SEQUENCE LISTING

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<120> Method for generating gene hybrids

<130> EV001P

<160> 59

<170> PatentIn version 3.5

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tggtgggttg gttgggttga gaagggagca gaggtttact ttttcgcatt taacatggat 720

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Ala Leu Ala Ser Ser Ile Thr Glu Asn Thr Phe Trp Asn Lys Glu Phe
20 25 30

eolf-seql

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Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
        35                  40                  45

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

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

Gly Val Ile Lys Asn Glu His Gln Ile Phe Lys Trp Asp Gly Lys Pro
                85                  90                  95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Ser Leu Arg Gly Ala Ile
            100                 105                 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
        115                 120                 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Asn Gln
    130                 135                 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Gly Gln Leu Arg
145                 150                 155                 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Phe Leu Asn
                165                 170                 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
            180                 185                 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
    210                 215                 220

Trp Val Glu Lys Gly Ala Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225                 230                 235                 240

Ile Asp Asn Glu Asn Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
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Ile Met Ala Ser Glu Gly Ile Ile Gly Gly
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aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcagattttc aaatgggacg gaaagccaag agccatgaaa 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagcggt tcccgtattt 360

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tggtgggttg gttgggttga gaagggagca gaggtttact ttttcgcatt taacatggat 720

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Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Ile Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
100 105 110

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Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
        115                 120                 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Asn Gln
    130                 135                 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Ser Glu Gly Gln Leu Arg
145                 150                 155                 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Phe Leu Asn
                165                 170                 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
            180                 185                 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
    210                 215                 220

Trp Val Glu Lys Gly Ala Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225                 230                 235                 240

Ile Asp Asn Glu Asn Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
                245                 250                 255

Ile Met Ala Ser Glu Gly Ile Ile Gly Gly
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ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca      180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact      240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag      300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt      360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aataccttaa aaaattttcc      420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaaga ccagcttaga      480

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Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
130 135 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Asp Gln Leu Arg
145 150 155 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Tyr Leu Asn
165 170 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
180 185 190

eolf-seql

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
210 215 220

Trp Val Glu Lys Glu Thr Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
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Ile Asp Asn Glu Ser Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
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Ile Arg Glu Ser Glu Gly Ile Ile Gly Gly
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ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcacca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aataccttaa aaaattttcc 420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaagg tcagcttaga 480

atttccgcag ttaatcaagt ggagtttcta gagtctctat ttttaaataa attgtcagca 540

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tggtgggttg gttgggttga gaagggagca gaggtttact ttttcgcatt taacatggat 720

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eolf-seql

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            20                  25                  30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
        35                  40                  45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Pro Lys Glu Tyr Leu
    50                  55                  60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
                85                  90                  95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
            100                 105                 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
        115                 120                 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
    130                 135                 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Gly Gln Leu Arg
145                 150                 155                 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Phe Leu Asn
                165                 170                 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
            180                 185                 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
    210                 215                 220

Trp Val Glu Lys Gly Ala Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225                 230                 235                 240

Ile Asp Asn Glu Asn Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
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Ile Met Ala Ser Glu Gly Ile Ile Gly Gly
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ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aataccttaa aaaattttcc 420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaaga ccagcttaga 480

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tggtgggttg ggtgggttga gaaggagaca gaggtttact ttttcgcctt taacatggat 720

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Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

eolf-seql

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
130 135 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Asp Gln Leu Arg
145 150 155 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Tyr Leu Asn
165 170 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
180 185 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
210 215 220

Trp Val Glu Lys Glu Thr Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
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Met Asp Asn Glu Ser Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
245 250 255

Ile Met Glu Ser Glu Gly Ile Ile Gly Gly
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aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcagattttc aaatgggacg gaaagccaag agccatgaaa 300

caatgggaaa gagacttgag cttaagaggg gcaatacaag tttcagcggt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aatatcttaa aaaattttca 420

tatggtaacc agaatatcag tggtggcatt gacaaattct ggttggaggg tcagcttaga 480

atttccgcag ttaatcaagt ggagtttcta gagtctctat ttttaaataa attgtcagca 540

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tggtgggttg gttgggttga gaagggagca gaggtttact ttttcgcatt taacatggat 720

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35 40 45

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

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

Gly Val Ile Lys Asn Glu His Gln Ile Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Ser Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Asn Gln
130 135 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Gly Gln Leu Arg
145 150 155 160

eolf-seq1

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Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Phe Leu Asn
                165                 170                 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
            180                 185                 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
    210                 215                 220

Trp Val Glu Lys Gly Ala Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225                 230                 235                 240

Ile Asp Asn Glu Asn Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
                245                 250                 255

Ile Met Ala Ser Glu Gly Ile Ile Gly Gly
            260                 265
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aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact      240

ggtgtcataa ggaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag      300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt      360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga ataccttaa aaaattttcc       420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaaga ccagcttaga      480

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tctaaagaaa atcagctaat agtaaaagag gctttggtaa cggaggctgc gcctgaatat      600

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tggtgggttg ggtgggttga gaaggagaca gaggtttact ttttcgcatt taacatggat      720

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            20                  25                  30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
        35                  40                  45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
    50                  55                  60

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

Gly Val Ile Arg Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
                85                  90                  95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
            100                 105                 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
        115                 120                 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
    130                 135                 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Asp Gln Leu Arg
145                 150                 155                 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Tyr Leu Asn
                165                 170                 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
            180                 185                 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
    210                 215                 220

Trp Val Glu Lys Glu Thr Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225                 230                 235                 240
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eolf-seql

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Ile Met Ala Ser Glu Gly Ile Ile Gly Gly
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ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagagact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aataccttaa aaaattttcc 420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaaga ccagcttaga 480

atttccgcag ttaatcaagt ggagtttcta gagtctctat atttaaataa attgtcagca 540

tctaaagaaa accagctaat agtaaaagag gcaatagtta cagaagcaac tccagaatat 600

atagttcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

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<210> 16
<211> 267
<212> PRT
<213> Artificial

<220>
<223> protein hybrid OXA11/OXA5

<400> 16

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

Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

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Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
     50                  55                  60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
                85                  90                  95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
            100                 105                 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
        115                 120                 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
    130                 135                 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Asp Gln Leu Arg
145                 150                 155                 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Tyr Leu Asn
                165                 170                 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Ile
            180                 185                 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
    210                 215                 220

Trp Val Glu Lys Glu Thr Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225                 230                 235                 240

Ile Asp Asn Glu Ser Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
                245                 250                 255

Ile Met Glu Ser Glu Gly Ile Ile Ile Gly Gly
            260                 265
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<210> 17
<211> 801
<212> DNA
<213> Artificial

<220>
<223> gene hybrid OXA11/OXA5

<400> 17

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tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc      120
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ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aataccttaa aaaattttcc 420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaaga ccagcttaga 480

atttccgcag ttaatcaagt ggagtttcta gagtctctat atttaaataa attgtcagca 540

tctaaagaaa accagctaat agtaaaagag gctttggtaa cggaggcggc acctgaatat 600

ctagtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg ggtgggtaga gaaaggaact gaggtttact ttttcgcctt tagcatggat 720

atagacaacg aaagtaagtt gccgctaaga aaatccattc ccaccaaaat catggaaagt 780

gagggcatca ttggtggcta a 801

<210> 18
<211> 266
<212> PRT
<213> Artificial

<220>
<223> protein hybrid OXA11/OXA7

<400> 18

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

Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

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Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
130 135 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Asp Gln Leu Arg
145 150 155 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Tyr Leu Asn
165 170 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
180 185 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
210 215 220

Trp Val Glu Lys Gly Thr Glu Val Tyr Phe Phe Ala Phe Ser Met Asp
225 230 235 240

Ile Asp Asn Glu Ser Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
245 250 255

Ile Met Glu Ser Glu Gly Ile Ile Gly Gly
260 265

<210> 19
<211> 804
<212> DNA
<213> Artificial

<220>
<223> gene hybris OXA11/OXA5

<400> 19
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tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc 120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aataccttaa aaaattttcc 420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaaga ccagcttaga 480

atttccgcag ttaatcaagt ggagtttcta gagtctctat atttaaataa attgtcagca 540

tctaaagaaa accagctaat agtaaaagag gctttggtaa cggaggcggc acctgaatat 600

ctagtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg ggtgggttga gaaggagaca gaggtttact ttttcgcctt taacatggat 720

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gaaggcatca tcattggtgg ctaa 804

<210> 20
<211> 267
<212> PRT
<213> Artificial

<220>
<223> protein hybrid OXA11/OXA5

<400> 20

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

Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
130 135 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Asp Gln Leu Arg
145 150 155 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Tyr Leu Asn
165 170 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
180 185 190

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

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Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
210 215 220

Trp Val Glu Lys Glu Thr Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225 230 235 240

Ile Asp Asn Glu Ser Lys Leu Pro Ser Arg Lys Ser Ile Ser Thr Lys
245 250 255

Ile Met Ala Ser Glu Gly Ile Ile Ile Gly Gly
260 265

<210> 21
<211> 801
<212> DNA
<213> Artificial

<220>
<223> gene hybrid OXO11/OXO5

<400> 21
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tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc 120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagtg agaatgcaga aataccttaa aaaattttcc 420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaaga ccagcttaga 480

atttccgcag ttaatcaagt ggagtctcta gagtctctat atttaaataa attgtcagca 540

tctaaagaaa accagctaat agtaaaagag gctttggtaa cggaggcggc acctgaatat 600

ctagtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg ggtgggttga gaaggagaca gaggtttact ttttcgcctt taacatggat 720

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gagggcatca ttggtggcta a 801

<210> 22
<211> 266
<212> PRT
<213> Artificial

<220>
<223> protein hybrid OXO11/OXO5

<400> 22

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

Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
130 135 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Asp Gln Leu Arg
145 150 155 160

Ile Ser Ala Val Asn Gln Val Glu Ser Leu Glu Ser Leu Tyr Leu Asn
165 170 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
180 185 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
210 215 220

Trp Val Glu Lys Glu Thr Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225 230 235 240

Ile Asp Asn Glu Ser Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
245 250 255

Ile Met Glu Ser Glu Gly Ile Ile Gly Gly
260 265

<210> 23
<211> 804
<212> DNA
<213> Artificial

<220>
<223> gene hybrid OXO11/OXO5

<400> 23
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tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc 120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aataccttaa aaaattttcc 420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaaga ccagcttaga 480

atttccgcag ttaatcaaga ggagtttcta gagtctctat atttaaataa attgtcagca 540

tctaaagaaa accagctaat agtaaaagag gctttggtaa cggaggcggc acctgaatat 600

ctagtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg ggtgggttga gaaggagaca gaggtttact ttttcgcctt taacatggat 720

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gagggcatca tcattggtgg ctaa 804

<210> 24
<211> 267
<212> PRT
<213> Artificial

<220>
<223> protein hybrid OXO11/OXO5

<400> 24

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

Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

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Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
            100                 105                 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
        115                 120                 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
    130                 135                 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Asp Gln Leu Arg
145                 150                 155                 160

Ile Ser Ala Val Asn Gln Glu Glu Phe Leu Glu Ser Leu Tyr Leu Asn
                165                 170                 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
            180                 185                 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
    210                 215                 220

Trp Val Glu Lys Glu Thr Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225                 230                 235                 240

Ile Asp Asn Glu Ser Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
                245                 250                 255

Ile Met Glu Ser Glu Gly Ile Ile Ile Gly Gly
            260                 265
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<210> 25
<211> 800
<212> DNA
<213> Artificial

<220>
<223> gene hybrid OXO11/OXO5

<400> 25

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tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc     120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca     180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact     240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag     300

caatgggaaa gagacttgag cttaagaggg gcaatacaag tttcagctgt tcccgtattt     360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga gataccttaa aaaattttcc     420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaaga ccagcttaga     480
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atttccgcag ttaatcaagt ggagtttcta gagtctctat atttaaataa attgtcagca 540

tctaaagaaa accagctaat agtaaaagag gctttggtaa cggaggcggc acctgaatat 600

ctagtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg ggtgggttgg gaaggagaca gaggtttact ttttcgcctt taacatggat 720

atagacaacg aaagtaagtt gccgctaaga aatccattcc caccaaaatc atggaaagtg 780

agggcatcat tggtggctaa 800

<210> 26
<211> 266
<212> PRT
<213> Artificial

<220>
<223> protein hybrid OXO11/OXO5

<400> 26

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

Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Ser Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

Glu Val Arg Met Gln Arg Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
130 135 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Asp Gln Leu Arg
145 150 155 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Tyr Leu Asn
165 170 175

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Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
180 185 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
210 215 220

Trp Val Gly Lys Glu Thr Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225 230 235 240

Ile Asp Asn Glu Ser Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
245 250 255

Ile Met Glu Ser Glu Gly Ile Ile Gly Gly
260 265

<210> 27
<211> 802
<212> DNA
<213> Artificial

<220>
<223> gene hybrid OXO11/OXO5

<400> 27
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tcaattacag aaaatacgtt ttggaacaaa gagttctctg ccgaagccgt caatggtgtt 120

ttttcgtgct ttgtaaaagt agcagtaaat cctgcgctac caataactta gctcgtgcat 180

caaaggaata tcttccagca tcaacattta agatccccaa cgcaattatc ggcctagaaa 240

ctggtgtcat aaagaatgag catcaggttt tcaaatggga cggaaagcca agagccatga 300

aacaatggga aagagacttg agcttaagag gggcaataca agtttcagcg gttcccgtat 360

ttcaacaaat cgccagagaa gttggcgaag taagaatgca gaaatatctt aaaaaatttt 420

catatggtaa ccagaatatc agtggtggca ttgacaaatt ctggttggag ggtcagctta 480

gaatttccgc agttaatcaa gtggagtttc tagagtctct atttttaaat aaattgtcag 540

catcaaaaga aaatcagcta atagtaaaag aggctttggt aacggaggct gcgcctgaat 600

atcttgtgca ttcaaaaact ggtttttctg gtgtgggaac tgagtcaaat cctggtgtcg 660

catggtgggt tggttgggtt gagaagggag cagaggttta ctttttcgca tttaacatgg 720

atatagacaa cgaaaataag ttgccgctaa gaaaatccat tcccaccaaa tcatggcaag 780

tgagggcatc attggtggct aa 802

<210> 28
<211> 266
<212> PRT
<213> Artificial

<220>

<223> protein hybrid OX011/OX05

<400> 28

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

Ala Leu Ala Ser Ser Ile Thr Glu Asn Thr Phe Trp Asn Lys Glu Phe
            20                  25                  30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
        35                  40                  45

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

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
                85                  90                  95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Ser Leu Arg Gly Ala Ile
            100                 105                 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
        115                 120                 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Asn Gln
    130                 135                 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Gly Gln Leu Arg
145                 150                 155                 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Phe Leu Asn
                165                 170                 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
            180                 185                 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
    210                 215                 220

Trp Val Glu Lys Gly Ala Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225                 230                 235                 240

Ile Asp Asn Glu Asn Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
                245                 250                 255
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Ile Met Ala Ser Glu Gly Ile Ile Gly Gly
260 265

<210> 29
<211> 801
<212> DNA
<213> Artificial

<220>
<223> gene hybrid OXO11/OXO5

<400> 29
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tcaattacag aaaatacgtt ttggaacaaa gagttctctg ccgaagccgt caatggtgtt 120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcagattttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aataccttaa aaaattttca 420

tatggtaacc agaatatcag tggtggcatt gacaaattct ggttggaggg tcagcttaga 480

attcccgcag ttaatcaagt ggagtttcta gagtctctat ttttaaataa attgtcagca 540

tcaaaagaaa atcagctaat agtaaaagag gctttggtaa cggaggcggc acctgaatat 600

cttgtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg gttgggttga gaagggagca gaggtttact ttttcgcatt taacatggat 720

atagacaacg aaaataagtt gccgctaaga aaatccattc ccaccaaaat catggcaagt 780

gagggcatca ttggtggcta a 801

<210> 30
<211> 266
<212> PRT
<213> Artificial

<220>
<223> protein hybrid OXO11/OXO5

<400> 30

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

Ala Leu Ala Ser Ser Ile Thr Glu Asn Thr Phe Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

eolf-seql

```
Pro Ala Ser Thr Phe Lys Ile Pro Asn Ala Ile Ile Gly Leu Glu Thr
65                  70                  75                  80

Gly Val Ile Lys Asn Glu His Gln Ile Phe Lys Trp Asp Gly Lys Pro
                85                  90                  95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
            100                 105                 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
        115                 120                 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Asn Gln
    130                 135                 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Gly Gln Leu Arg
145                 150                 155                 160

Ile Pro Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Phe Leu Asn
                165                 170                 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
            180                 185                 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
    210                 215                 220

Trp Val Glu Lys Gly Ala Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225                 230                 235                 240

Ile Asp Asn Glu Asn Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
                245                 250                 255

Ile Met Ala Ser Glu Gly Ile Ile Gly Gly
            260                 265
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<210> 31
<211> 801
<212> DNA
<213> Artificial

<220>
<223> gene hybrid OX011/OX05

<400> 31

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tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc      120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca      180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact      240
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ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aataccttaa aaaattttcc 420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaaga ccagcttaga 480

atttccgcag ttaatcaagt ggagtttcta gagtctctat atttaaataa attgtcagca 540

tctaaagaaa accagctaat agtaaaagag gctttggtaa cggaggcggc acctgaatat 600

ctagtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg ggtgggttga gaaggagaca gaggtttact ttttcgcctt taacatggat 720

atagacaacg aaagtaagtt gccgctaaga aaatccattc ccaccaaaat catggaaagt 780

gagggcatca ttggtggcta a 801

<210> 32
<211> 266
<212> PRT
<213> Artificial

<220>
<223> protein hybrid OXO11/OXO5

<400> 32

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

Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
130 135 140

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Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Asp Gln Leu Arg
145 150 155 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Tyr Leu Asn
165 170 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
180 185 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
210 215 220

Trp Val Glu Lys Glu Thr Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225 230 235 240

Ile Asp Asn Glu Ser Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
245 250 255

Ile Met Glu Ser Glu Gly Ile Ile Gly Gly
260 265

<210> 33
<211> 801
<212> DNA
<213> Artificial

<220>
<223> gene hybrid OXO11/OXO5

<400> 33
atgaaaacat ttgccgcata tgtaattatc gcgtgtcttt cgagtacggc attagctggt 60

tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc 120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga ataccttaa aaaattttcc 420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaaga ccagcttaga 480

atttccgcag ttaatcaagt ggagtttcta gagtctctat atttaaataa attgtcagca 540

tctaaagaaa accagctaat agtaaaagag gctttggtaa cggaggcggc acctgaacat 600

ctagtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg ggtgggttga gaaggagaca gaggtttact ttttcgcctt taacatggac 720

atagacaacg aaagtaagtt gccgctaaga aaatccattc ccaccaaaat catggaaagt 780

gagggcatca ttggtggcta a 801

<210> 34
<211> 266
<212> PRT
<213> Artificial

<220>
<223> protein hybrid OXO11/OXO5

<400> 34

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

Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
130 135 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Asp Gln Leu Arg
145 150 155 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Tyr Leu Asn
165 170 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
180 185 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
210 215 220

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Trp Val Glu Lys Glu Thr Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225 230 235 240

Ile Asp Asn Glu Ser Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
245 250 255

Ile Met Glu Ser Glu Gly Ile Ile Gly Gly
260 265

<210> 35
<211> 804
<212> DNA
<213> Artificial

<220>
<223> gene hybrid OXO11/OXO5

<400> 35
atgaaaacat ttgccgcata tttaattatc gcgtgtcttt cgagtacggc attagctggt 60

tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc 120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aataccttaa aaaattttcc 420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaaga ccagcttaga 480

atttccgcag ttaatcaagt ggagtttcta gagtctctat atttaaataa attgtcagca 540

tctaaagaaa accagctaat agtaaaagag gctttggtaa cggaggcggc acctgaatat 600

ctagtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg ggtgggttga gaaggagaca gaggtttact ttttcgcctt taacatggat 720

atagacaacg aaagtaagtt gccgctaaga aaatccattc ccaccaaaat catggaaagt 780

gagggcatca tcattggtgg ctta 804

<210> 36
<211> 267
<212> PRT
<213> Artificial

<220>
<223> protein hybrid OXO11/OXO5

<400> 36

Met Lys Thr Phe Ala Ala Tyr Leu Ile Ile Ala Cys Leu Ser Ser Thr
1 5 10 15

Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

eolf-seql

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
130 135 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Asp Gln Leu Arg
145 150 155 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Tyr Leu Asn
165 170 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
180 185 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
210 215 220

Trp Val Glu Lys Glu Thr Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225 230 235 240

Ile Asp Asn Glu Ser Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
245 250 255

Ile Met Glu Ser Glu Gly Ile Ile Ile Gly Gly
260 265

<210> 37
<211> 804
<212> DNA
<213> Artificial

<220>
<223> gene hybrid OXO11/OXO5

<400> 37
atgaaaacat ttgccgcata tgtaattatc gcgtgtcttt cgagtacggc attagctggt 60

tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc 120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttctgctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga ataccttaa aaaattttcc 420

tatggcagcc agaatatcag tggtggcatt gacaaattct ggttggaaga ccagcttaga 480

atttccgcag ttaatcaagt ggagtttcta gagtctctat atttaaataa attgtcagca 540

tctaaagaaa accagctaat agtaaaagag gctttggtaa cggaggcggc acctgaatat 600

ctagtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg ggtgggttga gaaggagact gaggtttact tttttgcttc taacatggac 720

atagacaatg agagtaaatt gccgtcaaga aaatccattt caacgaaaat catggcaagt 780

gaaggcatca tcattggtgg ctaa 804

<210> 38
<211> 267
<212> PRT
<213> Artificial

<220>
<223> protein hybrid OXO11/OXO5

<400> 38

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

Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
100 105 110

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Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Ser Gln
130 135 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Asp Gln Leu Arg
145 150 155 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Tyr Leu Asn
165 170 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
180 185 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
210 215 220

Trp Val Glu Lys Glu Thr Glu Val Tyr Phe Phe Ala Ser Asn Met Asp
225 230 235 240

Ile Asp Asn Glu Ser Lys Leu Pro Ser Arg Lys Ser Ile Ser Thr Lys
245 250 255

Ile Met Ala Ser Glu Gly Ile Ile Ile Gly Gly
260 265

<210> 39
<211> 801
<212> DNA
<213> Saccharomyces cerevisiae

<400> 39
atgaaaacat ttgccgcata tgtaattatc gcgtgtcttt cgagtacggc attagctggt 60

tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc 120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aataccttaa aaaattttcc 420

tatggcagcc agaatatcag tggtggcatt gacaaatcct ggttggaaga ccagcttaga 480

atttccgcag ttaatcaagt ggagtttcta gagtctctat atttaaataa attgtcagca 540

tctaaagaaa accagctaat agtaaaagag gctttggtaa cggaggcggc acctgaatat 600

ctagtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg ggtgggttga gaaggagaca gaggtttact ttttcgcctt taacatggat 720

atagacaacg aaagtaagtt gccgctaaga aaatccattc ccaccaaaat catggaaagt 780

gagggcatca ttggtggcta a 801

<210> 40
<211> 801
<212> DNA
<213> Saccharomyces cerevisiae

<400> 40
atgaaaacat ttgccgcata tgtaattact gcgtgtcttt caagtacggc attagctagt 60

tcaattacag aaaatacgtt ttggaacaaa gagttctctg ccgaagccgt caatggtgtt 120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca ataacttagc tcgtgcacca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcagattttc aaatgggacg gaaaaccaag agccatgaaa 300

caatgggaaa gagacttgag cttaagaggg gcaatacaag tttcagcggt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aatatcttaa aaaattttca 420

tatggtaacc agaatatcag tggcggcatt gacaaattct ggtcggaggg tcagcttaga 480

atttccgcag ttaatcaagt ggagtttcta gagtctctat ttttaaataa attgtcagca 540

tcaaaagaaa atcagctaat agtaaaagag gctttggtaa cggaggctgc gcctgaatat 600

cttgtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg gttgggttga gaagggagca gaggtttact ttttcgcatt taacatggat 720

atagacaacg aaaataagtt gccgctaaga aaatccattc ccaccaaaat catggcaagt 780

gagggcatca ttggtggcta a 801

<210> 41
<211> 804
<212> DNA
<213> Saccharomyces cerevisiae

<400> 41
atgaaaacca tagccgcata cttagttact tcctgttttt caagcaccgc gctctcaaag 60

tctatttctg aaaatttggt gtggaataaa gaattttcta gtgaatccgt acatggcgtt 120

tttgtacttt gtaaaagtag tagcaattcc tgtactacaa ataatgcggc acgtgcatct 180

acagcctata ttccagcatc aacattcaaa attcctaatg ctctaatagg tcttgaaacc 240

ggcgccataa aagatgaacg gcagattttc aaatgggacg gcaagcccag agccatgaaa 300

caatgggaaa aagacttaag gctaaggggc gctatacagg tttctgcggt tccggtattt 360

caacaaattg ccagagaagt tggcgaaatg agaatgcaaa gatatcttaa cctgttttca 420

tacggtaacg ccaatatagg gggaggcatt gacaaattct ggctagaggg tcagcttaga 480

atcccagcat tcaatcaaga taaatctttа gagtcgctct tcctgaataa tttgccagca 540

tcaaaagcaa atcaactaat agtaaaagag gcaatagtta cagaagctac gccagaatat 600

attgttcatt caaaaactgg gtattccggt gttggcacag aatcaagtcc tggtgtcgct 660

tggtgggttg gttgggtagg gaaaggagct gaggtttact tttttgcatt taacatggac 720

atagacaatg agaataaatt gccgtcaaga aaatccattt caacgaaaat catggcaagt 780

gaaggcatca tcattggtgg ctaa 804

<210> 42
<211> 827
<212> DNA
<213> Artificial Sequence

<220>
<223> OUL3-05-II

<400> 42
atgaaaacat ttgccgcata tgtaattatc gcgtgtcttt cgagtacggc attagctggt 60

tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc 120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacattcaaa attcctaatg ctctaatagg tcttgaaacc 240

ggcgccataa aagatgaacg gcaggttttc aaatgggacg gcaagcccag agccatgaag 300

caatgggaaa aagacttaaa gctaaggggc gctatacagg tttctgctgt tccggtattt 360

caacaaattg ccagagaagt tggcgaaata agaatgcaaa aataccttaa cctgttttca 420

tacggcaacg ccaatatagg gggaggcatt gacaaattct ggctagaagg tcagcttaga 480

atctcagcat tcaatcaagt taaattttta gagtcgctct acctgaataa tttgccagca 540

tcaaaagcaa accaactaat agtaaaagag gcaatagtta cagaagcaac tccagaatat 600

atagttcatt caaaaactgg gtattccggt gttggcacag aatcaagtcc tggtgtcgct 660

tggtgggttg gttgggtaga gaaaggaact gaggtttact tttttgcttt taacatggac 720

atagacaatg agagtaaatt gccgtcaaga aaatccattc ccaccaaaat catggcaagt 780

gagggcatca ttggtggcta agctgtgaag atcccagcaa aggctta 827

<210> 43
<211> 266
<212> PRT
<213> Artificial

<220>
<223> OUL3-05-II

<400> 43

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

Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Ala Ile Lys Asp Glu Arg Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Lys Asp Leu Lys Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

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

Asn Ile Gly Gly Gly Ile Asp Lys Phe Trp Leu Glu Gly Gln Leu Arg
145 150 155 160

Ile Ser Ala Phe Asn Gln Val Lys Phe Leu Glu Ser Leu Tyr Leu Asn
165 170 175

Asn Leu Pro Ala Ser Lys Ala Asn Gln Leu Ile Val Lys Glu Ala Ile
180 185 190

Val Thr Glu Ala Thr Pro Glu Tyr Ile Val His Ser Lys Thr Gly Tyr
195 200 205

Ser Gly Val Gly Thr Glu Ser Ser Pro Gly Val Ala Trp Trp Val Gly
210 215 220

Trp Val Glu Lys Gly Thr Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225 230 235 240

Ile Asp Asn Glu Ser Lys Leu Pro Ser Arg Lys Ser Ile Pro Thr Lys
245 250 255

Ile Met Ala Ser Glu Gly Ile Ile Gly Gly
260 265

<210> 44
<211> 801
<212> DNA
<213> Artificial

<220>
<223> OUL3-05-III

<400> 44
atgaaaacat ttgccgcata tttagttctc gcgtgtcttt cgagtacggc attagctggt 60

tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc 120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg tctagaaact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaaata agaatgcaga aatatcttaa aaaattttca 420

tatggtaacc agaatatcag tggtggcatt gacaaattct ggctagaagg tcagcttaga 480

atctcagcat tcaatcaagt taaattttta gagtcgctct acctgaataa tttgccagca 540

tcaaaagaaa atcagctaat agtaaaagag gctttggtaa cggaggctgc gcctgaatat 600

cttgtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg gttgggttga gaagggagca gaggtttact ttttcgcatt taacatggat 720

atagacaacg aaaataagtt gccgctaaga aaatccattc ccaccaaaat catggcaagt 780

gagggcatca ttggtggcta a 801

<210> 45
<211> 266
<212> PRT
<213> Artificial

<220>
<223> OUL3-05-III

<400> 45

Met Lys Thr Phe Ala Ala Tyr Leu Val Leu Ala Cys Leu Ser Ser Thr
1 5 10 15

Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

Glu Ile Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Asn Gln
130 135 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Gly Gln Leu Arg
145 150 155 160

Ile Ser Ala Phe Asn Gln Val Lys Phe Leu Glu Ser Leu Tyr Leu Asn
165 170 175

Asn Leu Pro Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
180 185 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
210 215 220

Trp Val Glu Lys Gly Ala Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225 230 235 240

Ile Asp Asn Glu Asn Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
245 250 255

Ile Met Ala Ser Glu Gly Ile Ile Gly Gly
260 265

<210> 46
<211> 801
<212> DNA
<213> Artificial Sequence

<220>
<223> OUL3-05-IV

<400> 46
atgaaaacat ttgccgcata tgtaattatc gcgtgtcttt cgagtacggc attagctagt 60

tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc 120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaaata agaatgcaga aatatcttaa aaaattttca 420

tatggtaacc agaatatcag tggtggcatt gacaaattct ggttggaggg tcagcttaga 480

atttccgcag ttaatcaagt ggagtttcta gagtctctat ttttaaataa attgtcagca 540

tcaaaagaaa atcagctaat agtaaaagag gctttggtaa cggaggctgc gcctgaatat 600

cttgtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg gttgggttga gaagggagca gaggtttact ttttcgcatt taacatggat 720

atagacaacg aaaataagtt gccgctaaga aaatccattc ccaccaaaat catggcaagt 780

gagggcatca ttggtggcta a 801

<210> 47
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> OUL3_05_IV

<400> 47

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

Ala Leu Ala Ser Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

Glu Ile Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Asn Gln
130 135 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Gly Gln Leu Arg
145 150 155 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Phe Leu Asn
165 170 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
180 185 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
210 215 220

Trp Val Glu Lys Gly Ala Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225 230 235 240

Ile Asp Asn Glu Asn Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
245 250 255

Ile Met Ala Ser Glu Gly Ile Ile Gly Gly
260 265

<210> 48
<211> 801
<212> DNA
<213> Artificial Sequence

<220>
<223> OUL3-05-IX

<400> 48
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tttgtacttt gtaaaagtag tagcaattcc tgtactacaa ataatgcggc acgtgcatct 180

acagcctata ttccagcatc aacattcaaa attcctaatg ctctaatagg tcttgaaacc 240

ggcgccataa aagatgaacg gcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttaaa gctaaggggc gctatacagg tttctgctgt tccggtattt 360

caacaaattg ccagagaagt tggcgaaata agaatgcaaa aataccttaa cctgttttca 420

tacggcaacg ccaatatagg gggaggcatt gacaaattct ggctagaagg tcagcttaga 480

atctcagcat tcaatcaagt taaattttta gagtcgctct acctgaataa attgtcagca 540

tcaaaagaaa accaactaat agtaaaagag gcaatagtta cagaagcaac tccagaatat 600

atagttcatt caaaaactgg tttttctggt gttggcacag aatcaagtcc tggtgtcgct 660

tggtgggttg gttgggtaga gaaaggaact gaggtttact tttttgcttt taacatggac 720

atagacaatg agagtaaatt gccgtcaaga aaatccattc ccaccaaaat catggcaagt 780

gagggcatca ttggtggcta a 801

<210> 49
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> OUL3-05-IX

<400> 49

Met Lys Thr Leu Ala Ala Tyr Leu Val Leu Val Phe Tyr Ala Ser Thr
1 5 10 15

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Ala Leu Ser Glu Ser Ile Thr Glu Asn Leu Ala Trp Asn Lys Glu Phe
            20                  25                  30

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

Asn Ser Cys Thr Thr Asn Asn Ala Ala Arg Ala Ser Thr Ala Tyr Ile
    50                  55                  60

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

Gly Ala Ile Lys Asp Glu Arg Gln Val Phe Lys Trp Asp Gly Lys Pro
                85                  90                  95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Lys Leu Arg Gly Ala Ile
            100                 105                 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
        115                 120                 125

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

Asn Ile Gly Gly Gly Ile Asp Lys Phe Trp Leu Glu Gly Gln Leu Arg
145                 150                 155                 160

Ile Ser Ala Phe Asn Gln Val Lys Phe Leu Glu Ser Leu Tyr Leu Asn
                165                 170                 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Ile
            180                 185                 190

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

Ser Gly Val Gly Thr Glu Ser Ser Pro Gly Val Ala Trp Trp Val Gly
    210                 215                 220

Trp Val Glu Lys Gly Thr Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225                 230                 235                 240

Ile Asp Asn Glu Ser Lys Leu Pro Ser Arg Lys Ser Ile Pro Thr Lys
                245                 250                 255

Ile Met Ala Ser Glu Gly Ile Ile Gly Gly
            260                 265
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<210> 50
<211> 801
<212> DNA

<213> Artificial Sequence

<220>
<223> OUL3-05-X

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tcaattacag aaaatacgtc ttggaacaaa gagttctctg ccgaagccgt caatggtgtc 120

ttcgtgcttt gtaaaagtag cagtaaatcc tgcgctacca atgacttagc tcgtgcatca 180

aaggaatatc ttccagcatc aacatttaag atccccaacg caattatcgg cctagaaact 240

ggtgtcataa agaatgagca tcaggttttc aaatgggacg gaaagccaag agccatgaag 300

caatgggaaa gagacttgac cttaagaggg gcaatacaag tttcagctgt tcccgtattt 360

caacaaatcg ccagagaagt tggcgaagta agaatgcaga aatatcttaa aaaattttca 420

tatggtaacc agaatatcag tggtggcatt gacaaattct ggttggaagg tcagcttaga 480

atttccgcag ttaatcaagt ggagtttcta gagtctctat ttttaaataa attgtcagca 540

tcaaaagaaa atcagctaat agtaaaagag gctttggtaa cggaggctgc gcctgaatat 600

cttgtgcatt caaaaactgg tttttctggt gtgggaactg agtcaaatcc tggtgtcgca 660

tggtgggttg gttgggttga gaagggagca gaggtttact ttttcgcatt taacatggat 720

atagacaacg aaaataagtt gccgctaaga aaatccattc ccaccaaaat catggcaagt 780

gagggcatca ttggtggcta a 801

<210> 51
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> OUL3-05-X

<400> 51

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

Ala Leu Ala Gly Ser Ile Thr Glu Asn Thr Ser Trp Asn Lys Glu Phe
20 25 30

Ser Ala Glu Ala Val Asn Gly Val Phe Val Leu Cys Lys Ser Ser Ser
35 40 45

Lys Ser Cys Ala Thr Asn Asp Leu Ala Arg Ala Ser Lys Glu Tyr Leu
50 55 60

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

Gly Val Ile Lys Asn Glu His Gln Val Phe Lys Trp Asp Gly Lys Pro
85 90 95

Arg Ala Met Lys Gln Trp Glu Arg Asp Leu Thr Leu Arg Gly Ala Ile
100 105 110

Gln Val Ser Ala Val Pro Val Phe Gln Gln Ile Ala Arg Glu Val Gly
115 120 125

Glu Val Arg Met Gln Lys Tyr Leu Lys Lys Phe Ser Tyr Gly Asn Gln
130 135 140

Asn Ile Ser Gly Gly Ile Asp Lys Phe Trp Leu Glu Gly Gln Leu Arg
145 150 155 160

Ile Ser Ala Val Asn Gln Val Glu Phe Leu Glu Ser Leu Phe Leu Asn
165 170 175

Lys Leu Ser Ala Ser Lys Glu Asn Gln Leu Ile Val Lys Glu Ala Leu
180 185 190

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

Ser Gly Val Gly Thr Glu Ser Asn Pro Gly Val Ala Trp Trp Val Gly
210 215 220

Trp Val Glu Lys Gly Ala Glu Val Tyr Phe Phe Ala Phe Asn Met Asp
225 230 235 240

Ile Asp Asn Glu Asn Lys Leu Pro Leu Arg Lys Ser Ile Pro Thr Lys
245 250 255

Ile Met Ala Ser Glu Gly Ile Ile Gly Gly
260 265

<210> 52
<211> 1056
<212> DNA
<213> Kluyveromyces

<400> 52
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gtcaagtact ccggtgtgtg ccacactgac ttgcacgcct accacggtga ctggccattg 180

ccagttaagt tgcctctagt cggtggccac gagggtgccg gtgtcgttgt cgccatgggt 240

gagaacgtca agggctggaa ggtcggtgac ttggccggta tcaagtggtt gaacggctcc 300

tgtatgtcct gtgagtcctg tgagttgggt aacgagtcca actgtccaga ggctgacttg 360

tccggttaca cccacgacgg ttctttccag cagtacgcta ctgccgatgc cgtccaggcc 420

gctaagatcc cagctggcgc tgaccttgct gagatcgccc caatcctgtg tgccggtatc 480

actgtctaca aggctttgaa gtctgctaac ttgcaggccg gtgactgggt tgccatctcc 540

ggtgccgccg gtggtttggg ttccctagcc gtccagtacg ccaaggccat gggttaccgt 600

gtcttgggta tcgacggtgg tgaggagaag gagcagctct tcagacagtt gggtggtgag 660

gtcttcatcg acttcagaac ctgcaaggac atcgagggtg agatcatcaa ggccaccaac 720

ggtggtgctc acggtgtcat caacgtctct gtctccgagg ccgccatcga gtcctctacc 780

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aacagagctg acaccagaga ggctctagac ttcttcgtcc gtggtttggt cagatctcca 960

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attgttggca gatacgttgt cgacacctcc aactaa 1056

<210> 53
<211> 1045
<212> DNA
<213> Saccharomyces

<400> 53
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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 ccgacttggc ccaagtcgcc cccatcttgt gtgctggtat caccgtctac 480

aaggctttga agtctgctaa cttgatggcc ggtcactggg ttgctatctc cggtgctgct 540

ggtggtctag gttctttggc tgttcaatac gccaaggcta tgggttacag agtcttgggt 600

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gacttcacta aggaaaagga cattgtcggt gtgttctaaa ggccactgac ggtggtgctc 720

acggtgtcat caacgtttcc gttccgaagc cgctattgaa gcttctacca gatacgttag 780

agctaacggt accaccgttt tggtcggtat gccagctggt gccaagtgtt gttctgatgt 840

cttcaaccaa gtcgtcaagt ccatctctat tgttggttct tacgtcggta acagagctga 900

caccagagaa gctttggact tcttcgccag aggtttggtc aagtctccaa tcaaggttgt 960

cggcttgtct accttgccag aaatttacga aaagatggaa aagggtcaaa tcgttggtag 1020

atacgttgtt gacacttcta ataa 1045

<210> 54
<211> 1047
<212> DNA
<213> Artificial

<220>
<223> Clon A02

<400> 54
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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 aactgtccag aggctgactt gtccggttac 360

acccacgacg gttctttcca gcagtacgct actgccgatg ccgtccaggc cgctaagatc 420

ccagctggcg ctgaccttgc tgagatcgcc ccaatcctgt gtgccggtat cactgtctac 480

aaggctttga agtctgctaa cttgcaggcc ggtgactggg ttgccatctc cggtgccgcc 540

ggtggtttgg gttccctagc cgtccagtac gccaaggcca tgggttaccg tgtcttgggt 600

atcgacggtg gtgaggagaa ggagcagctc ttcagacagt tgggtggtga ggtcttcatc 660

gacttcagaa cctgcaagga catcgagggt gagatcatca aggccaccaa cggtggcgct 720

cacggtgtca tcaacgtctc tgtctccgag gccgccatcg agtcctctac caactacgtc 780

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gttttcaacc aggtcgtcaa gtccatctct atcgtcggtt cttacgtcgg taacagagct 900

gacaccagag aggctctaga cttcttcgtc cgtggtttgg tcagatctcc aatcaaggtt 960

gtcggtctat ctactctacc agagattttc gagaagatgg agaagggcca aattgttggc 1020

agatacgttg tcgacacctc caactaa 1047

<210> 55
<211> 1060
<212> DNA
<213> Artificial

<220>
<223> Clon A03

<400> 55
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cggtaagttg gaatacaaag atattccagt tccaaagcca aaggccaacg aattgttgat 120

caacgttaaa tactctggtg tctgtcacac tgacttgcac gcttggcacg gtgactggcc 180

attgccagtt aagctaccat tagtcggtgg tcacgaaggt gccggtgtcg ttgtcgccat 240

gggtgagaac gtcaagggct ggaaggtcgg tgacttggcc ggtatcaagt ggttgaacgg 300

ctcctgtatg tcctgtgagt cctgtgagtt gggtaacgag tccaactgtc cagaggctga 360

cttgtccggt tacacccacg acggttcttt ccagcagtac gctactgccg atgccgtcca 420

ggccgctaag atcccagctg gcgctgacct tgctgagatc gccccaatcc tgtgtgccgg 480

tatcactgtc tacaaggctt tgaagtctgc taacttgcag gccggtgact gggttgccat 540

ctccggtgcc gccggtggtt tgggttccct agccgtccag tacgccaagg ccatgggtta 600

ccgtgtcttg ggtatcgacg gtggtgagga gaaggagcag ctcttcagac agttgggtgg 660

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gtgcaagtct gacgttttca accaggtcgt caagtccatc tctatcgtcg gttcttacgt 900

cggtaacaga gctgacacca gagaggctct agacttcttc gtccgtggtt tggtcagatc 960

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ccaaattgtt ggcagatacg ttgtcgacac ctccaactaa 1060

<210> 56
<211> 1047
<212> DNA
<213> Artificial

<220>
<223> Clon A05

<400> 56
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tccggtgtgt gccacactga cttgcacgcc taccacggtg actggccatt gccagttaag 180

ttgcctctag tcggtggcca cgagggtgcc ggtgtcgttg tcgccatggg tgagaacgtc 240

aagggctgga aggtcggtga cttggccggt atcaagtggt tgaacggctc ctgtatgtcc 300

tgtgagtcct gtgagttggg taacgagtcc aactgtccag aggctgactt gtccggttac 360

acccacgacg gttctttcca gcagtacgct actgccgatg ccgtccaggc cgctaagatc 420

ccagctggcg ctgaccttgc tgagatcgcc ccaatcctgt gtgccggtat cactgtctac 480

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cacggtgtca tcaacgtctc tgtctccgag gccgccatcg agtcctctac caactacgtc 780

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gttttcaacc aggtcgtcaa gtccatctct atcgtcggtt cttacgtcgg taacagagct 900

gacaccagag aggctctaga cttcttcgtc cgtggtttgg tcagatctcc aatcaaggtt 960

gtcggtctat ctactctacc agagattttc gagaagatgg agaagggcca aattgttggc 1020

agatacgttg tcgacacctc caactaa 1047

<210> 57
<211> 1047
<212> DNA

<213> Artificial

<220>
<223> Clon A06

<400> 57
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tacaaagata ttccagttcc aaagccaaag gccaacgaat tgttgatcaa cgttaaatac 120

tctggtgtct gtcacactga cttgcacgct tggcacggtg actggccatt gccagttaag 180

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aagggctgga agatcggtga ctacgccggt atcaaatggt tgaacggttc ttgtatggcc 300

tgtgaatact gtgaattggg taacgagtcc aactgtccag aggctgactt gtctggttac 360

acccacgacg gttctttcca acaatacgct actgccgatg ccgtccaggc cgctaagatc 420

ccagctggcg ctgaccttgc tgagatcgcc ccaatcctgt gtgccggtat cactgtctac 480

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gttttcaacc aggtcgtcaa gtccatctct atcgtcggtt cttacgtcgg taacagagct 900

gacaccagag aggctctaga cttcttcgtc cgtggtttgg tcagatctcc aatcaaggtt 960

gtcggtctat ctactctacc agagattttc gagaagatgg agaagggcca aattgttggc 1020

agatacgttg tcgacacctc caactaa 1047

<210> 58
<211> 1049
<212> DNA
<213> Artificial

<220>
<223> Clon A10

<400> 58
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tacaaggaca tcgatgtccc aaccccaaag gccaacgagc ttttggtcaa cgtcaagtac 120

tccggtgtgt gccacactga cttgcacgcc taccacggtg actggccatt gccagttaag 180

ttgcctctag tcggtggcca cgagggtgcc ggtgtcgttg tcgccatggg tgagaacgtc 240

aagggctgga aggtcggtga cttggccggt atcaagtggt tgaacggctc ctgtatgtcc 300

tgtgagtcct gtgagttggg taacgagtcc aactgtccag aggctgactt gtccggttac 360

acccacgacg gttctttcca gcagtacgct actgccgatg ccgtccaggc cgctaagatc 420

ccagctggcg ctgaccttgc tgagatcgcc ccaatcctgt gtgccggtat cactgtctac 480

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ggtggtttgg gttccctagc cgtccagtac gccaaggcca tgggtttacc gtgtcttggg 600

tatcgacggt ggtgaggaga aggagcagct cttcagacag ttgggtggtg gaggtcttca 660

tcgacttcag aacctgcaag gacatcgagg gtgagatcat caagcccacc aacggtggtg 720

ctcacggtgt catcaacgtc tctgtctccg aggccgccat cgagtcctct accaactacg 780

tcagagccaa cggtaccgtc gtcttggtcg gtttgccagc tggcgccaag tgcaagtctg 840

acgttttcaa ccaggtcgtc aagtccatct ctatcgtcgg ttcttacgtc ggtaacagag 900

ctgacaccag agaggctcta gacttcttcg tccgtggttt ggtcagatct ccaatcaagg 960

ttgtcggtct atctactcta ccagagattt tcgagaagat ggagaagggc caaattgttg 1020

gcagatacgt tgtcgacacc tccaactaa 1049

<210> 59
<211> 1047
<212> DNA
<213> Artificial

<220>
<223> Clon A11

<400> 59
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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 gcagtacgct actgccgatg ccgtccaggc cgctaagatc 420

ccagctggcg ctgaccttgc tgagatcgcc ccaatcctgt gtgccggtat cactgtctac 480

aaggctttga agtctgctaa cttgcaggcc ggtgactggg ttgccatctc cggtgccgcc 540

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gttttcaacc aggtcgtcat gtccatctct atcgtcggtt cttacgtcgg taacagagct 900

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