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<151> 2019-04-01

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Val Tyr Leu Pro Gly Ile Tyr Pro Arg Asn Met Lys Leu Asp Ser Lys
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Arg Ala Ile Val Pro Cys Ala Asn Ile Leu Gly Gly Gly Ser Ser Ile
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Asn Phe Met Met Tyr Thr Arg Gly Ser Ala Ser Asp Tyr Asp Asp Phe

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

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

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

Arg Ala Ala Gly Val Lys Pro Leu Val Asn Leu Pro Gly Val Gly Arg
    290                 295                 300

Asn Phe Gln Asp His Tyr Cys Phe Phe Ser Pro Tyr Arg Ile Lys Pro
305                 310                 315                 320

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

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

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

Leu Ser Gln Met Asp Glu Ser Phe Gln Glu Gly Tyr Arg Glu Tyr Phe
    370                 375                 380

Glu Asp Lys Pro Asp Lys Pro Val Met His Tyr Ser Ile Ile Ala Gly
385                 390                 395                 400

Phe Phe Gly Asp His Thr Lys Ile Pro Pro Gly Lys Tyr Met Thr Met
                405                 410                 415

Phe His Phe Leu Glu Tyr Pro Phe Ser Arg Gly Ser Ile His Ile Thr
            420                 425                 430

Ser Pro Asp Pro Tyr Ala Ala Pro Asp Phe Asp Pro Gly Phe Met Asn
        435                 440                 445
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Asp Glu Arg Asp Met Ala Pro Met Val Trp Ala Tyr Lys Lys Ser Arg
    450                 455                 460

Glu Thr Ala Arg Arg Met Asp His Phe Ala Gly Glu Val Thr Ser His
465                 470                 475                 480

His Pro Leu Phe Pro Tyr Ser Ser Glu Ala Arg Ala Leu Glu Met Asp
                485                 490                 495

Leu Glu Thr Ser Asn Ala Tyr Gly Gly Pro Leu Asn Leu Ser Ala Gly
            500                 505                 510

Leu Ala His Gly Ser Trp Thr Gln Pro Leu Lys Lys Pro Thr Ala Lys
        515                 520                 525

Asn Glu Gly His Val Thr Ser Asn Gln Val Glu Leu His Pro Asp Ile
    530                 535                 540

Glu Tyr Asp Glu Glu Asp Asp Lys Ala Ile Glu Asn Tyr Ile Arg Glu
545                 550                 555                 560

His Thr Glu Thr Thr Trp His Cys Leu Gly Thr Cys Ser Ile Gly Pro
                565                 570                 575

Arg Glu Gly Ser Lys Ile Val Lys Trp Gly Gly Val Leu Asp His Arg
            580                 585                 590

Ser Asn Val Tyr Gly Val Lys Gly Leu Lys Val Gly Asp Leu Ser Val
        595                 600                 605

Cys Pro Asp Asn Val Gly Cys Asn Thr Tyr Thr Thr Ala Leu Leu Ile
    610                 615                 620

Gly Glu Lys Thr Ala Thr Leu Val Gly Glu Asp Leu Gly Tyr Thr Gly
625                 630                 635                 640

Glu Ala Leu Asp Met Thr Val Pro Gln Phe Lys Leu Gly Thr Tyr Glu
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645 650 655

Lys Thr Gly Leu Ala Arg Phe
660

<210> 10
<211> 1992
<212> DNA
<213> Komagataella pastoris

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gagaacaacc tcaacaaccc atgggtttac cttccaggta tttacccaag aaacatgaag 180

ttggactcca agactgcatc cttctacact tctaaccctt ctcctcactt gaacggtaga 240

agagctattg ttccatgtgc taacgtcttg ggtggtggtt cttccattaa cttcatgatg 300

tacaccagag gttctgcttc tgattatgac gacttccaag ccgagggctg gaaaaccaag 360

gacttgcttc cattgatgaa aaagaccgag acctaccaaa gagcttgcaa caaccctgac 420

attcacgggt tcgaaggtcc aatcaaggtt tctttcggta actacaccta cccagtttgc 480

caggacttct tgagagcttc tgaatcccaa ggtattccat acgttgacga cttggaagac 540

ttggttactg ctcacggtgc tgaacactgg ctgaaatgga tcaacagaga cactggtcgt 600

cgttccgact ccgctcatgc atttgtccac tctactatga gaaaccacga caacttgtac 660

ttgatttgta acacaaaggt tgacaagatt attgtcgaag acggaagagc tgctgctgtt 720

agaactgttc caagcaagcc tttgaaccca aagaagccaa gtcacaagat ctaccgtgct 780

agaaagcaaa tcgttttgtc ttgtggtacc atctcatctc ctttggttct gcaaagatcc 840

ggtttcggtg acccaatcaa gttgagagcc gctggtgtta agcctttggt caacttgcct 900

ggtgtcggaa gaaacttcca agaccactac tgtttcttca gtccttacag aatcaagcct 960

cagtacgaat ctttcgatga cttcgtgcgt ggtgatgctg agatccaaaa gagagttttc 1020

gaccaatggt acgccaatgg tactggtcct cttgccacta acggtatcga agccggtgtc 1080

aagattagac caacaccaga ggaactgtct caaatggacg aatctttcca agagggttac 1140

agagaatact ttgaggacaa gccagacaag ccagttatgc actactccat tattgctggt 1200

ttcttcggtg accacaccaa gattcctcct ggaaagtaca tgaccatgtt ccacttttg 1260

gaatacccat tctccagagg ttccattcac attacctctc cagatccata cgcagctcca 1320

gacttcgacc caggtttcat gaacgatgaa agagacatgg ctcctatggt ctgggcctac 1380

aagaagtcta gagagacagc tagaagaatg gaccactttg ccggtgaggt tacttctcac 1440

cacccattgt tcccatactc atccgaggcc agagctttgg agatggattt ggagacctcc 1500

aatgcctacg gtggaccttt gaacttgtct gctggtcttg cccacggttc ttggactcaa 1560

cctttgaaga agccaactgc aaagaacgaa ggccatgtta cctccaacca agtcgagctt 1620

catccagaca tcgagtacga cgaggaggac gacaaggcca ttgaaaacta catccgtgag 1680

cacactgaga ccacatggca ctgtctggga acctgttcca tcggtccaag agagggttcc 1740

aagatcgtca aatggggtgg tgttttggac cacagatcca acgtttacgg agtcaagggc 1800

ctgaaggttg gtgacttgtc tgtctgtcca gacaatgttg gttgtaacac ctacaccacc 1860

gctcttttga tcggtgagaa gactgccact ttggttggag aagacttagg atacaccggt 1920

gaagccttag acatgactgt tcctcagttc aagttgggca cttacgagaa gaccggtctt 1980

gctagattct aa 1992

<210> 11
<211> 663
<212> PRT
<213> Komagataella pastoris

<400> 11

Met Ala Ile Pro Glu Glu Phe Asp Ile Leu Val Leu Gly Gly Gly Ser
1 5 10 15

Ser Gly Ser Cys Ile Ala Gly Arg Leu Ala Asn Leu Asp His Ser Leu
20 25 30

Lys Val Gly Leu Ile Glu Ala Gly Glu Asn Asn Leu Asn Asn Pro Trp
35 40 45

```
Val Tyr Leu Pro Gly Ile Tyr Pro Arg Asn Met Lys Leu Asp Ser Lys
    50                  55                  60

Thr Ala Ser Phe Tyr Thr Ser Asn Pro Ser Pro His Leu Asn Gly Arg
65                  70                  75                  80

Arg Ala Ile Val Pro Cys Ala Asn Ile Leu Gly Gly Gly Ser Ser Ile
                85                  90                  95

Asn Phe Met Met Tyr Thr Arg Gly Ser Ala Ser Asp Tyr Asp Asp Phe
            100                 105                 110

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

Thr Glu Thr Tyr Gln Arg Ala Cys Asn Asn Pro Glu Ile His Gly Phe
    130                 135                 140

Glu Gly Pro Ile Lys Val Ser Phe Gly Asn Tyr Thr Tyr Pro Val Cys
145                 150                 155                 160

Gln Asp Phe Leu Arg Ala Thr Glu Ser Gln Gly Ile Pro Tyr Val Asp
                165                 170                 175

Asp Leu Glu Asp Leu Glu Thr Ala His Gly Ala Glu His Trp Leu Lys
            180                 185                 190

Trp Ile Asn Arg Asp Thr Gly Arg Arg Ser Asp Ser Ala His Ala Phe
        195                 200                 205

Val His Ser Thr Met Arg Asn His Asp Asn Leu Tyr Leu Ile Cys Asn
    210                 215                 220

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

Arg Thr Val Pro Ser Lys Pro Leu Asn Ala Lys Lys Pro Thr His Lys
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                245                 250                 255

Val Tyr Arg Ala Arg Lys Gln Ile Val Leu Ser Cys Gly Thr Ile Ser
            260                 265                 270

Ser Pro Leu Val Leu Gln Arg Ser Gly Phe Gly Asp Pro Ile Lys Leu
        275                 280                 285

Arg Ala Ala Gly Val Lys Pro Leu Val Asn Leu Pro Gly Val Gly Arg
    290                 295                 300

Asn Phe Gln Asp His Tyr Cys Phe Phe Ser Pro Tyr Arg Ile Lys Pro
305                 310                 315                 320

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

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

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

Leu Ser Gln Met Asp Glu Ser Phe Gln Glu Gly Tyr Arg Glu Tyr Phe
    370                 375                 380

Glu Asp Lys Pro Asp Lys Pro Val Met His Tyr Ser Ile Ile Ala Gly
385                 390                 395                 400

Phe Phe Gly Asp His Thr Lys Ile Pro Pro Gly Lys Tyr Met Thr Met
                405                 410                 415

Phe His Phe Leu Glu Tyr Pro Phe Ser Arg Gly Ser Ile His Ile Thr
            420                 425                 430

Ser Pro Asp Pro Tyr Ala Thr Pro Asp Phe Asp Pro Gly Phe Met Asn
        435                 440                 445
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```
Asp Glu Arg Asp Met Ala Pro Met Val Trp Ser Tyr Lys Lys Ser Arg
    450                 455                 460

Glu Thr Ala Arg Lys Met Asp His Phe Ala Gly Glu Val Thr Ser His
465                 470                 475                 480

His Pro Leu Phe Pro Tyr Ser Ser Glu Ala Arg Ala Tyr Glu Met Asp
                485                 490                 495

Leu Glu Thr Ser Asn Ala Tyr Gly Gly Pro Leu Asn Leu Thr Ala Gly
            500                 505                 510

Leu Ala His Gly Ser Trp Thr Gln Pro Leu Lys Lys Pro Ala Ala Arg
        515                 520                 525

Asn Glu Gly His Val Thr Ser Asn Gln Val Glu Leu His Pro Asp Ile
    530                 535                 540

Glu Tyr Asp Glu Glu Asp Asp Lys Ala Ile Glu Asn Tyr Ile Arg Glu
545                 550                 555                 560

His Thr Glu Thr Thr Trp His Cys Leu Gly Thr Cys Ser Ile Gly Pro
                565                 570                 575

Arg Glu Gly Ser Lys Ile Val Lys Trp Gly Gly Val Leu Asp His Arg
            580                 585                 590

Ser Asn Val Tyr Gly Val Lys Gly Leu Lys Val Gly Asp Leu Ser Val
        595                 600                 605

Cys Pro Asp Asn Val Gly Cys Asn Thr Tyr Thr Thr Ala Leu Leu Ile
    610                 615                 620

Gly Glu Lys Thr Ala Thr Leu Val Gly Glu Asp Leu Gly Tyr Thr Gly
625                 630                 635                 640

Asp Ala Leu Asp Met Thr Val Pro Gln Phe Lys Leu Gly Thr Tyr Glu
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645 650 655

Lys Thr Gly Leu Ala Arg Phe
660

<210> 12
<211> 1992
<212> DNA
<213> Komagataella pastoris

<400> 12
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attgccggaa gattggccaa cttggaccac tctttgaaag ttggtcttat cgaggccggt 120

gagaacaatc ttaacaaccc ttgggtctac cttccaggta tttacccaag aaacatgaaa 180

ttggactcca agaccgcttc tttctacacc tccaacccat ctcctcattt gaatggtaga 240

agagctattg tcccatgtgc taacatcttg ggtggtggtt cttccatcaa cttcatgatg 300

tacaccagag gttccgcttc tgattacgat gacttcgaag ctgagggctg gaaaaccaag 360

gatttgcttc ctttgatgaa gaagactgag acctaccaaa gagcttgcaa caaccctgag 420

atccacggtt tcgaaggtcc aatcaaggtt tctttcggta actacactta cccggtttgt 480

caagacttct tgagagcaac tgaatcccaa ggtattccat acgttgacga cttggaagac 540

ttggagactg ctcatggtgc cgaacactgg ttgaaatgga tcaacagaga cactggtcgt 600

cgttccgact ctgctcatgc tttcgtccat tctactatga gaaaccatga taacttgtac 660

ttgatctgca acaccaaggt tgacaagatt attgttgaag acggaagagc tgctggtgtc 720

agaaccgtcc caagtaaacc tttgaacgca aagaagccaa ctcacaaggt ttaccgtgct 780

agaaagcaga tcgttttgtc ttgtggtacc atttcttccc ctctggtttt gcaaagatcc 840

ggttttggtg atccaatcaa attgagagcc gctggtgtta agcctttggt caacttgcca 900

ggtgttggaa ggaacttcca ggaccattac tgcttcttct ctccttacag aatcaagccc 960

caatacgagt cttttgatga cttcgtccgt ggtgacgcta acatccaaaa gaaggtattc 1020

gaccaatggt acgctaacgg tactggtcca ttggccacca atggtattga agccggtgtc 1080

aagatcagac caactccaga ggaattatct caaatggacg agtcgttcca ggagggttac 1140

agagagtact ttgaagacaa accagacaaa ccagttatgc actattccat cattgctggt 1200

ttcttcggtg accacaccaa gattccgcct ggaaagtaca tgaccatgtt ccacttcttg 1260

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gactttgacc caggtttcat gaatgatgaa agagacatgg ctcctatggt ttggtcttac 1380

aagaagtcca gagagactgc cagaaagatg gatcactttg ctggtgaggt tacttcccac 1440

caccctctgt tcccatactc atccgaggcc agagcttacg agatggactt ggagacctcc 1500

aacgcctacg gtggaccact gaacttgact gctggtcttg ctcacggttc ttggactcag 1560

cctttgaaga agcctgccgc aagaaacgaa ggacatgtta cctctaacca agttgagctt 1620

catccagaca ttgaatacga tgaggaggat gacaaggcca ttgagaacta catccgtgag 1680

cacactgaga ccacatggca ctgtctcgga acctgttcca tcggtccaag agaaggttcc 1740

aagatagtca aatggggtgg tgttttggac cacagatcca acgtttacgg agtcaagggc 1800

ctgaaggttg gtgacttgtc tgtctgccca gacaatgttg gttgtaacac ctacaccacc 1860

gctcttttaa tcggtgaaaa gactgcaacc ttggtgggtg aagacttagg atacacaggt 1920

gatgccttag acatgactgt tcctcagttc aagttgggca cttacgagaa gactggtctt 1980

gctagattct ag 1992

<210> 13
<211> 664
<212> PRT
<213> Ogataea methanolica

<400> 13

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

Thr Val Ala Leu Ile Glu Gly Gly Glu Asn Asn Ile Asn Asn Pro Trp
35 40 45

```
Val Tyr Leu Pro Gly Val Tyr Pro Arg Asn Met Arg Leu Asp Ser Lys
    50                  55                  60

Thr Ala Thr Phe Tyr Ser Ser Arg Pro Ser Pro His Leu Asn Gly Arg
65                  70                  75                  80

Arg Ala Ile Val Pro Cys Ala Asn Ile Leu Gly Gly Gly Ser Ser Ile
                85                  90                  95

Asn Phe Leu Met Tyr Thr Arg Ala Ser Ala Ser Asp Tyr Asp Asp Trp
            100                 105                 110

Glu Ser Glu Gly Trp Thr Thr Asp Glu Leu Leu Pro Leu Met Lys Lys
        115                 120                 125

Ile Glu Thr Tyr Gln Arg Pro Cys Asn Asn Arg Glu Leu His Gly Phe
    130                 135                 140

Asp Gly Pro Ile Lys Val Ser Phe Gly Asn Tyr Thr Tyr Pro Asn Gly
145                 150                 155                 160

Gln Asp Phe Ile Arg Ala Ala Glu Ser Gln Gly Ile Pro Phe Val Asp
                165                 170                 175

Asp Ala Glu Asp Leu Lys Cys Ser His Gly Ala Glu His Trp Leu Lys
            180                 185                 190

Trp Ile Asn Arg Asp Leu Gly Arg Arg Ser Asp Ser Ala His Ala Tyr
        195                 200                 205

Ile His Pro Thr Met Arg Asn Lys Gln Asn Leu Phe Leu Ile Thr Ser
    210                 215                 220

Thr Lys Cys Glu Lys Ile Ile Ile Glu Asn Gly Val Ala Thr Gly Val
225                 230                 235                 240

Lys Thr Val Pro Met Lys Pro Thr Gly Ser Pro Lys Thr Gln Val Ala
```

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                245                 250                 255

Arg Thr Phe Lys Ala Arg Lys Gln Ile Ile Val Ser Cys Gly Thr Ile
            260                 265                 270

Ser Ser Pro Leu Val Leu Gln Arg Ser Gly Ile Gly Ser Ala His Lys
        275                 280                 285

Leu Arg Gln Val Gly Ile Lys Pro Ile Val Asp Leu Pro Gly Val Gly
    290                 295                 300

Met Asn Phe Gln Asp His Tyr Cys Phe Phe Thr Pro Tyr His Val Lys
305                 310                 315                 320

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

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

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

Glu Leu Ala Thr Ala Asp Asp Glu Phe Arg Ala Ala Tyr Asp Asp Tyr
    370                 375                 380

Phe Gly Asn Lys Pro Asp Lys Pro Leu Met His Tyr Ser Leu Ile Ser
385                 390                 395                 400

Gly Phe Phe Gly Asp His Thr Lys Ile Pro Asn Gly Lys Tyr Met Cys
                405                 410                 415

Met Phe His Phe Leu Glu Tyr Pro Phe Ser Arg Gly Phe Val His Val
            420                 425                 430

Val Ser Pro Asn Pro Tyr Asp Ala Pro Asp Phe Asp Pro Gly Phe Met
        435                 440                 445
```

```
Asn Asp Pro Arg Asp Met Trp Pro Met Val Trp Ser Tyr Lys Lys Ser
    450                 455                 460

Arg Glu Thr Ala Arg Arg Met Asp Cys Phe Ala Gly Glu Val Thr Ser
465                 470                 475                 480

His His Pro His Tyr Pro Tyr Asp Ser Pro Ala Arg Ala Ala Asp Met
                485                 490                 495

Asp Leu Glu Thr Thr Lys Ala Tyr Ala Gly Pro Asp His Phe Thr Ala
            500                 505                 510

Asn Leu Tyr His Gly Ser Trp Thr Val Pro Ile Glu Lys Pro Thr Pro
        515                 520                 525

Lys Asn Ala Ala His Val Thr Ser Asn Gln Val Glu Lys His Arg Asp
    530                 535                 540

Ile Glu Tyr Thr Lys Glu Asp Asp Ala Ala Ile Glu Asp Tyr Ile Arg
545                 550                 555                 560

Glu His Thr Glu Thr Thr Trp His Cys Leu Gly Thr Cys Ser Met Ala
                565                 570                 575

Pro Arg Glu Gly Ser Lys Val Val Pro Thr Gly Gly Val Val Asp Ser
            580                 585                 590

Arg Leu Asn Val Tyr Gly Val Glu Lys Leu Lys Val Ala Asp Leu Ser
        595                 600                 605

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

Ile Gly Glu Lys Ala Ser Thr Leu Val Ala Glu Asp Leu Gly Tyr Ser
625                 630                 635                 640

Gly Asp Ala Leu Lys Met Thr Val Pro Asn Phe Lys Leu Gly Thr Tyr
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645 650 655

Glu Glu Ala Gly Leu Ala Arg Phe
660

<210> 14
<211> 1995
<212> DNA
<213> Ogataea methanolica

<400> 14
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gaaaacaaca tcaacaaccc atgggtttac ttaccaggtg tttatccaag aaacatgaga 180

ttagactcaa agactgctac tttttactct tcaagaccat caccacactt gaacggtaga 240

agagctattg ttccatgtgc taacatcttg ggtggtggtt cttccatcaa cttcttgatg 300

tacaccagag cctctgcctc cgattacgat gattgggaat ctgaaggttg gactaccgat 360

gaattattac cactaatgaa gaagattgaa acttatcaaa gaccatgtaa caacagagaa 420

ttgcacggtt tcgatggtcc aattaaggtt tcatttggta actatactta tccaaacggt 480

caagatttca ttagagctgc cgaatctcaa ggtattccat ttgttgatga tgctgaagat 540

ttgaaatgtt cccacggtgc tgagcactgg ttgaagtgga tcaacagaga cttaggtaga 600

agatccgatt ctgctcatgc ttacattcac ccaaccatga gaaacaagca aaacttgttc 660

ttgattactt ccaccaagtg tgaaaagatt atcattgaaa acggtgttgc tactggtgtt 720

aagactgttc caatgaagcc aactggttct ccaaagaccc aagttgctag aactttcaag 780

gctagaaagc aaattattgt ttcttgtggt actatctcat caccattagt tttgcaaaga 840

tctggtatcg gttccgctca caagttgaga caagttggta ttaaaccaat tgttgactta 900

ccaggtgttg gtatgaactt ccaagatcac tactgtttct tcactccata ccatgtcaag 960

ccagatactc catcattcga tgactttgtt agaggtgata aagctgttca aaaatctgct 1020

ttcgaccaat ggtatgctaa caaggatggt ccattaacca ctaatggtat tgaggcaggt 1080

gttaagatta gaccaactga agaagaatta gccactgctg atgacgaatt cagagctgct 1140

tatgatgact actttggtaa caagccagat aagccattaa tgcactactc tctaatttct 1200

ggtttctttg gtgaccacac caagattcca aacggtaagt acatgtgcat gttccacttc 1260

ttggaatatc cattctccag aggtttcgtt cacgttgttt ctccaaaccc atacgatgct 1320

cctgactttg atccaggttt catgaacgat ccaagagata tgtggccaat ggtttggtct 1380

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caccacccac actacccata cgactcacca gccagagctg ctgacatgga cttggaaact 1500

actaaagctt atgctggtcc agaccacttt actgctaact tgtaccacgg ttcatggact 1560

gttccaattg aaaagccaac tccaaagaac gctgctcacg ttacttctaa ccaagttgaa 1620

aaacatcgtg acatcgaata caccaaggag gatgatgctg ctatcgaaga ttacatcaga 1680

gaacacactg aaaccacatg gcattgtctt ggtacttgtt caatggctcc aagagaaggt 1740

tctaaggttg tcccaactgg tggtgttgtt gactccagat taaacgttta cggtgttgaa 1800

aagttgaagg ttgctgattt atcaatttgc ccagataatg ttggttgtaa cacttactct 1860

actgctttgt taatcggtga aaaggcttct accttagttg ctgaagactt gggctactct 1920

ggtgatgctt tgaagatgac tgttccaaac ttcaaattgg gtacttatga agaagctggt 1980

ctagctagat tctag 1995

<210> 15
<211> 663
<212> PRT
<213> Ogataea methanolica

<400> 15

Met Ala Ile Pro Glu Glu Phe Asp Ile Ile Val Val Gly Gly Gly Ser
1 5 10 15

Ala Gly Cys Pro Thr Ala Gly Arg Leu Ala Asn Leu Asp Pro Asn Leu
20 25 30

Thr Val Ala Leu Ile Glu Ala Gly Glu Asn Asn Ile Asn Asn Pro Trp
35 40 45

```
Val Tyr Leu Pro Gly Val Tyr Pro Arg Asn Met Arg Leu Asp Ser Lys
    50                  55                  60

Thr Ala Thr Phe Tyr Ser Ser Arg Pro Ser Pro His Leu Asn Gly Arg
65                  70                  75                  80

Arg Ala Ile Val Pro Cys Ala Asn Ile Leu Gly Gly Gly Ser Ser Ile
                85                  90                  95

Asn Phe Met Met Tyr Thr Arg Gly Ser Ala Ser Asp Tyr Asp Asp Trp
            100                 105                 110

Glu Ser Glu Gly Trp Thr Thr Asp Glu Leu Leu Pro Leu Met Lys Arg
        115                 120                 125

Leu Glu Thr Tyr Gln Arg Pro Cys Asn Asn Pro Asp Leu His Gly Phe
    130                 135                 140

Asp Gly Pro Ile Lys Val Ser Phe Gly Asn Tyr Thr Tyr Pro Asn Cys
145                 150                 155                 160

Gln Asp Phe Leu Arg Ala Ala Glu Ser Gln Gly Ile Pro Phe Val Asp
                165                 170                 175

Asp Ala Glu Asp Leu Lys Thr Ser His Ala Ser Gln His Trp Leu Lys
            180                 185                 190

Trp Ile Asn Arg Asp Leu Gly Arg Arg Ser Asp Ala Ala His Ala Tyr
        195                 200                 205

Ile His Pro Thr Met Arg Asn Lys Ser Asn Leu Tyr Leu Ile Thr Ser
    210                 215                 220

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

Gln Val Val Pro Ser Lys Pro Leu Asn Pro Glu Lys Pro Ala Ala Lys
```

```
               245                 250                 255

Ile Tyr Lys Ala Arg Lys Gln Ile Ile Leu Ser Cys Gly Thr Ile Ser
            260                 265                 270

Thr Pro Leu Val Leu Gln Arg Ser Gly Ile Gly Ser Ala His Lys Leu
        275                 280                 285

Arg Gln Ala Gly Ile Lys Pro Ile Val Asp Leu Pro Gly Val Gly Met
    290                 295                 300

Asn Phe Gln Asp His Tyr Cys Phe Phe Thr Pro Tyr His Val Lys Pro
305                 310                 315                 320

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

Lys Ser Ala Phe Asp Gln Trp Tyr Ala Asn Lys Asp Gly Pro Leu Thr
            340                 345                 350

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

Leu Ala Thr Ala Asp Glu Asp Phe Gln Leu Gly Tyr Ala Ser Tyr Phe
    370                 375                 380

Glu Asn Lys Pro Asp Lys Pro Leu Met His Tyr Ser Leu Ile Ser Gly
385                 390                 395                 400

Phe Phe Gly Asp His Thr Lys Ile Pro Asn Gly Lys Tyr Met Thr Met
                405                 410                 415

Phe His Phe Leu Glu Tyr Pro Phe Ser Arg Gly Phe Val His Val Val
            420                 425                 430

Ser Pro Ser Pro Tyr Asp Ala Pro Asp Phe Asp Pro Gly Phe Met Asn
        435                 440                 445
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```
Asp Pro Lys Asp Met Trp Pro Met Val Trp Ala Tyr Lys Met Ser Arg
    450                 455                 460

Glu Thr Ala Arg Arg Met Glu Cys Phe Ala Gly Glu Val Thr Ser His
465                 470                 475                 480

His Pro Lys Tyr Pro Tyr Asp Ser Pro Ala Arg Ala Lys Asp Leu Asp
                485                 490                 495

Leu Glu Thr Cys Lys Ala Tyr Ala Gly Pro Asp His Phe Thr Ala Asn
            500                 505                 510

Leu Tyr His Gly Ser Trp Thr Ile Pro Leu Glu Lys Pro Thr Pro Lys
        515                 520                 525

Asn Thr Ser His Val Thr Ser Asn Gln Val Glu Leu His Ala Gln Leu
    530                 535                 540

Glu Tyr Ser Lys Glu Asp Asp Ile Ala Ile Glu Asn Tyr Ile Lys Glu
545                 550                 555                 560

His Val Glu Thr Thr Trp His Cys Leu Gly Thr Cys Ser Met Ala Pro
                565                 570                 575

Arg Glu Gly Ser Ser Ile Val Pro Thr Gly Gly Val Val Asp Glu Arg
            580                 585                 590

Leu Asn Val Tyr Asp Val Ala His Leu Lys Cys Ala Asp Leu Ser Ile
        595                 600                 605

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

Gly Glu Lys Ala Ser Met Ile Val Ala Glu Asp Leu Gly Tyr Ser Gly
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Ala Glu Leu Asp Met Thr Ile Pro Gly Phe Lys Leu Gly Thr Tyr Glu
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645 650 655

Ser Thr Gly Leu Gly Arg Phe
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<210> 16
<211> 1992
<212> DNA
<213> Ogataea methanolica

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ttagactcca aaactgcaac tttctactct tctagacctt ccccacattt aaatggtaga 240

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gaattattgc cattgatgaa aagattagaa acttatcaaa gaccatgtaa caaccctgat 420

ttgcacggtt tcgacggccc tatcaaggtc tccttcggta actacactta tcctaactgt 480

caagatttct taagagccgc tgaatctcaa ggtattccat ttgttgatga tgctgaagat 540

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gcgttactgg ttggtgaaaa ggcttctatg attgttgctg aagatttagg ttactctgga 1920

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cggagacaag acaaaacaac cctttgtcct gctcttttct ttctcacacc gcgtgggtgt 240

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cctggcttca aataacagcc tgctgctatc tgtgaccaga ttgggacacc cccctccct 360

ccgaatgatc catcaccttt tgtcgtactc cgacaatgat ccttccctgt catcttctgg 420

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<213> Ogataea methanolica

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tacaattttg tcaatgtttg tttgataacc caaggtggaa cgtttccagt tagacctgtt 480

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<211> 664
<212> PRT
<213> Ogataea polymorpha

<400> 19

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35 40 45

Trp Val Tyr Leu Pro Gly Val Tyr Pro Arg Asn Met Arg Leu Asp Ser
50 55 60

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

Arg Arg Ala Ile Val Pro Cys Ala Asn Ile Leu Gly Gly Gly Ser Ser
85 90 95

Ile Asn Phe Leu Met Tyr Thr Arg Ala Ser Ala Ser Asp Tyr Asp Asp
100 105 110

Trp Glu Ser Glu Gly Trp Ser Thr Asp Glu Leu Leu Pro Leu Ile Lys

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        115                 120                 125

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

Cys Gln Asp Phe Leu Arg Ala Ala Glu Ser Gln Gly Ile Pro Val Val
                165                 170                 175

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

Lys Trp Ile Asn Arg Asp Leu Gly Arg Arg Ser Asp Ser Ala His Ala
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Tyr Val His Pro Thr Met Arg Asn Lys Gln Ser Leu Phe Leu Ile Thr
    210                 215                 220

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

Val Arg Thr Val Pro Met Lys Pro Leu Asn Pro Lys Lys Pro Val Ser
                245                 250                 255

Arg Thr Phe Arg Ala Arg Lys Gln Ile Val Ile Ser Cys Gly Thr Ile
            260                 265                 270

Ser Ser Pro Leu Val Leu Gln Arg Ser Gly Ile Gly Ala Ala His His
        275                 280                 285

Leu Arg Ser Val Gly Val Lys Pro Ile Val Asp Leu Pro Gly Val Gly
    290                 295                 300

Glu Asn Phe Gln Asp His Tyr Cys Phe Phe Thr Pro Tyr Tyr Val Lys
305                 310                 315                 320
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Pro Asp Val Pro Thr Phe Asp Asp Phe Val Arg Gly Asp Pro Val Ala
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Gln Lys Ala Ala Phe Asp Gln Trp Tyr Ser Asn Lys Asp Gly Pro Leu
            340                 345                 350

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

Glu Leu Ala Thr Ala Asp Glu Asp Phe Arg Arg Gly Tyr Ala Glu Tyr
    370                 375                 380

Phe Glu Asn Lys Pro Asp Lys Pro Leu Met His Tyr Ser Val Ile Ser
385                 390                 395                 400

Gly Phe Phe Gly Asp His Thr Lys Ile Pro Asn Gly Lys Phe Met Thr
                405                 410                 415

Met Phe His Phe Leu Glu Tyr Pro Phe Ser Arg Gly Phe Val Arg Ile
            420                 425                 430

Thr Ser Ala Asn Pro Tyr Asp Ala Pro Asp Phe Asp Pro Gly Phe Leu
        435                 440                 445

Asn Asp Glu Arg Asp Leu Trp Pro Met Val Trp Ala Tyr Lys Lys Ser
    450                 455                 460

Arg Glu Thr Ala Arg Arg Met Glu Ser Phe Ala Gly Glu Val Thr Ser
465                 470                 475                 480

His His Pro Leu Phe Lys Val Asp Ser Pro Ala Arg Ala Arg Asp Leu
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Asp Leu Glu Thr Cys Ser Ala Tyr Ala Gly Pro Lys His Leu Thr Ala
            500                 505                 510

Asn Leu Tyr His Gly Ser Trp Thr Val Pro Ile Asp Lys Pro Thr Pro
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Lys Asn Asp Phe His Val Thr Ser Asn Gln Val Gln Leu His Ser Asp
    530                 535                 540

Ile Glu Tyr Thr Glu Glu Asp Asp Glu Ala Ile Val Asn Tyr Ile Lys
545                 550                 555                 560

Glu His Thr Glu Thr Thr Trp His Cys Leu Gly Thr Cys Ser Met Ala
                565                 570                 575

Pro Arg Glu Gly Ser Lys Ile Ala Pro Lys Gly Gly Val Leu Asp Ala
            580                 585                 590

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

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

Ile Gly Glu Lys Ala Ala Thr Leu Val Ala Glu Asp Leu Gly Tyr Ser
625                 630                 635                 640

Gly Ser Asp Leu Asp Met Thr Ile Pro Asn Phe Arg Leu Gly Thr Tyr
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Glu Glu Thr Gly Leu Ala Arg Phe
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<211> 1995
<212> DNA
<213> Ogataea polymorpha

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aacctcaagg ttgcggacct ttctgtttgt cccgacaacg ttggatgcaa cacctactct 1860

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<210> 21
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<212> DNA
<213> Ogataea polymorpha

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<212> PRT
<213> Artificial Sequence

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<222> (3)..(3)
<223> X at position 3 is either F or L

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> X at position 16 is either A or T

<400> 22

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Val Val Ser Ala
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<210> 23
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Leader sequence

<220>
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<223> X at position 3 is either F or L

<220>
<221> MISC_FEATURE

<222> (16)..(16)
<223> X at position 16 is either A or T

<400> 23

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Leu His Lys Arg
        35

<210> 24
<211> 85
<212> PRT
<213> Saccharomyces cerevisiae

<400> 24

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Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
            20   25   30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
        35   40   45

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

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65   70   75   80

Ser Leu Glu Lys Arg
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<210> 25
<211> 1991

<212> DNA
<213> Artificial Sequence

<220>
<223> AOX1 split marker cassette 1

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tgccagcacc accaatctca gaggtacccc taacaaactt aataaaatct tgggtatcaa 180

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ttcgtctcgc tcaggcgcaa tcacgaatga ataacggttt ggttgatgcg agtgattttg 1920

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<212> DNA
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tttcttggta tttcccactc ctcttcagag tacagaagat taagtgagac gttcgtttgt 1200

gcaagcttca acgatgccaa aagggtataa taagcgtcat ttgcagcatt gtgaagaaaa 1260

ctatgtggca agccaagcct gcgaagaatg tattttaagt ttgactttga tgtattcact 1320

tgattaagcc ataattctcg agtatctatg attggaagta tgggaatggt gatacccgca 1380

ttcttcagtg tcttgaggtc tcctatcaga ttatgcccaa ctaaagcaac cggaggagga 1440

gatttcatgg taaatttctc tgacttttgg tcatcagtag actcgaactg tgagactatc 1500

tcggttatga cagcagaaat gtccttcttg gagacagtaa atgaagtccc accaataaag 1560

aaatccttgt tatcaggaac aaacttcttg tttcgaactt tttcggtgcc ttgaactata 1620

aaatgtagag tggatatgtc gggtaggaat ggagcgggca aatgcttacc ttctggacct 1680

tcaagaggta tgtagggttt gtagatactg atgccaactt cagtgacaac gttgctattt 1740

cgttcaaacc attccgaatc cagagaaatc aaagttgttt gtctactatt gatccaagcc 1800

agtgcggtct tgaaactgac aatagtgtgc tcgtgttttg aggtcatctt tgt 1853

<210> 27
<211> 2038

<212> DNA
<213> Artificial Sequence

<220>
<223> AOX2 split marker cassette 1

<400> 27
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cgcagatgat gagcgtggtt gcattgctgg atttgacaac actggtttcg tgctgggaac 120

ttcatcctcg ttgtttaatc agtttattct gcaactgaat acgagtgatc tttcaggagc 180

aatttaccaa atcattgagc attttctgac tggacttagc gaagacgaag acgacattgc 240

tatctattcc cccaaccctt tctacaaaag tacgtatgca ggagtaggtg ccattgcgga 300

aaatgacacc ctttacttgg ttgatggtgg agaggataac caaaacgtcc ctctgcagcc 360

tctacttcaa aaggagcgtg acgttgatat catctttgcg tttgacaaca gtgcagacac 420

tgacctctct tggccaaacg gttcatcatt agtcaacacc tacatgagac agttttcttc 480

tcaagcaaat ggaacaacgt tcccttatgt acctgatacc accactttcc taaacttgaa 540

tctttcgagt aagccaacct tctttggttg tgatgctaga aatttgacag acattgttga 600

aggcacggat cacattcctc ccctggttgt ttatctggcc aatagacctt tctcgtattg 660

gagtaacact tcaactttca agttagacta ctctgaatcc gagaagagag gaatgatcca 720

aaacggtttt gaagtgtcgt ctcgtttgaa catgactatt gatgaagaat ggcgtacttg 780

tgttggatgt gcaatcattc gtagacagca ggagagatcc aatgcaacac aaacagagca 840

atgtagaaga tgttttgaga attattgttg gaacggtgat attgacactt ccaccgaaga 900

tatccccgtt aattttacca ctactggagc aaccaatgag gagaatgaca actccacttc 960

aatatcatcg gccaattcgg tagcaccttc caaactttgg taccaagcac cattgctgtt 1020

ggtcggcctt gtcgcattct tcatctagta cgtacgctgc aggtcgacaa cccttaatat 1080

aacttcgtat aatgtatgct atacgaagtt attaggtcta gatcggtacc gacatggagg 1140

cccagaatac cctccttgac agtcttgacg tgcgcagctc aggggcatga tgtgactgtc 1200

gcccgtacat ttagcccata catccccatg tataatcatt tgcatccata cattttgatg 1260

gccgcacggc gcgaagcaaa aattacggct cctcgctgca gacctgcgag cagggaaacg 1320

ctcccctcac agacgcgttg aattgtcccc acgccgcgcc cctgtagaga aatataaaag 1380

gttaggattt gccactgagg ttcttctttc atatacttcc ttttaaaatc ttgctaggat 1440

acagttctca catcacatcc gaacataaac aaccatgggt aaggaaaaga ctcacgtttc 1500

gaggccgcga ttaaattcca acatggatgc tgatttatat gggtataaat gggctcgcga 1560

taatgtcggg caatcaggtg cgacaatcta tcgattgtat gggaagcccg atgcgccaga 1620

gttgtttctg aaacatggca aaggtagcgt tgccaatgat gttacagatg agatggtcag 1680

actaaactgg ctgacggaat ttatgcctct tccgaccatc aagcatttta tccgtactcc 1740

tgatgatgca tggttactca ccactgcgat ccccggcaaa acagcattcc aggtattaga 1800

agaatatcct gattcaggtg aaaatattgt tgatgcgctg gcagtgttcc tgcgccggtt 1860

gcattcgatt cctgtttgta attgtccttt taacagcgat cgcgtatttc gtctcgctca 1920

ggcgcaatca cgaatgaata acggtttggt tgatgcgagt gattttgatg acgagcgtaa 1980

tggctggcct gttgaacaag tctggaaaga aatgcataag cttttgccat tctcaccg 2038

<210> 28
<211> 1944
<212> DNA
<213> Artificial Sequence

<220>
<223> AOX2 split marker cassette 2

<400> 28
aagcccgatg cgccagagtt gtttctgaaa catggcaaag gtagcgttgc caatgatgtt 60

acagatgaga tggtcagact aaactggctg acggaattta tgcctcttcc gaccatcaag 120

cattttatcc gtactcctga tgatgcatgg ttactcacca ctgcgatccc cggcaaaaca 180

gcattccagg tattagaaga atatcctgat tcaggtgaaa atattgttga tgcgctggca 240

gtgttcctgc gccggttgca ttcgattcct gtttgtaatt gtccttttaa cagcgatcgc 300

gtatttcgtc tcgctcaggc gcaatcacga atgaataacg gtttggttga tgcgagtgat 360

tttgatgacg agcgtaatgg ctggcctgtt gaacaagtct ggaaagaaat gcataagctt 420

ttgccattct caccggattc agtcgtcact catggtgatt tctcacttga taaccttatt 480

tttgacgagg ggaaattaat aggttgtatt gatgttggac gagtcggaat cgcagaccga 540

taccaggatc ttgccatcct atggaactgc ctcggtgagt tttctccttc attacagaaa 600

cggctttttc aaaaatatgg tattgataat cctgatatga ataaattgca gtttcatttg 660

atgctcgatg agtttttcta atcagtactg acaataaaaa gattcttgtt ttcaagaact 720

tgtcatttgt atagtttttt tatattgtag ttgttctatt ttaatcaaat gttagcgtga 780

tttatatttt ttttcgcctc gacatcatct gcccagatgc gaagttaagt gcgcagaaag 840

taatatcatg cgtcaatcgt atgtgaatgc tggtcgctat actggtacca ttcgagaacc 900

cttaatataa cttcgtataa tgtatgctat acgaagttat taggtgatat cagatccact 960

tcctcttacg gctttctttc ccaaaaaatc attggggaaa tgtgcccctc atcagagtcc 1020

aatgacccat gaataaagtt tcttgtactg tttaagacga tgaattgcaa cgataatccg 1080

agcagtttac ggggtacatc acgtgctttg catatgatct cggagtcgga tcagttccgg 1140

atgtgatgta ttaccccata gtttcaaact ctaatgcagc cgccaagtgc catacaccct 1200

ccatcaatct atgcttaaag tttttcacca tcgttgggtg gtgatgatga ctcgcttagt 1260

ctctgctgtt cgatattaac tttgtaagga tcgcccttgg atggaaaatt gaggggttgt 1320

aacctgaatt tgcaggctac ttacattgga cttttgagaa ggctggacgg ttgatgaaga 1380

gggctgggtg cagaggaatg gaaaaaaatt tagttgagag gactgcttga aattttagga 1440

aatggagtcc tttaagctga caaaacttca aggatgggga ttttcatgta gctttttcat 1500

gccttcgaca agctaaagga aggtaattga ttctggataa atggatattt gatctgcttt 1560

agcagatgtc aaagttctac tagtgatagt ctggtatctc gtagccttca attgggcgta 1620

tcttactcga agtgttatat ttttagctga cgagacgaag aacgagagag tattgacaca 1680

ttcagaggta agacaatatg tcgtattatc aaaataagta tcgaacctct attaggagcc 1740

tactggctca aatgtgcaac cttagtggtg attgtctctg cttcttgatc acaatctgtc 1800

gtgtttgaga gtgccgatgt atgattttta gtaaatgttt ttcagaaaag gcgctaagta 1860

aataaccagt aagtaataaa taacgtaaaa gtgatttgaa tcataaaaga atcaagatag 1920

aggtcaaagc atagataatc cccc 1944

<210> 29
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 29
ggctggaaat agatgtaggg ag 22

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 30
tcgcatctcc gcaaatttct c 21

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 31
gatcccattc cctatccatg t 21

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 32
ctctcccccc tcgtaatctt 20

<210> 33
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> enhanced green fluorescent protein (eGFP)

<400> 33
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac 60

ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcga tgccacctac 120

ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180

ctcgtgacca ccctgaccta cggcgtgcag tgcttcagcc gctaccccga ccacatgaag 240

cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc 300

ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg 360

gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420

aagctggagt acaactacaa cagccacaac gtctatatca tggccgacaa gcagaagaac 480

ggcatcaagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540

gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac 600

tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc 660

ctgctggagt tcgtgaccgc cgccgggatc actctcggca tggacgagct gtacaagtaa 720

<210> 34
<211> 1830
<212> DNA
<213> Artificial Sequence

<220>
<223> Human serum albumin (HSA) with its native secretion leader

<400> 34
atgaagtggg ttactttcat ctccttgttg ttcttgttct cctcagctta ctccagaggt 60

gttttcagaa gagatgctca caagtccgag gttgctcaca gattcaagga cttgggtgaa 120

gagaacttca aggctttggt tttgatcgct ttcgctcagt acttgcagca gtgtccattc 180

gaggaccacg ttaagttggt taacgaggtt actgagttcg ctaagacttg tgttgctgac 240

gaatccgctg agaactgtga taagtccttg cacactttgt tcggtgacaa gttgtgtact 300

gttgctactt tgagagaaac ttacggtgag atggctgact gttgtgctaa gcaagagcct 360

gagagaaacg agtgtttctt gcaacacaag gacgacaacc caaacttgcc aagattggtt 420

agaccagagg ttgacgttat gtgtactgct ttccacgaca acgaagagac tttcttgaag 480

aagtacttgt acgagatcgc tagaagacac ccatacttct acgctccaga gttgttgttc 540

ttcgctaaga gatacaaggc tgctttcact gagtgttgtc aggctgctga taaggctgct 600

tgtttgttgc caaagttgga cgagttgaga gatgagggta aggcttcttc cgctaagcag 660

agattgaagt gtgcttcctt gcagaagttc ggagagagag cttttaaggc ttgggctgtt 720

gctagattgt cccagagatt cccaaaggct gagttcgctg aggtttccaa gttggttact 780

gacttgacta aggttcacac agagtgttgt cacggtgact tgttggaatg tgctgatgac 840

agagctgact tggctaagta catctgtgag aaccaggatt ccatctcctc caagttgaaa 900

gaatgttgtg agaagccttt gttggagaag tcccactgta tcgctgaggt tgaaaacgac 960

gaaatgccag ctgacttgcc atctttggct gctgacttcg ttgaatccaa ggacgtctgc 1020

aagaactacg ctgaggctaa ggacgttttc ttgggtatgt tcttgtatga gtacgctaga 1080

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ttgaaccagt tgtgtgtctt gcacgaaaag acaccagttt ccgacagagt tactaagtgt 1500

tgtactgaat ccttggttaa cagaagacct tgtttctccg ctttggaggt tgacgagact 1560

tacgttccaa aagagttcaa cgctgagact ttcactttcc acgctgacat ctgtactttg 1620

tccgagaaag agagacagat caagaagcag actgctttgg ttgagttggt taagcacaag 1680

ccaaaggcta caaaagagca gttgaaggct gttatggacg acttcgctgc tttcgttgag 1740

aaatgttgta aggctgacga caaagagact tgtttcgctg aagagggtaa gaagttggtt 1800

gctgcttccc aagctgcttt gggtctgtaa 1830

<210> 35
<211> 1056
<212> DNA
<213> Artificial Sequence

<220>
<223> variable region of a camelid antibody (VHH) with the S. cerevisiae alpha-mating factor leader

<400> 35
atgagattcc catctatttt caccgctgtc ttgttcgctg cctcctctgc attggctgcc 60

cctgttaaca ctaccactga agacgagact gctcaaattc agctgaagc agttatcggt 120

tactctgacc ttgagggtga tttcgacgtc gctgttttgc ctttctctaa ctccactaac 180

aacggtttgt tgttcattaa caccactatc gcttccattg ctgctaagga agagggtgtc 240

tctctcgaga agagacaagc cggtggttca ttaagattgt cctgtgctgc ctctggtaga 300

actttcactt ctttcgcaat gggttggttt agacaagcac ctggaaaaga gagagagttt 360

gttgcttcta tctccagatc cggtacttta actagatacg ctgactctgc caagggtaga 420

ttcactattt ctgttgacaa cgccaagaac actgtttctt tgcaaatgga caaccttaac 480

ccagatgaca ccgcagtcta ttactgtgcc gctgacttgc acagaccata cggtccagga 540

acccaaagat ccgatgagta cgattcttgg ggtcagggaa ctcaagtcac tgtctcttca 600

ggtggtggat ctggtggtgg aggttcaggt ggtggaggat ccggtggtgg tggttctggt 660

ggtggtggat ctggtggagg tgaagttcaa cttgtcgaat ccggtggtgc acttgtccaa 720

cctggtggat ctcttagact ttcttgtgcc gcctccggtt ttcctgttaa ccgttactct 780

atgcgttggt acagacaagc ccctggaaaa gaacgtgaat gggttgccgg aatgtcctca 840

gctggtgaca gatcctccta cgaagattct gtgaagggac gtttcaccat ctccagagat 900

gacgcccgta acaccgttta ccttcaaatg aactccctta agcctgagga tactgccgtc 960

tactattgta acgtgaatgt cggatttgaa tactggggac agggaaccca agttactgtc 1020

tcttccggtg gacatcacca ccaccatcac taatag 1056

<210> 36
<211> 991
<212> DNA
<213> Pichia pastoris

<400> 36
gcaaggcaac tgagaaattg aatagtggtt tcaagcccgc tgacttttg tattatctca 60

atgtcggtgt ttcacagtcc ccagaagggg gctttgcctt caagggagac ggaagagaca 120

tcgtcaaccc tggggagaag tatttcaaat ggcgcaagtt cgctaatttt tacgattaag 180

cagtgctgta tggggtagtt aataaatcgg gaatatcctt ctgacgtgac tgtaacaaat 240

ctctttttac gtggtgcgca tactggacag aggcagagtc tcaatttctt cttttgagac 300

aggctactac agcctgtgat tcctcttggt acttggattt gcttttatct ggctccgttg 360

ggaactgtgc ctgggttttg aagtatcttg tggatgtgtt tctaacactt tttcaatctt 420

cttggagtga gaatgcagga ctttgaacat cgtctagctc gttggtaggt gaaccgtttt 480

accttgcatg tggttaggag ttttctggag taaccaagac cgtcttatca tcgccgtaaa 540

atcgctctta ctgtcgctaa taatcccgct ggaagagaag ttcgaacaga agtagcacgc 600

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cgatcaactt gccggctgtt gctggagaga tgacaccagt tgtggcatgg ccaattggta 720

ttcagccgta ccactgtatg gaaaatgaga ttatcttgtt cttgatctag tttcttgcca 780

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cgcagatacc agagatctgc cgatccttcc ccaacaatag gagcttacta cgccatacat 900

atagcctatc tattttcact ttcgcgtggg tgcttctata taaacggttc cccatcttcc 960

gtttcatact acttgaattt taagcactaa a 991

<210> 37
<211> 864
<212> DNA
<213> Pichia pastoris

<400> 37

ctttctttg ggcaaggaaa aatcaagaaa aagcagaggt taaagttttc aggggaatgg 60

caattgcttt atatatggga gaaagttaac tacgtcggtg ctgtaggcgt agagagcgac 120

tggagaatgc gtgatgaggt cgtctctttt cgccccccct tggcggggta aaaattgcac 180

tactgcagaa ttactacacc cctattccga ggagacggag tgcgacaaaa atggtaaagt 240

tcaccctagt ctgcgacttt taattgacgg acaccggcgt ttacatgcga aaaaaactaa 300

agtgcgcgca tttcacggcc gagggggtc ccacttggga ctgagagggg gtgggatctg 360

aaatcgagga ggtatcaaga ccccccgttt ctcaactccc taatcaaaaa ttacgaagtc 420

ctcgttggaa aggagttaaa ataattaagc ggggtcggac gccataccga ggttatcttg 480

caggcatttt actaatattg gaattcggag ctcaacttgc aaccaggcag ggtttagcta 540

tgtaatcaat gtaatcaata taataaagca ctaccacatc gaaggtttgg gagggaggcc 600

aatagtgtcc cccacagggt gctgatatcg cgattcttgg gtgaggagac acatatttca 660

ctcctctcac caaccaacca agcggctcct cgcaagatga tttatccgat tatccggaca 720

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ttctttttt ttcttcttat tgtc 864

<210> 38
<211> 1000
<212> DNA
<213> Pichia pastoris

<400> 38
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gctagacgaa ggagacttca gaggtgaaaa gtttgcaaga agagagctgc gggaaataaa 120

ttttcaattt aaggacttga gtgcgtccat attcgtgtac gtgtccaact gttttccatt 180

acctaagaaa aacataaaga ttaaaaagat aaacccaatc gggaaacttt agcgtgccgt 240

ttcggattcc gaaaaacttt tggagcgcca gatgactatg gaaagaggag tgtaccaaaa 300

tggcaagtcg ggggctactc accggatagc caatacattc tctaggaacc agggatgaat 360

ccaggttttt gttgtcacgg taggtcaagc attcacttct taggaatatc tcgttgaaag 420

ctacttgaaa tcccattggg tgcggaacca gcttctaatt aaatagttcg atgatgttct 480

ctaagtggga ctctacggct caaacttcta cacagcatca tcttagtagt cccttcccaa 540

aacaccattc taggtttcgg aacgtaacga aacaatgttc ctctcttcac attgggccgt 600

tactctagcc ttccgaagaa ccaataaaag ggaccggctg aaacgggtgt ggaaactcct 660

gtccagttta tggcaaaggc tacagaaatc ccaatcttgt cgggatgttg ctcctcccaa 720

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ttatttctcc tccagatgag actctccttc ttttctccgc tagttatcaa actataaacc 960

tattttacct caaatacctc caacatcacc cacttaaaca 1000

<210> 39
<211> 549
<212> DNA
<213> Pichia pastoris

<400> 39
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tgtttgcatc tcttatcacc acaccatcct cctcatctgg ccttcaattg tggggaacaa 120

ctagcatccc aacaccagac taactccacc cagatgaaac cagttgtcgc ttaccagtca 180

atgaatgttg agctaacgtt ccttgaaact cgaatgatcc cagccttgct gcgtatcatc 240

cctccgctat tccgccgctt gctccaacca tgtttccgcc tttttcgaac aagttcaaat 300

acctatcttt ggcaggactt ttcctcctgc ctttttttagc ctcaggtctc ggttagcctc 360

taggcaaatt ctggtcttca tacctatatc aacttttcat cagatagcct ttgggttcaa 420

aaaagaacta aagcaggatg cctgatatat aaatcccaga tgatctgctt ttgaaactat 480

tttcagtatc ttgattcgtt tacttacaaa caactattgt tgattttatc tggagaataa 540

tcgaacaaa 549

<210> 40

<211> 1000
<212> DNA
<213> Pichia pastoris

<400> 40
attactgttt tgggcaatcc tgttgataag acgcattcta gagttgtttc atgaaagggt 60

tacgggtgtt gattggtttg agatatgcca gaggacagat caatctgtgg tttgctaaac 120

tggaagtctg gtaaggactc tagcaagtcc gttactcaaa aagtcatacc aagtaagatt 180

acgtaacacc tgggcatgac tttctaagtt agcaagtcac caagagggtc ctatttaacg 240

tttggcggta tctgaaacac aagacttgcc tatcccatag tacatcatat tacctgtcaa 300

gctatgctac cccacagaaa taccccaaaa gttgaagtga aaaaatgaaa attactggta 360

acttcacccc ataacaaact taataatttc tgtagccaat gaaagtaaac cccattcaat 420

gttccgagat ttagtatact tgcccctata agaaacgaag gatttcagct tccttacccc 480

atgaacagaa atcttccatt taccccccac tggagagatc cgcccaaacg aacagataat 540

agaaaaaaga aattcggaca aatagaacac tttctcagcc aattaaagtc attccatgca 600

ctccctttag ctgccgttcc atccctttgt tgagcaacac catcgttagc cagtacgaaa 660

gaggaaactt aaccgatacc ttggagaaat ctaaggcgcg aatgagttta gcctagatat 720

ccttagtgaa gggttgttcc gatacttctc cacattcagt catagatggg cagctttgtt 780

atcatgaaga gacggaaacg ggcattaagg gttaaccgcc aaattatata aagacaacat 840

gtccccagtt taaagttttt ctttcctatt cttgtatcct gagtgaccgt tgtgtttaat 900

ataacaagtt cgttttaact taagaccaaa accagttaca acaaattata acccctctaa 960

acactaaagt tcactcttat caaactatca aacatcaaaa 1000

<210> 41
<211> 1000
<212> DNA
<213> Pichia pastoris

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catggcaacg aaaaaggggt cttcattgtt caacatgaat tcgtatccac ctttaatgta 240

gtcataaagc tgctgaagtt ccgaatcagt gatggaactg tctacagtga caatatagga 300

gttctcaatc accttatatc cagtcgaata tatctggata gggtcgggtc tcactgtgga 360

agattcaaat gggttagatc cctgtaattt cagcgatgga gactcagtat gatggggcaa 420

ggaaaacggc aattggatat tcaattggtc aagagatggt atcaaaagcg agtgtgccag 480

ggtagccacg gtagccactg atgctaatct gataattttc atttctggag tgtcaaaaca 540

gtagtgataa aaggctatga aggaggttgt ctaggggctc gcggaggaaa gtgattcaaa 600

cagacctgcc aaaaagagaa aaaagaggga atccctgttc tttccaatgg aaatgacgta 660

actttaactt gaaaaatacc ccaaccagaa gggttcaaac tcaacaagga ttgcgtaatt 720

cctacaagta gcttagagct gggggagaga caactgaagg cagcttaacg ataacgcggg 780

gggattggtg cacgactcga aaggaggtat cttagtcttg taacctcttt tttccagagg 840

ctattcaaga ttcataggcg atatcgatgt ggagaagggt gaacaatata aaaggctgga 900

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<213> Pichia pastoris

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ttatttaatc agataattgt ggggcattgt gacttgactt ttaccaggac ttcaaacctc 240

aaccatttaa acagttatag aagacgtacc gtcacttttg cttttaatgt gatctaaatg 300

tgatcacatg aactcaaact aaaatgatat cttttactgg acaaaaatgt tatcctgcaa 360

acagaaagct ttcttctatt ctaagaagaa catttacatt ggtgggaaac ctgaaaacag 420

aaaataaata ctccccagtg accctatgag caggattttt gcatccctat tgtaggcctt 480

tcaaactcac acctaatatt tcccgccact cacactatca atgatcactt cccagttctc 540

ttcttcccct attcgtacca tgcaaccctt acacgccttt tccatttcgg ttcggatgcg 600

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acccaaattc taccttgata aggtaattga ttaatttcat aaat 704

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ccccgttgtt gagaaaccca gaaaattgaa tgttcaacca atccagacga tcaataagaa 180

aaaaggccca aaggctactt ccaaacctgc tgccgccaaa cctgctcctt caaaagccgg 240

tcccaaggga ggtaagaagg tgagaaagcc aaagaagaca gttgaagaat tggatcagga 300

aatggctgac tactttgaaa ataagaatta gcccaacaaa atatgtacaa gtattatata 360

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atctccggac ttacgagtca aataactatc cgcagttcct tggaactcag actttcttcc 480

ataagcggtc atatcatctt tggactgtgg gaatcctgga cgaatctttg aaatgtcata 540

atcttgctct ctatctccaa gcacagcgtc cggtaaatgc tggttcttct ttctcagatg 600

aatcttggat ttaacaaata aagccgtgcc tatggctaat gtactcaaaa acaaagtctg 660

cttccagaat ttcgcaaacg atggaatgcc atttcctgta aatgtactca ttgaacctat 720

gtttgattaa agttggtgtg aagtcatcaa acgagagtaa aatcagatac tcgtgcaccg 780

gccaaaattg actgagctaa tctctgcagg cttgacatcc gaacacaaca aataggcgac 840

aaatcttaac tatctaatcg taggctatgg tagaactttg tgggggtaga ggaagactac 900

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<213> Pichia pastoris

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tgaataccgt aacatagtga ctattggaag acactgctat catattatat ttcggataaa 180

aatccaaacc ccagaccgac ctcttgagtc tcaactccaa gtcagccgca actttaatta 240

tccgtggatt gggagctagt ttggacaacg catcagtata atataacttt acggttccat 300

tatcagacgc tattgcaaga acttcctttc cattgatctc gccaatgcgg cagtaattga 360

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gcacggtgct aatggtagtt atccaacgga gctgaggtag tcgatatatc tggatatgcc 480

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ttagttaaaa ctatcatcca atcacaagat gcgggctgga aagacttgct cccgaaggat 780

aatcttctgc ttctatctcc cttcctcata tggtttcgca gggctcatgc cccttcttcc 840

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gctccaactt tgcttgttca tacaattctt gatattcaca 1000

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<211> 1000
<212> DNA
<213> Pichia pastoris

<400> 45

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ttgtcatcaa ccacgctgcc gcttgcaaag gagaactgaa catgaaggtt gttagggttt 180

gttatattgg aataagtggt ggatttgttg aaggcgaacg caccaaagct acatccgtcc 240

tgagcacact gtgaatttgt cacggaattg accaagaggt cagacgatcc tgtatcccat 300

tgagccgtta tgctttgtgg gggaaaccct atttctatcg tactaagaaa accaatggtg 360

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agggcaacag caactaacat atcttcattg atgaaacgtt gtgatcggtg tgacttttat 480

agtaaaagct acaactgttt gaaataccaa gatatcattg tgaatggctc aaaagggtaa 540

tacatctgaa aaacctgaag tgtggaaaat tccgatggag ccaactcatg ataacgcaga 600

agtcccattt tgccatcttc tcttggtatg aaacggtaga aaatgatccg agtatgccaa 660

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ggcggacccg ctcacagtca tttcaggaca atcaccacag gaatcaacta cttctcccag 840

tcttccttgc gtgaagcttc aagcctacaa cataacactt cttacttaat ctttgattct 900

cgaattgttt acccaatctt gacaacttag cctaagcaat actctggggt tatatatagc 960

aattgctctt cctcgctgta gcgttcattc catctttcta 1000

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<211> 1001
<212> DNA
<213> Pichia pastoris

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cgatacccga aattttgacg attttaccaa tatgacttga agacaagtct ctcattgaaa 360

ccttattatc gttactaagc aaaacgagct gacaagaagg gaaggtggtc ggtatttcct 420

cgttgttcaa atatatgatt ctcctggcaa tatctgtgat ggcctgttca aaaagtggaa 480

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tgtagatgta ctgattttcc atacgaaact ccaaaatgaa cgaacggaat gccttaatga 660

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ctctatcaaa ggacattgca acaaagtata aacggttgtg agcgggaaaa agatgtgtag 780

gtaattgtcg tagatgagac tgattcagta gaaaacgcgt cctgcactat ttttttcttt 840

cttcattaca tttcctaatc gggacaaaat gaatctaaag acgtggttat gtagtacacg 900

catcgatagg ctatccccat accaaaacac tattttaccc catccttgac aggttataaa 960

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aacggagcgt cacctagagt cagtttccaa gtcaattaca gaaagtttgg aaacagaaga 180

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gaaccttcaa gcttacattg atgattagag caatgatata aacaacaatt gagtgacagg 480

tctactttgt tctcaaaagg ccataaccat ctgtttgcat ctcttatcac cacaccatcc 540

tcctcatctg gccttcaatt gtggggaaca actagcatcc caacaccaga ctaactccac 600

ccagatgaaa ccagttgtcg cttaccagtc aatgaatgtt gagctaacgt tccttgaaac 660

tcgaatgatc ccagccttgc tgcgtatcat ccctccgcta ttccgccgct tgctccaacc 720

atgtttccgc ctttttcgaa caagttcaaa tacctatctt tggcaggact tttcctcctg 780

cctttttag cctcaggtct cggttagcct ctaggcaaat tctggtcttc atacctatat 840

caacttttca tcagatagcc tttgggttca aaaaagaact aaagcaggat gcctgatata 900

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<210> 48
<211> 1000
<212> DNA
<213> Pichia pastoris

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agtgcgtacg ccacttattc ggggccaata gctaaaccca ggtttgctgg cagcaaattc 720

aactgtagat tgaatctctc taacaataat ggtgttcaat cccctggctg gtcacgggga 780

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<211> 1000
<212> DNA
<213> Pichia pastoris

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ccgggtattt ttttaatctt tttagtctaa gatagcctcc ccagatatta ccgagttggg 180

ccatttgggg cggtatcggt ggtatctgat ggtagcgcgt ttttacatgc ctgtgcattg 240

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ggtctcaaca aaatggaact caattatatc ctcatcaccg gaactgtttc gaaaacttca 960

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<211> 350
<212> PRT
<213> Komagataella phaffii

<400> 50

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35 40 45

Asp Leu His Ala Trp Lys Gly Asp Trp Pro Leu Asp Asn Lys Leu Pro
50 55 60

Leu Val Gly Gly His Glu Gly Ala Gly Val Val Val Ala Tyr Gly Glu
65 70 75 80

Asn Val Thr Gly Trp Glu Ile Gly Asp Tyr Ala Gly Ile Lys Trp Leu
85 90 95

Asn Gly Ser Cys Leu Asn Cys Glu Tyr Cys Ile Gln Gly Ala Glu Ser
100 105 110

Ser Cys Ala Lys Ala Asp Leu Ser Gly Phe Thr His Asp Gly Ser Phe
115 120 125

Gln Gln Tyr Ala Thr Ala Asp Ala Thr Gln Ala Ala Arg Ile Pro Lys
130 135 140

Glu Ala Asp Leu Ala Glu Val Ala Pro Ile Leu Cys Ala Gly Ile Thr
145 150 155 160

Val Tyr Lys Ala Leu Lys Thr Ala Asp Leu Arg Ile Gly Gln Trp Val
165 170 175

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Ala Ile Ser Gly Ala Gly Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr
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Ala Lys Ala Leu Gly Leu Arg Val Leu Gly Ile Asp Gly Gly Ala Asp
        195                 200                 205

Lys Gly Glu Phe Val Lys Ser Leu Gly Ala Glu Val Phe Val Asp Phe
    210                 215                 220

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

Gly Pro His Gly Val Ile Asn Val Ser Val Ser Pro His Ala Ile Asn
                245                 250                 255

Gln Ser Val Gln Tyr Val Arg Thr Leu Gly Lys Val Val Leu Val Gly
            260                 265                 270

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

Lys Ser Ile Glu Ile Lys Gly Ser Tyr Val Gly Asn Arg Glu Asp Ser
    290                 295                 300

Ala Glu Ala Ile Asp Leu Phe Thr Arg Gly Leu Val Lys Ala Pro Ile
305                 310                 315                 320

Lys Ile Ile Gly Leu Ser Glu Leu Ala Lys Val Tyr Glu Gln Met Glu
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Ala Gly Ala Ile Ile Gly Arg Tyr Val Val Asp Thr Ser Lys
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<212> DNA
<213> Komagataella phaffii

<400> 51

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<210> 52
<211> 350
<212> PRT
<213> Komagataella pastoris

<400> 52

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Asn Gly Gly Pro Leu Glu Tyr Lys Asp Ile Pro Val Pro Lys Pro Lys
20 25 30

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        35                  40                  45

Asp Leu His Ala Trp Lys Gly Asp Trp Pro Leu Asp Asn Lys Leu Pro
    50                  55                  60

Leu Val Gly Gly His Glu Gly Ala Gly Val Val Val Ala Leu Gly Glu
65                  70                  75                  80

Asn Val Thr Gly Trp Asn Ile Gly Asp Tyr Ala Gly Ile Lys Trp Leu
                85                  90                  95

Asn Gly Ser Cys Leu Asn Cys Glu Tyr Cys Ile Gln Gly Ala Glu Ser
            100                 105                 110

Ser Cys Ala Lys Ala Asp Leu Ser Gly Phe Thr His Asp Gly Ser Phe
        115                 120                 125

Gln Gln Tyr Ala Thr Ala Asp Ala Thr Gln Ala Ala Arg Ile Pro Lys
    130                 135                 140

Glu Val Asp Leu Ala Glu Val Ala Pro Ile Leu Cys Ala Gly Ile Thr
145                 150                 155                 160

Val Tyr Lys Ala Leu Lys Thr Ala Asp Leu Arg Ile Gly Gln Trp Val
                165                 170                 175

Ala Ile Ser Gly Ala Gly Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr
            180                 185                 190

Ala Lys Ala Leu Gly Leu Arg Val Leu Gly Ile Asp Gly Gly Ala Asp
        195                 200                 205

Lys Gly Glu Phe Val Lys Ser Leu Gly Ala Glu Val Tyr Val Asp Phe
    210                 215                 220
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Thr Lys Thr Lys Asp Val Val Ala Glu Val Gln Lys Ala Thr Asn Gly
225                 230                 235                 240


Gly Pro His Gly Val Ile Asn Val Ser Val Ser Pro His Ala Ile Asn
                245                 250                 255


Gln Ser Val Gln Tyr Ala Arg Thr Leu Gly Lys Ile Val Leu Val Gly
            260                 265                 270


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


Lys Ser Ile Glu Ile Lys Gly Ser Tyr Val Gly Asn Arg Glu Asp Ser
    290                 295                 300


Ala Glu Ala Ile Asp Leu Phe Ala Arg Gly Leu Val Lys Ala Pro Ile
305                 310                 315                 320


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


Ala Gly Ala Ile Ile Gly Arg Tyr Val Val Asp Thr Ser Lys
            340                 345                 350


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aacaagcttc ctttggtcgg tggtcacgaa ggtgctggtg tcgttgtcgc tttaggtgag      240

aacgtcactg gatggaacat cggtgactac gctggtatca aatggttgaa cggttcttgt      300

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<210> 54
<211> 349
<212> PRT
<213> Ogataea parapolymorpha

<400> 54

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

Asn Glu Ile Leu Val Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp
35 40 45

Leu His Ala Trp Lys Gly Asp Trp Pro Leu Asp Thr Lys Leu Pro Leu
50 55 60

Val Gly Gly His Glu Gly Ala Gly Val Val Val Ala Lys Gly Ala Asn
65 70 75 80

```
Val Thr Asn Phe Glu Ile Gly Asp Tyr Ala Gly Ile Lys Trp Leu Asn
                85                  90                  95

Gly Ser Cys Met Gly Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro Asn
            100                 105                 110

Cys Pro Glu Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe Gln
        115                 120                 125

Gln Tyr Ala Thr Ala Asp Ala Val Gln Ala Ala Lys Ile Pro Lys Gly
    130                 135                 140

Thr Asn Leu Ala Asp Val Ala Pro Ile Leu Cys Ala Gly Val Thr Val
145                 150                 155                 160

Tyr Lys Ala Leu Lys Thr Ala Glu Leu Ser Pro Gly Gln Trp Val Ala
                165                 170                 175

Ile Ser Gly Ala Gly Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala
            180                 185                 190

Val Ala Met Gly Leu Arg Val Leu Gly Ile Asp Gly Gly Asp Glu Lys
        195                 200                 205

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

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

Pro His Gly Val Ile Asn Val Ser Val Ser Pro Ala Ala Ile Ser Gln
                245                 250                 255

Ser Cys Gln Tyr Val Arg Thr Leu Gly Lys Val Val Leu Val Gly Leu
            260                 265                 270
```

```
Pro Ala Gly Ala Val Cys Glu Ser Pro Val Phe Glu His Val Ile Lys
        275                 280                 285

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

Glu Ser Ile Asp Phe Phe Val Arg Gly Lys Val Lys Ala Pro Ile Lys
305                 310                 315                 320

Val Val Gly Leu Ser Glu Leu Pro Lys Val Phe Glu Leu Met Glu Gln
                325                 330                 335

Gly Lys Ile Ala Gly Arg Tyr Val Leu Asp Thr Ser Lys
            340                 345
```

<210> 55
<211> 1050
<212> DNA
<213> Ogataea parapolymorpha

<400> 55

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atgacttcca ttccaaagac tcaaaaggcc gttgttttcg agaccaacgg tggtcctctt       60

ctctacaagg acatccctgt tccacaacca aagccaaatg agattcttgt caacgtcaag      120

tactccggtg tttgccacac cgatctccac gcttggaagg gtgactggcc attggacacc      180

aaacttccac tggtcggtgg tcacgagggt gctggtgttg ttgttgctaa gggtgccaac      240

gttaccaact ttgaaatcgg tgactacgct ggtatcaaat ggttgaacgg ctcgtgcatg      300

ggttgtgagt tctgtcaaca aggtgcagag ccaaactgtc ctgaggccga cctttccggt      360

tacacgcacg acggttcttt ccaacaatac gccactgctg atgctgtcca ggctgccaag      420

attccaaagg gaactaacct ggctgacgtt gctccaattc tctgtgctgg tgtcactgtg      480

tacaaggcat tgaagactgc cgaattgagc ccaggccaat gggttgctat ctctggtgct      540

ggtggaggat tgggttctct tgccgttcaa tacgctgtcg ccatgggcct gagagtcctg      600

ggtatcgatg gtggtgacga aaaggctaag ctcttcgaga gcttgggcgg agaagtcttc      660

atcgatttca ccaaggaaaa ggacattgtc ggagccgtcc agaaggcaac caacggtggt      720
```

ccacacggtg ttatcaacgt ttctgtgtct ccagcagcta tctctcaatc ctgccaatac 780

gtgagaactc ttggtaaggt tgttcttgtt ggtcttccag ccggtgctgt ttgcgagtct 840

ccagttttcg agcacgttat caagtctatc cagattagag gttcctacgt tggtaacaga 900

caggacactg ccgagtcgat tgacttcttc gtcagaggca aggttaaggc tccaatcaag 960

gttgttggcc tttctgagct gccaaaggtg ttcgagttga tggagcaagg aaagattgct 1020

ggaagatacg ttcttgacac ttccaaatag 1050

<210> 56
<211> 382
<212> PRT
<213> Ogataea parapolymorpha

<400> 56

Met Met Ser Ile Ser Arg Val Ala Ala Leu Arg Asn Gln Phe Ala Arg
1 5 10 15

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

Ser Ala Pro Thr Ile Pro Lys Thr Gln Met Gly Cys Val Phe Glu Thr
35 40 45

Asn Gly Gly Pro Ile Glu Tyr Lys Glu Ile Pro Val Pro Lys Pro Lys
50 55 60

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

Asp Leu His Ala Trp Lys Gly Asp Trp Pro Leu Pro Val Lys Leu Pro
85 90 95

Leu Val Gly Gly His Glu Gly Ala Gly Val Val Val Ala Lys Gly Glu
100 105 110

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

```
Asn Gly Ser Cys Met Gly Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro
    130                 135                 140

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

Gln Gln Tyr Ala Thr Ala Asp Ala Val Gln Ala Ala Lys Leu Pro Pro
                165                 170                 175

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

Val Tyr Lys Ala Leu Lys Thr Ala Ala Leu Arg Pro Gly Gln Ile Val
        195                 200                 205

Ala Ile Ser Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr
    210                 215                 220

Ala Val Ala Met Gly Leu Arg Val Leu Gly Ile Asp Gly Gly Glu Gln
225                 230                 235                 240

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

Thr Lys Glu Lys Asp Ile Val Ser Ala Ile Gln Lys Ile Thr Asn Gly
            260                 265                 270

Gly Pro His Gly Val Ile Asn Val Ser Val Ser Pro Ala Ala Ile Ser
        275                 280                 285

Gln Ser Cys Gln Tyr Val Arg Thr Leu Gly Lys Val Val Leu Val Gly
    290                 295                 300

Leu Pro Ala Gly Ala Val Cys Glu Ser Pro Val Phe Glu His Val Val
305                 310                 315                 320
```

```
Lys Ser Ile Gln Ile Lys Gly Ser Tyr Val Gly Asn Arg Gln Asp Thr
                325                 330                 335

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

Gln Ile Ala Gly Leu Ser Glu Leu Pro Glu Val Phe Lys Lys Met Glu
        355                 360                 365

Glu Gly Lys Ile Leu Gly Arg Tyr Val Leu Asp Thr Ser Lys
    370                 375                 380
```

<210> 57
<211> 1149
<212> DNA
<213> Ogataea parapolymorpha

<400> 57

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atgatgtcta tttcgagagt tgctgctttg agaaaccaat ttgctcggct agccaagccc       60

gctgttgtcc agcaggtctt cagacactct actgcctctg ctccaaccat cccaaagacc      120

cagatgggat gtgtttttga aaccaacggt ggtccaattg agtacaagga gatccctgtt      180

ccaaagccaa agcctaacga gattttggtc cacgtcaagt actctggtgt gtgccacact      240

gacttgcacg cctggaaggg tgactggcca ctgcctgtca aactcccact tgtgggtggt      300

cacgagggtg ccggtgttgt cgttgccaag ggtgagaacg ttaaaaactt cgagatcggc      360

gacttggccg gtatcaagtg gctgaacggc tcgtgtatgg gttgtgagtt ctgtcaacag      420

ggtgccgaac caaactgtcc agacgctgac ctgtccggtt acacgcacga cggttctttc      480

caacaatacg ccactgctga cgctgtccag gccgctaagc tgcctcctgg aactgacctc      540

gctgctgttg ctcctatttt gtgtgctggt gtcactgttt acaaggcctt gaagactgct      600

gctctgcgtc caggacagat cgttgccatt tccggtgccg ccggtggatt gggttctctt      660

gccgttcaat acgctgtcgc catgggcctg agagttctgg gtattgacgg tggtgagcaa      720

aagggcgagt tcatcaagaa gctcggtgcc gaattctacg tcgacttcac caaggagaag      780

gacattgtgt ctgccatcca gaagatcacc aacggcggtc cacacggtgt catcaacgtt      840
```

tctgtctctc cagctgctat ctcccagtct tgtcaatacg tgagaaccct cggtaaggtt 900

gttctggtcg gtcttccagc cggcgctgtt tgcgagtctc ctgtctttga gcacgtcgtc 960

aagtccatcc agatcaaggg atcttacgtt ggtaacagac aagacactgc cgaggccgtg 1020

gacttcttca ccagaggcct tgtcaagtct ccattccaga ttgctggtct ttccgagctg 1080

ccagaggtct tcaagaagat ggaggagggc aagatcttgg gcagatacgt ccttgacact 1140

tctaaatag 1149

<210> 58
<211> 349
<212> PRT
<213> Ogataea polymorpha

<400> 58

Met Pro Ser Ile Pro Lys Thr Gln Lys Ala Ile Val Phe Glu Thr Asn
1 5 10 15

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

Asn Glu Ile Leu Val Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp
35 40 45

Leu His Ala Trp Lys Gly Asp Trp Pro Leu Ala Thr Lys Leu Pro Leu
50 55 60

Val Gly Gly His Glu Gly Ala Gly Val Val Val Ala Lys Gly Ala Asn
65 70 75 80

Val Thr Asn Phe Glu Ile Gly Asp Tyr Ala Gly Ile Lys Trp Leu Asn
85 90 95

Gly Ser Cys Met Gly Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro Asn
100 105 110

Cys Pro Asp Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe Gln
115 120 125

```
Gln Tyr Ala Thr Ala Asp Ala Val Gln Ala Ala Lys Ile Pro Lys Gly
    130                 135                 140

Thr Asn Leu Ala Asp Val Ala Pro Ile Leu Cys Ala Gly Val Thr Val
145                 150                 155                 160

Tyr Lys Ala Leu Lys Thr Ala Glu Leu Ser Pro Gly Gln Trp Val Ala
                165                 170                 175

Ile Ser Gly Ala Gly Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala
            180                 185                 190

Val Ala Met Gly Leu Arg Val Leu Gly Ile Asp Gly Gly Asp Glu Lys
        195                 200                 205

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

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

Pro His Gly Val Ile Asn Val Ser Val Ser Pro Ala Ala Ile Ser Gln
                245                 250                 255

Ser Cys Gln Tyr Val Arg Thr Leu Gly Lys Val Val Leu Val Gly Leu
            260                 265                 270

Pro Ala Gly Ala Val Cys Glu Ser Pro Val Phe Glu His Val Ile Lys
        275                 280                 285

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

Glu Ser Ile Asp Phe Phe Val Arg Gly Lys Val Lys Ala Pro Ile Lys
305                 310                 315                 320
```

Val Val Gly Leu Ser Glu Leu Pro Lys Val Phe Glu Leu Met Glu Gln
325 330 335

Gly Lys Ile Ala Gly Arg Tyr Val Leu Asp Thr Ser Lys
340 345

<210> 59
<211> 1050
<212> DNA
<213> Ogataea polymorpha

<400> 59
atgccttcca ttccaaagac tcaaaaggcc attgttttcg aaaccaacgg tggtcctctt 60

ctatacaagg acatccctgt tccacagcca aagccaaatg aaatccttgt caacgtcaag 120

tactctggtg tgtgccacac cgacttgcac gcctggaagg gtgactggcc attggccacc 180

aaacttccac tggtcggtgg tcacgagggt gctggtgttg ttgttgccaa gggtgccaac 240

gttaccaact ttgagatcgg cgactacgct ggtatcaaat ggctgaacgg ctcgtgtatg 300

ggttgtgagt tctgtcaaca aggtgcagaa ccaaactgtc cagacgccga cctttccggt 360

tacacgcacg acggttcctt ccaacaatac gccactgctg atgctgtcca ggctgccaag 420

attccaaagg gaactaacct ggccgatgtt gctccaattc tctgtgctgg tgtcactgtg 480

tacaaggcat tgaagactgc cgaattgagc ccaggccagt gggtcgctat ctctggtgct 540

ggtggaggat tgggttctct tgccgttcaa tacgctgtcg ctatgggcct gagagttctg 600

ggtatcgatg gtggtgacga aaaggccaag ctcttcgaga gcttgggcgg agaagtcttc 660

atcgatttca caaaggaaaa ggacattgtc ggagccgtcc agaaggctac caacggtggt 720

ccacacggtg tcatcaacgt ttccgtgtct ccagcagcta tctctcaatc ctgccaatac 780

gtgagaactc ttggtaaggt tgttcttgtt ggtcttccag caggtgctgt ttgcgagtct 840

ccagttttcg agcacgttat caagtctatc cagattagag gttcctacgt tggtaacaga 900

caggacactg cggagtcgat cgacttcttc gtcagaggca aggttaaggc tccaatcaag 960

gttgttggtc tttctgagct gccaaaagtg ttcgagttga tggagcaagg aaagattgca 1020

ggaagatacg tcctcgacac ttccaaatag 1050

<210> 60
<211> 381
<212> PRT
<213> Ogataea polymorpha

<400> 60

Met Ser Ile Ser Arg Val Ala Ala Leu Arg Asn Gln Phe Ala Arg Leu
1   5   10   15

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

Ala Pro Thr Ile Pro Lys Thr Gln Met Gly Cys Val Phe Glu Thr Asn
        35   40   45

Gly Gly Pro Ile Glu Tyr Lys Glu Ile Pro Val Pro Lys Pro Lys Pro
    50   55   60

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

Leu His Ala Trp Lys Gly Asp Trp Pro Leu Pro Val Lys Leu Pro Leu
                85   90   95

Val Gly Gly His Glu Gly Ala Gly Val Val Val Ala Lys Gly Glu Asn
            100   105   110

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

Gly Ser Cys Met Gly Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro Asn
    130   135   140

Cys Pro Asp Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe Gln
145   150   155   160

Gln Tyr Ala Thr Ala Asp Ala Val Gln Ala Ala Lys Leu Pro Pro Gly
                165   170   175

```
Thr Asp Leu Ala Ala Val Ala Pro Ile Leu Cys Ala Gly Val Thr Val
            180                 185                 190

Tyr Lys Ala Leu Lys Thr Ala Ala Leu Arg Pro Gly Gln Ile Val Ala
        195                 200                 205

Ile Ser Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala
    210                 215                 220

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

Gly Glu Phe Ile Lys Lys Leu Gly Ala Glu Phe Tyr Val Asp Phe Thr
                245                 250                 255

Lys Glu Lys Asp Ile Val Ser Ala Ile Gln Lys Val Thr Asn Gly Gly
            260                 265                 270

Pro His Gly Val Ile Asn Val Ser Val Ser Pro Ala Ala Ile Ser Gln
        275                 280                 285

Ser Cys Gln Tyr Val Arg Thr Leu Gly Lys Val Val Leu Val Gly Leu
    290                 295                 300

Pro Ala Gly Ala Val Cys Glu Ser Pro Val Phe Glu His Val Val Lys
305                 310                 315                 320

Ser Ile Gln Ile Lys Gly Ser Tyr Val Gly Asn Arg Gln Asp Thr Ala
                325                 330                 335

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

Ile Ala Gly Leu Ser Glu Leu Pro Glu Val Phe Lys Lys Met Glu Glu
        355                 360                 365
```

Gly Lys Ile Leu Gly Arg Tyr Val Leu Asp Thr Ser Lys
370 375 380

<210> 61
<211> 1146
<212> DNA
<213> Ogataea polymorpha

<400> 61
atgtctattt cgagagttgc tgcattgaga aaccaatttg ctcgtctagc caagccggct 60

gtagtccagc aggtcttcag acactccact gcctctgctc caaccatccc aaagacccag 120

atgggatgtg tttttgaaac caacggcggt ccaattgagt acaaggagat cccagttcca 180

aagccaaagc caaacgagat tctggtccac gtcaagtact ctggtgtgtg ccacaccgac 240

ttgcacgcct ggaagggtga ctggccactg cctgtcaaac tcccacttgt gggtggtcac 300

gagggtgccg gtgttgtcgt tgccaagggt gagaacgtta aaaacttcga gatcggcgac 360

ttggccggta tcaaatggct gaacggctcg tgtatgggtt gtgagttctg tcaacagggt 420

gccgaaccaa actgtcctga cgccgacctt tccggttaca cacacgacgg ttctttccaa 480

caatacgcca ctgctgacgc tgtccaggcc gctaagctgc ctccaggaac tgacctcgct 540

gctgttgctc caattttgtg tgctggtgtg actgtttaca aggccttgaa gactgctgct 600

ttgcgtccag gtcagattgt tgctatttcc ggtgccgccg gtggattggg ttctcttgcc 660

gttcaatacg ctgtcgccat gggtctgaga gttctgggta ttgacggtgg tgagcagaag 720

ggcgagttca tcaagaagct cggtgccgaa ttctacgtcg acttcaccaa ggagaaggac 780

attgtgtctg ccatccagaa ggtcaccaat ggcggtccac acggtgtcat caacgtgtct 840

gtgtctccag ctgctatctc ccagtcttgt caatacgtga gaaccctcgg taaggttgtt 900

ctggttggtc ttccagccgg cgctgtttgc gaatctcctg tctttgagca cgtcgtcaag 960

tccatccaga tcaagggatc ttatgttggt aacagacaag acactgccga ggccgtggac 1020

ttcttcacca gaggccttgt ccgttctcca ttccaaattg ccggtctttc cgagctgcct 1080

gaggtcttca agaagatgga ggagggcaag atcttgggta gatatgtcct tgacacttct 1140

aaataa 1146

<210> 62
<211> 348
<212> PRT
<213> Saccharomyces cerevisiae

<400> 62

Met Ser Ile Pro Glu Thr Gln Lys Ala Ile Ile Phe Tyr Glu Ser Asn
1 5 10 15

Gly Lys Leu Glu Tyr Lys Asp Ile Pro Val Pro Lys Pro Lys Ala Asn
20 25 30

Glu Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp Leu
35 40 45

His Ala Trp His Gly Asp Trp Pro Leu Pro Val Lys Leu Pro Leu Val
50 55 60

Gly Gly His Glu Gly Ala Gly Val Val Val Gly Met Gly Glu Asn Val
65 70 75 80

Lys Gly Trp Lys Ile Gly Asp Tyr Ala Gly Ile Lys Trp Leu Asn Gly
85 90 95

Ser Cys Met Ala Cys Glu Tyr Cys Glu Leu Gly Asn Glu Ser Asn Cys
100 105 110

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

Tyr Ala Thr Ala Asp Ala Val Gln Ala Ala His Ile Pro Gln Gly Thr
130 135 140

Asp Leu Ala Glu Val Ala Pro Val Leu Cys Ala Gly Ile Thr Val Tyr
145 150 155 160

Lys Ala Leu Lys Ser Ala Asn Leu Arg Ala Gly His Trp Val Ala Ile
165 170 175

```
Ser Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala Lys
            180                 185                 190

Ala Met Gly Tyr Arg Val Leu Gly Ile Asp Gly Gly Pro Gly Lys Glu
        195                 200                 205

Glu Leu Phe Thr Ser Leu Gly Gly Glu Val Phe Ile Asp Phe Thr Lys
    210                 215                 220

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

His Gly Ile Ile Asn Val Ser Val Ser Glu Ala Ala Ile Glu Ala Ser
                245                 250                 255

Thr Arg Tyr Cys Arg Ala Asn Gly Thr Val Val Leu Val Gly Leu Pro
            260                 265                 270

Ala Gly Ala Lys Cys Ser Ser Asp Val Phe Asn His Val Val Lys Ser
        275                 280                 285

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

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

Val Gly Leu Ser Ser Leu Pro Glu Ile Tyr Glu Lys Met Glu Lys Gly
                325                 330                 335

Gln Ile Ala Gly Arg Tyr Val Val Asp Thr Ser Lys
            340                 345
```

<210> 63
<211> 1047
<212> DNA
<213> Saccharomyces cerevisiae

<400> 63
atgtctattc cagaaactca aaaagccatt atcttctacg agtccaacgg taagttggaa 60

tacaaagata ttccagttcc aaagccaaag gccaacgaat tgttgatcaa cgttaaatac 120

tctggtgtct gtcacactga cttgcacgct tggcacggtg actggccatt gccagttaag 180

ctaccattag tcggtggtca cgaaggtgcc ggtgtcgttg tcggcatggg tgaaaacgtt 240

aagggctgga agatcggtga ctacgccggt atcaaatggt tgaacggttc ttgtatggcc 300

tgtgaatact gtgaattggg taacgaatcc aactgtcctc acgctgactt gtctggttac 360

acccacgacg gttctttcca acaatacgct accgctgacg ctgttcaagc cgctcacatt 420

cctcaaggta ctgacttggc tgaagtcgcc ccagttttgt gtgctggtat caccgtctac 480

aaggctttga agtctgccaa cttgagagca ggccactggg tggccatttc tggtgctgct 540

ggtggtctag gttctttggc tgttcaatat gctaaggcga tgggttacag agtcttaggt 600

attgatggtg gtccaggaaa ggaagaattg tttacctcgc tcggtggtga agtattcatc 660

gacttcacca aagagaagga cattgttagc gcagtcgtta aggctaccaa cggcggtgcc 720

cacggtatca tcaatgtttc cgtttccgaa gccgctatcg aagcttctac cagatactgt 780

agggcgaacg gtactgttgt cttggttggt ttgccagccg gtgcaaagtg ctcctctgat 840

gtcttcaacc acgttgtcaa gtctatctcc attgtcggct cttacgtggg gaacagagct 900

gataccagag aagccttaga tttctttgcc agaggtctag tcaagtctcc aataaaggta 960

gttggcttat ccagtttacc agaaatttac gaaaagatgg agaagggcca aattgctggt 1020

agatacgttg ttgacacttc taaataa 1047

<210> 64
<211> 349
<212> PRT
<213> Candida maltosa

<400> 64

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

```
Gly Gly Lys Leu Glu Tyr Lys Asp Ile Pro Val Pro Lys Pro Lys Pro
            20                  25                  30

Asn Glu Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp
        35                  40                  45

Leu His Ala Trp Lys Gly Asp Trp Pro Leu Ala Thr Lys Leu Pro Leu
    50                  55                  60

Val Gly Gly His Glu Gly Ala Gly Val Val Val Ala Ile Gly Asp Asn
65                  70                  75                  80

Val Lys Asn Trp Lys Val Gly Asp Phe Ala Gly Val Lys Trp Leu Asn
                85                  90                  95

Gly Ser Cys Leu Asn Cys Glu Tyr Cys Gln Gln Gly Ala Glu Pro Asn
            100                 105                 110

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

Gln Tyr Ala Thr Ala Asp Ala Val Gln Ala Ala Arg Ile Pro Ala Gly
    130                 135                 140

Thr Asp Leu Ala Thr Val Ala Pro Ile Leu Cys Ala Gly Val Thr Val
145                 150                 155                 160

Tyr Lys Ala Leu Lys Thr Ala Asn Leu Gln Pro Gly Gln Trp Val Ala
                165                 170                 175

Ile Ser Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala
            180                 185                 190

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

Gly Gln Phe Val Lys Ser Leu Gly Ala Glu Thr Phe Ile Asp Phe Thr
    210                 215                 220
```

```
Lys Glu Lys Asp Val Val Gly Ala Val Gln Lys Ala Thr Asn Gly Gly
225                 230                 235                 240


Pro His Gly Val Ile Asn Val Ser Val Ser Asp Arg Ala Ile Asn Gln
                245                 250                 255


Ser Val Glu Tyr Val Arg Thr Leu Gly Lys Val Val Leu Val Gly Leu
            260                 265                 270


Pro Ala Gly Ala Lys Val Thr Ala Pro Val Phe Asp Ser Val Val Lys
        275                 280                 285


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


Glu Ala Val Asp Phe Phe Ser Arg Gly Leu Ile Lys Cys Pro Ile Lys
305                 310                 315                 320


Ile Val Gly Leu Ser Glu Leu Pro Glu Val Tyr Lys Leu Met Glu Glu
                325                 330                 335


Gly Lys Ile Leu Gly Arg Tyr Val Leu Asp Thr Ser Lys
            340                 345


<210>  65
<211>  1050
<212>  DNA
<213>  Candida maltosa

<400>  65
atgtcttcta ttccaactac tcaaaaagct attatcttcg aaaccaacgg cggtaaatta       60

gaatacaaag atatcccagt cccaaaacca aaaccaaatg aattgttgat caatgttaaa      120

tactccggtg tttgtcacac tgatttgcac gcttggaaag gtgattggcc attagccacc      180

aaattaccat tggtcggtgg tcacgaaggt gctggtgttg tcgttgctat tggtgacaat      240

gtcaagaact ggaaagttgg tgatttcgcc ggtgtcaaat ggttgaatgg ttcttgtttg      300
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aactgtgaat actgtcaaca aggtgctgaa ccaaactgtg ctcaagctga cttgtccggt 360

tacacccacg atggttcttt ccaacaatac gccactgccg atgcagttca agcggctaga 420

attccagctg gtactgattt agccaccgtt gctccaatct tgtgtgctgg tgttaccgtt 480

tacaaggctt tgaagactgc caacttacaa ccaggtcaat gggttgccat ttccggtgcc 540

gctggtggtt taggttcttt ggctgttcaa tacgctaaag ctatgggtta cagagtcttg 600

gccattgacg gtggtgaaga taaaggtcaa tttgttaaat ctttgggtgc tgaaactttt 660

atcgatttta ccaaagaaaa ggatgttgtt ggtgctgtcc aaaaagctac caacggtggt 720

ccacatggtg tcattaacgt ctctgtttcc gacagagcta tcaaccaatc cgttgaatac 780

gttagaactt taggtaaagt tgttttggtt ggtttaccag ctggtgctaa agtcactgct 840

ccagtctttg actccgtcgt taaatccatt gaaattaaag gttcttatgt tggtaacaga 900

aaagacactg ccgaagccgt tgatttcttc tctagaggtt tgattaaatg tccaatcaag 960

attgttggtt tatctgaatt accagaagtt tacaaattga tggaagaagg taaaatcttg 1020

ggtagatacg ttttggacac ctccaaataa 1050

<210> 66
<211> 379
<212> PRT
<213> Kluyveromyces marxianus

<400> 66

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

Ala Leu Gly Gly Ser Arg Arg Leu Phe Val Arg Leu Asn Ser Ser Phe
20 25 30

Ala Ile Pro Glu Ser Gln Lys Gly Val Ile Phe Tyr Glu Asn Gly Gly
35 40 45

Lys Leu Glu Tyr Lys Asp Leu Pro Val Pro Lys Pro Lys Pro Asn Glu
50 55 60

```
Ile Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp Leu His
65                  70                  75                  80

Ala Trp Lys Gly Asp Trp Pro Leu Pro Val Lys Leu Pro Leu Val Gly
                85                  90                  95

Gly His Glu Gly Ala Gly Val Val Val Ala Lys Gly Glu Asn Val Thr
            100                 105                 110

Asn Phe Glu Ile Gly Asp Tyr Ala Gly Ile Lys Trp Leu Asn Gly Ser
        115                 120                 125

Cys Met Ser Cys Glu Leu Cys Glu Gln Gly Tyr Glu Ser Asn Cys Leu
    130                 135                 140

Gln Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe Gln Gln Tyr
145                 150                 155                 160

Ala Thr Ala Asp Ala Val Gln Ala Ala Gln Ile Pro Lys Gly Thr Asp
                165                 170                 175

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

Ala Leu Lys Thr Ala Asp Leu Gln Pro Gly Gln Trp Ile Ala Ile Ser
        195                 200                 205

Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala Lys Ala
    210                 215                 220

Met Gly Leu Arg Val Leu Gly Ile Asp Gly Gly Pro Gly Lys Glu Glu
225                 230                 235                 240

Leu Phe Lys Ser Leu Gly Gly Glu Val Phe Ile Asp Phe Thr Lys Ser
                245                 250                 255

Lys Asp Met Val Ala Asp Ile Gln Glu Ala Thr Asn Gly Gly Pro His
            260                 265                 270
```

```
Gly Val Ile Asn Val Ser Val Ser Glu Ala Ala Ile Ser Met Ser Thr
        275                 280                 285

Glu Tyr Val Arg Pro Thr Gly Val Val Val Leu Val Gly Leu Pro Ala
    290                 295                 300

His Ala Tyr Val Lys Ser Glu Val Phe Ser His Val Val Lys Ser Ile
305                 310                 315                 320

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

Ile Asp Phe Phe Thr Arg Gly Leu Val Lys Ser Pro Ile Lys Val Val
            340                 345                 350

Gly Leu Ser Glu Leu Pro Lys Val Tyr Glu Leu Met Glu Ala Gly Lys
        355                 360                 365

Ile Leu Gly Arg Tyr Val Val Asp Thr Ser Lys
    370                 375
```

<210> 67
<211> 1140
<212> DNA
<213> Kluyveromyces marxianus

<400> 67

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atgttcagac tagcacgcgc tcagaccagc attaccacca ctagcaaggc tctaggtggc       60

tccagaagac tattcgtcag actaaactcc tctttcgcca tcccagaatc ccaaaagggt      120

gtgattttct acgaaaacgg cggtaagttg gaatacaagg accttccagt tccaaagcca      180

aagccaaatg aaatcttgat caacgtcaag tactccggtg tgtgtcacac tgatttgcac      240

gcctggaagg gtgactggcc attgccagtt aagttgcctt tggtcggtgg tcacgaaggt      300

gccggtgtcg tcgttgccaa gggtgaaaac gttaccaact tcgagatcgg tgactacgca      360

ggtatcaagt ggttgaacgg ttcttgtatg tcttgtgaac tctgtgaaca aggttacgaa      420
```

tccaactgtt tgcaagctga cttgtctggt tacacccacg acggttcctt ccaacaatat 480

gccactgctg acgctgttca agctgcccaa attccaaagg gtaccgattt ggctgaaatc 540

gccccaatct tgtgtgccgg tgtcaccgtc tacaaggctc taaagaccgc tgacttgcaa 600

ccaggtcaat ggatcgctat ctccggtgct gccggtggtc ttggttccct agccgtgcaa 660

tacgccaagg caatgggtct aagagttcta ggtatcgacg gtggtccagg taaggaagaa 720

ttgttcaaga gcttgggtgg tgaagtcttc attgacttca caaagtccaa ggacatggtc 780

gcagacatcc aggaagccac caacggtggt cctcacggtg tgatcaacgt ctccgtctcc 840

gaggccgcta tctccatgtc caccgagtac gtcagaccaa ccggtgtggt cgttctagtc 900

ggtttgccag cccacgctta cgtcaagtcc gaagtcttct cccacgtcgt caagtctatc 960

tctattaagg gttcttacgt cggtaacaga gcagacacca gagaagctat tgacttcttc 1020

accagaggtt tggtcaagtc tccaatcaag gttgttggtt tgtctgaatt gccaaaggtt 1080

tatgaattga tggaagctgg taagatcttg ggtagatacg tcgttgacac ttccaaataa 1140

<210> 68
<211> 350
<212> PRT
<213> Escherichia coli

<400> 68

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

Asn Gly Gly Gln Leu Val Tyr Lys Asp Tyr Pro Val Pro Thr Pro Lys
20 25 30

Pro Asn Glu Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr
35 40 45

Asp Leu His Ala Trp Lys Gly Asp Trp Pro Leu Ala Thr Lys Leu Pro
50 55 60

Leu Val Gly Gly His Glu Gly Ala Gly Val Val Val Gly Met Gly Glu
65 70 75 80

```
Asn Val Lys Gly Trp Lys Ile Gly Asp Phe Ala Gly Ile Lys Trp Leu
                85                  90                  95

Asn Gly Ser Cys Met Ser Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro
            100                 105                 110

Asn Cys Gly Glu Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe
        115                 120                 125

Glu Gln Tyr Ala Thr Ala Asp Ala Val Gln Ala Ala Lys Ile Pro Ala
    130                 135                 140

Gly Thr Asp Leu Ala Asn Val Ala Pro Ile Leu Cys Ala Gly Val Thr
145                 150                 155                 160

Val Tyr Lys Ala Leu Lys Thr Ala Asp Leu Ala Ala Gly Gln Trp Val
                165                 170                 175

Ala Ile Ser Gly Ala Gly Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr
            180                 185                 190

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

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

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

Gly Pro His Gly Ala Ile Asn Val Ser Val Ser Glu Lys Ala Ile Asp
                245                 250                 255

Gln Ser Val Glu Tyr Val Arg Pro Leu Gly Lys Val Val Leu Val Gly
            260                 265                 270
```

```
Leu Pro Ala His Ala Lys Val Thr Ala Pro Val Phe Asp Ala Val Val
        275                 280                 285

Lys Ser Ile Glu Ile Lys Gly Ser Tyr Val Gly Asn Arg Lys Asp Thr
    290                 295                 300

Ala Glu Ala Ile Asp Phe Phe Ser Arg Gly Leu Ile Lys Cys Pro Ile
305                 310                 315                 320

Lys Ile Val Gly Leu Ser Asp Leu Pro Glu Val Phe Lys Leu Met Glu
                325                 330                 335

Glu Gly Lys Ile Leu Gly Arg Tyr Val Leu Asp Thr Ser Lys
            340                 345                 350
```

<210> 69
<211> 1053
<212> DNA
<213> Escherichia coli

<400> 69

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atgtctgaac aaatcccaaa aactcaaaaa gccgttgtct ttgataccaa tggtggtcaa       60

ttagtctaca aggattaccc agttccaact ccaaagccaa atgaattgtt aatcaacgtc      120

aaatactctg gtgtctgtca cactgattta cacgcttgga aaggtgactg gccattggct      180

actaaattgc cattagttgg tggtcacgaa ggtgccggtg tcgttgtcgg tatgggtgaa      240

aacgtcaaag gatggaaaat cggtgacttt gccggtatca aatggttgaa cggttcttgt      300

atgagttgtg aattctgtca acaaggtgct gaaccaaact gtggtgaagc tgacttgtct      360

ggttacactc acgatggttc attcgaacaa tacgctactg ctgatgctgt ccaagccgct      420

aaaattccag ctggtactga tttagccaat gtcgcaccaa tcttatgtgc tggtgttact      480

gtttacaaag ccttaaagac tgctgactta gcagctggcc aatgggttgc tatctccggt      540

gctggtggtg gtttaggttc tttggccgtt caatacgcca gagccatggg tttgagagtt      600

gttgctattg acggtggtga cgaaaaaggt gaatttgtta aatcattggg tgctgaagct      660

tacgttgatt tcaccaaaga taaagatatt gttgaagctg ttaagaaggc tactgatggt      720
```

ggtccacacg gtgctatcaa tgtctctgtt tctgaaaaag ccattgacca atctgttgaa 780

tatgttagac cattaggtaa agttgttttg gttggtttac cagctcacgc taaagtcact 840

gctccagttt tcgatgctgt tgtcaaatcc attgaaatca aaggttctta cgttggtaac 900

agaaaagata ctgctgaagc tattgacttc ttctccagag gtttaatcaa atgcccaatc 960

aagattgtcg gtttatctga cttgccagaa gtcttcaaat tgatggaaga aggtaaaatc 1020

ttgggtagat acgtcttgga caccagtaaa taa 1053

<210> 70
<211> 353
<212> PRT
<213> Fusarium graminearum

<400> 70

Met Ala Ala Pro Gln Ile Pro Ser Gln Gln Trp Ala Gln Ile Phe Glu
1 5 10 15

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

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

Thr Asp Leu His Ala Trp Gln Gly Asp Trp Pro Leu Asp Thr Lys Leu
50 55 60

Pro Leu Val Gly Gly His Glu Gly Ala Gly Val Val Val Ala Arg Gly
65 70 75 80

Glu Leu Val Lys Asp Val Lys Ile Gly Glu Lys Val Gly Ile Lys Trp
85 90 95

Leu Asn Gly Ser Cys Leu Ser Cys Ser Tyr Cys Gln Asn Ala Asp Glu
100 105 110

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

```
Phe Gln Gln Tyr Ala Ile Ala Lys Ala Ile His Val Ala Arg Ile Pro
    130                 135                 140

Glu Glu Cys Asp Leu Glu Ala Ile Ser Pro Ile Leu Cys Ala Gly Ile
145                 150                 155                 160

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

Leu Ala Ile Val Gly Ala Gly Gly Gly Leu Gly Ser Ile Ala Val Gln
            180                 185                 190

Tyr Ala Lys Ala Met Gly Ile His Ala Ile Ala Ile Asp Gly Gly Glu
        195                 200                 205

Glu Lys Glu Lys Met Cys Met Ser Leu Gly Ala Gln Thr Phe Ile Asp
    210                 215                 220

Phe Thr Lys Thr Lys Asn Ile Val Ala Asp Val Lys Ala Thr Thr Asn
225                 230                 235                 240

Asp Gly Leu Gly Pro His Ala Ala Leu Leu Val Ala Ala Ala Glu Lys
                245                 250                 255

Pro Phe Gln Gln Ala Thr Gln Tyr Ile Arg Ser Lys Gly Thr Val Val
            260                 265                 270

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

Thr Val Val Arg Met Ile Gln Ile Lys Gly Ser Tyr Val Gly Asn Arg
    290                 295                 300

Ala Asp Thr Ala Glu Ala Ile Asp Phe Phe Arg Arg Gly Leu Ile Lys
305                 310                 315                 320
```

Val Pro Phe Lys Thr Val Gly Leu Ser Glu Leu Asn Glu Val Phe Lys
325 330 335

Leu Met Lys Ala Gly Gln Val Ala Gly Arg Tyr Val Val Asp Thr Ser
340 345 350

Arg

<210> 71
<211> 1062
<212> DNA
<213> Fusarium graminearum

<400> 71
atggccgctc cccagattcc ttcccagcag tgggctcaga tcttcgagaa gaccgccggt 60

cccatcgagt acaagcagat tcccgtccag aagcctggcc ccgatgaggt tctcgtcaac 120

gtcaagttct ccggtgtctg ccacactgac ctccacgcct ggcagggtga ctggcccctc 180

gacaccaagc tgccccttgt cggtggccac gagggtgccg gtgttgtcgt tgcccgcggc 240

gagcttgtca aggatgtcaa gattggcgag aaggtcggta tcaagtggct caacggttct 300

tgcttgagct gctcttactg ccaaaacgcc gatgagtctc tctgcgctga ggctcttctc 360

tccggttaca ccgtcgatgg atctttccag caatacgcca tcgccaaggc tatccacgtt 420

gctcgcatcc ctgaggagtg tgaccttgag gccatctccc ccattctctg cgccggtatc 480

accgtctaca agggtatcaa ggagtccggt gtcaaggccg gccagtctct tgctatcgtc 540

ggtgctggtg gtggtctcgg ttccatcgct gttcagtacg ccaaggctat gggtatccat 600

gccattgcca ttgatggtgg tgaggagaag gagaagatgt gcatgtctct cggtgcccaa 660

accttcatcg acttcacaaa gactaagaac atcgtcgctg atgtcaaggc tactaccaac 720

gatggccttg gccctcacgc tgctctcctc gtcgctgctg ccgagaagcc cttccaacag 780

gctacccaat acatccgatc caagggtacc gtcgtctgca tcggtctccc cgctggtgct 840

cagttctctg cccccgtctt cgacactgtc gttcgcatga ttcagatcaa gggatcttat 900

gtcggtaacc gtgccgatac tgctgaggcc atcgacttct tccgccgtgg tctcatcaag 960

gttcccttca agactgttgg tctctctgag ctcaacgagg tcttcaagct catgaaggct 1020

ggccaagttg ctggtcgcta tgtcgttgac accagccgat aa 1062

<210> 72
<211> 1966
<212> DNA
<213> Artificial Sequence

<220>
<223> Adh2 split marker cassette 1

<400> 72
cgtatctacc gatgatggca ccagcctcca tctgttcgta gaccttagca agttcagaca 60

gaccgataat cttgatagga gccttgacca aacctctggt gaacaagtcg atggcctcgg 120

cactgtcctc tctgtttcca acgtaagatc ccttgatctc gatggacttc agaacgtgcc 180

agaaaacgtc agagttgaca acggcaccag atggcagacc aaccaaaaca accttaccca 240

aagttctaac gtattggaca gattggttga tagcatgtgg ggaaacggag acgttaataa 300

caccgtgtgg accaccgttg gtgagctttt ggacttcagc aacgacgtcc ttagtcttag 360

tgaagtcgac gaagacctca gcacccaagg acttgacaaa ttcacccttg tcggcaccac 420

catcaatacc caaaactctc aaacccagag ccttggcgta ttgaacggca agagaaccca 480

gtcctccacc agcaccagaa atggcaaccc attggccaat acgcaagtca gcggtcttaa 540

gagccttgta aacggtgata ccagcacaca gaattggggc aacttcagcc aagtcagcct 600

cctttggaat tctggcggct tgggtggcat cagcagtagc atactgctgg aaagatccgt 660

cgtgggtgaa accagacagg tcagccttgg cacaactgga ttcagcacct tggatacagt 720

actcacagtt caaacaagaa ccgttcaacc atttgatacc agcgtagtca ccgatagtgg 780

atctgatatc acctaataac ttcgtatagc atacattata cgaagttata ttaagggttc 840

tcgaatggta ccttgctcac atgttgatct ccagcttgca aattaaagcc ttcgagcgtc 900

ccaaaacctt ctcaagcaag gttttcagta taatgttaca tgcgtacacg cgtctgtaca 960

gaaaaaaaag aaaaatttga aatataaata acgttcttaa tactaacata actataaaaa 1020

aataaatagg gacctagact tcaggttgtc taactccttc cttttcggtt agagcggatg 1080

tgggggggagg gcgtgaatgt aagcgtgaca taactaatta catgatatcg acaaaggaaa 1140

aggggggacgg atctccgagg taaaatagaa caactacaat ataaaaaaac tatacaaatg 1200

acaagttctt gaaaacaaga atctttttat tgtcagtact gattattcct ttgccctcgg 1260

acgagtgctg gggcgtcggt ttccactatc ggcgagtact tctacacagc catcggtcca 1320

gacggccgcg cttctgcggg cgatttgtgt acgcccgaca gtcccggctc cggatcggac 1380

gattgcgtcg catcgaccct gcgcccaagc tgcatcatcg aaattgccgt caaccaagct 1440

ctgatagagt tggtcaagac caatgcggag catatacgcc cggagccgcg gcgatcctgc 1500

aagctccgga tgcctccgct cgaagtagcg cgtctgctgc tccatacaag ccaaccacgg 1560

cctccagaag aagatgttgg cgacctcgta ttgggaatcc ccgaacatcg cctcgctcca 1620

gtcaatgacc gctgttatgc ggccattgtc cgtcaggaca ttgttggagc cgaaatccgc 1680

gtgcacgagg tgccggactt cggggcagtc ctcggcccaa agcatcagct catcgagagc 1740

ctgcgcgacg gacgcactga cggtgtcgtc catcacagtt tgccagtgat acacatgggg 1800

atcagcaatc gcgcatatga aatcacgcca tgtagtgtat tgaccgattc cttgcggtcc 1860

gaatgggccg aacccgctcg tctggctaag atcggccgca gcgatcgcat ccatggcctc 1920

cgcgaccggc tgcagaacag cgggcagttc ggtttcaggc aggtct 1966

<210> 73
<211> 2069
<212> DNA
<213> Artificial Sequence

<220>
<223> Adh2 split marker cassette 2

<220>
<221> misc_feature
<222> (1099)..(1099)
<223> n is a, c, g, or t

<400> 73
agatgttggc gacctcgtat tgggaatccc cgaacatcgc ctcgctccag tcaatgaccg 60

ctgttatgcg gccattgtcc gtcaggacat tgttggagcc gaaatccgcg tgcacgaggt 120

gccggacttc ggggcagtcc tcggcccaaa gcatcagctc atcgagagcc tgcgcgacgg 180

acgcactgac ggtgtcgtcc atcacagttt gccagtgata cacatgggga tcagcaatcg 240

cgcatatgaa atcacgccat gtagtgtatt gaccgattcc ttgcggtccg aatgggccga 300

acccgctcgt ctggctaaga tcggccgcag cgatcgcatc catggcctcc gcgaccggct 360

gcagaacagc gggcagttcg gtttcaggca ggtcttgcaa cgtgacaccc tgtgcacggc 420

gggagatgca ataggtcagg ctctcgctga attccccaat gtcaagcact tccggaatcg 480

ggagcgcggc cgatgcaaag tgccgataaa cataacgatc tttgtagaaa ccatcggcgc 540

agctatttac ccgcaggaca tatccacgcc ctcctacatc gaagctgaaa gcacgagatt 600

cttcgccctc cgagagctgc atcaggtcgg agacgctgtc gaacttttcg atcagaaact 660

tctcgacaga cgtcgcggtg agttcaggct ttttacccat ggtttagttc ctcaccttgt 720

cgtattatac tatgccgata tactatgccg atgattaatt gtcaacaccg cccttagatt 780

agattgctat gctttctttc taatgagcaa gaagtaaaaa aagttgtaat agaacaagaa 840

aaatgaaact gaaacttgag aaattgaaga ccgtttatta acttaaatat caatgggagg 900

tcatcgaaag agaaaaaaat caaaaaaaaa aaattttcaa gaaaaagaaa cgtgataaaa 960

atttttattg ccttttttaga cgaagaaaaa gaaacgaggc ggtctctttt ttcttttcca 1020

aacctttagt acgggtaatt aacgacaccc tagaggaaga aagaggggaa atttagtatg 1080

ctgtgcttgg gggttttgna aatggtacgg cgatgcgcgg aatccgagaa aatctggaag 1140

agtaaaaaag gagtagaaac attttgaagc tatggtgtgt ggtaccgatc tagacctaat 1200

aacttcgtat agcatacatt atacgaagtt atattaaggg ttgtcgacct gcagcgtacg 1260

gcacgaattc gcaccccgga gagcgctcac ccccgttttc aaacagcggg gggagcacaa 1320

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attctcccaa atggaaaacg agattggaca atttgtggag ttggaaaggg gggtgggaat 1440

caacgaaatt agcagattca tgggcaattg gcaggactgg gcagaagggg tgagaattgc 1500

aatcgaatgg aacaggcact cccgttgcga aatcaaaaaa gtctcgctat ctgaactgat 1560

ttttttaag cagcaactta cggtcaatac atctccgatg gaggaatttt tcacccctcg 1620

ctaactagat gggccccttc taagaaattt gggtttaagg ttgggcagtc agtcagtgca 1680

ccaatgctaa ctgccatttg tccaaagagg ggtgcaagga tgagggaccg ttgagaataa 1740

gatttggggt gttaatcggt gatactgatt tgtcaaagag tggggaggac tgctgggcat 1800

tgttcacccc cctagttgtt agagttcgat agccggccga atcacccccc tcttcttaca 1860

taatcattgt cactatgtgg ggtctctaca gtctcaccct gcgatccggg acgacgccgc 1920

gaaattaggg ggcaagtctc ctccgggcat gcaatattgg taacaggatc aattgatgcg 1980

agaaaagttg gagggggtgt aaaattcaag cccacaaagt cacaccctta tgcctgtaga 2040

ggggcaatcg gagagcagcc atggggtgt 2069

<210> 74
<211> 1850
<212> DNA
<213> Artificial Sequence

<220>
<223> Adh900 split marker cassette 1

<400> 74
cactccagtt gggccattac cgaacatttt gccattgtag gcgattagta agtattaaca 60

agacagctga ctatacgttt attctcaaac aatatttccc tttttggttt tgacctcgct 120

ttaatcaatt tttcagacct gatcccacct acttttcttc ggcctcaact tcaatctgac 180

tcttctctct caattggtac caaccagcca gaaaatgtcc ttccgttact tgaaacggca 240

tttctctaca gctacaaacg caattgctct ccttagcaga cctgaattca aaataggtcg 300

aattgtggac gtcgtgaaac atccaaatgc agacaaactt tatgtctcgt cgatttctgt 360

gggaaacaat tatgcctcgg gtacatccaa caccctaacc gtttgcagcg gcttggtgga 420

ctacttttca gttcccgaat tgcttcagcg acgggtcgtt gtggtcacaa acctcaagcc 480

atcgaagatg agaggtgtaa catcggaggc aatgcttttg gcaggggaaa agtcggggaa 540

agtggaattg gtcgagccgc caatgtccgg gagagagggc gaatcactcc acttcgaagg 600

tgtagaaatt acatcagagg agagcgccaa tcaattgcat ttgcctgcta agcgattgaa 660

gaagtcagag tggagtcaac tggcggaagg tctacagaca aatgaccagc gtgaagtggt 720

cttccacagc caaattggct ccaaacgaat ttacgcttta gtaggagcga gtactgaaaa 780

atgcacgtta gcgactcttg cgcaggccgt cgtacgataa gggcaatatg gttgagaacg 840

ttcctcaccc aaataaaatc atcgtacgct gcaggtcgac aacccttaat ataacttcgt 900

ataatgtatg ctatacgaag ttattaggtc tagatcggta ccgacatgga ggcccagaat 960

accctccttg acagtcttga cgtgcgcagc tcaggggcat gatgtgactg tcgcccgtac 1020

atttagccca tacatcccca tgtataatca tttgcatcca tacattttga tggccgcacg 1080

gcgcgaagca aaaattacgg ctcctcgctg cagacctgcg agcagggaaa cgctcccctc 1140

acagacgcgt tgaattgtcc ccacgccgcg cccctgtaga gaaatataaa aggttaggat 1200

ttgccactga ggttcttctt tcatatactt ccttttaaaa tcttgctagg atacagttct 1260

cacatcacat ccgaacataa acaaccatgg gtaaggaaaa gactcacgtt tcgaggccgc 1320

gattaaattc caacatggat gctgatttat atgggtataa atgggctcgc gataatgtcg 1380

ggcaatcagg tgcgacaatc tatcgattgt atgggaagcc cgatgcgcca gagttgtttc 1440

tgaaacatgg caaaggtagc gttgccaatg atgttacaga tgagatggtc agactaaact 1500

ggctgacgga atttatgcct cttccgacca tcaagcattt tatccgtact cctgatgatg 1560

catggttact caccactgcg atccccggca aaacagcatt ccaggtatta gaagaatatc 1620

ctgattcagg tgaaaatatt gttgatgcgc tggcagtgtt cctgcgccgg ttgcattcga 1680

ttcctgtttg taattgtcct tttaacagcg atcgcgtatt tcgtctcgct caggcgcaat 1740

cacgaatgaa taacggtttg gttgatgcga gtgattttga tgacgagcgt aatggctggc 1800

ctgttgaaca agtctggaaa gaaatgcata agcttttgcc attctcaccg 1850

<210> 75
<211> 1993
<212> DNA
<213> Artificial Sequence

<220>
<223> Adh900 split marker cassette 2

<400> 75
aagcccgatg cgccagagtt gtttctgaaa catggcaaag gtagcgttgc caatgatgtt 60

acagatgaga tggtcagact aaactggctg acggaattta tgcctcttcc gaccatcaag 120

cattttatcc gtactcctga tgatgcatgg ttactcacca ctgcgatccc cggcaaaaca 180

gcattccagg tattagaaga atatcctgat tcaggtgaaa atattgttga tgcgctggca 240

gtgttcctgc gccggttgca ttcgattcct gtttgtaatt gtccttttaa cagcgatcgc 300

gtatttcgtc tcgctcaggc gcaatcacga atgaataacg gtttggttga tgcgagtgat 360

tttgatgacg agcgtaatgg ctggcctgtt gaacaagtct ggaaagaaat gcataagctt 420

ttgccattct caccggattc agtcgtcact catggtgatt tctcacttga taaccttatt 480

tttgacgagg ggaaattaat aggttgtatt gatgttggac gagtcggaat cgcagaccga 540

taccaggatc ttgccatcct atggaactgc ctcggtgagt tttctccttc attacagaaa 600

cggctttttc aaaaatatgg tattgataat cctgatatga ataaattgca gtttcatttg 660

atgctcgatg agtttttcta atcagtactg acaataaaaa gattcttgtt ttcaagaact 720

tgtcatttgt atagtttttt tatattgtag ttgttctatt ttaatcaaat gttagcgtga 780

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cttaatataa cttcgtataa tgtatgctat acgaagttat taggtgatat cagatccact 960

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ggacaaacgg aaatgccatg gctccaggga aaggcattcc tattgcaaac ctagaccgtc 1860

gaacctctcc tatcgcctac cagtcaccca gctatcccta ggcaactcat ctccttcaag 1920

cggattgcaa cctgctaagc caaattagat ctggccacag aaatgccgca atatttcttg 1980

gctctcccct ccc 1993

<210> 76
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 76
gaattgagcc aaaaaaggag agg 23

<210> 77
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 77
gatggaatag gagactaggt gtg 23

<210> 78
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 78

tggttgagac gtttgtattg 20

<210> 79
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 79
tgggttggga gtttagtg 18

<210> 80
<211> 1053
<212> DNA
<213> Artificial Sequence

<220>
<223> ADH2 coding sequence

<400> 80
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ctagagtaca aggacattcc agtcccaaag ccaaagtcaa acgaactttt gatcaacgtt 120

aagtactccg gtgtctgtca cactgatttg cacgcctgga agggtgactg gccattggac 180

aacaagcttc ctttggttgg tggtcacgaa ggtgctggtg tcgttgtcgc ttacggtgag 240

aacgtcactg gatgggagat cggtgactac gctggtatca aatggttgaa cggttcttgt 300

ttgaactgtg agtactgtat ccaaggtgct gaatccagtt gtgccaaggc tgacctgtct 360

ggtttcaccc acgacggatc tttccagcag tatgctactg ctgatgccac ccaagccgcc 420

agaattccaa aggaggctga cttggctgaa gttgccccaa ttctgtgtgc tggtatcacc 480

gtttacaagg ctcttaagac cgctgacttg cgtattggcc aatgggttgc catttctggt 540

gctggtggag gactgggttc tcttgccgtt caatacgcca aggctctggg tttgagagtt 600

ttgggtattg atggtggtgc cgacaagggt gaatttgtca agtccttggg tgctgaggtc 660

ttcgtcgact tcactaagac taaggacgtc gttgctgaag tccaaaagct caccaacggt 720

ggtccacacg gtgttattaa cgtctccgtt tccccacatg ctatcaacca atctgtccaa 780

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tctgacgttt tctggcacgt tctgaagtcc atcgagatca agggatctta cgttggaaac 900

agagaggaca gtgccgaggc catcgacttg ttcaccagag gtttggtcaa ggctcctatc 960

aagattatcg gtctgtctga acttgctaag gtctacgaac agatggaggc tggtgccatc 1020

atcggtagat acgttgtgga cacttccaaa taa 1053

<210> 81
<211> 1083
<212> DNA
<213> Artificial Sequence

<220>
<223> ADH900 coding sequence

<400> 81
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cctaaaccaa ctatcttgca cccaacagat gtcatcgtta agacggtggc tactaccatc 120

tgcggaacag acttgcacat cttgaaaggt gatgttccag aggtcaaacc tgaaaccgtc 180

ttgggtcatg aagcaattgg agtcgtcgaa tctatcggtg ataacgtcaa aaacttcagc 240

attggtgata aggtgctggt ttcatgcatc accagttgtg gaagctgtta ctactgtaag 300

agaaacttgc agagtcattg caagaccggt ggatggaaat taggtcacga tttgaacggt 360

acgcaggctg agtttgtccg tatcccatat ggagacttct cattgcaccg tattcctcat 420

gaagcagatg aaaaggcagt tctgatgctg tctgacatct tacctactgc ttacgaagtt 480

ggtgttcttg ccggaaatgt ccaaaaggga gactcagttg ccattgtcgg cgccggtcca 540

gttggtcttg ccgctctgct gactgtcaaa gcctttgagc cttctgaaat tattatgatt 600

gacactaacg atgaaagact gagtgcctcc ttgaaattgg gagccaccaa ggcagtcaac 660

ccaaccaagg tcagcagtgt caaagatgct gtttatgata ttgtcaatgc cactgtccgc 720

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tctctagacc ctacaccact ggttacacat gagttcaagt tcagtgaatt tgagaaggcc 1020

tatgagactt ctcaaaatgc tgccaccacc aaagccatca agattttctt atctgccgat 1080

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<210> 82
<211> 1080
<212> DNA
<213> Artificial Sequence

<220>
<223> Adh2_GG_cured

<400> 82
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aacggcggtc ccctagagta caaggacatt ccagtcccaa agccaaagtc aaacgaactt 120

ttgatcaacg ttaagtactc cggtgtctgt cacactgatt tgcacgcctg gaagggtgac 180

tggccattgg acaacaagct tcctttggtt ggtggtcacg aaggtgctgg tgtcgttgtc 240

gcttacggtg agaacgtcac tggatgggag atcggtgact acgctggtat caaatggttg 300

aacggttctt gtttgaactg tgagtactgt atccaaggtg ctgaatccag ttgtgccaag 360

gctgacctgt ctggtttcac ccacgacgga tctttccagc agtatgctac tgctgatgcc 420

acccaagccg ccagaattcc aaaggaggct gacttggctg aagttgcccc aattctgtgt 480

gctggtatca ccgtttacaa ggctcttaag accgctgact tgcgtattgg ccaatgggtt 540

gccatttctg gtgctggtgg aggactgggt tctcttgccg ttcaatacgc caaggctctg 600

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ggtgctgagg tgttcgtcga cttcactaag actaaggacg tcgttgctga agtccaaaag 720

ctcaccaacg gtggtccaca cggtgttatt aacgtctccg tttccccaca tgctatcaac 780

caatctgtcc aatacgttag aactttgggt aaggttgttt tggttggtct gccatctggt 840

gccgttgtca actctgacgt tttctggcac gttctgaagt ccatcgagat caagggatct 900

tacgttggaa acagagagga cagtgccgag gccatcgact tgttcaccag aggtttggtc 960

aaggctccta tcaagattat cggtctgtct gaacttgcta aggtctacga acagatggag 1020

gctggtgcca tcatcggtag atacgttgtg gacacttcca ataagctta gagaccgatc 1080

<210> 83
<211> 1110
<212> DNA
<213> Artificial Sequence

<220>
<223> Adh900_GG_cured

<400> 83
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tggaaaaact tccctaaacc aactatcttg cacccaacag atgtcatcgt taagacggtg 120

gctactacca tctgcggaac agacttgcac atcttgaaag gtgatgttcc agaggtcaaa 180

cctgaaaccg tcttgggtca tgaagcaatt ggagtcgtcg aatctatcgg tgataacgtc 240

aaaaacttca gcattggtga taaggtgctg gtttcatgca tcaccagttg tggaagctgt 300

tactactgta agagaaactt gcagagtcat tgcaagaccg gtggatggaa attaggtcac 360

gatttgaacg gtacgcaggc tgagtttgtc cgtatcccat atggagactt ctcattgcac 420

cgtattcctc atgaagcaga tgaaaaggca gttctgatgc tgtctgacat cttacctact 480

gcttacgaag ttggtgttct tgccggaaat gtccaaaagg gagactcagt tgccattgtc 540

ggcgccggtc cagttggtct tgccgctctg ctgactgtca aagcctttga gccttctgaa 600

attattatga ttgacactaa cgatgaaaga ctgagtgcct ccttgaaatt gggagccacc 660

aaggcagtca acccaaccaa ggtcagcagt gtcaaagatg ctgtttatga tattgtcaat 720

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ttatctgccg attaagctta gagaccgatc 1110

<210> 84
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 84
ttgatctttt ctacggggtg g 21

<210> 85
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 85
ggtgttttga agtggtacgg 20