

117549337_1
SEQUENCE LISTING

<110> LALLEMAND HUNGARY LIQUIDITY MANAGEMENT LLC
BASF SE

<120> PROCESS FOR DISPLACING AN EXOGENOUS ENZYME

<130> N420746WO

<150> 62/941967

<151> 2019-11-29

<150> 63/078139

<151> 2020-09-14

<150> 63/078135

<151> 2020-09-14

<160> 37

<170> PatentIn version 3.5

<210> 1

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Glucoamylase from *Rasamsonia emersonii* (Uniprot Q9C1V4)
associated with the signal sequence of *Saccharomyces cerevisiae*
alpha-mating factor 1

<220>

<221> SIGNAL

<222> (1)..(19)

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Ser Phe Leu Ala Thr Glu Thr Pro Ile Ala Leu Gln Gly Val Leu Asn
35 40 45

Asn Ile Gly Pro Asn Gly Ala Asp Val Ala Gly Ala Ser Ala Gly Ile

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50

55

60

Val Val Ala Ser Pro Ser Arg Ser Asp Pro Asn Tyr Phe Tyr Ser Trp
 65 70 75 80

Thr Arg Asp Ala Ala Leu Thr Ala Lys Tyr Leu Val Asp Ala Phe Ile
 85 90 95

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

Gln Ala Lys Val Gln Thr Ile Ser Asn Pro Ser Gly Asp Leu Ser Thr
 115 120 125

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

Gly Pro Trp Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr
 145 150 155 160

Ala Leu Ile Ala Tyr Ala Asn Tyr Leu Ile Asp Asn Gly Glu Ala Ser
 165 170 175

Thr Ala Asp Glu Ile Ile Trp Pro Ile Val Gln Asn Asp Leu Ser Tyr
 180 185 190

Ile Thr Gln Tyr Trp Asn Ser Ser Thr Phe Asp Leu Trp Glu Glu Val
 195 200 205

Glu Gly Ser Ser Phe Phe Thr Thr Ala Val Gln His Arg Ala Leu Val
 210 215 220

Glu Gly Asn Ala Leu Ala Thr Arg Leu Asn His Thr Cys Ser Asn Cys
 225 230 235 240

Val Ser Gln Ala Pro Gln Val Leu Cys Phe Leu Gln Ser Tyr Trp Thr
 245 250 255

Gly Ser Tyr Val Leu Ala Asn Phe Gly Gly Ser Gly Arg Ser Gly Lys

260

265

270

Asp Val Asn Ser Ile Leu Gly Ser Ile His Thr Phe Asp Pro Ala Gly
 275 280 285

Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys Ser Ala Arg Ala Leu Ala
 290 295 300

Asn His Lys Val Val Thr Asp Ser Phe Arg Ser Ile Tyr Ala Ile Asn
 305 310 315 320

Ser Gly Ile Ala Glu Gly Ser Ala Val Ala Val Gly Arg Tyr Pro Glu
 325 330 335

Asp Val Tyr Gln Gly Gly Asn Pro Trp Tyr Leu Ala Thr Ala Ala Ala
 340 345 350

Ala Glu Gln Leu Tyr Asp Ala Ile Tyr Gln Trp Lys Lys Ile Gly Ser
 355 360 365

Ile Ser Ile Thr Asp Val Ser Leu Pro Phe Phe Gln Asp Ile Tyr Pro
 370 375 380

Ser Ala Ala Val Gly Thr Tyr Asn Ser Gly Ser Thr Thr Phe Asn Asp
 385 390 395 400

Ile Ile Ser Ala Val Gln Thr Tyr Gly Asp Gly Tyr Leu Ser Ile Val
 405 410 415

Glu Lys Tyr Thr Pro Ser Asp Gly Ser Leu Thr Glu Gln Phe Ser Arg
 420 425 430

Thr Asp Gly Thr Pro Leu Ser Ala Ser Ala Leu Thr Trp Ser Tyr Ala
 435 440 445

Ser Leu Leu Thr Ala Ser Ala Arg Arg Gln Ser Val Val Pro Ala Ser
 450 455 460

Trp Gly Glu Ser Ser Ala Ser Ser Val Pro Ala Val Cys Ser Ala Thr

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<210> 3

<211> 598

<212> PRT

<213> Rasamsonia emersonii

<400> 3

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20 25 30

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

Ser Pro Ser Arg Ser Asp Pro Asn Tyr Phe Tyr Ser Trp Thr Arg Asp
50 55 60

Ala Ala Leu Thr Ala Lys Tyr Leu Val Asp Ala Phe Ile Ala Gly Asn
65 70 75 80

Lys Asp Leu Glu Gln Thr Ile Gln Gln Tyr Ile Ser Ala Gln Ala Lys
85 90 95

Val Gln Thr Ile Ser Asn Pro Ser Gly Asp Leu Ser Thr Gly Gly Leu
100 105 110

Gly Glu Pro Lys Phe Asn Val Asn Glu Thr Ala Phe Thr Gly Pro Trp
115 120 125

Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Leu Ile
130 135 140

Ala Tyr Ala Asn Tyr Leu Ile Asp Asn Gly Glu Ala Ser Thr Ala Asp
145 150 155 160

Glu Ile Ile Trp Pro Ile Val Gln Asn Asp Leu Ser Tyr Ile Thr Gln
 165 170 175

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

Ser Phe Phe Thr Thr Ala Val Gln His Arg Ala Leu Val Glu Gly Asn
 195 200 205

Ala Leu Ala Thr Arg Leu Asn His Thr Cys Ser Asn Cys Val Ser Gln
 210 215 220

Ala Pro Gln Val Leu Cys Phe Leu Gln Ser Tyr Trp Thr Gly Ser Tyr
 225 230 235 240

Val Leu Ala Asn Phe Gly Gly Ser Gly Arg Ser Gly Lys Asp Val Asn
 245 250 255

Ser Ile Leu Gly Ser Ile His Thr Phe Asp Pro Ala Gly Gly Cys Asp
 260 265 270

Asp Ser Thr Phe Gln Pro Cys Ser Ala Arg Ala Leu Ala Asn His Lys
 275 280 285

Val Val Thr Asp Ser Phe Arg Ser Ile Tyr Ala Ile Asn Ser Gly Ile
 290 295 300

Ala Glu Gly Ser Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Val Tyr
 305 310 315 320

Gln Gly Gly Asn Pro Trp Tyr Leu Ala Thr Ala Ala Ala Ala Glu Gln
 325 330 335

Leu Tyr Asp Ala Ile Tyr Gln Trp Lys Lys Ile Gly Ser Ile Ser Ile
 340 345 350

Thr Asp Val Ser Leu Pro Phe Phe Gln Asp Ile Tyr Pro Ser Ala Ala
 355 360 365

Val Gly Thr Tyr Asn Ser Gly Ser Thr Thr Phe Asn Asp Ile Ile Ser
 370 375 380

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

Thr Pro Ser Asp Gly Ser Leu Thr Glu Gln Phe Ser Arg Thr Asp Gly
 405 410 415

Thr Pro Leu Ser Ala Ser Ala Leu Thr Trp Ser Tyr Ala Ser Leu Leu
 420 425 430

Thr Ala Ser Ala Arg Arg Gln Ser Val Val Pro Ala Ser Trp Gly Glu
 435 440 445

Ser Ser Ala Ser Ser Val Pro Ala Val Cys Ser Ala Thr Ser Ala Thr
 450 455 460

Gly Pro Tyr Ser Thr Ala Thr Asn Thr Val Trp Pro Ser Ser Gly Ser
 465 470 475 480

Gly Ser Ser Thr Thr Thr Ser Ser Ala Pro Cys Thr Thr Pro Thr Ser
 485 490 495

Val Ala Val Thr Phe Asp Glu Ile Val Ser Thr Ser Tyr Gly Glu Thr
 500 505 510

Ile Tyr Leu Ala Gly Ser Ile Pro Glu Leu Gly Asn Trp Ser Thr Ala
 515 520 525

Ser Ala Ile Pro Leu Arg Ala Asp Ala Tyr Thr Asn Ser Asn Pro Leu
 530 535 540

Trp Tyr Val Thr Val Asn Leu Pro Pro Gly Thr Ser Phe Glu Tyr Lys
 545 550 555 560

Phe Phe Lys Asn Gln Thr Asp Gly Thr Ile Val Trp Glu Asp Asp Pro
 565 570 575

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Asn Arg Ser Tyr Thr Val Pro Ala Tyr Cys Gly Gln Thr Thr Ala Ile
580 585 590

Leu Asp Asp Ser Trp Gln
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<211> 1797
<212> DNA
<213> Artificial Sequence

<220>
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<210> 5

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal sequence of *Saccharomyces cerevisiae* alpha-mating factor 1

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Ala Leu Ala

<210> 6

<211> 618

<212> PRT

<213> *Rasamsonia emersonii*

<220>

<221> SIGNAL

<222> (1)..(20)

<400> 6

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Ala Ala Phe Ala Arg Ala Pro Val Ala Ala Arg Ala Thr Gly Ser Leu
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Asp Ser Phe Leu Ala Thr Glu Thr Pro Ile Ala Leu Gln Gly Val Leu
 35 40 45

Asn Asn Ile Gly Pro Asn Gly Ala Asp Val Ala Gly Ala Ser Ala Gly
 50 55 60

Ile Val Val Ala Ser Pro Ser Arg Ser Asp Pro Asn Tyr Phe Tyr Ser
 65 70 75 80

Trp Thr Arg Asp Ala Ala Leu Thr Ala Lys Tyr Leu Val Asp Ala Phe
 85 90 95

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

Ala Gln Ala Lys Val Gln Thr Ile Ser Asn Pro Ser Gly Asp Leu Ser
 115 120 125

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

Thr Gly Pro Trp Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala
 145 150 155 160

Thr Ala Leu Ile Ala Tyr Ala Asn Tyr Leu Ile Asp Asn Gly Glu Ala
 165 170 175

Ser Thr Ala Asp Glu Ile Ile Trp Pro Ile Val Gln Asn Asp Leu Ser
 180 185 190

Tyr Ile Thr Gln Tyr Trp Asn Ser Ser Thr Phe Asp Leu Trp Glu Glu
 195 200 205

Val Glu Gly Ser Ser Phe Phe Thr Thr Ala Val Gln His Arg Ala Leu
 210 215 220

Val Glu Gly Asn Ala Leu Ala Thr Arg Leu Asn His Thr Cys Ser Asn
 225 230 235 240

Cys Val Ser Gln Ala Pro Gln Val Leu Cys Phe Leu Gln Ser Tyr Trp
 245 250 255

Thr Gly Ser Tyr Val Leu Ala Asn Phe Gly Gly Ser Gly Arg Ser Gly
 260 265 270

Lys Asp Val Asn Ser Ile Leu Gly Ser Ile His Thr Phe Asp Pro Ala
 275 280 285

Gly Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys Ser Ala Arg Ala Leu
 290 295 300

Ala Asn His Lys Val Val Thr Asp Ser Phe Arg Ser Ile Tyr Ala Ile
 305 310 315 320

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

Glu Asp Val Tyr Gln Gly Gly Asn Pro Trp Tyr Leu Ala Thr Ala Ala
 340 345 350

Ala Ala Glu Gln Leu Tyr Asp Ala Ile Tyr Gln Trp Lys Lys Ile Gly
 355 360 365

Ser Ile Ser Ile Thr Asp Val Ser Leu Pro Phe Phe Gln Asp Ile Tyr
 370 375 380

Pro Ser Ala Ala Val Gly Thr Tyr Asn Ser Gly Ser Thr Thr Phe Asn
 385 390 395 400

Asp Ile Ile Ser Ala Val Gln Thr Tyr Gly Asp Gly Tyr Leu Ser Ile
 405 410 415

Val Glu Lys Tyr Thr Pro Ser Asp Gly Ser Leu Thr Glu Gln Phe Ser
 420 425 430

Arg Thr Asp Gly Thr Pro Leu Ser Ala Ser Ala Leu Thr Trp Ser Tyr
 435 440 445

Ala Ser Leu Leu Thr Ala Ser Ala Arg Arg Gln Ser Val Val Pro Ala
 450 455 460

Ser Trp Gly Glu Ser Ser Ala Ser Ser Val Pro Ala Val Cys Ser Ala
 465 470 475 480

Thr Ser Ala Thr Gly Pro Tyr Ser Thr Ala Thr Asn Thr Val Trp Pro
 485 490 495

Ser Ser Gly Ser Gly Ser Ser Thr Thr Thr Ser Ser Ala Pro Cys Thr
 500 505 510

Thr Pro Thr Ser Val Ala Val Thr Phe Asp Glu Ile Val Ser Thr Ser
 515 520 525

Tyr Gly Glu Thr Ile Tyr Leu Ala Gly Ser Ile Pro Glu Leu Gly Asn
 530 535 540

Trp Ser Thr Ala Ser Ala Ile Pro Leu Arg Ala Asp Ala Tyr Thr Asn
 545 550 555 560

Ser Asn Pro Leu Trp Tyr Val Thr Val Asn Leu Pro Pro Gly Thr Ser
 565 570 575

Phe Glu Tyr Lys Phe Phe Lys Asn Gln Thr Asp Gly Thr Ile Val Trp
 580 585 590

Glu Asp Asp Pro Asn Arg Ser Tyr Thr Val Pro Ala Tyr Cys Gly Gln
 595 600 605

Thr Thr Ala Ile Leu Asp Asp Ser Trp Gln
 610 615

<210> 7
 <211> 1854
 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 8

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal sequence associated with Rasamsonia emersonii
glucoamylase from(Uniprot Q9C1V4)

<400> 8

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Ala Ala Phe Ala
20

<210> 9

<211> 508

<212> PRT

<213> Artificial Sequence

<220>

<223> Glucoamylase from Saccharomycopsis fibuligera associated with the

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signal sequence of *Saccharomyces cerevisiae* alpha-mating factor 1

<220>

<221> SIGNAL

<222> (1)..(19)

<400> 9

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
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Ala Leu Ala Asn Thr Gly His Phe Gln Ala Tyr Ser Gly Tyr Thr Val
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Asn Arg Ala Asn Phe Thr Gln Trp Ile His Glu Gln Pro Ala Val Ser
35 40 45

Trp Tyr Tyr Leu Leu Gln Asn Ile Asp Tyr Pro Glu Gly Gln Phe Lys
50 55 60

Ala Ala Lys Pro Gly Val Val Val Ala Ser Pro Ser Thr Ser Glu Pro
65 70 75 80

Asp Tyr Phe Tyr Gln Trp Thr Arg Asp Thr Ala Ile Thr Phe Leu Ser
85 90 95

Leu Ile Ala Glu Val Glu Asp His Ser Phe Ser Asn Thr Thr Leu Ala
100 105 110

Lys Val Val Glu Tyr Tyr Ile Ser Asn Thr Tyr Thr Leu Gln Arg Val
115 120 125

Ser Asn Pro Ser Gly Asn Phe Asp Ser Pro Asn His Asp Gly Leu Gly
130 135 140

Glu Pro Lys Phe Asn Val Asp Asp Thr Ala Tyr Thr Ala Ser Trp Gly
145 150 155 160

Arg Pro Gln Asn Asp Gly Pro Ala Leu Arg Ala Tyr Ala Ile Ser Arg
165 170 175

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Tyr Leu Asn Ala Val Ala Lys His Asn Asn Gly Lys Leu Leu Leu Ala
 180 185 190

Gly Gln Asn Gly Ile Pro Tyr Ser Ser Ala Ser Asp Ile Tyr Trp Lys
 195 200 205

Ile Ile Lys Pro Asp Leu Gln His Val Ser Thr His Trp Ser Thr Ser
 210 215 220

Gly Phe Asp Leu Trp Glu Glu Asn Gln Gly Thr His Phe Phe Thr Ala
 225 230 235 240

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

Tyr Asn Asp Pro Gly Phe Thr Ser Trp Leu Glu Lys Gln Lys Asp Ala
 260 265 270

Leu Asn Ser Tyr Ile Asn Ser Ser Gly Phe Val Asn Ser Gly Lys Lys
 275 280 285

His Ile Val Glu Ser Pro Gln Leu Ser Ser Arg Gly Gly Leu Asp Ser
 290 295 300

Ala Thr Tyr Ile Ala Ala Leu Ile Thr His Asp Ile Gly Asp Asp Asp
 305 310 315 320

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

Tyr Tyr Leu Leu Val Asp Asn Lys Asn Arg Tyr Lys Ile Asn Gly Asn
 340 345 350

Tyr Lys Ala Gly Ala Ala Val Gly Arg Tyr Pro Glu Asp Val Tyr Asn
 355 360 365

Gly Val Gly Thr Ser Glu Gly Asn Pro Trp Gln Leu Ala Thr Ala Tyr
 370 375 380

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Ala Gly Gln Thr Phe Tyr Thr Leu Ala Tyr Asn Ser Leu Lys Asn Lys
385 390 395 400

Lys Asn Leu Val Ile Glu Lys Leu Asn Tyr Asp Leu Tyr Asn Ser Phe
405 410 415

Ile Ala Asp Leu Ser Lys Ile Asp Ser Ser Tyr Ala Ser Lys Asp Ser
420 425 430

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

Leu Leu Gln Phe Gly Asp Ser Phe Leu Lys Val Leu Leu Asp His Ile
450 455 460

Asp Asp Asn Gly Gln Leu Thr Glu Glu Ile Asn Arg Tyr Thr Gly Phe
465 470 475 480

Gln Ala Gly Ala Val Ser Leu Thr Trp Ser Ser Gly Ser Leu Leu Ser
485 490 495

Ala Asn Arg Ala Arg Asn Lys Leu Ile Glu Leu Leu
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<210> 10
<211> 1527
<212> DNA
<213> Artificial Sequence

<220>
<223> Encoding SEQ ID NO: 9

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 aacacctaca ccttgcaaag agtttctaata ccatccggta acttcgattc tccaaatcat 420
 gatggtttgg gtgaacctaa gttcaacgtt gatgatactg cttatacagc ttcttgggggt 480
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 aagaacttgg tcatcgaaaa gttgaactac gacttgtaca actccttcat tgctgatttg 1260
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 ttggatcaca tcgatgacaa cgggtcaattg actgaagaaa tcaacagata caccggtttt 1440
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 agaaacaagt tgatcgaatt attgtga 1527

<210> 11

<211> 616

<212> PRT

<213> Artificial Sequence

<220>

<223> Glucoamylase from *Rasamsonia emersonii* (Uniprot A0A0F4YWQ6)
 associated with the signal sequence of *Saccharomyces cerevisiae*
 alpha-mating factor 1

<220>

<221> SIGNAL

<222> (1)..(19)

<400> 11

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Ala Leu Ala Arg Ala Pro Val Ala Ala Arg Ala Ser Gly Ser Leu Asp
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Ser Phe Leu Ala Thr Glu Thr Pro Ile Ala Leu Gln Gly Val Leu Asn
 35 40 45

Asn Ile Gly Pro Asn Gly Ala Asp Val Ala Gly Ala Ser Ala Gly Ile
 50 55 60

Val Val Ala Ser Pro Ser Arg Ser Asp Pro Asp Tyr Phe Tyr Ser Trp
 65 70 75 80

Thr Arg Asp Ala Ala Leu Thr Ala Lys Tyr Leu Val Asp Ala Phe Ile
 85 90 95

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

Gln Ala Gln Val Gln Thr Ile Ser Asn Pro Ser Gly Asp Leu Ser Thr
 115 120 125

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

Gly Pro Trp Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr
 145 150 155 160

Ala Leu Ile Ala Tyr Ala Asn Tyr Leu Ile Asp Asn Gly Gln Ala Ser
 165 170 175

117549337_1

Thr Ala Asp Glu Ile Ile Trp Pro Ile Val Gln Asn Asp Leu Ser Tyr
 180 185 190

Val Thr Gln Tyr Trp Asn Ser Ser Thr Phe Asp Leu Trp Glu Glu Val
 195 200 205

Glu Gly Ser Ser Phe Phe Thr Thr Ala Val Gln His Arg Ala Leu Val
 210 215 220

Glu Gly Asn Ala Leu Ala Thr Arg Leu Asn His Thr Cys Pro Asn Cys
 225 230 235 240

Val Ser Gln Ala Pro Gln Val Leu Cys Phe Leu Gln Ser Tyr Trp Thr
 245 250 255

Gly Ser Tyr Val Leu Ala Asn Phe Gly Gly Ser Gly Arg Ser Gly Lys
 260 265 270

Asp Val Asn Ser Ile Leu Gly Ser Ile His Thr Phe Asp Pro Ala Gly
 275 280 285

Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys Ser Ala Arg Ala Leu Ala
 290 295 300

Asn His Lys Val Val Thr Asp Ser Phe Arg Ser Val Tyr Ala Val Asn
 305 310 315 320

Ser Gly Ile Ala Glu Gly Ser Ala Val Ala Val Gly Arg Tyr Pro Glu
 325 330 335

Asp Val Tyr Gln Gly Gly Asn Pro Trp Tyr Leu Ala Thr Ala Ala Ala
 340 345 350

Ala Glu Gln Leu Tyr Asp Ala Ile Tyr Gln Trp Asn Lys Ile Gly Ser
 355 360 365

Ile Ser Ile Thr Asp Val Ser Leu Ala Phe Phe Gln Asp Ile Tyr Pro
 370 375 380

117549337_1

Ser Ala Ala Val Gly Thr Tyr Asn Ser Gly Ser Ser Thr Phe Asn Asp
 385 390 395 400

Ile Ile Ser Ala Val Gln Thr Tyr Ala Asp Gly Tyr Leu Ser Ile Ile
 405 410 415

Glu Lys Tyr Thr Pro Ser Asp Gly Ser Leu Thr Glu Gln Phe Ser Arg
 420 425 430

Ser Asp Gly Thr Pro Leu Ser Ala Ser Gly Leu Thr Trp Ser Tyr Ala
 435 440 445

Ser Leu Leu Thr Ala Ala Ala Arg Arg Gln Ser Ile Val Pro Ala Ser
 450 455 460

Trp Gly Glu Ser Ser Ala Ser Ser Val Pro Ala Val Cys Ser Ala Thr
 465 470 475 480

Ser Ala Thr Gly Pro Tyr Ser Thr Ala Thr Asn Thr Ala Trp Pro Ser
 485 490 495

Ser Gly Ser Gly Pro Ser Thr Thr Thr Ser Val Pro Cys Thr Thr Pro
 500 505 510

Thr Ser Val Ala Val Thr Phe Asp Glu Ile Val Ser Thr Thr Tyr Gly
 515 520 525

Glu Thr Ile Tyr Leu Ala Gly Ser Ile Pro Glu Leu Gly Asn Trp Ser
 530 535 540

Pro Ser Ser Ala Ile Pro Leu Arg Ala Asp Ala Tyr Thr Ser Ser Asn
 545 550 555 560

Pro Leu Trp Tyr Val Thr Leu Asn Leu Pro Ala Gly Thr Ser Phe Glu
 565 570 575

Tyr Lys Phe Phe Lys Lys Glu Thr Asp Gly Thr Ile Val Trp Glu Asp
 580 585 590

117549337_1

Asp Pro Asn Arg Ser Tyr Thr Val Pro Ala Tyr Cys Gly Gln Thr Thr
 595 600 605

Ala Ile Leu Asp Asp Ser Trp Gln
 610 615

<210> 12
 <211> 1848
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encoding SEQ ID NO: 11

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 attgcattgc aaggggttct aaacaacatt ggaccgaacg gggcagacgt ggctggtgct 180
 tccgcaggga tcgtggttgc gtctccatca agaagcgacc ctgactactt ttatagttgg 240
 acgagagatg cggcattaac agcgaagtat ttagttgatg cattcatcgc cggaaataag 300
 gatttagagc agactataca agaatatatc tcagcgcaag cacaagtcca aacgatatcc 360
 aacccatcag gggacttgtc aacaggaggt ctgggtgagc cgaagtttaa tgtgaacgag 420
 actgcgttca ctgggccttg gggtcgtccc cagagggatg ggccagcttt gcgtgccacg 480
 gctctgattg cttacgcaaa ttaccttatc gacaatgggtc aggcaagtac cgctgatgaa 540
 ataatttggc cgattgtcca gaacgacctt tcatacgtta ccagttattg gaactcttcc 600
 acattcgatt tgtgggagga agtcgaagga tccagcttct ttacaactgc cgttcagcac 660
 agggcctttgg ttgaaggtaa tgccttggca acgcgtttga accatactg ccctaattgc 720
 gtgtcccaag ctccacaggt tttgtgtttc ctacagagct attggactgg ctctacgtc 780
 ctagcgaatt ttggcggcag tgggagatcc ggaaaagacg tgaacagcat cttggggagc 840
 attcacactt tcgaccagc tgggggctgc gatgatagta cgtttcagcc atgttccgcc 900
 cgtgcattgg cgaatcataa ggtggtaact gacagtttta ggtcagtata cgcggttaat 960
 tccgggattg ctgaaggag tgctgtagcg gtgggaaggt atccagagga cgtttatcag 1020
 ggtggtaatc cctggtacct ggctaccgcc gctgctgctg aacaactgta tgacgccatt 1080

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tatcagtgga acaaaattgg ttctatatcc atcaccgacg tctcactagc ctttttccag 1140
 gatatatatc caagcgccgc tgtcggaaca tacaactccg gttcatcaac gttcaatgat 1200
 ataatctccg ctgtgcaaac ctacgcggac ggttacttat ctattatcga aaaatacacg 1260
 ccaagtgacg gtagcctgac tgagcaatth agtcgttctg acggtactcc attatctgca 1320
 agcggactaa cgtggagcta cgcaagccta cttacagcgg cgcctcgtag acaatcaatt 1380
 gtcccagcca gttgggggtga gagttctgcg agttctgttc ctgcggtgtg tagtgcgacg 1440
 tcagcgaccg gcccttatag caccgcaaca aatacggctt ggccgagttc cgggtctggt 1500
 ccaagcacia cgaccagtgt cccctgcaca acccctacat cagtggccgt cacttttgac 1560
 gaaatcgtca gtacgacgta cggtgaaact atttatcttg cgggggtcaat accggagcta 1620
 gggaattggt caccgagttc cgcgattcct ttaagggcag acgcgtatac cagtagcaac 1680
 ccgttgtggt atgttacact taatctaccc gcgggcacta gcttcgagta caaattcttt 1740
 aaaaaagaaa cggacggcac gattgtttgg gaggacgacc caaacgttc ttacactgta 1800
 ccggcttatt gcggccagac aacagcgatc ttagacgaca gttggcag 1848

<210> 13
 <211> 597
 <212> PRT
 <213> Rasamsonia emersonii

<400> 13

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

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

Ser Pro Ser Arg Ser Asp Pro Asp Tyr Phe Tyr Ser Trp Thr Arg Asp
 50 55 60

Ala Ala Leu Thr Ala Lys Tyr Leu Val Asp Ala Phe Ile Ala Gly Asn

65		70		75		80
Lys	Asp	Leu	Glu	Gln	Thr	Ile
			85			
				Gln	Glu	Tyr
					90	
				Ile	Ser	Ala
						Gln
						Ala
						Gln
Val	Gln	Thr	Ile	Ser	Asn	Pro
			100			
				Ser	Gly	Asp
					105	
				Leu	Ser	Thr
						Gly
						Gly
						Leu
Gly	Glu	Pro	Lys	Phe	Asn	Val
			115			
				Asn	Glu	Thr
					120	
				Ala	Phe	Thr
						Gly
						Pro
						Trp
Gly	Arg	Pro	Gln	Arg	Asp	Gly
						130
						135
						Pro
						Ala
						Leu
						Arg
						Ala
						Thr
						Ala
						Leu
						Ile
Ala	Tyr	Ala	Asn	Tyr	Leu	Ile
					145	
						150
						Asp
						Asn
						Gly
						Gln
						Ala
						Ser
						Thr
						Ala
						Asp
Glu	Ile	Ile	Trp	Pro	Ile	Val
				165		
						Gln
						Asn
						Asp
						Leu
						Ser
						Tyr
						Val
						Thr
						Gln
Tyr	Trp	Asn	Ser	Ser	Thr	Phe
			180			
						185
						Leu
						Trp
						Glu
						Glu
						Val
						Glu
						Gly
						Ser
Ser	Phe	Phe	Thr	Thr	Ala	Val
			195			
						Gln
						His
						Arg
						Ala
						Leu
						Val
						Glu
						Gly
						Asn
Ala	Leu	Ala	Thr	Arg	Leu	Asn
					210	
						215
						His
						Thr
						Cys
						Pro
						Asn
						Cys
						Val
						Ser
						Gln
Ala	Pro	Gln	Val	Leu	Cys	Phe
					225	
						230
						Gln
						Ser
						Tyr
						Trp
						Thr
						Gly
						Ser
						Tyr
Val	Leu	Ala	Asn	Phe	Gly	Gly
					245	
						250
						Arg
						Ser
						Gly
						Lys
						Asp
						Val
						Asn
Ser	Ile	Leu	Gly	Ser	Ile	His
			260			
						265
						Pro
						Ala
						Gly
						Gly
						Cys
						Asp
Asp	Ser	Thr	Phe	Gln	Pro	Cys
						Ala
						Arg
						Ala
						Leu
						Ala
						Asn
						His
						Lys

275

280

285

Val Val Thr Asp Ser Phe Arg Ser Val Tyr Ala Val Asn Ser Gly Ile
 290 295 300

Ala Glu Gly Ser Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Val Tyr
 305 310 315 320

Gln Gly Gly Asn Pro Trp Tyr Leu Ala Thr Ala Ala Ala Ala Glu Gln
 325 330 335

Leu Tyr Asp Ala Ile Tyr Gln Trp Asn Lys Ile Gly Ser Ile Ser Ile
 340 345 350

Thr Asp Val Ser Leu Ala Phe Phe Gln Asp Ile Tyr Pro Ser Ala Ala
 355 360 365

Val Gly Thr Tyr Asn Ser Gly Ser Ser Thr Phe Asn Asp Ile Ile Ser
 370 375 380

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

Thr Pro Ser Asp Gly Ser Leu Thr Glu Gln Phe Ser Arg Ser Asp Gly
 405 410 415

Thr Pro Leu Ser Ala Ser Gly Leu Thr Trp Ser Tyr Ala Ser Leu Leu
 420 425 430

Thr Ala Ala Ala Arg Arg Gln Ser Ile Val Pro Ala Ser Trp Gly Glu
 435 440 445

Ser Ser Ala Ser Ser Val Pro Ala Val Cys Ser Ala Thr Ser Ala Thr
 450 455 460

Gly Pro Tyr Ser Thr Ala Thr Asn Thr Ala Trp Pro Ser Ser Gly Ser
 465 470 475 480

Gly Pro Ser Thr Thr Thr Ser Val Pro Cys Thr Thr Pro Thr Ser Val

Ala Val Thr Phe Asp Glu Ile Val Ser Thr Thr Tyr Gly Glu Thr Ile
500 505 510

Tyr Leu Ala Gly Ser Ile Pro Glu Leu Gly Asn Trp Ser Pro Ser Ser
515 520 525

Ala Ile Pro Leu Arg Ala Asp Ala Tyr Thr Ser Ser Asn Pro Leu Trp
530 535 540

Tyr Val Thr Leu Asn Leu Pro Ala Gly Thr Ser Phe Glu Tyr Lys Phe
545 550 555 560

Phe Lys Lys Glu Thr Asp Gly Thr Ile Val Trp Glu Asp Asp Pro Asn
565 570 575

Arg Ser Tyr Thr Val Pro Ala Tyr Cys Gly Gln Thr Thr Ala Ile Leu
580 585 590

Asp Asp Ser Trp Gln
595

<210> 14
<211> 1791
<212> DNA
<213> Artificial Sequence

<220>
<223> Encoding SEQ ID NO: 13

<400> 14
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gcttccgcag ggatcgtgggt tgcgtctcca tcaagaagcg accctgacta cttttatagt 180
tggacgagag atgcggcatt aacagcgaag tatttagttg atgcattcat cgccggaaat 240
aaggatttag agcagactat acaagaatat atctcagcgc aagcacaagt ccaaacgata 300
tccaacccat caggggactt gtcaacagga ggtctgggtg agccgaagtt taatgtgaac 360

117549337_1

gagactgcgt tcactgggcc ttggggtcgt cccagaggg atgggccagc tttgcgtgcc 420
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 gaaataattt ggccgattgt ccagaacgac ctttcatacg ttaccagta ttggaactct 540
 tccacattcg atttgtggga ggaagtcgaa ggatccagct tctttacaac tgccgttcag 600
 cacagggtt tggttgaagg taatgccttg gcaacgcgtt tgaaccatac gtgccctaata 660
 tgcgtgtccc aagctccaca ggTTTTgtgt ttcctacaga gctattggac tggctcctac 720
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 caggatatat atccaagcgc cgctgtcgga acatacaact ccggttcac aacgttcaat 1140
 gatataatct ccgctgtgca aacctacgcg gacggttact tatctattat cgaaaaatac 1200
 acgccaagt acggtagcct gactgagcaa tttagtcgtt ctgacggtac tccattatct 1260
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 gacgaaatcg tcagtacgac gtacggtgaa actatttatc ttgcggggtc aataccggag 1560
 ctagggaatt ggtcaccgag ttccgcgatt cttttaaggg cagacgcgta taccagtagc 1620
 aaccgttgt ggtatgttac acttaatcta cccgcgggca ctagcttcga gtacaaattc 1680
 tttaaaaaag aaacggacgg cacgattgtt tgggaggacg acccaaaccg ttcttacact 1740
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<210> 15
 <211> 617
 <212> PRT

<213> Rasamsonia emersonii

<220>

<221> SIGNAL

<222> (1)..(20)

<400> 15

Met Ala Ser Leu Val Ala Gly Ala Leu Cys Val Leu Gly Leu Thr Pro
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Ala Ala Phe Ala Arg Ala Pro Val Ala Ala Arg Ala Ser Gly Ser Leu
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Asp Ser Phe Leu Ala Thr Glu Thr Pro Ile Ala Leu Gln Gly Val Leu
 35 40 45

Asn Asn Ile Gly Pro Asn Gly Ala Asp Val Ala Gly Ala Ser Ala Gly
 50 55 60

Ile Val Val Ala Ser Pro Ser Arg Ser Asp Pro Asp Tyr Phe Tyr Ser
 65 70 75 80

Trp Thr Arg Asp Ala Ala Leu Thr Ala Lys Tyr Leu Val Asp Ala Phe
 85 90 95

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

Ala Gln Ala Gln Val Gln Thr Ile Ser Asn Pro Ser Gly Asp Leu Ser
 115 120 125

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

Thr Gly Pro Trp Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala
 145 150 155 160

Thr Ala Leu Ile Ala Tyr Ala Asn Tyr Leu Ile Asp Asn Gly Gln Ala
 165 170 175

117549337_1

Ser Thr Ala Asp Glu Ile Ile Trp Pro Ile Val Gln Asn Asp Leu Ser
 180 185 190

Tyr Val Thr Gln Tyr Trp Asn Ser Ser Thr Phe Asp Leu Trp Glu Glu
 195 200 205

Val Glu Gly Ser Ser Phe Phe Thr Thr Ala Val Gln His Arg Ala Leu
 210 215 220

Val Glu Gly Asn Ala Leu Ala Thr Arg Leu Asn His Thr Cys Pro Asn
 225 230 235 240

Cys Val Ser Gln Ala Pro Gln Val Leu Cys Phe Leu Gln Ser Tyr Trp
 245 250 255

Thr Gly Ser Tyr Val Leu Ala Asn Phe Gly Gly Ser Gly Arg Ser Gly
 260 265 270

Lys Asp Val Asn Ser Ile Leu Gly Ser Ile His Thr Phe Asp Pro Ala
 275 280 285

Gly Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys Ser Ala Arg Ala Leu
 290 295 300

Ala Asn His Lys Val Val Thr Asp Ser Phe Arg Ser Val Tyr Ala Val
 305 310 315 320

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

Glu Asp Val Tyr Gln Gly Gly Asn Pro Trp Tyr Leu Ala Thr Ala Ala
 340 345 350

Ala Ala Glu Gln Leu Tyr Asp Ala Ile Tyr Gln Trp Asn Lys Ile Gly
 355 360 365

Ser Ile Ser Ile Thr Asp Val Ser Leu Ala Phe Phe Gln Asp Ile Tyr
 370 375 380

117549337_1

Pro Ser Ala Ala Val Gly Thr Tyr Asn Ser Gly Ser Ser Thr Phe Asn
385 390 395 400

Asp Ile Ile Ser Ala Val Gln Thr Tyr Ala Asp Gly Tyr Leu Ser Ile
405 410 415

Ile Glu Lys Tyr Thr Pro Ser Asp Gly Ser Leu Thr Glu Gln Phe Ser
420 425 430

Arg Ser Asp Gly Thr Pro Leu Ser Ala Ser Gly Leu Thr Trp Ser Tyr
435 440 445

Ala Ser Leu Leu Thr Ala Ala Ala Arg Arg Gln Ser Ile Val Pro Ala
450 455 460

Ser Trp Gly Glu Ser Ser Ala Ser Ser Val Pro Ala Val Cys Ser Ala
465 470 475 480

Thr Ser Ala Thr Gly Pro Tyr Ser Thr Ala Thr Asn Thr Ala Trp Pro
485 490 495

Ser Ser Gly Ser Gly Pro Ser Thr Thr Thr Ser Val Pro Cys Thr Thr
500 505 510

Pro Thr Ser Val Ala Val Thr Phe Asp Glu Ile Val Ser Thr Thr Tyr
515 520 525

Gly Glu Thr Ile Tyr Leu Ala Gly Ser Ile Pro Glu Leu Gly Asn Trp
530 535 540

Ser Pro Ser Ser Ala Ile Pro Leu Arg Ala Asp Ala Tyr Thr Ser Ser
545 550 555 560

Asn Pro Leu Trp Tyr Val Thr Leu Asn Leu Pro Ala Gly Thr Ser Phe
565 570 575

Glu Tyr Lys Phe Phe Lys Lys Glu Thr Asp Gly Thr Ile Val Trp Glu
580 585 590

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Asp Asp Pro Asn Arg Ser Tyr Thr Val Pro Ala Tyr Cys Gly Gln Thr
595 600 605

Thr Ala Ile Leu Asp Asp Ser Trp Gln
610 615

<210> 16

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal sequence associated with Rasamsonia emersonii glucoamylase
(Uniprot A0A0F4YWQ6)

<400> 16

Met Ala Ser Leu Val Ala Gly Ala Leu Cys Val Leu Gly Leu Thr Pro
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Ala Ala Phe Ala
20

<210> 17

<211> 471

<212> PRT

<213> Rhizomucor pusillus

<220>

<221> SIGNAL

<222> (1)..(21)

<400> 17

Met Lys Phe Ser Ile Ser Leu Ser Ala Ala Ile Val Leu Phe Ala Ala
1 5 10 15

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

Arg Ala Thr Ser Asp Asp Trp Lys Ser Lys Ala Ile Tyr Gln Leu Leu
35 40 45

117549337_1

Thr Asp Arg Phe Gly Arg Ala Asp Asp Ser Thr Ser Asn Cys Ser Asn
 50 55 60

Leu Ser Asn Tyr Cys Gly Gly Thr Tyr Glu Gly Ile Thr Lys His Leu
 65 70 75 80

Asp Tyr Ile Ser Gly Met Gly Phe Asp Ala Ile Trp Ile Ser Pro Ile
 85 90 95

Pro Lys Asn Ser Asp Gly Gly Tyr His Gly Tyr Trp Ala Thr Asp Phe
 100 105 110

Tyr Gln Leu Asn Ser Asn Phe Gly Asp Glu Ser Gln Leu Lys Thr Leu
 115 120 125

Ile Gln Ala Ala His Glu Arg Gly Met Tyr Val Met Leu Asp Val Val
 130 135 140

Ala Asn His Ala Gly Pro Thr Ser Asn Gly Tyr Ser Gly Tyr Thr Phe
 145 150 155 160

Gly Asp Ala Ser Leu Tyr His Pro Lys Cys Thr Ile Asp Tyr Asn Asp
 165 170 175

Gln Thr Ser Ile Glu Gln Cys Trp Val Ala Asp Glu Leu Pro Asp Ile
 180 185 190

Asp Thr Glu Asn Ser Asp Asn Val Ala Ile Leu Asn Asp Ile Val Ser
 195 200 205

Gly Trp Val Gly Asn Tyr Ser Phe Asp Gly Ile Arg Ile Asp Thr Val
 210 215 220

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

Val Phe Ala Thr Gly Glu Val Phe Asn Gly Asp Pro Ala Tyr Val Gly
 245 250 255

117549337_1

Pro Tyr Gln Lys Tyr Leu Pro Pro Leu Ile Asn Tyr Pro Met Tyr Tyr
 260 265 270

Ala Leu Asn Asp Val Phe Val Ser Lys Ser Lys Gly Phe Ser Arg Ile
 275 280 285

Ser Glu Met Leu Gly Ser Asn Arg Asn Ala Phe Glu Asp Thr Ser Val
 290 295 300

Leu Thr Thr Phe Val Asp Asn His Asp Asn Pro Arg Phe Leu Asn Ser
 305 310 315 320

Gln Ser Asp Lys Ala Leu Phe Lys Asn Ala Leu Thr Tyr Val Leu Leu
 325 330 335

Gly Glu Gly Ile Pro Ile Val Tyr Tyr Gly Ser Glu Gln Gly Phe Ser
 340 345 350

Gly Gly Ala Asp Pro Ala Asn Arg Glu Val Leu Trp Thr Ala Asn Tyr
 355 360 365

Asp Thr Ser Ser Asp Leu Tyr Gln Phe Ile Lys Thr Val Asn Ser Val
 370 375 380

Arg Met Lys Ser Asn Lys Thr Val Tyr Met Asp Ile Tyr Val Gly Asp
 385 390 395 400

Asn Ala Tyr Ala Phe Lys His Gly Asp Ala Leu Val Val Leu Asn Asn
 405 410 415

Tyr Gly Ser Gly Ser Thr Asn Gln Val Ser Phe Ser Val Ser Gly Lys
 420 425 430

Phe Asp Ser Gly Ala Ser Leu Met Asp Ile Val Ser Asn Ile Thr Thr
 435 440 445

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

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Pro Ala Ile Phe Thr Ser Ala
465 470

<210> 18
<211> 615
<212> PRT
<213> Aspergillus luchuensis

<220>
<221> SIGNAL
<222> (1)..(21)

<400> 18

Met Asp Gly Trp Trp Ile Ile Ser Leu Leu Val Val Thr Leu Gly Phe
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Ser Thr Val Asn Ala Ala Ser Arg Asp Gln Trp Ile Gly Arg Ser Ile
20 25 30

Tyr Gln Ile Val Thr Asp Arg Phe Ala Arg Ser Asp Asn Ser Thr Thr
35 40 45

Ala Ala Cys Asp Ala Ala Gln Gly Asn Tyr Cys Gly Gly Ser Phe Gln
50 55 60

Gly Ile Ile Asn Lys Leu Asp Tyr Ile His Asp Leu Gly Phe Asp Ala
65 70 75 80

Val Gly Leu Ala Leu Gln Ser Ser Val Pro His Thr Phe Cys Asn Ser
85 90 95

Ser His Ile Gln Val Ser Arg Tyr Gly Ser Leu Gln Arg Lys Pro Arg
100 105 110

Phe Pro Pro Glu Gln Gln Ile Ser Gln Phe Ile Ala Tyr His Gly Tyr
115 120 125

Trp Pro Asn Asp Leu Tyr Ser Ile Asn Ser His Phe Gly Thr Pro Lys
130 135 140

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Glu Leu Gln Ala Leu Ser Ser Ala Leu His Asn Arg Gly Met Tyr Leu
 145 150 155 160

Met Leu Asp Ile Val Val Gly Asp Met Ala Trp Ala Gly Asn Ser Ser
 165 170 175

Thr Val Asp Tyr Ser Thr Phe Asn Pro Phe Asp Asp Glu Lys Tyr Phe
 180 185 190

His Asp Phe Lys Leu Leu Ser Ser Asp Pro Thr Asn Glu Thr Cys Val
 195 200 205

Leu Asp Cys Trp Met Gly Asp Thr Val Val Ser Leu Pro Asp Leu Arg
 210 215 220

Asn Glu Asp Asp Gln Val Gln Asn Ile Leu Gly Ser Trp Ile Ser Gly
 225 230 235 240

Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Ser Val Leu
 245 250 255

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

Phe Thr Ile Gly Glu Gly Ala Thr Ala Asp Ala Ala Asp Val Cys Pro
 275 280 285

Leu Gln Pro Ser Leu Asn Gly Leu Leu Asn Tyr Pro Phe Leu Ser Arg
 290 295 300

Val Asp Leu Leu Arg Tyr Tyr Ile Leu Thr Asn Ala Phe Asn Thr Thr
 305 310 315 320

Asn Gly Asn Leu Ser Thr Ile Thr Glu Ser Ile Ser Tyr Thr Lys Gly
 325 330 335

Gln Cys Glu Asp Val Leu Ala Leu Gly Thr Phe Thr Ala Asn Gln Asp
 340 345 350

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Val Pro Arg Phe Gly Ser Tyr Thr Ser Asp Ile Ser Gln Tyr Ala Gly
 355 360 365

Gly Arg His Pro His Pro Tyr Val Pro Ile Pro Thr Pro His Arg Arg
 370 375 380

Gln Asp Phe Ser Asp Thr Thr Asp Asp Gln Asn Thr Val Tyr Tyr Gly
 385 390 395 400

Glu Glu Gln His Leu Thr Gly Ser Tyr Asn Pro Val Asn Arg Glu Ala
 405 410 415

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

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

Gln Tyr Thr Gln Asn Ser Gln Ser Gly Ser Asp Tyr Leu Ser Tyr Leu
 450 455 460

Ser Ala Pro Ile Tyr Asn Ser Thr His Ile Leu Ala Thr Arg Lys Gly
 465 470 475 480

Phe Ala Gly Asn Gln Val Val Ser Val Val Ser Asn Leu Gly Ala Lys
 485 490 495

Pro Ala Ser Lys Ala Ala Thr Lys Ile Thr Leu Gly Ser Asp Glu Thr
 500 505 510

Gly Phe Gln Ser Lys Gln Asn Val Thr Glu Ile Leu Ser Cys Lys Thr
 515 520 525

Tyr Val Thr Asp Ser Ser Gly Asn Leu Ala Val Asp Leu Ser Ser Asp
 530 535 540

Gly Gly Pro Arg Val Tyr Tyr Pro Thr Asp Ser Leu Lys Asp Ser Thr
 545 550 555 560

117549337_1

Asp Ile Cys Asp Asp Gln Thr Lys Ser Ala Thr Pro Ser Ser Ser Ala
565 570 575

Ala Ser Ser Val Ser Pro Asn Gln Ser Lys Gly Ser Glu Thr Cys Leu
580 585 590

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

Ala Thr Ser Tyr Ala Phe Ile
610 615

<210> 19

<211> 549

<212> PRT

<213> Aspergillus oryzae

<220>

<221> SIGNAL

<222> (1)..(23)

<400> 19

Met Val Ser Ser Ser Ser Leu Gly Arg Phe Ala Val Leu Val Thr Ser
1 5 10 15

Leu Val Gly Ser Ala Val Ala Ala Thr Thr Ala Glu Trp Lys Ser Arg
20 25 30

Ser Val Tyr Gln Thr Met Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser
35 40 45

Thr Thr Ala Pro Cys Asn Thr Thr Gln Gly Leu Tyr Cys Gly Gly Thr
50 55 60

Trp Arg Gly Thr Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe
65 70 75 80

Asp Ala Val Met Ile Ser Pro Ile Val Glu Asn Ile Glu Gly Arg Val
85 90 95

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Ser Tyr Gly Glu Ala Tyr His Gly Tyr Trp Pro Leu Asp Leu Tyr Ser
 100 105 110

Leu Asn Ser His Phe Gly Thr His Gln Asp Leu Leu Asp Leu Ser Glu
 115 120 125

Ala Leu His Ser Arg Gly Met Tyr Leu Met Met Asp Thr Val Ile Asn
 130 135 140

Asn Met Ala Tyr Met Thr Asn Gly Lys Asp Pro Ala Lys Asn Ile Asp
 145 150 155 160

Tyr Ser Val Phe Thr Pro Phe Asn Asp Ser Ser Tyr Phe His Pro Tyr
 165 170 175

Cys Lys Ile Thr Asp Trp Asn Asn Tyr Thr Asn Ala Gln Leu Cys Gln
 180 185 190

Thr Gly Asp Asp Lys Val Ala Leu Pro Asp Leu Phe Thr Glu His Glu
 195 200 205

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

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

Gly Phe Leu Lys Asn Phe Gly Asp Ala Ile Gly Ala Phe Met Thr Gly
 245 250 255

Glu Val Leu Gln Gln Glu Val Asp Thr Ile Cys Lys Tyr Gln Asn Asn
 260 265 270

Tyr Ile Gly Ser Val Pro Asn Tyr Pro Ile Tyr Tyr Ser Val Leu Lys
 275 280 285

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

117549337_1

Met Lys Asn Ser Cys Asp Asp Val Thr Ala Leu Ala Ser Phe Ser Glu
 305 310 315 320

Asn His Asp Val Ala Arg Phe Ala Ser Met Thr Asp Asp Met Ala Leu
 325 330 335

Ala Lys Asn Val Leu Thr Phe Thr Ile Leu Tyr Asp Gly Val Pro Met
 340 345 350

Ile Tyr Gln Gly Gln Glu Gln His Leu Asp Gly Pro Gly Thr Pro Asp
 355 360 365

Asn Arg Glu Ala Ile Trp Leu Thr Lys Tyr Asn Thr Asp Ala Glu Leu
 370 375 380

Tyr Lys Leu Ile Ala Lys Leu Asn Thr Ile Arg Lys His Ala Tyr Lys
 385 390 395 400

Leu Asp Pro Asn Tyr Val Ser Leu Gln Thr Tyr Pro Ile Phe Arg Gly
 405 410 415

Gly Ser Glu Leu Gly Phe Arg Lys Gly Val Glu Gly Arg Gln Val Val
 420 425 430

Met Leu Leu Ser Thr Gln Gly Ser Asn Ser Ser Ala Tyr Asn Leu Thr
 435 440 445

Leu Pro Val Ser Phe Asn Gly Gly Val Gln Val Met Asp Val Leu Asn
 450 455 460

Cys Val Asn Tyr Thr Val Asn Pro Gln Ser Glu Leu Ile Val Pro Met
 465 470 475 480

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

Ser Gly Leu Cys Gly Tyr Thr Thr Ala Asn Val Ser Phe Val Glu Leu
 500 505 510

117549337_1

Lys Thr Lys Gly Ala Ala Ala Ala Met Ser Leu Gly Ala Lys Thr Thr
515 520 525

Ser Ser Ala Ala His Gly Val Leu Leu Ser Val Leu Leu Ser Ser Leu
530 535 540

Val Ala Val Leu Leu
545

<210> 20
<211> 515
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)..(19)

<400> 20

Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
1 5 10 15

Ile Ser Ala Gln Tyr Ser Pro Asn Thr Gln Gln Gly Arg Thr Ser Ile
20 25 30

Val His Leu Phe Glu Trp Arg Trp Val Asp Ile Ala Leu Glu Cys Glu
35 40 45

Arg Tyr Leu Ala Pro Lys Gly Phe Gly Gly Val Gln Val Ser Pro Pro
50 55 60

Asn Glu Asn Val Ala Ile Tyr Asn Pro Phe Arg Pro Trp Trp Glu Arg
65 70 75 80

Tyr Gln Pro Val Ser Tyr Lys Leu Cys Thr Arg Ser Gly Asn Glu Asp
85 90 95

Glu Phe Arg Asn Met Val Thr Arg Cys Asn Asn Val Gly Val Arg Ile
100 105 110

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Tyr Val Asp Ala Val Ile Asn His Met Cys Gly Asn Ala Val Ser Ala
 115 120 125

Gly Thr Ser Ser Thr Cys Gly Ser Tyr Phe Asn Pro Gly Ser Arg Asp
 130 135 140

Phe Pro Ala Val Pro Tyr Ser Gly Trp Asp Phe Asn Asp Gly Lys Cys
 145 150 155 160

Lys Thr Gly Ser Gly Asp Ile Glu Asn Tyr Asn Asp Ala Thr Gln Val
 165 170 175

Arg Asp Cys Arg Leu Thr Gly Leu Leu Asp Leu Ala Leu Glu Lys Asp
 180 185 190

Tyr Val Arg Ser Lys Ile Ala Glu Tyr Met Asn His Leu Ile Asp Ile
 195 200 205

Gly Val Ala Gly Phe Arg Leu Asp Ala Ser Lys His Met Trp Pro Gly
 210 215 220

Asp Ile Lys Ala Ile Leu Asp Lys Leu His Asn Leu Asn Ser Asn Trp
 225 230 235 240

Phe Pro Ala Gly Ser Lys Pro Phe Ile Tyr Gln Glu Val Ile Asp Leu
 245 250 255

Gly Gly Glu Pro Ile Lys Ser Ser Asp Tyr Phe Gly Asn Gly Arg Val
 260 265 270

Thr Glu Phe Lys Tyr Gly Ala Lys Leu Gly Thr Val Ile Arg Lys Trp
 275 280 285

Asn Gly Glu Lys Met Ser Tyr Leu Lys Asn Trp Gly Glu Gly Trp Gly
 290 295 300

Phe Val Pro Ser Asp Arg Ala Leu Val Phe Val Asp Asn His Asp Asn
 305 310 315 320

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Gln Arg Gly His Gly Ala Gly Gly Ala Ser Ile Leu Thr Phe Trp Asp
 325 330 335

Ala Arg Leu Tyr Lys Met Ala Val Gly Phe Met Leu Ala His Pro Tyr
 340 345 350

Gly Phe Thr Arg Val Met Ser Ser Tyr Arg Trp Pro Arg Gln Phe Gln
 355 360 365

Asn Gly Asn Asp Val Asn Asp Trp Val Gly Pro Pro Asn Asn Asn Gly
 370 375 380

Val Ile Lys Glu Val Thr Ile Asn Pro Asp Thr Thr Cys Gly Asn Asp
 385 390 395 400

Trp Val Cys Glu His Arg Trp Arg Gln Ile Arg Asn Met Val Ile Phe
 405 410 415

Arg Asn Val Val Asp Gly Gln Pro Phe Thr Asn Trp Tyr Asp Asn Gly
 420 425 430

Ser Asn Gln Val Ala Phe Gly Arg Gly Asn Arg Gly Phe Ile Val Phe
 435 440 445

Asn Asn Asp Asp Trp Ser Phe Ser Leu Thr Leu Gln Thr Gly Leu Pro
 450 455 460

Ala Gly Thr Tyr Cys Asp Val Ile Ser Gly Asp Lys Ile Asn Gly Asn
 465 470 475 480

Cys Thr Gly Ile Lys Ile Tyr Val Ser Asp Asp Gly Lys Ala His Phe
 485 490 495

Ser Ile Ser Asn Ser Ala Glu Asp Pro Phe Ile Ala Ile His Ala Glu
 500 505 510

Ser Lys Leu
 515

<210> 21
 <211> 555
 <212> PRT
 <213> Aspergillus niger

<220>
 <221> SIGNAL
 <222> (1)..(25)

<400> 21

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

Ala Ser Trp Leu Gly Ser Ser Leu Ala Ala Ser Thr Glu Gln Trp Lys
 20 25 30

Ser Arg Ser Ile Tyr Gln Thr Met Thr Asp Arg Phe Ala Arg Thr Asp
 35 40 45

Gly Ser Thr Thr Ser Pro Cys Asn Thr Thr Glu Gly Leu Tyr Cys Gly
 50 55 60

Gly Thr Trp Arg Gly Met Ile Asn His Leu Asp Tyr Ile Gln Gly Met
 65 70 75 80

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

Arg Val Glu Tyr Gly Glu Ala Tyr His Gly Tyr Trp Pro Val Asp Leu
 100 105 110

Tyr Ser Leu Asn Ser His Phe Gly Thr His Gln Asp Leu Leu Asp Leu
 115 120 125

Ser Asp Ala Leu His Ala Arg Asp Met Tyr Leu Met Met Asp Thr Val
 130 135 140

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

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Ile Asp Tyr Ser Thr Leu Thr Pro Phe Asn Ser Ser Ser Tyr Tyr His
 165 170 175

Pro Tyr Cys Lys Ile Thr Asp Trp Asn Asn Phe Thr Asn Ala Gln Leu
 180 185 190

Cys Gln Thr Gly Asp Asn Ile Val Ala Leu Pro Asp Leu Tyr Thr Glu
 195 200 205

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

Ser Thr Tyr Ser Ile Asp Gly Leu Arg Ile Asp Ala Ala Lys His Val
 225 230 235 240

Asn Pro Gly Phe Leu Lys Asn Phe Gly Asp Ala Leu Asp Ile Phe Met
 245 250 255

Thr Gly Glu Val Leu Gln Gln Glu Val Ser Thr Ile Cys Asp Tyr Gln
 260 265 270

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

Leu Lys Ala Phe Thr Leu Gly Asn Thr Ser Ala Leu Ala Thr Gln Val
 290 295 300

Gln Ser Met Lys Asn Ser Cys Asn Asp Val Thr Ala Leu Ser Ser Phe
 305 310 315 320

Ser Glu Asn His Asp Val Ala Arg Phe Ala Ser Met Thr His Asp Met
 325 330 335

Ala Leu Ala Lys Asn Ile Leu Thr Phe Thr Leu Leu Phe Asp Gly Val
 340 345 350

Pro Met Ile Tyr Gln Gly Gln Glu Gln His Leu Asp Gly Pro Gly Ser
 355 360 365

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Pro Glu Asn Arg Glu Ala Ile Trp Leu Ser Glu Tyr Asn Thr Asp Ala
 370 375 380

Glu Leu Tyr Lys Leu Ile Gly Lys Leu Asn Ala Ile Arg Lys His Ala
 385 390 395 400

Tyr Arg Leu Asp Asn His Tyr Pro Asp Val Glu Thr Tyr Pro Ile Phe
 405 410 415

Glu Gly Gly Ser Glu Leu Gly Phe Arg Lys Gly Ile Glu Gly Arg Gln
 420 425 430

Val Val Met Leu Leu Ser Thr Gln Gly Thr Asn Ser Ser Ala Tyr Asn
 435 440 445

Leu Ser Met Pro Val Ser Phe Thr Gly Gly Thr Val Val Thr Glu Ile
 450 455 460

Leu Asn Cys Val Asn Tyr Thr Val Asn Thr Gln Ser Glu Leu Val Val
 465 470 475 480

Pro Met Asp Lys Gly Glu Pro Arg Val Phe Phe Pro Ala Asp Leu Met
 485 490 495

Pro Gly Ser Gly Leu Cys Gly Leu Pro Val Ala Asn Val Thr Tyr Ala
 500 505 510

Ala Leu Arg Thr Gln Gly Ala Ala Ala Ala Glu Ala Ala Leu Ser Leu
 515 520 525

Gly Ile Lys Thr Asp Ala Ala Ser Ser Ala Leu Leu Ser Leu Gly Leu
 530 535 540

Ser Val Val Ala Gly Leu Ile Val Gly Met Trp
 545 550 555

<210> 22

<211> 567

<212> PRT

<213> Aspergillus niger

<220>

<221> SIGNAL

<222> (1)..(22)

<400> 22

Met Asp Asp Gly Trp Trp Ile Ile Ser Leu Leu Val Val Thr Leu Gly
 1 5 10 15

Ile Pro Thr Val Asn Ala Ala Ser Arg Asp Gln Trp Ile Gly Arg Ser
 20 25 30

Ile Tyr Gln Ile Val Thr Asp Arg Phe Ala Arg Ser Asp Asn Ser Thr
 35 40 45

Thr Ala Ala Cys Asp Ala Ala Leu Gly Asn Tyr Cys Gly Gly Ser Phe
 50 55 60

Gln Gly Ile Ile Asn Lys Leu Asp Tyr Ile Gln Glu Leu Gly Phe Asp
 65 70 75 80

Ala Ile Trp Ile Ser Pro Ala Gln Ser Gln Ile Ser Ala Arg Thr Ala
 85 90 95

Asp Leu Ser Ala Tyr His Gly Tyr Trp Pro Asn Asp Leu Tyr Ser Ile
 100 105 110

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

Leu His Asp Arg Gly Met Tyr Leu Met Leu Asp Ile Val Val Gly Asp
 130 135 140

Met Ala Trp Ala Gly Asn His Ser Thr Val Asp Tyr Ser Asn Phe Asn
 145 150 155 160

Pro Phe Asn Asp Gln Lys Phe Phe His Asp Phe Lys Leu Leu Ser Ser
 165 170 175

117549337_1

Asp Pro Thr Asn Glu Thr Cys Val Leu Asp Cys Trp Met Gly Asp Thr
 180 185 190

Val Val Ser Leu Pro Asp Leu Arg Asn Glu Asp Gln Gln Val Gln Asn
 195 200 205

Ile Leu Gly Thr Trp Ile Ser Gly Leu Val Ser Asn Tyr Ser Ile Asp
 210 215 220

Gly Leu Arg Ile Asp Ser Val Leu Asn Ile Ala Pro Asp Phe Phe Ser
 225 230 235 240

Asn Phe Thr Lys Ser Ser Gly Val Phe Thr Val Gly Glu Gly Ala Thr
 245 250 255

Ala Asp Ala Ala Asp Val Cys Pro Leu Gln Pro Ser Leu Asn Gly Leu
 260 265 270

Leu Asn Tyr Pro Leu Tyr Tyr Ile Leu Thr Asp Ala Phe Asn Thr Thr
 275 280 285

Asn Gly Asn Leu Ser Thr Ile Thr Glu Ser Ile Ser Tyr Thr Lys Gly
 290 295 300

Gln Cys Glu Asp Val Leu Ala Leu Gly Thr Phe Thr Ala Asn Gln Asp
 305 310 315 320

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

Ile Leu Thr Ser Ser Met Leu Thr Asp Gly Ile Pro Ile Leu Tyr Tyr
 340 345 350

Gly Glu Glu Gln His Leu Thr Gly Ser Tyr Asn Pro Val Asn Arg Glu
 355 360 365

Ala Leu Trp Leu Thr Asn Tyr Ser Met Arg Ser Thr Ser Leu Pro Thr
 370 375 380

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

Glu Gln Tyr Thr Gln Lys Ser Gln Ser Gly Ser Asp Tyr Leu Ser Tyr
405 410 415

Leu Ser Ala Pro Ile Tyr Asn Ser Thr His Ile Leu Ala Thr Arg Lys
420 425 430

Gly Phe Ala Gly Asn Gln Ile Val Ser Val Val Ser Asn Leu Gly Ala
435 440 445

Lys Pro Ala Ser Lys Ala Thr Thr Lys Ile Thr Leu Gly Ser Asp Glu
450 455 460

Thr Gly Phe Gln Ser Lys Gln Asn Val Thr Glu Ile Leu Ser Cys Lys
465 470 475 480

Thr Tyr Val Thr Asp Ser Ser Gly Asn Leu Ala Val Asp Leu Ser Ser
485 490 495

Asp Gly Gly Pro Arg Val Tyr Tyr Pro Thr Asp Ser Leu Lys Asp Ser
500 505 510

Thr Asp Ile Cys Gly Asp Gln Thr Lys Ser Ala Thr Pro Ser Ser Ser
515 520 525

Ala Ala Ser Ser Ala Ser Leu Thr Gln Ser Lys Gly Ser Glu Thr Cys
530 535 540

Leu Phe Gly Val Pro Leu Gly Ile Ser Thr Leu Val Val Thr Val Ala
545 550 555 560

Met Ala Thr Ser Tyr Val Phe
565

<210> 23
<211> 550
<212> PRT
<213> Aspergillus niger

<220>

<221> SIGNAL

<222> (1)..(29)

<400> 23

Met Met Phe Arg Lys Ser Ala Ser Leu Leu Gly Gln Arg Leu Met Ala
 1 5 10 15

Val Cys Leu Leu Cys Trp Cys Val Ser Leu Ala Thr Ala Ala Ser Thr
 20 25 30

Glu Glu Trp Lys Thr Arg Ser Ile Tyr Gln Thr Met Thr Asp Arg Phe
 35 40 45

Ala Leu Thr Asn Gly Ser Thr Thr Ala Pro Cys Asn Thr Thr Val Ala
 50 55 60

Asn Tyr Cys Gly Gly Ser Trp Gln Gly Thr Ile Asp Lys Leu Asp Tyr
 65 70 75 80

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

Asn Ile Ala Gly Arg Ser Lys Asp Gly Glu Ala Tyr His Gly Tyr Trp
 100 105 110

Pro Leu Asp Leu Tyr Glu Ile Asn Ser His Phe Gly Thr Arg Glu Glu
 115 120 125

Leu Leu Lys Leu Ser Glu Glu Ile His Ala Arg Gly Met Tyr Leu Leu
 130 135 140

Leu Asp Val Val Ile Asn Asn Met Ala Tyr Met Thr Asp Gly Glu Asp
 145 150 155 160

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

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Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asn Trp Asn Asn Tyr Thr
 180 185 190

Asp Ala Gln Trp Cys Gln Thr Gly Asp Asn Tyr Thr Ala Leu Pro Asp
 195 200 205

Leu Tyr Thr Glu His Thr Ala Val Gln Asn Ile Leu Met Asp Trp Ser
 210 215 220

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

Ala Lys Ser Leu Thr Pro Ser Phe Leu Pro Thr Tyr Ala Ser Thr Val
 245 250 255

Gly Gly Phe Met Thr Gly Glu Val Met Asp Ser Asn Ala Thr Asn Val
 260 265 270

Cys Lys Tyr Gln Thr Asp Tyr Leu Pro Ser Leu Pro Asn Tyr Pro Leu
 275 280 285

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

Leu Glu Glu Ile Ala Thr Ile Asn Asp Leu Cys Pro Asp Thr Phe Ala
 305 310 315 320

Met Val Asn Phe Ile Glu Asp Gln Asp Val Asp Arg Trp Ala Tyr Met
 325 330 335

Asn Asp Asp Ile Met Leu Ala Lys Thr Ala Leu Thr Phe Met Met Leu
 340 345 350

Tyr Asp Gly Ile Pro Leu Val Tyr Gln Gly Leu Glu Gln Ala Ile Ala
 355 360 365

Tyr Ser Asn Arg Ala Ala Leu Trp Leu Thr Asp Phe Asp Thr Asn Ala
 370 375 380

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Thr Leu Tyr Lys His Ile Lys Lys Leu Asn Ala Ile Arg Lys His Ala
385 390 395 400

Ile Asn Leu Asp Ser Ser Tyr Ile Ser Ser Lys Thr Tyr Pro Ile Tyr
405 410 415

Gln Gly Gly Ser Glu Leu Ala Phe Trp Lys Gly Asn Asn Gly Arg Gln
420 425 430

Val Ile Met Val Leu Ser Thr Ala Gly Ser Asn Gly Ser Ala Tyr Thr
435 440 445

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

Leu Asn Cys Val Asn Tyr Thr Val Asn Thr Tyr Ser Gln Leu Val Val
465 470 475 480

Asp Met Asp Lys Gly Glu Pro Arg Val Phe Phe Pro Ala Ser Met Met
485 490 495

Pro Gly Ser Gly Leu Cys Gly Tyr Asn Thr Ser Asn Val Thr Tyr Ser
500 505 510

Glu Leu Arg Leu Ala Ala Val Gly Ser Ser Ser Ser Ala Gly Ser His
515 520 525

Ser Val Ile Pro Ser Ala Phe Ala Ser Leu Phe Met Ala Ile Val Ala
530 535 540

Phe Leu Ala Phe Arg Ala
545 550

<210> 24
<211> 524
<212> PRT
<213> Aspergillus niger

<220>
<221> SIGNAL

<222> (1)..(16)

<400> 24

Met Thr Ile Phe Leu Phe Leu Ala Ile Phe Val Ala Thr Ala Leu Ala
 1 5 10 15

Ala Thr Pro Ala Glu Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
 20 25 30

Asp Arg Phe Ala Arg Thr Asp Asn Ser Thr Thr Ala Ser Cys Asp Leu
 35 40 45

Ser Ala Arg Gln Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn Gln
 50 55 60

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
 65 70 75 80

Val Thr Ala Gln Ile Pro Gln Asp Thr Gly Tyr Gly Gln Ala Tyr His
 85 90 95

Gly Tyr Trp Gln Gln Asp Ala Tyr Ala Leu Asn Ser His Tyr Gly Thr
 100 105 110

Ala Asp Asp Leu Lys Ala Leu Ala Ser Ala Leu His Ser Arg Gly Met
 115 120 125

Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly His Asn Gly Thr
 130 135 140

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

Tyr Phe His Asn Leu Cys Trp Ile Ser Asp Tyr Asn Asn Gln Thr Asn
 165 170 175

Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ala Leu Pro Asp Leu
 180 185 190

117549337_1

Asp Thr Thr Ser Thr Glu Val Lys Asn Met Trp Tyr Asp Trp Val Glu
 195 200 205

Ser Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Val Asp Thr Val
 210 215 220

Lys Asn Val Gln Lys Asn Phe Trp Pro Gly Tyr Asn Asn Ala Ser Gly
 225 230 235 240

Val Tyr Cys Ile Gly Glu Val Phe Asp Gly Asp Ala Ser Tyr Thr Cys
 245 250 255

Pro Tyr Gln Glu Asp Leu Asp Gly Val Leu Asn Tyr Pro Met Tyr Tyr
 260 265 270

Pro Leu Leu Arg Ala Phe Glu Ser Thr Asn Gly Ser Ile Ser Asp Leu
 275 280 285

Tyr Asn Met Ile Asn Thr Val Lys Ser Thr Cys Arg Asp Ser Thr Leu
 290 295 300

Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Asn Tyr
 305 310 315 320

Thr Ser Asp Met Ser Leu Ala Lys Asn Ala Ala Thr Phe Thr Ile Leu
 325 330 335

Ala Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ser
 340 345 350

Gly Gly Asn Asp Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
 355 360 365

Lys Thr Thr Ser Glu Leu Tyr Thr His Ile Ala Ala Ser Asn Lys Ile
 370 375 380

Arg Thr His Ala Ile Lys Gln Asp Thr Gly Tyr Leu Thr Tyr Lys Asn
 385 390 395 400

117549337_1

Tyr Pro Ile Tyr Gln Asp Thr Ser Thr Leu Ala Met Arg Lys Gly Tyr
405 410 415

Asn Gly Thr Gln Thr Ile Thr Val Leu Ser Asn Leu Gly Ala Ser Gly
420 425 430

Ser Ser Tyr Thr Leu Ser Leu Pro Gly Thr Gly Tyr Thr Ala Gly Gln
435 440 445

Lys Ile Thr Glu Ile Tyr Thr Cys Thr Asn Leu Thr Val Asn Ser Asn
450 455 460

Gly Ser Val Pro Val Pro Met Lys Ser Gly Leu Pro Arg Ile Leu Tyr
465 470 475 480

Pro Ala Asp Lys Leu Val Asn Gly Ser Ser Phe Cys Ser Ser Ala Ile
485 490 495

Thr Val Phe Lys Asp Ala Gly Gly Gly Val Leu Phe Phe Ser Tyr Thr
500 505 510

Val Ile Phe Ala Gln Val Leu Ile Ala Ile Met Thr
515 520

<210> 25
<211> 632
<212> PRT
<213> Aspergillus fischeri

<220>
<221> SIGNAL
<222> (1)..(23)

<400> 25

Met Lys Trp Ile Ser Pro Leu Leu Pro Leu Ser Leu Ser Leu Cys Leu
1 5 10 15

Leu Gly Gln Ala Ala His Ala Leu Thr Pro Ala Glu Trp Arg Ser Gln
20 25 30

117549337_1

Ser Ile Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Glu Asp Asn Ser
 35 40 45

Thr Thr Ala Ala Cys Asp Val Thr Gln Arg Leu Tyr Cys Gly Gly Ser
 50 55 60

Trp Gln Gly Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe
 65 70 75 80

Thr Ala Ile Trp Ile Thr Pro Val Thr Gln Gln Phe Tyr Glu Asn Thr
 85 90 95

Gly Asp Gly Thr Ser Tyr His Gly Tyr Trp Gln Gln Asn Ile Tyr Glu
 100 105 110

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

Ala Leu His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn
 130 135 140

His Met Gly Tyr Asp Gly Ala Gly Asn Ser Val Asp Tyr Ser Val Phe
 145 150 155 160

Thr Pro Phe Asp Ser Ser Thr Tyr Phe His Thr Tyr Cys Leu Ile Ser
 165 170 175

Asp Tyr Asn Asn Gln Asn Asn Val Glu Asp Cys Trp Leu Gly Asp Thr
 180 185 190

Thr Val Ser Leu Pro Asp Leu Asp Thr Thr Asn Thr Ala Val Arg Thr
 195 200 205

Ile Trp Tyr Asp Trp Val Lys Gly Leu Val Ala Asn Tyr Ser Ile Asp
 210 215 220

Gly Leu Arg Ile Asp Thr Val Lys His Val Glu Lys Asp Phe Trp Pro
 225 230 235 240

117549337_1

Asp Tyr Asn Asp Ala Ala Gly Val Tyr Cys Val Gly Glu Val Phe Ser
 245 250 255

Gly Asp Pro Ser Tyr Thr Cys Pro Tyr Gln Asn Tyr Met Asp Gly Val
 260 265 270

Leu Asn Tyr Pro Ile Tyr Tyr Gln Leu Leu Tyr Ala Phe Gln Ser Thr
 275 280 285

Ser Gly Ser Ile Ser Asn Leu Tyr Asn Met Ile Ser Ser Val Asp Ser
 290 295 300

Asp Cys Ala Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp
 305 310 315 320

Asn Pro Arg Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn
 325 330 335

Val Ile Ser Phe Met Phe Phe Ser Asp Gly Ile Pro Ile Val Tyr Ala
 340 345 350

Gly Gln Glu Gln His Tyr Ser Gly Gly Ala Asp Pro Ala Asn Arg Glu
 355 360 365

Ala Val Trp Leu Ser Gly Tyr Ser Thr Ser Ala Thr Leu Tyr Ser Trp
 370 375 380

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

Ala Tyr Ile Thr Ser Lys Asn Asn Pro Phe Tyr Tyr Asp Ser Asn Thr
 405 410 415

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

Leu Ser Asn Lys Gly Ser Ser Gly Ser Ser Tyr Thr Leu Ser Leu Ser
 435 440 445

117549337_1

Gly Thr Gly Tyr Ser Ala Gly Ala Thr Leu Val Glu Met Tyr Thr Cys
450 455 460

Thr Thr Leu Thr Val Asp Ser Ser Gly Asn Leu Ala Val Pro Met Ala
465 470 475 480

Ser Gly Leu Pro Arg Val Leu Val Pro Ser Ser Trp Val Ser Gly Ser
485 490 495

Gly Leu Cys Gly Asp Ser Ile Ser Thr Ile Ala Thr Thr Thr Thr Ser
500 505 510

Thr Thr Lys Thr Thr Thr Val Ala Thr Thr Thr Ala Cys Ala Ser Ala
515 520 525

Thr Ala Leu Pro Ile Leu Phe Glu Glu Leu Val Thr Thr Thr Tyr Gly
530 535 540

Glu Thr Ile Tyr Leu Thr Gly Ser Ile Ser Gln Leu Gly Asn Trp Asp
545 550 555 560

Thr Ser Ser Ala Ile Ala Leu Ser Ala Ser Lys Tyr Thr Ser Ser Asn
565 570 575

Pro Glu Trp Tyr Ala Thr Val Thr Leu Pro Val Gly Thr Ser Phe Gln
580 585 590

Tyr Lys Phe Phe Lys Lys Glu Ser Asp Gly Ser Ile Val Trp Glu Ser
595 600 605

Asp Pro Asn Arg Ser Tyr Thr Val Pro Ala Gly Cys Ala Gly Thr Thr
610 615 620

Val Thr Val Ser Asp Thr Trp Arg
625 630

<210> 26

<211> 640

<212> PRT

<213> Aspergillus luchuensis

<220>

<221> SIGNAL

<222> (1)..(21)

<400> 26

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

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

Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr
 35 40 45

Ala Thr Cys Asn Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln
 50 55 60

Gly Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala
 65 70 75 80

Ile Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ser Asp
 85 90 95

Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Tyr Val Asn
 100 105 110

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

His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met
 130 135 140

Gly Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro
 145 150 155 160

Phe Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp
 165 170 175

117549337_1

Asp Asn Leu Thr Met Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val
 180 185 190

Ser Leu Pro Asp Leu Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp
 195 200 205

Tyr Asp Trp Val Ala Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu
 210 215 220

Arg Ile Asp Ser Val Glu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr
 225 230 235 240

Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn
 245 250 255

Pro Ala Leu Asp Cys Pro Tyr Gln Lys Tyr Leu Asp Gly Val Leu Asn
 260 265 270

Tyr Pro Ile Tyr Trp Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly
 275 280 285

Ser Ile Ser Asn Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys
 290 295 300

Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro
 305 310 315 320

Arg Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu
 325 330 335

Ser Tyr Ile Phe Leu Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu
 340 345 350

Glu Gln His Tyr Ser Gly Gly Asp Val Pro Tyr Asn Arg Glu Ala Thr
 355 360 365

Trp Leu Ser Gly Tyr Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala
 370 375 380

117549337_1

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

Ile Thr Tyr Lys Asn Asp Pro Ile Tyr Thr Asp Ser Asn Thr Ile Ala
 405 410 415

Met Arg Lys Gly Thr Ser Gly Ser Gln Ile Ile Thr Val Leu Ser Asn
 420 425 430

Lys Gly Ser Ser Gly Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly
 435 440 445

Tyr Thr Ser Gly Thr Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val
 450 455 460

Thr Val Asp Ser Asn Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu
 465 470 475 480

Pro Arg Val Leu Leu Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys
 485 490 495

Gly Gly Ser Gly Asn Thr Thr Thr Thr Thr Thr Ala Ala Thr Ser Thr
 500 505 510

Ser Lys Ala Thr Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr
 515 520 525

Ser Ser Ser Cys Thr Ala Thr Ser Thr Thr Leu Pro Ile Thr Phe Glu
 530 535 540

Glu Leu Val Thr Thr Thr Tyr Gly Glu Glu Val Tyr Leu Ser Gly Ser
 545 550 555 560

Ile Ser Gln Leu Gly Glu Trp His Thr Ser Asp Ala Val Lys Leu Ser
 565 570 575

Ala Asp Asp Tyr Thr Ser Ser Asn Pro Glu Trp Ser Val Thr Val Ser
 580 585 590

117549337_1

Leu Pro Val Gly Thr Thr Phe Glu Tyr Lys Phe Ile Lys Val Asp Glu
595 600 605

Gly Gly Ser Val Thr Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
610 615 620

Pro Glu Cys Gly Ser Gly Ser Gly Glu Thr Val Val Asp Thr Trp Arg
625 630 635 640

<210> 27
<211> 576
<212> PRT
<213> Gloeophyllum trabeum

<220>
<221> SIGNAL
<222> (1)..(17)

<400> 27

Met Tyr Arg Phe Leu Val Cys Ala Leu Gly Leu Leu Gly Thr Val Leu
1 5 10 15

Ala Gln Ser Val Asp Ser Tyr Val Gly Ser Glu Gly Pro Ile Ala Lys
20 25 30

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

Ala Ala Ala Gly Val Val Val Ala Ser Pro Ser Lys Ser Asp Pro Asp
50 55 60

Tyr Trp Tyr Thr Trp Thr Arg Asp Ser Ser Leu Val Phe Lys Ser Leu
65 70 75 80

Ile Asp Gln Tyr Thr Thr Gly Ile Asp Ser Thr Ser Ser Leu Arg Ser
85 90 95

Leu Ile Asp Ser Phe Val Ile Ala Glu Ala Asn Ile Gln Gln Val Ser
100 105 110

117549337_1

Asn Pro Ser Gly Thr Leu Thr Thr Gly Gly Leu Gly Glu Pro Lys Phe
 115 120 125

Asn Val Asp Glu Thr Ala Phe Thr Gly Ala Trp Gly Arg Pro Gln Arg
 130 135 140

Asp Gly Pro Ala Leu Arg Ala Thr Ala Leu Ile Thr Tyr Gly Asn Trp
 145 150 155 160

Leu Leu Ser Asn Gly Asn Thr Thr Trp Val Thr Ser Thr Leu Trp Pro
 165 170 175

Ile Ile Gln Asn Asp Leu Asn Tyr Val Val Gln Tyr Trp Asn Gln Thr
 180 185 190

Thr Phe Asp Leu Trp Glu Glu Val Asn Ser Ser Ser Phe Phe Thr Thr
 195 200 205

Ala Val Gln His Arg Ala Leu Arg Glu Gly Ala Ala Phe Ala Thr Lys
 210 215 220

Ile Gly Gln Thr Ser Ser Val Ser Ser Tyr Thr Thr Gln Ala Ala Asn
 225 230 235 240

Leu Leu Cys Phe Leu Gln Ser Tyr Trp Asn Pro Thr Ser Gly Tyr Ile
 245 250 255

Thr Ala Asn Thr Gly Gly Gly Arg Ser Gly Lys Asp Ala Asn Thr Leu
 260 265 270

Leu Ala Ser Ile His Thr Tyr Asp Pro Ser Ala Gly Cys Asp Ala Thr
 275 280 285

Thr Phe Gln Pro Cys Ser Asp Lys Ala Leu Ser Asn Leu Lys Val Tyr
 290 295 300

Val Asp Ser Phe Arg Ser Val Tyr Ser Ile Asn Ser Gly Ile Ala Ser
 305 310 315 320

117549337_1

Asn Ala Ala Val Ala Thr Gly Arg Tyr Pro Glu Asp Ser Tyr Gln Gly
 325 330 335

Gly Asn Pro Trp Tyr Leu Thr Thr Phe Ala Val Ala Glu Gln Leu Tyr
 340 345 350

Asp Ala Leu Asn Val Trp Ala Ala Gln Gly Ser Leu Asn Val Thr Ser
 355 360 365

Ile Ser Leu Pro Phe Phe Gln Gln Phe Ser Ser Ser Val Thr Ala Gly
 370 375 380

Thr Tyr Ala Ser Ser Ser Thr Thr Tyr Thr Thr Leu Thr Ser Ala Ile
 385 390 395 400

Lys Ser Phe Ala Asp Gly Phe Val Ala Ile Asn Ala Gln Tyr Thr Pro
 405 410 415

Ser Asn Gly Gly Leu Ala Glu Gln Phe Ser Arg Ser Asn Gly Ser Pro
 420 425 430

Val Ser Ala Val Asp Leu Thr Trp Ser Tyr Ala Ser Ala Leu Thr Ala
 435 440 445

Phe Glu Ala Arg Asn Asn Thr Gln Phe Ala Gly Trp Gly Ala Val Gly
 450 455 460

Leu Thr Val Pro Thr Ser Cys Ser Ser Asn Ser Gly Gly Gly Gly Gly
 465 470 475 480

Ser Thr Val Ala Val Thr Phe Asn Val Asn Ala Gln Thr Val Trp Gly
 485 490 495

Glu Asn Ile Tyr Ile Thr Gly Ser Val Asp Ala Leu Ser Asn Trp Ser
 500 505 510

Pro Asp Asn Ala Leu Leu Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser
 515 520 525

117549337_1

Ile Thr Val Asn Leu Pro Ala Ser Thr Ala Ile Gln Tyr Lys Tyr Ile
 530 535 540

Arg Lys Asn Asn Gly Ala Val Thr Trp Glu Ser Asp Pro Asn Asn Ser
 545 550 555 560

Ile Thr Thr Pro Ala Ser Gly Ser Val Thr Glu Asn Asp Thr Trp Arg
 565 570 575

<210> 28
 <211> 632
 <212> PRT
 <213> Trichoderma reesii

<220>
 <221> SIGNAL
 <222> (1)..(20)

<400> 28

Met His Val Leu Ser Thr Ala Val Leu Leu Gly Ser Val Ala Val Gln
 1 5 10 15

Lys Val Leu Gly Arg Pro Gly Ser Ser Gly Leu Ser Asp Val Thr Lys
 20 25 30

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

Asn Leu Leu Cys Asn Val Gly Pro Asp Gly Cys Arg Ala Phe Gly Thr
 50 55 60

Ser Ala Gly Ala Val Ile Ala Ser Pro Ser Thr Ile Asp Pro Asp Tyr
 65 70 75 80

Tyr Tyr Met Trp Thr Arg Asp Ser Ala Leu Val Phe Lys Asn Leu Ile
 85 90 95

Asp Arg Phe Thr Glu Thr Tyr Asp Ala Gly Leu Gln Arg Arg Ile Glu
 100 105 110

117549337_1

Gln Tyr Ile Thr Ala Gln Val Thr Leu Gln Gly Leu Ser Asn Pro Ser
 115 120 125

Gly Ser Leu Ala Asp Gly Ser Gly Leu Gly Glu Pro Lys Phe Glu Leu
 130 135 140

Thr Leu Lys Pro Phe Thr Gly Asn Trp Gly Arg Pro Gln Arg Asp Gly
 145 150 155 160

Pro Ala Leu Arg Ala Ile Ala Leu Ile Gly Tyr Ser Lys Trp Leu Ile
 165 170 175

Asn Asn Asn Tyr Gln Ser Thr Val Ser Asn Val Ile Trp Pro Ile Val
 180 185 190

Arg Asn Asp Leu Asn Tyr Val Ala Gln Tyr Trp Asn Gln Thr Gly Phe
 195 200 205

Asp Leu Trp Glu Glu Val Asn Gly Ser Ser Phe Phe Thr Val Ala Asn
 210 215 220

Gln His Arg Ala Leu Val Glu Gly Ala Thr Leu Ala Ala Thr Leu Gly
 225 230 235 240

Gln Ser Gly Ser Ala Tyr Ser Ser Val Ala Pro Gln Val Leu Cys Phe
 245 250 255

Leu Gln Arg Phe Trp Val Ser Ser Gly Gly Tyr Val Asp Ser Asn Ile
 260 265 270

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

Ser Ile His Thr Phe Asp Pro Asn Leu Gly Cys Asp Ala Gly Thr Phe
 290 295 300

Gln Pro Cys Ser Asp Lys Ala Leu Ser Asn Leu Lys Val Val Val Asp
 305 310 315 320

117549337_1

Ser Phe Arg Ser Ile Tyr Gly Val Asn Lys Gly Ile Pro Ala Gly Ala
 325 330 335

Ala Val Ala Ile Gly Arg Tyr Ala Glu Asp Val Tyr Tyr Asn Gly Asn
 340 345 350

Pro Trp Tyr Leu Ala Thr Phe Ala Ala Ala Glu Gln Leu Tyr Asp Ala
 355 360 365

Ile Tyr Val Trp Lys Lys Thr Gly Ser Ile Thr Val Thr Ala Thr Ser
 370 375 380

Leu Ala Phe Phe Gln Glu Leu Val Pro Gly Val Thr Ala Gly Thr Tyr
 385 390 395 400

Ser Ser Ser Ser Ser Thr Phe Thr Asn Ile Ile Asn Ala Val Ser Thr
 405 410 415

Tyr Ala Asp Gly Phe Leu Ser Glu Ala Ala Lys Tyr Val Pro Ala Asp
 420 425 430

Gly Ser Leu Ala Glu Gln Phe Asp Arg Asn Ser Gly Thr Pro Leu Ser
 435 440 445

Ala Leu His Leu Thr Trp Ser Tyr Ala Ser Phe Leu Thr Ala Thr Ala
 450 455 460

Arg Arg Ala Gly Ile Val Pro Pro Ser Trp Ala Asn Ser Ser Ala Ser
 465 470 475 480

Thr Ile Pro Ser Thr Cys Ser Gly Ala Ser Val Val Gly Ser Tyr Ser
 485 490 495

Arg Pro Thr Ala Thr Ser Phe Pro Pro Ser Gln Thr Pro Lys Pro Gly
 500 505 510

Val Pro Ser Gly Thr Pro Tyr Thr Pro Leu Pro Cys Ala Thr Pro Thr
 515 520 525

117549337_1

Ser Val Ala Val Thr Phe His Glu Leu Val Ser Thr Gln Phe Gly Gln
 530 535 540

Thr Val Lys Val Ala Gly Asn Ala Ala Ala Leu Gly Asn Trp Ser Thr
 545 550 555 560

Ser Ala Ala Val Ala Leu Asp Ala Val Asn Tyr Ala Asp Asn His Pro
 565 570 575

Leu Trp Ile Gly Thr Val Asn Leu Glu Ala Gly Asp Val Val Glu Tyr
 580 585 590

Lys Tyr Ile Asn Val Gly Gln Asp Gly Ser Val Thr Trp Glu Ser Asp
 595 600 605

Pro Asn His Thr Tyr Thr Val Pro Ala Val Ala Cys Val Thr Gln Val
 610 615 620

Val Lys Glu Asp Thr Trp Gln Ser
 625 630

<210> 29
 <211> 574
 <212> PRT
 <213> Trametes cingulata

<220>
 <221> SIGNAL
 <222> (1)..(22)

<400> 29

Met Arg Phe Thr Leu Leu Thr Ser Leu Leu Gly Leu Ala Leu Gly Ala
 1 5 10 15

Phe Ala Gln Ser Ser Ala Ala Asp Ala Tyr Val Ala Ser Glu Ser Pro
 20 25 30

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

117549337_1

Ser Asn Gly Ala Lys Ala Gly Ile Val Ile Ala Ser Pro Ser Thr Ser
 50 55 60

Asn Pro Asn Tyr Leu Tyr Thr Trp Thr Arg Asp Ser Ser Leu Val Phe
 65 70 75 80

Lys Ala Leu Ile Asp Gln Phe Thr Thr Gly Glu Asp Thr Ser Leu Arg
 85 90 95

Thr Leu Ile Asp Glu Phe Thr Ser Ala Glu Ala Ile Leu Gln Gln Val
 100 105 110

Pro Asn Pro Ser Gly Thr Val Ser Thr Gly Gly Leu Gly Glu Pro Lys
 115 120 125

Phe Asn Ile Asp Glu Thr Ala Phe Thr Asp Ala Trp Gly Arg Pro Gln
 130 135 140

Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Ile Ile Thr Tyr Ala Asn
 145 150 155 160

Trp Leu Leu Asp Asn Lys Asn Thr Thr Tyr Val Thr Asn Thr Leu Trp
 165 170 175

Pro Ile Ile Lys Leu Asp Leu Asp Tyr Val Ala Ser Asn Trp Asn Gln
 180 185 190

Ser Thr Phe Asp Leu Trp Glu Glu Ile Asn Ser Ser Ser Phe Phe Thr
 195 200 205

Thr Ala Val Gln His Arg Ala Leu Arg Glu Gly Ala Thr Phe Ala Asn
 210 215 220

Arg Ile Gly Gln Thr Ser Val Val Ser Gly Tyr Thr Thr Gln Ala Asn
 225 230 235 240

Asn Leu Leu Cys Phe Leu Gln Ser Tyr Trp Asn Pro Thr Gly Gly Tyr
 245 250 255

117549337_1

Ile Thr Ala Asn Thr Gly Gly Gly Arg Ser Gly Lys Asp Ala Asn Thr
 260 265 270

Val Leu Thr Ser Ile His Thr Phe Asp Pro Ala Ala Gly Cys Asp Ala
 275 280 285

Val Thr Phe Gln Pro Cys Ser Asp Lys Ala Leu Ser Asn Leu Lys Val
 290 295 300

Tyr Val Asp Ala Phe Arg Ser Ile Tyr Ser Ile Asn Ser Gly Ile Ala
 305 310 315 320

Ser Asn Ala Ala Val Ala Thr Gly Arg Tyr Pro Glu Asp Ser Tyr Met
 325 330 335

Gly Gly Asn Pro Trp Tyr Leu Thr Thr Ser Ala Val Ala Glu Gln Leu
 340 345 350

Tyr Asp Ala Leu Ile Val Trp Asn Lys Leu Gly Ala Leu Asn Val Thr
 355 360 365

Ser Thr Ser Leu Pro Phe Phe Gln Gln Phe Ser Ser Gly Val Thr Val
 370 375 380

Gly Thr Tyr Ala Ser Ser Ser Ser Thr Phe Lys Thr Leu Thr Ser Ala
 385 390 395 400

Ile Lys Thr Phe Ala Asp Gly Phe Leu Ala Val Asn Ala Lys Tyr Thr
 405 410 415

Pro Ser Asn Gly Gly Leu Ala Glu Gln Tyr Ser Arg Ser Asn Gly Ser
 420 425 430

Pro Val Ser Ala Val Asp Leu Thr Trp Ser Tyr Ala Ala Ala Leu Thr
 435 440 445

Ser Phe Ala Ala Arg Ser Gly Lys Thr Tyr Ala Ser Trp Gly Ala Ala
 450 455 460

117549337_1

Gly Leu Thr Val Pro Thr Thr Cys Ser Gly Ser Gly Gly Ala Gly Thr
465 470 475 480

Val Ala Val Thr Phe Asn Val Gln Ala Thr Thr Val Phe Gly Glu Asn
485 490 495

Ile Tyr Ile Thr Gly Ser Val Pro Ala Leu Gln Asn Trp Ser Pro Asp
500 505 510

Asn Ala Leu Ile Leu Ser Ala Ala Asn Tyr Pro Thr Trp Ser Ser Thr
515 520 525

Val Asn Leu Pro Ala Ser Thr Thr Ile Glu Tyr Lys Tyr Ile Arg Lys
530 535 540

Phe Asn Gly Ala Val Thr Trp Glu Ser Asp Pro Asn Asn Ser Ile Thr
545 550 555 560

Thr Pro Ala Ser Gly Thr Phe Thr Gln Asn Asp Thr Trp Arg
565 570

<210> 30
<211> 579
<212> PRT
<213> Athelia rolfsil

<220>
<221> SIGNAL
<222> (1)..(18)

<400> 30

Met Phe Arg Ser Leu Leu Ala Leu Ala Ala Cys Ala Val Ala Ser Val
1 5 10 15

Ser Ala Gln Ser Ala Ser Ala Thr Ala Tyr Leu Thr Lys Glu Ser Ala
20 25 30

Val Ala Lys Asn Gly Val Leu Cys Asn Ile Gly Ser Gln Gly Cys Met
35 40 45

117549337_1

Ser Glu Gly Ala Tyr Ser Gly Ile Val Ile Ala Ser Pro Ser Lys Thr
 50 55 60

Ser Pro Asp Tyr Leu Tyr Thr Trp Thr Arg Asp Ser Ser Leu Val Phe
 65 70 75 80

Lys Met Leu Ile Asp Gln Tyr Thr Asn Gly Leu Asp Thr Thr Leu Arg
 85 90 95

Thr Leu Ile Asp Glu Phe Val Ser Ala Glu Ala Thr Ile Gln Gln Thr
 100 105 110

Ser Asn Ser Ser Gly Thr Val Ser Thr Gly Gly Leu Gly Glu Pro Lys
 115 120 125

Phe Asn Ile Asp Glu Thr Ala Phe Thr Gly Ala Trp Gly Arg Pro Gln
 130 135 140

Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Ile Met Thr Tyr Ala Thr
 145 150 155 160

Tyr Leu Tyr Asn Asn Gly Asn Thr Ser Tyr Val Thr Asn Thr Leu Trp
 165 170 175

Pro Ile Ile Lys Leu Asp Leu Asp Tyr Val Asn Ser Asp Trp Asn Gln
 180 185 190

Thr Thr Phe Asp Leu Trp Glu Glu Val Asp Ser Ser Ser Phe Phe Thr
 195 200 205

Thr Ala Val Gln His Arg Ala Leu Val Gln Gly Ala Ala Phe Ala Thr
 210 215 220

Leu Ile Gly Gln Thr Ser Ser Ala Ser Thr Tyr Ser Ala Thr Ala Pro
 225 230 235 240

Ser Ile Leu Cys Phe Leu Gln Ser Tyr Trp Asn Thr Asn Gly Tyr Trp
 245 250 255

117549337_1

Thr Ala Asn Thr Gly Gly Gly Arg Ser Gly Lys Asp Ala Asn Thr Ile
 260 265 270

Leu Ala Ser Ile His Thr Phe Asp Ala Ser Ala Gly Cys Ser Ala Ala
 275 280 285

Thr Ser Gln Pro Cys Ser Asp Val Ala Leu Ala Asn Leu Lys Val Tyr
 290 295 300

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

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

Gly Asn Pro Trp Tyr Leu Cys Thr Leu Ala Val Ala Glu Gln Leu Tyr
 340 345 350

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

Val Ser Leu Ala Phe Phe Gln Gln Phe Asp Ser Ser Ile Thr Ala Gly
 370 375 380

Thr Tyr Ala Ser Ser Ser Ser Val Tyr Thr Ser Leu Ile Ser Asp Ile
 385 390 395 400

Gln Ala Phe Ala Asp Glu Phe Val Asp Ile Val Ala Lys Tyr Thr Pro
 405 410 415

Ser Ser Gly Phe Leu Ser Glu Gln Tyr Asp Lys Ser Thr Gly Ala Gln
 420 425 430

Asp Ser Ala Ala Asn Leu Thr Trp Ser Tyr Ala Ala Ala Ile Thr Ala
 435 440 445

Tyr Gln Ala Arg Asn Gly Phe Thr Gly Ala Ser Trp Gly Ala Lys Gly
 450 455 460

117549337_1

Val Ser Thr Ser Cys Ser Thr Gly Ala Thr Ser Pro Gly Gly Ser Ser
465 470 475 480

Gly Ser Val Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly
485 490 495

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

Pro Ala Asn Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser
515 520 525

Ala Thr Ile Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val
530 535 540

Asn Ile Asp Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg
545 550 555 560

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

Asp Glu Ser

<210> 31
<211> 604
<212> PRT
<213> Rhizopus oryzae

<220>
<221> SIGNAL
<222> (1)..(25)

<400> 31

Met Gln Leu Phe Asn Leu Pro Leu Lys Val Ser Phe Phe Leu Val Leu
1 5 10 15

Ser Tyr Phe Ser Leu Leu Val Ser Ala Ala Ser Ile Pro Ser Ser Ala
20 25 30

117549337_1

Ser Val Gln Leu Asp Ser Tyr Asn Tyr Asp Gly Ser Thr Phe Ser Gly
 35 40 45

Lys Ile Tyr Val Lys Asn Ile Ala Tyr Ser Lys Lys Val Thr Val Ile
 50 55 60

Tyr Ala Asp Gly Ser Asp Asn Trp Asn Asn Asn Gly Asn Thr Ile Ala
 65 70 75 80

Ala Ser Tyr Ser Ala Pro Ile Ser Gly Ser Asn Tyr Glu Tyr Trp Thr
 85 90 95

Phe Ser Ala Ser Ile Asn Gly Ile Lys Glu Phe Tyr Ile Lys Tyr Glu
 100 105 110

Val Ser Gly Lys Thr Tyr Tyr Asp Asn Asn Asn Ser Ala Asn Tyr Gln
 115 120 125

Val Ser Thr Ser Lys Pro Thr Thr Thr Thr Ala Thr Ala Thr Thr Thr
 130 135 140

Thr Ala Pro Ser Thr Ser Thr Thr Thr Pro Pro Ser Arg Ser Glu Pro
 145 150 155 160

Ala Thr Phe Pro Thr Gly Asn Ser Thr Ile Ser Ser Trp Ile Lys Lys
 165 170 175

Gln Glu Gly Ile Ser Arg Phe Ala Met Leu Arg Asn Ile Asn Pro Pro
 180 185 190

Gly Ser Ala Thr Gly Phe Ile Ala Ala Ser Leu Ser Thr Ala Gly Pro
 195 200 205

Asp Tyr Tyr Tyr Ala Trp Thr Arg Asp Ala Ala Leu Thr Ser Asn Val
 210 215 220

Ile Val Tyr Glu Tyr Asn Thr Thr Leu Ser Gly Asn Lys Thr Ile Leu
 225 230 235 240

117549337_1

Asn Val Leu Lys Asp Tyr Val Thr Phe Ser Val Lys Thr Gln Ser Thr
 245 250 255

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

Ser Gly Tyr Thr Gly Ala Trp Gly Arg Pro Gln Asn Asp Gly Pro Ala
 275 280 285

Glu Arg Ala Thr Thr Phe Ile Leu Phe Ala Asp Ser Tyr Leu Thr Gln
 290 295 300

Thr Lys Asp Ala Ser Tyr Val Thr Gly Thr Leu Lys Pro Ala Ile Phe
 305 310 315 320

Lys Asp Leu Asp Tyr Val Val Asn Val Trp Ser Asn Gly Cys Phe Asp
 325 330 335

Leu Trp Glu Glu Val Asn Gly Val His Phe Tyr Thr Leu Met Val Met
 340 345 350

Arg Lys Gly Leu Leu Leu Gly Ala Asp Phe Ala Lys Arg Asn Gly Asp
 355 360 365

Ser Thr Arg Ala Ser Thr Tyr Ser Ser Thr Ala Ser Thr Ile Ala Asn
 370 375 380

Lys Ile Ser Ser Phe Trp Val Ser Ser Asn Asn Trp Ile Gln Val Ser
 385 390 395 400

Gln Ser Val Thr Gly Gly Val Ser Lys Lys Gly Leu Asp Val Ser Thr
 405 410 415

Leu Leu Ala Ala Asn Leu Gly Ser Val Asp Asp Gly Phe Phe Thr Pro
 420 425 430

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

117549337_1

Ala Ser Leu Tyr Pro Ile Asn Lys Asn Leu Pro Ser Tyr Leu Gly Asn
450 455 460

Ser Ile Gly Arg Tyr Pro Glu Asp Thr Tyr Asn Gly Asn Gly Asn Ser
465 470 475 480

Gln Gly Asn Ser Trp Phe Leu Ala Val Thr Gly Tyr Ala Glu Leu Tyr
485 490 495

Tyr Arg Ala Ile Lys Glu Trp Ile Gly Asn Gly Gly Val Thr Val Ser
500 505 510

Ser Ile Ser Leu Pro Phe Phe Lys Lys Phe Asp Ser Ser Ala Thr Ser
515 520 525

Gly Lys Lys Tyr Thr Val Gly Thr Ser Asp Phe Asn Asn Leu Ala Gln
530 535 540

Asn Ile Ala Leu Ala Ala Asp Arg Phe Leu Ser Thr Val Gln Leu His
545 550 555 560

Ala His Asn Asn Gly Ser Leu Ala Glu Glu Phe Asp Arg Thr Thr Gly
565 570 575

Leu Ser Thr Gly Ala Arg Asp Leu Thr Trp Ser His Ala Ser Leu Ile
580 585 590

Thr Ala Ser Tyr Ala Lys Ala Gly Ala Pro Ala Ala
595 600

<210> 32
<211> 612
<212> PRT
<213> Aspergillus oryzae

<220>
<221> SIGNAL
<222> (1)..(19)

<400> 32

117549337_1

Met Val Ser Phe Ser Ser Cys Leu Arg Ala Leu Ala Leu Gly Ser Ser
 1 5 10 15

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

Trp Leu Ser Thr Glu Ala Asn Phe Ser Arg Gln Ala Ile Leu Asn Asn
 35 40 45

Ile Gly Ala Asp Gly Gln Ser Ala Gln Gly Ala Ser Pro Gly Val Val
 50 55 60

Ile Ala Ser Pro Ser Lys Ser Asp Pro Asp Tyr Phe Tyr Thr Trp Thr
 65 70 75 80

Arg Asp Ser Gly Leu Val Met Lys Thr Leu Val Asp Leu Phe Arg Gly
 85 90 95

Gly Asp Ala Asp Leu Leu Pro Ile Ile Glu Glu Phe Ile Ser Ser Gln
 100 105 110

Ala Arg Ile Gln Gly Ile Ser Asn Pro Ser Gly Ala Leu Ser Ser Gly
 115 120 125

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

Ala Trp Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala
 145 150 155 160

Met Ile Ser Phe Gly Glu Trp Leu Val Glu Asn Ser His Thr Ser Ile
 165 170 175

Ala Thr Asp Leu Val Trp Pro Val Val Arg Asn Asp Leu Ser Tyr Val
 180 185 190

Ala Gln Tyr Trp Ser Gln Ser Gly Phe Asp Leu Trp Glu Glu Val Gln
 195 200 205

117549337_1

Gly Thr Ser Phe Phe Thr Val Ala Val Ser His Arg Ala Leu Val Glu
 210 215 220

Gly Ser Ser Phe Ala Lys Thr Val Gly Ser Ser Cys Pro Tyr Cys Asp
 225 230 235 240

Ser Gln Ala Pro Gln Val Arg Cys Tyr Leu Gln Ser Phe Trp Thr Gly
 245 250 255

Ser Tyr Ile Gln Ala Asn Phe Gly Gly Gly Arg Ser Gly Lys Asp Ile
 260 265 270

Asn Thr Val Leu Gly Ser Ile His Thr Phe Asp Pro Gln Ala Thr Cys
 275 280 285

Asp Asp Ala Thr Phe Gln Pro Cys Ser Ala Arg Ala Leu Ala Asn His
 290 295 300

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

Arg Ala Glu Asn Gln Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Ser
 325 330 335

Tyr Tyr Asn Gly Asn Pro Trp Phe Leu Thr Thr Leu Ala Ala Ala Glu
 340 345 350

Gln Leu Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Ile Gly Ser Leu Ala
 355 360 365

Ile Thr Asp Val Ser Leu Pro Phe Phe Lys Ala Leu Tyr Ser Ser Ala
 370 375 380

Ala Thr Gly Thr Tyr Ala Ser Ser Thr Thr Val Tyr Lys Asp Ile Val
 385 390 395 400

Ser Ala Val Lys Ala Tyr Ala Asp Gly Tyr Val Gln Ile Val Gln Thr
 405 410 415

117549337_1

Tyr Ala Ala Ser Thr Gly Ser Met Ala Glu Gln Tyr Thr Lys Thr Asp
 420 425 430

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

Leu Thr Ala Asn Asn Arg Arg Asn Ala Val Val Pro Ala Pro Trp Gly
 450 455 460

Glu Thr Ala Ala Thr Ser Ile Pro Ser Ala Cys Ser Thr Thr Ser Ala
 465 470 475 480

Ser Gly Thr Tyr Ser Ser Val Val Ile Thr Ser Trp Pro Thr Ile Ser
 485 490 495

Gly Tyr Pro Gly Ala Pro Asp Ser Pro Cys Gln Val Pro Thr Thr Val
 500 505 510

Ser Val Thr Phe Ala Val Lys Ala Thr Thr Val Tyr Gly Glu Ser Ile
 515 520 525

Lys Ile Val Gly Ser Ile Ser Gln Leu Gly Ser Trp Asn Pro Ser Ser
 530 535 540

Ala Thr Ala Leu Asn Ala Asp Ser Tyr Thr Thr Asp Asn Pro Leu Trp
 545 550 555 560

Thr Gly Thr Ile Asn Leu Pro Ala Gly Gln Ser Phe Glu Tyr Lys Phe
 565 570 575

Ile Arg Val Gln Asn Gly Ala Val Thr Trp Glu Ser Asp Pro Asn Arg
 580 585 590

Lys Tyr Thr Val Pro Ser Thr Cys Gly Val Lys Ser Ala Val Gln Ser
 595 600 605

Asp Val Trp Arg
 610

<210> 33
 <211> 630
 <212> PRT
 <213> Ophiostoma floccosum

<220>
 <221> SIGNAL
 <222> (1)..(18)

<400> 33

Met Lys Leu Ser Ser Leu Leu Pro Leu Ala Phe Leu Gly Gln Ala Val
 1 5 10 15

Asn Ala Leu Ser Pro Ala Glu Trp Arg Lys Gln Ser Ile Tyr Phe Leu
 20 25 30

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

Asn Thr Gly Asp Arg Ala Tyr Cys Gly Gly Ser Trp Gln Gly Val Ile
 50 55 60

Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile
 65 70 75 80

Thr Pro Val Thr Gly Gln Phe Tyr Glu Ser Thr Gly Asp Gly Thr Ser
 85 90 95

Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Ser His Leu
 100 105 110

Gly Asp Gln Asn Asp Leu Lys Ala Leu Ser Ala Ala Leu His Ala Arg
 115 120 125

Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp
 130 135 140

Gly Ala Gly Ser Asn Val Asp Tyr Ser Val Phe Asp Ala Phe Pro Ser
 145 150 155 160

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Ser Ser Tyr Phe His Ser Tyr Cys Glu Ile Ser Asn Tyr Asp Asp Gln
 165 170 175

Ser Asn Val Glu Asp Cys Trp Leu Gly Asp Thr Thr Val Ser Leu Pro
 180 185 190

Asp Leu Asn Thr Glu Leu Thr Ser Val Arg Ser Ile Trp Asn Ser Trp
 195 200 205

Val Ala Gly Leu Val Ala Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp
 210 215 220

Thr Val Lys His Val Glu Thr Ser Phe Trp Pro Gly Tyr Asn Asp Ala
 225 230 235 240

Ala Gly Val Tyr Cys Val Gly Glu Val Phe Asp Gly Asp Pro Ala Tyr
 245 250 255

Thr Cys Ala Tyr Gln Asn Tyr Met Asp Gly Val Leu Asn Tyr Pro Ile
 260 265 270

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

Asn Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ala Asp Pro
 290 295 300

Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala
 305 310 315 320

Ser Tyr Thr Ser Asp Tyr Ser Leu Ala Gln Asn Ala Ile Ser Phe Leu
 325 330 335

Phe Phe Ser Asp Gly Ile Pro Ile Val Tyr Ser Gly Gln Glu Gln His
 340 345 350

Tyr Ser Gly Gly Ala Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser
 355 360 365

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Gly Tyr Ser Thr Thr Ala Thr Leu Tyr Lys His Ile Lys Thr Thr Asn
 370 375 380

Gln Ile Arg Ser Leu Ile Ile Gly Lys Asp Ser Ser Trp Ala Thr Ser
 385 390 395 400

Ala Asn Ser Pro Phe Tyr Gln Asp Ser Asn Thr Ile Ala Met Leu Lys
 405 410 415

Gly Ser Ala Ser Gly Ser Lys Val Leu Thr Val Leu Ser Asn Lys Gly
 420 425 430

Ala Ser Gly Ser Ser Tyr Thr Leu Ser Leu Gly Ser Thr Gly Tyr Ser
 435 440 445

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

Asp Ser Ser Gly Asn Val Pro Val Pro Met Ala Ser Gly Leu Pro Arg
 465 470 475 480

Val Leu Val Pro Ser Ser Trp Val Ser Gly Ser Gly Leu Cys Gly Thr
 485 490 495

Ala Val Thr Thr Gly Thr Ala Thr Ala Thr Gly Thr Ser Thr Lys Ala
 500 505 510

Thr Thr Ala Thr Ala Thr Thr Ala Thr Ser Cys Thr Ala Ala Thr Ala
 515 520 525

Val Ser Val Val Phe Asn Glu Leu Ala Thr Thr Thr Tyr Gly Glu Asn
 530 535 540

Val Tyr Ile Ile Gly Ser Thr Ser Gln Leu Gly Ser Trp Ser Thr Ala
 545 550 555 560

Asn Ala Ile Ala Leu Ser Ser Ser Asp Tyr Thr Ser Ser Asn Pro Leu
 565 570 575

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Trp His Val Thr Val Ser Leu Pro Ala Gly Ser Ser Phe Thr Tyr Lys
 580 585 590

Phe Ile Lys Lys Glu Ser Asp Gly Thr Phe Val Trp Glu Ser Asp Pro
 595 600 605

Asn Arg Ser Tyr Thr Val Pro Thr Gly Cys Ser Gly Leu Ser Ala Thr
 610 615 620

Val Ser Ala Thr Trp Arg
 625 630

<210> 34
 <211> 620
 <212> PRT
 <213> Trichocladium griseum

<220>
 <221> SIGNAL
 <222> (1)..(19)

<400> 34

Met His Thr Phe Ser Lys Leu Leu Val Leu Gly Ser Ala Val Gln Ser
 1 5 10 15

Ala Leu Gly Arg Pro His Gly Ser Ser Arg Leu Gln Glu Arg Ala Ala
 20 25 30

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

Leu Ala Asn Ile Gly Pro Asn Gly Lys Ala Ala Pro Gly Ala Ala Ala
 50 55 60

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

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

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Leu Gly His Asn Tyr Asn Thr Thr Leu Gln Gln Val Ser Asn Pro Ser
 100 105 110

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

Asp Leu Thr Ala Phe Thr Gly Glu Trp Gly Arg Pro Gln Arg Asp Gly
 130 135 140

Pro Pro Leu Arg Ala Ile Ala Leu Ile Gln Tyr Ala Lys Trp Leu Ile
 145 150 155 160

Ala Asn Gly Tyr Lys Ser Thr Ala Lys Ser Val Val Trp Pro Val Val
 165 170 175

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

Asp Leu Trp Glu Glu Val Pro Gly Ser Ser Phe Phe Thr Ile Ala Ser
 195 200 205

Ser His Arg Ala Leu Thr Glu Gly Ala Tyr Leu Ala Ala Gln Leu Asp
 210 215 220

Thr Glu Cys Pro Pro Cys Thr Thr Val Ala Pro Gln Val Leu Cys Phe
 225 230 235 240

Gln Gln Ala Phe Trp Asn Ser Lys Gly Asn Tyr Val Val Ser Thr Ser
 245 250 255

Thr Ala Gly Glu Tyr Arg Ser Gly Lys Asp Ala Asn Ser Ile Leu Ala
 260 265 270

Ser Ile His Asn Phe Asp Pro Glu Ala Gly Cys Asp Asn Leu Thr Phe
 275 280 285

Gln Pro Cys Ser Glu Arg Ala Leu Ala Asn His Lys Ala Tyr Val Asp
 290 295 300

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Ser Phe Arg Asn Leu Tyr Ala Ile Asn Lys Gly Ile Ala Gln Gly Lys
 305 310 315 320

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

Pro Trp Tyr Leu Ala Asn Phe Ala Ala Ala Glu Gln Leu Tyr Asp Ala
 340 345 350

Ile Tyr Val Trp Asn Lys Gln Gly Ser Ile Thr Val Thr Ser Val Ser
 355 360 365

Leu Pro Phe Phe Arg Asp Leu Val Ser Ser Val Ser Thr Gly Thr Tyr
 370 375 380

Ser Lys Ser Ser Ser Thr Phe Thr Asn Ile Val Asn Ala Val Lys Ala
 385 390 395 400

Tyr Ala Asp Gly Phe Ile Glu Val Ala Ala Lys Tyr Thr Pro Ser Asn
 405 410 415

Gly Ala Leu Ala Glu Gln Tyr Asp Arg Asn Thr Gly Lys Pro Asp Ser
 420 425 430

Ala Ala Asp Leu Thr Trp Ser Tyr Ser Ala Phe Leu Ser Ala Ile Asp
 435 440 445

Arg Arg Ala Gly Leu Val Pro Pro Ser Trp Arg Ala Ser Val Ala Lys
 450 455 460

Ser Gln Leu Pro Ser Thr Cys Ser Arg Ile Glu Val Ala Gly Thr Tyr
 465 470 475 480

Val Ala Ala Thr Ser Thr Ser Phe Pro Ser Lys Gln Thr Pro Asn Pro
 485 490 495

Ser Ala Ala Pro Ser Pro Ser Pro Tyr Pro Thr Ala Cys Ala Asp Ala
 500 505 510

117549337_1

Ser Glu Val Tyr Val Thr Phe Asn Glu Arg Val Ser Thr Ala Trp Gly
515 520 525

Glu Thr Ile Lys Val Val Gly Asn Val Pro Ala Leu Gly Asn Trp Asp
530 535 540

Thr Ser Lys Ala Val Thr Leu Ser Ala Ser Gly Tyr Lys Ser Asn Asp
545 550 555 560

Pro Leu Trp Ser Ile Thr Val Pro Ile Lys Ala Thr Gly Ser Ala Val
565 570 575

Gln Tyr Lys Tyr Ile Lys Val Gly Thr Asn Gly Lys Ile Thr Trp Glu
580 585 590

Ser Asp Pro Asn Arg Ser Ile Thr Leu Gln Thr Ala Ser Ser Ala Gly
595 600 605

Lys Cys Ala Ala Gln Thr Val Asn Asp Ser Trp Arg
610 615 620

<210> 35
<211> 639
<212> PRT
<213> Aspergillus awamori

<220>
<221> SIGNAL
<222> (1)..(18)

<400> 35

Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Ser Gly
1 5 10 15

Leu Ala Ser Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
20 25 30

Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
35 40 45

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Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
 50 55 60

Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
 65 70 75 80

Gly Leu Val Ile Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
 85 90 95

Asp Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ser Gln Ala Ile Val
 100 105 110

Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Gly Leu Gly
 115 120 125

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

Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile Gly
 145 150 155 160

Phe Arg Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Ala Ala Thr Glu
 165 170 175

Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln Tyr
 180 185 190

Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser Ser
 195 200 205

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

Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln Ala
 225 230 235 240

Pro Gln Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Glu Tyr Ile
 245 250 255

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Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Thr Asn Thr Leu
 260 265 270

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

Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu Val
 290 295 300

Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser Asp
 305 310 315 320

Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Lys Asp Ser Tyr Tyr Asn
 325 330 335

Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu Tyr
 340 345 350

Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Ile Thr Asp
 355 360 365

Val Ser Leu Asp Phe Phe Gln Ala Leu Tyr Ser Asp Ala Ala Thr Gly
 370 375 380

Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala Val
 385 390 395 400

Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala Ala
 405 410 415

Ser Asn Gly Ser Leu Ser Glu Gln Tyr Asp Lys Ser Asp Gly Asp Glu
 420 425 430

Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr Ala
 435 440 445

Asn Asn Arg Arg Asn Ser Val Met Pro Pro Ser Trp Gly Glu Thr Ser
 450 455 460

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Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ser Gly Thr
465 470 475 480

Tyr Ser Ser Val Thr Val Thr Ser Ser Pro Ser Ile Val Ala Thr Gly
485 490 495

Gly Thr Thr Thr Thr Ala Thr Thr Thr Gly Phe Gly Gly Val Thr Ser
500 505 510

Thr Ser Lys Thr Thr Thr Thr Ala Ser Lys Thr Ser Thr Thr Thr Ser
515 520 525

Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu
530 535 540

Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile
545 550 555 560

Ser Gln Leu Gly Asp Trp Asp Thr Ser Asp Gly Ile Ala Leu Ser Ala
565 570 575

Asp Lys Tyr Thr Ser Ser Asn Pro Leu Trp Tyr Val Thr Val Thr Leu
580 585 590

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

Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro
610 615 620

Gln Ala Cys Gly Glu Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625 630 635

<210> 36
<211> 639
<212> PRT
<213> Aspergillus niger

<220>
<221> SIGNAL

<222> (1)..(18)

<400> 36

Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
 1 5 10 15

Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Trp Asp Ser Trp Leu Ser
 20 25 30

Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
 35 40 45

Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
 50 55 60

Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
 65 70 75 80

Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
 85 90 95

Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
 100 105 110

Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
 115 120 125

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

Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
 145 150 155 160

Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
 165 170 175

Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
 180 185 190

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Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Val Asn Gly Ser Ser
 195 200 205

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

Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln Ala
 225 230 235 240

Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe Ile
 245 250 255

Leu Ala Asn Phe Asp Ser Ser Arg Ser Ala Lys Asp Ala Asn Thr Leu
 260 265 270

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

Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
 290 295 300

Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
 305 310 315 320

Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
 325 330 335

Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
 340 345 350

Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
 355 360 365

Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Thr Gly
 370 375 380

Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala Val
 385 390 395 400

117549337_1

Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala Ala
 405 410 415

Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu Gln
 420 425 430

Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr Ala
 435 440 445

Asn Asn Arg Arg Asn Val Val Pro Ser Ala Ser Trp Gly Glu Thr Ser
 450 455 460

Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly Thr
 465 470 475 480

Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr Gly
 485 490 495

Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr Ser
 500 505 510

Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr Ser
 515 520 525

Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu
 530 535 540

Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile
 545 550 555 560

Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala
 565 570 575

Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu
 580 585 590

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

117549337_1

Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro
610 615 620

Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
625 630 635

<210> 37

<211> 515

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutated *Saccharomyces fibuligera* glucoamylase

<220>

<221> SIGNAL

<222> (1)..(26)

<400> 37

Met Ile Arg Leu Thr Val Phe Leu Thr Ala Val Phe Ala Ala Val Ala
1 5 10 15

Ser Cys Val Pro Val Glu Leu Asp Lys Arg Asn Thr Gly His Phe Gln
20 25 30

Ala Tyr Ser Gly Tyr Thr Val Asn Arg Ser Asn Phe Thr Gln Trp Ile
35 40 45

His Glu Gln Pro Ala Val Ser Trp Tyr Tyr Leu Leu Gln Asn Ile Asp
50 55 60

Tyr Pro Glu Gly Gln Phe Lys Ser Ala Lys Pro Gly Val Val Val Ala
65 70 75 80

Ser Pro Ser Thr Ser Glu Pro Asp Tyr Phe Tyr Gln Trp Thr Arg Asp
85 90 95

Thr Ala Ile Thr Phe Leu Ser Leu Ile Ala Glu Val Glu Asp His Ser
100 105 110

Phe Ser Asn Thr Thr Leu Ala Lys Val Val Glu Tyr Tyr Ile Ser Asn

115

120

125

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

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

Ala Tyr Thr Ala Ser Trp Gly Arg Pro Gln Asn Asp Gly Pro Ala Leu
 165 170 175

Arg Ala Tyr Ala Ile Ser Arg Tyr Leu Asn Ala Val Ala Lys His Asn
 180 185 190

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

Ala Ser Asp Ile Tyr Trp Lys Ile Ile Lys Pro Asp Leu Gln His Val
 210 215 220

Ser Thr His Trp Ser Thr Ser Gly Phe Asp Leu Trp Glu Glu Asn Gln
 225 230 235 240

Gly Thr His Phe Phe Thr Ala Leu Val Gln Leu Lys Ala Leu Ser Tyr
 245 250 255

Gly Ile Pro Leu Ser Lys Thr Tyr Asn Asp Pro Gly Phe Thr Ser Trp
 260 265 270

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

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

Ser Arg Gly Gly Leu Asp Ser Ala Thr Tyr Ile Ala Ala Leu Ile Thr
 305 310 315 320

His Asp Ile Gly Asp Asp Asp Thr Tyr Thr Pro Phe Asn Val Asp Asn

Ser Tyr Val Leu Asn Ser Leu Tyr Tyr Leu Leu Val Asp Asn Lys Asn
 340 345 350

Arg Tyr Lys Ile Asn Gly Asn Tyr Lys Ala Gly Ala Ala Val Gly Arg
 355 360 365

Tyr Pro Glu Asp Val Tyr Asn Gly Val Gly Thr Ser Glu Gly Asn Pro
 370 375 380

Trp Gln Leu Ala Thr Ala Tyr Ala Gly Gln Thr Phe Tyr Thr Leu Ala
 385 390 395 400

Tyr Asn Ser Leu Lys Asn Lys Lys Asn Leu Val Ile Glu Lys Leu Asn
 405 410 415

Tyr Asp Leu Tyr Asn Ser Phe Ile Ala Asp Leu Ser Lys Ile Asp Ser
 420 425 430

Ser Tyr Ala Ser Lys Asp Ser Leu Thr Leu Thr Tyr Gly Ser Asp Asn
 435 440 445

Tyr Lys Asn Val Ile Lys Ser Leu Leu Gln Phe Gly Asp Ser Phe Leu
 450 455 460

Lys Val Leu Leu Asp His Ile Asp Asp Asn Gly Gln Leu Thr Glu Glu
 465 470 475 480

Ile Asn Arg Tyr Thr Gly Phe Gln Ala Gly Ala Val Ser Leu Thr Trp
 485 490 495

Ser Ser Gly Ser Leu Leu Ser Ala Asn Arg Ala Arg Asn Lys Leu Ile
 500 505 510

Glu Leu Leu
 515