

SEQUENCE LISTING

<110> DSM IP Assets B.V.

<120> Optimization of C-5 sterol desaturation

<130> 32960-WO-PCT

<160> 22

<170> PatentIn version 3.5

<210> 1

<211> 1155

<212> DNA

<213> Pichia pastoris

<400> 1

```

atggacattg ctttgagat tctagacact ttgtctttg acaaagtcta tgcaaaacta    60
ctgcccattt ctctggtgca acatttgcca gatggctatt tgaagacttt gggacatttg    120
actggtgcca acaacaccat ggaatcactg ttcggaatag ctcaaacgt tgaccaagcg    180
tctaagaacc actggctgag aacagtgaat gactctattg ccttagcccg tcccggtagag    240
cgtctggtct acggtgtcaa cgctccttta cactttttg acgaaacagc gtatacatac    300
gcatcgatct tgggacgctc caatatcatt cgacaattca caactttgat gattctgatg    360
attcttttg gctgggggtt gtatttatct gtggcttcat ttcatacta cttgttttt    420
gataaagcca tttcaatca cccaagatac ctcaaaaacc agatgtctct ggagatccat    480
caagcgttga ctgctatacc tacgatggtt ttgcttacag ttcatggtt ttgattgag    540
ttgcgtggat actctaaatt atactttgat gtaaagagt ctactggagg atggaaggct    600
attatttggc aaatccttg cttcattatg ttaccgatt gttgtatcta cttattcat    660
cgttggttgc actggccatc cgtgtataag cgttgcaca agcctcacca caagtggatt    720
gtttgtacac ctttgctag tcatgccttc catccagttg atggttatgc acaatcacta    780
ccttaccatt tgtatggaat gttgtttcca ctacacaagg tgagctatct gatcttattt    840
gggcttgtga acttttgac tgttatgac catgatggag aatacctgtc cagagaccct    900
atagtcaatg gagctgcttg tcatacagtg catcacctat acttcaacta caattacggc    960

```

32960wo_ST25

cagttcaca cactttggga ccgctcttggg ggatcataca gaatgccaga caaggaactc 1020
 ttgataaga acaagaagaa agatgtaaag acatggcgtt cacaagtcaa gcaggccgat 1080
 tcgataagag aagacttaga gggaaaagaa gatttccgtg agtatggaac tgaggaaaaa 1140
 cttaaagca catag 1155

<210> 2
 <211> 384
 <212> PRT
 <213> Pichia pastoris

<400> 2

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

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

Tyr Leu Lys Thr Leu Gly His Leu Thr Gly Ala Asn Asn Thr Met Glu
 35 40 45

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

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

Arg Leu Val Tyr Gly Val Asn Ala Pro Leu His Phe Phe Asp Glu Thr
 85 90 95

Ala Tyr Thr Tyr Ala Ser Ile Leu Gly Arg Ser Asn Ile Ile Arg Gln
 100 105 110

Phe Thr Thr Leu Met Ile Leu Met Ile Leu Phe Gly Trp Gly Leu Tyr
 115 120 125

32960wo_ST25

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

Phe Asn His Pro Arg Tyr Leu Lys Asn Gln Met Ser Leu Glu Ile His
145 150 155 160

Gln Ala Leu Thr Ala Ile Pro Thr Met Val Leu Leu Thr Val Pro Trp
165 170 175

Phe Leu Ile Glu Leu Arg Gly Tyr Ser Lys Leu Tyr Phe Asp Val Asn
180 185 190

Glu Ser Thr Gly Gly Trp Lys Ala Ile Ile Trp Gln Ile Pro Cys Phe
195 200 205

Ile Met Phe Thr Asp Cys Cys Ile Tyr Phe Ile His Arg Trp Leu His
210 215 220

Trp Pro Ser Val Tyr Lys Arg Leu His Lys Pro His His Lys Trp Ile
225 230 235 240

Val Cys Thr Pro Phe Ala Ser His Ala Phe His Pro Val Asp Gly Tyr
245 250 255

Ala Gln Ser Leu Pro Tyr His Leu Tyr Gly Met Leu Phe Pro Leu His
260 265 270

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

Met Ile His Asp Gly Glu Tyr Leu Ser Arg Asp Pro Ile Val Asn Gly
290 295 300

Ala Ala Cys His Thr Val His His Leu Tyr Phe Asn Tyr Asn Tyr Gly
305 310 315 320

Gln Phe Thr Thr Leu Trp Asp Arg Leu Gly Gly Ser Tyr Arg Met Pro
Page 3

325

330

335

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

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

Lys Glu Asp Phe Arg Glu Tyr Gly Thr Glu Glu Lys Leu Lys Ser Thr
 370 375 380

<210> 3

<211> 939

<212> DNA

<213> *Penicillium roqueforti*

<400> 3

atggatattt tcttgacgt tctagatact ttggctctcg accggtgcta cgcagtactc 60

tcgccagacc caacagccat ctccaacaat gatactcaag ccaactgccca ttgaaccaa 120

catgtcgggg tatattacc tatgcagccc tcgaagtggg cggaggcaag cctctggaag 180

agagacgaca ttgccagaca agcattgtca ctgtacgtga ttatatggct ttgcgaatg 240

ataatgtacc tctcggtag ccttctcta tatcacacc tcttcgacaa aagactactc 300

caacacccgc gcttctcgc acaccaagtc aagctcgaga tcaaccaagg catctccgca 360

atcccagtca tggccctcct caccgtccca ttcttctag ctgagataag gggctggctg 420

aagctatatg atctcaccag cgactccccg ttctcggat acaccttgct ccagtatcca 480

ttgtcatct gcttcacaga tagtggcatt tactggatac accgtggtct gcatcatcct 540

agcgtctatc gctggcttca caagccacac cataaatggg cggtgccgac tccgttcgct 600

agtatgcgt ttcaccctct ggatggatgg gcgcagagtc tcccctacca tgttaccgg 660

ttgctcttc cgttcagaa gggagcatat ctgggactgt ttatgtttgt cactgtgtgg 720

acggtgctga ttcacgacgc tgagtacttg ccaacatcgg tggaatcaa cggcgcttct 780

tgtcacacga tgcatactt gtacttcaat tacaattacg ggcagtttac aacggcatgg 840

32960wo_ST25

gatcgctcgcg cgggaacata ccgaaagcct aaggggggata gtttcatgga aggtcagcaa 900

atggatggga aagggaaact cggaggtgaag tgtgaatag 939

<210> 4

<211> 312

<212> PRT

<213> *Penicillium roqueforti*

<400> 4

Met Asp Ile Phe Leu Asp Val Leu Asp Thr Leu Val Leu Asp Arg Cys

1 5 10 15

Tyr Ala Val Leu Ser Pro Asp Pro Thr Ala Ile Ser Asn Asn Asp Thr

20 25 30

Gln Ala Thr Ala His Leu Asn Gln His Val Gly Val Tyr Tyr Pro Met

35 40 45

Gln Pro Ser Lys Trp Ala Glu Ala Ser Leu Trp Lys Arg Asp Asp Ile

50 55 60

Ala Arg Gln Ala Leu Ser Leu Tyr Val Ile Ile Trp Leu Phe Ala Met

65 70 75 80

Ile Met Tyr Leu Leu Gly Ser Leu Leu Leu Tyr His Thr Leu Phe Asp

85 90 95

Lys Arg Leu Leu Gln His Pro Arg Phe Leu Ala His Gln Val Lys Leu

100 105 110

Glu Ile Asn Gln Gly Ile Ser Ala Ile Pro Val Met Ala Leu Leu Thr

115 120 125

Val Pro Phe Phe Leu Ala Glu Ile Arg Gly Trp Ser Lys Leu Tyr Asp

130 135 140

Leu Thr Ser Asp Ser Pro Phe Phe Gly Tyr Thr Leu Leu Gln Tyr Pro

32960wo_ST25

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

<210> 5
 <211> 903
 <212> DNA
 <213> Schizosaccharomyces pombe

<400> 5

32960wo_ST25

atggactacc tactcaacta tgctgaccaa tatgcgctgg attcgatata caatgctgta 60
tatccattag ctgcgacaa tatcgtaga cagtcgatca gttgtttt ttaactgg 120
ttggcggta tgttctgta ttaacattt gcgctgctt cctaccaatt tgtgttgat 180
aaaagtctga tggatcacc aaagttctta aaaaaccagg tttcatgga agttctaacg 240
gctttacaaa acttacctgg tatggcgta ttgacgggtc cgtggtttt ggctgagtg 300
catgggtaca gctactata cgacaacatc agtgattacg gttaaaata ctcttatgt 360
tcctacctc ttttgcac gttctcagat ttggcattt actgggctca tcgttcctt 420
catcaccgtt atgtataccc tcgtctcac aaactccatc ataagtgat tatctgact 480
ccatatgat cccatgctt caaatccgct gatggcttct tacaatctt tcctaccat 540
ctttcccct tttcttcc cctcacaag ttgacctact tggctcttt caccttgtc 600
aactctggt ccatcatgat tcacgatgg aaatacatc ccaacaacc catcatcaat 660
ggtgctgctc accataatgg ccatcacatt tatttcaact acaattacgg ccaattcacc 720
accctcttg atcgctcgg caactcttc cgggccccg atgaggcatg gttgacaaa 780
gatcttcgcc aaaacgagga tgttctcgt gtcgaattga tggagtacga ggctattcgt 840
aatgaagtg aaggtgatga tgatagagaa tacatcgcta actctgctaa gaagaacat 900
taa 903

<210> 6

<211> 300

<212> PRT

<213> Schizosaccharomyces pombe

<400> 6

Met Asp Tyr Leu Leu Asn Tyr Ala Asp Gln Tyr Ala Leu Asp Ser Ile
1 5 10 15

Tyr Asn Ala Val Tyr Pro Leu Ala Arg Asp Asn Ile Val Arg Gln Ser
20 25 30

Ile Ser Leu Phe Phe Leu Thr Trp Phe Gly Gly Met Phe Leu Tyr Leu

35

40

45

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

Asp His Pro Lys Phe Leu Lys Asn Gln Val Phe Met Glu Val Leu Thr
 65 70 75 80

Ala Leu Gln Asn Leu Pro Gly Met Ala Leu Leu Thr Val Pro Trp Phe
 85 90 95

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

Tyr Gly Leu Lys Tyr Phe Leu Cys Ser Leu Pro Leu Phe Val Met Phe
 115 120 125

Ser Asp Phe Gly Ile Tyr Trp Ala His Arg Phe Leu His His Arg Tyr
 130 135 140

Val Tyr Pro Arg Leu His Lys Leu His His Lys Trp Ile Ile Cys Thr
 145 150 155 160

Pro Tyr Ala Ser His Ala Phe Lys Ser Ala Asp Gly Phe Leu Gln Ser
 165 170 175

Leu Pro Tyr His Leu Phe Pro Phe Phe Phe Pro Leu His Lys Leu Thr
 180 185 190

Tyr Leu Ala Leu Phe Thr Phe Val Asn Phe Trp Ser Ile Met Ile His
 195 200 205

Asp Gly Lys Tyr Ile Ser Asn Asn Pro Ile Ile Asn Gly Ala Ala His
 210 215 220

His Asn Gly His His Ile Tyr Phe Asn Tyr Asn Tyr Gly Gln Phe Thr
 225 230 235 240

32960wo_ST25

Thr Leu Phe Asp Arg Leu Gly Asn Ser Phe Arg Ala Pro Asp Glu Ala
 245 250 255

Trp Phe Asp Lys Asp Leu Arg Gln Asn Glu Asp Val Leu Arg Val Glu
 260 265 270

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

Arg Glu Tyr Ile Ala Asn Ser Ala Lys Lys Asn His
 290 295 300

<210> 7

<211> 1098

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 7

atggattgg tctagaagt cgctgacat tatgtcttag acgacttga cgctaaagt 60
 ctgcccgtt cgttggcagc taatattcct gtcaagtggc agaaattgct aggggtgaac 120
 agtgggttca gcaattctac gattttgcag gagactttga actccaagaa tgccgtcaaa 180
 gaatgtagaa ggttctacgg gcaggtgcca ttctgtttg atatgtcgac gacgtctttt 240
 gcatcgctat tgctctgttc cagcatcttg agagaattcc tctactatg gggtattgtt 300
 acgatcttg gtttactact ttactattc acggctagtc tcagctacgt gtttgtgtt 360
 gacaagtcca tttcaacca tctcgttac ttgaaaaacc aaatggcaat ggaaatcaag 420
 ttggcagtca gtgctatccc atggatgtcg atgttgaccg ttccatggtt tggtatggaa 480
 ttgaacggcc attctaaact atacatgaag attgattatg aaaaccacgg tgtaaggaag 540
 ctcatatcg agtacttcac ttcatcttt ttactgatt gcggtgtgta ttagcgcac 600
 agatggttgc attggccaag ggtctaccgt gctctgcaca agcctcatca caagtggctg 660
 gtctgcacac ctttcgcatc tcattctttc catcctgtag acgggtttt gcaatccatc 720
 tcgtaccaca tctaccatt gattctgcca ttacacaagg ttcttattt gattctgttc 780

32960wo_ST25

acttttgta acttttggac tgttatgatt catgacggtc aatacctatc aaacaatcct 840
gccgtcaacg gtactgcctg ccacacgggt caccatctat attcaacta caactacggt 900
caattcacca ctctgtggga cagactaggg ggttcttacc gtagaccaga tgactcattg 960
tttgatccta agttaagaga tgctaaggag acctgggacg ctcaagtaa ggaagttgaa 1020
catttcatca aggaggtcga aggtgatgat aatgatagaa tctatgaaaa cgacccaaat 1080
accaagaaga acaactga 1098

<210> 8

<211> 365

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 8

Met Asp Leu Val Leu Glu Val Ala Asp His Tyr Val Leu Asp Asp Leu
1 5 10 15

Tyr Ala Lys Val Leu Pro Ala Ser Leu Ala Ala Asn Ile Pro Val Lys
20 25 30

Trp Gln Lys Leu Leu Gly Leu Asn Ser Gly Phe Ser Asn Ser Thr Ile
35 40 45

Leu Gln Glu Thr Leu Asn Ser Lys Asn Ala Val Lys Glu Cys Arg Arg
50 55 60

Phe Tyr Gly Gln Val Pro Phe Leu Phe Asp Met Ser Thr Thr Ser Phe
65 70 75 80

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

Trp Val Ile Val Thr Ile Phe Gly Leu Leu Leu Tyr Leu Phe Thr Ala
100 105 110

32960wo_ST25

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

Arg Tyr Leu Lys Asn Gln Met Ala Met Glu Ile Lys Leu Ala Val Ser
130 135 140

Ala Ile Pro Trp Met Ser Met Leu Thr Val Pro Trp Phe Val Met Glu
145 150 155 160

Leu Asn Gly His Ser Lys Leu Tyr Met Lys Ile Asp Tyr Glu Asn His
165 170 175

Gly Val Arg Lys Leu Ile Ile Glu Tyr Phe Thr Phe Ile Phe Phe Thr
180 185 190

Asp Cys Gly Val Tyr Leu Ala His Arg Trp Leu His Trp Pro Arg Val
195 200 205

Tyr Arg Ala Leu His Lys Pro His His Lys Trp Leu Val Cys Thr Pro
210 215 220

Phe Ala Ser His Ser Phe His Pro Val Asp Gly Phe Leu Gln Ser Ile
225 230 235 240

Ser Tyr His Ile Tyr Pro Leu Ile Leu Pro Leu His Lys Val Ser Tyr
245 250 255

Leu Ile Leu Phe Thr Phe Val Asn Phe Trp Thr Val Met Ile His Asp
260 265 270

Gly Gln Tyr Leu Ser Asn Asn Pro Ala Val Asn Gly Thr Ala Cys His
275 280 285

Thr Val His His Leu Tyr Phe Asn Tyr Asn Tyr Gly Gln Phe Thr Thr
290 295 300

Leu Trp Asp Arg Leu Gly Gly Ser Tyr Arg Arg Pro Asp Asp Ser Leu

305 310 315 320
 Phe Asp Pro Lys Leu Arg Asp Ala Lys Glu Thr Trp Asp Ala Gln Val
 325 330 335
 Lys Glu Val Glu His Phe Ile Lys Glu Val Glu Gly Asp Asp Asn Asp
 340 345 350
 Arg Ile Tyr Glu Asn Asp Pro Asn Thr Lys Lys Asn Asn
 355 360 365

<210> 9

<211> 1155

<212> DNA

<213> Artificial Sequence

<220>

<223> S. cerevisiae codon-optimized Pichia pastoris ERG3

<400> 9

atggatatcg ctttggaat cttggatacc ttgttttcg acaagggtta tgctaaattg 60
 ttgccaattt ccttggtcca acatttgcca gatgggtact tgaaaacctt gggtcatttg 120
 actggtgcca acaacaccat ggaatccttg ttcggtattg ctcaaactg tgaccaagcc 180
 tctaagaacc actggttgcg tactgttaac gattccattg ctttggccag acctggtgaa 240
 cgtttgggtc acggtgtcaa cgctccttg catttttcg atgaaaccgc ttatacttac 300
 gcttccatct tgggtcggtc caatatcatt cgtcaattca ctacttgat gatcttgatg 360
 attttgttcg gttgggggtt gtatttgtct gtcgcttctt ttcctatta cttgttttt 420
 gataaggcta tttcaacca tccaagatac ttgaagaacc aaatgctctt ggaaatccat 480
 caagccttga ctgctattcc taccatggtt ttgtgactg ttccatgggt ttgatcgaa 540
 ttgcgtggtt actctaagtt atacttgat gtaaatgaat ccaactggtg ttggaaggct 600
 attattggc aaatccttg ttcattatg ttaccgatt gttgtatcta cttattcat 660
 cgttggttgc actggccatc cgtttacaag cgtttgaca agcctcacca caagtggatt 720
 gttgtactc catttgcttc tcatgccttc catccagttg atggttatgc tcaatctttg 780

32960wo_ST25

ccttaccatt tgtatggtat gttgtttcca ttgcacaagg tttcctactt gatcttggtt 840
 ggtttggtca acttttggac tggtatgata catgatggtg aataactgtc ccgtgatcct 900
 attgtcaatg gtgctgcttg tcatactgtc catcacttgt acttcaacta caattacggt 960
 caattcacta ctttgtggga ccgtttgggt ggttcttaca gaatgccaga caaggaattg 1020
 ttcgataaga acaagaagaa agatgttaag acttggcggt ctcaagtcaa gcaagccgac 1080
 tctattagag aagacttga aggtaaagaa gatttccgtg aatacgggtac tgaagaaaaa 1140
 ttgaaatcca cctaa 1155

<210> 10
 <211> 939
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> S. cerevisiae codon-optimized Pencicillium roqueforti ERG3

<400> 10
 atggatattt tcttgacgt ttggatact ttggtcttg acagatgcta cgctgtcttg 60
 tccccagacc caactgccat ctccaacaat gatactcaag ccactgccca ttgaaccaa 120
 catgtcgggtg tctattacc tatgcaacct tccaagtggg ccgaagcctc cttgtggaag 180
 cgtgatgaca ttgccagaca agccttgtcc ttgtacgtca ttatttggtt gttcgctatg 240
 attatgtact tgttgggttc cttgttgtg taccatacct tgttcgacaa aagattgttg 300
 caacacccaa gattcttggc ccaccaagtc aagttggaaa tcaaccaagg tatctccgct 360
 atcccagtca tggccttggt gaccgtccca ttcttttgg ctgaaatccg tggttggtcc 420
 aagttgtatg acttgacctc cgactcccca ttctcggtt acaccttgtt gcaataccca 480
 ttgttcatct gcttactga ttccggtatt tactggattc accgtgggtt gcaccatcct 540
 tccgtctacc gttggttgca caagccacac cataaatggg ccgtccctac cccttccgct 600
 tcttatgctt tccaccctt ggacgggttg gcccaatcct tgccatacca tgtttacca 660
 ttgtgttcc cattgcaaaa ggggtgttac ttgggtttgt tcatgtttgt cactgtctgg 720

32960wo_ST25

accgtcttga tccatgacgc cgaatacttg ccaacctctg tcgttatcaa cggcgcctct 780
 tgtcacacca tgcatactt gtacttcaat tacaattacg gtcaattcac tactgcctgg 840
 gaccgtttgg ccggtactta ccgtaagcct aagggtgact ctttcatgga aggtcaacaa 900
 atggacggta aaggtaagtt gggcggtaag tgtgaataa 939

<210> 11
 <211> 990
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> S. cerevisiae codon-optimized Schizosaccharomyces pombe ERG3

<400> 11
 atggatgttg tcttgaata cgctgataaa tacgttttg acaccttta cggtaagatt 60
 gctgaatcct tcgattcctc ttctctttt gctaatactg ctgttaattc taccaccttg 120
 ggtttggctg aaaagggttaa cttgctatc acctccggtt tgtagatcg taacaatgtc 180
 tggcgtcaat tcacctcctt gttcttgatc acctggatta tgggtacttt gtcttacttt 240
 ttgtctgcct ctttgccta ttacgtttac ttgatcgtg aagaagccag acgtcacctt 300
 aagttttga aaaaccaaga aacttggaa ttgatggttg cttgaaaaa ctgccaggt 360
 atggctattt tgaccgctcc ttggttctta gctgaaattc gtggttatgg ttatgtttat 420
 gataagtgg atgaatatgg ttatttctat ttgttcttt ccatcgcctt gttcttgttg 480
 tttctgatt tttgattta ctggattcac cgtgcttgc atcatcgtg gttgtacgct 540
 cctttgcata agttgcatca caaatggatt gtccaactc cttactcttc tcacgctttt 600
 cattatttgg atggttactc tcaatccttg ccatatcata tgttccatt tttctccca 660
 ttaaacaat acgtttattt gttgtgttt ggtctgtta attactggac tgtcttgatc 720
 caccgacgta agtacttttc taacaacgct gtcgtaatg gtgctgctca tcacgctgct 780
 caccatatgt actttaacta taactatggg caattcttca ccttgttga tcgtttgtgc 840
 tcttcttaca gacaaccaga ccaagaatta ttcgatgccg aattgcgtaa cgaaaaattg 900
 caagaacaac gtatccgttt catggaaact gtccaatata ccgtcgaagg taaagatgac 960

cgtacttacg cttccaagaa ggataactaa 990

<210> 12

<211> 610

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 12

Met Thr Glu Thr Lys Asp Leu Leu Gln Asp Glu Glu Phe Leu Lys Ile
1 5 10 15

Arg Arg Leu Asn Ser Ala Glu Ala Asn Lys Arg His Ser Val Thr Tyr
20 25 30

Asp Asn Val Ile Leu Pro Gln Glu Ser Met Glu Val Ser Pro Arg Ser
35 40 45

Ser Thr Thr Ser Leu Val Glu Pro Val Glu Ser Thr Glu Gly Val Glu
50 55 60

Ser Thr Glu Ala Glu Arg Val Ala Gly Lys Gln Glu Gln Glu Glu Glu
65 70 75 80

Tyr Pro Val Asp Ala His Met Gln Lys Tyr Leu Ser His Leu Lys Ser
85 90 95

Lys Ser Arg Ser Arg Phe His Arg Lys Asp Ala Ser Lys Tyr Val Ser
100 105 110

Phe Phe Gly Asp Val Ser Phe Asp Pro Arg Pro Thr Leu Leu Asp Ser
115 120 125

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

Lys Gln Leu Lys Asn Leu Gln Leu Thr Lys Thr Lys Thr Lys Ala Thr
145 150 155 160

32960wo_ST25

Val Lys Thr Thr Val Lys Thr Thr Glu Lys Thr Asp Lys Ala Asp Ala
165 170 175

Pro Pro Gly Glu Lys Leu Glu Ser Asn Phe Ser Gly Ile Tyr Val Phe
180 185 190

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

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

Met Thr Thr Asp Leu Phe Thr Ile Ala Met Leu Asp Leu Ala Met Phe
225 230 235 240

Leu Cys Thr Phe Phe Val Val Phe Val His Trp Leu Val Lys Lys Arg
245 250 255

Ile Ile Asn Trp Lys Trp Thr Gly Phe Val Ala Val Ser Ile Phe Glu
260 265 270

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

Phe Asn Trp Val Thr Arg Ile Phe Leu Phe Leu His Ser Val Val Phe
290 295 300

Val Met Lys Ser His Ser Phe Ala Phe Tyr Asn Gly Tyr Leu Trp Asp
305 310 315 320

Ile Lys Gln Glu Leu Glu Tyr Ser Ser Lys Gln Leu Gln Lys Tyr Lys
325 330 335

Glu Ser Leu Ser Pro Glu Thr Arg Glu Ile Leu Gln Lys Ser Cys Asp
340 345 350

32960wo_ST25

Phe Cys Leu Phe Glu Leu Asn Tyr Gln Thr Lys Asp Asn Asp Phe Pro
355 360 365

Asn Asn Ile Ser Cys Ser Asn Phe Phe Met Phe Cys Leu Phe Pro Val
370 375 380

Leu Val Tyr Gln Ile Asn Tyr Pro Arg Thr Ser Arg Ile Arg Trp Arg
385 390 395 400

Tyr Val Leu Glu Lys Val Cys Ala Ile Ile Gly Thr Ile Phe Leu Met
405 410 415

Met Val Thr Ala Gln Phe Phe Met His Pro Val Ala Met Arg Cys Ile
420 425 430

Gln Phe His Asn Thr Pro Thr Phe Gly Gly Trp Ile Pro Ala Thr Gln
435 440 445

Glu Trp Phe His Leu Leu Phe Asp Met Ile Pro Gly Phe Thr Val Leu
450 455 460

Tyr Met Leu Thr Phe Tyr Met Ile Trp Asp Ala Leu Leu Asn Cys Val
465 470 475 480

Ala Glu Leu Thr Arg Phe Ala Asp Arg Tyr Phe Tyr Gly Asp Trp Trp
485 490 495

Asn Cys Val Ser Phe Glu Glu Phe Ser Arg Ile Trp Asn Val Pro Val
500 505 510

His Lys Phe Leu Leu Arg His Val Tyr His Ser Ser Met Gly Ala Leu
515 520 525

His Leu Ser Lys Ser Gln Ala Thr Leu Phe Thr Phe Phe Leu Ser Ala
530 535 540

32960wo_ST25

Val Phe His Glu Met Ala Met Phe Ala Ile Phe Arg Arg Val Arg Gly
545 550 555 560

Tyr Leu Phe Met Phe Gln Leu Ser Gln Phe Val Trp Thr Ala Leu Ser
565 570 575

Asn Thr Lys Phe Leu Arg Ala Arg Pro Gln Leu Ser Asn Val Val Phe
580 585 590

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

Thr Leu
610

<210> 13

<211> 1833

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 13

atgacggaga ctaaggattt gttgcaagac gaagagtttc ttaagatccg cagactcaat 60

tccgcagaag ccaacaaacg gcattcggtc acgtacgata acgtgatcct gccacaggag 120

tccatggagg ttctgccacg gtcgtctacc acgtcgctgg tggagccagt ggagtcgact 180

gaaggagtgg agtcgactga ggcggaacgt gtggcaggga agcaggagca ggaggaggag 240

taccctgtgg acgcccacat gcaaaagtac ctttcacacc tgaagagcaa gtctcggtcg 300

aggttccacc gaaaggatgc tagcaagtat gtgtcgtttt ttggggacgt gagttttgat 360

cctcgcccca cgctcctgga cagcgccatc aacgtgccct tccagacgac ttcaaaggt 420

ccggtgctgg agaaacagct caaaaattta cagttgacaa agaccaagac caaggccacg 480

gtgaagacta cggatgaagac tacggagaaa acggacaagg cagatgcccc cccaggagaa 540

aaactggagt cgaacttttc agggatctac gtgttcgcat ggatgttctt gggctggata 600

gcatcagggt gctgcacaga ttactatgcg tcgtacggca gtgcatggaa taagctggaa 660

atcgatcagt acatgacaac ggactgttgc acgatcgcaa tgttgactt ggcaatgttc 720

32960wo_ST25

```

ctgtgcactt tcttcgtggt ttctgtgcac tggctggtga aaaagcggat catcaactgg 780
aagtggactg gggtcgttc agtgagcatc ttcgagttgg ctttcatccc cgtgacgttc 840
ccattttacg tctactactt tgatttcaac tgggtcacga gaatcttct gttcctgcac 900
tccgtggtgt ttgttatgaa gagccactcg ttgcctttt acaacgggta tcttgggac 960
ataaagcagg aactcgagta ctcttccaaa cagttgcaaa aatacaagga atctttgtcc 1020
ccagagaccc gcgagattct gcaaaaaagt tgcgactttt gccttttga attgaactac 1080
cagaccaagg ataacgactt cccaacaac atcagttgca gcaatttct catgttctgt 1140
ttgtccccg tctcgtgta ccagatcaac tacccaagaa cgtcgcgcat cagatggagg 1200
tatgtgttg agaaggtgtg cgccatcatt ggcacatct tctcatgat ggtcacggca 1260
cagtttctca tgcacccggt ggccatgcgc tgtatccagt tccacaacac gccaccttc 1320
ggcggctgga tccccgccac gcaagagtgg ttccacctgc tcttcgacat gattccgggc 1380
ttcactgttc tgtacatgct cacgttttac atgatatggg acgctttatt gaattgcgtg 1440
gcgaggtga ccaggttgc ggacagatat ttctacggcg actggtggaa ttgcgtttcg 1500
ttgaagagt ttagcagaat ctggaacgtc cccgttcaca aattttact aagacacgtg 1560
taccacagct ccatgggccc attgcattg agcaagagcc aagctacatt atttacttt 1620
ttctgagtg ccgtgtcca cgaaatggcc atgttcgcca tttcagaag ggtagagga 1680
tatctgttca tgttccaact gtcgcagttt gtgtggactg cttgagcaa caccaagttt 1740
ctacgggcaa gaccgcagtt gtccaacgtt gtctttcgt ttggtgtctg ttcagggccc 1800
agtatcatta tgacgttgta cctgacctta tga 1833

```

<210> 14
 <211> 241
 <212> PRT
 <213> Ustilago maydis

<400> 14

Met Ala Ser His Arg Pro Arg Ser Asn Lys Ala Ala Asn Gly Ala Ser
 1 5 10 15

32960wo_ST25

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

Phe Cys Ala Leu Ile Ala Ala Leu Asp Ser Ile Arg Ser Ser Phe Tyr
35 40 45

Ile Phe Asp His Lys Ala Ile Tyr Lys Ile Ala Ser Thr Ala Val Ala
50 55 60

Asn His Pro Gly Asn Ala Thr Ala Ile Phe Asp Asp Val Leu Asp Asn
65 70 75 80

Leu Arg Ala Asp Pro Lys Leu Ala Pro Tyr Ile Asn Lys Asn His Phe
85 90 95

Ser Asp Glu Ser Glu Trp Met Phe Asn Asn Ala Gly Gly Ala Met Gly
100 105 110

Ser Met Phe Ile Ile His Ala Ser Val Thr Glu Tyr Leu Ile Phe Phe
115 120 125

Gly Thr Pro Val Gly Thr Glu Gly His Thr Gly Arg His Thr Ala Asp
130 135 140

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

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

Arg Gly Thr Val Lys Gln Tyr Met Met Pro Glu Asp Gly Cys Trp Ala
180 185 190

Leu Glu Leu Ala Gln Gly Trp Ile Pro Pro Met Leu Pro Phe Gly Leu
195 200 205

32960wo_ST25

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

Val Trp Ile Thr Ala Arg Glu Met Val Gly Asn Leu Leu Ile Gly Lys
 225 230 235 240

Phe

<210> 15

<211> 726

<212> DNA

<213> Ustilago maydis

<400> 15

atggcatcgc atagaccacg cagcaacaag gctgccaatg gtgcttcgac ttcacccaaa 60

cgagctgga taattgtctc agctgcgctc gttggcttct gcgctctcat cgccgctctc 120

gattcgatcc gatccagctt ctacatcttt gaccacaagg caatctacaa gatcgcatcg 180

actgcggtcg ccaaccatcc aggcaatgcg acggccatct ttgatgatgt cctcgacaac 240

cttcgtgccg accccaagct cgcgcccttac atcaacaaga atcatttcag cgacgagtca 300

gaatggatgt tcaacaatgc cgggtggtgct atgggtagca tgttcatcat tcatgcttcc 360

gtcaccgagt acctgatctt ctttggcact cccgtcggaa ccgagggtca cactggtcgt 420

cacacagccg atgactactt caacatcctt accggtaacc aatacgcttt cccagctggt 480

gcgctcaagg cggagcacta cctgcccga tcagtgcacc atcttcgccg cggaacggtc 540

aagcagtaca tgatgcctga agacgggtgc tgggcgctcg agcttgctca gggctggatc 600

ccacccatgc ttcccttgg tctcgccgat gtgctcagct cgacgctcga cctgcccacc 660

tttggtatca ctgtctggat cactgcacga gaaatggtg gcaatctgct catcggcaag 720

ttttga 726

<210> 16

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 16

tgttctgtac atgctcacgt ttac

25

<210> 17

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 17

cacacggtct cacaagacaa cgttggacaa ctgc

34

<210> 18

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 18

cacacggtct caatcaaacg aaaagacaac gttggac

37

<210> 19

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 19

cttgctgttt ggtgtctgtt cagggcccag tatcattatg acgttgacc tgaccttatg

60

actgca

66

<210> 20

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 20

gtcataaggt caggtacaac gtcataatga tactgggccc tgaacagaca ccaaacga 58

<210> 21

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 21

tgatgtctgt tcagggccca gtatcattat gacgtgtac ctgaccttat gactgca 57

<210> 22

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 22

gtcataaggt caggtacaac gtcataatga tactgggccc tgaacagac 49