

2014DE614-WO-PCT - sequence listing_ST25.txt
SEQUENCE LISTING

<110> Clariant Produkte (Deutschland) GmbH

<120> Polypeptides having xylanase activity with a high conversion rate of xylose-containing polysaccharides

<130> 2014DE614-WO-PCT

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 1185

<212> DNA

<213> Fomes fomentarius

<400> 1

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ggttccacct gcacgggtcat caatgcatac tattcgcaat gtcttcctgt ctctagcact	180
tctaccacca ctggcggcac gacaactacc gcgacaacta cgcctagctc gaccgccggc	240
ttgcacacgc ttgccaaagc gaagggcaaa ctgtactttg gtagtgcgac agataacccg	300
gaactctccg actcgggtata cgttacgctc ctctccaaca acaaggagtt cggccagatc	360
actcccggca acagcatgaa atgggacgcg actgagccgt cgcgcggaac cttccaattc	420
gcgaacggcg acaccatcgc caaccttgcc aaaaacaacg ggcagctcct gcgcggacac	480
aactgcgtgt ggcacagcca actcccgagc tgggtttcga acggcaactg gaccgctgcg	540
gagttgactg agatcattca gaccactgc agcactgttg tcggccacta caaggggtcaa	600
atctattcgt gggatgtcat caacgagcca ttcaacgagg acggtacctg gcgtaccagc	660
gtcttttaca acacctcaa cactactttc gtctcggtcg cactcaaggc cgcacgctcc	720
gcagacccgg acgccaagct gtacatcaac gactacaaca ttgagagcac aggcgcgaag	780
tcgaccgca tgctgaatct agtcaagcag ctgcaggcgg atggcgtgcc catcgacggt	840
gtcggcttgc aggcacacct cattgttggc tctgtcccga cgtcgttgca gaccgtgctg	900
gagcagttca ccgcgctcgg cgtcgaggtc gcgatcacgg agctcgacgt caggatgacg	960
cttcccgcga ccgatgcgt cctcgcgcag caggccaaag attatcagag tgctgtgcag	1020
gcgtgtgcta atgtgtccaa gtgcgttggc atcacgatat gggactacac cgacaagtac	1080
tcttgggttc ccagcgtctt ccaaggacag ggtgctgctc tcccttggga cgagaacttc	1140
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<210> 2

<211> 394

<212> PRT

<213> Fomes fomentarius

<400> 2

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1 5 10 15
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 20 25 30
 Ser Gly Pro Thr Thr Cys Val Ser Gly Ser Thr Cys Thr Val Ile Asn
 35 40 45
 Ala Tyr Tyr Ser Gln Cys Leu Pro Val Ser Ser Thr Ser Thr Thr Thr
 50 55 60
 Gly Gly Thr Thr Thr Thr Ala Thr Thr Thr Pro Ser Ser Thr Ala Gly
 65 70 75 80
 Leu His Thr Leu Ala Lys Ala Lys Gly Lys Leu Tyr Phe Gly Ser Ala
 85 90
 Thr Asp Asn Pro Glu Leu Ser Asp Ser Val Tyr Val Thr Leu Leu Ser
 100 105 110
 Asn Asn Lys Glu Phe Gly Gln Ile Thr Pro Gly Asn Ser Met Lys Trp
 115 120 125
 Asp Ala Thr Glu Pro Ser Arg Gly Thr Phe Gln Phe Ala Asn Gly Asp
 130 135 140
 Thr Ile Ala Asn Leu Ala Lys Asn Asn Gly Gln Leu Leu Arg Gly His
 145 150 155 160
 Asn Cys Val Trp His Ser Gln Leu Pro Ser Trp Val Ser Asn Gly Asn
 165 170 175
 Trp Thr Ala Ala Glu Leu Thr Glu Ile Ile Gln Thr His Cys Ser Thr
 180 185 190
 Val Val Gly His Tyr Lys Gly Gln Ile Tyr Ser Trp Asp Val Ile Asn
 195 200 205
 Glu Pro Phe Asn Glu Asp Gly Thr Trp Arg Thr Ser Val Phe Tyr Asn
 210 215 220
 Thr Leu Asn Thr Thr Phe Val Ser Val Ala Leu Lys Ala Ala Arg Ser
 225 230 235 240
 Ala Asp Pro Asp Ala Lys Leu Tyr Ile Asn Asp Tyr Asn Ile Glu Ser
 245 250 255
 Thr Gly Ala Lys Ser Thr Ala Met Leu Asn Leu Val Lys Gln Leu Gln
 260 265 270
 Ala Asp Gly Val Pro Ile Asp Gly Val Gly Leu Gln Ala His Leu Ile

275

280

285

Val Gly Ser Val Pro Thr Ser Leu Gln Thr Val Leu Glu Gln Phe Thr
 290 295 300

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

Leu Pro Ala Thr Asp Ala Leu Leu Ala Gln Gln Ala Lys Asp Tyr Gln
 325 330 335

Ser Val Val Gln Ala Cys Ala Asn Val Ser Lys Cys Val Gly Ile Thr
 340 345 350

Ile Trp Asp Tyr Thr Asp Lys Tyr Ser Trp Val Pro Ser Val Phe Gln
 355 360 365

Gly Gln Gly Ala Ala Leu Pro Trp Asp Glu Asn Phe Asn Ile Lys Pro
 370 375 380

Ala Tyr Asn Gly Ile Val Ala Ala Leu Thr
 385 390

<210> 3
 <211> 1128
 <212> DNA
 <213> Fomes fomentarius

<400> 3
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 ggcttgaca cgcttgcaa agcgaagggc aaactgtact ttggtagtgc gacagataac 240
 ccggaactct ccgactcgtt atacgttacg ctctcttcca acaacaagga gttcggccag 300
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 ttgcggaacg gcgacacat cgccaacctt gccaaaaaca acgggcagct cctgcgcgga 420
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 caaatctatt cgtgggatgt catcaacgag ccattcaacg aggacggtac ctggcggtacc 600
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 tccgcagacc cggacgcaa gctgtacatc aacgactaca acattgagag cacaggcgcg 720
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caggcgtgtg ctaatgtgtc caagtgcgtt ggcatacaga tatgggacta caccgacaag 1020
tactcttggg ttcccagcgt cttccaagga cagggtgctg ctctcccttg ggacgagaac 1080
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<210> 4
<211> 375
<212> PRT
<213> Fomes fomentarius

<400> 4

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Thr Thr Cys Val Ser Gly Ser Thr Cys Thr Val Ile Asn Ala Tyr Tyr
20 25 30

Ser Gln Cys Leu Pro Val Ser Ser Thr Ser Thr Thr Thr Gly Gly Thr
35 40 45

Thr Thr Thr Ala Thr Thr Thr Pro Ser Ser Thr Ala Gly Leu His Thr
50 55 60

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

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

Glu Phe Gly Gln Ile Thr Pro Gly Asn Ser Met Lys Trp Asp Ala Thr
100 105 110

Glu Pro Ser Arg Gly Thr Phe Gln Phe Ala Asn Gly Asp Thr Ile Ala
115 120 125

Asn Leu Ala Lys Asn Asn Gly Gln Leu Leu Arg Gly His Asn Cys Val
130 135 140

Trp His Ser Gln Leu Pro Ser Trp Val Ser Asn Gly Asn Trp Thr Ala
145 150 155 160

Ala Glu Leu Thr Glu Ile Ile Gln Thr His Cys Ser Thr Val Val Gly
165 170 175

His Tyr Lys Gly Gln Ile Tyr Ser Trp Asp Val Ile Asn Glu Pro Phe
180 185 190

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

Thr Thr Phe Val Ser Val Ala Leu Lys Ala Ala Arg Ser Ala Asp Pro

210

215

220

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

Lys Ser Thr Ala Met Leu Asn Leu Val Lys Gln Leu Gln Ala Asp Gly
 245 250 255

Val Pro Ile Asp Gly Val Gly Leu Gln Ala His Leu Ile Val Gly Ser
 260 265 270

Val Pro Thr Ser Leu Gln Thr Val Leu Glu Gln Phe Thr Ala Leu Gly
 275 280 285

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

Thr Asp Ala Leu Leu Ala Gln Gln Ala Lys Asp Tyr Gln Ser Val Val
 305 310 315 320

Gln Ala Cys Ala Asn Val Ser Lys Cys Val Gly Ile Thr Ile Trp Asp
 325 330 335

Tyr Thr Asp Lys Tyr Ser Trp Val Pro Ser Val Phe Gln Gly Gln Gly
 340 345 350

Ala Ala Leu Pro Trp Asp Glu Asn Phe Asn Ile Lys Pro Ala Tyr Asn
 355 360 365

Gly Ile Val Ala Ala Leu Thr
 370 375

<210> 5

<211> 1206

<212> DNA

<213> Artificial sequence coding tFFxyn1 mature protein fusion with the Trichoderma reesei CBHI signal peptide and C-terminal 6x-His-TAG

<220>

<223> Artificial sequence coding tFFxyn1 mature protein fusion with the Trichoderma reesei CBHI signal peptide and C-terminal 6x-His-TAG

<400> 5

atgtatcggg agttggccgt catctcggcc ttcttgcca cagcacgggc tcaagcccag	60
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acctgcacgg tcatcaatgc atactattcg caatgtcttc ctgtctctag cacttctacc	180
accactggcg gcacgacaac taccgcgaca actacgccta gctcgaccgc cggcttgac	240
acgcttgcca aagcgaaggg caaactgtac tttggtagtg cgacagataa cccggaactc	300
tccgactcgg tatacgttac gtcctctcc aacaacaagg agttcgcca gatcactccc	360
ggcaacagca tgaaatggga cgcgactgag ccgtcgcgcg gaaccttcca attcgcaac	420

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ggcgacacca tcgccaacct tgccaaaaac aacgggcagc tcctgcgcgg acacaactgc	480
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ccggacgcca agctgtacat caacgactac aacattgaga gcacaggcgc gaagtcgacc	780
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gttcccagcg ttttccaagg acagggtgct gctctccctt gggacgagaa cttcaatatc	1140
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<210> 6

<211> 1431

<212> DNA

<213> Artificial sequence coding yFfxyn1 mature protein fusion with the Saccharomyces cerevisiae MFalpha signal peptide and C-terminal 6x-HIS-TAG

<220>

<223> Artificial sequence coding yFfxyn1 mature protein fusion with the Saccharomyces cerevisiae MFalpha signal peptide and C-terminal 6x-HIS-TAG

<400> 6

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tacttagatt tagaagggga tttcgatggt gctgttttgc ctttttccaa cagcacaagt	180
aacgggttat tgtttataaa tactactatt gccagcattg ctgctaaaga agaaggggta	240
tctttggata aacgtgaggc ggaagcacc tctcaagccc agacatgggg ccagtgcggg	300
ggtcaaggct ggtcaggacc cagcactgac gtgtcggggt ccacctgcac ggtcatcaat	360
gcatactatt cgcaatgtct tcctgtctct agcacttcta ccaccactgg cggcacgaca	420
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ggcaaactgt actttggtag tgcgacagat aaccgggaac tctccgactc ggtatacgtt	540
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gacgcgactg agccgtcgcg cggaaccttc caattcgcga acggcgacac catcgccaac	660
cttgccaaaa acaacgggca gctcctgcgc ggacacaact gcgtgtggca cagccaactc	720
ccgagctggg tttcgaacgg caactggacc gctgcggagt tgactgagat cattcagacc	780
cactgcagca ctgttgcggt ccactacaag ggtcaaattc attcgtggga tgtcatcaac	840

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gagccattca acgaggacgg tacctggcgt accagcgtct tctacaacac cctcaacact 900
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 ggacaggggtg ctgctctccc ttgggacgag aacttcaata tcaagcctgc gtacaacggc 1380
 atcgtcgcag ccctgacagg atctggccat caccaccatc atcactaata a 1431

<210> 7

<211> 384

<212> PRT

<213> tFfxyn1 mature protein fusion with the Trichoderma reesei CBHI signal peptide and C-terminal 6x-His-TAG

<400> 7

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 1 5 10 15

Thr Thr Cys Val Ser Gly Ser Thr Cys Thr Val Ile Asn Ala Tyr Tyr
 20 25 30

Ser Gln Cys Leu Pro Val Ser Ser Thr Ser Thr Thr Thr Gly Gly Thr
 35 40 45

Thr Thr Thr Ala Thr Thr Thr Pro Ser Ser Thr Ala Gly Leu His Thr
 50 55 60

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

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

Glu Phe Gly Gln Ile Thr Pro Gly Asn Ser Met Lys Trp Asp Ala Thr
 100 105 110

Glu Pro Ser Arg Gly Thr Phe Gln Phe Ala Asn Gly Asp Thr Ile Ala
 115 120 125

Asn Leu Ala Lys Asn Asn Gly Gln Leu Leu Arg Gly His Asn Cys Val
 130 135 140

Trp His Ser Gln Leu Pro Ser Trp Val Ser Asn Gly Asn Trp Thr Ala
 145 150 155 160

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Ala Glu Leu Thr Glu Ile Ile Gln Thr His Cys Ser Thr Val Val Gly
165 170 175

His Tyr Lys Gly Gln Ile Tyr Ser Trp Asp Val Ile Asn Glu Pro Phe
180 185 190

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

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

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

Lys Ser Thr Ala Met Leu Asn Leu Val Lys Gln Leu Gln Ala Asp Gly
245 250 255

Val Pro Ile Asp Gly Val Gly Leu Gln Ala His Leu Ile Val Gly Ser
260 265 270

Val Pro Thr Ser Leu Gln Thr Val Leu Glu Gln Phe Thr Ala Leu Gly
275 280 285

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

Thr Asp Ala Leu Leu Ala Gln Gln Ala Lys Asp Tyr Gln Ser Val Val
305 310 315 320

Gln Ala Cys Ala Asn Val Ser Lys Cys Val Gly Ile Thr Ile Trp Asp
325 330 335

Tyr Thr Asp Lys Tyr Ser Trp Val Pro Ser Val Phe Gln Gly Gln Gly
340 345 350

Ala Ala Leu Pro Trp Asp Glu Asn Phe Asn Ile Lys Pro Ala Tyr Asn
355 360 365

Gly Ile Val Ala Ala Leu Thr Gly Ser Gly His His His His His His
370 375 380

<210> 8
<211> 216
<212> PRT
<213> Thermomyces lanuginosus

<400> 8

Ser Phe Pro Ala Gly Asn Ala Thr Glu Leu Glu Lys Arg Gln Thr Thr
1 5 10 15

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Pro Asn Ser Glu Gly Trp His Asp Gly Tyr Tyr Tyr Ser Trp Trp Ser
20 25 30

Asp Gly Gly Ala Gln Ala Thr Tyr Thr Asn Leu Glu Gly Gly Thr Tyr
35 40 45

Glu Ile Ser Trp Gly Asp Gly Gly Asn Leu Val Gly Gly Lys Gly Trp
50 55 60

Asn Pro Gly Leu Asn Ala Arg Ala Ile His Phe Glu Gly Val Tyr Gln
65 70 75 80

Pro Asn Gly Asn Ser Tyr Leu Ala Val Tyr Gly Trp Thr Arg Asn Pro
85 90 95

Leu Val Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asp Pro Ser
100 105 110

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

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

Gln Thr Phe Asp Gln Tyr Trp Ser Val Arg Gln Asp Lys Arg Thr Ser
145 150 155 160

Gly Thr Val Gln Thr Gly Cys His Phe Asp Ala Trp Ala Arg Ala Gly
165 170 175

Leu Asn Val Asn Gly Asp His Tyr Tyr Gln Ile Val Ala Thr Glu Gly
180 185 190

Tyr Phe Ser Ser Gly Tyr Ala Arg Ile Thr Val Ala Asp Val Gly Gly
195 200 205

Ser Gly His His His His His His
210 215

<210> 9

<211> 215

<212> PRT

<213> Trichoderma reesei

<400> 9

Ser Cys Arg Pro Ala Ala Glu Val Glu Ser Val Ala Val Glu Lys Arg
1 5 10 15

Gln Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
20 25 30

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Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
35 40 45

Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
50 55 60

Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
65 70 75 80

Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
85 90 95

Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
100 105 110

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

Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
130 135 140

Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
145 150 155 160

Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
165 170 175

Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
180 185 190

Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser Gly Ser
195 200 205

Gly His His His His His His
210 215

<210> 10
<211> 219
<212> PRT
<213> Trichoderma reesei

<400> 10

Met Pro Thr Gly Leu Glu Pro Glu Ser Ser Val Asn Val Thr Glu Arg
1 5 10 15

Gly Met Tyr Asp Phe Val Leu Gly Ala His Asn Asp His Arg Arg Arg
20 25 30

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

Tyr Ser Pro Ser Asn Thr Gly Phe Ser Val Asn Trp Asn Thr Gln Asp
Page 10

50

55

60

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

Asn Phe Gly Gly Ser Phe Ser Val Asn Ser Gly Thr Gly Leu Leu Ser
85 90 95

Val Tyr Gly Trp Ser Thr Asn Pro Leu Val Glu Tyr Tyr Ile Met Glu
100 105 110

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

Ser Asp Gly Ala Thr Tyr Thr Ile Trp Glu Asn Thr Arg Val Asn Glu
130 135 140

Pro Ser Ile Gln Gly Thr Ala Thr Phe Asn Gln Tyr Ile Ser Val Arg
145 150 155 160

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

Ala Trp Ala Ser Leu Gly Leu His Leu Gly Gln Met Asn Tyr Gln Val
180 185 190

Val Ala Val Glu Gly Trp Gly Gly Ser Gly Ser Ala Ser Gln Ser Val
195 200 205

Ser Asn Gly Ser Gly His His His His His His
210 215

<210> 11

<211> 465

<212> PRT

<213> Trichoderma reesei

<400> 11

Trp Ser Tyr Ala Thr Lys Ser Gln Tyr Arg Ala Asn Ile Lys Ile Asn
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Ala Arg Gln Thr Tyr Gln Thr Met Ile Gly Gly Gly Cys Ser Gly Ala
20 25 30

Phe Gly Ile Ala Cys Gln Gln Phe Gly Ser Ser Gly Leu Ser Pro Glu
35 40 45

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

Leu Ser Ile Val Arg Asn Asp Ile Gly Ser Ser Pro Gly Thr Thr Ile
65 70 75 80

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Leu Pro Thr Cys Pro Ala Thr Pro Gln Asp Lys Phe Asp Tyr Val Trp
 85 90 95
 Asp Gly Ser Asp Asn Cys Gln Phe Asn Leu Thr Lys Thr Ala Leu Lys
 100 105 110
 Tyr Asn Pro Asn Leu Tyr Val Tyr Ala Asp Ala Trp Ser Ala Pro Gly
 115 120 125
 Cys Met Lys Thr Val Gly Thr Glu Asn Leu Gly Gly Gln Ile Cys Gly
 130 135 140
 Val Arg Gly Thr Asp Cys Lys His Asp Trp Arg Gln Ala Tyr Ala Asp
 145 150 155 160
 Tyr Leu Val Gln Tyr Val Arg Phe Tyr Lys Glu Glu Gly Ile Asp Ile
 165 170 175
 Ser Leu Leu Gly Ala Trp Asn Glu Pro Asp Phe Asn Pro Phe Thr Tyr
 180 185 190
 Glu Ser Met Leu Ser Asp Gly Tyr Gln Ala Lys Asp Phe Leu Glu Val
 195 200 205
 Leu Tyr Pro Thr Leu Lys Lys Ala Phe Pro Lys Val Asp Val Ser Cys
 210 215 220
 Cys Asp Ala Thr Gly Ala Arg Gln Glu Arg Asn Ile Leu Tyr Glu Leu
 225 230 235 240
 Gln Gln Ala Gly Gly Glu Arg Tyr Phe Asp Ile Ala Thr Trp His Asn
 245 250 255
 Tyr Gln Ser Asn Pro Glu Arg Pro Phe Asn Ala Gly Gly Lys Pro Asn
 260 265 270
 Ile Gln Thr Glu Trp Ala Asp Gly Thr Gly Pro Trp Asn Ser Thr Trp
 275 280 285
 Asp Tyr Ser Gly Gln Leu Ala Glu Gly Leu Gln Trp Ala Leu Tyr Met
 290 295 300
 His Asn Ala Phe Val Asn Ser Asp Thr Ser Gly Tyr Thr His Trp Trp
 305 310 315 320
 Cys Ala Gln Asn Thr Asn Gly Asp Asn Ala Leu Ile Arg Leu Asp Arg
 325 330 335
 Asp Ser Tyr Glu Val Ser Ala Arg Leu Trp Ala Phe Ala Gln Tyr Phe
 340 345 350

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

Glu Asn Val Tyr Val Thr Ala Tyr Val Asn Lys Asn Gly Thr Val Ala
370 375 380

Ile Pro Val Ile Asn Ala Ala His Phe Pro Tyr Asp Leu Thr Ile Asp
385 390 395 400

Leu Glu Gly Ile Lys Lys Arg Lys Leu Ser Glu Tyr Leu Thr Asp Asn
405 410 415

Ser His Asn Val Thr Leu Gln Ser Arg Tyr Lys Val Ser Gly Ser Ser
420 425 430

Leu Lys Val Thr Val Glu Pro Arg Ala Met Lys Thr Phe Trp Leu Glu
435 440 445

Pro Gln Ser Thr Phe Ala Val Ile Gly Ser Gly His His His His His
450 455 460

His
465

<210> 12
<211> 777
<212> PRT
<213> Trichoderma reesei

<400> 12

Gln Asn Asn Gln Thr Tyr Ala Asn Tyr Ser Ala Gln Gly Gln Pro Asp
1 5 10 15

Leu Tyr Pro Glu Thr Leu Ala Thr Leu Thr Leu Ser Phe Pro Asp Cys
20 25 30

Glu His Gly Pro Leu Lys Asn Asn Leu Val Cys Asp Ser Ser Ala Gly
35 40 45

Tyr Val Glu Arg Ala Gln Ala Leu Ile Ser Leu Phe Thr Leu Glu Glu
50 55 60

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

Leu Pro Asn Tyr Gln Val Trp Asn Glu Ala Leu His Gly Leu Asp Arg
85 90 95

Ala Asn Phe Ala Thr Lys Gly Gly Gln Phe Glu Trp Ala Thr Ser Phe
100 105 110

2014DE614-WO-PCT - sequence listing_ST25.txt

Pro Met Pro Ile Leu Thr Thr Ala Ala Leu Asn Arg Thr Leu Ile His
115 120 125

Gln Ile Ala Asp Ile Ile Ser Thr Gln Ala Arg Ala Phe Ser Asn Ser
130 135 140

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

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

Phe Leu Ser Ser Ala Tyr Thr Tyr Glu Tyr Ile Thr Gly Ile Gln Gly
180 185 190

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

Ala Gly Tyr Asp Leu Glu Asn Trp Asn Asn Gln Ser Arg Leu Gly Phe
210 215 220

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

Phe Leu Ala Ala Ala Arg Tyr Ala Lys Ser Arg Ser Leu Met Cys Ala
245 250 255

Tyr Asn Ser Val Asn Gly Val Pro Ser Cys Ala Asn Ser Phe Phe Leu
260 265 270

Gln Thr Leu Leu Arg Glu Ser Trp Gly Phe Pro Glu Trp Gly Tyr Val
275 280 285

Ser Ser Asp Cys Asp Ala Val Tyr Asn Val Phe Asn Pro His Asp Tyr
290 295 300

Ala Ser Asn Gln Ser Ser Ala Ala Ala Ser Ser Leu Arg Ala Gly Thr
305 310 315 320

Asp Ile Asp Cys Gly Gln Thr Tyr Pro Trp His Leu Asn Glu Ser Phe
325 330 335

Val Ala Gly Glu Val Ser Arg Gly Glu Ile Glu Arg Ser Val Thr Arg
340 345 350

Leu Tyr Ala Asn Leu Val Arg Leu Gly Tyr Phe Asp Lys Lys Asn Gln
355 360 365

Tyr Arg Ser Leu Gly Trp Lys Asp Val Val Lys Thr Asp Ala Trp Asn
370 375 380

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

Gly Thr Leu Pro Leu Ser Lys Lys Val Arg Ser Ile Ala Leu Ile Gly
405 410 415

Pro Trp Ala Asn Ala Thr Thr Gln Met Gln Gly Asn Tyr Tyr Gly Pro
420 425 430

Ala Pro Tyr Leu Ile Ser Pro Leu Glu Ala Ala Lys Lys Ala Gly Tyr
435 440 445

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

Gly Phe Ala Lys Ala Ile Ala Ala Ala Lys Lys Ser Asp Ala Ile Ile
465 470 475 480

Tyr Leu Gly Gly Ile Asp Asn Thr Ile Glu Gln Glu Gly Ala Asp Arg
485 490 495

Thr Asp Ile Ala Trp Pro Gly Asn Gln Leu Asp Leu Ile Lys Gln Leu
500 505 510

Ser Glu Val Gly Lys Pro Leu Val Val Leu Gln Met Gly Gly Gly Gln
515 520 525

Val Asp Ser Ser Ser Leu Lys Ser Asn Lys Lys Val Asn Ser Leu Val
530 535 540

Trp Gly Gly Tyr Pro Gly Gln Ser Gly Gly Val Ala Leu Phe Asp Ile
545 550 555 560

Leu Ser Gly Lys Arg Ala Pro Ala Gly Arg Leu Val Thr Thr Gln Tyr
565 570 575

Pro Ala Glu Tyr Val His Gln Phe Pro Gln Asn Asp Met Asn Leu Arg
580 585 590

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

Lys Pro Val Tyr Glu Phe Gly Ser Gly Leu Phe Tyr Thr Thr Phe Lys
610 615 620

Glu Thr Leu Ala Ser His Pro Lys Ser Leu Lys Phe Asn Thr Ser Ser
625 630 635 640

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

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Val Phe Thr Phe Glu Ala Asn Ile Lys Asn Ser Gly Lys Thr Glu Ser
660 665 670

Pro Tyr Thr Ala Met Leu Phe Val Arg Thr Ser Asn Ala Gly Pro Ala
675 680 685

Pro Tyr Pro Asn Lys Trp Leu Val Gly Phe Asp Arg Leu Ala Asp Ile
690 695 700

Lys Pro Gly His Ser Ser Lys Leu Ser Ile Pro Ile Pro Val Ser Ala
705 710 715 720

Leu Ala Arg Val Asp Ser His Gly Asn Arg Ile Val Tyr Pro Gly Lys
725 730 735

Tyr Glu Leu Ala Leu Asn Thr Asp Glu Ser Val Lys Leu Glu Phe Glu
740 745 750

Leu Val Gly Glu Glu Val Thr Ile Glu Asn Trp Pro Leu Glu Glu Gln
755 760 765

Gln Ile Lys Asp Ala Thr Pro Asp Ala
770 775

<210> 13
<211> 849
<212> PRT
<213> Talaromyces emersonii
<400> 13

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

Asn Gly Gln Gly Asp Trp Ala Glu Ala Tyr Glu Lys Ala Val Lys Phe
20 25 30

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

Gly Trp Glu Gln Asp Arg Cys Val Gly Gln Val Gly Ser Ile Pro Arg
50 55 60

Leu Gly Phe Pro Gly Leu Cys Met Gln Asp Ser Pro Leu Gly Val Arg
65 70 75 80

Asp Thr Asp Tyr Asn Ser Ala Phe Pro Ala Gly Val Asn Val Ala Ala
85 90 95

Thr Trp Asn Arg Asp Leu Ala Tyr Arg Arg Gly Gln Ala Met Gly Glu
100 105 110

2014DE614-WO-PCT - sequence listing_ST25.txt

Glu His Arg Gly Lys Gly Val Asp Val Gln Leu Gly Pro Val Ala Gly
115 120 125

Pro Leu Gly Arg Ser Pro Asp Ala Gly Arg Asn Trp Glu Gly Phe Ala
130 135 140

Pro Asp Pro Val Leu Thr Gly Asn Met Met Ala Ser Thr Ile Gln Gly
145 150 155 160

Ile Gln Asp Ala Gly Val Ile Ala Cys Ala Lys His Phe Ile Leu Tyr
165 170 175

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

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

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

Cys Ser Tyr Asn Gln Val Asn Asn Ser Tyr Ala Cys Ser Asn Ser Tyr
225 230 235 240

Thr Met Asn Lys Leu Leu Lys Ser Glu Leu Gly Phe Gln Gly Phe Val
245 250 255

Met Thr Asp Trp Gly Gly His His Ser Gly Val Gly Ser Ala Leu Ala
260 265 270

Gly Leu Asp Met Ser Met Pro Gly Asp Ile Ala Phe Asp Ser Gly Thr
275 280 285

Ser Phe Trp Gly Thr Asn Leu Thr Val Ala Val Leu Asn Gly Ser Val
290 295 300

Pro Glu Trp Arg Val Asp Asp Met Ala Val Arg Ile Met Ser Ala Tyr
305 310 315 320

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

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

Asn Thr Lys Ile Asn Glu His Val Asp Val Arg Gly Asn His Ala Glu
355 360 365

Ile Ile His Glu Ile Gly Ala Ala Ser Ala Val Leu Leu Lys Asn Lys
370 375 380

2014DE614-WO-PCT - sequence listing_ST25.txt

Gly Gly Leu Pro Leu Thr Gly Thr Glu Arg Phe Val Gly Val Phe Gly
385 390 395 400

Glu Asp Ala Gly Ser Asn Pro Trp Gly Val Asn Gly Cys Ser Asp Arg
405 410 415

Gly Cys Asp Asn Gly Thr Leu Ala Met Gly Trp Gly Ser Gly Thr Ala
420 425 430

Asn Phe Pro Tyr Leu Val Thr Pro Glu Gln Ala Ile Glu Arg Glu Val
435 440 445

Val Ser Arg Asn Gly Thr Phe Thr Ala Ile Thr Asp Asn Gly Ala Leu
450 455 460

Glu Gln Met Ala Ala Val Ala Ser Gln Ala Asp Val Cys Leu Val Phe
465 470 475 480

Ala Asn Ala Asp Ser Gly Glu Gly Tyr Ile Asn Val Asp Gly Asn Glu
485 490 495

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

His Asn Val Thr Ala Asn Cys Asn Asn Thr Val Val Val Leu His Thr
515 520 525

Val Gly Pro Val Leu Ile Asp Asp Trp Tyr Asp His Pro Asn Val Thr
530 535 540

Ala Ile Leu Trp Ala Gly Leu Pro Gly Gln Glu Ser Gly Asn Ser Leu
545 550 555 560

Val Asp Val Leu Tyr Gly Arg Val Asn Pro Gly Gly Lys Thr Pro Phe
565 570 575

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

Pro Asn Asn Gly Lys Gly Ala Pro Gln Gln Asp Phe Thr Glu Gly Ile
595 600 605

Phe Ile Asp Tyr Arg Arg Phe Asp Lys Tyr Asn Ile Thr Pro Ile Tyr
610 615 620

Glu Phe Gly Phe Gly Leu Ser Tyr Thr Thr Phe Glu Phe Ser Glu Leu
625 630 635 640

Asn Val Gln Pro Ile Asn Thr Pro Pro Tyr Thr Pro Ala Ser Gly Phe
645 650 655

2014DE614-WO-PCT - sequence listing_ST25.txt

Thr Lys Ala Ala Gln Ser Phe Gly Pro Ser Ser Asn Ala Ser Asp Asn
660 665 670

Leu Tyr Pro Ser Asp Ile Glu Arg Val Pro Leu Tyr Ile Tyr Pro Trp
675 680 685

Leu Asn Ser Thr Asp Leu Lys Ala Ser Ala Asn Asp Pro Asp Tyr Gly
690 695 700

Leu Pro Asn Asp Lys Tyr Val Pro Pro Asn Ala Thr Asn Gly Asn Pro
705 710 715 720

Gln Pro Ile Asn Pro Ala Gly Gly Ala Pro Gly Gly Asn Pro Ser Leu
725 730 735

Tyr Glu Pro Val Ala Arg Val Ser Ala Ile Ile Thr Asn Thr Gly Lys
740 745 750

Val Thr Gly Asp Glu Val Pro Gln Leu Tyr Val Ser Leu Gly Gly Pro
755 760 765

Asp Asp Ala Pro Lys Val Leu Arg Gly Phe Asp Arg Ile Thr Leu Ala
770 775 780

Pro Gly Gln Gln Thr Leu Trp Thr Thr Thr Leu Thr Arg Arg Asp Ile
785 790 795 800

Ser Asn Trp Asp Pro Val Thr Gln Asn Trp Val Val Thr Asn Tyr Thr
805 810 815

Lys Thr Val Tyr Val Gly Asn Ser Ser Arg Asn Leu Pro Leu Gln Ala
820 825 830

Pro Leu Lys Pro Tyr Pro Gly Ile Gly His Gly His His His His His
835 840 845

His

<210> 14
<211> 332
<212> PRT
<213> Trichoderma reesei

<400> 14

His Gly His Ile Asn Asp Ile Val Ile Asn Gly Val Trp Tyr Gln Ala
1 5 10 15

Tyr Asp Pro Thr Thr Phe Pro Tyr Glu Ser Asn Pro Pro Ile Val Val
20 25 30

Gly Trp Thr Ala Ala Asp Leu Asp Asn Gly Phe Val Ser Pro Asp Ala

35

40

45

Tyr Gln Asn Pro Asp Ile Ile Cys His Lys Asn Ala Thr Asn Ala Lys
 50 55 60

Gly His Ala Ser Val Lys Ala Gly Asp Thr Ile Leu Phe Gln Trp Val
 65 70 75 80

Pro Val Pro Trp Pro His Pro Gly Pro Ile Val Asp Tyr Leu Ala Asn
 85 90 95

Cys Asn Gly Asp Cys Glu Thr Val Asp Lys Thr Thr Leu Glu Phe Phe
 100 105 110

Lys Ile Asp Gly Val Gly Leu Leu Ser Gly Gly Asp Pro Gly Thr Trp
 115 120 125

Ala Ser Asp Val Leu Ile Ser Asn Asn Asn Thr Trp Val Val Lys Ile
 130 135 140

Pro Asp Asn Leu Ala Pro Gly Asn Tyr Val Leu Arg His Glu Ile Ile
 145 150 155 160

Ala Leu His Ser Ala Gly Gln Ala Asn Gly Ala Gln Asn Tyr Pro Gln
 165 170 175

Cys Phe Asn Ile Ala Val Ser Gly Ser Gly Ser Leu Gln Pro Ser Gly
 180 185 190

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

Asn Ile Tyr Thr Ser Pro Leu Asn Tyr Ile Ile Pro Gly Pro Thr Val
 210 215 220

Val Ser Gly Leu Pro Thr Ser Val Ala Gln Gly Ser Ser Ala Ala Thr
 225 230 235 240

Ala Thr Ala Ser Ala Thr Val Pro Gly Gly Gly Ser Gly Pro Thr Ser
 245 250 255

Arg Thr Thr Thr Thr Ala Arg Thr Thr Gln Ala Ser Ser Arg Pro Ser
 260 265 270

Ser Thr Pro Pro Ala Thr Thr Ser Ala Pro Ala Gly Gly Pro Thr Gln
 275 280 285

Thr Leu Tyr Gly Gln Cys Gly Gly Ser Gly Tyr Ser Gly Pro Thr Arg
 290 295 300

Cys Ala Pro Pro Ala Thr Cys Ser Thr Leu Asn Pro Tyr Tyr Ala Gln

305

Cys Leu Asn Ala Ser Ala His His His His His His
325 330