Ala Thr
1               5                   10                  15

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

Ser Leu Asn Phe His Gly Thr Lys Glu Arg Ile Lys Lys Met Phe Asp
        35                  40                  45

Lys Ile Glu Leu Ser Val Ser Ser Tyr Asp Thr Ala Trp Val Ala Met
    50                  55                  60

Val Pro Ser Pro Asp Cys Pro Glu Thr Pro Cys Phe Pro Glu Cys Thr
65                  70                  75                  80

Lys Trp Ile Leu Glu Asn Gln Leu Gly Asp Gly Ser Trp Ser Leu Pro
                85                  90                  95

His Gly Asn Pro Leu Leu Val Lys Asp Ala Leu Ser Ser Thr Leu Ala
```

100 105 110

Cys Ile Leu Ala Leu Lys Arg Trp Gly Ile Gly Glu Glu Gln Ile Asn
115 120 125

Lys Gly Leu Arg Phe Ile Glu Leu Asn Ser Ala Ser Val Thr Asp Asn
130 135 140

Glu Gln His Lys Pro Ile Gly Phe Asp Ile Ile Phe Pro Gly Met Ile
145 150 155 160

Glu Tyr Ala Lys Asp Leu Asp Leu Asn Leu Pro Leu Lys Pro Thr Asp
165 170 175

Ile Asn Ser Met Leu His Arg Arg Ala Leu Glu Leu Thr Ser Gly Gly
180 185 190

Gly Lys Asn Leu Glu Gly Arg Arg Ala Tyr Leu Ala Tyr Val Ser Glu
195 200 205

Gly Ile Gly Lys Leu Gln Asp Trp Glu Met Ala Met Lys Tyr Gln Arg
210 215 220

Lys Asn Gly Ser Leu Phe Asn Ser Pro Ser Thr Thr Ala Ala Ala Phe
225 230 235 240

Ile His Ile Gln Asp Ala Glu Cys Leu His Tyr Ile Arg Ser Leu Leu
245 250 255

Gln Lys Phe Gly Asn Ala Val Pro Thr Ile Tyr Pro Leu Asp Ile Tyr
260 265 270

Ala Arg Leu Ser Met Val Asp Ala Leu Glu Arg Leu Gly Ile Asp Arg
275 280 285

His Phe Arg Lys Glu Arg Lys Phe Val Leu Asp Glu Thr Tyr Arg Phe
290 295 300

Trp Leu Gln Gly Glu Glu Glu Ile Phe Ser Asp Asn Ala Thr Cys Ala
305 310 315 320

Leu Ala Phe Arg Ile Leu Arg Leu Asn Gly Tyr Asp Val Ser Leu Glu
325 330 335

Asp His Phe Ser Asn Ser Leu Gly Gly Tyr Leu Lys Asp Ser Gly Ala
340 345 350

Ala Leu Glu Leu Tyr Arg Ala Leu Gln Leu Ser Tyr Pro Asp Glu Ser
355 360 365

Leu Leu Glu Lys Gln Asn Ser Arg Thr Ser Tyr Phe Leu Lys Gln Gly

370 375 380

Leu Ser Asn Val Ser Leu Cys Gly Asp Arg Leu Arg Lys Asn Ile Ile
385 390 395 400

Gly Glu Val His Asp Ala Leu Asn Phe Pro Asp His Ala Asn Leu Gln
405 410 415

Arg Leu Ala Ile Arg Arg Arg Ile Lys His Tyr Ala Thr Asp Asp Thr
420 425 430

Arg Ile Leu Lys Thr Ser Tyr Arg Cys Ser Thr Ile Gly Asn Gln Asp
435 440 445

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

Arg Glu Glu Phe Lys His Ile Glu Arg Trp Val Val Glu Arg Arg Leu
465 470 475 480

Asp Lys Leu Lys Phe Ala Arg Gln Lys Glu Ala Tyr Cys Tyr Phe Ser
485 490 495

Ala Ala Ala Thr Leu Phe Ala Pro Glu Leu Ser Asp Ala Arg Met Ser
500 505 510

Trp Ala Lys Asn Gly Val Leu Thr Thr Val Val Asp Asp Phe Phe Asp
515 520 525

Val Gly Gly Ser Glu Glu Glu Leu Val Asn Leu Ile Glu Leu Ile Glu
530 535 540

Arg Trp Asp Val Asn Gly Ser Ala Asp Phe Cys Ser Glu Glu Val Glu
545 550 555 560

Ile Ile Tyr Ser Ala Ile His Ser Thr Ile Ser Glu Ile Gly Asp Lys
565 570 575

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

Trp Leu Asp Leu Leu Lys Ser Met Leu Thr Glu Ala Gln Trp Ser Ser
595 600 605

Asn Lys Ser Val Pro Thr Leu Asp Glu Tyr Met Thr Thr Ala His Val
610 615 620

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

Pro Lys Leu Ser Glu Glu Val Ala Gly His Pro Glu Leu Leu Asn Leu

645 650 655

Tyr Lys Val Met Ser Thr Cys Gly Arg Leu Leu Asn Asp Trp Arg Ser
660 665 670

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

Met Ile His Ser Gly Gly Ala Ser Thr Glu Glu Glu Thr Ile Glu His
690 695 700

Phe Lys Gly Leu Ile Asp Ser Gln Arg Arg Gln Leu Leu Gln Leu Val
705 710 715 720

Leu Gln Glu Lys Asp Ser Ile Ile Pro Arg Pro Cys Lys Asp Leu Phe
725 730 735

Trp Asn Met Ile Lys Leu Leu His Thr Phe Tyr Met Lys Asp Asp Gly
740 745 750

Phe Thr Ser Asn Glu Met Arg Asn Val Val Lys Ala Ile Ile Asn Glu
755 760 765

Pro Ile Ser Leu Asp Glu Leu
770 775

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<211> 2358
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<220>
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<400> 31
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ggattggact cagaagtaca gacaagagct aacaatgtga gctttgagca aacaaaggag 120

aagattagga agatgttgga gaaagtggag ctttctgttt cggcctacga tactagttgg 180

gtagcaatgg ttccatcacc gagctcccaa aatgctccac ttttcccaca gtgtgtgaaa 240

tggttattgg ataatcaaca tgaagatgga tcttggggac ttgataacca tgaccatcaa 300

tctcttaaga aggatgtgtt atcatctaca ctggctagta tcctcgcgtt aaagaagtgg 360

ggaattggtg aaagacaaat aaacaagggt ctccagttta ttgagctgaa ttctgcatta 420

gtcactgatg aaaccataca gaaaccaaca gggtttgata ttatatttcc tgggatgatt 480

aaatatgcta gagatttgaa tctgacgatt ccattgggct cagaagtggt ggatgacatg 540

atacgaaaaa gagatctgga tcttaaatgt gatagtgaaa agttttcaaa gggaagagaa 600

gcatatctgg cctatgtttt agaggggaca agaaacctaa aagattggga tttgatagtc 660

aaatatcaaa ggaaaaatgg gtcactgttt gattctccag ccacaacagc agctgctttt 720

actcagtttg ggaatgatgg ttgtctccgt tatctctgtt ctctccttca gaaattcgag 780

gctgcagttc cttcagttta tccatttgat caatatgcac gccttagtat aattgtcact 840

cttgaaagct taggaattga tagagatttc aaaaccgaaa tcaaaagcat attggatgaa 900

acctatagat attggcttcg tggggatgaa gaaatatgtt tggacttggc cacttgtgct 960

ttggctttcc gattattgct tgctcatggc tatgatgtgt cttacgatcc gctaaaacca 1020

tttgcagaag aatctggttt ctctgatact ttggaaggat atgttaagaa tacgttttct 1080

gtgttagaat tatttaaggc tgctcaaagt tatccacatg aatcagcttt gaagaagcag 1140

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ttggatctgc tcaagtctat gttgagagaa gccgagtggt ccagtgacaa gtcaacacca 1860

agcttggagg attacatgga aaatgcgtac atatcatttg cattaggacc aattgtcctc 1920

ccagctacct atctgatcgg acctccactt ccagagaaga cagtcgatag ccaccaatat 1980

aatcagctct acaagctcgt gagcactatg ggtcgtcttc taaatgacat acaaggtttt 2040

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gacaatcgca gcaaagaagt gatcatagaa tcgatgaaag gtttagcaga gagaaagagg 2160

gaagaattgc ataagctagt tttggaggag aaaggaagtg tggttccaag ggaatgcaaa 2220

gaagcgttct tgaaaatgag caaagtgttg aacttatttt acaggaagga cgatggattc 2280

acatcaaatg atctgatgag tcttgttaaa tcagtgatct acgagcctgt tagcttacag 2340

aaagaatctt taacttga 2358

<210> 32
<211> 785
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<213> Arabidopsis thaliana

<400> 32

Met Ser Ile Asn Leu Arg Ser Ser Gly Cys Ser Ser Pro Ile Ser Ala
1 5 10 15

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Thr Leu Glu Arg Gly Leu Asp Ser Glu Val Gln Thr Arg Ala Asn Asn
            20                  25                  30

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                 320

Leu Ala Phe Arg Leu Leu Leu Ala His Gly Tyr Asp Val Ser Tyr Asp
                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

Trp Ile Val Glu Asn Arg Leu Gln Glu Leu Lys Phe Ala Arg Gln Lys
                485                 490                 495

Leu Ala Tyr Cys Tyr Phe Ser Gly Ala Ala Thr Leu Phe Ser Pro Glu
            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

Val Lys Ser Val Ile Tyr Glu Pro Val Ser Leu Gln Lys Glu Ser Leu
770 775 780

Thr
785

<210> 33
<211> 513
<212> PRT
<213> Stevia rebaudiana

<400> 33

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

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
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> 34
<211> 509
<212> PRT
<213> Arabidopsis thaliana

<400> 34

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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

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
    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> 35
<211> 525
<212> PRT
<213> Fusarium fujikuroi

<400> 35

```
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

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
            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> 36
<211> 499
<212> PRT

<213> Trametes versicolor

<400> 36

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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

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
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> 37
<211> 1678
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 37
aaacaaagaa tgattcaagt tctaacaccg atccttctct tcctcatttt cttcgttttc 60

tggaaggttt acaagcacca gaaaaccaaa atcaatcttc caccgggaag cttcggatgg 120

ccatttctgg gcgaaactct ggcactccta cgtgcaggtt gggactcaga gccggagaga 180

tttgttcgtg aacggatcaa gaaacacgga agtcctctag tgtttaagac gtcgttgttt 240

ggcgaccgtt ttgcggtgtt gtgtggacct gccggaaaca agttcctgtt ctgcaacgag 300

aacaagctgg tggcgtcgtg gtggccggtt ccggtgagga agcttttcgg caagtctctg 360

ctcacgattc gtggtgatga agctaagtgg atgaggaaga tgttgttatc gtatctcggt 420

cctgatgctt tcgcaactca ttatgccgtc accatggacg tcgtcacccg tcggcatatc 480

gacgttcatt ggcgagggaa ggaagaggtg aacgtattcc aaaccgttaa gttatatgcc 540

tttgagcttg catgtcgttt attcatgaac ctagacgacc caaaccacat tgcaaaactc 600

ggttccttgt tcaacatttt cttgaaaggc atcattgagc ttccaatcga cgtcccaggg 660

acacgatttt atagctccaa aaaagcagca gcagctatca ggattgaact aaaaaaattg 720

attaaagcaa gaaaactgga actgaaagaa gggaaggcat catcttcaca agacctctta 780

tcacatttgc ttacatctcc agatgaaaat ggtatgtttc taaccgaaga agagattgta 840

gacaacatct tgttactact ctttgcgggt catgatacct cggctctttc aatcactttg 900

ctcatgaaga ctcttggcga acattctgat gtttatgaca aggtgttaaa agagcaacta 960

gagatatcga agacgaaaga agcatgggag tccctgaaat gggaggacat acaaaagatg 1020

aaatactcct ggagtgttat atgtgaagtc atgagactaa atccacctgt tataggaacc 1080

tatagagagg cccttgtgga tattgattat gcgggttata ccatccccaa aggatggaag 1140

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ggggggccta gaatgtgttt agggaaagaa tttgctcgat tggaagtact tgcgtttctt 1320

cacaatattg tcaccaattt caaatgggac ctgttgatac ctgatgagaa aatagaatat 1380

gatcccatgg ctaccccagc aaaggggctt ccaattcgtc ttcatcccca tcaagtttga 1440

ttacttcaag catgaatcag tgatgtgaag gtaaaccata atggatctta ttggtagtta 1500

cagattatgt gtttttatgg catgaagaag ttatgataaa taaaattgtg ttattctaca 1560

acttatgtaa tttgtgcctg taagtaactg aatctattaa tgttttatgt gacatgaaac 1620

ataaatgtat aattagtaaa ttttctgctc aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1678

<210> 38
<211> 476
<212> PRT
<213> Stevia rebaudiana

<400> 38

```
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
    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 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

Lys Gly Leu Pro Ile Arg Leu His Pro His Gln Val
465 470 475

<210> 39
<211> 476
<212> PRT
<213> Stevia rebaudiana

<400> 39

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
    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

Lys Gly Leu Pro Ile Arg Leu His Pro His Gln Val
465 470 475

<210> 40
<211> 525
<212> PRT
<213> Arabidopsis thaliana

<400> 40

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
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

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> 41
<211> 526
<212> PRT
<213> Vitis vinifera

<400> 41

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
                165                 170                 175

Lys Asn Glu Ser Gly Leu Val Ser Val Glu Met Lys Gln Trp Phe Gly
            180                 185                 190

Asp Leu Thr Leu Asn Val Ile Leu Arg Met Val Ala Gly Lys Arg Tyr
        195                 200                 205

Phe Ser Ala Ser Asp Ala Ser Glu Asn Lys Gln Ala Gln Arg Cys Arg
    210                 215                 220

Arg Val Phe Arg Glu Phe Phe His Leu Ser Gly Leu Phe Val Val Ala
225                 230                 235                 240

Asp Ala Ile Pro Phe Leu Gly Trp Leu Asp Trp Gly Arg His Glu Lys
                245                 250                 255

Thr Leu Lys Lys Thr Ala Ile Glu Met Asp Ser Ile Ala Gln Glu Trp
            260                 265                 270

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

Gln Asp Phe Met Asp Val Met Gln Ser Val Leu Asp Gly Lys Asn Leu
    290                 295                 300

Gly Gly Tyr Asp Ala Asp Thr Ile Asn Lys Ala Thr Cys Leu Thr Leu
305                 310                 315                 320

Ile Ser Gly Gly Ser Asp Thr Thr Val Val Ser Leu Thr Trp Ala Leu
                325                 330                 335
```

```
Ser Leu Val Leu Asn Asn Arg Asp Thr Leu Lys Lys Ala Gln Glu Glu
            340                 345                 350

Leu Asp Ile Gln Val Gly Lys Glu Arg Leu Val Asn Glu Gln Asp Ile
        355                 360                 365

Ser Lys Leu Val Tyr Leu Gln Ala Ile Val Lys Glu Thr Leu Arg Leu
    370                 375                 380

Tyr Pro Pro Gly Pro Leu Gly Gly Leu Arg Gln Phe Thr Glu Asp Cys
385                 390                 395                 400

Thr Leu Gly Gly Tyr His Val Ser Lys Gly Thr Arg Leu Ile Met Asn
                405                 410                 415

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 Ser Cys Ser Leu Tyr Asn
        515                 520                 525


<210>  42
<211>  479
<212>  PRT
<213>  Medicago truncatula

<400>  42

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
            100                 105                 110

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

Ser Ile Lys Met Arg Lys Leu Leu Pro Gln Phe Phe Lys Pro Glu Ala
    130                 135                 140

Leu Gln Arg Tyr Val Gly Val Met Asp Val Ile Ala Gln Arg His Phe
145                 150                 155                 160

Val Thr His Trp Asp Asn Lys Asn Glu Ile Thr Val Tyr Pro Leu Ala
                165                 170                 175

Lys Arg Tyr Thr Phe Leu Leu Ala Cys Arg Leu Phe Met Ser Val Glu
            180                 185                 190

Asp Glu Asn His Val Ala Lys Phe Ser Asp Pro Phe Gln Leu Ile Ala
        195                 200                 205

Ala Gly Ile Ile Ser Leu Pro Ile Asp Leu Pro Gly Thr Pro Phe Asn
    210                 215                 220

Lys Ala Ile Lys Ala Ser Asn Phe Ile Arg Lys Glu Leu Ile Lys Ile
225                 230                 235                 240

Ile Lys Gln Arg Arg Val Asp Leu Ala Glu Gly Thr Ala Ser Pro Thr
                245                 250                 255

Gln Asp Ile Leu Ser His Met Leu Leu Thr Ser Asp Glu Asn Gly Lys
            260                 265                 270

Ser Met Asn Glu Leu Asn Ile Ala Asp Lys Ile Leu Gly Leu Leu Ile
        275                 280                 285

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

Leu Gly Glu Leu Pro His Ile Tyr Asp Lys Val Tyr Gln Glu Gln Met
305                 310                 315                 320
```

Glu Ile Ala Lys Ser Lys Pro Ala Gly Glu Leu Leu Asn Trp Asp Asp
325 330 335

Leu Lys Lys Met Lys Tyr Ser Trp Asn Val Ala Cys Glu Val Met Arg
340 345 350

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> 43
<211> 522
<212> PRT
<213> Stevia rebaudiana

<400> 43

Met Gly Leu Phe Pro Leu Glu Asp Ser Tyr Ala Leu Val Phe Glu Gly
1 5 10 15

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 His Pro
35 40 45

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

Leu Ala Leu Ala Ser Leu Ala Asp Arg Cys Gly Pro Ile Phe Thr Ile
65 70 75 80

```
Arg Leu Gly Ile Arg Arg Val Leu Val Val Ser Asn Trp Glu Ile Ala
                85                  90                  95

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

Tyr Leu Ala Ala Lys Ile Leu Gly Phe Asn Tyr Val Ser Phe Ser Phe
        115                 120                 125

Ala Pro Tyr Gly Pro Tyr Trp Val Gly Ile Arg Lys Ile Ile Ala Thr
    130                 135                 140

Lys Leu Met Ser Ser Ser Arg Leu Gln Lys Leu Gln Phe Val Arg Val
145                 150                 155                 160

Phe Glu Leu Glu Asn Ser Met Lys Ser Ile Arg Glu Ser Trp Lys Glu
                165                 170                 175

Lys Lys Asp Glu Glu Gly Lys Val Leu Val Glu Met Lys Lys Trp Phe
            180                 185                 190

Trp Glu Leu Asn Met Asn Ile Val Leu Arg Thr Val Ala Gly Lys Gln
        195                 200                 205

Tyr Thr Gly Thr Val Asp Asp Ala Asp Ala Lys Arg Ile Ser Glu Leu
    210                 215                 220

Phe Arg Glu Trp Phe His Tyr Thr Gly Arg Phe Val Val Gly Asp Ala
225                 230                 235                 240

Phe Pro Phe Leu Gly Trp Leu Asp Leu Gly Gly Tyr Lys Lys Thr Met
                245                 250                 255

Glu Leu Val Ala Ser Arg Leu Asp Ser Met Val Ser Lys Trp Leu Asp
            260                 265                 270

Glu His Arg Lys Lys Gln Ala Asn Asp Asp Lys Lys Glu Asp Met Asp
        275                 280                 285

Phe Met Asp Ile Met Ile Ser Met Thr Glu Ala Asn Ser Pro Leu Glu
    290                 295                 300

Gly Tyr Gly Thr Asp Thr Ile Ile Lys Thr Thr Cys Met Thr Leu Ile
305                 310                 315                 320

Val Ser Gly Val Asp Thr Thr Ser Ile Val Leu Thr Trp Ala Leu Ser
                325                 330                 335

Leu Leu Leu Asn Asn Arg Asp Thr Leu Lys Lys Ala Gln Glu Glu Leu
            340                 345                 350
```

Asp Met Cys Val Gly Lys Gly Arg Gln Val Asn Glu Ser Asp Leu Val
355 360 365

Asn Leu Ile Tyr Leu Glu Ala Val Leu Lys Glu Ala Leu Arg Leu Tyr
370 375 380

Pro Ala Ala Phe Leu Gly Gly Pro Arg Ala Phe Leu Glu Asp Cys Thr
385 390 395 400

Val Ala Gly Tyr Arg Ile Pro Lys Gly Thr Cys Leu Leu Ile Asn Met
405 410 415

Trp Lys Leu His Arg Asp Pro Asn Ile Trp Ser Asp Pro Cys Glu Phe
420 425 430

Lys Pro Glu Arg Phe Leu Thr Pro Asn Gln Lys Asp Val Asp Val Ile
435 440 445

Gly Met Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Tyr Cys
450 455 460

Pro Gly Thr Arg Leu Ala Leu Gln Met Leu His Ile Val Leu Ala Thr
465 470 475 480

Leu Leu Gln Asn Phe Glu Met Ser Thr Pro Asn Asp Ala Pro Val Asp
485 490 495

Met Thr Ala Ser Val Gly Met Thr Asn Ala Lys Ala Ser Pro Leu Glu
500 505 510

Val Leu Leu Ser Pro Arg Val Lys Trp Ser
515 520

<210> 44
<211> 710
<212> PRT
<213> Stevia rebaudiana

<400> 44

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
100 105 110

Gly Thr Ala Glu Gly Phe Ala Lys Ala Leu Val Glu Glu Ala Lys Val
115 120 125

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

Ala Asp Asp Asp Glu Tyr Glu Glu Lys Leu Lys Lys Glu Ser Leu 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 Asn Phe Tyr Lys Trp Phe Thr Glu Gly Asp Asp Lys Gly Glu Trp
180 185 190

Leu Lys Lys Leu Gln Tyr Gly Val Phe Gly Leu Gly Asn Arg Gln Tyr
195 200 205

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

Met Gly Ala Lys Arg Leu Val Pro Val Gly Leu Gly Asp Asp Asp Gln
225 230 235 240

Cys Ile Glu Asp Asp Phe Thr Ala Trp Lys Glu Leu Val Trp Pro Glu
245 250 255

Leu Asp Gln Leu Leu Arg Asp Glu Asp Asp Thr Ser Val Thr Thr Pro
260 265 270

Tyr Thr Ala Ala Val Leu Glu Tyr Arg Val Val Tyr His Asp Lys Pro
275 280 285

Ala Asp Ser Tyr Ala Glu Asp Gln Thr His Thr Asn Gly His Val Val
290 295 300

His Asp Ala Gln His Pro Ser Arg Ser Asn Val Ala Phe Lys Lys Glu
305 310 315 320

Leu His Thr Ser Gln Ser Asp Arg Ser Cys Thr His Leu Glu Phe Asp
325 330 335

Ile Ser His Thr Gly Leu Ser Tyr Glu Thr Gly Asp His Val Gly Val

340 345 350

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

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> 45
<211> 692
<212> PRT
<213> Arabidopsis thaliana

<400> 45

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

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

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

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> 46
<211> 713
<212> PRT
<213> Fusarium fujikuroi

<400> 46

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

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

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
                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> 47
<211> 480
<212> PRT
<213> Stevia rebaudiana

<400> 47

```
Met Asp Ala Met Ala Thr Thr Glu Lys Lys Pro His Val Ile Phe Ile
1               5                   10                  15
```

```
Pro Phe Pro Ala Gln Ser His Ile Lys Ala Met Leu Lys Leu Ala Gln
            20                  25                  30

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

Ala Ala Cys Gly Phe Met Gly Phe Tyr His Ile His Ser Leu Ile Glu
145                 150                 155                 160

Lys Gly Phe Ala Pro Leu Lys Asp Ala Ser Tyr Leu Thr Asn Gly Tyr
                165                 170                 175

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
    210                 215                 220

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
                245                 250                 255

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
        275                 280                 285
```

```
Gln Ser Lys Glu Pro Asn Ser Val Val Tyr Val Asn Phe Gly Ser Thr
    290                 295                 300

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
                325                 330                 335

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

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
    370                 375                 380

Glu Ser Leu Ser Ala Gly Val Pro Met Ile Cys Trp Pro Tyr Ser Trp
385                 390                 395                 400

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
    450                 455                 460

Ser Leu Asn Ile Asp Lys Met Val Lys Glu Ile Thr Val Leu Ala Arg
465                 470                 475                 480
```

<210> 48
<211> 787
<212> PRT
<213> Stevia rebaudiana

<400> 48

```
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

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

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
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> 49
<211> 527
<212> PRT
<213> Streptomyces clavuligerus

<400> 49

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

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
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```
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
            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 Gly 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


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<212>  PRT
<213>  Bradyrhizobium diazoefficiens

<400>  50

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

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
370 375 380

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

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gcaggaaggt ggagaagggc cttggctaga gcacagcaca catcagaatc cgcagctgtc 180

gcaaagggca gcagtttgac ccctatagtg agaactgacg ctgagtcaag gagaacaaga 240

tggccaaccg atgacgatga cgccgaacct ttagtggatg agatcagggc aatgcttact 300

tccatgtctg atggtgacat ttccgtgagc gcatacgata cagcctgggt cggattggtt 360

ccaagattag acggcggtga aggtcctcaa tttccagcag ctgtgagatg gataagaaat 420

aaccagttgc ctgacggaag ttggggcgat gccgcattat tctctgccta tgacaggctt 480

atcaataccc ttgcctgcgt tgtaactttg acaaggtggt ccctagaacc agagatgaga 540

ggtagaggac tatctttttt gggtaggaac atgtggaaat tagcaactga agatgaagag 600

tcaatgccta ttggcttcga attagcattt ccatctttga tagagcttgc taagagccta 660

ggtgtccatg acttccctta tgatcaccag gccctacaag gaatctactc ttcaagagag 720

atcaaaatga agaggattcc aaaagaagtg atgcataccg ttccaacatc aatattgcac 780

agtttggagg gtatgcctgg cctagattgg gctaaactac ttaaactaca gagcagcgac 840

ggaagttttt tgttctcacc agctgccact gcatatgctt taatgaatac cggagatgac 900

aggtgtttta gctacatcga tagaacagta aagaaattca acggcggcgt ccctaatgtt 960

tatccagtgg atctatttga acatatttgg gccgttgata gacttgaaag attaggaatc 1020

tccaggtact tccaaaagga gatcgaacaa tgcatggatt atgtaaacag gcattggact 1080

gaggacggta tttgttgggc aaggaactct gatgtcaaag aggtggacga cacagctatg 1140

gcctttagac ttcttaggtt gcacggctac agcgtcagtc ctgatgtgtt taaaaacttc 1200

gaaaaggacg gtgaattttt cgcatttgtc ggacagtcta atcaagctgt taccggtatg 1260

tacaacttaa acagagcaag ccagatatcc ttcccaggcg aggatgtgct tcatagagct 1320

ggtgccttct catatgagtt cttgaggaga aaagaagcag agggagcttt gagggacaag 1380

tggatcattt ctaaagatct acctggtgaa gttgtgtata ctttggattt tccatggtac 1440

ggcaacttac ctagagtcga ggccagagac tacctagagc aatacggagg tggtgatgac 1500

gtttggattg gcaagacatt gtataggatg ccacttgtaa acaatgatgt atatttggaa 1560

ttggcaagaa tggatttcaa ccactgccag gctttgcatc agttagagtg gcaaggacta 1620

aaaagatggt atactgaaaa taggttgatg gactttggtg tcgcccaaga agatgccctt 1680

agagcttatt ttcttgcagc cgcatctgtt tacgagcctt gtagagctgc cgagaggctt 1740

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tcattcagag aaaggttaga gcattctctt aggtgtagac ctagtgaaga gacagatggc 1860

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cacaagttgt taagatctgc ttgggccgag tgggttaggg aaaaggcaga cgctgccgat 2040

agcgtgtgca atggtagttc tgcagtagaa caagagggat caagaatggt ccatgataaa 2100

cagacctgtc tattattggc tagaatgatc gaaatttctg ccggtagggc agctggtgaa 2160

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gtggatgacg aattgaagtt gaggattaga gagttcgttc aatatttgct tagactaggt 2340

gaaaaaaaga ctggatctag cgaaaccagg caaacatttt taagtatagt gaaatcatgt 2400

tactatgctg ctcattgccc acctcatgtc gttgatagac acattagtag agtgattttc 2460

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<211> 827
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<213> Zea mays

<400> 52

Met Val Leu Ser Ser Ser Cys Thr Thr Val Pro His Leu Ser Ser Leu
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Ala Val Val Gln Leu Gly Pro Trp Ser Ser Arg Ile Lys Lys Lys Thr
20 25 30

Asp Thr Val Ala Val Pro Ala Ala Ala Gly Arg Trp Arg Arg Ala Leu
35 40 45

Ala Arg Ala Gln His Thr Ser Glu Ser Ala Ala Val Ala Lys Gly Ser
50 55 60

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

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

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

Pro Glu Met Arg Gly Arg Gly Leu Ser Phe Leu Gly Arg Asn Met Trp
180 185 190

```
Lys Leu Ala Thr Glu Asp Glu Glu Ser Met Pro Ile Gly Phe Glu Leu
        195                 200                 205

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
        275                 280                 285

Ala Thr Ala Tyr Ala Leu Met Asn Thr Gly Asp Asp Arg Cys Phe Ser
    290                 295                 300

Tyr Ile Asp Arg Thr Val Lys Lys Phe Asn Gly Gly Val Pro Asn Val
305                 310                 315                 320

Tyr Pro Val Asp Leu Phe Glu His Ile Trp Ala Val Asp Arg Leu Glu
                325                 330                 335

Arg Leu Gly Ile Ser Arg Tyr Phe Gln Lys Glu Ile Glu Gln Cys Met
            340                 345                 350

Asp Tyr Val Asn Arg His Trp Thr Glu Asp Gly Ile Cys Trp Ala Arg
        355                 360                 365

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

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
```

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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
                485                 490                 495

Gly Gly Asp Asp Val Trp Ile Gly Lys Thr Leu Tyr Arg Met Pro Leu
            500                 505                 510

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
    530                 535                 540

Thr Glu Asn Arg Leu Met Asp Phe Gly Val Ala Gln Glu Asp Ala Leu
545                 550                 555                 560

Arg Ala Tyr Phe Leu Ala Ala Ala Ser Val Tyr Glu Pro Cys Arg Ala
                565                 570                 575

Ala Glu Arg Leu Ala Trp Ala Arg Ala Ala Ile Leu Ala Asn Ala Val
            580                 585                 590

Ser Thr His Leu Arg Asn Ser Pro Ser Phe Arg Glu Arg Leu Glu His
        595                 600                 605

Ser Leu Arg Cys Arg Pro Ser Glu Glu Thr Asp Gly Ser Trp Phe Asn
    610                 615                 620

Ser Ser Ser Gly Ser Asp Ala Val Leu Val Lys Ala Val Leu Arg Leu
625                 630                 635                 640

Thr Asp Ser Leu Ala Arg Glu Ala Gln Pro Ile His Gly Gly Asp Pro
                645                 650                 655

Glu Asp Ile Ile His Lys Leu Leu Arg Ser Ala Trp Ala Glu Trp Val
            660                 665                 670

Arg Glu Lys Ala Asp Ala Ala Asp Ser Val Cys Asn Gly Ser Ser Ala
        675                 680                 685

Val Glu Gln Glu Gly Ser Arg Met Val His Asp Lys Gln Thr Cys Leu
    690                 695                 700

Leu Leu Ala Arg Met Ile Glu Ile Ser Ala Gly Arg Ala Ala Gly Glu
705                 710                 715                 720

Ala Ala Ser Glu Asp Gly Asp Arg Arg Ile Ile Gln Leu Thr Gly Ser
                725                 730                 735
```

Ile Cys Asp Ser Leu Lys Gln Lys Met Leu Val Ser Gln Asp Pro Glu
740 745 750

Lys Asn Glu Glu Met Met Ser His Val Asp Asp Glu Leu Lys Leu Arg
755 760 765

Ile Arg Glu Phe Val Gln Tyr Leu Leu Arg Leu Gly Glu Lys Lys Thr
770 775 780

Gly Ser Ser Glu Thr Arg Gln Thr Phe Leu Ser Ile Val Lys Ser Cys
785 790 795 800

Tyr Tyr Ala Ala His Cys Pro Pro His Val Val Asp Arg His Ile Ser
805 810 815

Arg Val Ile Phe Glu Pro Val Ser Ala Ala Lys
820 825

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cttcttcttt ccttaccatc tcaggatctc ctctcaatgt cgctagagac aaatccagaa 180

gcggttccat acattgttca aagcttcgaa ctcaagaata cattaattct caagaggttc 240

aacatgattt gcctctaata catgagtggc aacagcttca aggagaagat gctcctcaga 300

ttagtgttgg aagtaatagt aatgcattca aagaagcagt gaagagtgtg aaaacgatct 360

tgagaaacct aacggacggg gaaattacga tatcggctta cgatacagct tgggttgcat 420

tgatcgatgc cggagataaa actccggcgt ttccctccgc cgtgaaatgg atcgccgaga 480

accaactttc cgatggttct tggggagatg cgtatctctt ctcttatcat gatcgtctca 540

tcaataccct tgcatgcgtc gttgctctaa gatcatggaa tctctttcct catcaatgca 600

acaaaggaat cacgtttttc cgggaaaata ttgggaagct agaagacgaa aatgatgagc 660

atatgccaat cggattcgaa gtagcattcc catcgttgct tgagatagct cgaggaataa 720

acattgatgt accgtacgat tctccggtct taaaagatat atacgccaag aaagagctaa 780

agcttacaag gataccaaaa gagataatgc acaagatacc aacaacattg ttgcatagtt 840

tggaggggat gcgtgattta gattgggaaa agctcttgaa acttcaatct caagacggat 900

ctttcctctt ctctccttcc tctaccgctt ttgcattcat gcagacccga gacagtaact 960

gcctcgagta tttgcgaaat gccgtcaaac gtttcaatgg aggagttccc aatgtctttc 1020

ccgtggatct tttcgagcac atatggatag tggatcggtt acaacgttta gggatatcga 1080

gatactttga agaagagatt aaagagtgtc ttgactatgt ccacagatat tggaccgaca 1140

atggcatatg ttgggctaga tgttcccatg tccaagacat cgatgataca gccatggcat 1200

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aagagggaga gtttttctgc tttgtggggc aatcaaacca agcagtaacc ggtatgttca 1320

acctataccg ggcatcacaa ttggcgtttc caagggaaga gatattgaaa aacgccaaag 1380

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gcttgcctcg agtagagacg agattctata ttgatcaata tggtggagaa aacgacgttt 1560

ggattggcaa gactctttat aggatgccat acgtgaacaa taatggatat ctggaattag 1620

caaaacaaga ttacaacaat tgccaagctc agcatcagct cgaatgggac atattccaaa 1680

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gggctaagtc aagtgtattg gttaaagcca tttcttcttc ttttggggaa tcctctgact 1860

ccagaagaag cttctccgat cagtttcatg aatacattgc caatgctcga cgaagtgatc 1920

atcactttaa tgacaggaac atgagattgg accgaccagg atcggttcag gccagtcggc 1980

ttgccggagt gttaatcggg actttgaatc aaatgtcttt tgacctttc atgtctcatg 2040

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tatatggaga tgaaggagaa ggagagctca tggtgaagat gataattcta atgaagaaca 2160

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tatgtggcga tcatctccaa actcacatct ccaaagtctt gtttcaaaaa gtctagtaac 2460

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<211> 802
<212> PRT
<213> Arabidopsis thaliana

<400> 54

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Leu Ser Ser Thr Lys Thr Thr Ile Ser Ser Ser Phe Leu Thr Ile Ser
20 25 30

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

His Cys Ser Lys Leu Arg Thr Gln Glu Tyr Ile Asn Ser Gln Glu Val
    50                  55                  60

Gln His Asp Leu Pro Leu Ile His Glu Trp Gln Gln Leu Gln Gly Glu
65                  70                  75                  80

Asp Ala Pro Gln Ile Ser Val Gly Ser Asn Ser Asn Ala Phe Lys Glu
                85                  90                  95

Ala Val Lys Ser Val Lys Thr Ile Leu Arg Asn Leu Thr Asp Gly Glu
            100                 105                 110

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

Gly Asp Lys Thr Pro Ala Phe Pro Ser Ala Val Lys Trp Ile Ala Glu
    130                 135                 140

Asn Gln Leu Ser Asp Gly Ser Trp Gly Asp Ala Tyr Leu Phe Ser Tyr
145                 150                 155                 160

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

Trp Asn Leu Phe Pro His Gln Cys Asn Lys Gly Ile Thr Phe Phe Arg
            180                 185                 190

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

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

Asn Ile Asp Val Pro Tyr Asp Ser Pro Val Leu Lys Asp Ile Tyr Ala
225                 230                 235                 240

Lys Lys Glu Leu Lys Leu Thr Arg Ile Pro Lys Glu Ile Met His Lys
                245                 250                 255

Ile Pro Thr Thr Leu Leu His Ser Leu Glu Gly Met Arg Asp Leu Asp
            260                 265                 270

Trp Glu Lys Leu Leu Lys Leu Gln Ser Gln Asp Gly Ser Phe Leu Phe
        275                 280                 285

Ser Pro Ser Ser Thr Ala Phe Ala Phe Met Gln Thr Arg Asp Ser Asn
    290                 295                 300
```

```
Cys Leu Glu Tyr Leu Arg Asn Ala Val Lys Arg Phe Asn Gly Gly Val
305                 310                 315                 320

Pro Asn Val Phe Pro Val Asp Leu Phe Glu His Ile Trp Ile Val Asp
                325                 330                 335

Arg Leu Gln Arg Leu Gly Ile Ser Arg Tyr Phe Glu Glu Glu Ile Lys
            340                 345                 350

Glu Cys Leu Asp Tyr Val His Arg Tyr Trp Thr Asp Asn Gly Ile Cys
        355                 360                 365

Trp Ala Arg Cys Ser His Val Gln Asp Ile Asp Asp Thr Ala Met Ala
    370                 375                 380

Phe Arg Leu Leu Arg Gln His Gly Tyr Gln Val Ser Ala Asp Val Phe
385                 390                 395                 400

Lys Asn Phe Glu Lys Glu Gly Glu Phe Phe Cys Phe Val Gly Gln Ser
                405                 410                 415

Asn Gln Ala Val Thr Gly Met Phe Asn Leu Tyr Arg Ala Ser Gln Leu
            420                 425                 430

Ala Phe Pro Arg Glu Glu Ile Leu Lys Asn Ala Lys Glu Phe Ser Tyr
        435                 440                 445

Asn Tyr Leu Leu Glu Lys Arg Glu Arg Glu Glu Leu Ile Asp Lys Trp
    450                 455                 460

Ile Ile Met Lys Asp Leu Pro Gly Glu Ile Gly Phe Ala Leu Glu Ile
465                 470                 475                 480

Pro Trp Tyr Ala Ser Leu Pro Arg Val Glu Thr Arg Phe Tyr Ile Asp
                485                 490                 495

Gln Tyr Gly Gly Glu Asn Asp Val Trp Ile Gly Lys Thr Leu Tyr Arg
            500                 505                 510

Met Pro Tyr Val Asn Asn Asn Gly Tyr Leu Glu Leu Ala Lys Gln Asp
        515                 520                 525

Tyr Asn Asn Cys Gln Ala Gln His Gln Leu Glu Trp Asp Ile Phe Gln
    530                 535                 540

Lys Trp Tyr Glu Glu Asn Arg Leu Ser Glu Trp Gly Val Arg Arg Ser
545                 550                 555                 560

Glu Leu Leu Glu Cys Tyr Tyr Leu Ala Ala Ala Thr Ile Phe Glu Ser
                565                 570                 575
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Glu Arg Ser His Glu Arg Met Val Trp Ala Lys Ser Ser Val Leu Val
            580                 585                 590

Lys Ala Ile Ser Ser Ser Phe Gly Glu Ser Ser Asp Ser Arg Arg Ser
        595                 600                 605

Phe Ser Asp Gln Phe His Glu Tyr Ile Ala Asn Ala Arg Arg Ser Asp
    610                 615                 620

His His Phe Asn Asp Arg Asn Met Arg Leu Asp Arg Pro Gly Ser Val
625                 630                 635                 640

Gln Ala Ser Arg Leu Ala Gly Val Leu Ile Gly Thr Leu Asn Gln Met
                645                 650                 655

Ser Phe Asp Leu Phe Met Ser His Gly Arg Asp Val Asn Asn Leu Leu
            660                 665                 670

Tyr Leu Ser Trp Gly Asp Trp Met Glu Lys Trp Lys Leu Tyr Gly Asp
        675                 680                 685

Glu Gly Glu Gly Glu Leu Met Val Lys Met Ile Ile Leu Met Lys Asn
    690                 695                 700

Asn Asp Leu Thr Asn Phe Phe Thr His Thr His Phe Val Arg Leu Ala
705                 710                 715                 720

Glu Ile Ile Asn Arg Ile Cys Leu Pro Arg Gln Tyr Leu Lys Ala Arg
                725                 730                 735

Arg Asn Asp Glu Lys Glu Lys Thr Ile Lys Ser Met Glu Lys Glu Met
            740                 745                 750

Gly Lys Met Val Glu Leu Ala Leu Ser Glu Ser Asp Thr Phe Arg Asp
        755                 760                 765

Val Ser Ile Thr Phe Leu Asp Val Ala Lys Ala Phe Tyr Tyr Phe Ala
    770                 775                 780

Leu Cys Gly Asp His Leu Gln Thr His Ile Ser Lys Val Leu Phe Gln
785                 790                 795                 800

Lys Val
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<211> 983
<212> PRT
<213> Diaporthe amygdali

<400> 55

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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

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
            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                 395                 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                 480

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                 560

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

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

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> 56
<211> 881
<212> PRT
<213> Physcomitrella patens

<400> 56

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

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

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

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
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> 57
<211> 952
<212> PRT
<213> Gibberella fujikuroi

<400> 57

```
Met Pro Gly Lys Ile Glu Asn Gly Thr Pro Lys Asp Leu Lys Thr Gly
1               5                   10                  15

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

Ser His His Ser Tyr Tyr Gly Leu Cys Ser Thr Ser Cys Gln Val Tyr
        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
        115                 120                 125

Glu His Gly Val Thr Ser Leu Lys Arg Gln Leu Ala Val Trp Asn Asp
    130                 135                 140

Val Glu Asp Thr Asn His Ile Gly Val Glu Phe Ile Ile Pro Ala Leu
145                 150                 155                 160

Leu Ser Met Leu Glu Lys Glu Leu Asp Val Pro Ser Phe Glu Phe Pro
                165                 170                 175

Cys Arg Ser Ile Leu Glu Arg Met His Gly Glu Lys Leu Gly His Phe
            180                 185                 190

Asp Leu Glu Gln Val Tyr Gly Lys Pro Ser Ser Leu Leu His Ser Leu
        195                 200                 205

Glu Ala Phe Leu Gly Lys Leu Asp Phe Asp Arg Leu Ser His His Leu
    210                 215                 220

Tyr His Gly Ser Met Met Ala Ser Pro Ser Ser Thr Ala Ala Tyr Leu
225                 230                 235                 240
```

```
Ile Gly Ala Thr Lys Trp Asp Asp Glu Ala Glu Asp Tyr Leu Arg His
                245                 250                 255

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

Phe Pro Thr Thr His Phe Glu Cys Ser Trp Ile Ile Ala Thr Leu Leu
        275                 280                 285

Lys Val Gly Phe Thr Leu Lys Gln Ile Asp Gly Asp Gly Leu Arg Gly
    290                 295                 300

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

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

Leu Ala Leu Ser Leu Val Asn Gln Pro Val Ser Pro Asp Ile Met Ile
            340                 345                 350

Lys Val Phe Glu Gly Lys Asp His Phe Thr Thr Phe Gly Ser Glu Arg
        355                 360                 365

Asp Pro Ser Leu Thr Ser Asn Leu His Val Leu Leu Ser Leu Leu Lys
    370                 375                 380

Gln Ser Asn Leu Ser Gln Tyr His Pro Gln Ile Leu Lys Thr Thr Leu
385                 390                 395                 400

Phe Thr Cys Arg Trp Trp Trp Gly Ser Asp His Cys Val Lys Asp Lys
                405                 410                 415

Trp Asn Leu Ser His Leu Tyr Pro Thr Met Leu Leu Val Glu Ala Phe
            420                 425                 430

Thr Glu Val Leu His Leu Ile Asp Gly Gly Glu Leu Ser Ser Leu Phe
        435                 440                 445

Asp Glu Ser Phe Lys Cys Lys Ile Gly Leu Ser Ile Phe Gln Ala Val
    450                 455                 460

Leu Arg Ile Ile Leu Thr Gln Asp Asn Asp Gly Ser Trp Arg Gly Tyr
465                 470                 475                 480

Arg Glu Gln Thr Cys Tyr Ala Ile Leu Ala Leu Val Gln Ala Arg His
                485                 490                 495

Val Cys Phe Phe Thr His Met Val Asp Arg Leu Gln Ser Cys Val Asp
            500                 505                 510
```

```
Arg Gly Phe Ser Trp Leu Lys Ser Cys Ser Phe His Ser Gln Asp Leu
        515                 520                 525

Thr Trp Thr Ser Lys Thr Ala Tyr Glu Val Gly Phe Val Ala Glu Ala
    530                 535                 540

Tyr Lys Leu Ala Ala Leu Gln Ser Ala Ser Leu Glu Val Pro Ala Ala
545                 550                 555                 560

Thr Ile Gly His Ser Val Thr Ser Ala Val Pro Ser Ser Asp Leu Glu
                565                 570                 575

Lys Tyr Met Arg Leu Val Arg Lys Thr Ala Leu Phe Ser Pro Leu Asp
            580                 585                 590

Glu Trp Gly Leu Met Ala Ser Ile Ile Glu Ser Ser Phe Phe Val Pro
        595                 600                 605

Leu Leu Gln Ala Gln Arg Val Glu Ile Tyr Pro Arg Asp Asn Ile Lys
    610                 615                 620

Val Asp Glu Asp Lys Tyr Leu Ser Ile Ile Pro Phe Thr Trp Val Gly
625                 630                 635                 640

Cys Asn Asn Arg Ser Arg Thr Phe Ala Ser Asn Arg Trp Leu Tyr Asp
                645                 650                 655

Met Met Tyr Leu Ser Leu Leu Gly Tyr Gln Thr Asp Glu Tyr Met Glu
            660                 665                 670

Ala Val Ala Gly Pro Val Phe Gly Asp Val Ser Leu Leu His Gln Thr
        675                 680                 685

Ile Asp Lys Val Ile Asp Asn Thr Met Gly Asn Leu Ala Arg Ala Asn
    690                 695                 700

Gly Thr Val His Ser Gly Asn Gly His Gln His Glu Ser Pro Asn Ile
705                 710                 715                 720

Gly Gln Val Glu Asp Thr Leu Thr Arg Phe Thr Asn Ser Val Leu Asn
                725                 730                 735

His Lys Asp Val Leu Asn Ser Ser Ser Ser Asp Gln Asp Thr Leu Arg
            740                 745                 750

Arg Glu Phe Arg Thr Phe Met His Ala His Ile Thr Gln Ile Glu Asp
        755                 760                 765

Asn Ser Arg Phe Ser Lys Gln Ala Ser Ser Asp Ala Phe Ser Ser Pro
    770                 775                 780
```

```
Glu Gln Ser Tyr Phe Gln Trp Val Asn Ser Thr Gly Gly Ser His Val
785                 790                 795                 800

Ala Cys Ala Tyr Ser Phe Ala Phe Ser Asn Cys Leu Met Ser Ala Asn
                805                 810                 815

Leu Leu Gln Gly Lys Asp Ala Phe Pro Ser Gly Thr Gln Lys Tyr Leu
            820                 825                 830

Ile Ser Ser Val Met Arg His Ala Thr Asn Met Cys Arg Met Tyr Asn
        835                 840                 845

Asp Phe Gly Ser Ile Ala Arg Asp Asn Ala Glu Arg Asn Val Asn Ser
    850                 855                 860

Ile His Phe Pro Glu Phe Thr Leu Cys Asn Gly Thr Ser Gln Asn Leu
865                 870                 875                 880

Asp Glu Arg Lys Glu Arg Leu Leu Lys Ile Ala Thr Tyr Glu Gln Gly
                885                 890                 895

Tyr Leu Asp Arg Ala Leu Glu Ala Leu Glu Arg Gln Ser Arg Asp Asp
            900                 905                 910

Ala Gly Asp Arg Ala Gly Ser Lys Asp Met Arg Lys Leu Lys Ile Val
        915                 920                 925

Lys Leu Phe Cys Asp Val Thr Asp Leu Tyr Asp Gln Leu Tyr Val Ile
    930                 935                 940

Lys Asp Leu Ser Ser Ser Met Lys
945                 950
```

<210> 58
<211> 361
<212> PRT
<213> Stevia rebaudiana

<400> 58

```
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

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> 59
<211> 342
<212> PRT
<213> Fusarium fujikuroi

<400> 59

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

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

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> 60
<211> 300
<212> PRT
<213> Mus musculus

<400> 60

```
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

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> 61
<211> 339
<212> PRT
<213> Thalassiosira pseudonana

<400> 61

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
                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


Arg Lys Asn
```

<210> 62
<211> 355
<212> PRT
<213> Streptomyces clavuligerus

<400> 62

```
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
    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>  63
<211>  330
<212>  PRT
<213>  Sulfolobus acidocaldarius

<400>  63

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
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```
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                 330
```

<210> 64
<211> 297
<212> PRT
<213> Synechococcus sp.

<400> 64

```
Met Val Ala Gln Thr Phe Asn Leu Asp Thr Tyr Leu Ser Gln Arg Gln
1               5                  10                  15

Gln Gln Val Glu Glu Ala Leu Ser Ala Ala Leu Val Pro Ala Tyr Pro
            20                  25                  30

Glu Arg Ile Tyr Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys
        35                  40                  45

Arg Leu Arg Pro Ile Leu Cys Leu Ala Ala Cys Glu Leu Ala Gly Gly
    50                  55                  60

Ser Val Glu Gln Ala Met Pro Thr Ala Cys Ala Leu Glu Met Ile His
65                  70                  75                  80

Thr Met Ser Leu Ile His Asp Asp Leu Pro Ala Met Asp Asn Asp Asp
                85                  90                  95

Phe Arg Arg Gly Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Ile
            100                 105                 110

Ala Ile Leu Ala Gly Asp Ala Leu Leu Ala Tyr Ala Phe Glu His Ile
        115                 120                 125

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

Ala Arg Ile Gly His Ala Val Ala Ala Thr Gly Leu Val Gly Gly Gln
145                 150                 155                 160

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

Glu Tyr Ile His Ser His Lys Thr Gly Ala Leu Leu Glu Ala Ser Val
            180                 185                 190

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

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

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> 65
<211> 371
<212> PRT
<213> Arabidopsis thaliana

<400> 65

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

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> 66
<211> 473
<212> PRT
<213> Stevia rebaudiana

<400> 66

```
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 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 Gly Tyr Arg
        195                 200                 205

Met Gly Met 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 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

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>  67
<211>  459
<212>  PRT
<213>  Ipomoea purpurea

<400>  67

Met Gly Ser Gln Ala Thr Thr Tyr His Met Ala Met Tyr Pro Trp Phe
1               5                   10                  15

Gly Val Gly His Leu Thr Gly Phe Phe Arg Leu Ala Asn Lys Leu Ala
            20                  25                  30

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

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

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

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

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

Val Val Phe Tyr Asp Phe Thr His Trp Leu Pro Ser Leu Ala Arg Lys
        115                 120                 125

Ile Gly Ile Lys Ser Val Phe Tyr Ser Thr Ile Ser Pro Leu Met His
    130                 135                 140

Gly Tyr Ala Leu Ser Pro Glu Arg Arg Val Val Gly Lys Gln Leu Thr
145                 150                 155                 160

Glu Ala Asp Met Met Lys Ala Pro Ala Ser Phe Pro Asp Pro Ser Ile
                165                 170                 175

Lys Leu His Ala His Glu Ala Arg Gly Phe Thr Ala Arg Thr Val Met
            180                 185                 190

Lys Phe Gly Gly Asp Ile Thr Phe Phe Asp Arg Ile Phe Thr Ala Val
        195                 200                 205

Ser Glu Ser Asp Gly Leu Ala Tyr Ser Thr Cys Arg Glu Ile Glu Gly
    210                 215                 220

Gln Phe Cys Asp Tyr Ile Glu Thr Gln Phe Gln Lys Pro Val Leu Leu
225                 230                 235                 240

Ala Gly Pro Ala Leu Pro Val Pro Ser Lys Ser Thr Met Glu Gln Lys
                245                 250                 255

Trp Ser Asp Trp Leu Gly Lys Phe Lys Glu Gly Ser Val Ile Tyr Cys
            260                 265                 270

Ala Phe Gly Ser Glu Cys Thr Leu Arg Lys Asp Lys Phe Gln Glu Leu
        275                 280                 285

Leu Trp Gly Leu Glu Leu Thr Gly Met Pro Phe Phe Ala Ala Leu Lys
    290                 295                 300

Pro Pro Phe Glu Thr Glu Ser Val Glu Ala Ala Ile Pro Glu Glu Leu
305                 310                 315                 320

Lys Glu Lys Ile Gln Gly Arg Gly Ile Val His Gly Glu Trp Val Gln
                325                 330                 335

Gln Gln Leu Phe Leu Gln His Pro Ser Val Gly Cys Phe Val Ser His
            340                 345                 350

Cys Gly Trp Ala Ser Leu Ser Glu Ala Leu Val Asn Asp Cys Gln Ile
        355                 360                 365
```

Val Leu Leu Pro Gln Val Gly Asp Gln Ile Ile Asn Ala Arg Ile Met
370 375 380

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
420 425 430

Leu Arg Gly Phe Leu Met Asn Ala Asp Leu Asp Ser Lys Tyr Met Asp
435 440 445

Ser Phe Asn Gln Lys Leu Gln Asp Leu Leu Gly
450 455

<210> 68
<211> 1380
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 68
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ttgactggtt tcttccgttt ggcaaacaaa ttagctggca aaggacatag aatctcattt 120

ctaattccta aaaacactca atctaagtta gaatctttca accttcatcc acacttaatc 180

tcttttgtgc ctatcgttgt cccaagtata ccaggcctgc cacctggtgc agagactaca 240

tcagatgttc ctttcccaag tacacatttg ctaatggaag caatggacaa gactcaaaac 300

gatatagaga ttatcctgaa ggatcttaaa gtagatgttg ttttctatga ttttactcac 360

tggttgcctt ctctggccag aaagattggc attaagagtg tcttttactc caccatttct 420

cctttaatgc atggatatgc tttatcacca gaaagacgtg tagttggtaa gcaattgaca 480

gaggcagata tgatgaaggc cccagcttct ttcccagacc catccattaa gctacatgca 540

catgaagcta ggggttttac agccagaacc gttatgaaat tcggtggtga catcaccttt 600

ttcgatagaa tattcacagc agtttccgaa agtgatggcc tggcctactc tacttgtaga 660

gagatcgagg gacaattctg tgattacatt gaaacacaat tccagaagcc agtcttgtta 720

gccggtccag ctttgccagt cccatccaaa tccactatgg aacaaaagtg gtcagattgg 780

ttggggaaat tcaaggaagg ctccgtcatc tactgtgctt tcgggtctga atgtacattg 840

agaaaggaca aatttcagga acttttatgg ggtttggaat tgacaggaat gcctttcttc 900

gctgctctga agccaccttt tgagactgag tctgttgagg ctgctatccc tgaggaacta 960

aaggaaaaga ttcagggaag aggtatagta catggagaat gggtacaaca acaattgttt 1020

cttcaacacc catctgtcgg gtgcttcgtt tctcactgcg gctgggcaag tttatctgaa 1080

gcccttgtta atgattgtca aatcgtgtta cttccacaag ttggcgatca gattatcaac 1140

gccagaataa tgtcagtatc acttaaagtg ggcgtggaag ttgaaaaggg tgaggaggac 1200

ggtgtctttt caagagaatc tgtgtgcaag gctgttaaag cagtaatgga tgaaaaatct 1260

gaaatcggta gagaagtcag aggtaatcat gataaactga ggggtttctt gatgaatgca 1320

gacttagatt caaagtacat ggattcattc aatcaaaagc tacaagattt gctaggttaa 1380

<210> 69
<211> 438
<212> PRT
<213> Bellis perennis

<400> 69

Met Asp Ser Lys Ile Asp Ser Lys Thr Phe Arg Val Val Met Leu Pro
1 5 10 15

Trp Leu Ala Tyr Ser His Ile Ser Ser Phe Leu Val Phe Ala Lys Arg
20 25 30

Leu Thr Asn His Asn Phe His Ile Tyr Ile Cys Ser Ser Gln Thr Asn
35 40 45

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
65 70 75 80

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

Arg Asp Ile Pro Lys Gly Gly Ser Lys Tyr Ile Glu Arg Phe Val Asp
180 185 190

Cys Met Arg Arg Ser Cys Glu Ile Ile Leu Val Arg Ser Thr Met Glu

195 200 205

Leu Glu Gly Lys Tyr Ile Asp Tyr Leu Ser Lys Thr Leu Gly Lys Lys
210 215 220

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
245 250 255

Val Val Phe Val Cys Phe Gly Ser Glu Tyr Ile Leu Ser Asp Asn Glu
260 265 270

Ile Glu Asp Ile Ala Tyr Gly Leu Glu Leu Ser Gln Val Ser Phe Val
275 280 285

Trp Ala Ile Arg Ala Lys Thr Ser Ala Leu Asn Gly Phe Ile Asp Arg
290 295 300

Val Gly Asp Lys Gly Leu Val Ile Asp Lys Trp Val Pro Gln Ala Asn
305 310 315 320

Ile Leu Ser His Ser Ser Thr Gly Gly Phe Ile Ser His Cys Gly Trp
325 330 335

Ser Ser Thr Met Glu Ser Ile Arg Tyr Gly Val Pro Ile Ile Ala Met
340 345 350

Pro Met Gln Phe Asp Gln Pro Tyr Asn Ala Arg Leu Met Glu Thr Val
355 360 365

Gly Ala Gly Ile Glu Val Gly Arg Asp Gly Glu Gly Arg Leu Lys Arg
370 375 380

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

Glu Ser Ile Arg Glu Lys Ala Lys Glu Leu Gly Glu Ile Met Lys Lys
405 410 415

Asn Met Glu Ala Glu Val Asp Gly Ile Val Ile Glu Asn Leu Val Lys
420 425 430

Leu Cys Glu Met Asn Asn
435

<210> 70
<211> 1317
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 70
atggattcta aaatcgattc aaagacattc agagtcgtta tgttgccttg gcttgcatac 60

tcacacattt catcattcct agtgtttgcc aagagactaa caaatcataa cttccacatc 120

tacatttgtt cctctcaaac aaatatgcaa tacctgaaaa acaacttgac gtctcagtat 180

tcaaaatcta tacaactgat tgagttgaat cttccatcta gttccgaatt gcctctgcag 240

tatcatacta ctcacggact accaccacac cttacgaaaa cattgtctga tgattatcaa 300

aagtccggac ctgactttga aaccattttg atcaaattga acccacatct ggtaatctac 360

gactttaatc aactttgggc tccagaggtt gctagtacac ttcatattcc atccatacag 420

ttactgtctg gttgcgtcgc cttatatgcc ttagacgccc atctgtacac aaagccacta 480

gacgaaaact tggctaagtt tcctttccca gaaatctatc ctaaaaacag agatattcct 540

aagggaggta gtaaatacat cgaaaggttc gtagactgta tgagaagatc ttgtgaaatc 600

atattagtca gaagtaccat ggaacttgaa ggaaaataca ttgattactt gtctaagaca 660

ttagggaaaa aggtgttgcc agtagggcct ctggtgcaag aggcttcttt gttgcaagat 720

gatcatatat ggattatgaa gtggttagac aaaaaggagg agtcatccgt cgtgtttgtt 780

tgttttggtt ctgagtacat cttatcagac aacgaaatag aagatattgc ttatggccta 840

gagttgtccc aagtaagttt cgtttgggca ataagagcta agacttctgc cttaaatggc 900

ttcattgata gagtgggtga taaaggctta gtcatcgata aatgggttcc acaggctaac 960

atcttatctc actcttctac tggtggattc attagtcatt gcggttggtc atcaacaatg 1020

gaatctatta gatatggggt tcctattatc gccatgccaa tgcaattcga tcaaccttac 1080

aatgctaggt tgatggaaac tgttggtgca ggtatcgaag ttggcagaga tggcgaaggt 1140

agattgaaaa gagaagagat tgctgccgtg gttagaaagg tcgttgttga agattctggg 1200

gaatccataa gggagaaggc aaaggaattg ggagaaatca tgaaaaaaaa catggaggcc 1260

gaagtagatg gtatagtgat tgaaaatcta gttaagctat gtgagatgaa caattaa 1317

<210> 71
<211> 477
<212> PRT
<213> Arabidopsis thaliana

<400> 71

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

Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly
20 25 30

Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val
35 40 45

```
Lys Cys Ser Val Lys Val Gln Gln Gln Gln Pro Pro Pro Ala Trp
    50                  55                  60

Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro
65                  70                  75                  80

Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr
                85                  90                  95

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

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

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

Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly
145                 150                 155                 160

Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val
                165                 170                 175

Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala
            180                 185                 190

Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile
        195                 200                 205

Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys
    210                 215                 220

Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln
225                 230                 235                 240

Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly
                245                 250                 255

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

Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr
        275                 280                 285

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

His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His
305                 310                 315                 320
```

Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val
325 330 335

Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr
340 345 350

Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg
355 360 365

Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn
370 375 380

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

Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu
405 410 415

Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val
420 425 430

Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser
435 440 445

Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala
450 455 460

Asn Val Gln Leu Ser Ser Gly Ala Arg Pro Val His Ala
465 470 475

<210> 72
<211> 440
<212> PRT
<213> Leishmania infantum

<400> 72

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

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

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> 73
<211> 527
<212> PRT
<213> Saccharomyces cerevisiae

<400> 73

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
                165                 170                 175

Thr Ser Tyr His Ile Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala
            180                 185                 190

Ser Ala Met Arg Gly Cys Lys Ala Ile Asn Ala Gly Gly Gly Ala Thr
        195                 200                 205

Thr Val Leu Thr Lys Asp Gly Met Thr Arg Gly Pro Val Val Arg Phe
    210                 215                 220

Pro Thr Leu Lys Arg Ser Gly Ala Cys Lys Ile Trp Leu Asp Ser Glu
225                 230                 235                 240

Glu Gly Gln Asn Ala Ile Lys Lys Ala Phe Asn Ser Thr Ser Arg Phe
                245                 250                 255

Ala Arg Leu Gln His Ile Gln Thr Cys Leu Ala Gly Asp Leu Leu Phe
            260                 265                 270

Met Arg Phe Arg Thr Thr Thr Gly Asp Ala Met Gly Met Asn Met Ile
        275                 280                 285

Ser Lys Gly Val Glu Tyr Ser Leu Lys Gln Met Val Glu Glu Tyr Gly
    290                 295                 300

Trp Glu Asp Met Glu Val Val Ser Val Ser Gly Asn Tyr Cys Thr Asp
305                 310                 315                 320

Lys Lys Pro Ala Ala Ile Asn Trp Ile Glu Gly Arg Gly Lys Ser Val
                325                 330                 335

Val Ala Glu Ala Thr Ile Pro Gly Asp Val Val Arg Lys Val Leu Lys
            340                 345                 350

Ser Asp Val Ser Ala Leu Val Glu Leu Asn Ile Ala Lys Asn Leu Val
        355                 360                 365

Gly Ser Ala Met Ala Gly Ser Val Gly Gly Phe Asn Ala His Ala Ala
    370                 375                 380

Asn Leu Val Thr Ala Val Phe Leu Ala Leu Gly Gln Asp Pro Ala Gln
385                 390                 395                 400

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

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> 74
<211> 1226
<212> PRT
<213> Ganoderma lucidum

<400> 74

```
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

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

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

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
        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

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>  75
<211>  888
<212>  PRT
<213>  Bos taurus

<400>  75

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


Pro Trp Glu Val Ile Val Gly Thr Val Thr Leu Thr Ile Cys Met Met
            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


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
            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

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
885

<210> 76
<211> 567
<212> PRT
<213> Artemisia annua

<400> 76

Met Asp Leu Arg Arg Lys Leu Pro Pro Lys Pro Pro Ser Ser Thr Thr
1 5 10 15

Thr Lys Gln Pro Ser His Arg Ser His Ser Pro Thr Pro Ile Pro Lys
20 25 30

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 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

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
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
545 550 555 560

Ser Ala Ile Ala Ser Lys Val
565

<210> 77
<211> 435
<212> PRT
<213> Trypanosoma cruzi

<400> 77

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

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
            420                 425                 430

Lys Lys Lys
        435
```

<210> 78
<211> 426
<212> PRT
<213> Staphylococcus aureus

<400> 78

```
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

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
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<210> 79
<211> 481
<212> PRT
<213> Arabidopsis thaliana

<400> 79

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

Gly His Val Ile Pro Val Ile Glu Leu Gly Lys Arg Leu Ser Ala Asn
            20                  25                  30

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

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

Pro Ser Pro Asp Ile Tyr Gly Leu Val Asp Pro Asp Asp His Val Val
65                  70                  75                  80

Thr Lys Ile Gly Val Ile Met Arg Ala Ala Val Pro Ala Leu Arg Ser
                85                  90                  95

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

Phe Gly Thr Asp Ala Leu Cys Leu Ala Lys Glu Phe Asn Met Leu Ser
        115                 120                 125

Tyr Val Phe Ile Pro Thr Asn Ala Arg Phe Leu Gly Val Ser Ile Tyr
    130                 135                 140

Tyr Pro Asn Leu Asp Lys Asp Ile Lys Glu Glu His Thr Val Gln Arg
145                 150                 155                 160

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

Leu Asp Ala Tyr Leu Val Pro Asp Glu Pro Val Tyr Arg Asp Phe Val
            180                 185                 190

Arg His Gly Leu Ala Tyr Pro Lys Ala Asp Gly Ile Leu Val Asn Thr
        195                 200                 205
```

```
Trp Glu Glu Met Glu Pro Lys Ser Leu Lys Ser Leu Leu Asn Pro Lys
    210                 215                 220

Leu Leu Gly Arg Val Ala Arg Val Pro Val Tyr Pro Ile Gly Pro Leu
225                 230                 235                 240

Cys Arg Pro Ile Gln Ser Ser Glu Thr Asp His Pro Val Leu Asp Trp
                245                 250                 255

Leu Asn Glu Gln Pro Asn Glu Ser Val Leu Tyr Ile Ser Phe Gly Ser
            260                 265                 270

Gly Gly Cys Leu Ser Ala Lys Gln Leu Thr Glu Leu Ala Trp Gly Leu
        275                 280                 285

Glu Gln Ser Gln Gln Arg Phe Val Trp Val Val Arg Pro Pro Val Asp
    290                 295                 300

Gly Ser Cys Cys Ser Glu Tyr Val Ser Ala Asn Gly Gly Gly Thr Glu
305                 310                 315                 320

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

Asp Arg Gly Phe Val Val Pro Ser Trp Ala Pro Gln Ala Glu Ile Leu
            340                 345                 350

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

Thr Leu Glu Ser Val Val Gly Gly Val Pro Met Ile Ala Trp Pro Leu
    370                 375                 380

Phe Ala Glu Gln Asn Met Asn Ala Ala Leu Leu Ser Asp Glu Leu Gly
385                 390                 395                 400

Ile Ala Val Arg Leu Asp Asp Pro Lys Glu Asp Ile Ser Arg Trp Lys
                405                 410                 415

Ile Glu Ala Leu Val Arg Lys Val Met Thr Glu Lys Glu Gly Glu Ala
            420                 425                 430

Met Arg Arg Lys Val Lys Lys Leu Arg Asp Ser Ala Glu Met Ser Leu
        435                 440                 445

Ser Ile Asp Gly Gly Gly Leu Ala His Glu Ser Leu Cys Arg Val Thr
    450                 455                 460

Lys Glu Cys Gln Arg Phe Leu Glu Arg Val Val Asp Leu Ser Arg Gly
465                 470                 475                 480
```

Ala

<210> 80
<211> 513
<212> PRT
<213> Arabidopsis thaliana

<400> 80

Met Gly Ala Tyr Glu Thr Glu Lys Pro Thr Lys Asp Ala Ala Ala Leu
1 5 10 15

Glu Thr Gln Ser Pro Glu Asp Phe Asp Gln Pro Ser Pro Leu Arg Lys
20 25 30

Ile Ile Ser Val Ala Ser Ile Ala Ala Gly Val Gln Phe Gly Trp Ala
35 40 45

Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln Leu Leu Gly Ile Pro
50 55 60

His Lys Trp Ser Ser Leu Ile Trp Leu Cys Gly Pro Val Ser Gly Met
65 70 75 80

Ile Val Gln Pro Ile Val Gly Phe His Ser Asp Arg Cys Arg Ser Lys
85 90 95

Phe Gly Arg Arg Arg Pro Phe Ile Ala Thr Gly Ala Ala Leu Val Ala
100 105 110

Val Ala Val Phe Leu Ile Gly Tyr Ala Ala Asp Phe Gly Tyr Lys Met
115 120 125

Gly Asp Lys Leu Glu Glu Lys Val Lys Val Arg Ala Ile Gly Ile Phe
130 135 140

Ala Leu Gly Phe Trp Ile Leu Asp Val Ala Asn Asn Thr Leu Gln Gly
145 150 155 160

Pro Cys Arg Ala Phe Leu Ala Asp Leu Ala Ala Gly Asp Ala Lys Arg
165 170 175

Thr Arg Val Ala Asn Ala Phe Phe Ser Phe Phe Met Ala Val Gly Asn
180 185 190

Val Leu Gly Tyr Ala Ala Gly Ser Tyr Thr Asn Leu His Lys Met Phe
195 200 205

Pro Phe Thr Met Thr Lys Ala Cys Asp Ile Tyr Cys Ala Asn Leu Lys
210 215 220

Thr Cys Phe Phe Leu Ser Ile Thr Leu Leu Leu Ile Val Thr Val Thr

225 230 235 240

Ser Leu Trp Tyr Val Asn Asp Lys Gln Trp Ser Pro Pro Pro Arg Asn
245 250 255

Ala Asp Asp Asp Glu Lys Thr Ser Ser Val Pro Leu Phe Gly Glu Ile
260 265 270

Phe Gly Ala Phe Lys Val Met Lys Arg Pro Met Trp Met Leu Leu Ile
275 280 285

Val Thr Ala Leu Asn Trp Ile Ala Trp Phe Pro Phe Leu Leu Phe Asp
290 295 300

Thr Asp Trp Met Gly Arg Glu Val Phe Gly Gly Asp Ser Asp Gly Asn
305 310 315 320

Glu Arg Ser Lys Lys Leu Tyr Ser Leu Gly Val Gln Ser Gly Ala Met
325 330 335

Gly Leu Met Phe Asn Ser Ile Val Leu Gly Phe Met Ser Leu Gly Val
340 345 350

Glu Trp Ile Gly Arg Lys Leu Gly Gly Ala Lys Arg Leu Trp Gly Ile
355 360 365

Val Asn Phe Ile Leu Ala Ala Gly Leu Ala Met Thr Val Leu Val Thr
370 375 380

Lys Phe Ala Glu Asp His Arg Lys Thr Ala Gly Asp Leu Ala Gly Pro
385 390 395 400

Ser Ala Ser Val Lys Ala Gly Ala Leu Ser Leu Phe Ala Val Leu Gly
405 410 415

Ile Pro Leu Ala Ile Thr Phe Ser Thr Pro Phe Ala Leu Ala Ser Ile
420 425 430

Phe Ser Ser Cys Ser Gly Ala Gly Gln Gly Leu Ser Leu Gly Val Leu
435 440 445

Asn Leu Ala Ile Val Ile Pro Gln Met Ile Val Ser Leu Gly Gly Gly
450 455 460

Pro Phe Asp Ala Leu Phe Gly Gly Gly Asn Leu Pro Ala Phe Ile Val
465 470 475 480

Ala Ala Ile Ala Ala Ala Ile Ser Gly Val Leu Ala Leu Thr Val Leu
485 490 495

Pro Ser Pro Pro Pro Asp Ala Pro Lys Ala Thr Thr Met Gly Gly Phe

500 505 510

His

<210> 81
<211> 806
<212> PRT
<213> Coffea arabica

<400> 81

Met Ala Glu Arg Val Leu Thr Arg Val His Ser Leu Arg Glu Arg Leu
1 5 10 15

Asp Ala Thr Leu Ala Ala His Arg Asn Asp Val Leu Leu Phe Met Ser
20 25 30

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

Ala Glu Phe Glu Glu Ile Asn Lys Asp Gly Lys Gln Lys Ile His Asp
50 55 60

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

Pro Pro Trp Val Ala Leu Ala Ile Arg Leu Arg Pro Gly Val Trp Glu
85 90 95

Tyr Val Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val
100 105 110

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

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

Pro Lys Pro Thr Leu Thr Lys Tyr Ile Gly Asp Gly Val Glu Phe Leu
145 150 155 160

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

Pro Leu Leu Asp Phe Leu Arg Val His Gln Tyr Lys Gly Lys Thr Met
180 185 190

Met Leu Asn Asp Arg Ile Lys Asp Leu Asn Thr Leu Gln Ala Val Leu
195 200 205

Arg Lys Ala Glu Glu Tyr Leu Thr Thr Leu Ser Ala Asp Thr Pro Tyr
210 215 220

```
Ser Glu Phe Glu His Lys Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp
225                 230                 235                 240

Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Cys Met Leu Leu Asp
                245                 250                 255

Leu Leu Gly Ala Pro Asp Ser Cys Thr Leu Glu Lys Phe Leu Gly Arg
            260                 265                 270

Ile Pro Met Val Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe
        275                 280                 285

Ala Gln Glu Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val
    290                 295                 300

Tyr Ile Leu Asp Gln Val Pro Ala Leu Glu Arg Glu Met Leu Lys Arg
305                 310                 315                 320

Ile Lys Glu Gln Gly Leu Asp Val Lys Pro Arg Ile Leu Ile Ile Thr
                325                 330                 335

Arg Leu Leu Pro Asp Ala Pro Gly Thr Thr Cys Gly Gln Arg Leu Glu
            340                 345                 350

Lys Val Tyr Gly Ser Glu Tyr Ser His Ile Leu Arg Val Pro Phe Arg
        355                 360                 365

Thr Glu Lys Gly Val Val Arg Lys Trp Ile Ser Arg Phe Glu Val Trp
    370                 375                 380

Pro Tyr Met Glu Thr Phe Thr Glu Asp Val Ala Lys Glu Val Thr Ala
385                 390                 395                 400

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

Asn Leu Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys
            420                 425                 430

Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp Ile
        435                 440                 445

Tyr Leu Ser Lys Phe Asp Glu Lys Tyr His Phe Ser Cys Gln Phe Thr
    450                 455                 460

Ala Asp Leu Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr
465                 470                 475                 480

Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu Ser
                485                 490                 495
```

```
His Met Ala Phe Thr Met Pro Gly Leu Tyr Arg Val Val His Gly Ile
            500                 505                 510

Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Thr
        515                 520                 525

Asn Leu Tyr Phe Pro His Thr Glu Lys Glu Lys Arg Leu Thr Ser Phe
    530                 535                 540

His Pro Glu Ile Glu Glu Leu Leu Phe Ser Asp Val Glu Asn Glu Glu
545                 550                 555                 560

His Leu Cys Val Leu Lys Asp Lys Lys Lys Pro Ile Leu Phe Thr Met
                565                 570                 575

Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val Glu Leu Tyr
            580                 585                 590

Ala Lys Asn Pro Lys Leu Arg Glu Leu Val Asn Leu Val Val Val Gly
        595                 600                 605

Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu Gln Ala Glu Met
    610                 615                 620

Lys Lys Met Tyr Ser Leu Ile Glu Thr Tyr Asn Leu Asn Gly Gln Phe
625                 630                 635                 640

Arg Trp Ile Ser Ser Gln Met Asn Arg Val Arg Asn Gly Glu Leu Tyr
                645                 650                 655

Arg Tyr Ile Ala Asp Thr Arg Gly Ala Phe Val Gln Pro Ala Phe Tyr
            660                 665                 670

Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu Pro
        675                 680                 685

Thr Phe Ala Thr Asn His Gly Gly Pro Ala Glu Ile Ile Ile His Gly
    690                 695                 700

Lys Ser Gly Phe His Ile Asp Pro Tyr His Gly Glu Gln Val Ser Glu
705                 710                 715                 720

Leu Leu Ala Asn Phe Phe Glu Arg Cys Lys Lys Glu Pro Ser Tyr Trp
                725                 730                 735

Asp Thr Ile Ser Ala Gly Gly Leu Lys Arg Ile Gln Glu Lys Tyr Thr
            740                 745                 750

Trp Gln Ile Tyr Ser Asp Arg Leu Leu Thr Leu Ala Gly Val Tyr Gly
        755                 760                 765
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Phe Trp Lys Cys Val Ser Lys Leu Asp Arg Gln Glu Ile Arg Arg Tyr
770 775 780

Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Leu Ala Glu Ala Val
785 790 795 800

Pro Leu Ala Val Asp Gln
805

<210> 82
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 82
tgaattcgtt aacgaattc 19

<210> 83
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<212> DNA
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<220>
<223> Synthetic oligonucleotide

<400> 83
tgaattcgtt aacgaactc 19

<210> 84
<211> 19
<212> DNA
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<220>
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<400> 84
tgaattcgtt aacgaagtc 19

<210> 85
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<212> DNA
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<220>
<223> Synthetic oligonucleotide

<400> 85
tgaattcgtt aacgaaatt 19

<210> 86
<211> 473
<212> PRT
<213> Stevia rebaudiana

<400> 86

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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 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 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 Val 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
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> 87
<211> 21
<212> DNA
<213> Artificial sequence

<220>
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<400> 87
cggtaggtat tgattgtaat t 21

<210> 88
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<220>
<223> Synthetic oligonucleotide

<400> 88
cttttcggtt agagcggatg t 21

<210> 89
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 89
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tggcttgctt tcggtcatat actgccttac ctacaactat caaaactgat agctgaaaaa 120

ggacataaag tgtcattcct ttcaacaact agaaacattc aaagattatc ttcccacata 180

tcaccattga ttaacgtcgt tcaattgaca cttccaagag tacaggaatt accagaagat 240

gctgaagcta caacagatgt gcatcctgaa gatatccctt acttgaaaaa ggcatccgat 300

ggattacagc ctgaggtcac tagattcctt gagcaacaca gtccagattg gatcatatac 360

gactacactc actattggtt gccttcaatt gcagcatcac taggcatttc tagggcacat 420

ttcagtgtaa ccacaccttg ggccattgct tacatgggtc catccgctga tgctatgatt 480

aacggcagtg atggtagaac taccgttgaa gatttgacaa ccccaccaaa gtggtttcca 540

tttccaacta aagtctgttg gagaaaacac gacttagcaa gactggttcc atacaaggca 600

ccaggaatct cagacggcta tagaatgggt ttagtcctta aagggtctga ctgcctattg 660

tctaagtgtt accatgagtt tgggacacaa tggctaccac ttttggaaac attacaccaa 720

gttcctgtcg taccagttgg tctattacct ccagaaatcc ctggtgatga gaaggacgag 780

acttgggttt caatcaaaaa gtggttagac gggaagcaaa aaggctcagt ggtatatgtg 840

gcactgggtt ccgaagtttt agtatctcaa acagaagttg tggaacttgc cttaggtttg 900

gaactatctg gattgccatt tgtctgggcc tacagaaaac caaaaggccc tgcaaagtcc 960

gattcagttg aattgccaga cggctttgtc gagagaacta gagatagagg gttggtatgg 1020

acttcatggg ctccacaatt gagaatcctg agtcacgaat ctgtgtgcgg tttcctaaca 1080

cattgtggtt ctggttctat agttgaagga ctgatgtttg gtcatccact tatcatgttg 1140

ccaatctttg gtgaccagcc tttgaatgca cgtctgttag aagataaaca agttggaatt 1200

gaaatcccac gtaatgagga agatggatgt ttaaccaagg agtctgtggc cagatcatta 1260

cgttccgttg tcgttgaaaa ggaaggcgaa atctacaagg ccaatgcccg tgaactttca 1320

aagatctaca atgacacaaa agtagagaag gaatatgttt ctcaatttgt agattaccta 1380

gagaaaaacg ctagagccgt agctattgat catgaatcct aa 1422

<210> 90

<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 90
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ggtcacaagg tttcattctt gtctaccacc agaaacatcc aaagattgtc ctctcatatc 180

tccccattga tcaacgttgt tcaattgact ttgccaagag tccaagaatt gccagaagat 240

gctgaagcta ctactgatgt tcatccagaa gatatccctt acttgaaaaa ggcttccgat 300

ggtttacaac cagaagttac tagattcttg gaacaacatt ccccagattg gatcatctac 360

gattatactc attactggtt gccatccatt gctgcttcat tgggtatttc tagagcccat 420

ttctctgtta ctactccatg ggctattgct tatatgggtc catctgctga tgctatgatt 480

aacggttctg atggtagaac taccgttgaa gatttgacta ctccaccaaa gtggtttcca 540

tttccaacaa aagtctgttg gagaaaacac gatttggcta gattggttcc atacaaagct 600

ccaggtattt ctgatggtta cagaatgggt atggttttga aaggttccga ttgcttgttg 660

tctaagtgct atcatgaatt cggtactcaa tggttgcctt tgttggaaac attgcatcaa 720

gttccagttg ttccagtagg tttgttgcca ccagaaattc caggtgacga aaaagacgaa 780

acttgggttt ccatcaaaaa gtggttggat ggtaagcaaa agggttctgt tgtttatgtt 840

gctttgggtt ccgaagcttt ggtttctcaa accgaagttg ttgaattggc tttgggtttg 900

gaattgtctg gtttgccatt tgtttgggct tacagaaaac ctaaaggtcc agctaagtct 960

gattctgttg aattgccaga tggtttcgtt gaaagaacta gagatagagg tttggtttgg 1020

acttcttggg ctccacaatt gagaattttg tctcatgaat ccgtctgtgg tttcttgact 1080

cattgtggtt ctggttctat cgttgaaggt ttgatgtttg gtcacccatt gattatgttg 1140

ccaatctttg gtgaccaacc attgaacgct agattattgg aagataagca agtcggtatc 1200

gaaatcccaa gaaatgaaga agatggttgc ttgaccaaag aatctgttgc tagatctttg 1260

agatccgttg tcgttgaaaa agaaggtgaa atctacaagg ctaacgctag agaattgtcc 1320

aagatctaca acgataccaa ggtcgaaaaa gaatacgttt cccaattcgt tgactacttg 1380

gaaaagaatg ctagagctgt tgccattgat catgaatctt ga 1422

<210> 91
<211> 1503
<212> DNA
<213> Stevia rebaudiana

<400> 91
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acccaacttc gtcgtaaatc cgccaatcta ccgccgacgg tgttcccatc catccccata 120

atcggtcatc tctacctcct caaaaaacca ctctatagaa cactagccaa aattgccgcc 180

aaatacggcc ctatcctcca actccaacta gggtaccgcc gtgtcctcgt aatctcctcc 240

ccttccgccg ccgaagaatg cttcaccaac aacgacgtta tcttcgccaa ccgtccgaag 300

acgctattcg gaaaaattgt agggggtacc agcctcgggt cgctgtcgta cggcgaccag 360

tggcgcaacc tccgccgcgt tgcatccatc gagattctat cagtccaccg gctcaacgag 420

tttcacgaca tacgtgttga cgaaaaccgg cttctgatcc gtaaactaag atccagttct 480

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ttccgggaga tactcgatga gacacttttg ctcgcgggtg cttctaatgt tggggattac 660

ttgccgattc tgaattggtt gggggtgaag agcttggaga agaagctaat cgcattgcag 720

aaaaagagag atgatttctt tcagggactg atcgagcaag ttcggaaatc tagaggggct 780

aaagtgggaa aaggaaggaa gacgatgatc gagttgttgt tatccctaca agaatctgaa 840

cctgagtatt acactgacgc catgatccga tcatttgtgc tgggtttatt agcagcaggg 900

agtgatacat cggctggaac tatggaatgg gcgatgtctc ttttggtaaa ccacccgcac 960

gtattaaaaa aggcacaggc tgaaattgat cgagtcatcg gcaacaaccg tctaattgat 1020

gagtccgaca tagggaatat accttacatt ggttgcatca taaacgagac gctcagattg 1080

taccctgcgg gcccgttgct atttccccat gagtcatcag cggactgtgt tatcagcggg 1140

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aaggtgtggg acgaccctga gacattcaaa ccggaaagat tccaagggct tgaagggaca 1260

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tga 1503

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<211> 436
<212> PRT
<213> Archaeoglobus fulgidus

<400> 92

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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

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

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
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Arg Leu Arg Ser
435

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<400> 93

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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

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Val His Thr Phe Ala Asp Thr Pro Arg Gly Pro Met Leu Val Ala His
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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
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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
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Met Arg Ala Leu Ala Thr Glu Gly Ile Gln Arg Gly His Met Ala Leu
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His Ala Arg Asn Ile Ala Val Val Ala Gly Ala Arg Gly Asp Glu Val
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tcagtcgctg ggttgctgaa caagacctca ctggacccta gagatatcga tcatatcgtt 180

tggggtaatg ttgtacttca aggatcagct cataactgcg ccagagaaat agttatcgac 240

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<400> 97

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aattggattg atggcagagg taaatcagtg gttgcagaag ccactttatt ggctgatgtt 840

gtcgaagata ctctgaaatg tacagtcgat tctttggtat ccttgaatat cgacaaaaac 900

cttgttgggt cagctatggc tggttctgtt ggaggtttta acgcccaggc tgcaaacgct 960

gtggcagcca ttttcattgc aaccggtcaa gatcctgctc aagtggtaga aagttcaatg 1020

tgtatcacta caatgtccaa ggtaggtaac gatctattga tctctgtgac catgccttct 1080

atcgaggtcg gggtcgtggg aggagggact ggtcttgctg cccaaagagg atgcttagag 1140

ttaatagggt gcggaggccc atctaaggag tctcctggta ctaatgccca acttctaagt 1200

agagttgttg cagctggcgt tttatcagcc gaactttcct tgatgtccgg actggcagca 1260

ggtcatctat tgtcagcaca tatgagattg aacagaaaga agaaataa 1308

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<211> 1281
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 100
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gatgaagagg tagcaaactc attgatagaa aatgtcatcg cacagggcgc actgcctgtt 180

ggtttactac caaatatcat cgttgatgac aaagcatacg tcgtgcctat gatggtggaa 240

gagccatctg ttgttgccgc tgcttcatac ggcgctaaat tggtgaacca 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 aaggttttcg ttgatactaa ggatgctatg 540

ggcgctaata tgttaaacac aatcctagaa gcaatcacag ccttttgaa aaacgaattc 600

ccacaatctg atatcttgat gtctatcctt tccaaccacg caacagccag tgttgtcaag 660

gtccagggtg aaatagacgt taaggatttg gcaagaggag aacgtactgg agaagaggtc 720

gctaagagaa tggaaagagc atctgtgtta gctcaagtgg acattcatag agcagcaaca 780

cacaataagg gtgttatgaa tggcattcat gctgtagtct tggctacagg taatgatact 840

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gctacatgga gatacgatca agagagacaa aggttaatag gaactataga agttccaatg 960

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ttgcaataca agtctttagc catcgtagtc ggggctaagg gcgatgaaat tgctcaggta 1200

gccgaagcac taaagcaaga gccaagagca aacactcaag ttgcagagag aattttgcaa 1260

gatttgagaa gtcaacaata a 1281

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

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gaatttgcag ggttatctga tgaggaagtg aaagctgttt tgtcacaagg tttacctttg 180

gacgtagctg atagaatgat cgaaaatgtg atcggtacat ttgaattacc acttggtata 240

gcaaccaatt tccttattga tggcaaggat tatctaatcc ctatggctat agaggaacca 300

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aatgcagcta agttcgaagt tctacgtcaa aaagacgaaa tcatagaaag agcaaatgag 480

tgtgatccaa tgttggtgaa tttgggcggt ggatgtaaag atatagaagc aagggtgatc 540

gatacaatca tgggtaagat gctaattgtt catctgatcg ttgatgttaa agacgctatg 600

ggtgcaaatg ctgtcaacac tatgtgtgaa aaagttgctc ctttcatcga acgtattact 660

gggggaaagg tctatcttag aatcatttcc aacttggctg catatagact tgctagagca 720

aaggccgttt ttgacaaaga cgttattggc ggagaggagg ttgtagaagg gatcatgctt 780

gcatacgcct tcgctgccgc tgacccattt cgttgcgcca cccacaataa gggtatcatg 840

aatggcatat cagccttaat gatcgctaca ggaaacgact ttagagccat tgaagcagga 900

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accaaagtca acccactagc caagatctct cttaagatac taggagtgaa cactgctgaa 1080

gagttagcca gagtcgcagc cgctctaggt ttggctcaaa actttgctgc cttaagagcc 1140

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atggctggag ctactggaga tgaggttgac agagttgtag agattatggt gagagatggc 1260

aaaatcagat tggactacgc taaggaagta ttggagagac tgcgttccta a 1311

<210> 102
<211> 1287
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 102
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cacattggcc aacttttggg actaagtcat gacgacgttt ccctttagc aaacgccggt 120

gctttaccaa tggatatcgc taatggtatg attgaaaatg taatcgggac ctttgaactg 180

ccatatgcag tggccagtaa ctttcagatc aatggccgtg acgtcttagt accattagtt 240

gtggaggaac ctagtatcgt tgctgcagcc tcttacatgg caaagttagc tagagccaat 300

ggtgggttca ctacatcttc atctgctcca ctaatgcatg cacaagtaca aattgtcggc 360

attcaggatc cactaaacgc aagattgtct ttactgcgta gaaaggatga gatcatagaa 420

ttagccaata ggaaggacca acttctgaat tcattgggcg gtggttgcag agacatagag 480

gtgcatacat ttgccgatac tccaagagga ccaatgcttg tagcacacct tattgtcgat 540

gtgcgtgatg ccatgggagc taatactgtt aacactatgg ctgaagcagt agcacctctg 600

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 acgcttgtag atccggacat 900

tacggttcat taacaacatg ggaaaaagat aacaatggac acttggtcgg gacattggaa 960

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tctttgagga tacttggtgt caaaactgct caagcactag ccgaaattgc cgttgctgtt 1080

ggtttggcac aaaacttggg tgcaatgcgt gctttagcta cagaaggcat ccaaagagga 1140

catatggctc tacacgctag aaacattgca gttgttgcag gagccagagg tgatgaggtt 1200

gattgggtgg ctagacaact tgtcgaatat catgatgtca gagcagacag ggctgtggca 1260

ttactgaaac agaagagagg tcaataa 1287

<210> 103
<211> 2355
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 103
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ttatcagcaa ttcatacagc tagtacatcc catggtggcc aaaccaaccc tacgaatctg 120

ataatcgata cgaccaagga gagaatacaa aaacaattca aaaatgttga aatttcagtt 180

tcttcttatg atactgcgtg ggttgccatg gttccatcac ctaattctcc aaagtctcca 240

tgtttcccag aatgtttgaa ttggctgatt aacaaccagt tgaatgatgg atcttggggt 300

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ttggcttgca tcgtggccct aaagagatgg aacgtaggtg aggatcagat taacaagggg 420

cttagtttca ttgaatctaa cttggcttcc gcgactgaaa aatctcaacc atctccaata 480

ggattcgata tcatctttcc aggtctgtta gagtacgcca aaaatctaga tatcaactta 540

ctgtctaagc aaactgattt ctcactaatg ttacacaaga gagaattaga acaaaagaga 600

tgtcattcaa acgaaatgga tggttaccta gcttatatct ctgaaggtct tggtaatctt 660

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cttgaaacat atcatgcgtc acatatcctt taccaagagg acttatcatc tggaaaacaa 1140

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cgtattaaca caagacgtaa catccagctt tacaacgtag acaatactag aatcttgaaa 1320

accacttacc attcttccaa catatcaaac actgattacc taagattagc tgttgaagat 1380

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ttcaagttaa tgtccacaca aggcagatta cttaatgata ttcattcttt caaaagagag 2040

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gaggagcaaa gataa 2355

<210> 104
<211> 2355
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 104
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ctttctgcaa ttcatactgc cagtactagt catggaggtc aaacaaaccc aacaaatttg 120

ataatcgata ctactaagga gagaatccaa aagctattca aaaatgttga aatctcagta 180

tcatcttatg acaccgcatg ggttgcaatg gtgccatcac ctaattcccc aaaaagtcca 240

tgttttccag agtgcttgaa ttggttaatc aataatcagt taaacgatgg ttcttggggt 300

ttagtcaacc acactcataa ccacaatcat ccattattga aggactcttt atcatcaaca 360

ttagcctgta ttgttgcatt gaaaagatgg aatgtaggtg aagatcaaat caacaagggt 420

ttatcattca tagaatccaa tctagcttct gctaccgaca aatcacaacc atctccaatc 480

gggttcgaca taatcttccc tggtttgctg gagtatgcca aaaaccttga tatcaactta 540

ctgtctaaac aaacagattt ctctttgatg ctacacaaaa gagagttaga gcagaaaaga 600

tgccattcta acgaaattga cgggtactta gcatatatct cagaaggttt gggtaatttg 660

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ttcaagttaa tgtcaacaca aggcagactt ctgaacgata tccactcctt caaaagagaa 2040

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tggaatatgt gccatgttct taacttcttt tacgctaatg atgatggctt cactggaaat 2280

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gaggaacaaa gataa 2355

<210> 105
<211> 1773
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 105
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ttctcatccg gtggccatgc tttgagattc gggagtagtc tgccatgttg gagaaggacc 120

cctacccaaa gatctacttc ttcctctact actagaccag ctgccgaagt gtcatcaggt 180

aagagtaaac aacatgatca ggaagctagt gaagcgacta tcagacaaca attacaactt 240

gtggatgtcc tggagaatat gggaatatcc agacattttg ctgcagagat aaagtgcata 300

ctagacagaa cttacagatc ttggttacaa agacacgagg aaatcatgct ggacactatg 360

acatgtgcta tggcttttag aatcctaaga ttgaacggat acaacgtttc atcagatgaa 420

ctataccacg ttgtagaggc atctggtctg cataattctt tgggtgggta tcttaacgat 480

accagaacac tacttgaatt acacaaggct tcaacagtta gtatctctga ggatgaatct 540

atcttagatt caattggctc tagatccaga acattgctta gagaacaatt ggagtctggt 600

ggcgcactga gaaagccttc tttattcaaa gaggttgaac atgcactgga tggacctttt 660

tacaccacac ttgatagact tcatcatagg tggaatattg aaaacttcaa cattattgag 720

caacacatgt tggagactcc atacttatct aaccagcata catcaaggga tatcctagca 780

ttgtcaatta gagatttttc ctcctcacaa ttcacttatc aacaagagct acagcatctg 840

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tacttttacc tatcagccgc aggcaccatg ttttctcctg agctttctga tgcgagaaca 960

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gttttaccag ctttgtattt cgttggtcca aagatttcag aaagtatagt aaaggaccca 1380

gaatatgatg aattgttcaa actaatgtca acatgtggta gattgttgaa tgacgtgcaa 1440

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ggaggcccaa tgtctatttc agacgcaaag aggaaattac aaaagcctat tgatacgtgt 1560

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gaactattct ggaaaatgtg taaagtgtgc tatttctttt actcaacaac tgatgggttt 1680

tctagtcaag tcgaaagagc aaaagaggta gacgctgtca taaatgagcc actgaagttg 1740

caaggttctc atacactggt atctgatgtt taa 1773

<210> 106
<211> 2232
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 106
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ttcatagaac tcaactctgc tagtgtaacc gataacgaac aacacaaacc aattggattt 360

gacattatct ttccaggtat gattgaatac gctatagact tagacctgaa tctaccacta 420

aaaccaactg acattaactc catgttgcat cgtagagccc ttgaattgac atcaggtgga 480

ggcaaaaatc tagaaggtag aagagcttac ttggcctacg tctctgaagg aatcggtaag 540

ctgcaagatt gggaaatggc tatgaaatac caacgtaaaa acggatctct gttcaatagt 600

ccatcaacaa ctgcagctgc attcatccat atacaagatg ctgaatgcct ccactatatt 660

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aggattctaa aaacttccta cagatgctca acaatcggta accaagattt tctaaaactt 1260

gcagtggaag atttcaatat ctgtcaatca atacaaagag aggaattcaa gcatattgaa 1320

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tgggccaaaa atggtgtatt gacaactgtg gttgatgatt tcttcgatgt cggaggctct 1500

gaagaggaat tagttaactt gatagaattg atcgagcgtt gggatgtgaa tggcagtgca 1560

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cttccagcct tatacttcgt tggcccaaag ttgtcagaag aggttgcagg tcatcctgaa 1860

ctactaaacc tctacaaagt cacatctact tgtggcagac tactgaatga ttggagaagt 1920

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ggtggtgctt ctacagaaga ggaaacaatc gaacatttca aaggtttgat tgattctcag 2040

agaaggcaac tgttacaatt ggtgttgcaa gagaaggata gtatcatacc tagaccatgt 2100

aaagatctat tttggaatat gattaagtta ttacacactt tctacatgaa agatgatggc 2160

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gatgaattat ga 2232

<210> 107
<211> 1542
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 107
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agatcccaat caaatcatct tccaagagtg cctgaagtcc caggtgttcc attgttagga 180

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gagatagcca aggaggcatt ggtgaccaga ttccaatcca tatctacaag gaacttatct 360

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tatcataaaa cagttaagag acacatactg accgccgtct tgggtcctaa tgcacagaaa 480

aagcatagaa ttcacagaga tatcatgatg gataacatat ctactcaact tcatgaattc 540

gtgaaaaaca acccagaaca ggaagaggta gaccttagaa aaatctttca atctgagtta 600

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ggagcaatcg atgttgattg gagagacttc tttccatacc taaagtgggt cccaaacaaa 780

aagttcgaaa atactattca acaaatgtac atcagaagag aagctgttat gaaatcttta 840

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ggttccttgc aagccctttt aactgcatct attgggattg ggagaatggt tcaagagttc 1440

gaatggaaac tgaaggatat gactcaagag gaagtgaaca cgataggcct aactacacaa 1500

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<210> 108
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 108
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gagaaaaagc ctcataaaac tttcactaga tggtcagaga tatatggacc tatctactct 240

ataaagatgg gttcttcatc tcttattgta ttgaacagta cagaaactgc taaggaagca 300

atggtcacta gattttcatc aatatctacc agaaaattgt caaacgccct aacagttcta 360

acctgcgata agtctatggt cgccacttct gattatgatg acttccacaa attagttaag 420

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gatgctttga ttgaaaatgt gagttccaag ctacatgcac acgctagaga tcatccacaa 540

gagccagtta actttagagc aattttcgaa cacgaattgt ttggtgtagc attaaagcaa 600

gccttcggta aagacgtaga atccatatac gtcaaggagt taggcgtaac attatcaaaa 660

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ccattagttc ctattagata cgcccacgaa gatacacaaa tcggtggcta ccatgttcca 1200

gctgggtccg aaattgctat aaacatctac gggtgcaaca tggacaaaaa gagatgggaa 1260

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ttgcataaaa caatggcttt cggagctggc aaaagagtgt gtgccggtgc tctacaagcc 1380

tccctaatgg ctggtatcgc tattggtaga ttggtccaag agttcgaatg gaaacttaga 1440

gatggtgaag aggaaaatgt cgatacttat gggttaacat ctcaaaagtt atacccacta 1500

atggcaatca tcaatcctag aagatcctaa 1530

<210> 109
<211> 1578
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 109
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gcatggttat gttcttatgt gatacatgtt ttatcatctt cctctacagt aaaagtgcca 180

gttgttggat acaggtctgt attcgaacct acatggttgc ttagacttag attcgtctgg 240

gaaggtggct ctatcatagg tcaagggtac aataagttta aagactctat tttccaagtt 300

aggaaattgg gaactgatat tgtcattata ccacctaact atattgatga agtgagaaaa 360

ttgtcacagg acaagactag atcagttgaa cctttcatta atgattttgc aggtcaatac 420

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actccaaaat tggtttcctt gaccaaggtc atgaaggaag agttggatta tgctttaaca 540

aaagagatgc ctgatatgaa aaatgacgaa tgggtagaag tagatatcag tagtataatg 600

gtgagattga tttccaggat ctccgccaga gtctttctag ggcctgaaca ctgtcgtaac 660

caggaatggt tgactactac agcagaatat tcagaatcac ttttcattac agggtttatc 720

ttaagagttg tacctcatat cttaagacca ttcatcgccc ctctattacc ttcatacagg 780

actctactta gaaacgtttc aagtggtaga agagtcatcg gtgacatcat aagatctcag 840

caaggggatg gtaacgaaga tatactttcc tggatgagag atgctgccac aggagaggaa 900

aagcaaatcg ataacattgc tcagagaatg ttaattcttt ctttagcatc aatccacact 960

actgcgatga ccatgacaca tgccatgtac gatctatgtg cttgccctga gtacattgaa 1020

ccattaagag atgaagttaa atctgttgtt ggggcttctg gctgggacaa gacagcgtta 1080

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tcacttagag atgaatga 1578

<210> 110
<211> 1500
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 110
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agatggtaca gagatccatt gagatccatc ccaacagttg gtggttccga tttgcctatt 120

ctatcttaca tcggcgcact aagatggaca agacgtggca gagagatact tcaagaggga 180

tatgatggct acagaggatc tacattcaaa atcgcgatgt tagaccgttg gatcgtgatc 240

gcaaatggtc ctaaactagc tgatgaagtc agacgtagac cagatgaaga gttaaacttt 300

atggacggat taggagcatt cgtccaaact aagtacacct taggtgaagc tattcataac 360

gatccatacc atgtcgatat cataagagaa aaactaacaa gaggccttcc agccgtgctt 420

cctgatgtca ttgaagagtt gacacttgcg gttagacagt acattccaac agaaggtgat 480

gaatgggtgt ccgtaaactg ttcaaaggcc gcaagagata ttgttgctag agcttctaat 540

agagtctttg taggtttgcc tgcttgcaga aaccaaggtt acttagattt ggcaatagac 600

tttacattgt ctgttgtcaa ggatagagcc atcatcaata tgtttccaga attgttgaag 660

ccaatagttg gcagagttgt aggtaacgcc accagaaatg ttcgtagagc tgttcctttt 720

gttgctccat tggtggagga aagacgtaga cttatggaag agtacggtga agactggtct 780

gaaaaaccta atgatatgtt acagtggata atggatgaag ctgcatccag agatagttca 840

gtgaaggcaa tcgcagagag attgttaatg gtgaacttcg cggctattca tacctcatca 900

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aactatgatg taaagttgcc tggtgacggt aaacgtccat tgaacatgta ttggggtcca 1440

acagttttgc ctgcaccagc aggccaagta ttgttcagaa agagacaagt tagtctataa 1500

<210> 111
<211> 1578
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 111
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cctaaagcat ctggtgaaat cattccaatt acaggaatca tattgaatct gctatctggc 180

tcaagtggtc tacctattat cttagcactt gcctctttag cagacagatg tggtcctatt 240

ttcaccatta ggctgggtat taggagagtg ctagtagtat caaattggga aatcgctaag 300

gagattttca ctacccacga tttgatagtt tctaatagac caaaatactt agccgctaag 360

attcttggtt tcaattatgt ttcattctct ttcgctccat acggcccata ttgggtcgga 420

atcagaaaga ttattgctac aaaactaatg tcttcttcca gacttcagaa gttgcaattt 480

gtaagagttt ttgaactaga aaactctatg aaatctatca gagaatcatg gaaggagaaa 540

aaggatgaag agggaaaggt attagttgag atgaaaaagt ggttctggga actgaatatg 600

aacatagtgt taaggacagt tgctggtaaa caatacactg gtacagttga tgatgccgat 660

gcaaagcgta tctccgagtt attcagagaa tggtttcact acactggcag atttgtcgtt 720

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gaagcaaatt caccacttga aggatacggc actgatacta ttatcaagac cacatgtatg 960

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ttgttaaaca acagagatac tttgaaaaag gcacaagagg aattagatat gtgcgtaggt 1080

aaaggaagac aagtcaacga gtctgatctt gttaacttga tatacttgga agcagtgctt 1140

aaagaggctt taagacttta cccagcagcg ttcttaggcg gaccaagagc attcttggaa 1200

gattgtactg ttgctggtta tagaattcca aagggcacct gcttgttgat taacatgtgg 1260

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ttgacaccta atcaaaagga tgttgatgtg atcggtatgg atttcgaatt gataccattt 1380

ggtgccggca gaagatattg tccaggtact agattggctt tacagatgtt gcatatcgta 1440

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actgcttctg ttggcatgac aaatgccaaa gcatcacctt tagaagtctt gctatcacct 1560

cgtgttaaat ggtcctaa 1578

<210> 112
<211> 1431
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 112
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tacaaacatc aaaagactaa aatcaatcta ccaccaggtt ccttcggctg gccatttttg 120

ggtgaaacct tagccttact tagagcaggc tgggattctg agccagaaag attcgtaaga 180

gagcgtatca aaaagcatgg atctccactt gttttcaaga catcactatt tggagacaga 240

ttcgctgttc tttgcggtcc agctggtaat aagtttttgt tctgcaacga aaacaaatta 300

gtggcatctt ggtggccagt ccctgtaagg aagttgttcg gtaaaagttt actcacaata 360

agaggagatg aagcaaaatg gatgagaaaa atgctattgt cttacttggg tccagatgca 420

tttgccacac attatgccgt tactatggat gttgtaacac gtagacatat tgatgtccat 480

tggaggggca aggaggaagt taatgtattt caaacagtta agttgtacgc attcgaatta 540

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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

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accttaggtg aacacagtga tgtgtacgac aaggttttga aggaacaatt agaaatttcc 960

aaaacaaagg aggcttggga atcactaaag tgggaagata tccagaagat gaagtactca 1020

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gcgttggttg atatcgacta tgctggttac actatcccaa aaggatggaa gttgcattgg 1140

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gttaccaact ttaagtggga tcttctaatc cctgatgaga agatcgaata tgatccaatg 1380

gctactccag ctaagggctt gccaattaga cttcatccac accaagtcta a 1431

<210> 113
<211> 1578
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 113
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tcactgaagc tacaaggtgt 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 tctaatggtc ctcattgggc ccatcagcgt 480

agaattatcg cctacgagtt tactcatgat aagatcaagg gtatggttgg tttgatggtt 540

gagtctgcta tgcctatgtt gaataagtgg gaggagatgg taaagagagg cggagaaatg 600

ggatgcgaca taagagttga tgaggacttg aaagatgttt cagcagatgt gattgcaaaa 660

gcctgtttcg gatcctcatt ttctaaaggt aaggctattt tctctatgat aagagatttg 720

cttacagcta tcacaaagag aagtgttcta ttcagattca acggattcac tgatatggtc 780

tttgggagta aaaagcatgg tgacgttgat atagacgctt tagaaatgga attggaatca 840

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tctcctacct accaacatag tcctagtcac aaacttttag tagaaccaca acatggggtg 1560

gtaattagag tggtttaa 1578

<210> 114
<211> 1590
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 114
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gctaatgatc aagtgtcttc ttcaagacct gaactattag cttctaagtt gttgggttat 360

aactacgcca tgtttggttt ttcaccatac ggttcatact ggagagaaat gagaaagatc 420

atctctctcg aattactatc taattccaga ttggaactat tgaaagatgt tagagcctca 480

gaagttgtca catctattaa ggaactatac aaattgtggg cggaaaagaa gaatgagtca 540

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<210> 115
<211> 1440
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 115
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aaaccagaag cacttcaaag atacgtcggc gttatggatg taatcgcaca aagacatttt 480

gtcactcact gggacaacaa aaatgagatc acagtttatc cacttgctaa aagatacact 540

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tcagacccat tccaactaat cgctgcaggc atcatttcac ttcctatcga tcttcctggt 660

actccattca acaaggccat aaaggcttca aatttcatta gaaaagagct gataaagatt 720

atcaaacaaa gacgtgttga tctggcagag ggtacagcat ctccaaccca ggatatcttg 780

tcacatatgc tattaacatc tgatgaaaac ggtaaatcta tgaacgagtt gaacattgcc 840

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ctagtgaagt acttaggaga attaccacat atctacgata aagtctacca agagcaaatg 960

gaaattgcca agtccaaacc tgctggggaa ttgttgaatt gggatgactt gaaaaagatg 1020

aagtattcat ggaatgtggc atgtgaggta atgagattgt caccaccttt acaaggtggt 1080

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cataatctgg tcaaacgttt taagtgggaa aaggttattc cagacgaaaa gattattgtc 1380

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<211> 2133
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 116
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attgggtgtc ttgtatttct aatgtggaga cgttcatcct ctaaaaagct ggtacaagat 240

ccagttccac aagttatcgt tgtaaagaag aaagagaagg agtcagaggt tgatgacggg 300

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gcattagtcg aggaagcaaa agtgagatat gaaaagacct ctttcaaggt tatcgatcta 420

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atgtctggaa gatacttaag agatgtttgg taa 2133

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

<220>
<223> Synthetic oligonucleotide

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<210> 118
<211> 2142
<212> DNA
<213> Artificial Sequence

<220>
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gctgcaggtg gtgcttccaa gcctggcaga actagaaaca tcgtcgaagc tatggaggaa 180

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gaagattatg acttcgataa cttagacact gttccatctg ataacatcgt tatgtttgta 360

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gttgcgttcg gtctgggcaa caatacctac gaacactaca actcaatggt caggaacgtt 540

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cacttggaag gtacagcgaa aggtccattc aactcccaca acccatatat cgcaccaatt 840

gcagaatcat acgaactttt ctcagctaag gatagaaatt gtctgcatat ggaaattgat 900

atttctggta gtaatctaaa gtatgaaaca ggcgaccata tcgcgatctg gcctaccaac 960

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caacacagac tgaaggaaag atcaaaggaa gtttctgatc ttctatccca aaaagcatac 1920

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atcatagcag aaggccgtgg tgtatcagaa gccaagggtg aggaaattgt caaaaacatg 2040

agatcagcaa atcaatacca agtgtgttct gatttcgtaa ctttacactg taaagagaca 2100

acatacgcga attcagaatt gcaagaggat gtctggagtt aa 2142

<210> 119
<211> 2364
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 119
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gacatcaact tcagatgtaa agcagtttct aaagagtact ctgatctgtt gcagaaagat 180

gaggcttctt tcacaaaatg ggacgatgac aaggtgaaag atcatcttga taccaacaaa 240

aacttatacc caaatgatga gattaaggaa tttgttgaat cagtaaaggc tatgttcggt 300

agtatgaatg acggggagat aaacgtctct gcatacgata ctgcatgggt tgctttggtt 360

caagatgtcg atggatcagg tagtcctcag ttcccttctt ctttagaatg gattgccaac 420

aatcaattgt cagatggatc atggggagat catttgctgt tctcagctca cgatagaatc 480

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gaaaaaggtt tgaattttct gagagaaaac atttgcaaat tagaagatga aaacgcagaa 600

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gtttttagtg acacaccaga tgatttggat caagatatga aacaaacatt cctgacagtg 2280

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aaagttttcg aaatcgtaat ttga 2364

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<211> 1584
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 120
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gctacccaac tgctaactga gtccgcagaa gatgcatggg gtgaagtcag tgtgtcagaa 120

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

<220>
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<400> 121
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gaattgtact gtcctactag agtcgtaaga gtagctgagc tagctggcct gtggttagca 1500

ttaagatggg gtagaagagt attagctgaa ggtgctggtg ctgcacctta a 1551

<210> 122
<211> 2952
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 122
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<211> 2646
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

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caatgcttga aaaagaggag atgccttagg ccaaccgaat ccgtactaga atcatctcct 180

ggctctggtt catatagaat agtaactggc ccttctggaa ttaaccctag ttctaacggg 240

cacttgcaag agggttcctt gactcacagg ttaccaatac caatggaaaa atctatcgat 300

aacttccaat ctactctata tgtgtcagat atttggtctg aaacactaca gagaactgaa 360

tgtttgctac aagtaactga aaacgtccag atgaatgagt ggattgagga aattagaatg 420

tactttagaa atatgacttt aggtgaaatt tccatgtccc cttacgacac tgcttgggtg 480

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aagagaatcc acttgaatat ggctaaaatc atgcatgcct tctacaagga tactgatgga 2580

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<211> 2859
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 124
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tctgctgcta agagtttact agatcgagct ttcaaaagtc atcattccta ctacggatta 120

tgctcaactt catgtcaagt ttatgataca gcttgggttg caatgattcc aaaaacaaga 180

gataatgtaa aacagtggtt gtttccagaa tgtttccatt acctcttaaa aacacaagcc 240

gcagatggct catggggttc attgcctaca acacagacag cgggtatcct agatacagcc 300

tcagctgtgc tggcattatt gtgccacgca caagagcctt tacaaatatt ggatgtatct 360

ccagatgaaa tggggttgag aatagaacac ggtgtcacat ccttgaaacg tcaattagca 420

gtttggaatg atgtggagga caccaaccat attggcgtcg agtttatcat accagcctta 480

ctttccatgc tagaaaagga attagatgtt ccatcttttg aatttccatg taggtccatc 540

ttagagagaa tgcacgggga gaaattaggt catttcgacc tggaacaagt ttacggcaag 600

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ggcttaagag gtttatcaac catcttactt gaggcgcttc gtgatgagaa tggtgtcata 960

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ggtggtgaat tgtctagtct gtttgatgaa tcctttaagt gtaagattgg tcttagcatc 1380

tttcaagcgg tacttagaat aatcctcacc caagacaacg acggctcttg gagaggatac 1440

agagaacaga cgtgttacgc aatattggct ttagttcaag cgagacatgt atgctttttc 1500

actcacatgg ttgacagact gcaatcatgt gttgatcgag gtttctcatg gttgaaatct 1560

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gcactagagg ccttggaaag acagagtaga gatgatgccg gagacagagc tggatctaaa 2760

gatatgagaa agttgaaaat cgttaagtta ttctgtgatg ttacggactt atacgatcag 2820

ctctacgtta tcaaagattt gtcatcctct atgaagtaa 2859

<210> 125
<211> 1086
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 125
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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 tgcatctgtc 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 acacaaggtc tacggggagg aaatggcagt attgaccggc 540

gatgctttac taagtttatc tttcgaacat atagctactg ctacaaaggg tgtatcaaag 600

gatagaatcg tcagagctat aggggagttg gcccgttcag ttggctccga aggtttagtg 660

gctggacaag ttgtagatat cttgtcagag ggtgctgatg ttggattaga tcacctagaa 720

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ctactattcc aagttgtgga tgacattttg gatgttacaa 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> 126
<211> 1029
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 126
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aaattagaaa ttactgtcca aatgatggac acataccatt acagagaaac gcctccagat 120

tcctcatctt ctgaaggcgg ttcattgtct agatacgacg agagaagagt ctctttgcct 180

ctcagtcata atgctgcctc tccagatatt gtatcacaac tatgtttttc cactgcaatg 240

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aactatatcc taacattacc atcaaaagga attagaggtg cctttatcga ttccctgaac 360

gtatggttgg aggttccaga ggatgaaaca tcagtcatca aggaagttat tggtatgctc 420

cacaactctt cattaatcat tgatgacttc caagataatt ctccacttag aagaggaaag 480

ccatctaccc atacagtctt cggccctgcc caggctatca atactgctac ttacgttata 540

gttaaagcaa tcgaaaagat acaagacata gtgggacacg atgcattggc agatgttacg 600

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ggcaagtact cactaacact tattcatgcc ctccaaactg attcatccga tctactgacc 960

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tggaaatga 1029

<210> 127
<211> 903
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 127
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caactaccag gaaagcaagt ccgttctaaa ctatcacaag cgttcaatca ctggttaaaa 120

gttcctgaag ataagttaca aatcattatt gaagtcacag aaatgctaca caatgcttct 180

ttactgatcg atgatataga ggattcttcc aaactgagaa gaggttttcc tgtcgctcat 240

tccatatacg gggtaccaag tgtaatcaac tcagctaatt acgtctactt cttgggattg 300

gaaaaagtat tgacattaga tcatccagac gctgtaaagc tattcaccag acaacttctt 360

gaattgcatc aaggtcaagg tttggatatc tattggagag acacttatac ttgcccaaca 420

gaagaggagt acaaagcaat ggttctacaa aagactggcg gtttgttcgg acttgccgtt 480

ggtctgatgc aacttttctc tgattacaag gaggacttaa agcctctgtt ggataccttg 540

ggcttgtttt tccagattag agatgactac gctaacttac attcaaagga atattcagaa 600

aacaaatcat tctgtgaaga tttgactgaa gggaagttta gttttccaac aatccacgcc 660

atttggtcaa gaccagaatc tactcaagtg caaaacattc tgcgtcagag aacagagaat 720

attgacatca aaaagtattg tgttcagtac ttggaagatg ttggttcttt tgcttacaca 780

agacatacac ttagagaatt agaggcaaaa gcatacaagc aaatagaagc ctgtggaggc 840

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taa 903

<210> 128
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 128
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ggtaaaccaa caaaccatgt cgttttcggc gaagatgtag ctattcttgc aggtgactct 480

ttattgtcaa cttccttcga gcacgtcgct agagaaacaa aaggagtgtc agcagaaaag 540

atcgtggatg ttatcgctag attaggcaaa tctgttggtg ccgagggcct tgctggcggt 600

caagttatgg acttagaatg tgaagctaaa ccaggtacca cattagacga cttgaaatgg 660

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gagagtaagg catacgcaag acaactaatc gatgaagcca aggaaagttt ggctcctttt 960

ggagatagag ctgccccttt attggccatt gcagatttca ttattgatag aaagaattga 1020

<210> 129
<211> 1068
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 129
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gaaagacaag gtgccttggg tagaagacgt ggagctggct ctactggctg tgcccgtgct 120

gctgctggtg ttcaccgtag aagaggagga ggcgaggctg atccatcagc tgctgtgcat 180

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gcagcttaca caatggaacg tccactgcac attggtgcag ccctggctgg ggcaagacca 660

gaactattag cagggctttc agcatacgcc ttgccagctg gagaagcctt ccaattggca 720

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agactaagat gcgtattggt agcaactggt gcaagagccg aagccgaaag acttattaca 960

gagagaagag atcaagcatt aactgcattg aacgcattaa cactgccacc tcctttagct 1020

gaggcattag caagattgac attagggtct acagctcatc ctgcctaa 1068

<210> 130
<211> 993
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 130
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ttaacagctg atgaaaaaga gctaggaaaa cctgttttca gtgatatcag agaaggtaaa 720

aagaccatat tagtcattaa gactttagaa ttgtgtaagg aagacgagaa aaagattgtg 780

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<213> Zea mays

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35 40 45

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

Ala Trp Val Gly Leu Val Pro Arg Leu Asp Gly Gly Glu Gly Pro Gln
65 70 75 80

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Phe Pro Ala Ala Val Arg Trp Ile Arg Asn Asn Gln Leu Pro Asp Gly
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Ser Trp Gly Asp Ala Ala Leu Phe Ser Ala Tyr Asp Arg Leu Ile Asn
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Thr Leu Ala Cys Val Val Thr Leu Thr Arg Trp Ser Leu Glu Pro Glu
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Met Arg Gly Arg Gly Leu Ser Phe Leu Gly Arg Asn Met Trp Lys Leu
    130                 135                 140

Ala Thr Glu Asp Glu Glu Ser Met Pro Ile Gly Phe Glu Leu Ala Phe
145                 150                 155                 160

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

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

Met Lys Arg Ile Pro Lys Glu Val Met His Thr Val Pro Thr Ser Ile
        195                 200                 205

Leu His Ser Leu Glu Gly Met Pro Gly Leu Asp Trp Ala Lys Leu Leu
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Lys Leu Gln Ser Ser Asp Gly Ser Phe Leu Phe Ser Pro Ala Ala Thr
225                 230                 235                 240

Ala Tyr Ala Leu Met Asn Thr Gly Asp Asp Arg Cys Phe Ser Tyr Ile
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Asp Arg Thr Val Lys Lys Phe Asn Gly Gly Val Pro Asn Val Tyr Pro
            260                 265                 270

Val Asp Leu Phe Glu His Ile Trp Ala Val Asp Arg Leu Glu Arg Leu
        275                 280                 285

Gly Ile Ser Arg Tyr Phe Gln Lys Glu Ile Glu Gln Cys Met Asp Tyr
    290                 295                 300

Val Asn Arg His Trp Thr Glu Asp Gly Ile Cys Trp Ala Arg Asn Ser
305                 310                 315                 320

Asp Val Lys Glu Val Asp Asp Thr Ala Met Ala Phe Arg Leu Leu Arg
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Leu His Gly Tyr Ser Val Ser Pro Asp Val Phe Lys Asn Phe Glu Lys
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Asp Gly Glu Phe Phe Ala Phe Val Gly Gln Ser Asn Gln Ala Val Thr
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Gly Met Tyr Asn Leu Asn Arg Ala Ser Gln Ile Ser Phe Pro Gly Glu
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Asp Val Leu His Arg Ala Gly Ala Phe Ser Tyr Glu Phe Leu Arg Arg
385                 390                 395                 400

Lys Glu Ala Glu Gly Ala Leu Arg Asp Lys Trp Ile Ile Ser Lys Asp
                405                 410                 415

Leu Pro Gly Glu Val Val Tyr Thr Leu Asp Phe Pro Trp Tyr Gly Asn
            420                 425                 430

Leu Pro Arg Val Glu Ala Arg Asp Tyr Leu Glu Gln Tyr Gly Gly Gly
        435                 440                 445

Asp Asp Val Trp Ile Gly Lys Thr Leu Tyr Arg Met Pro Leu Val Asn
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Asn Asp Val Tyr Leu Glu Leu Ala Arg Met Asp Phe Asn His Cys Gln
465                 470                 475                 480

Ala Leu His Gln Leu Glu Trp Gln Gly Leu Lys Arg Trp Tyr Thr Glu
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Asn Arg Leu Met Asp Phe Gly Val Ala Gln Glu Asp Ala Leu Arg Ala
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Tyr Phe Leu Ala Ala Ala Ser Val Tyr Glu Pro Cys Arg Ala Ala Glu
        515                 520                 525

Arg Leu Ala Trp Ala Arg Ala Ala Ile Leu Ala Asn Ala Val Ser Thr
    530                 535                 540

His Leu Arg Asn Ser Pro Ser Phe Arg Glu Arg Leu Glu His Ser Leu
545                 550                 555                 560

Arg Cys Arg Pro Ser Glu Glu Thr Asp Gly Ser Trp Phe Asn Ser Ser
                565                 570                 575

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

Ser Leu Ala Arg Glu Ala Gln Pro Ile His Gly Gly Asp Pro Glu Asp
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Ile Ile His Lys Leu Leu Arg Ser Ala Trp Ala Glu Trp Val Arg Glu
    610                 615                 620
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Gln Glu Gly Ser Arg Met Val His Asp Lys Gln Thr Cys Leu Leu Leu
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Ala Arg Met Ile Glu Ile Ser Ala Gly Arg Ala Ala Gly Glu Ala Ala
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Ser Glu Asp Gly Asp Arg Arg Ile Ile Gln Leu Thr Gly Ser Ile Cys
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Asp Ser Leu Lys Gln Lys Met Leu Val Ser Gln Asp Pro Glu Lys Asn
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Glu Glu Met Met Ser His Val Asp Asp Glu Leu Lys Leu Arg Ile Arg
705                 710                 715                 720

Glu Phe Val Gln Tyr Leu Leu Arg Leu Gly Glu Lys Lys Thr Gly Ser
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Ser Glu Thr Arg Gln Thr Phe Leu Ser Ile Val Lys Ser Cys Tyr Tyr
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Ala Ala His Cys Pro Pro His Val Val Asp Arg His Ile Ser Arg Val
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Ile Phe Glu Pro Val Ser Ala Ala Lys
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gcaggagaat catatttgga aacattcaaa caagttgggt ctaaatcact agctgactta      300

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