eolf-seql

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agcaaattta cacattgcca ctaaacgtct aaacccttgt aatttgtttt tgttttacta 960
tgtgtgttat gtatttgatt tgcgataaat ttttatattt ggtactaaat ttataacacc 1020
ttttatgcta acgtttgcca acacttagca atttgcaagt tgattaattg attctaaatt 1080
atttttgtct tctaaataca 1100

<210> 213
<211> 1226
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 213
gttaattata gatatatttt aggtagtatt agcaatttac acttccaaaa gactatgtaa 60
gttgtaaata tgatgcgttg atctcttcat cattcaatgg ttagtcaaaa aaataaaagc 120
ttaactagta aactaaagta gtcaaaaatt gtactttagt ttaaaatatt acatgaataa 180
tccaaaacga catttatgtg aaacaaaaac aatatgtcga ggcgatcgca gtacttaatc 240
agtgatcagt aactaaattc agtacattaa agacgtccgc aatgtgttat taagttgtct 300

aagcgtcaat ttgttgtcgg caagatctct gacactcaac taaaatgttg gattttccct 360
ttcaggtgta tgctcacaag gtctataaat atcttgagac tccactgctg tctctgagtg 420
agataagaga caacgaccgt attgtcgcat ataggttcaa ccagatgcac agaggaccag 480
gaaaagccaa actagagatt cttcactcgg agcagaaaca gtaagcattc gagaattctt 540
taggttctgt ctatctttca aatctcacag gtctgatttt ggcagagacg cagagatttc 600
tggaaagtta tttggaattc cccttgttac ttatgtcaac tcagaacgac atagtggaag 660
tgacattgat gcaattattt ctggattgct atcaccgcta caccggactc attcatcatc 720
tggaagctta gaggatacta cagttggtga aaaagagttt tctttcagcg tcttctggtt 780
agatcgttat tcttccagtc tcaagccact tgagtccgat tttgttccga atcctcttag 840
tgctacaagg ctcgtagtca agtgggacga gaaagagcat gaaaaatatg attcaagcag 900
ctacttgaat gatctacctg aggtttataa agcaacttcc tcggtggcgg aaaaggtttc 960
tttgttttca tgcttggaag cctttctagc agaagagcct ctcggaccag atgatatgtg 1020
gtgttgtcct gcttgcaaag aacacaggca agcgaacaag aagctgaact tgtggaagtt 1080
gccagagatt cttgtgttcc acctaaaacg gttcgcctat accagatttt taaagagtaa 1140
gattgatacg ttcgtggatt ttccgattca tgacttagat ttaagcaagt acgtgaagaa 1200
taaagagggt gagtcgtatc tttacg 1226

<210> 214
<211> 2100
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 214
acatcatctt gcaaccgact tgaataatca cgtccaccaa cctaacaaca gaggagaaga 60
ggttatcatc gcagatggct ccctcttctc atcgcagatg gctcaggtct tccaatcaca 120
catattggtt cctccattga tcacaaaaat tttaaaggaa tttttaacat tttttgtaat 180
ttaaagttgt tttaaaaatt tcaaagtata atatataaga aaaaatctaa tttttattat 240
tatatggtta atgtgattgt ttattttttt aataatataa aattaaacaa aaatgaggaa 300
agatgcaaaa gttgttatca aatctttatt attcataatc attaattgtc atatatatgt 360
tagttatatt aggtaattcc gtagctttta tttaaggaaa aaatacacac tgtttttatt 420
ttgggttaat ataactttcc ctagtaattg gattttacac caacattttt tcaattgatt 480
cttaagctgc catgtaagct aaatttgcat actaattaag tgacacctaa gtagggtttc 540
tttttaatta gtacaaactt aatgttacaa ttttttaaat gatcttcaat taatatatag 600
gggataagac acaacctcct cttatgattg tgtaatatta atagtcctca tataccttca 660
attatttata tgcagtagta gatgcagtat gaagggaaga ggtgtgattc ggagatgcag 720
tagtagtcaa ttggaaccga agaatgagag gaggaggagt gtgggttatt gtcgctgcca 780
gatgatgtgg ctttggattg cctggttcag gtgtcgagac tggacctggt gggcttagcc 840
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cggctgggta acttggaccc atatttgtgc gtatttatac actccaagcc caaggtggtt 960
cgtcctccac accctgcaac attggctcaa accggtccat tcaagcttgt atccggctcc 1020
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tgattttaaa actggaacgt gagagttttt gtttgtattt acgcccaaga tgcccctcaa 1320
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gcctaaccca gaaaatagaa acgattggtt tttatttgag gtaataatgt gccgtggtat 1500
cggcgggaga atactgtggc gttggccaga tgagattctt tagaaagaag tcaaaggttt 1560
ggaagagctg cagcaacaac acatcatcaa aatctgctcc ttctctgaga agacgattgc 1620
catcttctgg gatgcccggt ggcctcaaca aggtctagga gctttggtat gccgagattt 1680
ccatgaagag acaccaggga gacgaggggt ggtggaaggt ttgggggaac attgagagtt 1740
ccgctgctgt tatctcagac tcatcgcata gttcctttaa cttgttatat gctgctactg 1800
tctttgcctg aattactatt ctcaagcaat cctttggttt tttatataat ttgtttctat 1860
tttatctttt gattgcaaca tgttatcaca aaccaaacta atcggtaacg ttattgctta 1920
aacatatcat aagctaagca aatcacacac ctccccaatc catggatatg ttctctcttt 1980
tctcaatcaa tttgtttaca ctcaaacact gatagtttaa actgaaggcg ggaaacgaca 2040
atctgatcac tgattagtaa ctaaggcctt taattaatct agaggcgcgc cgggcccccc 2100

<210> 215

<211> 2065
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 215
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cgttgtgtta tattcagtct aaaacaaggc gcctactacc ggtaattccc gggattagcg 120
gccgctagtc tgtgcgcact tgtatcctgc aggtcaatcg tttaaacact gtacggaccg 180
tggcctaata ggccggtacc caactttatt atacatagtt gataattcac tggccggatg 240
taccgaattc gcggccgcaa gcttgtacac tagtacgcgt caattggcga tcgcagtact 300
taatcagtga tcagtaacta aattcagtac atcaaccgta tttagtttta atttttataa 360
gatttttaca caattataac tttgtttaaa ttaaaatttt attataatat ttttaggtaa 420
ataaaaagtg tggttctaat ggtaaatttc tctgtctgct ccatctatga catcttttgc 480
ggttatcacc tttgctcttt gttagcatca tgtttttttgt aacttttta attctggttt 540
gtggcagtgg gctccttttc atctgttttg gcaatgacac agctggttgc ttttgaaatc 600
atgctctgtg tttatggctg gtgtgttgtt tatgatacat ttggttgtgt ccctgaatcc 660
ttgtgttgca gttgtttatg atagatttgg ttgtgtccta ctattgtttg cgttcggatt 720
gcgattttgg actggacttg gtttcttagt tgtatttcat ttcgaaaaat tgtaactcgt 780
tatatttttt ttttcttttt gttcttaggg aagaatgatt attgctcatt tatgtgatga 840
gctgaaagaa ctgaaaacaa ttatgtgcat ggtaatattc ctttgcactt gcaaacgcaa 900
taaccgcaag attgaatgat gggtaggtaa attttttttt ttttttttgt ttatggtcat 960
tgcataacat acttttattg gaaattgtct tctcttaaga atgaatgggt ggtttgagac 1020
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ttatttttttg ctgtaatata ataatggaaa tgataaaaat gtataactat agatttttca 1320
gatagatgtt taatgtaata ttccatttct tatattgtac atttaattat tatttatttt 1380
tcttatatta tatatttatt tattttaatt attttgcctt tcatcaaatg gtaatattat 1440
gatagatgtt taatgtaata tttatttttc ttctattgta tatttacatc tttttatgtt 1500
ttcttataat ttaatataaa aatgtaaaac tatacatttt taaatagatg tttaatgtag 1560
tatttccatt tcttatattg tgtatttact tattttaatt ttcttccttt tatatcaaat 1620
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tgtttttata atgtattaat gtcgtgtggc atcttttgga agaaggattt tatgttgaga 1740
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acgggcgggt taattacact aaactatttc atattagaat atattttaat tttataaaat 1860
atttgaatat ttactttata ttaaaataat aaatacaatc tatttttatt tctttttatt 1920
ctaagatcat atcataactt ttattaaaat tttttggttt taattataaa gatcaataac 1980
atttttttct gagaaaacaa aattaataaa ttaaagttaa tgaacattta atgatttata 2040
tttttctatt tgatttatat ttcaa 2065

<210> 216
<211> 1500
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 216
atgtatgtgt agattcttgt aattttgcaa taataaaaaa atgtggctta gattaaaaaa 60
aagagttata tatgttgttt ttacattagg tgaggactct gttgtaaaaa aaatgtgatt 120
tgtttttttа tagatgtggt aattttatat atatctcaag gtctcttgtg gattagatag 180
agagtgaatg attaaatgtt tttaaagtgg gctctcctat tgcaataatc taaaaataaa 240
ggtttgtttg ttatacacaa taatttttaa gagagaattt taaacaaaaa atattactcc 300
aatcaaaaat agcattttct aaaaaatatc tcattctcaa ttgatataat ttcttctttt 360
catttgttca ttttatacta cttatttttg gtttaagaaa cttctaaaaa accttcaact 420
gaaaatgctt ttatgcttct aacatttatt tcaaagactt ctgatttatg tttggaacaa 480
atgaaataga gaagcaattc catgaattga agtgattaat gtatgttttg caacaattaa 540
aaatgttgct tgtaagtttg caacaattta aaaataaaaa ggtctaatct gtttttcatt 600

tttcattttt tcacatttag gtgatgagta gttgtagtat aacttaaatg gtggtttgtc 660
ttgttatatt tggttgtcat ttctttattt caagatcttt gatttttttt ttttacaaaa 720
cacatggaat gaattccatg catttgttaa ttgttttgga attttttttg tactctattt 780
aggtgttagg actctactgt agtatgacct aacatagtgg tgatatgttg atcaaatttt 840
gtgtgacatt tatatgaagg tcttttgatt tatatttagt aaaatgaaat agagagggaa 900
gtttatatga aggtctccag aaattgaagt gactcatgaa tgtttagtta agtaaagatc 960
aatggacttt catcaccaaa tatatatttt ttaaactata caaaaaaaaa tccttttttat 1020
tttaaagaag tttaattata tttaaaaatg atttaaatgt acgtaataat tataaacaga 1080
atattctttt gtagagtgga cctaatgcaa gtaggcaaga tccgacaaaa caagttaaag 1140
acacacccca ccaaaagcaa ccaagagaga cgtctttaat gtactgaatt tagtaactga 1200
aggcgggaaa cgacaatctg atcactgatt agtaactaag gcctttaatt aatctagagg 1260
cgcgccgggc cccctgcagg gagctcggcc ggccaattta aattgatatc ggtacatcga 1320
ttacgccaag ctatcaactt tgtatagaaa agttgccatg attacgccaa gcttggccac 1380
taaggcaaat ttcgcgccct gcagcaaatt tacacattgc cactaaacgt ctaaaccctt 1440
gtaatttgtt tttgttttac tatgtgtgtt atgtatttga tttgcgataa atttttatat 1500

<210> 217
<211> 1948
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 217
cggccgagct ccctgcaggg ggcccggcgc gcctctagat taattaaagg ccttagttac 60
taatcagtga tcagattgtc gtttcccgcc ttcagtttaa actatcagtg ttgctttagt 120
ggtcaatcaa aagatgaaca gtatcttctc gatcgatgat ttctccgatc ccttttggga 180
atcttctccg cctctcgatt cggactcggc caaggccctc acggcggagg aatggaccgt 240
ggagatgttt ttcgaagaga tcgcttcctc cgtgacctct gcgcctgtcg gatccaacaa 300
caacaacaac aacgcgatcg tcggagtttc gtcggcgcag tctcttcctt ccgtctccgg 360
acagaacgat ttcgaggaag acagtcggtt tctccgtcgc gaatcagatg attaccgtcg 420
cgttcttgag aacaagctcg agactgagtg tgcagctact gttgtagctc ttagggtttg 480
tcttctgttt ctctttttttt tatattgcat gtgtaagaag aagaagaaga tctgaatctt 540
aaagctttgt ttgttctctc tgcttgtgtt gtgtaggctg gttctgtgaa gcctgaagat 600
tcgactggtt ctcctgagac tctgtttcaa ccagctctgt ctagtcctct tactcaaggt 660
aataggtgct catcatgcaa attagttttt tacactacat agcttgtctc ttagcttcac 720
catgtttgaa attttttatg ccaagaaagt gttctaaaaa tcggtctagg cgcctagtcg 780
gcaaatcggg tctgtacgaa atgatttttt caaatcgatt tgaaaatcgg tctagacgtc 840
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atgatgacgc tgccgttggc aatagaatac taaaagccga catcgagaca ctaagagcta 1680
aggtaataac accttctttt ttttcataac cacactaatg ttttgttact ataactaatt 1740
gtatttgatc aaggtgaaaa tggcggaaga gacggttaag agagtaacag gaatgaaccc 1800
tatgcttctc ggtagatcaa atggacataa caacaacaac aatagaatgc cattaactgg 1860
taatagcagg atgggtggtt cttcatgcat cccacctttt caaccgcaat caaatccaaa 1920
catgggggga ctaacaacaa ccattcta 1948

<210> 218
<211> 1600
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 218
caagaccaca agattgcatc tctttgaaag tctcttcagc ccttttgaaa tctccttggc 60
aacaaaatcc attaacaaga gatgagtaag tcaccacgtt tggcttacac ttggtcttac 120
ccatgtctcg aaaaatcttt aaggcggtag tcatatcctg ttgcttcacg tacccatcga 180
tgattgtgga ataagtgaac tcatcaggta caagtctttc ttcggtcatc ctattcatac 240
acatcaatgc ctcattcaac attccggatc tgcaaaaccc ctttatcata gcgttgtggt 300
gcacgacatc aaccttcaca ccctttttcaa ttgagagaga ggaaaccttc tttgcttcct 360
caaaatcacc gcttctgatg aatccatcta tgagggtagc atacacataa gcatccggtg 420
aaattttccg gtctaacatc tccaagaaga ggagcttggc agatgaaaac ccacctctct 480
tacacaaccc actcatcaac atattgtaga tggcagcatc cggtgaaact cctctctcta 540
tcattttacc tttcatctta attgcatcat ccatatgacc tgaagcgaca agaccatgga 600
taagaatccc atacgtaact atatctggtt tgcaacctct ctcagccatc tgcagaagca 660
acttagaagc aatatcatac tctttgactc tgcaataacc ttgtattaga ggggcatagg 720
ttatattgtt ccgaaccaac cctctctttg cagcttcatc caaaatccca acagcatctt 780
ccatcctacc ttctttacat aaacgattga tcaaaatatt atatgttgct atatcaggct 840
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atttgatctg tgtttttttg gccttaatac taaatcctta cataagcttt gttgcttctc 1440
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tggaagttgt tgagaggttc tacggagagt tggatggaaa ggtttcccaa ggagtgaacg 1560
ctttgttggg atctttcgga gttgagttga ctgatacccc 1600

<210> 219
<211> 955
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 219
ttttgaacaa gtaaatccaa aaaaaaaaaa aaaaatctca actcaacact aaattatttt 60
aatgtataaa agatgcttaa aacatttggc ttaaaagaaa gaagctaaaa acatagagaa 120
ctcttgtaaa ttgaagtatg aaaatatact gaattgggta ttatatgaat ttttctgatt 180
taggattcac atgatccaaa aaggaaatcc agaagcacta atcagacatt ggaagtagga 240
ttaatcagtg atcagtaact attaaattca attaaccgcg gacatctaca tttttgaatt 300
gaaaaaaaat tggtaattac tctttctttt tctccatatt gaccatcata ctcattgctg 360
atccatgtag atttcccgga catgaagcca tttgtcaacg tcgttgtttg atttcgttaa 420
ggggagagca gtccaagtgt gtttttaatc tcagataggc ctaacatcta gatttatttc 480
agactaaccc aaaaccgaaa cttttgcatt caagtcatct ttcgtgttga ttcgtaattc 540
tttttttcac attcaacttt ttggtagcag caggttcaga agattcattc ggtttttcaa 600
tgtttcagag taacactaga tttgtttcag attaaaccga aaaatcggat tcgttcagaa 660
gttttatttg gtatgactat gttccggtat gtgatcaata agaaccactt gagttcggtc 720
gagttgtttt ttttttttga acttttgtat ctgatcagtt cggatagact cgaaaaagga 780
aaagtaaagt ctaatagaca tcaatatttt gacaaaatat caaaaaatca atatacaata 840
ctaaaagggg atataagcca tggagagggt atccacgtaa gataggaaaa tcaaccaatc 900
agagaaccca aaattttcac atcatctcaa ttatttttcg taaaaaatac aatac 955

<210> 220
<211> 2199
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 220
aaactgaaac tttcaaattc caaagttcga tcagtgtttc taataatcag caaacctgtt 60
gaagaagaca aagtaattgg caaagtaaat tccattattt catacctct tctttgattc 120
tagtgaagaa gacaaatcaa aatattaatc ttctgctaaa aaactgaaac tttcaagttc 180
caaatttcca aaaaacacat ttctccttaa tagacctttt aacatcaatt caaactacag 240
tccacaagct tttcacatga actggcacaa taaactgcat tcatattctt tggttctagt 300
gaagaagacg catcaaaaac tgtagcagct aaaaaaaaaa ctgaaacttt caagttccaa 360
agttgtacca gtgtttctaa taatgagcaa acctgttgaa agcttttgac ggttttgcca 420
agactcttgc caatctcagg aagcttctta ggtccgaaca gcaacgcagc gactccagcg 480
atcacagcta gctcagggac accgagacca aacagagcat tacaagttag tgcatttctc 540
ctctgctccg gtcggaacgc cactagagaa cgggtgtatg gtcgagtcgt cacagtgaag 600
cagttgtagt agaaggaaga gcgagatgat gagagaggca aagaaactgc tgtgagagaa 660
gaaagagtcg caacatttgt cgccattact gctatcttct ggttctgatg ttatgtgtgt 720
tttctatgag tttttatcca attaaatatt cagaaatgtt atagaaacta aattaatctt 780
cttattgtct caactctaca tgcagtacaa aactcatctc atacgtagaa aagtagaaat 840
taataggaaa actagatcat cactcgcccg ggcggacgga tttttattcc tttgcaaacg 900
cggattgtaa tttttttatt gtaatgcaaa aattgctata aaacttgtat tttgattttt 960
tttgtgaatt atgaagttaa tttttttaaa acaattatta cataattgct cagtgaattt 1020
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tcacttaaaa gaagctgtta tgtttctaat ttaataagat agatttttaa taccatgttt 1140
aaaatatata ttataaaccc atgaactatg ttattttgta tgaatactta cttaaattta 1200
tgtttagaat ttataaaatt gtacataaaa ttatttaact cttgatgctt attattggtt 1260
gatgatatat tctctaataa attatttaat tattcaatat tgacatgtca agctgtttaa 1320
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acccacgatt ttcgtggtta cttgttagtc catatctcaa attaccattc taccgttaat 1560
gaggagtatt tatttttga aaatacaatg gcattttaag taatatgcca tgtaaaagta 1620
agggtaaata ttagcagtga tcctgaatta ataatattga tactagcaaa tgttttatta 1680
ttatcaaatt tgcagataaa catgattaat tctactaagt tcactaacag gaattaaata 1740
gttttagaaa atttagggag tgtattcaaa gtttaaggtg atttgtatta aaatgacagt 1800
tattcaaaca tgatttttaa atattcaaaa atctagtgtt attaaaattg ttatttgata 1860
aactacccag tcagcatcat cacaccaaaa gttaggcccg aatagtttga aattagaaag 1920
ctcgcaattg aggtctacag gccaaattcg ctcttagccg tacaatatta ctcaccggtg 1980
cgatgccccc catcgtaggt gaaggtggaa attaatggcg cgcctgatca ctgattagta 2040
actattacgt aagcctacgt agcgtcacgt gacgttagct aacgctacgt agcctcagct 2100
gacgttacgt aagcctacgt agcgtcacgt gagcttagct aacgctacct aggctcagct 2160
gacgttacgt aacgctagct agcgtcactc ctgcagcaa 2199

<210> 221
<211> 1748
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 221
aaacattttt tcagattttg aacaagtaaa tccaaaaaaa aaaaaaaaaa tctcaactca 60
acactaaatt attttaatgt ataaaagatg cttaaaacat ttggcttaaa agaaagaagc 120
taaaaacata gagaactctt gtaaattgaa gtatgaaaat atactgaatt gggtattata 180
tgaatttttc tgatttagga ttcacatgat ccaaaaagga aatccagaag cactaatcag 240
acattggaag taggattaat cagtgatcag taactattaa attcaattaa ccgcggacat 300
ctacattttt ttactgctat tctttcatat tagcaactgg ttgattactg aattagtaca 360
gatgtaacta acatatatat tggatattat tattatccaa aagagctatt caacctttta 420
agcatatgta tatacatgtt taattgattt tattagtatt tcttgctctt gttgttttgc 480
ttatattttt gtaatgattt atttatttt agttatttag ttttatcaaa gtggtgatta 540
agagaagcca catgactaat accttgttct ccaacttttt ggttaaaata aatttatcta 600
agatatattt tgatcgattg atatgaatgt tattataaca tttacaattt aaaaaataca 660

gtttttctt tctcatttac attgtttcct ttaggggtga acacttctgg ttattttatc 720
ggttcagttt agattcggtt cgatttggtt aattcagttt tataaatttt tccaactgga 780
gtaaccataa ttaattatgg tttgaatcgg tttaatttac cttaatcaga tccagtttaa 840
ttttttttt aaaaaataat attttataac acatggtgga tataaaaaat gaactatgta 900
aattaaatct aataaaaaac tgaaacacaa tcttaaaaaa ccacaaaagt ttataagaac 960
acaatcaaac caaaataaat agaaaactaa aaacccaaca ttgttaacac agttaatagt 1020
gactttagtt ttagaattta gtatattgta tattgctatt atgtttaatg taaataataa 1080
caaaaataca ttgtttttt ggttcagttc ggtttggttt gttcgagttg agaaaatctt 1140
aaatcaacct atttgataat agacgttggt ttggttcgga tcgatttcgg ttcggttggt 1200
ttgatttgac tcggtgttca ctgaatacaa tttattctat aacttatttg tcatacttta 1260
ttatcctgta atagagttcc ggtttaattt ggggtttggt ttgtgtttga tccggttttg 1320
ttaactcggg tttgataaaa ctccgaatta aatttggttt ggttggtacg ttttagttcg 1380
gtttaatttc caaatctata acacttgaca aaactcacat cctcgctctt ccttccccca 1440
accctaacaa aaaccttcac gctggggaga aaaaaagcaa caaccttcac cgtcgtctgc 1500
tgctcctcac caccgcgccg tcgaaaattg acctctaccc attactaggt aagcttccca 1560
gacccatcct acatcctcaa ttcactaaac aaacgctaaa gtctctacct ttatctcctc 1620
caatcgtaga tctaaagcta tggctatctc ccaagatctc tacccttccc aagaagacct 1680
cgtctacgag gaagagatcc tccgaaaccc cttcagcctc aagctctggt ggcgctacct 1740
catctcca 1748

<210> 222
<211> 1500
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 222
aaagagaaag caaagtggct tcgccgtgat cgccgagaga ggtcagaagt aaattaaaaa 60
aaaaaaaaaa tcaagagcta aggctcgaga gagatggcgt catcatagac taatcaccgt 120
tagaagatta gtaggaaaaa aaaagatgac acagagacga aagatcttaa cagttgaaca 180
cgtggcggaa aagcgaaatc cgatttaaca gatcggaaaa taaaaaccgg cgagattaaa 240
gaagaaagga gatagagaga agaggtacct tagatccgga tcctgtagat gtggagcagc 300
tcgcttggag actggtgtcc tcgaatccat cagccgaggg agacgcagat ccgccgccgc 360
tccacgagag cggcgtcttc ggactgcctc tagcggaatc aacatccttc ttcaacgaaa 420
cgacaccaaa tcttgacgac cgagaccgcc gttgacggac tccccaccgc aacggaggaa 480
ggttcgtcga tggatcttcc gaaaccaccg tcccagcatg cttcagccgg ataagaagct 540
ccacgaccat ctcgtcgtcc gtcatcgccg ccgccaccca ctcatcgttg accaacatct 600
tagccgctgc cgatgtaact ttcttcatcg acgctaactg atcaaatcta cagctcccgg 660
agaaaaaggg aatcagatac agtatagaag gagcgagaga gaatgaaaga gaagttacag 720
aagagagaga gaaaatgacg aagaaagaca gagggaagtt tgatgtatcg atatagagga 780
gagaaaaaaa gatacatggg tggtgttata tacgaggcta tctaacatta ttcttctttt 840
tatttttatt tttatttta tttttccttg tttcattttc atttatattt tgatttattt 900
tccattttgg aaatatttta atcaaataca atgtgggacc ttcttggaaa gtatatctaa 960
aattatatgt gaagattctc ctaataaaat tatatgtgaa gattctccta ataaacctcc 1020
agtcagcatc atcacaccaa aagttaggcc cgaatagttt gaaattagaa agctcgcaat 1080
tgaggtctac aggccaaatt cgctcttagc cgtacaatat tactcaccgg tgcgatgccc 1140
cccatcgtag gtgaaggtgg aaattaatgg cgcgcctgat cactgattag taactattac 1200
gtaagcctac gtagcgtcac gtgacgttag ctaacgctac gtagcctcag ctgacgttac 1260
gtaagcctac gtagcgtcac gtgagcttag ctaacgctac ctaggctcag ctgacgttac 1320
gtaacgctag ctagcgtcac tcctgcagca aatttacaca ttgccactaa acgtctaaac 1380
ccttgtaatt tgtttttgtt ttactatgtg tgttatgtat ttgatttgcg ataaattttt 1440
atatttggta ctaaatttat aacacctttt atgctaacgt ttgccaacac ttagcaattt 1500

<210> 223
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<220>
<221> misc_feature
<222> (578)..(578)
<223> n is a, c, g, or t

<400> 223
actcttgtaa attgaagtat gaaaatatac tgaattgggt attatatgaa tttttctgat 60
ttaggattca catgatccaa aaaggaaatc cagaagcact aatcagacat tggaagtagg 120
attaatcagt gatcagtaac tattaaattc aattaaccgc ggacatctac atttttgaat 180
tgaaaaaaaa ttggtaatta ctcttttctt ttctccatat tgaccatcat actcattgct 240
gatccatgta gatttcccgg ttctttttct cagactactc actgcccgaa gccactacta 300
ctacacacat tattatctct ctcacatctc tactatttac tcttggattc cgcaaagtaa 360
gtaaaaaaaa aagaaagcaa actctgcttc tcaaatctct ctctacccat ttgctctctc 420
acattttcct ttgaccaaaa ctgaatcttt acttcaagca gcgtaaggtg ctcgctcctt 480
tttgttcctc tgactttggt tttgatatga agttttcatg aaactctttc attacacttg 540
ctttttgaaa aaaaatgatg tagctttcct ggaaaatnta gtttcttttc attatcttgg 600
gatcttgtga tagattaaat gttatgttta cagttcttca tacctggtgg tcaaactctc 660
tttttctttg tttttgtaag ttttaaggtt taatgtttaa agctatttct gtgatgcact 720
gtgattgttt gctaatgctt tactttaatc aatctgatga ttgtttgctt cactcaagtg 780
gtttttataa attagattct ccttttttcat ggaaaaaaat tcatccagga atccaaatag 840
attttatttt tttgcttgtc ttgtctttga gtggagtatt aaatctattt actttatatt 900
aaattttttt ttatgtaaaa agatatttaa actcaattat gtgattcatg atagtagttc 960
ttcaacgtct actaggtccc ctccttttcac gccaataatg gaggagatga tgaaatttaa 1020
catacaaaat tacagtttaa ccctcttgtg ttccatttag gattaagaat ctggtaggga 1080
cataaaacgt aaatctacca tattgtgtgc tgcttgtgta gtttgtgtag gacccttggt 1140
taccaacctt catgatgata ggttgtgaac attacatagt caagaggagt tccctttttt 1200
tatgacttta ttatagtcaa acaacttgag tagttaacat caatggtttc aatgtcaaga 1260
tatgagttaa gtctttcttt attttgtttg gttttatttg ggtaaaactc cagaaatgaa 1320
agc 1323

<210> 224
<211> 1100
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 224
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tatgaatcgt ttgcttttac cacaagctgc tcgatcaatc ttttagagtt ttcaaatcta 120
aatttaacac aaaaaaatca atttttagtt tttgaattat gtttccattg ctgcgacagc 180
ttaaaaaata atccattttt tatcgtcttc catcatttgt ctccagcttt cggagtggaa 240
atgagttctc ttagactcaa gttggagatg atttcaaatt ggggcgttgg aggaactttc 300
attctttaac agtttataaa gtttgtaaat catttacaaa gtttttaaat catttataaa 360
tgtttataaa ttatttgtaa gagcatataa accatttata aggtttataa aggtatgtaa 420
ataatttatg agggtttata aaatgtttat taagttcata aaaaggtttt ataaagttta 480
gaaacaattt ataacgactt attaatcatt tataaagagt ctataaacgt tttataaagg 540
gtatgtaaat gttttataga cccttataaa gtttgtaaac cctaatagaa ccccgacatg 600
aagtttataa aagaacagtt taggcccgaa tagtttgaaa ttagaaagct cgcaattgag 660
gtctacaggc caaattcgct cttagccgta caatattact caccggtgcg atgcccccca 720
tcgtaggtga aggtggaaat taatggcgcg cctgatcact gattagtaac tattacgtaa 780
gcctacgtag cgtcacgtga cgttagctaa cgctacgtag cctcagctga cgttacgtaa 840
gcctacgtag cgtcacgtga gcttagctaa cgctacctag gctcagctga cgttacgtaa 900
cgctagctag cgtcactcct gcagcaaatt tacacattgc cactaaacgt ctaaaccctt 960
gtaatttgtt tttgttttac tatgtgtgtt atgtatttga tttgcgataa atttttatat 1020
ttggtactaa atttataaca ccttttatgc taacgtttgc caacacttag caatttgcaa 1080
gttgattaat tgattctaaa 1100

<210> 225
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 225
atatactgaa ttgggtatta tatgaatttt tctgatttag gattcacatg atccaaaaag 60
gaaatccaga agcactaatc agacattgga agtaggatta atcagtgatc agtaactatt 120
aaattcaatt aaccgcggac atctacattt ttgaattgaa aaaaaattgg taattactct 180
ttctttttct ccatattgac catcatactc attgctgatc catgtagatt tcccggacat 240
gaagccattt acaatccatg tccttataaa tggtttatat actcttataa ataatttgct 300
tcttcatgcc tcaagaatat tactactttc aagaatagga aaatctgtgt actaaaaact 360
tcatctcggg ttctatcata ttgtggtact atcagtaggt gactctgtgt ttctatctgc 420
aacataaaag catgaaacta ataagattgt acaattattt tataagtctt tataaatgta 480
aacaatgtaa taaaatctca gacattaaat gaataagttt tgactattat tttataagtc 540
cttgaaagta ttaaattgta ataaacacct caaatatttt gatacttcca gcaatgagga 600
agtcttgagt actagaaacg tcaattcgtg tatgtatcat gtttgacata attaattgtg 660
atctatgcct ttccatttgt aacataaaaa catgaactca ataatttcta tacaataatt 720
tttttaagtt cttatgaaaa tgtaaaagga gttctaaata tctcaagggc attaccatag 780
acaaccttgt ttcgcacaat caaagagtgt gtacatatat gtttgcaata taaaaacacg 840
aaactttgtg attgtgtcaa agtaaataac aaagccttat aaataaaaca tgaccaaaga 900
gttaacctca gaaattgttg cacaaaaacg aagaaatctt ccaatttctt tatgtttgct 960
cataaaagag gccacttgga gatcatttct aataaaaact gaaagaacct cttttgtacc 1020
aaagaacctc ttttgtgtat tatttataaa ctcttataaa attgtatcca ttaataaaag 1080
tttataatta tttataagta tttacaaatt gtagcacaca caagatagca attgatgtag 1140
cttcctcggc taaaacatga tttcctgtaa caataccctt tctagctgat ctcaaggcaa 1200
aagtgaacat ttgtttcatc gcgttacttc ctcctggcat atctagtgaa agagccacgt 1260
ccttcaacaa gggatatatt gcctcaccct ctctgtagac tgtacagaga ccatgcttgt 1320
gatcagaatc aaacaaactc atttcaaggt ttagttttat aaatactact acttacctta 1380
actcttgtgg atttagaagg gaatgagaga agc 1413

<210> 226
<211> 2200
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 226
agctccccag aacaaaataa aaatcgaaac tttgacacta cgaaacgatc aattacgagt 60
gaaaagcgaa aaagaatcga actttaacaa caagagccgt cacaaaggaa gagtgtcaaa 120
ggtaccacag tattggacat cggtggtggc tcgaacaatc gttgagaaga cgaggagaag 180
aggaagaatc gcgattctcg acatcgttga tggaatctcg gaggggtgat cgatgatcaa 240
aagcccaaag gaggttaaac caggagcgga gcagagtaac tttacttctc ttttatattc 300
tcatggaatg taggcgtcat cgtgaccgtt cgtttagcta ggtcattctt gcctttacag 360
taaaacggac ggctagattt cgtttagaga agttatctga tatgaatgat tgcacctgat 420
tatccgtcat aacgaaccat caggattaac caactttgac tgcatacctt cttatttatg 480
acctcttctt ccttattttc ttaaagatat ttatgtaagg agaataaaat ttgaatacaa 540
ttctttttt catgttggca agatctaaca tggattgtgg tatacagatt cactaaaacc 600
tcgtcacttt gtagatagca agaataatgt atagtctaga taacaagaat aatgtacatt 660
tgttcatgaa attatactga tgaattaaga accatgaaag cacatacgtt aagtttcaat 720
ataaataaaa ctatttgtta aaaatagaca tctatttgta ataattagag actaattcat 780
ttacaaactg tataagtgca ttattgtatt attttatttg ttgcgtcatg tatcaatata 840
attaattttc ttccttcggt tgaaaaaata taatctttta ttttagcaaa gggtttaact 900
aaagaaatat aattgctatc aaatataaat aaattataat ctcattaaac tgttcatgtt 960
gtctcaagaa tataccatta aattttattt gtataaggaa ccaaataaca cccgtgaaac 1020
tttacaactt gaaagtaata gtgtactcta agaatgtcaa caaaagttga aatgtaatat 1080
aaataaagaa aagacacgaa gtcaaacatc tatcgaccgg taacagcgtc ggcgacaggt 1140
gtcatcgccg gagacggcaa tggagacgaa cggcatacgg gacacgtagg atgaatcatg 1200
agccaagggt caacgcactt gtcgtggaac aaatggttac aatccggcaa aaccctaatc 1260
atatctgtct tcttgtaatc cgcgagacat atagaacaac acgacgtcgc agtggcatcc 1320
ttttgcaagc tataacccac acgagcctct tcgcacggaa ccttagagca tgcgcaacgg 1380
aggatgaccc cgaatcctta gcgcttaatg gttccattag ttttaatata ataataatat 1440

taagcttaat aaacgagcct ctgccagtca gcatcatcac accaaaagtt aggcccgaat 1500
agtttgaaat tagaaagctc gcaattgagg tctacaggcc aaattcgctc ttagccgtac 1560
aatattactc accggtgcga tgccccccat cgtaggtgaa ggtggaaatt aatggcgcgc 1620
ctgatcactg attagtaact attacgtaag cctacgtagc gtcacgtgac gttagctaac 1680
gctacgtagc ctcagctgac gttacgtaag cctacgtagc gtcacgtgag cttagctaac 1740
gctacctagg ctcagctgac gttacgtaac gctagctagc gtcactcctg cagcaaattt 1800
acacattgcc actaaacgtc taaacccttg taatttgttt ttgttttact atgtgtgtta 1860
tgtatttgat ttgcgataaa tttttatatt tggtactaaa tttataacac cttttatgct 1920
aacgtttgcc aacacttagc aatttgcaag ttgattaatt gattctaaat tatttttgtc 1980
ttctaaatac atatactaat caactggaaa tgtaaatatt tgctaatatt tctactatag 2040
gagaattaaa gtgagtgaat atggtaccac aaggtttgga gatttaattg ttgcaatgct 2100
gcatggatgg catatacacc aaacattcaa taattcttga ggataataat ggtaccacac 2160
aagatttgag gtgcatgaac gtcacgtgga caaaaggttt 2200

<210> 227
<211> 3137
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 227
ctgatttagg attcacatga tccaaaaagg aaatccagaa gcactaatca gacattggaa 60
gtaggattaa tcagtgatca gtaactatta aattcaatta accgcggaca tctacatttt 120
tgaattgaaa aaaaattggt aattactctt tctttttctc catattgacc atcatactca 180
ttgctgatcc atgtagattt cccggacatg aagccattta caatgagtca aaaaaaagtt 240
gttttgatga gtcactgcta caataatgta agatgataaa actcagacct caatcacaga 300
ggcaaacaac aacactcatt agtcatgatt ttttacccaa acaaaaagat gttatagagc 360
tttaagaaaa aaaaaaatta aaattacaaa tcggtctggt aagagtggta gattgatttt 420
tagaagttta tattccttct ttttgggttc ggtaagaatg atcatcatgc ctgtcttgtc 480
ttttacaatt tccgtaaacg tgcaatgatg tcagattggt aaaagtagct cagctttagc 540
taagcaaatt cgaattagtc aaaattaact aatttaatca tcatatatgc ttccactgat 600
atgttttcac attgcaatat ggctcagctt acttaatatg atgatggtta agaagaaatc 660
gtcaatcata acgagcattt gactagtgcc catgagacct ggtgatatgt tgtttgattg 720
aagcagcaaa aaaaaaaaaa acacctaagc atgtatttta tatatctatg atggaaatta 780
tgcaatccag ggtctagtaa cataactgat gaagctataa aaaaaaaacc atatctaaaa 840
aactatttat acaaaggcaa ataaagtgaa ttgctgctct acatgtcggc cacagatggt 900
acggatccaa tgtctatgga aaatttgatg cacgttagct ccttcttttg cgcgtccagc 960
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tcaatctttt cctgatttaa tatgcacatt caaactagtc attcaatgtc tctatgcatt 1080
ggtcaaatac cactaaacta agcctaagac atccaatatg atacaagaga tgcttcaaga 1140
ttaggtagca agaaccaata aagaaaaagc gaatggaact tacaggagga gtgtaaccag 1200
gaagaacttg agaatgtgca accaagaagt ctccggtttc aacaggacaa gttgtctcag 1260
agcaaagttc atgagtctcg gagtgaatgt gccatccaaa gtatgtaact tcaatcacca 1320
gcttcccacc cgtaatccca cgccctttat taaaagaaaa acacatatca taaacaacac 1380
attcattatc atcacaaagg aaacatcttt ctatcattgg catcaaataa aaaaaagtaa 1440
aaaagaagta acctgtggtg gcagagatgg taaaggtagc tccgtagctg gctcgccttg 1500
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ctctgcaatt aacaaaatac attacactat caaggcagag agctccccag aacaaaataa 1620
aaatcgaaac tttgacacta cgaaacgatc aattacgagt gaaaagcgaa aaagaatcga 1680
actttaacaa caagagccgt cacaaaggaa gagtgtcaaa ggtaccacag tattggacat 1740
cggtggtggc tcgaacaatc gttgagaaga cgaggagaag aggaagaatc gcgattctcg 1800
acatcgttga tggaatctcg gaggggtgat cgatgatcaa aagcccaaag gaggttaaac 1860
caggagcgga gcagagtaac tttacttctc ttttatattc tcatggaatg taggcgtcat 1920
cgtgaccgtt cgtttagcta ggtcattctt gcctttacag taaaacggac ggctagattt 1980
cgtttagaga agttatctga tatgaatgat tgcacctgat tatccgtcat aacgaaccat 2040
caggattaac caactttgac tgcatacctt cttatttatg acctcttctt ccttattttc 2100
ttaaagatat ttatgtaagg agaataaaat ttgaatacaa ttctttttt catgttggca 2160
agatctaaca tggattgtgg tatacagatt cactaaaacc tcgtcacttt gtagatagca 2220
agaataatgt atagtctaga taacaagaat aatgtacatt tgttcatgaa attatactga 2280
tgaattaaga accatgaaag cacatacgtt aagtttcaat ataaataaaa ctatttgtta 2340
aaaatagaca tctatttgta ataattagag actaattcat ttacaaactg tataagtgca 2400

ttattgtatt attttatttg ttgcgtcatg tatcaatata attaattttc ttccttcggt 2460
tgaaaaaata taatctttta ttttagcaaa gggtttaact aaagaaatat aattgctatc 2520
aaatataaat aaattataat ctcattaaac tgttcatgtt gtctcaagaa tataccatta 2580
aatttttattt gtataaggaa ccaaataaca cccgtgaaac tttacaactt gaaagtaata 2640
gtgtactcta agaatgtcaa caaaagttga aatgtaatat aaataaagaa aagacacgaa 2700
gtcaaacatc tatcgaccgg taacagcgtc ggcgacaggt gtcatcgccg gagacggcaa 2760
tggagacgaa cggcatacgg gacacgtagg atgaatcatg agccaagggt caacgcactt 2820
gtcgtggaac aaatggttac aatccggcaa aaccctaatc atatctgtct tcttgtaatc 2880
cgcgagacat atagaacaac acgacgtcgc agtggcatcc ttttgcaagc tataacccac 2940
acgagcctct tcgcacggaa ccttagagca tgcgcaacgg aggatgaccc cgaatcctta 3000
gcgcttaatg gttccattag ttttaatata ataataatat taagcttaat aaacgtaagg 3060
attggtccat aattaggtgc tggacggact cgtcattgtg ttacgtgtcc gaatttgagt 3120
ggattcgggc cggcttt 3137

<210> 228
<211> 1100
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 228
tatttttgtt catgtcttat tttctttttt cctaatgtaa ctatgagagg cttaaaaact 60
gtaaaatcag caaaacaata tacaattaca gtaaaaaatg tcacatacta agttctatat 120
atgactacaa gtctacaact caactaatca tccacataaa taattagttt tgtcataatt 180
atattatagt aagtacctga agaaaagata aagccatttc tggacaacat catctcgtat 240
tggcatcttt atacgtggac gacaaaatct atcacaataa tagttgctag atatagatac 300
atgaattttg taatatgatt aattaattgg cgcttcataa ctaaaataac taataaaggg 360
taaatgttct taaagtttca taattaatta tgtttcagag tggttgcatt atagtagttt 420
aaaattcaga agtgtacgcg acgagaaaag agatttgctg gtgactattg catcatcttt 480
gacatggaaa aaatcttaga taagaatagt ttgaaattag aaagctcgca attgaggtct 540
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gccgtacaat attactcacc ggtgcgatgc cccccatcgt aggtgaaggt ggaaattaat 720
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<211> 811
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 229
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ccacaaatat atttttattt ataaaaaggt ggccattgta tactatgtgt gcgtatacag 300
gaataaaaat gtgtcaatgt atatgtaaac tgattccatc ttatatgtaa tgtgcgtgtg 360
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tatctcaaga ttctttcttt tttttctacg aatatcgcaa tctataatac cattaaatta 480
ttgtaacaaa attggttgac atttataaaa tgaaaaagaa gagaagagca tttaaacacg 540
actgatgaaa gtccaatgta gctagataaa ccacgcgtgg tggtcaatgc gttccattcc 600
aaaaggatcc gagttcgaat ccgcaccaca ccagattttc actgcgcgtg gccatgaagc 660

tttcgcattc tcgctcctga gaatggttct ccatttttt tttccagtgt agctagatac 720
cggtctgaat ctaggtttat aatatgctga caatgtaatg ataattaata catcaaaaca 780
tgtgtttctg aaccaaaata aaaacttttt t 811

<210> 230
<211> 2900
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 230
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cctttaaatg agtggaagat gagaaccatg tgatgaaaaa cctgcaaaac aagataaatt 180
agtaagaaaa acatgagaca gaaacaataa attgatataa agtttgatgt ttataagttc 240
aaagggatta aagagaggtt tgagagtttt agaacgagga acataccatt tttgttgcag 300
ccatttgaga ggagaagaga gaatgtgtaa atgtttttt atataaggag acaaaaattc 360
caataaggtt aaatattttt gatcagaaga cttactagac gacttacttg taagtcgccc 420
agaagacttc aatattttta gcgggaaact aaaatatttt tagcgggagt tagaagaccc 480
taaacataac ccttaaacta aattaactaa ctaaatactt cataaaatca aattaaactt 540
aaaaagtgtt tactatacac agaaataatc acatgtagat ataaatttaa tttttcaaaa 600
aaacatttaa gctttccaaa atctaaccct aagaatacat acaatactac aacatatgtt 660
gccaaaccct agaccaaaga atatcatgat tcactacttt cactcatcta tgttgaaaac 720
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<210> 231
<211> 1800
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 231
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atttttgaat tgaaaaaaaa ttggtaatta ctctttcttt ttctccatat tgaccatcat    180
actcattgct gatccatgta gatttcccgg acatgaagcc atttacaatt gaatatatcc    240
tcacatatga aatatatttt ttttttacaa attacaccta ttaaattata cttgatcggt    300
catctgatat atttgaaaga accctatcag ccagctattc ataatttaca taaaagaaaa    360
ttacgtgctt aaaatctctc taaaaaaaaa aaaagacaaa gacatcaaac tgatccatga    420
aagtaaaatg gagtgtattt taattttatc ttcagaccaa tgttatcaat gtagcccata    480
tattaatact aaaacaactt ctgcacaaac acacgaatca aagcctcgtg tttcatcgta    540
gctttagcta aaatttccca aaagcaaatt caatagtatt ttactaggtc aaacccacaa    600
gagaaaaaga aagtcaatcc caaggatcaa gaaatgagaa gtgagaggag aatgctttat    660
tgggtttgct aataactaat aagacatgaa gcagactgaa aacatctggt tttgtccaaa    720
aaagaaggaa gtcagattcc aaaactgcgc acctacattg tttaatactc actcacacat    780
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gatattctta tttcaactca atccacgagt aaatgtgtta gcaccacatc taaccatttg   1620
gagcttgtac tagctctatc tttccaaact taactttctt gagtgcttat ttatataaag   1680
catcagtata tggcccaacc caagaaaagc tgaacaaaat tagcaacaat agcaagggac   1740
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<210> 232
<211> 1600
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 232
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ctgaagaaga tgatgtgaat gagatggttg cttggagcaa tgatgaggat gaggaccttg    180
gttggcaaac aaatgaacct ataaggataa ataatgagct caaggtacct atccttcagc    240
atttcacatt tcataatcat agctgttagt ggttgagttc tttttattgt ctctaagcct    300
ttgttaactg tttgctaact ccaaaccctt tttaactttt gcaggagctt cctccagttc    360
cacctgtgga tgtcactttg gaaccacatc atgtcatgct tcctgttgga gttgttcttt    420
cggtatcata aaataaactc tacctgtgcg ctattgcttg ctaaacctaa aaccattgtg    480
atttctgatg ttccaggtac tgagcacacc actgacacaa gtaatagtgg agggaatgga    540
aaagcatagt cctttggccg aaggttctat cctatggata agtgaaagaa gaacgccatt    600
gggactggtg gatgagatct ttgcacaagt tgagtgccct tactatagtg tgaggttcaa    660
ttcagaaaac gaagtgccgg agggggttag tgaaggtaca cctgtctcat tcgttgctga    720
gtacgctcag catattctca atatcaagga actgcagaag aaaggttacg atgcatcagg    780
agataacgac gaggaggtag cagaggagct tgagttctca gatgatgaga aagaagcccg    840
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aatacataaa aatgcagaag atggaaaaga gagggatgat ggatgaccaa aaagatggta 900
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<210> 233
<211> 3284
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 233
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ggcctaactt ttggtgtgat gaaagtgtga gaatatttcc atattagaca attctgtaga 180
ttttatttaa tgaaagtgtg agaatatttt tttgtacact atttatcaat ttaataaaaa 240
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atatgtttgt tgtactaaca acaagatttc atacatttca aacgaaaaag agagattgat 420
gtgatcagta ttattgcttt tacaaaacta ttgaaggttc agcgagttct tagtaaagtc 480
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<210> 234
<211> 1700
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 234
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cggagaatat tattcataaa aatacgatag taacgggtga tatattcatt agaatgaacc 480
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ctaaaccctt gtaatttgtt 1700

<210> 235
<211> 1532
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 235
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gcatgtgtag ctcagatcct taccgccggt ttcggttcat tctaatgaat atatcacccg 180
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ccaataaaat ttaatcaatt caaatatttt tatttaatgt ttcttaaaag tataaaaaat 720
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tctcgcttga agaacaagat tggtatattt gttacaacgg gctagtttat caatatcttt 1140
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gaaagagcag aaagatcatc attcaacagt agaaagcgac gacaaagtcg aagctgttct 1260
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tctcgggtta ataaatattg caggagaagt tctgtaacag agcttgtgtc agtagattct 1440
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ggagatcttc tcttggcatc ggtatactct tc 1532

<210> 236
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 236
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gtgaccttag gtaacgctac gtagcgtcaa agctttacaa cgctacacaa aaatgcttgc 180
gtttcttctc tcattacgag aatatacttt tttcaatatt gcttcaaaaa ctttctgtca 240
tgtgaatttg attttagata tatgtttaaa aaatacttcc tccccgaaaa taagattttc 300
taaagtgttc gattattaag aattcattaa atatttataa tttaattttt ctttttacttt 360
attatacatt ttctaataac tttttaccaa taaaatttaa tcaattcaaa tatttttatt 420
taatgtttct taaaagtata aaaaatatct taatcatata gaaaatatat ttttgtggaa 480
caagtaaaaa tctaaaacat cttactttca ggaacggagg taatagatag ttacattaaa 540
ggtctcaaca ttactatttt aagtctattc acttgttttg cttgcttgct aaccaaacaa 600
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<210> 237
<211> 1600
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 237
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actacaaaat ataatagcct caattatctt caaaactaag ttgacattta attatgcttt 120
tgcaagatat ttacttttgt tgttcgatca tatttaatga ttattttggt tttgaaacaa 180
atattaacat tatatatatt gtgtctatat tgaactgttg taaattataa acatcaaaat 240
tttaatgtta tcttaattat aatttctaat actagtatat tcaaaaatca aaataaacat 300
attttataaa atagtgccag tacgtagtat gggagataat actagtggct ttataaaggg 360
aaacattgtc tctaaaatct cagataaaat gttaaaacac acttattcac aattatgaag 420
atttgaaata tctgaaattt caaattgatg cacttggtag aaagcaaagg ttcaacgcta 480
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catcgtaggt gaaggtggaa attaatggcg cgcctgatca ctgattagta actattacgt 1200
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atttggtact aaatttataa caccttttat gctaacgttt gccaacactt agcaatttgc 1500
aagttgatta attgattcta aattattttt gtcttctaaa tacatatact aatcaactgg 1560
aaatgtaaat atttgctaat atttctacta taggagaatt 1600

<210> 238
<211> 1677
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 238
taattgaaat tcgttattag ggttctaagc tgttttaaca gtcactgggt taatatctct 60
cgaatcttgc atggaaaatg ctcttaccat tggtttttaa ttgaaatgtg ctcatatggg 120
ccgtggtttc caaattaaat aaaactacga tgtcatcgag aagtaaaatc aactgtgtcc 180
acattatcag ttttgtgtat acgatgaaat agggtaattc aaaatctagc ttgatatgcc 240
ttttggttca ttttaacctt ctgtaaacat tttttcagat tttgaacaag taaatccaaa 300
aaaaaaaaaa aaaatctcaa ctcaacacta aattatttta atgtataaaa gatgcttaaa 360
acatttggct taaaagaaag aagctaaaaa catagagaac tcttgtaaat tgaagtatga 420
aaatatactg aattgggtat tatatgaatt tttctgattt aggattcaca tgatccaaaa 480
aggaaatcca gaagcactaa tcagacattg gaagtaggat taatcagtga tcagtaacta 540
ttaaattcaa ttaaccgcgg acatctacat ttttgaattg aaaaaaaatt ggtaattact 600
ctttcttttt ctccatattg accatcatac tcattgtaag acacacagat gaagaagtca 660
aatagctcga cattcctttg gtctggtcca gtgatgtcga ctcacaaagc gaagattgca 720
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ttaacgaaga acaaacgaca tttataatcc taagataatt ttttctaatt caaaaataat 1260
tttcgatttt caaaaaaaaa attgaaaaaa aaattgaaaa gaaaaattca aaacaaaatt 1320

atatgaaagt tcaaatttga aaaatgataa ttcaaaaaca taaaaaaata tatttttatt 1380
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<210> 239
<211> 5600
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 239
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tagttaaatt tatatgatat ttacttcagt aatattaaaa tattatatac atttttatta 180
tatttggttt agtaatatta aatggattct attttaaatt tcttatgaca atcaaaacca 240
cttagtgtga taatttctga aaaaaattgg caaaaaaatc aaaaatactt atcttattat 300
ttgtagtgat ttttctctct ctcatgttaa aattttgaat gtttaaagtc tttattatct 360
ttaataaata attagattaa atttttaata tataattacc cataatttaa aacaaatttc 420
attaatttta aaatcatcat tatctaaaaa gattatatat tatgttatcc aaaaatattt 480
tacatcataa tattttaaaa taaatataaa tttatgtata ttgttttatg tatatatgaa 540
tgtttttaag tttatttttac ataatcaaat atattttaca aaaataattt ttatcatata 600
taaaatttaa catttaatta attattaaat atttcaaaag tatgaatata acttattctc 660
atggttttta attgataata tatctattta caatttttg taaaattatt aaacccgcaa 720
gtatggacaa aacacctagt atatatattt ggaacaaaga atacagacaa aacacctagt 780
atatatattt ggaacaaaaa atatacgtac atattttata tacatgaata acttatatat 840
cacttagaaa taggataatc aattgacatt aaactctctt aaattatata ttgtatagaa 900
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<210> 240
<211> 1321
<212> DNA
<213> Artificial Sequence

<220>
<223> flanking sequence

<400> 240
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attgaaaagc attattttta tcgaaatgaa tctagtatac aatcaatatt tatgtttttt 120
catcagatac tttcctattt tttggcacct ttcatcggac tactgattta tttcaatgtg 180
tatgcatgca tgagcatgag tatacacatg tcttttaaaa tgcatgtaaa gcgtaacgga 240
ccacaaaaga ggatccatac aaatacatct catcgcttcc tctactattc tccgacacac 300
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ttttatatta tatacctact tcctctctct cgctctgtta tgttcgattt cgaaaggatt 420
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acgaggttga aattttcggg acttggaggg ctaaagtgga agagactgaa tctgaagatg 540
tcgtttctcg aaactttgag atacagaatc atgtctatca ttgaaggaat ggttttggtt 600
tctaagcttg ctttcttctt tctctgttgc ggttgcagat tttaacacgt tagttttttt 660
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t 1321

<210> 241
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 241
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tgacactcaa ctaaaatgtt ggattttccc tttcaggtgt 100

<210> 242
<211> 148
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 242
cacacacctc cccaatccat ggatatgttc tctcttttct caatcaattt gtttacactc 60
aaacactgat agtttaaact gaaggcggga aacgacaatc tgatcactga ttagtaacta 120
aggcctttaa ttaatctaga ggcgcgcc 148

<210> 243
<211> 147
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 243
ggcgcgcctc tagattaatt aaaggcctta gttactaatc agtgatcaga ttgtcgtttc 60
ccgccttcag tttaaactat cagtgttgct ttagtggtca atcaaaagat gaacagtatc 120
ttctcgatcg atgatttctc cgatccc 147

<210> 244
<211> 118
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 244
caccaaaagc aaccaagaga gacgtcttta atgtactgaa tttagtaact gaaggcggga 60
aacgacaatc tgatcactga ttagtaacta aggcctttaa ttaatctaga ggcgcgcc 118

<210> 245
<211> 110
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 245
gcggacatct acatttttga attgaaaaaa aattggtaat tactctttct ttttctccat 60
attgaccatc atactcattg taagacacac agatgaagaa gtcaaatagc 110

<210> 246
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 246
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tttatattat atacctactt cctctctctc gctct 95

<210> 247
<211> 101
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 247
ctctttcttt ttctccatat tgaccatcat actcattgct gatccatgta gatttcccgg 60
acatgaagcc atttgtcaac gtcgttgttt gatttcgtta a 101

<210> 248
<211> 197
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 248
caattaaccg cggacatcta catttttta ctgctattct ttcatattag caactggttg 60
attactgaat tagtacagat gtaactaaca tatatattgg atattattat tatccaaaag 120
agctattcaa ccttttaagc atatgtatat acatgtttaa ttgattttat tagtatttct 180
tgctcttgtt gttttgc 197

<210> 249
<211> 138
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 249
aattaaccgc ggacatctac atttttgaat tgaaaaaaaa ttggtaatta ctctttcttt 60
ttctccatat tgaccatcat actcattgct gatccatgta gatttcccgg ttctttttct 120
cagactactc actgcccg 138

<210> 250
<211> 137
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 250
ctctttcttt ttctccatat tgaccatcat actcattgct gatccatgta gatttcccgg 60
acatgaagcc atttacaatc catgtcctta taaatggttt atatactctt ataaataatt 120
tgcttcttca tgcctca 137

<210> 251
<211> 113
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 251
ctctttcttt ttctccatat tgaccatcat actcattgct gatccatgta gatttcccgg 60
acatgaagcc atttacaatg agtcaaaaaa aagttgtttt gatgagtcac tgc 113

<210> 252
<211> 160
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 252
ctctttcttt ttctccatat tgaccatcat actcattgct gatccatgta gatttcccgg 60
acatgaagcc atttactctg accctactcc acaaatatat ttttatttat aaaaaggtgg 120
ccattgtata ctatgtgtgc gtatacagga ataaaaatgt 160

<210> 253
<211> 169
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 253
ccatattgac catcatactc attgctgatc catgtagatt tcccggacat gaagccattt 60
acaattgaat atatcctcac atatgaaata tatttttttt ttacaaatta cacctattaa 120
attatacttg atcggtcatc tgatatattt gaaagaaccc tatcagcca 169

<210> 254
<211> 576
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 254
gacctcaatt gcgagctttc taatttcaaa ctattcgggc ctaacttttg gtgtgatgaa 60
agtgtgagaa tatttccata ttagacaatt ctgtagattt tatttaatga aagtgtgaga 120
atatttttt gtacactatt tatcaattta ataaaaaaat ataatataat ttaagatgaa 180
ccaacatatt tctctaaatt ctgaatttta ttttcatggt gacacgtgga tacgaaacaa 240
tgttgtaatg tttatcgatt aatatataat gtatgttata tgtttgttgt actaacaaca 300
agatttcata catttcaaac gaaaaagaga gattgatgtg atcagtatta ttgcttttac 360
aaaactattg aaggttcagc gagttcttag taaagtcgaa tccttgtaat aatctctgtt 420
ccaacgggca aacatgcagc tgttaaacta tcgacgccgt ttgacctatt ttttcttctt 480
ctttgttttc ttcctcattt gtacatgcgt gcaagcctac tgacggttgg atgccttggc 540
acgcacttca acaactctat atccttcctg gtgagg 576

<210> 255
<211> 189
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 255
cgtgccaagg catccaaccg tcagtaggct attctgtaga ttttatttaa tgaaagtgtg 60
agaatattta gacaattctg tagattttat ttaatgaaag tgtgagaata ttttttaag 120
gcccgaatag tttgaaatta gaaagctcgc aattgaggtc tacaggccaa attcgctctt 180
agccgtaca 189

<210> 256
<211> 91
<212> DNA
<213> Artificial Sequence

<220>
<223> amplicon

<400> 256
gcctacctag actcacgtga ccttaggtaa cgctacgtag cgtcaaagct ttacaacgct 60
acacaaaaat gcttgcgttt cttctctcat t 91

<210> 257
<211> 873
<212> DNA
<213> Artificial Sequence

<220>
<223> d6Elo(Pp) as by plasmid VC-LTM593-1qcz

<400> 257
atggaagttg ttgagaggtt ctacggagag ttggatggaa aggtttccca aggagtgaac 60
gctttgttgg gatctttcgg agttgagttg actgataccc caactactaa gggattgcca 120
ctcgttgatt ctccaactcc aattgtgttg ggagtgtctg tttacttgac catcgtgatc 180
ggaggattgc tttggatcaa ggctagagat ctcaagccaa gagcttctga gccattcttg 240
ttgcaagctt tggtgttggt gcacaacttg ttctgcttcg ctttgtctct ttacatgtgc 300
gtgggtatcg cttaccaagc tatcacctgg agatattcct tgtggggaaa cgcttataac 360
ccaaagcaca aggagatggc tatcctcgtt tacctcttct acatgtccaa gtacgtggag 420
ttcatggata ccgtgatcat gatcctcaag agatccacca gacagatttc tttcctccac 480
gtgtaccacc actcttctat ctcccttatc tggtgggcta ttgctcacca cgctccagga 540
ggagaggctt attggagtgc tgctctcaac tctggagtgc acgtgttgat gtacgcttac 600
tacttcttgg ctgcttgctt gagatcttcc ccaaagctca agaacaagta cctcttctgg 660
ggaagatacc tcacccaatt ccagatgttc cagttcatgc tcaacttggt gcaagcttac 720
tacgatatga aaaccaacgc tccatatcca caatggctca tcaagatcct cttctactac 780
atgatctccc tcttgttcct cttcggaaac ttctacgtgc aaaagtacat caagccatcc 840
gatggaaagc aaaagggagc taagaccgag tga 873

<210> 258
<211> 290
<212> PRT
<213> Physcomitrella patens

<220>
<223> d6Elo(Pp) as by plasmid VC-LTM593-1qcz

<400> 258
Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser
1 5 10 15
Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp
20 25 30
Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile
35 40 45
Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu
50 55 60
Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu
65 70 75 80
Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser
85 90 95
Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr
100 105 110
Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile
115 120 125
Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr
130 135 140
Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His
145 150 155 160
Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His
165 170 175
His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly
180 185 190
Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg
195 200 205
Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu
210 215 220
Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr
225 230 235 240
Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile
245 250 255
Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr
260 265 270
Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys
275 280 285
Thr Glu
290

<210> 259
<211> 1320
<212> DNA
<213> Artificial Sequence

<220>
<223> d5Des(Tc) as by plasmid VC-LTM593-1qcz

<400> 259
atgggaaaag gatctgaggg aagatctgct gctagagaga tgactgctga ggctaacgga 60
gataagagaa agaccatcct cattgaggga gtgttgtacg atgctaccaa cttcaaacac 120
ccaggaggtt ccattattaa cttcctcacc gagggagaag ctggagttga tgctacccaa 180
gcttacagag agttccatca gagatccgga aaggctgata agtacctcaa gtccctccca 240
aagttggatg cttctaaggt ggagtctagg ttctctgcta aggagcaggc tagaagggac 300

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gctatgacca gggattacgc tgctttcaga gaggagttgg ttgctgaggg atacttcgat    360
ccatctatcc cacacatgat ctacagagtg gtggagattg tggctttgtt cgctttgtct    420
ttctggttga tgtctaaggc ttctccaacc tctttggttt tgggagtggt gatgaacgga    480
atcgctcaag gaagatgcgg atgggttatg cacgagatgg gacacggatc tttcactgga    540
gttatctggc tcgatgatag gatgtgcgag ttcttctacg gagttggatg tggaatgtct    600
ggacactact ggaagaacca gcactctaag caccacgctg ctccaaacag attggagcac    660
gatgtggatt tgaacacctt gccactcgtt gctttcaacg agagagttgt gaggaaggtt    720
aagccaggat ctttgttggc tttgtggctc agagttcagg cttatttgtt cgctccagtg    780
tcttgcttgt tgatcggatt gggatggacc ttgtacttgc acccaagata tatgctcagg    840
accaagagac acatggagtt tgtgtggatc ttcgctagat atatcggatg gttctccttg    900
atgggagctt tgggatattc tcctggaact tctgtgggaa tgtacctctg ctctttcgga    960
cttggatgca tctacatctt cctccaattc gctgtgtctc acacccactt gccagttacc   1020
aacccagagg atcaattgca ctggcttgag tacgctgctg atcacaccgt gaacatctct   1080
accaagtctt ggttggttac ctggtggatg tctaacctca acttccaaat cgagcaccac   1140
ttgttcccaa ccgctccaca attcaggttc aaggagatct ctccaagagt tgaggctctc   1200
ttcaagagac acaacctccc ttactacgat ttgccataca cctctgctgt ttctactacc   1260
ttcgctaacc tctactctgt tggacactct gttggagctg ataccaagaa gcaggattga   1320
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<210> 260
<211> 439
<212> PRT
<213> Thraustochytrium sp.

<220>
<223> d5Des(Tc) as by plasmid VC-LTM593-1qcz

<400> 260

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Met Gly Lys Gly Ser Glu Gly Arg Ser Ala Ala Arg Glu Met Thr Ala
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Glu Ala Asn Gly Asp Lys Arg Lys Thr Ile Leu Ile Glu Gly Val Leu
            20                  25                  30
Tyr Asp Ala Thr Asn Phe Lys His Pro Gly Gly Ser Ile Ile Asn Phe
        35                  40                  45
Leu Thr Glu Gly Glu Ala Gly Val Asp Ala Thr Gln Ala Tyr Arg Glu
    50                  55                  60
Phe His Gln Arg Ser Gly Lys Ala Asp Lys Tyr Leu Lys Ser Leu Pro
65                  70                  75                  80
Lys Leu Asp Ala Ser Lys Val Glu Ser Arg Phe Ser Ala Lys Glu Gln
                85                  90                  95
Ala Arg Arg Asp Ala Met Thr Arg Asp Tyr Ala Ala Phe Arg Glu Glu
            100                 105                 110
Leu Val Ala Glu Gly Tyr Phe Asp Pro Ser Ile Pro His Met Ile Tyr
        115                 120                 125
Arg Val Val Glu Ile Val Ala Leu Phe Ala Leu Ser Phe Trp Leu Met
    130                 135                 140
Ser Lys Ala Ser Pro Thr Ser Leu Val Leu Gly Val Val Met Asn Gly
145                 150                 155                 160
Ile Ala Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly
                165                 170                 175
Ser Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Met Cys Glu Phe Phe
            180                 185                 190
Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln His
        195                 200                 205
Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val Asp Leu
    210                 215                 220
Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val Arg Lys Val
225                 230                 235                 240
Lys Pro Gly Ser Leu Leu Ala Leu Trp Leu Arg Val Gln Ala Tyr Leu
                245                 250                 255
Phe Ala Pro Val Ser Cys Leu Leu Ile Gly Leu Gly Trp Thr Leu Tyr
            260                 265                 270
Leu His Pro Arg Tyr Met Leu Arg Thr Lys Arg His Met Glu Phe Val
        275                 280                 285
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eolf-seql

Trp Ile Phe Ala Arg Tyr Ile Gly Trp Phe Ser Leu Met Gly Ala Leu
290 295 300
Gly Tyr Ser Pro Gly Thr Ser Val Gly Met Tyr Leu Cys Ser Phe Gly
305 310 315 320
Leu Gly Cys Ile Tyr Ile Phe Leu Gln Phe Ala Val Ser His Thr His
325 330 335
Leu Pro Val Thr Asn Pro Glu Asp Gln Leu His Trp Leu Glu Tyr Ala
340 345 350
Ala Asp His Thr Val Asn Ile Ser Thr Lys Ser Trp Leu Val Thr Trp
355 360 365
Trp Met Ser Asn Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr
370 375 380
Ala Pro Gln Phe Arg Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu
385 390 395 400
Phe Lys Arg His Asn Leu Pro Tyr Tyr Asp Leu Pro Tyr Thr Ser Ala
405 410 415
Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly
420 425 430
Ala Asp Thr Lys Lys Gln Asp
435

<210> 261
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> d6Des(Ot) as by plasmid VC-LTM593-1qcz

<400> 261
atgtgtgttg agaccgagaa caacgatgga atccctactg tggagatcgc tttcgatgga 60
gagagagaaa gagctgaggc taacgtgaag ttgtctgctg agaagatgga acctgctgct 120
ttggctaaga ccttcgctag aagatacgtg gttatcgagg gagttgagta cgatgtgacc 180
gatttcaaac atcctggagg aaccgtgatt ttctacgctc tctctaacac tggagctgat 240
gctactgagg ctttcaagga gttccaccac agatctagaa aggctaggaa ggctttggct 300
gctttgcctt ctagacctgc taagaccgct aaagtggatg atgctgagat gctccaggat 360
ttcgctaagt ggagaaagga gttggagagg gacggattct tcaagccttc tcctgctcat 420
gttgcttaca gattcgctga gttggctgct atgtacgctt tgggaaccta cttgatgtac 480
gctagatacg ttgtgtcctc tgtgttggtt tacgcttgct tcttcggagc tagatgtgga 540
tgggttcaac acgagggagg acactcttct ttgaccggaa acatctggtg ggataagaga 600
atccaagctt tcactgctgg attcggattg gctggatctg gagatatgtg gaactccatg 660
cacaacaagc accacgctac tcctcaaaaa gtgaggcacg atatggattt ggataccact 720
cctgctgttg ctttcttcaa caccgctgtg gaggataata gacctagggg attctctaag 780
tactggctca gattgcaagc ttggaccttc attcctgtga cttctggatt ggtgttgctc 840
ttctggatgt tcttcctcca cccttctaag gctttgaagg gaggaaagta cgaggagctt 900
gtgtggatgt tggctgctca cgtgattaga acctggacca ttaaggctgt tactggattc 960
accgctatgc aatcctacgg actcttcttg gctacttctt gggtttccgg atgctacttg 1020
ttcgctcact tctctacttc tcacacccac ttggatgttg ttcctgctga tgagcacttg 1080
tcttgggtta ggtacgctgt ggatcacacc attgatatcg atccttctca gggatgggtt 1140
aactggttga tgggatactt gaactgccaa gtgattcacc acctcttccc ttctatgcct 1200
caattcagac aacctgaggt gtccagaaga ttcgttgctt tcgctaagaa gtggaacctc 1260
aactacaagg tgatgactta tgctggagct tggaaggcta ctttgggaaa cctcgataat 1320
gtgggaaagc actactacgt gcacggacaa cactctggaa agaccgcttg a 1371

<210> 262
<211> 456
<212> PRT
<213> Ostreococcus tauri

<220>
<223> d6Des(Ot) as by plasmid VC-LTM593-1qcz

<400> 262

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Met Cys Val Glu Thr Glu Asn Asn Asp Gly Ile Pro Thr Val Glu Ile
1               5                  10                  15
Ala Phe Asp Gly Glu Arg Glu Arg Ala Glu Ala Asn Val Lys Leu Ser
            20                  25                  30
Ala Glu Lys Met Glu Pro Ala Ala Leu Ala Lys Thr Phe Ala Arg Arg
        35                  40                  45
Tyr Val Val Ile Glu Gly Val Glu Tyr Asp Val Thr Asp Phe Lys His
    50                  55                  60
Pro Gly Gly Thr Val Ile Phe Tyr Ala Leu Ser Asn Thr Gly Ala Asp
65                  70                  75                  80
Ala Thr Glu Ala Phe Lys Glu Phe His His Arg Ser Arg Lys Ala Arg
                85                  90                  95
Lys Ala Leu Ala Ala Leu Pro Ser Arg Pro Ala Lys Thr Ala Lys Val
            100                 105                 110
Asp Asp Ala Glu Met Leu Gln Asp Phe Ala Lys Trp Arg Lys Glu Leu
        115                 120                 125
Glu Arg Asp Gly Phe Phe Lys Pro Ser Pro Ala His Val Ala Tyr Arg
    130                 135                 140
Phe Ala Glu Leu Ala Ala Met Tyr Ala Leu Gly Thr Tyr Leu Met Tyr
145                 150                 155                 160
Ala Arg Tyr Val Val Ser Ser Val Leu Val Tyr Ala Cys Phe Phe Gly
                165                 170                 175
Ala Arg Cys Gly Trp Val Gln His Glu Gly Gly His Ser Ser Leu Thr
            180                 185                 190
Gly Asn Ile Trp Trp Asp Lys Arg Ile Gln Ala Phe Thr Ala Gly Phe
        195                 200                 205
Gly Leu Ala Gly Ser Gly Asp Met Trp Asn Ser Met His Asn Lys His
    210                 215                 220
His Ala Thr Pro Gln Lys Val Arg His Asp Met Asp Leu Asp Thr Thr
225                 230                 235                 240
Pro Ala Val Ala Phe Phe Asn Thr Ala Val Glu Asp Asn Arg Pro Arg
                245                 250                 255
Gly Phe Ser Lys Tyr Trp Leu Arg Leu Gln Ala Trp Thr Phe Ile Pro
            260                 265                 270
Val Thr Ser Gly Leu Val Leu Leu Phe Trp Met Phe Phe Leu His Pro
        275                 280                 285
Ser Lys Ala Leu Lys Gly Gly Lys Tyr Glu Glu Leu Val Trp Met Leu
    290                 295                 300
Ala Ala His Val Ile Arg Thr Trp Thr Ile Lys Ala Val Thr Gly Phe
305                 310                 315                 320
Thr Ala Met Gln Ser Tyr Gly Leu Phe Leu Ala Thr Ser Trp Val Ser
                325                 330                 335
Gly Cys Tyr Leu Phe Ala His Phe Ser Thr Ser His Thr His Leu Asp
            340                 345                 350
Val Val Pro Ala Asp Glu His Leu Ser Trp Val Arg Tyr Ala Val Asp
        355                 360                 365
His Thr Ile Asp Ile Asp Pro Ser Gln Gly Trp Val Asn Trp Leu Met
    370                 375                 380
Gly Tyr Leu Asn Cys Gln Val Ile His His Leu Phe Pro Ser Met Pro
385                 390                 395                 400
Gln Phe Arg Gln Pro Glu Val Ser Arg Arg Phe Val Ala Phe Ala Lys
                405                 410                 415
Lys Trp Asn Leu Asn Tyr Lys Val Met Thr Tyr Ala Gly Ala Trp Lys
            420                 425                 430
Ala Thr Leu Gly Asn Leu Asp Asn Val Gly Lys His Tyr Tyr Val His
        435                 440                 445
Gly Gln His Ser Gly Lys Thr Ala
    450                 455
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<210> 263
<211> 819
<212> DNA
<213> Artificial Sequence

<220>
<223> d6Elo(Tp) as by plasmid VC-LTM593-1qcz

<400> 263
atggatgctt ataacgctgc tatggataag attggagctg ctatcatcga ttggagtgat 60
ccagatggaa agttcagagc tgatagggag gattggtggt tgtgcgattt cagatccgct 120
atcaccattg ctctcatcta catcgctttc gtgatcttgg gatctgctgt gatgcaatct 180
ctcccagcta tggacccata ccctatcaag ttcctctaca acgtgtctca aatcttcctc 240
tgcgcttaca tgactgttga ggctggattc ctcgcttata ggaacggata caccgttatg 300
ccatgcaacc acttcaacgt gaacgatcca ccagttgcta acttgctctg gctcttctac 360
atctccaaag tgtgggattt ctgggatacc atcttcattg tgctcggaaa gaagtggaga 420
caactctctt tcttgcacgt gtaccaccac accaccatct tcctcttcta ctggttgaac 480
gctaacgtgc tctacgatgg agatatcttc ttgaccatcc tcctcaacgg attcattcac 540
accgtgatgt acacctacta cttcatctgc atgcacacca aggattctaa gaccggaaag 600
tctttgccaa tctggtggaa gtcatctttg accgctttcc aactcttgca attcaccatc 660
atgatgtccc aagctaccta cttggttttc cacggatgcg ataaggtttc cctcagaatc 720
accatcgtgt acttcgtgta cattctctcc cttttcttcc tcttcgctca gttcttcgtg 780
caatcctaca tggctccaaa gaagaagaag tccgcttga 819

<210> 264
<211> 272
<212> PRT
<213> Thalassiosira pseudonana

<220>
<223> d6Elo(Tp) as by plasmid VC-LTM593-1qcz

<400> 264
Met Asp Ala Tyr Asn Ala Ala Met Asp Lys Ile Gly Ala Ala Ile Ile
1 5 10 15
Asp Trp Ser Asp Pro Asp Gly Lys Phe Arg Ala Asp Arg Glu Asp Trp
20 25 30
Trp Leu Cys Asp Phe Arg Ser Ala Ile Thr Ile Ala Leu Ile Tyr Ile
35 40 45
Ala Phe Val Ile Leu Gly Ser Ala Val Met Gln Ser Leu Pro Ala Met
50 55 60
Asp Pro Tyr Pro Ile Lys Phe Leu Tyr Asn Val Ser Gln Ile Phe Leu
65 70 75 80
Cys Ala Tyr Met Thr Val Glu Ala Gly Phe Leu Ala Tyr Arg Asn Gly
85 90 95
Tyr Thr Val Met Pro Cys Asn His Phe Asn Val Asn Asp Pro Pro Val
100 105 110
Ala Asn Leu Leu Trp Leu Phe Tyr Ile Ser Lys Val Trp Asp Phe Trp
115 120 125
Asp Thr Ile Phe Ile Val Leu Gly Lys Lys Trp Arg Gln Leu Ser Phe
130 135 140
Leu His Val Tyr His His Thr Thr Ile Phe Leu Phe Tyr Trp Leu Asn
145 150 155 160
Ala Asn Val Leu Tyr Asp Gly Asp Ile Phe Leu Thr Ile Leu Leu Asn
165 170 175
Gly Phe Ile His Thr Val Met Tyr Thr Tyr Tyr Phe Ile Cys Met His
180 185 190
Thr Lys Asp Ser Lys Thr Gly Lys Ser Leu Pro Ile Trp Trp Lys Ser
195 200 205
Ser Leu Thr Ala Phe Gln Leu Leu Gln Phe Thr Ile Met Met Ser Gln
210 215 220
Ala Thr Tyr Leu Val Phe His Gly Cys Asp Lys Val Ser Leu Arg Ile
225 230 235 240
Thr Ile Val Tyr Phe Val Tyr Ile Leu Ser Leu Phe Phe Leu Phe Ala
245 250 255
Gln Phe Phe Val Gln Ser Tyr Met Ala Pro Lys Lys Lys Lys Ser Ala
260 265 270

<210> 265
<211> 1197
<212> DNA
<213> Artificial Sequence

<220>
<223> d12Des(Ps) as by plasmid VC-LTM593-1qcz

<400> 265
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aagcaaagac aattggctga ggctggatac actcacgttg agggtgctcc tgctcctttg 120
cctttggagt tgcctcactt ctctctcaga gatctcagag ctgctattcc taagcactgc 180
ttcgagagat ctttcgtgac ctccacctac tacatgatca agaacgtgtt gacttgcgct 240
gctttgttct acgctgctac cttcattgat agagctggag ctgctgctta tgttttgtgg 300
cctgtgtact ggttcttcca gggatcttac ttgactggag tgtgggttat cgctcacgag 360
tgtggacacc aggcttattg ctcttctgag gtggtgaaca acttgattgg actcgtgttg 420
cactctgctt tgttggtgcc ttaccactct tggagaatct ctcacagaaa gcaccactcc 480
aacactggat cttgcgagaa cgatgaggtt ttcgttcctg tgaccagatc tgtgttggct 540
tcttcttgga acgagacctt ggaggattct cctctctacc aactctaccg tatcgtgtac 600
atgttggttg ttggatggat gcctggatac ctcttcttca acgctactgg acctactaag 660
tactggggaa agtctaggtc tcacttcaac ccttactccg ctatctatgc tgatagggag 720
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ttcagagagg gagagtggaa ttggttgaga ggagctttgt gcactgtgga tagatcattt 960
ggtccattcc tcgattctgt ggtgcataga atcgtggata cccacgtttg ccaccatatc 1020
ttctccaaga tgcctttcta tcactgcgag gaggctacca acgctattaa gcctctcctc 1080
ggaaagttct acttgaagga tactactcct gttcctgttg ctctctggag atcttacacc 1140
cactgcaagt tcgttgagga tgatggaaag gtggtgttct acaagaacaa gttatag 1197

<210> 266
<211> 398
<212> PRT
<213> Phytophthora sojae

<220>
<223> d12Des(Ps) as by plasmid VC-LTM593-1qcz

<400> 266
Met Ala Ile Leu Asn Pro Glu Ala Asp Ser Ala Ala Asn Leu Ala Thr
1 5 10 15
Asp Ser Glu Ala Lys Gln Arg Gln Leu Ala Glu Ala Gly Tyr Thr His
20 25 30
Val Glu Gly Ala Pro Ala Pro Leu Pro Leu Glu Leu Pro His Phe Ser
35 40 45
Leu Arg Asp Leu Arg Ala Ala Ile Pro Lys His Cys Phe Glu Arg Ser
50 55 60
Phe Val Thr Ser Thr Tyr Tyr Met Ile Lys Asn Val Leu Thr Cys Ala
65 70 75 80
Ala Leu Phe Tyr Ala Ala Thr Phe Ile Asp Arg Ala Gly Ala Ala Ala
85 90 95
Tyr Val Leu Trp Pro Val Tyr Trp Phe Phe Gln Gly Ser Tyr Leu Thr
100 105 110
Gly Val Trp Val Ile Ala His Glu Cys Gly His Gln Ala Tyr Cys Ser
115 120 125
Ser Glu Val Val Asn Asn Leu Ile Gly Leu Val Leu His Ser Ala Leu
130 135 140
Leu Val Pro Tyr His Ser Trp Arg Ile Ser His Arg Lys His His Ser
145 150 155 160
Asn Thr Gly Ser Cys Glu Asn Asp Glu Val Phe Val Pro Val Thr Arg
165 170 175
Ser Val Leu Ala Ser Ser Trp Asn Glu Thr Leu Glu Asp Ser Pro Leu

```
            180                 185                 190
Tyr Gln Leu Tyr Arg Ile Val Tyr Met Leu Val Val Gly Trp Met Pro
        195                 200                 205
Gly Tyr Leu Phe Phe Asn Ala Thr Gly Pro Thr Lys Tyr Trp Gly Lys
    210                 215                 220
Ser Arg Ser His Phe Asn Pro Tyr Ser Ala Ile Tyr Ala Asp Arg Glu
225                 230                 235                 240
Arg Trp Met Ile Val Leu Ser Asp Ile Phe Leu Val Ala Met Leu Ala
                245                 250                 255
Val Leu Ala Ala Leu Val His Thr Phe Ser Phe Asn Thr Met Val Lys
            260                 265                 270
Phe Tyr Val Val Pro Tyr Phe Ile Val Asn Ala Tyr Leu Val Leu Ile
        275                 280                 285
Thr Tyr Leu Gln His Thr Asp Thr Tyr Ile Pro His Phe Arg Glu Gly
    290                 295                 300
Glu Trp Asn Trp Leu Arg Gly Ala Leu Cys Thr Val Asp Arg Ser Phe
305                 310                 315                 320
Gly Pro Phe Leu Asp Ser Val Val His Arg Ile Val Asp Thr His Val
                325                 330                 335
Cys His His Ile Phe Ser Lys Met Pro Phe Tyr His Cys Glu Glu Ala
            340                 345                 350
Thr Asn Ala Ile Lys Pro Leu Leu Gly Lys Phe Tyr Leu Lys Asp Thr
        355                 360                 365
Thr Pro Val Pro Val Ala Leu Trp Arg Ser Tyr Thr His Cys Lys Phe
    370                 375                 380
Val Glu Asp Asp Gly Lys Val Val Phe Tyr Lys Asn Lys Leu
385                 390                 395
```

<210> 267
<211> 1092
<212> DNA
<213> Artificial Sequence

<220>
<223> o3Des(Pir) as by plasmid VC-LTM593-1qcz

<400> 267

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atggcttcta catctgctgc tcaagacgct gctccttacg agttcccttc tctcactgag     60
atcaagaggg ctcttccttc tgagtgtttc gaggcttctg ttcctctttc tctctactac    120
accgctagat ctcttgctct tgctggatct ctcgctgttg ctctctctta cgctagagct    180
ttgcctcttg ttcaggctaa cgctcttctt gatgctactc tctgcactgg atacgttctt    240
ctccagggaa tcgttttctg gggattcttc accgttggtc acgattgtgg acacggagct    300
ttctctagat ctcacgtgct caacttctct gttggaaccc tcatgcactc tatcatcctt    360
acccctttcg agtcttggaa gctctctcac agacaccacc acaagaacac cggaaacatc    420
gataaggacg agatcttcta ccctcaaaga gaggctgatt ctcaccctgt ttctagacac    480
cttgtgatgt ctcttggatc tgcttggttc gcttaccttt tcgctggatt ccctcctaga    540
accatgaacc acttcaaccc ttgggaggct atgtatgtta gaagagtggc tgctgtgatc    600
atctctctcg gagttctttt cgctttcgct ggactctact cttacctcac cttcgttctt    660
ggattcacca ctatggctat ctactacttc ggacctctct tcatcttcgc taccatgctt    720
gttgttacca ctttcctcca ccacaacgat gaggagacac cttggtacgc tgattctgag    780
tggacttacg tgaagggaaa cctctcttct gtggacagat cttacggtgc tctcatcgac    840
aaccttagcc acaacatcgg aactcaccag atccaccacc tcttccctat catccctcac    900
tacaagctca acgatgctac tgctgctttc gctaaggctt tccctgagct tgttaggaaa    960
aacgctgctc ctatcatccc aactttcttc aggatggctg ctatgtacgc taagtacgga   1020
gttgttgaca ctgatgctaa gaccttcact ctcaaggagg ctaaggctgc tgctaagact   1080
aagtcatctt ga                                                       1092
```

<210> 268
<211> 363
<212> PRT
<213> Pythium irregulare

<220>

eolf-seql

<223> o3Des(Pir) as by plasmid VC-LTM593-1qcz

<400> 268

```
Met Ala Ser Thr Ser Ala Ala Gln Asp Ala Ala Pro Tyr Glu Phe Pro
1               5                  10                  15
Ser Leu Thr Glu Ile Lys Arg Ala Leu Pro Ser Glu Cys Phe Glu Ala
            20                  25                  30
Ser Val Pro Leu Ser Leu Tyr Tyr Thr Ala Arg Ser Leu Ala Leu Ala
        35                  40                  45
Gly Ser Leu Ala Val Ala Leu Ser Tyr Ala Arg Ala Leu Pro Leu Val
    50                  55                  60
Gln Ala Asn Ala Leu Leu Asp Ala Thr Leu Cys Thr Gly Tyr Val Leu
65                  70                  75                  80
Leu Gln Gly Ile Val Phe Trp Gly Phe Phe Thr Val Gly His Asp Cys
                85                  90                  95
Gly His Gly Ala Phe Ser Arg Ser His Val Leu Asn Phe Ser Val Gly
            100                 105                 110
Thr Leu Met His Ser Ile Ile Leu Thr Pro Phe Glu Ser Trp Lys Leu
        115                 120                 125
Ser His Arg His His His Lys Asn Thr Gly Asn Ile Asp Lys Asp Glu
    130                 135                 140
Ile Phe Tyr Pro Gln Arg Glu Ala Asp Ser His Pro Val Ser Arg His
145                 150                 155                 160
Leu Val Met Ser Leu Gly Ser Ala Trp Phe Ala Tyr Leu Phe Ala Gly
                165                 170                 175
Phe Pro Pro Arg Thr Met Asn His Phe Asn Pro Trp Glu Ala Met Tyr
            180                 185                 190
Val Arg Arg Val Ala Ala Val Ile Ile Ser Leu Gly Val Leu Phe Ala
        195                 200                 205
Phe Ala Gly Leu Tyr Ser Tyr Leu Thr Phe Val Leu Gly Phe Thr Thr
    210                 215                 220
Met Ala Ile Tyr Tyr Phe Gly Pro Leu Phe Ile Phe Ala Thr Met Leu
225                 230                 235                 240
Val Val Thr Thr Phe Leu His His Asn Asp Glu Glu Thr Pro Trp Tyr
                245                 250                 255
Ala Asp Ser Glu Trp Thr Tyr Val Lys Gly Asn Leu Ser Ser Val Asp
            260                 265                 270
Arg Ser Tyr Gly Ala Leu Ile Asp Asn Leu Ser His Asn Ile Gly Thr
        275                 280                 285
His Gln Ile His His Leu Phe Pro Ile Ile Pro His Tyr Lys Leu Asn
    290                 295                 300
Asp Ala Thr Ala Ala Phe Ala Lys Ala Phe Pro Glu Leu Val Arg Lys
305                 310                 315                 320
Asn Ala Ala Pro Ile Ile Pro Thr Phe Phe Arg Met Ala Ala Met Tyr
                325                 330                 335
Ala Lys Tyr Gly Val Val Asp Thr Asp Ala Lys Thr Phe Thr Leu Lys
            340                 345                 350
Glu Ala Lys Ala Ala Ala Lys Thr Lys Ser Ser
        355                 360
```

<210> 269
<211> 1086
<212> DNA
<213> Artificial Sequence

<220>
<223> o3Des(Pi) as by plasmid VC-LTM593-1qcz

<400> 269

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atggctacaa aggaggctta cgttttccca actctcaccg agatcaagag atctctccca     60
aaggattgct tcgaggcttc tgtgcctttg tctctctact acactgtgag atgcttggtt    120
attgctgtgg ctttgacctt cggattgaac tacgctagag ctttgccaga ggttgagtct    180
ttctgggctt tggatgctgc tttgtgcact ggatatatcc tcctccaggg aattgtgttc    240
```

```
tggggattct tcactgttgg acacgatgct ggacacggag ctttctctag ataccacctc    300
ttgaacttcg ttgtgggaac cttcatgcac tctctcatct tgaccccatt cgagtcttgg    360
aagttgaccc acagacacca ccacaagaac accggaaaca tcgatagaga tgaggtgttc    420
tacccacaga gaaaggctga tgatcaccca ttgtccagga acttgatctt ggctttggga    480
gctgcttggc ttgcttattt ggtggaggga ttcccaccaa gaaaggtgaa ccacttcaac    540
ccattcgagc cacttttgt gagacaagtg tccgctgtgg ttatctcttt gctcgctcac    600
ttcttcgttg ctggactctc tatctacttg tctctccagt tgggacttaa gaccatggct    660
atctactact acggaccagt tttcgtgttc ggatctatgt tggtgattac caccttcttg    720
caccacaacg atgaggagac tccatggtat gctgattctg agtggactta cgtgaaggga    780
aacttgtcct ctgtggatag atcttacggt gctctcatcg ataacctctc ccacaacatc    840
ggaactcacc agatccacca cctcttccca attatcccac actacaagct caagaaggct    900
actgctgctt tccaccaagc tttcccagag cttgtgagaa agtccgatga gccaatcatc    960
aaggctttct tcagagtggg aaggttgtat gctaactacg gagtggttga tcaagaggct   1020
aagctcttca ctttgaagga ggctaaggct gctactgaag ctgctgctaa gaccaagtct   1080
acctga                                                              1086
```

<210> 270
<211> 361
<212> PRT
<213> Phytophthora infestans

<220>
<223> o3Des(Pi) as by plasmid VC-LTM593-1qcz

<400> 270

```
Met Ala Thr Lys Glu Ala Tyr Val Phe Pro Thr Leu Thr Glu Ile Lys
1               5                  10                  15
Arg Ser Leu Pro Lys Asp Cys Phe Glu Ala Ser Val Pro Leu Ser Leu
            20                  25                  30
Tyr Tyr Thr Val Arg Cys Leu Val Ile Ala Val Ala Leu Thr Phe Gly
        35                  40                  45
Leu Asn Tyr Ala Arg Ala Leu Pro Glu Val Glu Ser Phe Trp Ala Leu
    50                  55                  60
Asp Ala Ala Leu Cys Thr Gly Tyr Ile Leu Leu Gln Gly Ile Val Phe
65                  70                  75                  80
Trp Gly Phe Phe Thr Val Gly His Asp Ala Gly His Gly Ala Phe Ser
                85                  90                  95
Arg Tyr His Leu Leu Asn Phe Val Val Gly Thr Phe Met His Ser Leu
            100                 105                 110
Ile Leu Thr Pro Phe Glu Ser Trp Lys Leu Thr His Arg His His His
        115                 120                 125
Lys Asn Thr Gly Asn Ile Asp Arg Asp Glu Val Phe Tyr Pro Gln Arg
    130                 135                 140
Lys Ala Asp Asp His Pro Leu Ser Arg Asn Leu Ile Leu Ala Leu Gly
145                 150                 155                 160
Ala Ala Trp Leu Ala Tyr Leu Val Glu Gly Phe Pro Pro Arg Lys Val
                165                 170                 175
Asn His Phe Asn Pro Phe Glu Pro Leu Phe Val Arg Gln Val Ser Ala
            180                 185                 190
Val Val Ile Ser Leu Leu Ala His Phe Phe Val Ala Gly Leu Ser Ile
        195                 200                 205
Tyr Leu Ser Leu Gln Leu Gly Leu Lys Thr Met Ala Ile Tyr Tyr Tyr
    210                 215                 220
Gly Pro Val Phe Val Phe Gly Ser Met Leu Val Ile Thr Thr Phe Leu
225                 230                 235                 240
His His Asn Asp Glu Glu Thr Pro Trp Tyr Ala Asp Ser Glu Trp Thr
                245                 250                 255
Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala Leu
            260                 265                 270
Ile Asp Asn Leu Ser His Asn Ile Gly Thr His Gln Ile His His Leu
        275                 280                 285
Phe Pro Ile Ile Pro His Tyr Lys Leu Lys Lys Ala Thr Ala Ala Phe
    290                 295                 300
```

eolf-seql

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

<210> 271
<211> 1560
<212> DNA
<213> Artificial Sequence

<220>
<223> d4Des(Tc) as by plasmid VC-LTM593-1qcz

<400> 271
atgactgttg gatacgacga ggagatccca ttcgagcaag ttagggctca taacaagcca 60
gacgacgctt ggtgtgctat tcacggacac gtgtacgacg ttaccaagtt cgcttcagtt 120
cacccaggag gagatattat cttgctcgct gctggaaagg aagctactgt cctctacgag 180
acctaccatg ttagaggagt gtctgacgct gtgctcagaa agtacagaat aggaaagttg 240
ccagacggac aaggaggagc taacgagaag gagaagagaa ccttgtctgg attgtcctct 300
gcttcttact acacctggaa ctccgatttc tacagagtga tgagggagag agttgtggct 360
agattgaagg agagaggaaa ggctagaaga ggaggatacg aactctggat caaggctttc 420
ttgctccttg ttggattctg gtcctctctt tactggatgt gcaccctcga tccatctttc 480
ggagctatct tggctgctat gtctttggga gtgttcgctg cttttgttgg aacctgcatc 540
caacacgatg gaaaccacgg agctttcgct caatctagat gggttaacaa ggtggcagga 600
tggactttgg atatgatcgg agcttctgga atgacttggg agttccaaca cgtgttggga 660
caccacccat acactaactt gatcgaggag gagaacggat tgcaaaaggt gtccggaaag 720
aagatggata ccaagttggc tgatcaagag tctgatccag atgtgttctc cacctaccca 780
atgatgagat tgcacccttg gcaccagaag aggtggtatc acaggttcca gcacatctac 840
ggacctttca tcttcggatt catgaccatc aacaaggtgg tgactcaaga tgttggagtg 900
gtgttgagaa agagactctt ccaaatcgat gctgagtgca gatatgcttc cccaatgtac 960
gttgctaggt tctggattat gaaggctttg accgtgttgt atatggttgc tttgccttgt 1020
tatatgcaag gaccttggca cggattgaaa ctcttcgcta tcgctcactt cacttgcgga 1080
gaggttttgg ctaccatgtt catcgtgaac cacattatcg agggagtgtc ttacgcttct 1140
aaggatgctg ttaagggaac tatggctcca ccaaagacta tgcacggagt gaccccaatg 1200
aacaacacta gaaaggaggt tgaggctgag gcttctaagt ctggagctgt ggttaagtct 1260
gtgccattgg atgattgggc tgctgttcag tgccaaacct ctgtgaactg gtctgttgga 1320
tcttggtttt ggaaccactt ctctggagga ctcaaccacc aaatcgagca ccacctcttc 1380
ccaggattgt ctcacgagac ctactaccac atccaagacg tggttcaatc tacctgtgct 1440
gagtacggag ttccatacca acacgagcca tctttgtgga ctgcttactg gaagatgctc 1500
gaacacctta gacaattggg aaacgaggag actcacgagt catggcagag agctgcttga 1560

<210> 272
<211> 519
<212> PRT
<213> Thraustochytrium sp.

<220>
<223> d4Des(Tc) as by plasmid VC-LTM593-1qcz

<400> 272
Met Thr Val Gly Tyr Asp Glu Glu Ile Pro Phe Glu Gln Val Arg Ala
1 5 10 15
His Asn Lys Pro Asp Asp Ala Trp Cys Ala Ile His Gly His Val Tyr
20 25 30
Asp Val Thr Lys Phe Ala Ser Val His Pro Gly Gly Asp Ile Ile Leu
35 40 45
Leu Ala Ala Gly Lys Glu Ala Thr Val Leu Tyr Glu Thr Tyr His Val
50 55 60
Arg Gly Val Ser Asp Ala Val Leu Arg Lys Tyr Arg Ile Gly Lys Leu

65 70 75 80
Pro Asp Gly Gln Gly Gly Ala Asn Glu Lys Glu Lys Arg Thr Leu Ser
85 90 95
Gly Leu Ser Ser Ala Ser Tyr Tyr Thr Trp Asn Ser Asp Phe Tyr Arg
100 105 110
Val Met Arg Glu Arg Val Val Ala Arg Leu Lys Glu Arg Gly Lys Ala
115 120 125
Arg Arg Gly Gly Tyr Glu Leu Trp Ile Lys Ala Phe Leu Leu Leu Val
130 135 140
Gly Phe Trp Ser Ser Leu Tyr Trp Met Cys Thr Leu Asp Pro Ser Phe
145 150 155 160
Gly Ala Ile Leu Ala Ala Met Ser Leu Gly Val Phe Ala Ala Phe Val
165 170 175
Gly Thr Cys Ile Gln His Asp Gly Asn His Gly Ala Phe Ala Gln Ser
180 185 190
Arg Trp Val Asn Lys Val Ala Gly Trp Thr Leu Asp Met Ile Gly Ala
195 200 205
Ser Gly Met Thr Trp Glu Phe Gln His Val Leu Gly His His Pro Tyr
210 215 220
Thr Asn Leu Ile Glu Glu Glu Asn Gly Leu Gln Lys Val Ser Gly Lys
225 230 235 240
Lys Met Asp Thr Lys Leu Ala Asp Gln Glu Ser Asp Pro Asp Val Phe
245 250 255
Ser Thr Tyr Pro Met Met Arg Leu His Pro Trp His Gln Lys Arg Trp
260 265 270
Tyr His Arg Phe Gln His Ile Tyr Gly Pro Phe Ile Phe Gly Phe Met
275 280 285
Thr Ile Asn Lys Val Val Thr Gln Asp Val Gly Val Val Leu Arg Lys
290 295 300
Arg Leu Phe Gln Ile Asp Ala Glu Cys Arg Tyr Ala Ser Pro Met Tyr
305 310 315 320
Val Ala Arg Phe Trp Ile Met Lys Ala Leu Thr Val Leu Tyr Met Val
325 330 335
Ala Leu Pro Cys Tyr Met Gln Gly Pro Trp His Gly Leu Lys Leu Phe
340 345 350
Ala Ile Ala His Phe Thr Cys Gly Glu Val Leu Ala Thr Met Phe Ile
355 360 365
Val Asn His Ile Ile Glu Gly Val Ser Tyr Ala Ser Lys Asp Ala Val
370 375 380
Lys Gly Thr Met Ala Pro Pro Lys Thr Met His Gly Val Thr Pro Met
385 390 395 400
Asn Asn Thr Arg Lys Glu Val Glu Ala Glu Ala Ser Lys Ser Gly Ala
405 410 415
Val Val Lys Ser Val Pro Leu Asp Asp Trp Ala Ala Val Gln Cys Gln
420 425 430
Thr Ser Val Asn Trp Ser Val Gly Ser Trp Phe Trp Asn His Phe Ser
435 440 445
Gly Gly Leu Asn His Gln Ile Glu His His Leu Phe Pro Gly Leu Ser
450 455 460
His Glu Thr Tyr Tyr His Ile Gln Asp Val Val Gln Ser Thr Cys Ala
465 470 475 480
Glu Tyr Gly Val Pro Tyr Gln His Glu Pro Ser Leu Trp Thr Ala Tyr
485 490 495
Trp Lys Met Leu Glu His Leu Arg Gln Leu Gly Asn Glu Glu Thr His
500 505 510
Glu Ser Trp Gln Arg Ala Ala
515

<210> 273
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> d4Des(Pl) as by plasmid VC-LTM593-1qcz

<400> 273
atgccaccta gtgctgctag tgaaggtggt gttgctgaac ttagagctgc tgaagttgct 60
agctacacta gaaaggctgt tgacgaaaga cctgacctca ctatagttgg tgacgctgtt 120
tacgacgcta aggcttttag ggacgagcac cctggtggtg ctcacttcgt tagccttttc 180
ggaggtaggg acgctactga ggcttttatg gaatatcacc gtagagcttg gcctaaggct 240
aggatgtcta agttcttcgt tggttcactt gacgctagcg agaagcctac tcaagctgat 300
tcagcttacc ttagactttg cgctgaggtt aacgctcttt tgcctaaggg tagcggagga 360
ttcgctcctc ctagctactg gcttaaggct gctgctcttg ttgttgctgc tgttagtata 420
gagggttata tgctccttag gggtaagacc cttttgctta gcgttttcct tggactcgtg 480
ttcgcttgga taggacttaa tattcagcac gacgctaatc acggtgctct tagtagacac 540
tcagtgatta actactgcct cggttacgct caggattgga taggtggtaa tatggtgctt 600
tggcttcaag agcacgttgt gatgcaccac ctccacacta acgacgttga cgctgatcct 660
gatcaaaagg ctcacggtgt tcttagactt aagcctactg acggttggat gccttggcac 720
gcacttcaac aactctatat ccttcctggt gaggctatgt acgcttttaa gcttcttttc 780
ttggacgccc ttgagcttct tgcttggagg tgggagggtg agaagattag ccctcttgct 840
agagctttgt tcgctcctgc tgttgcttgt aagcttggat tctgggctag attcgttgct 900
ctccctctct ggcttcaacc tactgttcac actgctttgt gtatctgtgc tactgtgtgt 960
actggtagct tctacctcgc cttcttcttc tttatctctc acaacttcga cggtgttggt 1020
agcgttggac ctaagggatc acttcctaga tcagctactt tcgttcaacg tcaggttgag 1080
actagctcta acgttggtgg ttactggctt ggagttctta acggtggact taactttcag 1140
atagagcacc acttgttccc taggcttcac cactcttact acgctcaaat agctcctgtg 1200
gttaggactc acatagagaa gctcggtttt aagtaccgtc acttccctac cgttggatct 1260
aaccttagct caatgcttca gcatatgggt aagatgggaa ctagacctgg tgctgagaag 1320
ggtggtaagg ctgagtag 1338

<210> 274
<211> 445
<212> PRT
<213> Pavlova lutheri

<220>
<223> d4Des(Pl) as by plasmid VC-LTM593-1qcz

<400> 274
Met Pro Pro Ser Ala Ala Ser Glu Gly Gly Val Ala Glu Leu Arg Ala
1 5 10 15
Ala Glu Val Ala Ser Tyr Thr Arg Lys Ala Val Asp Glu Arg Pro Asp
20 25 30
Leu Thr Ile Val Gly Asp Ala Val Tyr Asp Ala Lys Ala Phe Arg Asp
35 40 45
Glu His Pro Gly Gly Ala His Phe Val Ser Leu Phe Gly Gly Arg Asp
50 55 60
Ala Thr Glu Ala Phe Met Glu Tyr His Arg Arg Ala Trp Pro Lys Ala
65 70 75 80
Arg Met Ser Lys Phe Phe Val Gly Ser Leu Asp Ala Ser Glu Lys Pro
85 90 95
Thr Gln Ala Asp Ser Ala Tyr Leu Arg Leu Cys Ala Glu Val Asn Ala
100 105 110
Leu Leu Pro Lys Gly Ser Gly Gly Phe Ala Pro Pro Ser Tyr Trp Leu
115 120 125
Lys Ala Ala Ala Leu Val Val Ala Ala Val Ser Ile Glu Gly Tyr Met
130 135 140
Leu Leu Arg Gly Lys Thr Leu Leu Leu Ser Val Phe Leu Gly Leu Val
145 150 155 160
Phe Ala Trp Ile Gly Leu Asn Ile Gln His Asp Ala Asn His Gly Ala
165 170 175
Leu Ser Arg His Ser Val Ile Asn Tyr Cys Leu Gly Tyr Ala Gln Asp
180 185 190
Trp Ile Gly Gly Asn Met Val Leu Trp Leu Gln Glu His Val Val Met
195 200 205

eolf-seql

```
His His Leu His Thr Asn Asp Val Asp Ala Asp Pro Asp Gln Lys Ala
    210                 215                 220
His Gly Val Leu Arg Leu Lys Pro Thr Asp Gly Trp Met Pro Trp His
225                 230                 235                 240
Ala Leu Gln Gln Leu Tyr Ile Leu Pro Gly Glu Ala Met Tyr Ala Phe
                245                 250                 255
Lys Leu Leu Phe Leu Asp Ala Leu Glu Leu Leu Ala Trp Arg Trp Glu
            260                 265                 270
Gly Glu Lys Ile Ser Pro Leu Ala Arg Ala Leu Phe Ala Pro Ala Val
        275                 280                 285
Ala Cys Lys Leu Gly Phe Trp Ala Arg Phe Val Ala Leu Pro Leu Trp
    290                 295                 300
Leu Gln Pro Thr Val His Thr Ala Leu Cys Ile Cys Ala Thr Val Cys
305                 310                 315                 320
Thr Gly Ser Phe Tyr Leu Ala Phe Phe Phe Ile Ser His Asn Phe
                325                 330                 335
Asp Gly Val Gly Ser Val Gly Pro Lys Gly Ser Leu Pro Arg Ser Ala
            340                 345                 350
Thr Phe Val Gln Arg Gln Val Glu Thr Ser Ser Asn Val Gly Gly Tyr
        355                 360                 365
Trp Leu Gly Val Leu Asn Gly Gly Leu Asn Phe Gln Ile Glu His His
    370                 375                 380
Leu Phe Pro Arg Leu His His Ser Tyr Tyr Ala Gln Ile Ala Pro Val
385                 390                 395                 400
Val Arg Thr His Ile Glu Lys Leu Gly Phe Lys Tyr Arg His Phe Pro
                405                 410                 415
Thr Val Gly Ser Asn Leu Ser Ser Met Leu Gln His Met Gly Lys Met
            420                 425                 430
Gly Thr Arg Pro Gly Ala Glu Lys Gly Gly Lys Ala Glu
        435                 440                 445
```

<210> 275
<211> 903
<212> DNA
<213> Artificial Sequence

<220>
<223> d5Elo(Ot) as by plasmid VC-LTM593-1qcz

<400> 275

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atgtctgcta gcggagcttt gttgcctgct atagctttcg ctgcttacgc ttacgctacc     60
tacgcttatg ctttcgagtg gagccacgct aacggaatcg ataacgtgga tgctagagag    120
tggattggag ctttgtcttt gagactccct gcaattgcaa ccacaatgta cctcttgttc    180
tgccttgtgg gacctagatt gatggctaag agggaggctt ttgatcctaa gggatttatg    240
ctcgcttaca acgcttacca aaccgctttc aacgttgtgg tgctcggaat gttcgctaga    300
gagatctctg gattgggaca acctgtttgg ggatctacta tgccttggag cgataggaag    360
tccttcaaga ttttgttggg agtgtggctc cactacaaca ataagtacct cgagttgttg    420
gatactgtgt tcatggtggc taggaaaaag accaagcagc tctctttctt gcacgtgtac    480
caccacgctt tgttgatttg ggcttggtgg cttgtttgtc acctcatggc taccaacgat    540
tgcatcgatg cttatttcgg agctgcttgc aactctttca tccacatcgt gatgtactcc    600
tactacctca tgtctgcttt gggaattagg tgcccttgga agagatatat cacccaggct    660
cagatgttgc aattcgtgat cgtgttcgct cacgctgttt tcgtgctcag acaaaagcac    720
tgccctgtta ctttgccttg ggcacaaatg ttcgtgatga caaatatgtt ggtgctcttc    780
ggaaacttct acctcaaggc ttactctaac aagtctaggg gagatggagc ttcttctgtt    840
aagcctgctg agactactag agcaccttct gtgagaagaa ccaggtcaag gaagatcgat    900
tga                                                                  903
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<210> 276
<211> 300
<212> PRT
<213> Ostreococcus tauri

<220>

<223> d5Elo(Ot) as by plasmid VC-LTM593-1qcz

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Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
        35   40   45
Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly
    50   55   60
Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met
65   70   75   80
Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly
                85   90   95
Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser
            100   105   110
Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val
        115   120   125
Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe
    130   135   140
Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr
145   150   155   160
His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met
                165   170   175
Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser
            180   185   190
Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly
        195   200   205
Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln
    210   215   220
Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His
225   230   235   240
Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met
                245   250   255
Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser
            260   265   270
Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala
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Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp
    290   295   300

<210> 277
<211> 2013
<212> DNA
<213> Artificial Sequence

<220>
<223> AHAS as by plasmid VC-LTM593-1qcz

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<211> 670
<212> PRT
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<400> 278

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            20                  25                  30
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        35                  40                  45
Ser Arg Arg Arg Gly Ile Lys Ser Ser Ser Pro Ser Ser Ile Ser Ala
    50                  55                  60
Val Leu Asn Thr Thr Thr Asn Val Thr Thr Thr Pro Ser Pro Thr Lys
65                  70                  75                  80
Pro Thr Lys Pro Glu Thr Phe Ile Ser Arg Phe Ala Pro Asp Gln Pro
                85                  90                  95
Arg Lys Gly Ala Asp Ile Leu Val Glu Ala Leu Glu Arg Gln Gly Val
            100                 105                 110
Glu Thr Val Phe Ala Tyr Pro Gly Gly Thr Ser Met Glu Ile His Gln
        115                 120                 125
Ala Leu Thr Arg Ser Ser Ser Ile Arg Asn Val Leu Pro Arg His Glu
    130                 135                 140
Gln Gly Gly Val Phe Ala Ala Glu Gly Tyr Ala Arg Ser Ser Gly Lys
145                 150                 155                 160
Pro Gly Ile Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
                165                 170                 175
Ser Gly Leu Ala Asp Ala Leu Leu Asp Ser Val Pro Leu Val Ala Ile
            180                 185                 190
Thr Gly Gln Val Pro Arg Arg Met Ile Gly Thr Asp Ala Phe Gln Glu
        195                 200                 205
Thr Pro Ile Val Glu Val Thr Arg Ser Ile Thr Lys His Asn Tyr Leu
    210                 215                 220
Val Met Asp Val Glu Asp Ile Pro Arg Ile Ile Glu Glu Ala Phe Phe
225                 230                 235                 240
Leu Ala Thr Ser Gly Arg Pro Gly Pro Val Leu Val Asp Val Pro Lys
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eolf-seql

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Leu Pro Gly Tyr Met Ser Arg Met Pro Lys Pro Pro Glu Asp Ser His
275 280 285
Leu Glu Gln Ile Val Arg Leu Ile Ser Glu Ser Lys Lys Pro Val Leu
290 295 300
Tyr Val Gly Gly Gly Cys Leu Asn Ser Ser Asp Glu Leu Gly Arg Phe
305 310 315 320
Val Glu Leu Thr Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu Gly
325 330 335
Ser Tyr Pro Cys Asp Asp Glu Leu Ser Leu His Met Leu Gly Met His
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Gly Thr Val Tyr Ala Asn Tyr Ala Val Glu His Ser Asp Leu Leu Leu
355 360 365
Ala Phe Gly Val Arg Phe Asp Asp Arg Val Thr Gly Lys Leu Glu Ala
370 375 380
Phe Ala Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu
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Ile Gly Lys Asn Lys Thr Pro His Val Ser Val Cys Gly Asp Val Lys
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Asn Tyr Lys Lys Pro Arg Gln Trp Leu Ser Ser Gly Gly Leu Gly Ala
500 505 510
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515 520 525
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565 570 575
Arg Phe Tyr Lys Ala Asn Arg Ala His Thr Phe Leu Gly Asp Pro Ala
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595 600 605
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610 615 620
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<210> 279
<211> 60074
<212> DNA
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<220>
<223> vector VC-LTM593-1qcz rc

<400> 279

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<212> DNA
<213> Artificial sequence

<220>
<223> LBFLFK Locus 1 RB junction region

<400> 282
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<210> 283
<211> 20
<212> DNA
<213> Artificial sequence

<220>

<223> LBFLFK Locus 1 LB junction region

<400> 283
aagccatata tctgacccta 20

<210> 284
<211> 1100
<212> DNA
<213> Artificial sequence

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<223> LBFLFK Locus 1 flanking sequence up to and including the right
border of the T-DNA

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<212> DNA
<213> Artificial sequence

<220>
<223> LBFLFK Locus 1 flanking sequence up to and including the left
border of the T-DNA

<400> 285
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<223> LBFLFK Locus 1_Forward primer

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<223> LBFLFK Locus 1_Reverse primer

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<223> LBFLFK locus 1_Probe

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<212> DNA
<213> Artificial sequence

<220>
<223> LBFLFK Locus 2 RB junction region

<400> 291
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<210> 292
<211> 20
<212> DNA
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<220>
<223> LBFLFK Locus 2 LB junction region

<400> 292
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<210> 293
<211> 2900
<212> DNA
<213> Artificial sequence

<220>
<223> LBFLFK Locus 2 flanking sequence up to and including the right
border of the T-DNA

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<210> 294
<211> 1800
<212> DNA
<213> Artificial sequence

<220>
<223> LBFLFK Locus 2 flanking sequence up to and including the left
border of the T-DNA

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<223> LBFDAU Locus 1 RB junction region

<400> 300
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<210> 301
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<223> LBFDAU Locus 1 flanking sequence up to and including the right

border of the T-DNA

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<210> 303
<211> 1677
<212> DNA
<213> Artificial sequence

<220>
<223> LBFDAU Locus 1 flanking sequence up to and including the left border of the T-DNA

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agacctcaat tgcgagcttt ctaatttcaa actattcggg cctaactttt ggtgtgatga   4140
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gtatgacagg ttagattttg ttttgtatag ttgtatacat acttctttgt gatgttttgt 4680
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gcggatgggt tatgcacgag atgggacacg gatctttcac tggagttatc tggctcgatg 5520
ataggatgtg cgagttcttc tacggagttg gatgtggaat gtctggacac tactggaaga 5580
accagcactc taagcaccac 5600

<210> 312
<211> 1321
<212> DNA
<213> Artificial sequence

<220>
<223> LBFDAU Locus 2 flanking sequence up to and including the left
border of the T-DNA

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attgaaaagc attatttta tcgaaatgaa tctagtatac aatcaatatt tatgtttttt 120
catcagatac tttcctattt tttggcacct ttcatcggac tactgattta tttcaatgtg 180
tatgcatgca tgagcatgag tatacacatg tcttttaaaa tgcatgtaaa gcgtaacgga 240
ccacaaaaga ggatccatac aaatacatct catcgcttcc tctactattc tccgacacac 300
acactgagca tggtgcttaa acactctggt gagttctagt acttctgcta taatgttaaa 360
ttttatatta tatacctact tcctctctct cgctctgtta tgttcgattt cgaaaggatt 420
tcaagatcaa agatgatgag aaaaggtacc ttttcgatat ttaagacaag gaaagaaagg 480
acgaggttga aattttcggg acttggaggg ctaaagtgga agagactgaa tctgaagatg 540
tcgtttctcg aaactttgag atacagaatc atgtctatca ttgaaggaat ggttttggtt 600
tctaagcttg ctttcttctt tctctgttgc ggttgcagat tttaacacgt tagttttttt 660
tttttcgttt ttttgaacgt caacaatgtc ttttttgtac tctttagctc atgtgtaaaa 720
ttctaaattc ttccaataac atacccaaca aattattcgt atctgatttt tatagttttt 780
aacctgttaa tgtaattaat ctaagtgtaa tttttaggct aaatgttaaa ttttatatta 840
aagttttgta acttgaaatt acattcttct tatagcggat aaacagaaaa tgctcttaaa 900
caaatcctga aacaagtaaa aaatacaaca gaaaaatcta acgtttaatt cttaaaacct 960
caaaatcctt atttttacag ctttcaaagt ttaacagctg gaaacctgta gaaaatcaga 1020
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aatttgaaaa tttatcatca tcatgttaac ggaagttgtc tgtaaaagta gttgattacc 1200
tgttatcgtg taaagtagtt agtaatttct tgcttatttg aaaaatagag aacatttaac 1260
atgtattttt aaataggcac gaccatgcta ctgaacttta tgaaatgctt tggaatctta 1320
t 1321

<210> 313
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> LBFDAU Locus 2_Forward primer

<400> 313
cactgagcat ggtgcttaaa cac 23

<210> 314
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> LBFDAU Locus 2_Reverse primer

<400> 314
agagcgagag agaggaagta ggtatataa 29

<210> 315
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> LBFDAU locus 2_Probe

<400> 315
ctggtgagtt ctagtactt 19

<210> 316
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Primer for determining zygosity of LBFLFK Locus 1

<400> 316
agaagtgtac gcgacgaga 19

<210> 317
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Primer for determining zygosity of LBFLFK Locus 1

<400> 317
tcaggagcga gaatgcgaaa g 21

<210> 318
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Primer for determining zygosity of LBFLFK Locus 2

<400> 318
acccatacat acgcataagt g 21

<210> 319

<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Primer for determining zygosity of LBFLFK Locus 2

<400> 319
aatatatggg ctacattga 19

<210> 320
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Primer for determining zygosity of LBFDAU Locus 1

<400> 320
ggcaggcgtg atcttatt 18

<210> 321
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Primer for determining zygosity of LBFDAU Locus 1

<400> 321
cataatttgc agtcgctgat t 21

<210> 322
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Primer for determining zygosity of LBFDAU Locus 2

<400> 322
agataacgat acatccacga a 21

<210> 323
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Primer for determining zygosity of LBFDAU Locus 2

<400> 323
cgaacataac agagcgagag a 21

<210> 324
<211> 1197
<212> DNA
<213> Artificial Sequence

<220>
<223> d12Des(Ps) on LBFLFK Locus 1

<400> 324

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cctttggagt tgcctcactt ctctctcaga gatctcagag ctgctattcc taagcactgc    180
ttcgagagat ctttcgtgac ctccacctac tacatgatca agaacgtgtt gacttgcgct    240
gctttgttat acgctgctac cttcattgat agagctggag ctgctgctta tgttttgtgg    300
cctgtgtact ggttcttcca gggatcttac ttgactggag tgtgggttat cgctcacgag    360
tgtggacacc aggcttattg ctcttctgag gtggtgaaca acttgattgg actcgtgttg    420
cactctgctt tgttggtgcc ttaccactct tggagaatct ctcacagaaa gcaccactcc    480
aacactggat cttgcgagaa cgatgaggtt ttcgttcctg tgaccagatc tgtgttggct    540
tcttcttgga acgagacctt ggaggattct cctctctacc aactctaccg tatcgtgtac    600
atgttggttg ttggatggat gcctggatac ctcttcttca acgctactgg acctactaag    660
tactggggaa agtctaggtc tcacttcaac ccttactccg ctatctatgc tgatagggag    720
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ggtccattcc tcgattctgt ggtgcataga atcgtggata cccacgtttg ccaccatatc   1020
ttctccaaga tgcctttcta tcactgcgag gaggctacca acgctattaa gcctctcctc   1080
ggaaagttct acttgaagga tactactcct gttcctgttg ctctctggag atcttacacc   1140
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<210> 325
<211> 398
<212> PRT
<213> Artificial Sequence

<220>
<223> d12Des(Ps) on LBFLFK Locus 1

<400> 325

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            20                  25                  30
Val Glu Gly Ala Pro Ala Pro Leu Pro Leu Glu Leu Pro His Phe Ser
        35                  40                  45
Leu Arg Asp Leu Arg Ala Ala Ile Pro Lys His Cys Phe Glu Arg Ser
    50                  55                  60
Phe Val Thr Ser Thr Tyr Tyr Met Ile Lys Asn Val Leu Thr Cys Ala
65                  70                  75                  80
Ala Leu Leu Tyr Ala Ala Thr Phe Ile Asp Arg Ala Gly Ala Ala Ala
                85                  90                  95
Tyr Val Leu Trp Pro Val Tyr Trp Phe Phe Gln Gly Ser Tyr Leu Thr
            100                 105                 110
Gly Val Trp Val Ile Ala His Glu Cys Gly His Gln Ala Tyr Cys Ser
        115                 120                 125
Ser Glu Val Val Asn Asn Leu Ile Gly Leu Val Leu His Ser Ala Leu
    130                 135                 140
Leu Val Pro Tyr His Ser Trp Arg Ile Ser His Arg Lys His His Ser
145                 150                 155                 160
Asn Thr Gly Ser Cys Glu Asn Asp Glu Val Phe Val Pro Val Thr Arg
                165                 170                 175
Ser Val Leu Ala Ser Ser Trp Asn Glu Thr Leu Glu Asp Ser Pro Leu
            180                 185                 190
Tyr Gln Leu Tyr Arg Ile Val Tyr Met Leu Val Val Gly Trp Met Pro
        195                 200                 205
Gly Tyr Leu Phe Phe Asn Ala Thr Gly Pro Thr Lys Tyr Trp Gly Lys
    210                 215                 220
Ser Arg Ser His Phe Asn Pro Tyr Ser Ala Ile Tyr Ala Asp Arg Glu
225                 230                 235                 240
Arg Trp Met Ile Val Leu Ser Asp Ile Phe Leu Val Ala Met Leu Ala
                245                 250                 255
Val Leu Ala Ala Leu Val His Thr Phe Ser Phe Asn Thr Met Val Lys
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260 265 270
Phe Tyr Val Val Pro Tyr Phe Ile Val Asn Ala Tyr Leu Val Leu Ile
275 280 285
Thr Tyr Leu Gln His Thr Asp Thr Tyr Ile Pro His Phe Arg Glu Gly
290 295 300
Glu Trp Asn Trp Leu Arg Gly Ala Leu Cys Thr Val Asp Arg Ser Phe
305 310 315 320
Gly Pro Phe Leu Asp Ser Val Val His Arg Ile Val Asp Thr His Val
325 330 335
Cys His His Ile Phe Ser Lys Met Pro Phe Tyr His Cys Glu Glu Ala
340 345 350
Thr Asn Ala Ile Lys Pro Leu Leu Gly Lys Phe Tyr Leu Lys Asp Thr
355 360 365
Thr Pro Val Pro Val Ala Leu Trp Arg Ser Tyr Thr His Cys Lys Phe
370 375 380
Val Glu Asp Asp Gly Lys Val Val Phe Tyr Lys Asn Lys Leu
385 390 395

<210> 326
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> d4Des(Pl) on LBFLFK Locus 2

<400> 326
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tacgacgcta aggcttttag ggacgagcac cctggtggtg ctcacttcgt tagccttttc 180
ggaggtaggg acgctactga ggcttttatg gaatatcacc gtagagcttg gcctaaggct 240
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ttcgcttgga taggacttaa tattcagcac gacgctaatc acggtgctct tagtagacac 540
tcagtgatta actactgcct cggttacgct caggattgga taggtggtaa tatggtgctt 600
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gatcaaaagg ctcacggtgt tcttagactt aagcctactg acggttggat gccttggcac 720
gcacttcaac aactctatat ccttcctggt gaggctatgt acgctttaa gcttcttttc 780
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atagagcacc acttgttccc taggcttcac cactcttact acgctcaaat agctcctgtg 1200
gttaggactc acatagagaa gctcggtttt aagtaccgtc acttccctac cgttggatct 1260
aaccttagct caatgcttca gcatatgggt aagatgggaa ctagacctgg tgctgagaag 1320
ggtggtaagg ctgagtag 1338

<210> 327
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> d4Des(Pl) on LBFLFK Locus 2

<400> 327
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Ala Glu Val Ala Ser Tyr Thr Arg Lys Ala Val Asp Glu Arg Pro Asp

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            20                  25                  30
Leu Thr Ile Val Gly Asp Ala Val Tyr Asp Ala Lys Ala Phe Arg Asp
        35                  40                  45
Glu His Pro Gly Gly Ala His Phe Val Ser Leu Phe Gly Gly Arg Asp
    50                  55                  60
Ala Thr Glu Ala Phe Met Glu Tyr His Arg Arg Ala Trp Pro Lys Ala
65                  70                  75                  80
Arg Met Ser Lys Phe Phe Val Gly Ser Leu Asp Ala Ser Glu Lys Pro
                85                  90                  95
Thr Gln Ala Asp Ser Ser Tyr Leu Arg Leu Cys Ala Glu Val Asn Ala
            100                 105                 110
Leu Leu Pro Lys Gly Ser Gly Gly Phe Ala Pro Pro Ser Tyr Trp Leu
        115                 120                 125
Lys Ala Ala Ala Leu Val Val Ala Ala Val Ser Ile Glu Gly Tyr Met
    130                 135                 140
Leu Leu Arg Gly Lys Thr Leu Leu Leu Ser Val Phe Leu Gly Leu Val
145                 150                 155                 160
Phe Ala Trp Ile Gly Leu Asn Ile Gln His Asp Ala Asn His Gly Ala
                165                 170                 175
Leu Ser Arg His Ser Val Ile Asn Tyr Cys Leu Gly Tyr Ala Gln Asp
            180                 185                 190
Trp Ile Gly Gly Asn Met Val Leu Trp Leu Gln Glu His Val Val Met
        195                 200                 205
His His Leu His Thr Asn Asp Val Asp Ala Asp Pro Asp Gln Lys Ala
    210                 215                 220
His Gly Val Leu Arg Leu Lys Pro Thr Asp Gly Trp Met Pro Trp His
225                 230                 235                 240
Ala Leu Gln Gln Leu Tyr Ile Leu Pro Gly Glu Ala Met Tyr Ala Phe
                245                 250                 255
Lys Leu Leu Phe Leu Asp Ala Leu Glu Leu Leu Ala Trp Arg Trp Glu
            260                 265                 270
Gly Glu Lys Ile Ser Pro Leu Ala Arg Ala Leu Phe Ala Pro Ala Val
        275                 280                 285
Ala Cys Lys Leu Gly Phe Trp Ala Arg Phe Val Ala Leu Pro Leu Trp
    290                 295                 300
Leu Gln Pro Thr Val His Thr Ala Leu Cys Ile Cys Ala Thr Val Cys
305                 310                 315                 320
Thr Gly Ser Phe Tyr Leu Ala Phe Phe Phe Phe Ile Ser His Asn Phe
                325                 330                 335
Asp Gly Val Gly Ser Val Gly Pro Lys Gly Ser Leu Pro Arg Ser Ala
            340                 345                 350
Thr Phe Val Gln Arg Gln Val Glu Thr Ser Ser Asn Val Gly Gly Tyr
        355                 360                 365
Trp Leu Gly Val Leu Asn Gly Gly Leu Asn Phe Gln Ile Glu His His
    370                 375                 380
Leu Phe Pro Arg Leu His His Ser Tyr Tyr Ala Gln Ile Ala Pro Val
385                 390                 395                 400
Val Arg Thr His Ile Glu Lys Leu Gly Phe Lys Tyr Arg His Phe Pro
                405                 410                 415
Thr Val Gly Ser Asn Leu Ser Ser Met Leu Gln His Met Gly Lys Met
            420                 425                 430
Gly Thr Arg Pro Gly Ala Glu Lys Gly Gly Lys Ala Glu
        435                 440                 445
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<210> 328
<211> 398
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus

<220>

<221> misc_feature
<222> (94)..(94)
<223> Xaa can be any proteinogenic amino acid

<220>
<221> misc_feature
<222> (186)..(186)
<223> Xaa can be any proteinogenic amino acid

<400> 328

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Leu Ser Glu Ala Lys Gln Arg Glu Leu Ala Glu Ala Gly Tyr Lys His
            20                  25                  30
Val Glu Gly Ala Pro Ala Pro Leu Pro Leu Asp Leu Pro His Phe Ser
        35                  40                  45
Leu Arg Asp Leu Arg Ala Ala Ile Pro Lys His Cys Phe Glu Arg Ser
    50                  55                  60
Phe Ile Thr Ser Thr Tyr Tyr Met Ile Lys Asn Leu Leu Thr Cys Ala
65                  70                  75                  80
Ala Leu Phe Tyr Ala Ala Thr Tyr Ile Asp Gln Thr Gly Xaa Phe Ala
                85                  90                  95
Tyr Leu Leu Trp Pro Val Tyr Trp Phe Phe Gln Gly Ser Tyr Leu Thr
            100                 105                 110
Gly Ile Trp Val Ile Ala His Glu Cys Gly His Gln Ala Tyr Cys Ser
        115                 120                 125
Ser Glu Val Val Asn Asn Leu Ile Gly Leu Val Leu His Ser Ala Leu
    130                 135                 140
Leu Val Pro Tyr His Ser Trp Arg Ile Ser His Arg Lys His His Ser
145                 150                 155                 160
Asn Thr Gly Ser Cys Glu Asn Asp Glu Val Phe Val Pro Val Thr Arg
                165                 170                 175
Ser Val Ile Ala Ser Ser Trp Asp Glu Xaa Leu Glu Asp Ser Pro Leu
            180                 185                 190
Tyr Gln Leu Tyr Arg Ile Val Tyr Met Leu Val Val Gly Trp Met Pro
        195                 200                 205
Gly Tyr Leu Phe Phe Asn Ala Thr Gly Pro Thr Lys Tyr Trp Gly Lys
    210                 215                 220
Ser Arg Ser His Phe Asn Pro Tyr Ser Ala Ile Tyr Ser Asp Arg Glu
225                 230                 235                 240
Arg Trp Met Ile Val Leu Ser Asp Ile Phe Leu Val Leu Met Ile Gly
                245                 250                 255
Val Leu Ala Thr Leu Val Tyr Thr Phe Ser Phe Tyr Thr Met Leu Lys
            260                 265                 270
Phe Tyr Val Val Pro Tyr Phe Ile Val Asn Ala Tyr Leu Val Leu Ile
        275                 280                 285
Thr Tyr Leu Gln His Thr Asp Thr Tyr Ile Pro His Phe Arg Asp Ser
    290                 295                 300
Glu Trp Asn Trp Leu Arg Gly Ala Leu Cys Thr Val Asp Arg Ser Phe
305                 310                 315                 320
Gly Pro Tyr Leu Asp Ser Val Val His Arg Ile Val Asp Thr His Val
                325                 330                 335
Cys His His Ile Phe Ser Lys Met Pro Phe Tyr His Cys Glu Glu Ala
            340                 345                 350
Thr Asn Ala Ile Lys Pro Leu Leu Gly Lys Phe Tyr Leu Lys Asp Asp
        355                 360                 365
Thr Pro Val Pro Ile Ala Leu Trp Arg Ser Tyr Thr His Cys Lys Phe
    370                 375                 380
Val Glu Asp Asp Gly Lys Ile Val Phe Tyr Lys Asn Lys Leu
385                 390                 395
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<210> 329
<211> 398

<212> PRT
<213> Phytophthora sojae

<220>
<223> G5A275_PHYSP-Phytophthora_sojae

<400> 329
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20 25 30
Val Glu Gly Ala Pro Ala Pro Leu Pro Leu Glu Leu Pro His Phe Ser
35 40 45
Leu Arg Asp Leu Arg Ala Ala Ile Pro Lys His Cys Phe Glu Arg Ser
50 55 60
Phe Val Thr Ser Thr Tyr Tyr Met Ile Lys Asn Val Leu Thr Cys Ala
65 70 75 80
Ala Leu Phe Tyr Ala Ala Thr Phe Ile Asp Arg Ala Gly Ala Ala Ala
85 90 95
Tyr Val Leu Trp Pro Val Tyr Trp Phe Phe Gln Gly Ser Tyr Leu Thr
100 105 110
Gly Val Trp Val Ile Ala His Glu Cys Gly His Gln Ala Tyr Cys Ser
115 120 125
Ser Glu Val Val Asn Asn Leu Ile Gly Leu Val Leu His Ser Ala Leu
130 135 140
Leu Val Pro Tyr His Ser Trp Arg Ile Ser His Arg Lys His His Ser
145 150 155 160
Asn Thr Gly Ser Cys Glu Asn Asp Glu Val Phe Val Pro Val Thr Arg
165 170 175
Ser Val Leu Ala Ser Ser Trp Asn Glu Thr Leu Glu Asp Ser Pro Leu
180 185 190
Tyr Gln Leu Tyr Arg Ile Val Tyr Met Leu Val Val Gly Trp Met Pro
195 200 205
Gly Tyr Leu Phe Phe Asn Ala Thr Gly Pro Thr Lys Tyr Trp Gly Lys
210 215 220
Ser Arg Ser His Phe Asn Pro Tyr Ser Ala Ile Tyr Ala Asp Arg Glu
225 230 235 240
Arg Trp Met Ile Val Leu Ser Asp Ile Phe Leu Val Ala Met Leu Ala
245 250 255
Val Leu Ala Ala Leu Val His Thr Phe Ser Phe Asn Thr Met Val Lys
260 265 270
Phe Tyr Val Val Pro Tyr Phe Ile Val Asn Ala Tyr Leu Val Leu Ile
275 280 285
Thr Tyr Leu Gln His Thr Asp Thr Tyr Ile Pro His Phe Arg Glu Gly
290 295 300
Glu Trp Asn Trp Leu Arg Gly Ala Leu Cys Thr Val Asp Arg Ser Phe
305 310 315 320
Gly Pro Phe Leu Asp Ser Val Val His Arg Ile Val Asp Thr His Val
325 330 335
Cys His His Ile Phe Ser Lys Met Pro Phe Tyr His Cys Glu Glu Ala
340 345 350
Thr Asn Ala Ile Lys Pro Leu Leu Gly Lys Phe Tyr Leu Lys Asp Thr
355 360 365
Thr Pro Val Pro Val Ala Leu Trp Arg Ser Tyr Thr His Cys Lys Phe
370 375 380
Val Glu Asp Asp Gly Lys Val Val Phe Tyr Lys Asn Lys Leu
385 390 395

<210> 330
<211> 398
<212> PRT
<213> Phytophthora ramorum

<220>
<223> H3G9L1_PHYRM-Phytophthora_ramorum

<400> 330
Met Ala Ile Leu Asn Pro Glu Ala Asp Ser Ala Ala Lys Val Ala Ser
1   5   10   15
Asp Ser Glu Ala Lys Gln Arg Gln Leu Ala Glu Ala Gly Tyr Lys His
            20   25   30
Val Glu Gly Ala Pro Ala Pro Leu Pro Leu Glu Leu Pro His Phe Ser
        35   40   45
Leu Arg Glu Leu Arg Ala Ala Ile Pro Lys His Cys Phe Glu Arg Ser
    50   55   60
Phe Val Thr Ser Thr Tyr Tyr Ala Ile Lys Asn Met Leu Thr Cys Ala
65   70   75   80
Ala Leu Phe Tyr Ala Ala Ser Tyr Ile Asp Gln Thr Gly Ala Ala Ala
                85   90   95
Tyr Leu Leu Trp Pro Val Tyr Trp Phe Phe Gln Gly Ser Tyr Leu Thr
            100   105   110
Gly Ile Trp Val Val Ala His Glu Cys Gly His Gln Ala Tyr Cys Ser
        115   120   125
Ser Glu Val Val Asn Asn Ile Ile Gly Leu Val Leu His Ser Ala Leu
    130   135   140
Leu Val Pro Tyr His Ser Trp Arg Ile Ser His Arg Lys His His Ser
145   150   155   160
Asn Thr Gly Ser Cys Glu Asn Asp Glu Val Phe Val Pro Val Thr Arg
                165   170   175
Ser Val Ala Ala Ser Ser Trp Asp Glu Thr Leu Glu Asp Ser Pro Leu
            180   185   190
Tyr Gln Leu Tyr Arg Ile Val Tyr Met Leu Val Val Gly Trp Met Pro
        195   200   205
Gly Tyr Leu Phe Phe Asn Ala Thr Gly Pro Thr Lys Tyr Trp Gly Lys
    210   215   220
Pro Arg Ser His Phe Asn Pro Tyr Ser Ala Ile Tyr Ser Asp Arg Glu
225   230   235   240
Arg Trp Met Ile Val Leu Ser Asp Ile Phe Leu Ile Val Ala Leu Ser
                245   250   255
Thr Leu Ala Val Leu Val His Thr Phe Ser Leu Phe Thr Met Val Lys
            260   265   270
Phe Tyr Val Val Pro Tyr Phe Val Val Asn Ala Tyr Leu Val Leu Ile
        275   280   285
Thr Phe Leu Gln His Thr Asp Thr Tyr Ile Pro His Phe Arg Glu Gly
    290   295   300
Glu Trp Ser Trp Leu Arg Gly Ala Leu Cys Thr Val Asp Arg Ser Phe
305   310   315   320
Gly Lys Tyr Leu Asp Ser Val Val His Arg Ile Val Asp Thr His Val
                325   330   335
Cys His His Ile Phe Ser Lys Met Pro Phe Tyr His Cys Glu Glu Ala
            340   345   350
Thr Asn Ala Ile Lys Pro Leu Leu Gly Lys Phe Tyr Leu Lys Asp Thr
        355   360   365
Thr Pro Val Pro Met Ala Leu Trp Arg Ser Tyr Thr Tyr Cys Lys Phe
    370   375   380
Val Glu Asp Asp Gly Asn Val Val Phe Tyr Lys Asn Lys Leu
385   390   395

<210> 331
<211> 398
<212> PRT
<213> Phytophthora infestans

<220>
<223> G4XUM4_PHYIN-Phytophthora_infestans

<400> 331
Met Ala Ile Leu Asn Pro Glu Ala Glu Ser Ala Ala Lys Val Ala Thr
1   5   10   15
Leu Ser Glu Ala Lys Gln Arg Glu Leu Ala Glu Ala Gly Tyr Lys His
            20   25   30
Val Glu Gly Ala Pro Ala Pro Leu Pro Leu Asp Leu Pro His Phe Ser
        35   40   45
Leu Arg Asp Leu Arg Ala Ala Ile Pro Lys His Cys Phe Glu Arg Ser
    50   55   60
Phe Ile Thr Ser Thr Tyr Tyr Met Ile Lys Asn Leu Leu Thr Cys Ala
65   70   75   80
Ala Leu Phe Tyr Ala Ala Thr Tyr Ile Asp Gln Thr Gly Ser Phe Ala
                85   90   95
Tyr Leu Leu Trp Pro Val Tyr Trp Phe Phe Gln Gly Ser Tyr Leu Thr
            100   105   110
Gly Ile Trp Val Val Ala His Glu Cys Gly His Gln Ala Tyr Cys Ser
        115   120   125
Ser Glu Val Val Asn Asn Met Ile Gly Leu Val Leu His Ser Thr Leu
    130   135   140
Leu Val Pro Tyr His Ser Trp Arg Ile Ser His Arg Lys His His Ser
145   150   155   160
Asn Thr Gly Ser Cys Glu Asn Asp Glu Val Phe Val Pro Val Thr Arg
                165   170   175
Ser Val Ile Ala Ser Ser Trp Asp Glu Thr Leu Glu Asp Ser Pro Leu
            180   185   190
Tyr Gln Leu Tyr Arg Ile Val Tyr Met Leu Val Val Gly Trp Met Pro
        195   200   205
Gly Tyr Leu Phe Phe Asn Ala Thr Gly Pro Ser Lys Tyr Leu Gly Lys
    210   215   220
Ser Arg Ser His Phe Asn Pro Tyr Ser Ser Ile Tyr Ser Asp Arg Glu
225   230   235   240
Arg Trp Met Ile Val Leu Ser Asp Ile Phe Leu Val Leu Met Ile Gly
                245   250   255
Ala Leu Val Thr Leu Val Tyr Thr Phe Ser Phe Tyr Thr Met Leu Lys
            260   265   270
Phe Tyr Val Val Pro Tyr Phe Ile Val Asn Ala Tyr Leu Val Leu Ile
        275   280   285
Thr Tyr Leu Gln His Thr Asp Thr Tyr Ile Pro His Phe Arg Asp Ser
    290   295   300
Glu Trp Asn Trp Leu Arg Gly Ala Leu Cys Thr Val Asp Arg Ser Phe
305   310   315   320
Gly Pro Tyr Leu Asp Ser Val Val His Arg Ile Val Asp Thr His Ile
                325   330   335
Cys His His Ile Phe Ser Lys Met Pro Phe Tyr His Cys Glu Glu Ala
            340   345   350
Thr Asn Ala Ile Lys Pro Leu Leu Gly Lys Phe Tyr Leu Lys Asp Asp
        355   360   365
Thr Pro Val Pro Ile Ala Leu Trp Arg Ser Tyr Ile His Cys Lys Phe
    370   375   380
Val Glu Asp Asp Gly Lys Ile Val Phe Tyr Lys Asn Lys Leu
385   390   395

<210> 332
<211> 398
<212> PRT
<213> Hyaloperonospora arabidopsidis

<220>
<223> M4BXW8_HYAAE-Hyaloperonospora_arabidopsidis

<400> 332
Met Ala Ile Leu Asn Pro Asp Ser Glu Ser Pro Thr Lys Gln Val Ala
1   5   10   15

Asp Ser Glu Ala Lys Gln Arg Gln Leu Ala Glu Ala Gly Tyr Lys His
            20   25   30
Val Glu Gly Cys Pro Ala Pro Leu Pro Leu Glu Leu Pro His Phe Ser
        35   40   45
Leu Arg Asp Leu Arg Ala Ala Thr Pro Glu His Cys Phe Glu Arg Ser
    50   55   60
Phe Val Thr Ser Met Tyr His Leu Val Lys Asn Leu Leu Tyr Cys Gly
65   70   75   80
Ala Leu Leu Tyr Val Ala Thr Arg Leu Asp Asp Leu Gly Ala Ile Ala
                85   90   95
Tyr Leu Leu Trp Pro Val Tyr Trp Phe Phe Gln Gly Ser Tyr Leu Thr
            100   105   110
Gly Val Trp Val Ile Ala His Glu Cys Gly His Gln Ser Phe Cys Ser
        115   120   125
Ser Glu Thr Val Asn Asn Leu Ile Gly Leu Val Leu His Ser Ala Leu
    130   135   140
Leu Val Pro Tyr His Ser Trp Arg Ile Ser His Arg Lys His His Ser
145   150   155   160
Asn Thr Gly Ser Cys Glu Asn Asp Glu Val Phe Val Pro Val Thr Arg
                165   170   175
Ser Ala Ile Lys Ser Ser Trp Asn Glu Val Leu Glu Asp Ser Pro Leu
            180   185   190
Tyr Gln Leu Tyr Arg Ile Ala Phe Met Leu Val Val Gly Trp Met Pro
        195   200   205
Gly Tyr Leu Cys Phe Asn Ala Thr Gly Pro Ser Lys Tyr Trp Gly Lys
    210   215   220
Ala Arg Ser His Phe Asn Pro Phe Ser Thr Leu Tyr Ala Asp Arg Glu
225   230   235   240
Arg Trp Leu Ile Val Leu Ser Asp Val Ser Leu Val Leu Val Leu Ala
                245   250   255
Gly Leu Ala Gly Leu Val His Thr Leu Ser Leu Tyr Thr Met Val Lys
            260   265   270
Leu Tyr Phe Ala Pro Tyr Leu Ile Val Asn Val Tyr Leu Val Leu Ile
        275   280   285
Thr Phe Leu Gln His Thr Asp Thr Tyr Ile Pro His Phe Arg Glu Gly
    290   295   300
Glu Trp Thr Trp Leu Arg Gly Ala Leu Cys Thr Val Asp Arg Ser Phe
305   310   315   320
Gly Pro Tyr Leu Asp Ser Val Leu His His Ile Val Asp Thr His Val
                325   330   335
Val His His Ile Phe Ser Lys Met Pro Phe Tyr His Cys Glu Glu Ala
            340   345   350
Thr Lys Ala Ile Lys Pro Leu Leu Gly Lys Phe Tyr Leu Lys Asp Thr
        355   360   365
Thr Pro Phe Pro Leu Ala Met Trp Arg Ser Tyr Lys His Cys Lys Phe
    370   375   380
Val Glu Asp Asp Gly Lys Ile Val Phe Tyr Lys Asn Lys Leu
385   390   395

<210> 333
<211> 398
<212> PRT
<213> Phytophthora parasitica

<220>
<223> W2PDL4_PHYPN-Phytophthora_parasitica

<400> 333
Met Ala Ile Leu Asn Pro Glu Ala Glu Ser Ala Ala Lys Val Ala Ser
1   5   10   15
Leu Ser Glu Ala Lys Gln Arg Glu Leu Ala Glu Ala Gly Tyr Lys His
            20   25   30
Val Glu Gly Ala Pro Ala Pro Leu Pro Leu Asp Leu Pro His Phe Ser

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        35                  40                  45
Leu Arg Asp Leu Arg Ala Ala Ile Pro Lys His Cys Phe Glu Arg Ser
    50                  55                  60
Phe Ile Thr Ser Thr Tyr Tyr Met Ile Lys Asn Leu Leu Thr Cys Ala
65                  70                  75                  80
Ala Leu Phe Tyr Ala Ala Thr Tyr Ile Asp Gln Thr Gly Asn Phe Ala
                85                  90                  95
Tyr Leu Leu Trp Pro Val Tyr Trp Phe Phe Gln Gly Ser Tyr Leu Thr
            100                 105                 110
Gly Ile Trp Val Ile Ala His Glu Cys Gly His Gln Ala Tyr Cys Ser
        115                 120                 125
Ser Glu Val Val Asn Asn Leu Ile Gly Leu Val Leu His Ser Ala Leu
    130                 135                 140
Leu Val Pro Tyr His Ser Trp Arg Ile Ser His Arg Lys His His Ser
145                 150                 155                 160
Asn Thr Gly Ser Cys Glu Asn Asp Glu Val Phe Val Pro Val Thr Arg
                165                 170                 175
Ser Val Ile Ala Ser Ser Trp Asp Glu Asn Leu Glu Asp Ser Pro Leu
            180                 185                 190
Tyr Gln Leu Tyr Arg Ile Val Tyr Met Leu Val Val Gly Trp Met Pro
        195                 200                 205
Gly Tyr Leu Phe Phe Asn Ala Thr Gly Pro Thr Lys Tyr Trp Gly Lys
    210                 215                 220
Ser Arg Ser His Phe Asn Pro Tyr Ser Ala Ile Tyr Ser Asp Arg Glu
225                 230                 235                 240
Arg Trp Met Ile Val Leu Ser Asp Ile Phe Leu Val Leu Val Ile Gly
                245                 250                 255
Val Leu Ala Thr Leu Val Tyr Thr Phe Ser Phe Tyr Thr Met Leu Lys
            260                 265                 270
Phe Tyr Val Val Pro Tyr Phe Ile Val Asn Ala Tyr Leu Val Leu Ile
        275                 280                 285
Thr Tyr Leu Gln His Thr Asp Thr Tyr Ile Pro His Phe Arg Asp Ser
    290                 295                 300
Glu Trp Asn Trp Leu Arg Gly Ala Leu Cys Thr Val Asp Arg Ser Phe
305                 310                 315                 320
Gly Pro Tyr Leu Asp Ser Val Val His Arg Ile Val Asp Thr His Val
                325                 330                 335
Cys His His Ile Phe Ser Lys Met Pro Phe Tyr His Cys Glu Glu Ala
            340                 345                 350
Thr Asn Ala Ile Lys Pro Leu Leu Gly Lys Phe Tyr Leu Lys Asp Asp
        355                 360                 365
Thr Pro Val Pro Ile Ala Leu Trp Arg Ser Tyr Thr His Cys Lys Phe
    370                 375                 380
Val Glu Asp Asp Gly Lys Ile Val Phe Tyr Lys Asn Lys Leu
385                 390                 395

<210> 334
<211> 398
<212> PRT
<213> Phytophthora parasitica

<220>
<223> W2LW72_PHYPR-Phytophthora_parasitica

<400> 334
Met Ala Ile Leu Asn Pro Glu Ala Glu Ser Ala Ala Lys Val Ala Ser
1               5                   10                  15
Leu Ser Glu Ala Lys Gln Arg Glu Leu Ala Glu Ala Gly Tyr Lys His
            20                  25                  30
Val Glu Gly Ala Pro Ala Pro Leu Pro Leu Asp Leu Pro His Phe Ser
        35                  40                  45
Leu Arg Asp Leu Arg Ala Ala Ile Pro Lys His Cys Phe Glu Arg Ser
    50                  55                  60
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Phe Ile Thr Ser Thr Tyr Tyr Met Ile Lys Asn Leu Leu Thr Cys Ala
65                  70                  75                  80
Ala Leu Phe Tyr Ala Ala Thr Tyr Ile Asp Gln Thr Gly Asn Phe Ala
                85                  90                  95
Tyr Leu Leu Trp Pro Val Tyr Trp Phe Phe Gln Gly Ser Tyr Leu Thr
            100                 105                 110
Gly Ile Trp Val Ile Ala His Glu Cys Gly His Gln Ala Tyr Cys Ser
        115                 120                 125
Ser Glu Val Val Asn Asn Leu Ile Gly Leu Val Leu His Ser Ala Leu
    130                 135                 140
Leu Val Pro Tyr His Ser Trp Arg Ile Ser His Arg Lys His His Ser
145                 150                 155                 160
Asn Thr Gly Ser Cys Glu Asn Asp Glu Val Phe Val Pro Val Thr Arg
                165                 170                 175
Ser Val Ile Ala Ser Ser Trp Asp Glu Asn Leu Glu Asp Ser Pro Leu
            180                 185                 190
Tyr Gln Leu Tyr Arg Ile Val Tyr Met Leu Val Val Gly Trp Met Pro
        195                 200                 205
Gly Tyr Leu Phe Phe Asn Ala Thr Gly Pro Thr Lys Tyr Trp Gly Lys
    210                 215                 220
Ser Arg Ser His Phe Asn Pro Tyr Ser Ala Ile Tyr Ser Asp Arg Glu
225                 230                 235                 240
Arg Trp Met Ile Val Leu Ser Asp Ile Phe Leu Val Leu Met Ile Gly
                245                 250                 255
Val Leu Ala Thr Leu Val Tyr Thr Phe Ser Phe Tyr Thr Met Leu Lys
            260                 265                 270
Phe Tyr Val Val Pro Tyr Phe Ile Val Asn Ala Tyr Leu Val Leu Ile
        275                 280                 285
Thr Tyr Leu Gln His Thr Asp Thr Tyr Ile Pro His Phe Arg Asp Ser
    290                 295                 300
Glu Trp Asn Trp Leu Arg Gly Ala Leu Cys Thr Val Asp Arg Ser Phe
305                 310                 315                 320
Gly Pro Tyr Leu Asp Leu Val Val His Arg Ile Val Asp Thr His Val
                325                 330                 335
Cys His His Ile Phe Ser Lys Met Pro Phe Tyr His Cys Glu Glu Ala
            340                 345                 350
Thr Asn Ala Ile Lys Pro Leu Leu Gly Lys Phe Tyr Leu Lys Asp Asp
        355                 360                 365
Thr Pro Val Pro Ile Ala Leu Trp Arg Ser Tyr Thr His Cys Lys Phe
    370                 375                 380
Val Glu Asp Asp Gly Lys Ile Val Phe Tyr Lys Asn Lys Leu
385                 390                 395

<210> 335
<211> 398
<212> PRT
<213> Phytophthora parasitica

<220>
<223> W2ZYI2_PHYPR-Phytophthora_parasitica

<400> 335
Met Ala Ile Leu Asn Pro Glu Ala Glu Ser Ala Ala Lys Val Ala Ser
1               5                  10                  15
Leu Ser Glu Ala Lys Gln Arg Glu Leu Ala Glu Ala Gly Tyr Lys His
            20                  25                  30
Val Glu Gly Ala Pro Ala Pro Leu Pro Leu Asp Leu Pro His Phe Ser
        35                  40                  45
Leu Arg Asp Leu Arg Ala Ala Ile Pro Lys His Cys Phe Glu Arg Ser
    50                  55                  60
Phe Ile Thr Ser Thr Tyr Tyr Met Ile Lys Asn Leu Leu Thr Cys Ala
65                  70                  75                  80
Ala Leu Phe Tyr Ala Ala Thr Tyr Ile Asp Gln Thr Gly Asn Phe Thr
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                85                  90                  95
Tyr Leu Leu Trp Pro Val Tyr Trp Phe Phe Gln Gly Ser Tyr Leu Thr
            100                 105                 110
Gly Ile Trp Val Ile Ala His Glu Cys Gly His Gln Ala Tyr Cys Ser
        115                 120                 125
Ser Glu Val Val Asn Asn Leu Ile Gly Leu Val Leu His Ser Ala Leu
    130                 135                 140
Leu Val Pro Tyr His Ser Trp Arg Ile Ser His Arg Lys His His Ser
145                 150                 155                 160
Asn Thr Gly Ser Cys Glu Asn Asp Glu Val Phe Val Pro Val Thr Arg
                165                 170                 175
Ser Val Ile Ala Ser Ser Trp Asp Glu Asn Leu Glu Asp Ser Pro Leu
            180                 185                 190
Tyr Gln Leu Tyr Arg Ile Val Tyr Met Leu Val Val Gly Trp Met Pro
        195                 200                 205
Gly Tyr Leu Phe Phe Asn Ala Thr Gly Pro Thr Lys Tyr Trp Gly Lys
    210                 215                 220
Ser Arg Ser His Phe Asn Pro Tyr Ser Ala Ile Tyr Ser Asp Arg Glu
225                 230                 235                 240
Arg Trp Met Ile Val Leu Ser Asp Ile Phe Leu Val Leu Met Ile Gly
                245                 250                 255
Val Leu Ala Thr Leu Val Tyr Thr Phe Ser Phe Tyr Thr Met Leu Lys
            260                 265                 270
Phe Tyr Val Val Pro Tyr Phe Ile Val Asn Ala Tyr Leu Val Leu Ile
        275                 280                 285
Thr Tyr Leu Gln His Thr Asp Thr Tyr Ile Pro His Phe Arg Asp Ser
    290                 295                 300
Glu Trp Asn Trp Leu Arg Gly Ala Leu Cys Thr Val Asp Arg Ser Phe
305                 310                 315                 320
Gly Pro Tyr Leu Asp Ser Val Val His Arg Ile Val Asp Thr His Val
                325                 330                 335
Cys His His Ile Phe Ser Lys Met Pro Phe Tyr His Cys Glu Glu Ala
            340                 345                 350
Thr Asn Ala Ile Lys Pro Leu Leu Gly Lys Phe Tyr Leu Lys Asp Asp
        355                 360                 365
Thr Pro Val Pro Ile Ala Leu Trp Arg Ser Tyr Thr His Cys Lys Phe
    370                 375                 380
Val Glu Asp Asp Gly Lys Ile Val Phe Tyr Lys Asn Lys Leu
385                 390                 395

<210> 336
<211> 393
<212> PRT
<213> Saprolegnia spp.

<220>
<223> Q6UB74_9STRA-Saprolegnia

<400> 336
Met Cys Lys Gly Gln Ala Pro Ser Lys Ala Asp Val Phe His Ala Ala
1                   5                  10                  15
Gly Tyr Arg Pro Val Ala Gly Thr Pro Glu Pro Leu Pro Leu Glu Pro
            20                  25                  30
Pro Thr Ile Thr Leu Lys Asp Leu Arg Ala Ala Ile Pro Ala His Cys
        35                  40                  45
Phe Glu Arg Ser Ala Ala Thr Ser Phe Tyr His Leu Ala Lys Asn Leu
    50                  55                  60
Ala Ile Cys Ala Gly Val Phe Ala Val Gly Leu Lys Leu Ala Ala Ala
65                  70                  75                  80
Asp Leu Pro Leu Ala Ala Lys Leu Val Ala Trp Pro Ile Tyr Trp Phe
                85                  90                  95
Val Gln Gly Thr Tyr Phe Thr Gly Ile Trp Val Ile Ala His Glu Cys
            100                 105                 110
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Gly His Gln Ala Phe Ser Ala Ser Glu Ile Leu Asn Asp Thr Val Gly
        115                 120                 125
Ile Ile Leu His Ser Leu Leu Phe Val Pro Tyr His Ser Trp Lys Ile
    130                 135                 140
Thr His Arg Arg His His Ser Asn Thr Gly Ser Cys Glu Asn Asp Glu
145                 150                 155                 160
Val Phe Thr Pro Thr Pro Arg Ser Val Val Glu Ala Lys His Asp His
                165                 170                 175
Ser Leu Leu Glu Glu Ser Pro Leu Tyr Asn Leu Tyr Gly Ile Val Met
            180                 185                 190
Met Leu Leu Val Gly Trp Met Pro Gly Tyr Leu Phe Phe Asn Ala Thr
        195                 200                 205
Gly Pro Thr Lys Tyr Ala Gly Leu Ala Lys Ser His Phe Asn Pro Tyr
    210                 215                 220
Ala Ala Phe Phe Leu Pro Lys Glu Arg Leu Ser Ile Trp Trp Ser Asp
225                 230                 235                 240
Leu Cys Phe Leu Ala Ala Leu Tyr Gly Phe Gly Tyr Gly Val Ser Val
                245                 250                 255
Phe Gly Leu Leu Asp Val Ala Arg His Tyr Ile Val Pro Tyr Leu Ile
            260                 265                 270
Cys Asn Ala Tyr Leu Val Leu Ile Thr Tyr Leu Gln His Thr Asp Thr
        275                 280                 285
Tyr Val Pro His Phe Arg Gly Asp Glu Trp Asn Trp Leu Arg Gly Ala
    290                 295                 300
Leu Cys Thr Val Asp Arg Ser Phe Gly Ala Trp Ile Asp Ser Ala Ile
305                 310                 315                 320
His His Ile Ala Asp Thr His Val Thr His His Ile Phe Ser Lys Thr
                325                 330                 335
Pro Phe Tyr His Ala Ile Glu Ala Thr Asp Ala Ile Thr Pro Leu Leu
            340                 345                 350
Gly Lys Tyr Tyr Leu Ile Asp Pro Thr Pro Ile Pro Leu Ala Leu Trp
        355                 360                 365
Arg Ser Phe Thr His Cys Lys Tyr Val Glu Asp Asp Gly Asn Val Val
    370                 375                 380
Phe Tyr Lys Arg Lys Leu Glu Glu Lys
385                 390
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