SEQUENCE LISTING

<110> DA COSTA GARCIA, MIGUEL ANGELO
SOUSA DE SAO JOSE, CARLOS JORGE
RODRIGUES LEANDRO, CLARA ISABEL
RODRIGUES PARDAL DIAS ANTUNES MARCAL DA SILVA, FILIPA MARIA

<120> ANTIBACTERIAL PHAGE, PHAGE PEPTIDES AND METHODS OF USE THEREOF

<130> 16395-105003PC

<140>
<141>

<150> 61/384,015
<151> 2010-09-17

<160> 1300

<170> PatentIn version 3.5

<210> 1
<211> 113073
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 1
attatgcaaa ctaaacgaaa tcatacactc cactaattaa aggttgacaa catgaaacgc 60

tttgtaatat catctaaacc ggcggcaaaa ttgaacaaaa tggcaagctc ggaactggtc 120

aaaatgcagc gcgatatggc gcggcgttac cgctcttatc agcgcggagg tcagcaaggc 180

ttaccgatga tttgggataa catgatgcgt tatctaaaat ctttacaaaa taacgtttga 240

caatctgccg ataacgcttt attatagaat ctcaataagc aacaccgctc tttaaaaatt 300

tggaaaagtc gattctctca gtaagggtaa ttgagttttc tgttaacact ctagcagtaa 360

aagagtgtta accggataac ccaataaact aaactggagt aagaaacatg caaaacgtta 420

aaaccccaat gatcggtgat tccgttttta ttcctttcgt tactggcgac gtaagtaagc 480

cgggcgaaaa tgaaaaaatc ggatatatca aaggggcggc gatgatcccg tttgataaaa 540

ttaatgcggt atacgccgaa acggaaaaag caaaaaacag cgacgcgaag atttacagcg 600

tccgggtaga ttccggcgac gtggtgaaag tcattcgcaa agatgataaa tggttggctg 660

tcgcttaaca gccaataagt ttaaccccgg caaataatgg gatgcttccc ctatgttaga 720

cttccgatgt atattccatg cagcgcaagc aatgttatgg tgcgcaaatt aaacttatgt 780

gctggaactt atatcatgct ttgaacggca attgtgagtt aacacgaatc tatagcgtga 840

aatagacgta atagcgtaat tattaaaggc agcgtatata tacaatgccg ctttaaatag 900

ctttaaattg aaaactaaaa taaagagttt tcgttatata ttctagctag aatatatagc 960

ggctaacttt ctagccttaa cccttaaata aaactggaga tatatcatga ctgctactaa 1020

aaccgaaaaa ttcgcatgga acgaaacaaa cgccgctacc gccgttgaaa tgtacgaaaa 1080

gatcattgct tccgatggtc tggaggtggc taactcgcaa ggtcttattg atattgcaaa 1140

ggctgtaggt gctgaatcgc atgttaaagt gcgctctaaa ctggttagcg caaaggtgta 1200

tcagaagtcc gataagccgc gcaaagtcgg cggcggctcc tccctgcgta aagctcacta 1260

tgtgcgcgtt ctcactcagc acgccattgc tgacggcctg attgatgatg ccgatggtct 1320

ggcaagtctg gaacaaatga agctcgacca actggacgtt atcgcccgta tggttggcgt 1380

tcaggatgaa gtaaaagaat cagcagaata attataatgc gcctccctag cggggcgcat 1440

aattaaatat tttgtccccc ataactggag aaataaaaat ggctttaatt aaaggctccg 1500

ttattaaatt aacgggaacc gttgtggatg aattaatcca aacggggtat caggataata 1560

aggttatgac gcccccaagc gttaaagtac ctgaatatat tgttttgtgg gttaaccctg 1620

atgcggatac tttcgggatg gctattaacc gcgaagtctt taagccggaa atgctggaat 1680

tatcttcccg cgaaatttac cttctcaatt acgctttcag cgtagaagaa aaggaggttg 1740

taaaatgatc tttttcccta ctgaatcctt aattcttatc gctggctttt tcgccgccgc 1800

ttgtctctat ggttactata atttcatgga aataggcagc gaacaaacgg atttattacg 1860

ccgtgacttc tggttcaaga aagcgagtat ttgccgccgc tggtcaataa tctttattat 1920

tctagcggta actttcggaa tatcagcaag cattatcccg gcaatagttt agagtcgcaa 1980

attataacgc caccagcaac aaggcgttat atttggcaat tctgcctata tcccattaac 2040

tggagaattt agataatgat cattgcaatt gagaaacaaa aagctatttt aaccgctgct 2100

aacaacctca atttttgggg taaacgcctg cgcgctaaaa agctggagat ctgcgacgaa 2160

ttgagcaaag agcattacgg gacggcgaaa cactctagcg aaatttgcga ttggctggat 2220

agtaacaagc ctgttaaacc cgctgctgaa aaacgcgccc aacgtgttgc ggtggaagat 2280

tcccgccccg ttgccgctgg tcagcttaat tccagcgtcg aaagctggaa ggtaattccg 2340

ggccgccgtt ttctgctaac gtcgattcaa aataatacct tccctcatgc taatttctgg 2400

aaaactttac aggaggccgc gaaatatctc ggcgctactc tgttagtaag caaatacgcc 2460

tacaacaaaa aaggcttcca aaacgggcaa ggcaacgatg aactgaaata tgatgatgct 2520

ttctcagatt tcatttgtga tgaaaacgtg tttttgggca accgcgaaac cggattcgca 2580

ttcatggcgg aaattaatat tctgccaact gctgattttc cgctgtccgg ctttggcgag 2640

actgcgaccg cctacggcct gaaagggctg gctattggtc acgctaaaat caccgccgaa 2700

agtgtcccgg caatgaaggg cgacactgtg cgccgtatgt attcaactgg cacagcgacg 2760

ctgaaaaatt atattcagca aaaagcgggc caaaaggccg aagcgctgca taactatggc 2820

gctttgctgg tagagatcga cgacaacggc aacttctttg ctcgccaaat cgaaacgatg 2880

gacgaaagcg ggatgtttta cgatcttaat cataaattta ctgttaacgg tggcgaggag 2940

gtaacgggcc acgttgccgc gctgcaatat ggtgacattc acgccgaaaa gctggatcac 3000

gctgtcgcct ttgcttcatg ggggccgtgt gatgattctc tagtgaacgt cctgcgccct 3060

cgttaccaga ttgtgcatga tgtgcatgac tttacatcac gaaaccatca taaccgcgct 3120

agtggcgttt tccttgcgaa acaatatgcc gccggacgtg acaaggtaat tgacgatctt 3180

atcgataccg ggcgcgtact agaagcaatg gaacgtgaat tcagtcaaac ggtcattgtt 3240

gaatcgaacc acgatcttgc gctttctcgc tggctggatg atagtaaagc taacattcaa 3300

caagacccgg cgaacgccca tctttattat cgcctgaatg ctgcgattta tgaagcaatc 3360

gaaaacaagg acgatacttt taacgtacta gattacgccc tgcgcaatgt tgctggctgc 3420

gattttgctg cgatcttctt aaccacggat gaatctatga aaattgcggg catcgaatgc 3480

ggttcccacg gtcacaacgg cattaacggc gctcgcggca acccgaaggg attccgcaag 3540

ctcggcaaga tgaacactgg ccatacgcat acgcccagca tttacggcgg cgtttatacc 3600

gctggcgtcg ctggttccct cgatatgggt tacaacatcg gcgcgtctag ctggtcacaa 3660

acgcatttga tcacctatga aaacgggcaa cgtaccttga ttgactttaa agacggcgtt 3720

ttctttgcat aacaaaaaag ccggggtaat tgccccggca ataaataacc cataaataaa 3780

taaataagct ggagaaacaa atgaaactta ctttcatcta taacaatcgt aaatctttca 3840

ccgcgtccaa cgtcgtagaa aatagccttg ttatttcccg cgatagtgaa gggcgcccgc 3900

atgttagcta tcagaaagtt aacacggtgg acggcgacac tgttttaaaa gctctagccg 3960

ctatcctccc gcgccccgct gaatttaaag aatccggcat tgtgtcgcaa ttagtcgccg 4020

ccgattctat tctttatgag gctgatatct gcgagatcgt agagattgac gccgccgccg 4080

ctggccttat gtttatcgtc gtaagcgaaa atgattatga tgatacctat ctgctcggcg 4140

acgtgatgga ttattcttct agcgaatata cgccgccgct ggcaattgtc ccggtaatgg 4200

ctacccggat taaaccggct gaattagccg atgccttaac tttattcttc tgataattaa 4260

caaagcgagt tataatatag ctcgcttgat taattaccaa caaccccgaa accggagaaa 4320

tgaaaaatgg cttttaataa actggcaatt aaggcaatta agttatggga tttagacgga 4380

actgttatta attcctttgc ccgcgtgttc ccgtgtatgg atgataaagg gaacttagat 4440

ttaaacatgt accgggaaaa ggcttgcgta catgatgcaa ttatgaccga cactctttta 4500

ccgctggttg aatatatgcg ggcatcgctt aacgatccca ctgtattaaa cattattgtc 4560

accgctcgtt atatgggtaa gagtgactac tatttcctac gcaaacaacg tatccgggcg 4620

gggcgcggtg gtaatatcca gatactgtcc cgcgatgtat tgcaccgata tattggcgat 4680

gctgattata aagaggtgta ctattcgaaa gatggtatct ataaaacgca ttatttcgaa 4740

atgcttaaag ctgaatatcc gaacgctact atcactatga ttgacgataa tagaggcgtg 4800

ttggctgctg ctgctgctgc tggccttcaa acgatggacg ctaccgcaat taacgatatt 4860

ctatctattg gtgtgcgcct tgcgggtgag tcattcatag atgaagcgct ggatgatgat 4920

aatgattatc aatatctttg cgagcgttta gctcattgct gggaaggtat gaccgaagaa 4980

gaaagaagcg actacggaat taagccgcaa caatttattc aatcgttagc catcgcatca 5040

taagaaagct aatagtaccc tagcgaaata gttagggtac taatagttag ctaggggggt 5100

aatcggacta ccataccacc ccccgaccct ctaagcccac ctccatgtgt aactttatga 5160

aatttggaga aaaggctaaa gggagtactt aggcaaactt agaacgagca gcccgaatca 5220

aagctactac tgctactgcc gctgtcgcaa taagaacttc ccgagtcata cccgctatac 5280

gttgcaactg ccgcagttgt agctatgatt gctgcagtcg acccatcatc gctccgagaa 5340

cttcccgagt tcgatgaagg acttcccgaa actttccgag aattatccga gcctgcccgt 5400

ttttgcttgc gtttcgcgac ctgtggtgtc actggaggga tgtagtacgg gttgctcggg 5460

tcattccgaa gatcgttcat gactcgttgg tgttttgaga tcgctacttg acgttctgcc 5520

cgagtttgaa ggatctcttg atgcagactt ttgttacgaa gatctgccgc tactaccgcg 5580

ttccgcaggt catgtgcccg cacaccaaac caaactgctg ccaggaaaaa gaatgttgtg 5640

aaaattaata caatagtcat gttttacacc ataccccttag taatgtagat tttgtttgct 5700

gattctagtt ctgccttgca ttcagacagg tttaactgtg ccttatgcag caaacgggtt 5760

tgattgtcat aagacttctg cagcaccccg ttagtgcgtt ctagctgttt gattgcctta 5820

ccctgcttta cggtaatgac gaatagtacg attgagagta aaacaagtgc tcctataact 5880

acttccatag tggtcctcct agatggtttt aaaaaatctg gtttacttgg cggttgattt 5940

aatttataat aatattatat tataaaagtc acttgttagc aagtgagatt ttgaggtttt 6000

tatgggcttt tatgcaggaa ggataggcga caaaaaagtg ttgtctctta cctctggcaa 6060

caataaagac gttaataacc acactaatcc aggttgggat actatattcc atagcgatat 6120

gcctcacgtt gtagttttag aaactcacga aagagacctc tgggatggtg gtgattggta 6180

tcgttgtact agaatgccag acagaattat tcaggtactg tccgcagact acgacagggt 6240

tgtcttaact gaagttgagt ttgaggatgg caccagacgt ttcatttatg gtacatccct 6300

gggtgtgggc gctaaagcgt ataacgctta ctttagtaat actgtcggtt cccaggcttc 6360

tgcaggtact atggctagta tgaagactaa cgtttgtgct tctgcagact tacacatgga 6420

tattagtttc tatttcgaag agacgccagg tactattaac gagaagctac gagacggtac 6480

tgggtgtatg tacacctggg gcgttaactc agaatgggga gacagagggc ctgggccgcc 6540

ggttggagct cctatacgtc ctaactttga gactattatt aaagctggat gggtgctcta 6600

taggggggct tttagtggca atatagccgg ttctgtgtct ccgcccaata gacccttac 6660

tattggtgtt gatgctatgc gccacccgtg gatgcgtact actggtgtta acagtatatg 6720

tttgcgtggt gagactctca accgtaatat gtacggacat atggggccta gatatgggca 6780

gagctccaat cccgttggtg gtccttatgc tcataacatc cagactgagt cttatcagga 6840

ggttcagtac aaagcaggtt ttttccgtgg tccgcccaat aactttatgg ggtgggaaaa 6900

cacagataac aacaatgctg gtagtggttg gggtaacaat gccatttacc gtgacaataa 6960

cttccgtgtt cctaaacgtg ttcgctggta tattactaat atgaaataca atgggcaggg 7020

gttctacgca gagaacgtat ttggctcccg caaccaggag attaaaatca gccctagaga 7080

gttcattgta aacggtataa acctaatgaa cactgggtgg aagttcataa accagaacga 7140

tataaactac agcccaggta ataggcctga tatccgagtt attgcaacca acgtcgccag 7200

atttagtggc aaccctactg ttggtaataa tggatatgtt cactttaatc agcctctaac 7260

tcgaccagat aatggtgctg agtttggaca aggtaacgtg agtgagatgc atgtaaccac 7320

tgtaggggtt tacaatttta gatctgatgc acagtggtac gtaaaatcta acccgccgga 7380

aatcggaaac cagtggggtc cagtatggtc tgaatcaact cgacctctcc gcctagtggg 7440

cggtaccggc tctgctgata ttggagggaa cctacgtact agcggtaatg ctagtcacca 7500

cctggctacc ttgtggttag gggttaataa ctcccgaaat ggggcttgcg tcgtcactct 7560

agactggaaa aatgatgagt ggattgctgc tgcagggatt ggatgttata accctctaga 7620

agatcttacc cagtggagcg aggtggatag taggctgaga attttcggaa atcacttcca 7680

gaaacgtgtg catcaaatca tgtgtttgcc cgttaacatg tgtgtgccgt tccactttat 7740

acgcgggacc gtaacccagt gtggggttat tcctgggaac aacgccatgc aaatgaaggc 7800

tatgtgggca cctactacta ccaactctgc cactcagggc gattatgcca ttatctattg 7860

gctgatagct agggctgacg gtagtgttga agtttgggtt aacgttgaga tgagcaatat 7920

catgaatatg cgagtaattc ttcctgaggt taggattgct gtgcaaaggc ttgcctaaag 7980

gaggcaatat gagcaatgat ttaattgtac cagatacaat gtctccggaa ggcatgctag 8040

ttatagaggc ctacctggag tctggcagcg acgttgcgaa agcagcgtta gctgttggca 8100

tggaggaacc taaattccgg gagattatgc gtaaacctga ggtcaaagcg taccttacgg 8160

atatcttcat ggaatctggc ttccgtaacc gtgataaatt cttcggcatt ctagacactg 8220

ttctaactat gaaaatggag gaactggatg aaactggaat gggttcagag atggatatta 8280

tggatatcct caaactcatg cacaaaatga agatggatga gatgaagatg cagatcgagt 8340

atgagaaggt gaagcaagct aaagctccaa tacaccaaaa taatactcag atcaacctgg 8400

caggggtca cgactctaat tacacggacc ttctgtcacg cattgtggga gcaggtaagt 8460

aatggaaatc tcacgtagtt atattaatac gactgacgtg gtggattttg gtgttgataa 8520

acgattcttt aaattcccgg tgtccggctt gctggccacc gaggggatcg ttccaaatgg 8580

cccgcagtgc gcaatcataa acgcactgga agacccacgt caccgtttcg ttacagcatg 8640

cgtatcacgt cgtgttggca agtcgttcat tgcgtatact ctaggcttcc ttaaactcct 8700

agagccgaac gttaaggtgc tcgtagtagc tccgaactac tccctggcaa acatcgggtg 8760

ggcgcagatc aaaggtctga ttaagaaata cgggcttcaa actgagcgtg agaacgccaa 8820

agataaagag attgaacttg ctaacggttc gctctttaag ctggcttctg ctgcgcaggc 8880

tgactccgca gttggtcgtt catacgactt tattatcttt gacgaagcag cgatctccga 8940

cgttggtggg gacgcttttg atattcagct ccgtcctaca ctagacaaac ctaactctaa 9000

agctctgttt atctctactc ctcgtggcgg taactggttc aagcgcttct atgaacaggg 9060

attcagagag gatcttccgc aatgggtatc aatccacggt acataccgag ataaccctcg 9120

cgtatctctt gcagatatcg aggaagcacg taagactgta tctaagaact acttcaaaca 9180

ggagtatgag gcggacttct ccgtattcga aggtcagatt tacgacacct tcagcgtttc 9240

cgagcacgta caggatcttg caggtatggg gcacttcttt gctgcggacc atgagttcga 9300

aaccattcta ggtatcgacg ttggttacag agacccgaca gcagtactta ccattaagta 9360

ccactatgac caagatgtgt actacatcct tgaggagtac cagcaggcag agaagactac 9420

agcacagcat gccatgtaca tacaacactg catagaccgg tataacgtag accgtatctt 9480

cgttgactcc gcggctgcac agttccgaca ggacttagca tacgagcatg aaatatcctc 9540

tgctcctgcc aaaaaatctg ttctagatgg cctggcatgc ctagctgctc tattccagca 9600

gggtaagatc attgtcgacg cctcgtgcac tgcgttaatt cacgcactcc agaactacaa 9660

gtgggacttc caagaagggg aggaaaagct ctccagagag aaacctcgtc acgatgccaa 9720

ctctcactta tgtgacgcac tgcgttacgg catctactcg atttcccgtg gcaaataaga 9780

gctgagttgg aacggatagt agtgagtaca aattccgttc caactttata aaattcactt 9840

tacaatttcg tgtgtggcag ttataatata ttcatacctt gagagatctc atagacatca 9900

gggtgaatga gaggaatatt taattgctat acccgaagta gtattttccc aactaagagg 9960

aggaacactt tggcttccaa tgtaaaatat aagagagatg caatctccat aatgcgtgac 10020

ggaatcaaag cccagtacaa aagaggcaac tgttgcgcca tttgtgactc acaggaaaac 10080

ctggagctac accactactc gactgtggcc ttactagtta aaaactttgc taaagaattc 10140

caactggatt tcactgactc agaagtcgtc ctaagtaatc gggataagtt ctataaacat 10200

tattggcatg agctagtaga ggacacggtc accttatgtg tctttcatca tcagacctta 10260

cacaaggtct atacgaaaga acctccgttg ttttcagcta acaaacagaa gatttgggtt 10320

gagaaacaac gtgaaagatg tatgaatcca gaggcacctc gtacaagcaa cactggcgaa 10380

agatcaggct ttgcgaagtg gcttccgact gacgtcaaga ctgagaaatc aggattcgca 10440

aggttcctat aatggctatt cgtgactggt tagttactaa actaaaccgc ggacaacgca 10500

taatcaggga cttggaggat gttagtcacc gtactaacgt caagccattc acgactggca 10560

aagcctattc gtctattgag atccttaata gatccgcgaa catggtaatt gacagcgccg 10620

ctgagtgctc ctacaccgta ggtgaacagt ataaaacaat aacaacctat ggcacgatca 10680

ggagtaaaac tcttgagacg ctgcttaatg ttcgccctaa cccgtacatg gattccagta 10740

cttttagacg cctaatagtg tctgaccttc tattcgaagg gtgcgcgtat atccattggg 10800

acggttcgtc tctgtaccat ctgcctgctg ccctaatgga agtaaaagca gatgacaaaa 10860

aattcgttaa caaattcgtc tttaataata tgatcgacta tcgcgttgat gaaattatct 10920

tcatcaaaga taatggccag aatggtggta ttaactccca gattacgggt caatctcgtg 10980

tggctaccgt aattaactcg cttactaagc gtgagaaaat gcttgagttc aaggagaaat 11040

tcctggacaa tggtacggtt atcggtctta ttctagaaac agatgaaatc ctaaataaaa 11100

agctccgtga acgtaaacaa gaagagcttc agctggacta taaccctagt accggccaat 11160

caactgtgct cattctagac ggcgggatga aggctaagcc atactcccaa atctcctcct 11220

ttaaagatct cgatttcgag aacgatatcg ctcgttttaa taaagacgta tgtatcgctc 11280

tcggagtccc acaactattg atcgatgggg gtaacaacgc caatattcga ccgaacattg 11340

agctgttcta ctacatgact attgtgccta tgctcaataa agtatgtagc tctcttacgt 11400

tcttcttcgg ttttaaagta acgcccaata ctaaagacgt agtagcacta actcctgaca 11460

aggagaaaga ggctaaattc gtaactgcac tggtcaacaa cggtatcctt accggtaacg 11520

aaggtcgtat agagcttggt tacgaggagc tggctgacga gcagatgaag aaaattcgca 11580

tccctgccaa cgtagctgga tcagctaccg gagtaagtgg acaagaaggt ggcgctccca 11640

ataaagacga ggaaaaacaa tgattgacta taaagcatta aaagcactat tccctaatgg 11700

tctccccgag gcacataacg tgtttgcaac cgttaaggca catctcactt accagattct 11760

gcgtaaggag tatgggtacg ctgctactaa cagtaaaacc tgggatcagt ttaaggaagc 11820

ctacgcggaa gcaactaagc cagtaccggt agcttctgtt agtatcacgg gcgctcctgc 11880

atccttagac tatactaaga ctgtacagct tgccgcaact gtcctaccaa caaacgcaga 11940

taataaaact gtaacgtgga agactagtga tgctacccta gctactgtga gctcaacagg 12000

attagtaaca gccctgtcta aggcaggcac tgttaaaatt actgccactg caggtggtaa 12060

atctagtgaa gtgtctattc aggtcaaggc tcctgttgta gcagttaccg gtgtcactat 12120

gtcacctaag actattacaa tcgaagcagg taagaccggc aaacttactg gtaccgtagc 12180

cccggctaac gcaaccaata agtctgtaac ttacacttct gctgatacca ccaaagctac 12240

cgtagctgcg gacggtacgg taactgttcc tgctaacctg gctgcggata gtaccgtagt 12300

tattactgtt aaaacagctg acggcaataa gaccgacact gcaatagtaa cagttaaggt 12360

tcctacagcg ggtgtgtaat atctgttaac tggggagctt cggctcccca tttttctatg 12420

ctagtgcata actattttca gtgtaaccaa tttcgactac ctactaattc cacacaccgt 12480

gtgggatttt caaatatctt ttgacattcg cgatttggta tgtaataata gtatctgaaa 12540

actgaggaac aacacgaaag tgtttggagc aaacgatgca gaatattaat cttaatgctg 12600

agattaaatc tgttaaagct gtcggtgagg gtgataatcc tcctttaaaa atcaaagggt 12660

atgctaacac gattaccaaa gaccgcgccg gcgacgttat tctctccgaa gcgtggacta 12720

ccagtaacgc cctcaagaat tttatgaaga acccgatcat gcttttcggc cataaccata 12780

gccgcccaat tggtaagatc ctagacctgg taccaaccga gtccggactt atggttgagg 12840

gtgaggtaag tgctgctgat ctacagattt actcattaat acgtgatgag gttcttaaaa 12900

cgttctcggt aggcttctat attaaagacg ccgaatggga cgatatgact gaaacgttca 12960

ttattaaaga tctggagtta ctcgagatct ctgtagtctc ggttccctgc aaccaagact 13020

caacttttag cctttcgaag tctgtaaacc ataatgatta catggagctt cgtaagtctt 13080

ttgtaaaatc ttcgcaggtc cagcctgttg aacaacctga actttctaat ttagagaaat 13140

tcctagtagc cgctggttac gctaaaggat aatggagaaa taataatgtc ttacgatatc 13200

gcacaactgt ctaaagatct gggcctgggt gacattgctg agcagcttaa aggtctaacc 13260

gcctctcaga aagctgaaga agctcgcaaa tttgctgctg agcaggaagc taaagaactc 13320

aagcgtatgg aagacctggt tgctaaagca actggtgaag accgtaaaaa cctggcagaa 13380

gctctggagc ttgtaaaaaa cctggatgag aaatccaaac agtccgctga agcgttcgtt 13440

aaagcaatga actcccagca ggaagaaatc actggtctga aagaagaaat caaatctctg 13500

ctggccgctc gtgaaaatgg tcgctctttc gtagctgatg gcgttgctaa ggcaatgttt 13560

ggtaagcagg aagatttcga agacgaagtt gagaaactgg ttcttctgtc ctacgtaatg 13620

cagaaagatg tattcggtac taagcgtggc gaagcccacc tgaaagctgt taacggctct 13680

tcttctatcg aagtttctac cgaagcatac gaaaccatct tctccctgcg tatcctgcgt 13740

gacattcagg ctaaactgat tatcggtacc atgttcgaag aactgccgat gtctagcaaa 13800

ttgctgacca tgatggttga gccggaagct ggtgaagcta gctgggttga cgcctctact 13860

tacggtactc ctgctactgt tggtgcggaa gacaaaacca agctgtctga aatcaccttc 13920

aagacctaca aactggctgc taaagcgtat atgaccgacg aaacagaaga agatgctatc 13980

ttcactctgc tgccgatcat gcgtcgtcgt ctgattgaag ctcacgctat cgcaatcgaa 14040

aaggcgttcc tgaccggtac tggtgctgcg ggtactccga aaggcctgat ccagttcgct 14100

aaagacgatg gtaaagtggt tgctaccact gctaaagctg acggttctgt taaagttacc 14160

gctaaagaaa ttcacaagct gcgtcgttcg ctgggccgcc acggtctaga cctgaacaaa 14220

ctggctctgg ttgtttcgat ggatgcttac tacgatctga tcgaagacga agaattccag 14280

gacgttgcac aggttaccgc taccaccgct atcaaactgc agggtcaggt tggtcgtatc 14340

tacggtctgc cggtactggt ttctgagttc ttcccagcta aggctgcaag cgctgagttc 14400

tgtgtagttg tttaccgtga caacttcatc gttcctcgtc agcgtgcaat cactgttgag 14460

aaagagcgtc aggctgaacg tcagcgcgat gcgtactacg ttactcagcg tctgaacctg 14520

atgcgtttct tcgagaacgg cgtagttgct ggtgcttacg ctgcttaatt tggctatact 14580

gccgactaaa ggagagcttc ggctctcctt ttttattggg taaaatatgc aattcatgac 14640

agattctgat tggagaacat atggaggcct taaacgtcct gacttagagt caaatatccc 14700

aatgttaatc aaagcagcca atgctctgat tactcagctt ctaggtattg acgacactgc 14760

taacgttgta gacgttctgc ctactaaacc agcacgcaaa aagtacttcc tgtcttctcc 14820

cgtgcctagc acgatcacta aaattacgat taacgatcag gagatcgata agtcgcaata 14880

taagaactac ccggatggta cgctcttgct gaaattctcc cctccagagg ggtatatgga 14940

agtagagttt actcagaccg gcttcacctc gatccctgac gacctggtac tagcagcctg 15000

cttcctagtt gatcactggg tcaagaagga ctaccgcgag tctcgtacat tcggcggaga 15060

aaccgttact ttcaatacca ctaaatctgg cgtaccggaa cacattcgta ctataatcga 15120

agtataccgg aggctgtagt ggcgttgggc gatctagctc gacagatagt taaagaacag 15180

ctggacatta tgagtggtgg tagccactct accaagaaca ccgtgatata tagtgcggaa 15240

actatggata accacaaaga tggcaccata ggcaaggtat ccttccgatt taccaagccg 15300

gtatcggagg atttactgaa tgttcggacg tcctctattt taaaagctgt ctcgtcgtca 15360

cttaatctgg aaggtgacgt tggtgttatc gataaccttc taaatagtat cactggtaaa 15420

aaatccaaaa taggaagaaa acggtctacc ggtagggtag aggttaactt tggagatcct 15480

tcagatgctg acaacggtta cgctggtgct atttctggcg cttctgggcg tttcgtctca 15540

aacacaaacc ttagagcgtt acttgaactc gtagcgaaag aatacttagt caaggatatg 15600

aaaaaagctg gggcacccct taaatttaga acggggcgtt tcgctaattc cttgaagatt 15660

aaagacgtgc tgttaagaga agacgcaggg gcaaagactc ctgacctcaa catcacgtat 15720

aactacatgc ttaagcctta ctctgtgttc aaccctgccg tctctaccta ccgcggactt 15780

tccttacggc ctttccctgg tgctaggaac ccgcagaagc tgatcggcga ggcaatcgct 15840

aaggctgcaa gagaccttat ccattctaga taccggataa gagtaaatca gggtacataa 15900

tgaattacag aacaagtatt gctgatgccc tagtggaacg actgaagaag gacatggatg 15960

ggagtaatcc cacagagttc ttcactaata tgtatgggaa cgtatcccgc cagacttatt 16020

cgtttgagca gatcaatgag ttcccttaca tagcagtcca tgtgggtacc gaaactggaa 16080

actacctgcc gtctgcacag cagtgggttt accttgaaat tcctattctt atctatgata 16140

aagaaaagga tgatattaac atgcaacttg agaaactcat agcggatgta aaaacctcta 16200

ttgacactgg aggaaattta caatatacta taatgaaacc tgatggttca actatcgatt 16260

ctgaagccac tgacatgcag atcacgtcgg tgtccacaga cgagggtata ctgtccccgt 16320

ttggttttgc tcaagttaac gtaacagtcc ggtatatgcc tctgagaaga gcgctggata 16380

gataagttac agctcaggag aaatttaaat gtctgtacaa ctattacgta atacacgaat 16440

cttcgtgtca accgttacta cggggttcac taaggccaac actcaggaga tcctagttca 16500

ggatgatgtc tcctggagcc aggacagtaa ctccactgat attaccctaa atgaggctgg 16560

ccctaagccg acccgcggtt cgcagcgctt taacgattca ttgaacgctg ctgagtggag 16620

cttctccact tatatcctac cgtatgacga tgcaggtaaa cagatcctgc cggactacct 16680

actgtggcac ggactggcaa ctggagctgc cgtgaatcta gcaggtacta ctggcgtatt 16740

ccagaatgct actaacctgg ttgtcaactt taaagacaac gggtaccacg aactggccat 16800

gttgaacatc tacatcctaa ccgatagctc ttggtctgtg atccgtaact gccaggttgg 16860

gcaggctgag gttaacgtag atattgatga tatcgggcgt gtaacctggt caggtaatgg 16920

tactcgcttg gagaccctag cttctcagcc gttcgaccct aaaaccatag ggatagacga 16980

cgctctttat gctaagattc agagttctta tatcaagaac aaactgacca ttcttaagct 17040

gaagaacaac gctaccggcg gaaaaaccta taacatcccg atcacgggag gttctttcac 17100

tatgaacaac aacgtgacgt acctgactcc taacatcatg tctcgtgttg acgttccgat 17160

cggttcattc actggttcct tcgagctgac tggttccttg acagcgtata tgaatgatgc 17220

tgccaacggc tctatccagc tgtacaaaga tctggtttcc gacctgaaag ctgtgaacga 17280

cttcgaagtt gcaatcatcc tgggtggaga gtatgatact gctcgtccgg cagctgttct 17340

ggtggctaag cacgctaacc tgaacatccc gtcaatcgaa actgatgacg tgctgggtgt 17400

gtctattgag ttcaaggcta ttccgactca gatggacgca ggggatgaag gttatctggg 17460

cttctcttcc aagtacacca agacttcgat cgcgaagctg atcagctctg gtgacggtaa 17520

ccctgtcaca ccataaggat aactaatgct atactcccta atgcgggagt ctagagtagt 17580

catcgagtac gatggcaggg cgtacggatt tgacgccctg tctgattaca ctgctggaac 17640

gtcctacgaa gagtttaaag caaatcgtag gacgattcac agacgcagta actacgccta 17700

ttcgaagata actgctcagt ctccttcttc aatttctcta actcttaact tctctagcaa 17760

tgctctcgaa ggtctatttt tcgagttgat ggggtttata gagatagacg gaatgtatca 17820

gatgcccttg ttcagtaata atattgagcc taaaatgttc tccgtatata ttattaacaa 17880

gaacacgagc ttacgtttcg ataactgttt tgctaccacc tgcgactttt ctctagataa 17940

gagtgtcccg gtgctaaacg ttggtatcga gtcgggatac tttgaggaag taggccaccc 18000

actcaacagc tatacgcttg atcaaggtga ggtgctacca ttttcattac ctcaggtatc 18060

ttcgaatggg agagtgctcc caggacttat gtcagccggt atgtcattcc agcagcaatg 18120

cgaatggcga ggtgacagaa gtttattcga tatcaataag atttataata atagaagggc 18180

aatcgttaac gaattgaact catccgcttt gatatcgatg tactatgcaa agagtcttca 18240

gatagactct acgcataaca ttaaacctga tattggccta ccggtacaaa tcagaaataa 18300

atatattgtg gtggatttcc cttccactcg aatcacaaaa cgcctagact taaccgacgt 18360

gtacaagatc gattatgacg taatacctac tgagcaatca gatcctgtcc gaatcaagct 18420

aattggagaa taacaaatga gtattaacct aaaagatatt gcactggata ccaaacagat 18480

caccattgca taccctggcc taccacactt caaactgaaa gttaactacg tctcccgtaa 18540

gctctccaag aaaattctgg aagctgcaca agagaaccag tttgttaatg gtatcgctgt 18600

taaagtgcaa aacgatgaca aattcgcaga agagttcgtc aaagtggcta ttgcaggttg 18660

ggaaggtctg accgtcgcag atgttgagaa actaatgctg atcgaagttc cagaagatcg 18720

tctggaagac aaagtcgaat ttagtatcga caacgcgatg atgttggtgc gtaactccag 18780

tgccttcgag acttggatga acagcactgt cttccaccta gacacttttc gtggctcaaa 18840

atcggaacct actgcttaag gaaatagatg cctttgcaga acgatgtgtc aaaggagggg 18900

actccaaaat tacacgggag cagtatctga cgatgtgcga atccctcggg gaggaaccta 18960

accccgaggt acttaaacgt ttcgtagaga tccatgactt ccctgaaatc gcacagaccg 19020

ctctaacaat atataacaac ttatcggata actatatccc cggagattat ccaacctatt 19080

taggcaagga taagagtgct ttactagttt tcttcgatat ctacggagtc gaagacgctg 19140

atgagaagag ccttatactc caaatcatca atatattcga ctcacatgcc gtggcagcct 19200

ctcgtaaacg cgttgaagca gctattaaga agtctaaaat gaagtcttct agtaggtagt 19260

gagttacagt ttcctccaac gggcgttcca cgtgaggctt ggcctagggt taatgcccta 19320

ggccttttta ttggaaaaaa tcatgacaga tagactaata cgagaattac ttgtagatat 19380

caagcagcgt ggtggatcca aagccgctaa acaaatcagg gatgttgaag ctgctttaga 19440

cggggctgct cagagctcag agggtctaaa tacaagcttg ggcaaacttc ctgggtcttt 19500

cacggcgctg gaacgatctg tatcacgtac tgctaagtcg ctggagaaat tatcctcgac 19560

caccagcatt acagcattag cagcgtctat cggcatgcta agcggcaagt ttacctcgtt 19620

cgaggttgac ttggctaaat ccgtactaaa aatcaacgca aacctaaacg gggtgacttc 19680

cgccgctaac aaaatggcct ctggttttga cactgcagcc acttcttcgg ttgcggactt 19740

aaaccgcgtc aataaggctc ttcaggagtt agatgcgcac gcctcttcag tagctaaagt 19800

gttgcagacc ttgaaggcgg gggccgggtt agaatctatt agctctagtg ctgctaaggc 19860

tagtacggat cttagccacc tagtatctgg ggtggaaaag ataggtaacc aattagctag 19920

aatggcggag caagccgtgc tggcaggcag gtctcttcag gggctgaaag ccgactcctt 19980

aggggctgcc ggagagcatc tgagtaaggc tgcgtccggg atttccgtag ctgtatcttc 20040

tatgggcgaa gaggtgaaca agctaaacaa actacttctt gagttggcag taaaggctga 20100

tttagcgagt aaatctatag caaatattgc accagggacc aaactgaata gtctgggaac 20160

tgaaatccag aagattaata ctagtttagc cactgcagcc aatacctcgg tagctgagat 20220

atctaagatt aaagcagccc ttacgtcttt agtatcctct accgctacag ctgccgcttc 20280

aatgaaaacc gtaggaaccg gtagtggtct gagcaagcta atctcagaga tatcagcagc 20340

cacctcagct tccacttcgg atatctctaa agtaacagcc gctttaaaac agcttaacgt 20400

agatgctacg gcagcaggaa aagcactgca aagtattaaa gcaggcgcaa atctttcttc 20460

tgtacctaca gttgttggaa agataggtac ttcaatgacg cagttgcgtg ctcagttaga 20520

aggatctgta accggtatcg agaaaagcct aaatgatcta tctagagctt ttgccactat 20580

gggaggtacg ggaaacctga atccactggg taactccatc agaggtatga tcccgtcact 20640

cacccagctg gctaaggccg ctgtgcaagt taactccgct ctgtcaaaaa tacaggcagg 20700

caggggcgta cttcaattac ctacccaatt caaagcagta acggcctcat taaatgccct 20760

ggagactaaa ctggcctcta cgtctcaaat actagagcgc ggattctcca agggatttca 20820

ggatatggcg tctaaatcaa cctcgtcatc tacgagaatg attaacaact tccagaaagt 20880

ggtaccggag ctcaacgcta ttgaagctgc tgctatacgt tctgctgctg caatagacaa 20940

gctaatagcc aaacgtatac gcctcggaca agctggggga gggggtaacc ctgcagcgtt 21000

caatatgggt gccttagtag cggaaatgaa caggattgta acctccattg aagctatggg 21060

caacaaaatg aataccacca tggctgatat ggcacggagt acggacaagg tatctgacaa 21120

attaacagat ctaaactcgg gagttcggga tgttaatact ggtttaggtg ggttgaattc 21180

aacgttaacg ggtacgggta gcgctgctaa tagggcgtcc agagcgttgg gaaatacttc 21240

aggatctgct cgcggagcta ctaggaactt cgcagcacta gctatggtga ctggccctat 21300

gcctcttatc tacggtgcta tagcctctaa cgtatacgtg cttaaagcag cgttcgatca 21360

gctaaaactt ggagaccagc tgaaccgctt agaacagttt ggatctatcg taggagcgaa 21420

gacaggtaca cctattcagt cccttgctgt ggcactgcag gaagctaccg gccacgcggt 21480

atcctttgaa gaggcaatgc gtcaggcatc tactgcggcc gcgtatggtt tcgacgctaa 21540

acagattagc gagtttgctc tagttgcacg tagggcagcg gctactcttg gcgttgatat 21600

gaccgatgca ctcaaccgtg taatcaaggg tgtgtccaag caggaaattg agcttctaga 21660

cgaattaggt gtaaccatcc gtttaaatga tgcgtatgcc gaatacgtta aaatacttaa 21720

tgcggctaac actggtataa cgtataacat tcagggtcta acttccttcc agaagcagca 21780

ggcatatgct aatgcggtag tagcagagtc taccaaacgc ttcggctacc ttgatgaggt 21840

actacgagca accccatggg agcaatttgc ggctaatgcg gattctgcat tacgcaaggt 21900

tcaacaagca gctgctaaat atctaggtcc agttattgca tctataaacg cagcattcta 21960

tacgtctaag gcttcggtat ctgcagaggc agctactgcc cagcaagagt cgattaagca 22020

aatggacggt aaagactcta acgcagtggt catgaacctt gaggcttctc agaaaggctt 22080

ggatgatgca gtcaaagcaa aagaggaagt aaaaaataaa ctcgcagctc ttaataagga 22140

gataatggat agagaggcga agatggatat gtccactgca ctggccacag ccgccaacta 22200

tagtgggttc ggtaatctgc ttaccctggg agcctctaaa gctaacaaag aatttacaca 22260

acagactgca gatatgcgta gacaggcgta tatgttacag caggagttag cagattctgc 22320

gggagctatc caaaaatgga aagacgccag ggactccgct ctatctaagg ctcagaaaga 22380

gaacccagaa ctggcgggga aacttaatat agggcagaac gttgaagcaa gtaatggact 22440

atacaccttt gacaacgcag cattagacgg ggcagttgct ctacggaagg agttcaataa 22500

tataaagaaa acttccggag atctgagcaa cgatatccag aactttgcac aggactctaa 22560

cactgcgtct cgagctactg cagcactggg tgatgcactt aaggcggttg agtcattggc 22620

gggtggatct acggaaaaag ccaatcaaat gaccaaggac cttaatttgg gctattccac 22680

cgtaaccgag atgaacactg cgtataaagc catgtctaac tatcagaaga tagtgaatga 22740

tgaggctaag tctaagctag atgttgagaa acgtatagcg gaggtctacg ctgccactcg 22800

taataaggat aaggcggaag aagctggtag agccctagaa atgcagcaac ttagcgcgaa 22860

gaaagaggca ttgaaagctg tgctggcgac gaacaaggac aacaaggcta ttcaaaaaga 22920

gttgaccctg ttagagacgg aagagctcaa agtgaagaac cagggcatgg aagcgactaa 22980

gaaggagaaa ttctataagg ataagatagt aggcatagat cgagaaatag cactcctaaa 23040

taatcgcact atgacagatt ctcagtataa cgtggcgaac cttaaattaa atctacaagt 23100

agagaaagat aggttagcct tactgaagac tcaggcagat aaggagaagg aagccgaaca 23160

gtctagacgt aacattgcct ctattgaaag ggaaatctgg aaagagcagc ttgaccgtaa 23220

tgccaaaact gctgagatgc gtaaagaaga attcgagcgc aatcaaagca tgaagcctct 23280

aatgggagag tcacagaaaa tgcaggagca gctagcgttc taccaagaaa tgaaggaatt 23340

cacgaaaggt aacgctgatg aacaggcgcg ttggagcaag gaaattgcta acactactgc 23400

gcaaatggcg gctctcaaag ctcagcgtac tgcacagatg atggatcgcg taggacagtc 23460

cttgggcgca gactatacgc ctactactgg cctggagggg gaggataaga aattcgccga 23520

catggaaaac cagatggcgt catacgatac cgctatcggt aagctctctc agctaaattc 23580

ggaggctact gctactgctc aaagtatggg gaacttagct aacgctatga tccagttctc 23640

tcaaggatct ctggatacta cgtccatgat tgcagcgggc atgcagacag ttagccagat 23700

gatcagctac ggtactaacc agcagatttc agcaattgat gcagctatag cggcagagca 23760

gaagcgtgac ggtaaatctg agcagtctaa gaacaagatc aaaaagatgg aagcggagaa 23820

gattaaactt cagcaggaat ctgctaagaa gcaaatcatt atccagacag cagtagcggt 23880

aatgcaggca gcaacagctg ttccgtatcc gttctctatt cctctgatga tcgcggctgg 23940

gcttgcaggt gctctgtctc tagcacaggc gtctagtgct accggaatga ccgatatagc 24000

aggatctggt ggtgaaaccg cctcttacct aaccttaggt gagcgccaga aaaacgtaga 24060

cgttagcatg ggcgcaaacg caggtgaact atcttacgtt cgcggcgata aaggcatagg 24120

tagtgctaac ggatttatcc ctcgtgcaga aggtggtaat acctacccag gtgtctccta 24180

taagatgggt gaacacggaa cggaagttgc aactcctatg gtgcctacca aggtaactcc 24240

agcggataaa gtggcttctg aaacttcttc tggcggtgct agaagaccgg ttaatctgaa 24300

catccaggca atggacgcta agagctttat ggagtacgca ttggaaaacc ctgcggcatt 24360

ccaggcagct gtagagttag ccttgaatga acaagggctg agcttaaaga acctgaatta 24420

actaaactaa agggaggacg taattgtcct cccttctttt tggaatttat aaaattatct 24480

tgaaaatttt tcttgatatg actataatat taacattgag aggagaaaac aaaacatgag 24540

attaccagat ccctttacac atcctcagta taacggcctt gggtttgata aagctacgct 24600

gatcgataat gatccagtga tcagagacga gctaccaaac ggcaaggtta acgaagttaa 24660

aacagccact cagtactggg gtcttaacat tagttatcct gtgatgtttc ccgacgagta 24720

tgctgtactt tcgtcagcaa ttctagagta taagcgtacc agaggctatc tcgacgttat 24780

actcccacat tacgagtctt accgagtaag aggggatgcg aacaactgtc gcattgccgc 24840

tggacaaaaa ggctccacac tggttatcac caatacgaat tccttatctg gagaacctaa 24900

gccaggtgat ttattccagt taaccacaca tccaaaggtg tataagatta catcttttaa 24960

aaacgtagca ggagtatgga cacttaatct ataccctgat ctgttgctca ctaccaacgg 25020

ctccgagaga ccacgtttca atgggattct tttccaaact aaattaatga acggagattc 25080

attcagcgaa gagatcacag ttgatggtgt atacgacggg gttaacctag ttctgagaga 25140

aagtctatga gacagatcct tccttctgcg aaagcctacc ttgccaacaa tgacaagata 25200

cgattagcgt atcttgtctc tatcgaactc ccggggtcca cgggtaataa cgctgtttat 25260

gcttatatga cggactatat gagagatatc aactatggtg gtatactctt ccaatcaggg 25320

aaaattaaaa caattagcag ccacaaacaa aaccgtacgt taaccgtcgg cagtttgagc 25380

tttagtgtta ctggtacgga tgccaacgaa gtcattaagc tcgtgcaaag tggtgtatca 25440

tttttagatc gctctatttc tatatatcag gcgatcatcg acgacaatgg ggaaatcctt 25500

ccagtggacc cagatactaa tggcccctta ctcttcttta ggggtaagat tgtaggtggt 25560

ggtatcaaag aaagtaatac agtatccgga gttggtactt ctgttataac ctggaactgt 25620

tctaatgaat tctatgattt tgagcgggtt gctggacgct tcacagatga cgcttcccac 25680

cgaggacttg agattgtaaa tggagaatta ctgccttctc acggtgccaa acgaccggaa 25740

taccaagaag actatggatt cttccacgcc aacaagagcg ttaacttcct agctaaatat 25800

caagtaaaag aagaacgata caagctagaa tctaagaaga aattattcgg tctctccaag 25860

agctacagcc ttaaaaagta ttatgagact gttactaaag aagtagacct ggacttcaac 25920

cttgcagcca aatttattcc tgtagtatac ggtactcaaa aagttcctgg tatcccggtt 25980

ttcgcggata cagagagaaa caatccaaac gttgtgtacg tggtttacgc gttctgtgag 26040

ggtgagattg aaggattcct agacttccag tttggggacg cccccatgat ctgtactgat 26100

caaactgaca gtacatctcg tacatgcttt ggacaaaaaa gggtgtcggg agatactatg 26160

gcaagaattt ccacagggct cccatcaaca tctctctcca cgcatggtca agaatacaag 26220

tataatgacg gtaacggaga tatacgaatc tggacattcc atggcaagcc agaccaaacg 26280

gtagctacgg tactaagaga cattgctgct gctaacaatt tcttccttca aggagagaac 26340

ggtaatggtc cggagtactg ggattctagg tacaagttat tagacaccgc atacgctgtc 26400

atacgtttca ctatcacgga gaacagaact gatattcctg aagtatccgc agaattaagc 26460

ggacgcaaag tgaaagtata ccaggcagat ggttctgtta aaatggataa aacgagtcag 26520

aatggtgtgt ggcaaacatt tgactaccta acctccacca cctttggtgc aagtatcccg 26580

atagacagaa tggtgattgg tgactggaga aaagaggccg atctattaaa cattatagac 26640

acctcttatc aaactagttg gcaacctttc tggagatacg ttggatggga gagctggaca 26700

gccgaaaaca gacaaataat gcaaatgaac acaatcctgg ataactccaa ctctgtgttc 26760

aaaaacgtgc aggagctatt agaatccttc caggggggcgt tgaataacct atcaggtatc 26820

ttccgcatca ccgtagagaa agattcaaaa actccgctag aacttaattt cctagatact 26880

tatggggacc tggatctatc agatactaca ggccgtaata agtacaactc agttcaggca 26940

tctctgattg atcctaccct gaactggaaa accaactcta taacgttcta taattctaag 27000

tttaagaatg aagatcgtgg agttgacaag aaacttcaac tttcttttgc taacataacc 27060

aactactaca ctgctagaag cttggcagat agagagctta agaagtctcg ttactctcgc 27120

tctctgagtt tctctttacc ttacaaattc cttggtatag aacctaacga tcctgtagta 27180

ttcacctacg atcgttatgg ctggaataag aagttcttcc tagtagatga ggtggagaac 27240

acaagggatg gtaagataaa cgtaactctt caggagtatg gtgaggatgt atttattaac 27300

tcaacgcagg tggataacag tagcgaggcc gttcctgaaa tatccaataa cgtcctgcca 27360

ccaagagact ttaagtacac ccctacacca ggtggaatgg taggtgatgt tggcaaaaac 27420

ggagagcttt catggcttcc tagcttgaca cctaacgtag tctattactc gatacgtaaa 27480

tccgaccgcg tggatcctta tattgtgcag cagactgctt tcacacctaa cgttagaatg 27540

ttccaagata tcgtgggtga gcctgctggc ctgactattt tcgagatccg cgccgttgat 27600

attaatggtc gtcgtagctc tccagtaaca atttctgtag atttgaactc agctaaaaac 27660

cttagtatgg tggaaaactt ccgagtgctt aaccttgccc ctgaccctgc tgaatgggta 27720

ggacctgact tagagttagg gtgggacaag ctgcaagaag aggggctgat ttcagggatt 27780

ttctacacgc ttgaaataag ggacaacact aataaactgc ttagatccgc aaagatcacc 27840

agtttatata actacagcta cctgttgggc tataataagc tcgactacaa ggccaacaac 27900

tcgaatactt tggggattta cagagcactt cagccaagaa ttcaggcgga gggaccaaag 27960

ggcgagaagt cggttgcatg ggcatatatc taaatgattt caaacatagc accagctaaa 28020

atggtactgc agaatatcgt gaccggctat acgattgcga gtattcagca ctcaatcttt 28080

tccgattacg acgtaattgg tagaactttc tggctaacta cgggtggggt aactacccgt 28140

agggacttta ccggcgttga tacattcatt gccacaatta acaatctaat cgctggcgct 28200

acctactctg cccagggtgc tttctatgac tcgatggttg atgcagagct gatggctgct 28260

aaagtaggta tgaacctctc tagcaccatt aacttcaaga tgaaaactgc tccgaagatt 28320

accaaagtgt cctcttttgc agaatctgtt gacgtgggtg tgggtgctcc tatggttgtc 28380

gtagagcttt ctggggaggc cgaatacgtt accatcgaaa tgaaacctga gggctctagc 28440

acctggacta aatactaccg tggtccaatc actgagcaga tcatctttgg gggtgttcca 28500

gttggcagat acaatatccg ggtatctggt gttgtcacta tgccagatgg tgttactgtg 28560

gatgtttctg ggtatgatac ctggccgtca ctgtttaacc tgacctacaa cttcactcca 28620

ccgtctgccc caactaacct gcgtttcaaa actgcccaca tccaagatgg tatggagcgt 28680

tttgacgttc gcctggaatg ggattggact cgtggtacgg gtgctaacgt tcgtgaattt 28740

atcatccagt atattagtaa cgatgagttt gcaaaaactg gatggactaa ggccaacaag 28800

ctaaacgtgg gtgcagctaa agctggtact atcactagct tcccttacaa aatccgccac 28860

cgcttccgtg tactatcggt tgcttggggc ccagatactc agtctataac taactctaac 28920

gaggttactt atattataga cgagagcacc actttcgaca atgcattcat taacgagacc 28980

ggtgtagaaa tgacctacgc aggtatcaag ggtaaactct ggaactctaa caccaaacag 29040

tgggagcaga ctttcttagt cgatgctgct acaggtgcag tagttcttgg tacactcgat 29100

gaaaatggta aagcgccgat ttcattcgac cctgttaata agattgtaaa cgtcgatggt 29160

aaagttatca ctaaagacat taatgctgct aacgtaattc ttactaacct gaccggtaaa 29220

gataacccgg caatcttcac tcagggtaag aagtacggta ataacgcagg tggtgtctgg 29280

atgggtgttg acaacgttga cggtaaggcc aaatttgacc tcggtaataa cactcagtat 29340

gtgcgctggg acggtgatac tcttcgcatt tctggtaacg ttgtaatcgg tactcctgga 29400

ggcgatgtag accttgaaac cggtatgcag ggtaagcaga ctgtatttgc ttataaactt 29460

ggtacatctc tgccaagtcg cccgcttgac caagtttatc caccagctgg atggtccgca 29520

ttcccgccta accgcactgc tcagaatcag aacgtgtacg ttgtgcaggg tactctggat 29580

cctaagaaga gtcctcctgc tctagtagac ggtaccaact actcagctgc atcccagtgg 29640

tctggtgtcc caggtactgg tggtactgat ggttctaacg gtgattacac tgttcagatt 29700

taccagatca gtgctagtaa gcccacgaaa ccaggcaata tcaatgaccc tagcggttgg 29760

agtcgtaccc caccgactgg aacccctctt tggatgtgtt ctggtagatt caatggcgat 29820

actaacgctc taactgttga gggttggtca gacccgatcc gagtagacgg cgagaaaggg 29880

gctactggtg ctactggtgc tactggtcct caaggtcctc aaggtccggc aggtggttca 29940

gtagaagtac agtggtctaa agatggtact actaactggc atgcaaactt tactactggt 30000

gatatctaca tgcgtcagcg tgttggtaca ggtgggtgga gttcagctat ccgtgcagtt 30060

ggggaagatg gtactaatgg tactcctggg tctaagggta actacattgg gatgcgcttc 30120

cgagtggcgg ctgagaaacc tgccactccg actggccaga ccccttcagg ttggtcagat 30180

gcacctcctc agggaaaccc tctatggatg gttaaagctg agttcaacgg tcaaaccaac 30240

gccctagtag gtacgtggtc agaaccagtt cgtattgatg gcgaaggtat tggagtaaac 30300

ctgtatccgg ttaagaaaac actggatcag tggaccggaa tgagcaacgg tactatggtt 30360

aagaacccag ataccctcag ctttaccata accaacacag agagcactac ctcctctacc 30420

ggaccgggtg cacatcctgt tccgttccag ggttcacaag gtcctatagt tgagattcca 30480

gtaaagccga atacagcgta catcttcact tatgaggtta gtactgatag caccagcttt 30540

gttctgagag acctgttact agagttctct agcattaccg gaagttttac caacttccaa 30600

gagttactga ctggagccaa aggtaagcag gaagctaaga ttgtcactcg tgctgatact 30660

aagttcctga gcttccgtcc aggtgtccgc actgccggag ctacggttac ttattctaat 30720

ctaaaacttg aagaaggcat taaagctacc gcttacagcg tagaggcttc cgacagtatc 30780

ggtgagaaag gagaccaagg tactcagggt ccacaagggc ctcagggtaa tcagggtcca 30840

cagggtaatc aaggcccgca aggtgctaag ggtgataatg caaaaggatt cagcctctct 30900

tctctcggtc agacgtttac gtacgacgca gaaggtaaac tgaagtccga tgcaaccatc 30960

ctgttccagg ctttccgtca gaatactact gcaaacgtta cttggtcagc caaggacgag 31020

aaaggtggga acatcactct gacaagtact agcaatactg gtgctacact gaccgccgct 31080

aacttcaaaa catcgaagtc tgtagtagtt acagccgtct gtgatggtat caccgatcag 31140

atcactattg tgcgtctaga cgatggttcc aacgctctcg tagggcttct gaccaacgaa 31200

ggttccacag ttctagcgaa ctatgctggt tacgtgcaaa actatagtac tggttctggt 31260

gacttcaaag tattctatgg ggcgaaggat atcacctcag aatgcacctt cagtactatg 31320

gagaagaata accttgatgc tgatattact tcagcgggca aatatacttt aaaaggtatg 31380

ccggctggta ctgatgttat caacggctgg gtcgacttac gtgctgtaca ccctacttac 31440

ggtgccgtgg tccgcagagt ggcaactact aaatctatcc ttgcaaaagg ttatgatcgc 31500

gttattacca cttcattcga gaacggaaat aagggtacct ggtcgactgg tagtgtccaa 31560

ggggtttctg gtgccacaat tgtagccgca ggtttcagca aggccctagt gatctctgct 31620

agagactgta tagaagatgc taacgcattc cctgtagtag ctggtcagaa atatagactg 31680

ggcatgtgga taatggctag tgagtctaaa gtcaatatca acatgggaat gcgaattgta 31740

agggcggccg acggagttgt tgattggcaa ggaaccctta tgattgcaca aggtactgta 31800

gtacctggtg gctggtccta catcgaaaaa gagtttactg ttggcagttc taataccggt 31860

atagcaatgc cgtggatcca gatggctggg tcttctggta gtgacttagg taaagcttac 31920

gttaccgata ttcacatttt cgccctagaa atggatgggg agaaaggtga tactggtgca 31980

actggtgcta caggttctca aggtccacaa ggtccacagg gtaataaagg ggacaaaggt 32040

gatactggtg caactggtgc tcaaggccct gctggtagct ctgtaaacgt ccagtggtct 32100

aaggatgggt ctactaactg gcatgctggt ttccaacctg gcgatatttt catgcgtcag 32160

caggttaatg gagtttgggg cagtgctatt cgtgcagttg gcgaagacgg taaaaatggt 32220

gctgatggta ctgacggtga ctacatttca atgaagttta tcgttcagga taccaaacct 32280

ggcacaccta ctggtaacaa cccaggtagc tggagtgatg ctcctccagt tggtagccct 32340

ttatggatga ctaagggcac tatgaatgct agcggtcaac tacagggtac gtggtctaat 32400

ccggtccgcc tagacgggac tatcaaccct aacctgttcg cagtacgtaa gtggatggca 32460

gggatgactg gtacggaagc cggcacatct aagaacgata tcgagaagct agcgcatacc 32520

ttgactcgta cttccggaac tgataatacg gctccagggt gctatgcgac cccgtatcta 32580

ggtagtgggg cgttttccca tccagtgact ccaggtaaac gctacactct aacctataat 32640

atcgacgcgg ctagcgaggt ccagacccga gatactatat tctggcaggc taatccagac 32700

tcaggacaat ccacctacat agaggaactg aataccggga cgtctataaa ggttaagcgt 32760

acctttgtag ttcctacagg tatgaactac ctaaccctac gcccttctgc tctgacactt 32820

aacgtagcga ctacgtggag caagattaag ctggaagaag gcggagagaa aactgagtat 32880

caagtagaat actcagacag tatcggtata gtaggtaaat cagttttagt acagtggtct 32940

aaggatagct cttctagtaa ctggcatgat accttccaaa caggtgactt gttcatgcgt 33000

cagaacgttg acggtgtttg gggtcctgcg attcgtgcta taggtgagaa aggtgagatt 33060

ggtcctgacg gtaagaaagg taactacacc aatatcatct tccgtatttc ggatactaaa 33120

ccagctaaac ctactggtaa caaacctacg gattggtttg atgctccacc tgatggttcc 33180

cctctttgga tggcaacagc aacgtttaat ggggatacta acgctatcat tggtgcttgg 33240

tctgaccctg tgcgaatcga tgcttccggc gtaggcgaaa acttcttagc gttcaaagag 33300

tggatgatgt ctattcagag ggctgagggg acgggctctt cagttagcaa gaatccggac 33360

cagatgagat tccgggtaac agctgggcca tccagaaatg acgcgtacac tacccttac 33420

caaggaaccg gcacacattt tatagaagtg tcgcctaata ctgtgtatac tttatcattt 33480

gaaatggaaa ctgctgtgtc cactagaatg atgctgttgc agtttgataa tggtaatggg 33540

ggcacgcacg cacgtaacaa tcaggttata tcaaccagta ctggtataaa cagtctgact 33600

attactacgg gtgctaacac tacccacctg tctatgcgta tgtcaatctc taacatggga 33660

gagactaacg tactgatgaa acctaagctg gaactcgggg cgtttcctac ggcatacgtg 33720

gcgcatccta gtgatctact tggtaaagat ggtgctactg gagctactgg tcctcaaggt 33780

ccgcagggta acactggtgc tactggtgct acaggcccac aaggtagtaa aggtgacaca 33840

ggggctactg gtcctcaagg tcctcaaggt ccgaaaggta acgcaggtga aaacgctaaa 33900

ggattcgccc taacgtcaga ttatcagtca ttcgtgtatg atactgtagg ggacattaaa 33960

tccgctacta ctattctgtt caagggacta aaacagaata ctactgcagg gatcacgtgg 34020

agtgctgtaa ataatacggg agctgcagta acactgatga attctggaga taaccgtcag 34080

ctaaccgctg cgaacttcgg cgcctctaag tgggttacga taacagcaac ctgtgatggt 34140

ttatcagatc aaattactgt ggttcgtttg caggacggtg agaacgtgtt gaccgctgtt 34200

atgacaaatg aggcagctac ggtacttgct aactactccg gatattgcca gagttacgaa 34260

aacgccaaag gtcagatgag agtttggtac ggaagcaccg atgttactgg tcagtgcact 34320

ttctctgagg gcggaagaag taacgtaact cctagcatca actcagcaaa tgggaactac 34380

tccgttactg gtatgttgga tgggaccgat attaccgaag gttgggtgga cgttaaggct 34440

actcatccaa aatatggagc aattaccaag cgttttgcgg taactaaggt attcctagcc 34500

aagagctatg agatggttat caccaatacc ttcgagaatg gtaacaaagg ttcatgggca 34560

ggagctctgc agagtgtttc cggcccaaca aaccagagca tctctaaggc gctgcgtatc 34620

acagctagag ataacctaga gggtaggaac accatcccag tagcaggggg gcaaaaagtc 34680

cgtatcagat tctggtacaa cccactagga ttagaggaag ccatttttag agtaggcttt 34740

attgttcacc gcaaagatgg gggcaaaggt tacccctcca gaactgtggt tacgggcccc 34800

gctcctaata gctcctgggc gtacttcgat caagagttga ctctaagtgc taacgatgag 34860

ggtattgcct ggccgtggtt ccagttagat aacaaaactt ctggttcttc attagggtat 34920

atgcttgttg ctgacataca cttcgaagat ctatccatgg atggtgcaga cggagctact 34980

ggtcctcaag gtccgcaggg taacactggt gctacaggtc ctcaaggtaa caaggggat 35040

actggtccac agggtccaca aggtcctgca ggagcttcag ttggtgttca gtggtctaaa 35100

accggcaacg cgagcgattg gcacacaaac tatgctactg gcgacattta tatgcgtcag 35160

caagttaacg gtgtgtggtc ttcggcaatc cgcgcagttg gcgaggatgg gcgggttggt 35220

gctgatggta aatatacctc cctgagattc caagtagctg caactaaacc tgctagacct 35280

acagggaact ctccggctaa ctggtctgat tcacctccag aaggttcccc actctggatg 35340

gttaaaggtg agtttgactc cagcaaccaa cttcagggaa cctggtcaga tccagttcgt 35400

ctggacggtg agacggtcaa cctcaacctg tttgctaaca aagcatggat tgcgtctata 35460

acgggtgcca gtggtagtgg atctgttgta gccaaaaacc ctgacgaact acgcttacgc 35520

attaccgcag gttctggtgc aactgacgcg tataccatgc ctagtggtgg tgatggtacg 35580

ttcttcacta aagttaccgc aggtaagcgc tacactatgt cgttcgacac ggatagtgct 35640

ctggaaatga gaatgcatgt gttctttatc caggcaggag caaatactac tacctcatca 35700

ttctcttgga tagcgtcaac aactgctggc agaactagct ggtcgttcac tgttcctgca 35760

ggatgtgata gggtatctgt ccgtgtgtca ctgaacaaca acccaggtgg aaccaacgtt 35820

gtttccaata tcaagctgga agagggagat ttcgccacag cgttcattag gaacgagctg 35880

gatactattg gtgctgatgg ttcacaaggc ccacaaggtc cacagggtag taaaggtgat 35940

aaaggggaca caggagctac tggtccacaa ggtccgcagg gtccaaatgg tactagcgcc 36000

aaagcctttg ccttaacatc cgatagcctg tcctttagct tcgatactag tggtaacctg 36060

aaatctaatg gtactatcaa gatcgatagc tggagacaga ataccactgc tgcaataacc 36120

tggactgcca agaaccaagc agggagtaat ataactttag gtggcactgc tactaacaag 36180

actataacct ctgctcagtt cggaagctca gagtacgtaa cagtaaccgc gacgtgtgat 36240

ggaataaccg attccattac aatagttagg ctgcaagacg gggtgaactc tctagtcggg 36300

tacttaacta acgaagcggc taacctgtcg tgtaactcct acggttttgt gcagaattgg 36360

gatggcacta cgggtaactt taaggtgttc tacggaacgg tagatgttac cagtcagtgt 36420

accttcggag tggaggataa gagcaatctt aacggcaaca tagggtcaag cggttattat 36480

gcccctagcg ctatgccaaa cgggctggaa attacctctg ggtgggtaga ttataaggct 36540

acgcatccta agtacggaac acttattaag aggtttacac tcaaaaagag cctgcccggg 36600

attggttacg acagagtgtt cacggggtcc tttgactctg gtaacaatgg atcgtgggga 36660

cgtacggtag ttgacatcgc tacgggcagt cccggaggac acaccaaggc tatacagtgc 36720

acctctaggg acaccatgga aagtagtaac tggttcccta ctcgtaaggg gatgcgctac 36780

cgtgtaactg catgggtgaa caactctgag ggtgagtatc agctaaggtt aggcctccat 36840

acccagaact cttctggcag cgttaacact ggttacccaa ctatgctagc cgcatcagct 36900

aaggattccg agggatggaa actagtaact ggtattgtca cggtaggaga tgggtctact 36960

gcggagactg gtagggcaag accatttatc cagatgaatg gtagtgctag ccccttcggc 37020

aacgcttacg tagctgctat agcgatcgaa gacctatcta tggatggtgc agatggggca 37080

acagggccgc agggtccaca aggtaatact ggtgccactg gtccgcaagg tgataaaggg 37140

gatactggtc ctcagggtcc acagggtcct gcaggtaact ctgtaaacgt tcaatggtct 37200

aaggacgggt ctactaactg gcacagtacg ttcacttcag gtgatctgta catgcgtcag 37260

caggtgaatg gatcctgggg tcctgcgatc agagcagtag gtgagaacgg ggctaatggt 37320

acgccaggtt ctaagggtaa ctatgtgagt atgaagttcg ccgtaatggc tagcactcct 37380

agtaggcctt ctggtagtaa tccggctggc tggtcagata gccctcctcc aggtaacccg 37440

ttatggatga ttaaagcgga gtttaatggg gagactaatg ctattatagg taattggtca 37500

gatcctattc gcctagatgg ggatagtatt aacgagaacc tgttctactt taaagcctgg 37560

ttagactcga ttaccggagt tgcaggcaac ggttcatcta taggtaagaa ctacgagtta 37620

ctaagggcta ggataatcgc aggtacagga gttaccgatg cgtataccct cccatcagat 37680

ggatccgcct ccatgttcac ctaccttcct ccaagcacca catatacgat gtctttcgag 37740

actgataacg ctgtagaagt tcgttgtcac gtattttggt acgctaaggg aagcaatacc 37800

actggaggag tgctgaagac tattgcatct actactgcag gtttgagcag ctttaccttc 37860

accacgccgg ctaattcgga taggatatcc gttaggttct cagttaacga atctggggga 37920

aataacgttg taggaaggtg taagattgaa aagggagcct tcgtaacgtc atatgttcgt 37980

aaccagtatg acgctgtagg ggatcgtggt ccagggttct atactcaggc gatcacaaac 38040

ttaaccggat ggaacgatac tcaggcagca tctttcttcc agtcaacatt tggtggacct 38100

ccggttaagt atgacgtact aactcagtat aagtcgggct ctccgcagaa ctcctggact 38160

cgtcaatgga atggctcggc atggacagct cctgcattaa ctgttcatgg tgatatgatc 38220

gtctccggtt ctatcactgc tgataagatt attgcaaaca acgcgttcct ggcgcagatt 38280

ggtgttgaca tcctttacaa tagggccgcc gcactaagct ctaacccaga gggcacttac 38340

acaatgaaaa tagacctggc taacgggtac attcatataa ggtaacaaat gagcacggaa 38400

aacagagtag ttgatattat ccttgatcaa aacgtgtcat acggattgat gctacagttc 38460

atggatatcg atgactctgc gtacccagca acggaaaccc ctgtcaatct gacaggggta 38520

acccttaagt cttcaattaa agactctctg gaatccactg gggtaaaatt agcagatttc 38580

gtcgtaacag tagtaaacgc tacacaaggt caggcgtcgc taggattaac tgcggctacc 38640

gtggcaacaa tcgttagtaa agcaagtaaa gaacgagata aatataatcc tagacttcgg 38700

ttcgcaggtt actatgatgt aatcatgacc aaaggaacag gagctaccgc tacctcttat 38760

agagtcatgg aggggagcgt gtacgtcagt gatggagtaa ccgcgtaatg gctattacaa 38820

caagaattat tgcacaacag gttaccgctc ttgacggagc taactcaagg gtaagtaagt 38880

acccaaaatt taccgtacag ctaggatact cagttagttc tctggctgct acagaattac 38940

tagatgctgc cactagatcg gcagcatccg ccgccgccgc taaaacttcg gaaaccaatg 39000

ctaaggcttc tgaaaccgct agtaaaaatt cccagacagc agctaagact tcagaaacta 39060

acgcggcagc atccgcccaa gtagctcaga atttggcagg taaagcgtcc ctagtaacac 39120

cactaggagt gatgaccggc tcggcagaag ctaagattgc atctataaca atagccgcaa 39180

atcagtcttc tagcgttcac gtattatttg cgctctacgc tacaggtaat ggagccaaca 39240

gggatgatat atacaatatg gagatagtat ccctggcatt acctggtcct gtaacctctg 39300

taaccgcgga caacatcggc agcttcctta gtcatcgagt aataggtccg gccaacacta 39360

atggatttat ggtaggactt aaatctacta ttgagggtag caacgtgacc tatgatgtat 39420

acctcaaatc tcgtagtagt ttcagagacc ctaagatggc attcttatcc ggctccatat 39480

ctgttactcc acctaccgga cctttggtgg acggaacatc ccctgcgtgg aaaactacag 39540

gttttgatac tgatgttatc tatgtaaata gggcgcaagt aattgatgat ggcattagtt 39600

tagcccgcat caaacaacta gctataacta acggtaaaac cgatagctct atacttcttt 39660

tatcctattt aaatgaaaca ggtatactat ctaccaataa gaagtctatt tccctccggc 39720

caggaggtac gagtgactct agtattgcag ctacggagtt tctacctaac gggaatataa 39780

ttctgcctaa tggggatact gggaaccaaa ctattagttg gttaggtggt ccccgcatac 39840

gagtcaactc caacgggtct tttgttcttt ctactaataa tcccagtaat caaactagtg 39900

ggtttataac tttcaggcca caaggtgatc aagtaacttc cactgagctt cagattaggg 39960

atgatggtaa cattaagcag acagctccac agtcatcggc aggcaatgca cttatacgcc 40020

aggatgcggc tattcaacat atcatggata aggctccggc tgccggtatt actgctaacc 40080

ccctaagcga cttgaacgta atacctacgc ctgaaggtac agatccttgg ggagcagacg 40140

gtgtacgtgt attccaatca ggggtatcaa caaaaaatac tccggacgga actactggtc 40200

ggcttggaac tatcctcaac gttaggcaca cccagtaccg tataatgcag ttcttcatgc 40260

agagtaatgc tactgcacct attctgcata ttagatcatt aagggctgat cagggtaata 40320

ccccaccggc atggtttaaa gtttatacag aatactctaa acctaacatt cagtctgaca 40380

tagcaggtat tactatagac ggcaatggtt tcgttaagaa agcctccccg atcgccaagc 40440

tcatagccga aattcctagc aaagaggatt cattcttctg gacaggcgtg gaaactgtgg 40500

gaggttacgt agggtgtaac gcagaggctc aaggtgtatt tgctgtaaaa actggactag 40560

gcaagtatac tattaaaggg agtttaggct ggaacacgga aggatggaaa tttgagctac 40620

caagagatga taacggcaat atgttgtgct tcgtggaatc ggattggaat gaggaagaga 40680

aagagctaaa catacaggtg ttcacccgta agtttgatat taacacaggt aatatcatcg 40740

ctggtgaacc tatggagata ccacaaggtc gttggattga tctacgtctg gaaatgccaa 40800

aagtggaaat accagaagtg gaatttccag aagatccaga agtataataa aataaaaccc 40860

cagtcggagc aatccgctgg ggtttttcta tttacatctt accagaactt ccgaagccac 40920

cttcgccacg atcagtgtcg gtcagactat cgacaatttc aatgtcattg gggttataat 40980

gaggtacgat caccaactga cacagacgct caaagttatc aatcggttgt gtctcgttgc 41040

tcatattcaa caggttcatc ttgatggttc ctcgataatc tgagtcaatc acccctgttg 41100

tattggcaat cattagccga cgtttcccta gagaacttct cggaaccacg attcctaccc 41160

agccttcggg aatctcaacc gcaactccgg tatcaatcat caatgactcc ccaggaggta 41220

tggcacgcaa taggtcggaa gcacgatctc cgaagtaggc ccgtagatcc ataccggctg 41280

cttccgagct tccaacgtga ggtttacaat cggggtgaga taatttaata cgcattatac 41340

ttctcctgtg gcaatagccg taatgtcttt aacaaattga tcgtagatat cttgtcctgc 41400

tgcggcaact gcttccccac agaaacttgg gagatctact agagttaggt tacgttccat 41460

aagttcgcct gatttattca gagcctggac gaatttttga gttcctggga gcggtagtgc 41520

atcaataatg tctagcacgc taccatgttc ccggattagg ttgtagccac gtttttcgcc 41580

gataccttca acaccacgaa tgttatcccc catatcgccc ataatggctt ttaatgagat 41640

aaactgatct acagtatcta cgttatggtt gtcgaacata tctttctcgt gatattcttt 41700

acgagtagta aacgagaagc gggagatatt cggagcaagc agggtatccc agtcaccgtc 41760

tgtggagatg agccagatat gatcgtagtg atgacctatc agctgaataa tgaaagccgc 41820

catgtcatct gcttctactc cgcggattcg gaaagtaggg aattggcttg caataagatc 41880

aaacgcatcg tctaagtatt caaagaattg acgatccgcc tctacttccg cttcggagcg 41940

atcggcgtac ttagcgtctc ggttgcccttatactccggg aaaatattgg tacggaagat 42000

actcttccct ttatccccta gaacgatagt gtgcttcgca tcgtaggagt ttgccaaaga 42060

gttgatggtg tttgcaaagg atgctgcaat aggcttacca ctatctttct tgaagcggaa 42120

gcctaagttc gtaccgtcaa caatcataag attacggcgt gaggcgaggc gttgttctgc 42180

ctctcgtttc attgttcccc aggatttact catttaacta aatctccaat ttcacatgcg 42240

tttaaccacg gctcaaaaag accgataaca atttccattc cacgtttatt aactatgaaa 42300

tgtgctctac tcatgaggtt atcaatcata gggtcgctac tatccagagc gataagccat 42360

tgaccacgat ctttcttaaa gatcagggcg ggtttcatgt tcatttgctc accttcacgt 42420

gcggcttggg cccaccattt ttctagctgg gattctccaa cgtttaggat attgctatta 42480

aatttttcgt ctgcgtagtg tttgatctca aaacagtatt ggctcatttt acctacgcta 42540

ggtggcagat acacatcccc ctttagggag tgggattggc caaaagctcc tgaaccagga 42600

acacgttccc agtccaagga ggtatattta cgcagcatat cacggatttg gtattccgcg 42660

cgttttcctt tctcgcgact atctacggcc attaggcctc caaaattgat aagccagctt 42720

cgtcttgttt aacctcaatc ttatgtgcat acggatgtgt gtgcccgtga gatacgatga 42780

ttgagttcag ctgatcttct tcctgtagaa gttctacgag ggtattaatt ccatccgggt 42840

caatataact tacaacttca tcaaggaaga gcaggttgat attaacttta ctaatcgttg 42900

aaagcaacat tcgaattgct aatagcgtgg aaatattgat acggctctgc tgaccagtgg 42960

agcagttgac catagaagtc ctgttaccat cattgtagat gacaacctgt agcttcgtct 43020

cgtctaactc gaaccctaga gcaaatttac cgctggtcat gatagagaga taatgattga 43080

tcatctcttc aaataccttg acactatgct ccagcttata ccctaccaga tcttttagcc 43140

cggtaattaa gatatctaga tccgctactt cttctgcaac taaggacagt tcagcctgga 43200

tcttatcaaa ctcctgctcg gccttttgaa tctgttcacg cttagcttca tatttcgcat 43260

tttcacgtac aactgattcg ttatgggttc ttgcaagttc taccgaggat ctgccttgac 43320

gaatgctaga ctcaatagct ttgatacgct cagctaaccc gctagcgtct acgatttcat 43380

cctgcgttcc attgacctca tcaaattcct tgaggttttt gcgagcctgt tccagagcgt 43440

taaacttaga gatataatcc ttaaacgccc tatcttcctt cctaagttct tcaacttctg 43500

cttccagctt ttgacgttct ttatagagcg gatcatactc ctccttagtt cgtctcatag 43560

cttcttgggc ggcggaggta tctaagtgag ttccgcacgc agaacactga gttttacctg 43620

cggcattttt gaaatcgtag taacgtttct tcaaatcatc cgctctagtt gccacgaccg 43680

ttaggttacg cgtaacactc aggagttcct cagatttcga ggtgggcgca ggtaaatttt 43740

cgaatggtgc aaaagttttt tcggcagctt gtacggccat gtccaaagag ctacgttttg 43800

caatactggc tttttgcttc tgagccagtg ctaccttgac ttttgcttcg gttaattctt 43860

cgactagtgg ctcttcatcg aaaacaggga ttgggatctc tgattgaggt gcgccaagcg 43920

aggcttttga ggaaagtata gattgggcag ttcgcaggct accttccaat ccggacagtt 43980

ttgccgagac ggctttacgt cccgctttaa cacgttcaga aacttcctta tattgttcct 44040

gatcaaacag gttaacgagg aaagtcttgc gctgagcatc cgtagtcttg aggaagtcga 44100

gactggatcc aactgactga tatacgagct tagtaaatgt cgtaaaatca caggcgagta 44160

cctcttctat cagcttatac gtttgggttg cggtgtgtcc gctgatatct tcaccgtttt 44220

tagtgagagt tactttggcg gttgacttca caactttctt gacgttgtac acgtcaccgt 44280

cttttgtgaa ctgaccttct agcgtatagg ccttggagcc agtatgccag ttaaacaggt 44340

cgtccttctt gataccacgt gagttcttat tataaagaag ctcctctaga gctgtaccaa 44400

ttgttgattt acccagcccg ttacgcccga ttaactgagt tacgcggtga ttatcaaatt 44460

ctatcaccac gttctcagca tatgacataa aatggctgat tgtcaattta ttaattacta 44520

tcgacatact cagcggctct ctttaatatg cgtgttctag acgcttcgtc tagtttctgc 44580

acgtttgtga aataagtatc cagctcctgt agcagtgaca tatcgtctag atctaactta 44640

gcatctttgg tgacacggtt attgatcttc ttatctaaca gttcgctgtt ctttaacgtt 44700

ttgagttgtg atacgtcgcc ggtgacttcg tatataactc tgtcatacgc atcggcttcc 44760

attggctcgc cgacttcaat agtttttcgt atgagctgtg gaagatctcc cagttcaatc 44820

cacgaaaggt agtgctcatg gtctcttggc aagaccgtat cgatgataaa agctccgtta 44880

gttccttttg tcctttctct gtgaaacgaa gttgtaagcg gagatccggg atagagcagg 44940

tcaacatccc cgatcttttg gctgttcttg tagctgtgga gatcgcctgc aaatactttg 45000

gagtacccat gttcgacgaa tctttcgagg tagatttctg gtacgacatg aggcgggatt 45060

gcacctctga catgcgtgaa gcaaatgtct gaaactctgg gcttccaact agctttgtga 45120

aggctgctgt aagggatgat atcgaactct ggagatcggt agtctttgac gactttccaa 45180

agtccatctg ttgcgtcgct aattgctgct gcatagtgat ccaggcaaga aatcgtttta 45240

gatttcattt cgtggttccc ggtgtaaata ataccaggat gttggagggt agctaggaat 45300

gcaaacagta gttcaacttc ttctgaagac gggtctgaaa catccatgat gtcaccacca 45360

ataatgtgaa ggtcacatcc agtagctcca aacacttcgt ccagcttttc accgagaaga 45420

ataaaccgat ttttctgcca ttcctgagga acgttcttcg ctcctagctt gatgtgatga 45480

tctgctgaga aaagtatttt catagtcaaa ataaaaggga gccgaagctc cccttgtttg 45540

gattaatcga ggtcagaagc tgcttcgtga tcgatgttac cggagttcgc ggaaccttca 45600

ttacctttag attcgtcgcc ctcctcatct ttcttacctt ccagccatgc ctggattgct 45660

ttcttctgct catcatagga cggaaccggg taggtaacat ccagtttagg cacttttttcg 45720

aagccttcga attcgtctgc ttcgttgtac agagcctcac caatcagagc aacgtcggct 45780

tcatgcaggg cggcctcttt agaacccggc tgatttttag ccatctggaa ctgcattgca 45840

gcgatctgct gtacatcgta cttggtatcg aagccagtac cagatttgga gatagtgata 45900

tcgatctcac ccggatcttc cagattcagc tgggccatga tggagtggat accggtcagg 45960

atggttgcct taacttccat cagcttcagt ttgttatcag tacgatcgat aacaacggcc 46020

aggtagtttt tcttaggacg cagcggctga gccttaccat ctttcttctc cggatctttg 46080

aagcccatgt cgtgaaccgg atcggatgct ccacggatga aacgctcttt ttcacggtcg 46140

aaacgcaggc actcgaacgg agccggttta ccttccttat tctgaatcca gtacacataa 46200

cgcgggagaa cgccggaaac gatacgtaca acgttcttac cgttgttgaa cttcatgtag 46260

tccagtttgt cgccgttaga accgccagta gtagaacccc aagatttagt agccatattt 46320

aattttcctc gataaatgtc aattttgact tgttgattgc gattagtggg tggtgctcga 46380

taactgctct aggaacccac ggtggaatat attgcatatc cagtgatgta tccttcgaga 46440

agctatattc ggcatagttt ctaaaactca aaagtcctag atactcagcc aactgtcggt 46500

ctgacagctt tcgtttatta taaacgattg tatcttcgtt caagataaat gatctacccg 46560

ttaacataac atgagcttcg ggatcttcaa ccattcgtct gataatctgt acaatcagcg 46620

atgagttacc tcgtgctaat atgtaaattt tttcgtaatc ataaaacaac atgattatta 46680

tacaccattt tgagagaatt tagcaactaa gtttttattt ttctgcttcg gactttccga 46740

agattcagtt gctgttccca ttaatttata cagatattat atcgtatttt tgaggactca 46800

gcaactgaaa tttttaacta tttgcttaac tcttctttgt aaatctgtct ctcagttcaa 46860

tataaatatt atatcaaact ttggggttct tagcaaacag aattttatct aagtttgcca 46920

tattcttctc gttaaagtca agaacttccc acccattgag acgatatacc gcttctctac 46980

ccgccgcctg cttaaatcct acacctccta gcttcagatc cacgaggatt gggtctaact 47040

tatcatctgc catacgttgg acacgacctg ccaactgttc gattagagat tcgttattta 47100

ttaaagagcc taacactaaa cacgataaag catttaatga tacaccctcc gagaagatgc 47160

tttgggaagc cgctaacaca cacggaccgt cattggtcac gtcaatctgt acttgctccc 47220

tatcatcgag cgaagttaca ccggtgatcg tgtaggtctt cacacccctg agttccaaag 47280

cattcgtaac tctctcaatt agatctatac gatcggacac aaacaggact ttatggcctg 47340

ccatcgaata tagctcgcac aagtcaacaa cctgttgaaa gtattctggc tgcgaatata 47400

catcgttagc tcttatcgcc cacggcacat tcatatttcc agaaacctgc gtttttagcg 47460

caaacctatg gatagtaggt ggcatagtgt tatttaccgg aggactatat actttcgttc 47520

caaaatagtc cttaaacata acctgcaaac catccttacg ttttaatgta ccggatagcc 47580

cgattttata tcgtgccgaa gactgctcta gaaacttggt aaacgtggtg gcaacgcagt 47640

gatgcacttc gtcaacaata acggtgccga attcttttgc caaagcggct ccgtgtttgt 47700

taactgtctg tatattacta ataacgatag gagaatcgat attaaatttg ccagacccaa 47760

taactcctgg ctcaatccca aagaacttgc gtacctcctt ctcccacata gctcgaatgg 47820

tagtgttggt acatataact aacgttttct gcccaagttt atgggcgata gcaagagcaa 47880

ggattgtttt accgaaccca ggcttaccat taataataca cgtatcatta cagtcttcat 47940

atatagggag ctgatcccct ggtcgcaggg tgaacgatgg ctttggaata tccataggaa 48000

ccagagtacg tttatctacg atctctgtca ctttttgccc gaaagattct agaagatcta 48060

atctggttac gggaaaccac ttgatctctt tacctaccga tcctgagttc tggaacatta 48120

gaggatactt tgccccaggt ttaaagatct ggtatgaagt gtgttttaat aagtattccc 48180

acagttcgtt gctgggttta caatagattt tattagatat aactatcttc atatcttaac 48240

tctaagtcta ggagtttctg gctcctcttc gtgcgtgtca aaaataactg gtgaaccgcg 48300

aaccaacgcg tacgaaatat agttggcagg ttcactaagt aagaaaggat atggaacgtt 48360

cttgacataa cactggtact ttccgttgaa gattctagtt gatcctctaa cgcgttccgt 48420

gataatgttg taataagtcg taggtttcca tgttactatc ttacctgtgg agtcgatgaa 48480

atgctttagt ccagagttta ttatctgaga taagtacttg aactgtttct ttaaaggata 48540

gagcttataa ggtaaatttt cccgctcacc ataaagaaaa agccttcgct gagagaatgt 48600

cccaggaagg cttggattgt ccagcacata ccttgtaaat ctcgtctgga taacaatgta 48660

ctccccctct tggaagagta catcataagc ccttaaagca tatactggta agctaaagtt 48720

aagcaccaag aaccctgcga acgttgacaa tatctttgct gatttccggc aaaaacttaa 48780

tattggcgta cttatcgtga tcagggtggt tttcatcgtt agccgcaata gcagcgtagt 48840

cgaagtcctc cataccgata atactacgta ctttctcctc aaactccttg tcctcaatgc 48900

aagcaacaga aggacgctgt ttcttgatct taccacagga gtaatcacga gaaccgccag 48960

cctcggagtc agagtcgata ccaataggac agcccggaat actaatacca cggtctacct 49020

gaatgttacg gattagcatc tcgttatact gatcaactaa atcctcacga acaatggcaa 49080

ccacggagtc gtgaaccagc atgataatct tcatttcgtc ctgcagaccc agagagcgaa 49140

tctcattatc ggtatcgata gcgcctagca ggagactatc agaagatgca gactgaatga 49200

tggcgttgaa accagaacgc agttcttcac cctgtacacc acggtcttcg gagttaatgt 49260

tgtgcagacg acgcttacga ccaaagtggc tgtaaatgaa gccgttagtt tggatctggg 49320

catgagattt atcgatccat ttcttaagct gagggaatcg gccaaagtag gtttcgatgt 49380

actctttcgc atcaccagta gtacattcag tgtacggttt accggtcttc atgtgctctt 49440

ctaggagagc ttcgtttact gacgctgcta ctttagccgg gccagaaccg taaagaatac 49500

cgaatgaaat agcttttgca gcctgtcgta gtgcaggata cagtttttta acctcagtcg 49560

gtttacacgg cagagcaaat accatgtgtg caattgaacc gtggaagtct gagtagtttt 49620

ccgggtcgtt ctgcatgttg ataaacactt gctgcatgtt aatgtcacca gacagtacag 49680

cggcgtagta aatctcagca gttgttaagt cccatgcgat aatacgataa cctacagggg 49740

caacaataca acctttaata acagactcat cacgaggtaa ctgctgaagg ttcagcttac 49800

cagacgaact cagacgaccg gatgtagtca tatggatatg gaatccagta cgaatgcaac 49860

cgtcagcatc aatactgatc agcatcttct cgatatacgt cgagagcagc ttggagatct 49920

tacgaatctc tagcagagtc ttagctatcg gatgctggtc cgaaagctct ttcagggcat 49980

ctgcgccggt ggaatctgca cccgtatctg tcatgatacc cgtcggggtt aagccaacat 50040

aatcgaacag gagcttacga agctgtacaa cagaggctgc gttaaatact gagccctgat 50100

cttcctctag cttacgaact tctggatact catacagctt agcttttgca agctgtagcg 50160

cagtcattaa ctgaacctga gcctctttca gacgatcttt ggagatcggt acaccacggt 50220

cttccatacg ctgtaggaat acacatcccg gcatcagtac atcgtaatac agagacttca 50280

gtcgagggtt agcttcgact tttggcagga agaaattgga tagacgcagt gttgcatcgg 50340

tatccttcgc tgcgtaaggc cacatgatat caaacggaat gagatcatac gagaaatcct 50400

ctttcttgat cttatgcgtc ttgcaatacg tctccttgaa ctggtcgagt tcaaaatcgt 50460

agtcccccat atcggtatac ttcatcgcca aagatttcaa accgtgtgta ccacgtcgtt 50520

catctagggc gtagtgcatc agcatggtat cgtggaggcg tttctcttct gctgccttat 50580

caaaggatag acctaagtga tagcagtaga agtgcatatc aaacttcaag ttatggaaca 50640

caacgccatg ctccgggcta tcgaacagtt tctgtaagta atagacggta ttttctgtga 50700

tgacgtctgc atcaatatat acgccctgat actcttggtg ggagattgag atccccagca 50760

tgtaaccatc tcggcagtat agcgcactgg tttcggagtc atatgcgatc atgccaggac 50820

acatggtata caccatcttc acatacgctt cggcttcgtc cgggcactga atcgggcggt 50880

aatcccctgc tttagagcgt ttttcacgac cattgagaat ggcatgaatg ctctctactg 50940

tggcttcaaa tacaggcttc atttccggtt taaagtggag ctgggccgga ctgatacttg 51000

caatccagtt agcataccca tcatgctcaa cacgtttacc tgagtaatcg gaaatgccct 51060

ttttagctgc aaacttcaag aacgggtctg cacctaccag aataacgtaa tcaaaatctt 51120

ccggattgaa cgggttctcc ggtgttccga tagtgatatg tttcttgagc agtcgcccgg 51180

ttactttctc actagccatg aagaaggtct caacctcatg gtcaaagagt tcgaagtgtt 51240

tctgatagcg gacgttattc ggtgatttgt ctacaactgc gattttcatt gatttctcct 51300

attaggtaag caagtaaaac gtcagtgttt cttctcaaac ttacccaatt attatatcaa 51360

atcttgacat gttcagcaat caagatttct acgtttctga tgagttggtc gacttcttca 51420

gcatctaggt ctccagggtc tttgccctct ggaagcaaga agttacctat aattggtata 51480

attctagtct tatcacggat taatttggcc aacttcttag ccgcctcatt accggactta 51540

tcattgtcca atatgatgac tacgtgagta gtaccggcga tttggaacgg catgaattta 51600

tctgcaatgt tatctagtga gaactggtga gtaccaaaac aacatgaaac gttatggcaa 51660

cctttatctt ctagattcaa catgtcgaat ataccttcga ctaggattag ggctggggtg 51720

ttatagcgaa cagggaagat tgggggggag accttcttag gtctaatcat atatttcgga 51780

ggggcagagc tatccatatt acggcctaag aagaataagt ttctccctac ggcatccgta 51840

ataggaaaca ctacacgacc ttcccagtcc tctgtttgtt ggaatgcaaa gtatttcttg 51900

aaagtctctg ctttgatacc acgaaagtct tgatcgaata tcatggctga ttctggaatt 51960

tctagactgc gaccctcagt tcggaggtca ctaatcattc tgcgaactct caggagtcta 52020

ggcgacgtcc tgtactgttc ttcattgaag taatgaaaga tgcttggtat accacgacca 52080

aatccgcagc ttaggcagtg gaaaaccccg gaatcggggt caacacgcaa actaggatga 52140

gcatcctcat gatcaggatt gagacagcgg atgaggatgt ccccacccgt atctctgtat 52200

tcaatccctt tgagatctaa aagctcggtt attctactca taagtctctt gaggattctc 52260

cggtgggatt agtatcctca tccgaagcct ttttcctttt tggtttgtct ttcggtttat 52320

cgctttcaag tgggataaca aactctgctt ccatctgacg aatgtcctct agcttaaggt 52380

cagaagtctg atccatacgc agtgagttcc agttgatctt cggcatgaat gtcataccct 52440

cggagttacg agtttttacg aagtcgaact tgattgcacc gtcatgcccc tcgttctgtt 52500

tagcagcatt taggtttgca gccatatcac aggaatcgag aatacctctt gccatacggg 52560

cgttaccctg ttggtcaatc tggtaagggg ctacaccagc aacgttatgc ttttggcacg 52620

tagacttgaa tgtagaggag acaaccatct gctgcttcca atcgtacata tctagtgtct 52680

tcgtatccgg caaacgtacc tggttgatgt agtctagcag ggcgattgtt accttatctc 52740

catacttgga ggttagctta gttagttcaa catcgatggt tgctgtacta agttccggat 52800

catacacaat gatcatcgga gtgtgcaggg gtctttcctg cattagcata gtctccatgt 52860

catggaaatc actcatctcg ttgagcgtat aacgtgatac aaaatcgtta tatacttcca 52920

gaccgccttc aaacattttt gcacgagtct tcgcaagttt gttgagttca ataccttgta 52980

aggagtcatt gcgcatagcc ttagcggaaa caccggccat aatggctagg ttacgtctaa 53040

agacctcatt ctctggcatt tcgatggaga aatatggggc gatatccccg ttgtaatatt 53100

gggctacttg aatgttagaa cagatgattg atttacctgt accacgccat ccaccgagta 53160

gcagtgtttc ttttctggca attccgccaa gttgagcatc aaattcgttt gagatgccga 53220

gagagataag atttaacatg gagtcttctt ttctcttgaa aacacgcata gtatcggcgt 53280

tgaagacctt accagtcgtt gttactcgtt cctctagctt catgtgcaga gccgctactc 53340

gatcaagtaa ttctccctga tccagtatgg taatatcctg caacacatca gtttctagca 53400

gattcaggaa tagatcctgt gtgtattccg actctaggac atgaatcgca tgcgatatgt 53460

caacgtctgg aatctgagtg tttgctaaaa cagttagtgc ttgagacaac cttgcgtttc 53520

tgttagactc tagcattaga gcatctaacg aaggcattcc gttatgcttt ttgtaataat 53580

tctggacagc ttggtagatc gcggtaaatg cgtcattgaa gtgatctttg cgcagtctag 53640

agaatgtctc tagggccacc tgcttttgat cggaggctag gagcattttc aaaactactg 53700

cttggacgtt atacataaga tactctctac gccgcgttag cgtctactta aacgaaaaag 53760

gggagaggaa caaaattcct ctcccctcag gtcaaatcaa ttacttggcg gatttagcgt 53820

caagtttagc gcgcttagca acaccatcgt gatccttagc agagatacca cggcggctca 53880

gcatagactt aacaccacgc tcggatttac cagttgcttc tgcgatctca gcaacggtca 53940

tatcggcgat attcagacct tccagaacgt cttcgcgtgc cttagcatta gagacttcct 54000

ggaccggcat agcttcgata cggccttcac gcagcaggct cagagcttta ccacggatct 54060

gcttaacggt acgttcgaac tgagcagcga ttgcttcaac ggacgcgcca ctggcaacgg 54120

cattaatgaa agcagcttcc tgatccgggc taaagctacg tacagcagcg gccttttcag 54180

tcggcttaac agccgcagtc agttccaggc tcaggatttt accctgtact tgtttagcgg 54240

tataagcacc accaactaca gcagcagcga tttcagcgta ggtatactga cccggatgat 54300

cgttcaggaa tgcaaccagt tcatcttcct gacccggagt ccacggagat ttggttacgt 54360

cggatgcttt ctgtacttcg aagccttctt tacgcagttt agaaccaacc gaacgggcgg 54420

taacttcttt accagtttca gcagccagtt cagcagcgat gttagcaacg gcttcctgag 54480

agataacggt cgcgttcaga gcgttagctt tagcggtcag ggatgcagtg atttcttcgt 54540

tccaggttaa tttagccatt tttatttatt ctccagtaga attttaatcg tcaagacttc 54600

gatgcccagc gattgtgctt ttttgtatga agaagaaccg atcttggttt catcttcgca 54660

gattaagtag tttacagcct tagtcacgga ggttttcacc gtatacccaa gactttccag 54720

atatttggta gcgtccgcac gatttttgaa gtcgttgagc ttaccagtaa tgcaaagaac 54780

aactccgttg gattcagtcg ccggggtaac ttgagcttcc cgcgccccac tgaatttcca 54840

tggtagatta attacgttct gtcctgccgg tgtattcttc cacgaagcta agttttctcc 54900

agctttacct tccgctttca cagattggaa atcgttgtaa agctgggata atttcttagc 54960

agcaacttca ccgataagag ggatactaag agatccaaga accgaaccaa agtcaacatc 55020

ttgtctcagc ttagtttcca actctagctc aagtttcgtg gcgactttat cacctacagc 55080

tctgaccaaa tcttctttag tcaggaaaaa gagttctgaa actttcgtga tttccagttt 55140

agcaatcgtc tgtgggccaa agcccttaa cttcatcttt gagcagaagt tctcgattaa 55200

tttactgctt tgagctggac acatagactt gttacggcag aacaactgat cgttaactaa 55260

gtccagtttc gaaccacaag agtggcaatt cagtggaatt tcaattttca ttgattttct 55320

tcctcatcaa tttatataaa tattatagca agaaaatcag gactaagcaa tcgaaatttt 55380

tcagaattta gctcagtctc tcaccaaata tttctttccc tcaactgaat gataatagta 55440

tacaccctgg cgatgaaaat gtcaataact actttaaaaa atcatcacgg tgtatctatt 55500

gaatcaagtg ttactcgtaa acacgttcta cgatgcgagg gatgacccca ccactacgaa 55560

ttacgcgaat ctggcaaccg atttctaggt caagggcagt gatataacca acgttattca 55620

gggtagcttt tgaaatgaca gcgtcgtcga tgactaccgg ggtgaagtat ccgacaggag 55680

taactttacc ggaagcccca acttgccatt ctacccgttc gagcgtagta acctcgcctt 55740

catcatcttc tttgatggcg tacgcaccac gcgggaactt gttagtccaa cctgctgcgt 55800

taaattggtt gttgccatcc atacgaacca ccacgccgtc cgttgggaac caatctactc 55860

gactggagat atccagacag gtaacaaaac catcaccctg gaggatatgc atatctccac 55920

agaaagtagc ggtcaggcca actttgccgg tttcacactg aatactatat gccgtgaaca 55980

tcaggccacc ttccgcaata cgggagagaa actctccaga atctttcagg ttaatagcac 56040

cagaggcgaa gttacgcata ttttcaactt ctttggtgat gtgtacttca ccagtaatct 56100

gcaccggagt cttttgggag atccgtttag ggatgttcag taacttcaca ttatgagtta 56160

catcattacc taagacgccg ttaccacggg ttaacgcaga aacgaacttt ccgtcaatat 56220

acagaagtga aatagcacag ccatcgagct tcggcgtttc aatgccctgg aagggtactt 56280

cttcgccgcg gcctgggtac actttctgta gggagaacat acggaatagg tgaggtacat 56340

caccttagg gccaatttct tcctctagcg gaaaacgacg gattaaggca tcatactctt 56400

catcagagat aatcgacatg cctttgtagt acgcgtcttg gcacagctta ataaattctt 56460

taacgtgttg cattatttgg cctcgtagta atcgaacagc atctgagtct tcccttccca 56520

gtaaaagttt tcgcataccg cctggaaggt ggacattacc ctacgcttag attttggact 56580

gtacaattcg catactagta cgttcttctc ataccacatg cctagcatct ggaagcctga 56640

cattgtccgt actacaggtt tgcccttctc tttctctaac caggttagga ctagctcctg 56700

accctgaagt ggcgggctgg agtatgcgtt aagcgttatc ttttgcattc tttaatgcct 56760

cgttaacaat tctagacatg tgtgctctca gctgttgagt gtgagcatac gtcttagcag 56820

cttcggtcag cttattaact aattgagcga tttcatgatc tttcataaag atctccttta 56880

aactatgaga atattatatc aaggtttaaa acactaagca attgagattt taaagaaaaa 56940

gccagcaact tagtcgtcac tggcttgggt cttttgagat tcacggtaaa cttcatgaag 57000

aacctctgaa ttgcttagta ttttagtaaa tgcacggaat agcgtgctgg tcatttctaa 57060

cgtgtacggg aacgagaagc ctgatttagt agggaaccag ttatcttcaa tatctagtaa 57120

ccataatcgg aaaccaaagt ataaattgcc tctaaactcc gagacagtca tacgaatctg 57180

tcgcccttca tcttcaaaga taacgtggga ctgatcatca atatgtcctt cgtaatcctg 57240

acaaatgttt tgattcattt ttattgttct cagataaaca aaaagccccc gaaggggctg 57300

attgcgtctt aacgacctac tggagtagct cgatcaagtt cttggttgag gctggtgatg 57360

cgcttaatat tcgcaatcgg aatatagcgg aatttatcgc tagagcggct aaagaccagg 57420

atatgatctt tgtcagcggg ttccaggcct tcacggacga ttcgctcggc cagatattta 57480

tcttgcttag gatcgaactc agtcgtaccg tagaggtaag ttacccccttt ggtacgcagt 57540

ttggtgtatt gcatgcaaaa ctcaccgtgt ttctcacaga tagctacgac ttgtgcttta 57600

ttcattgcaa taccctctta tttagtgatt ttacggatag cttcagccag gtgagaggca 57660

gctttaccgg tcagtttgtc aacgatcgat tcgtccagga agccatcttc cagtccagcg 57720

tcgttaaatg cagcgcgcag ttcagcctga gcatcagact tagaagtacg gccaccagct 57780

ttaggggcat caccaccagt tttagcggta gacttaccag cttctttctt gacgtatacg 57840

ccagctttgg acagcttcat acgaaggccg ttcggggaaa caccgtgctc tttggcgatc 57900

tcagctacga tctccatgga aacgccagga cgctcatctt ccgggaagag ttcgattttg 57960

gcgacgtagg cagaagtcag ttcagcttcg agttcaggag accattgagt tggagtagac 58020

atatttatta cttccttatt tattgttaaa aagagttttt aagttttgtt tcagactatg 58080

agaatattat aacaagttac tgagctgcaa agcaaacaga attttctagg atttggttaa 58140

cagctaccaa accattaggg gacaaacgat acatcttcag caaaccacga tcgtatttgg 58200

taagccagcc attatcttct gcttcgtcca tgggaagtgc atagtgcaga tcccggatag 58260

ctgtagcacc ctcggaatag atctgaaata agttcaggag ttgatattta ctcaccttta 58320

cctctctttt ctagtttcag ggctgctttt acagcgttat taaccagttc agctacgtct 58380

tctttacccc acttgaaccc cagggacttg atatcaacac caagtgctac cagatgttcg 58440

acagacgcca gatcccaata catgtagtta acatactgct ggcgggcttc ggacagcagg 58500

taaacacgat acgcgcctac cggattatcc agagcttttt taacttcgcc aatacactga 58560

tagccaggaa cccaaacgtg ttcgcctact tcgaatacct ctttcattga ttcttctgga 58620

atcgcaggtg gaaagagcgg gtcaacctcg ccattaacac gaagcagagc accgtgagca 58680

gacagaacca ttctgatcat gtttgcggaa cggtagaaac gctcggcaat tgcctcaaaa 58740

ctatcacctg acaggtacga atcgataacg ttggccagtt cagccccttc gattttagta 58800

ccacgtttct ttttacgcat ttcagcggaa acacgctggt tatctttcca ttcctcgata 58860

aggcgttcca tcgtggagtt agacgctacg ccgaggattt cgcaagcgcc tttcttggtt 58920

ttgccttcct ctagccactg aatcgcttcc ttaaactttt cgtccgggat gctattagca 58980

tgaagttttt tgcggattgc catgttcttt atcctctctc gaatttatga aactattata 59040

atacagattt agcttctaag caatcgcgat tttcatagaa cgtagggtcg aaagtaacgt 59100

gcatgaattc agatagactc ttgtacccca tgttaagttc catgttgatg cgtatagaaa 59160

ggcgtgtctt tcgctgagcc tctagccaat catagatatt tggcatctgt gctaagcgaa 59220

taggtattac tctacacaat tctatctctt tagctttccg tgctttcgta tcgcgtttgg 59280

gaaacttcct tgtttcccag cgggcatcac gcttgctcat tacgtactcc aagttcgttt 59340

tgcgcttcat cggccagcgc cttctcctcg tccgtcataa actcatacgg tacagagata 59400

ccctcgatag aacagtacgt gcgataccag tctacgatct gctccgtctc catttcctta 59460

ttaataccca tttgggttaa gtacatacgg gcatatttag ggttggcaga ctgtcccgtc 59520

ctaataaaga agtccttctt gtgtttcttc agggcttcaa taaaggggct aatcgtcacg 59580

ttagaacact tcttaatatc cttccagaat atatcttgaa gtttatggaa gaactccgcc 59640

cgcttgtgtg gtttcttact aatccacatc tccgcatgtt cctgtgtgat actcttgata 59700

gagtccaggt ggaagtactt gaccaacatt agcttggctt cgtatgcgtc cgcatgacgt 59760

ggtgcacacc aatccggggt actactcaaa atagcagaga ctcgttcagc agtatactct 59820

gcggccgagc tatcaatctt accccagctt tcactgaaga tatcgatagt tgctccctga 59880

tccagcagat aataccgcag agtactgata aagttacggg actctagttc acgacgttta 59940

acatacagct gctgagctaa ttctagccaa ccctcatcga tgttatactg ctccgaaccc 60000

gcagagaatc cgctggtgga cttatcgatg aaatagaaga tattcttagc tccccggtcg 60060

cgcctgattg cctggaagcg catgtttggc gcctggttag cggtacgagt aataacgaat 60120

acgttgtcga agtaattaaa gtcaacacca ctcgttactg acggactgca cagtagacaa 60180

tcaatctgct gttcaattaa ctcattcgtt gtataatcca agatacgacg aatatctata 60240

tcagatgtag agtttgagtg aatctcttta acaatcgcac ctgtattgtt tcttagcgtc 60300

aggcctttct cgtttaactc atccggccca cagtcggaca ccagaataga tttctctccc 60360

atctctaggg acgtttggag ggcaacccaa atactggatt catcagggaa ctcatacgcc 60420

tgagcatccg agagcatctt acgatggtgt ttataataag agaccggctt gtcaaaatct 60480

atgagagatc catatgcctc aatggtttct gcgctgatat ccccgtcaga caggataacg 60540

acttttgcag atagcagaat ttcacgaaga actgagatac actcacgacg ttgtttaaca 60600

actggagcaa ataacaggtc attcataact gcgtcgcact catcgataaa gataacatcg 60660

atctgcccaa caaagttttt aaacttgtgg attgagtgaa tagtagtaga catacgatca 60720

atggcaccgc gcttgaagtt taacatatct acggacttat catactgtcc ggcttcaaac 60780

ttcttagcgt tagatgaaac cagggcacgg gtgttagtaa ctgcaaggaa attacctttc 60840

agctgatcac gttctagcca cttcgtcact gcggtggttt tacccgtacc tagagaagcc 60900

ttgataaacg ttaaatgccc ttccggtggt ggacggttga tcttcaaata attcatcccg 60960

tctgggctat cagaggtcaa cttgtgtaca ggaacgcctt taacattcga ctcaggaata 61020

tctcgcatcg agttgttcac aaacgctttt aatgcctgct tacgaccgtt attgaagtaa 61080

tcctgaagac tgcgggaatt atccttcgtg ttgatataat cggacaaagc tgaggtaatt 61140

tctttctcaa gccaggcgaa atcaacaccg tcctccagag ctctgtggta cagtttagga 61200

ataatacgca gataaacacc atcctctgct tcttccagct ctgcaatggt ttgttccact 61260

ttctcagagg ctacgcgctt gcctttaatc tgattaagta gggatagaaa ctcttcttta 61320

aattccccac gagtggcttc ataatctggc atagtattgg gcagttcaat cctagcaccg 61380

ttaactttaa ccagacgtgg cttaccctcc gctttaaacg gatcggtaaa ctgatcccgg 61440

aaaatcgggt cagcgaaata gtgtagctgt acagatgaat aataagctaa gtcggcaata 61500

tcaaaaccat acttctgccg agagctatca ttgagggacg taaatagaaa ctttaactga 61560

ccctgagtaa cgggaatatt actctctaat agcatgtgca tacgaatccc cggcttaatt 61620

ccagccgaag acgacgcatg ggcaataaac cctgcgttaa gcgggaacat gtcctcgctg 61680

atgctattta ataacttaat gacatgacgt cccataccca caatgtcaaa cctgtcgcat 61740

cctccggtat cagagattcc atcgacgtcc atagcaataa tattgctctt atggtcgatt 61800

ttgaagttag tacgtttacg acgcacggcc ttctctgcaa ctaagcatgt acctcgtact 61860

gctacgagat gtggatcttg agtgagctga accatcagct catacgcttc attaagattt 61920

ttggggtcaa ctgtatccac tacgttaaat ttgtagggca ttgaggctgg cttaccttct 61980

ggatgctcgt tagaaaactc cttcgcaaaa aggtaatcag ttgtcttcac ttccttccag 62040

tttccggaag cgggatcgcg ggaaaaaccc gcgtgtcctt ctagaataga aaacattacg 62100

ttttctccta tgttgaagaa taaagcgatc tcgaactatc aaggatagaa cagcttaaaa 62160

gtccactgac tcaacaaatt tccttataga tggaggggtg gtcacttcct cattgctaga 62220

actggccgct tcgcacaact cccacacagc atgtaatcgc cgctaagctc catgtggttg 62280

acccctattc gtcgctattg cgcagaggta cgttgctact tacagcttca cttcttggtc 62340

atttcagacc gcggtgctat ttgctccaca tgactaacga acaaatatct gagagcctcg 62400

cgatgccaac ctctcttacc cgcattctag atcaattatc tataattccg ttcggaatca 62460

atttcccaat aagccaaacc caaccaagca tgtagcagcc ggactgttct gtatgctcgg 62520

aagtgaatga gaggaattat gtcagttttg taactcacat catttctctc aacctatgaa 62580

tatattatat aaaaatcgtg gcgagattgc aagtaaaata tttaaatacg tggtaggtaa 62640

ctgggtttaa gcatagaaaa gaccagagga taatcccctg gtctaagcgt tcaactaggc 62700

attccaaccc ataatattaa ttgagttaga agaggcattt tgtttgccct cacgaagaac 62760

ctctggagca tacgtccaag gctcatcagc taccaagaac cccggagaaa tacctgcccc 62820

cggttcccgg aatgctgcaa aattagaggg gtggaacaca acgttgttca ccagaaccat 62880

tagccccaga tccgagaggt catcccaatc aaagaggatc tcataatcct gggccaaact 62940

acctttggac aaaccaacac acacgtcatg ctggatgatg aagcaaagct cctcgtccct 63000

caacgcggct cgcagcagat tctctgctac atcaatcaat tccttgggga tatccgccca 63060

ggagatacgt tccattttag gaatactcat ttagttaacc cttcaacttg gaaaccgaag 63120

cgacgcagca cctggatcca accgttaata ttttccggag cataataatc ttcattacgt 63180

ccgacccaaa tacctgctga aacacctgta accccaaccg ggatatagga ctcacgcagc 63240

agacacacgt agcctagtgc aaacaccagc cccatctcag tcagatcgcc ccagtctagg 63300

acttcatctt gatcttcgtc cataggaacc catagcccca ggtgcatgtt gtcataatcg 63360

aagtagacct ccatattatc gcaccacaca cgaagatggt ccagcagaga ctcttttacg 63420

tccagaggaa tttcagccca gggaactagc ccaacccctt gattaacaac cttttcattg 63480

accagcatat tcttccccca tttggatgaa ttcgtgccac tgctcagagt ccgctcgtaa 63540

aacctgatag tcgtccgata ggtgactcat atcttgtaca tcactgcgat aacaccaact 63600

accgttgggc cataacagga tatcatcggg atggtacata aattttctcc tccagccaag 63660

cctcaacttg acctatgaaa tgtttgttgc taaatacatt ggcagcagta tcataccaaa 63720

cggggatccc gcgttcttcg tacaaactct gctccaggta gttaataccg ttgttcacta 63780

cccacacctt agtacctcga ctatgggctg ggaatagttc ccaattaaag tcgattactt 63840

ggttactagc accaacaacg attaccagat cctgggttgt cagggtatca aacaggttga 63900

tctgccccat ataccacgga gcggtttccc cgaagaacgt aattgcaggc ttaacccact 63960

catacttacg gtaatcaacc gcagtgtacc cgatatcttc cacgatcaca tccttacctc 64020

ggcgatacat tatctccgta aggtagccat gagcatggat cacatcatca tggggaatgc 64080

cagcacgctc tagtagatca tccacgttag tagtaaagtt aacgacttga ccagggaagc 64140

gctcatacca ctcagcaatt ctcaagtgag caatgttagg ctccaccgta cccagctcct 64200

gtcgccgcat gttgtagaac tcatgggtta gctcgtacag gttgcgacta ggctcatcat 64260

cagatccctc agaaagggct tctaacgggg gcatagggtc gttcagatag tgaaacccct 64320

tatcgaacgc ctgaatattg catacttcgg ttagtttgta tttatcccac aggggagtga 64380

tggcaccctt acggaacgtt ggcactcaat ccagcaccac ttacgataat caatctacgc 64440

attacaggaa ctccatatag tttctcattt cttctttccg caactgctca gccttttcgg 64500

acaagcactc agaggttctg ggatcgactt tatctttcca caagtggtta cggcatcgca 64560

gaagttttac cacgtcttct cgggaaatag atccgtatgc tccagagtcc atcataaagt 64620

agatacgctt ttcatcagtt ttatggattt tcataaatcc tccgtttctc aattacaact 64680

atcttatcaa aaacggaggt atttagcaag tgatttattt caaattcatg tgtttgaccc 64740

tttgcattac ttcctgttgc ttaccagggt taaagggtct actaccagga ctacctaagt 64800

acccacaaac gcgacgggta accgagatat tccccgaccc acattgagga catacaaagc 64860

cgtgctctcc ggatacagac tctcctagat atccgcactc ttcacattca tcaactggaa 64920

tgttaacccc tatgtagtga gatttactta atccataatc aacaacccac tctagtgcag 64980

ggataaactt acgcatctcc ggaagttcca caaaggatat attaccccca ttggcgatgg 65040

tggtaaaatt agcctcatag tcaaacttca cgttaggggc aacttttgta cggacatcca 65100

ggtggtggct attagtcagg tatcccttat ccgttagcca gtcgtactca gggtactgtt 65160

cggcaatttt agtattgaac ctattgcaca gagactcact aggggtagca taaaggctga 65220

atccaagatt agtttcctca gctttttgt tacaacggtc tttcatgtgg ttgagaacct 65280

gtacagcaaa ttcaatcgca ggtggggaca tggggtcggt atcctcaaac attacttcaa 65340

ccagctcgtt aataccgata tatcccaaag acactgatgc cctgccttca aagatgggcc 65400

atacaagatc attggctttc aaccgtaccc caaaagctcc gtgcatatag agaattggtg 65460

cctgtttagc acgcacacgc ttcaaccgct caatagccca atcgtgggca gccatcgctt 65520

tatcaatgta ttcgtccaac aacttccaga acctatcgaa gtatccctca gactctacag 65580

caactagcgg caggttaatg gatacaaccc ctaggttatt gcgccccgca gtctccccgg 65640

actcaatagc tgaaaggaaa gaccgacaac ccatagggaa cttaaaatca cctgtaacag 65700

ccgttactct ttcataactc acgtaatccg ggtacatcct cttagaagtg caggtgagcg 65760

ccagctgttt gatatcgtag ttgggatcgc tgggagattt attaagcccc tctttaactg 65820

cgaaaataag tttaggaaat acagcagtat gccctgaagc acccaggcct cttatacgaa 65880

cttccagcat agctttctgc aacatgcgtg cctcccagga ttctcctaga ccaaacccaa 65940

atgtcacaaa tggctgctga ccattagagt tgaacaacgt attaacttcg tactctagcc 66000

cctggcacgc atcatatact tctttttctg tcatttcagt agcatacact gctgccttct 66060

tactatcgtg aagccaacgc tggccaatag ctaagtgctt atcataggac ttacggacat 66120

acggggcaaa gacctcgtca atacgatcga tagacgtacc cccatactga cacgagctta 66180

cctgggcaat aacttgggca gttactgcag ctgcagtaga gatagatttt ggagtttcaa 66240

tctctgctcc accaatttta gttccattct taaacatccc cgctaaatct accaggcagc 66300

agttagtata cccctgcgct cggtagtcca tatcgtgaat gtgtatctct cctctattat 66360

gagccgccaa taggtatgct ggaagctcct gtgctaccac atacttagag acttccccag 66420

ctatcatgtc cctctgtgta gggaattgct cgcttgcctt attggcatta ttaaacataa 66480

ggtcttcttc accctcgtta tcaaggatac tatagatatt atcaatcagg tctaattcgt 66540

tcatatattc ctccagttag gcatatatta taccaaatag acacaactat gtcaacctta 66600

ttttattata atcaacagta acttgatctg gatcatcaaa acaataaaaa ctggaaaatt 66660

ttatttgctt attcacccta ttttatatta ttcgtgtgcg cccgcgcatc gcgcgaataa 66720

aggaaaggat ccgtcctcca tatcatccta gaaaatttca gttgcaatcc acgccaaaac 66780

ttggtatact ggtattctaa attgataaac atggtcgaaa tttgaccctc tgtagacctc 66840

taaggagatc gcaatgagaa aagcagcacg tcgtaaggag tcgcgccgta acggtagcgc 66900

aaaacgtgaa cgtcacgaaa acgtcatccc cgttgatttt gaagcacggg aacgttttca 66960

accaaccgca aaagaactca agccgaagaa cgctgagcaa aagcactata ttagcaccat 67020

ccgtaacttt acggtgacag ttggtattgg agaagcaggt acgggtaaaa cgtttatccc 67080

atctgttctc gctgctcaag agttagcaac gcctggttct gtgtacgaga agttcatcct 67140

agtccgtccg aacgaacctc ttggtaaatc cctagggatg ttgccaggag atctgaacga 67200

gaagatggca ccgtggttag aaccaatcgc tgacggcttc aagtgggcct taggggaacg 67260

ttcttatcag gggctggttg aacgcaaggc aatccaatac cttgctatcg aacatgcacg 67320

cggtcgtacc ttcaacaatt cttatgtaat tgttgacgaa gctcaaaata tctccgtaga 67380

agcaatgaag tgtattctaa cccgcgtagg tcaggattgc aaattagtaa tctgtggcga 67440

cgtagcgcag aaagacatta aatccgactc tggtctgcaa ctgatcatgg atatctacga 67500

tcagtacgaa catgtgcctt tctccttagt agagttgcat gataacgtgc gttccgctga 67560

atccaaagca ttccaggcaa tctttaacga tatgggaatc taatatggtt actgaactga 67620

tcattggtta tggtgagggt attacctctg aagaaaactg gggctttgta ggcttcggtg 67680

aaggtatcac ttctcacgac gaacgtcctg acctctaact ctaggagcgc gtatgaacaa 67740

cgtatttaca ctgaacaact tccgcactcg taaaacgaaa gtgcatccag tatccctggc 67800

aacagtcaat aaatacaatg ctaactatcc tgaggatgag cggcgacacc atgccgcttt 67860

caagatagca aacgaatttc ctaaccaacc cctcggtact aaagagttag ttagtcgaat 67920

gaaaaaatta cacttttatt aaagtagacc gacacacagg cagcctcgaa aggggttgcc 67980

tgtttttgtc tgtaaaatct catttgcaaa atggccgaaa acaaagtaga atatctttta 68040

aatcctgaca acttccaaaa ggagttacca atgacccaac gtattgaata cgttatcaag 68100

cgtgacggta caaaagaacc gttcatggcc cagaagctga atgactgggc aaaatacatc 68160

ggaatccgaa gcgatgttcc gtggtctccg gtagcggtag ccgcagttaa gaacctgccg 68220

aaaggtgatg tacactcaga cgatctgcaa acaatgctga ttaagtctgc cgaatcaatg 68280

atcgagcgtg atcatcgtta cgaccgattc gccctagagc tgcgtttagc ccagctccgt 68340

aagaacctgt ttgattctta caccccgccg tctctgcgtt tcttccacga ccacatggta 68400

gagctgggag cgtgggaaga tatgagcggc tggatctctg acgaccagtt cgaagctcta 68460

aacgaagtta tcgaccacag ccgtgacgaa ctattcacta atgctggtct gaagcagttc 68520

atggataaat actctagacg taatatctat acggaagaga tctatgaaac tccgcagttt 68580

gcctacatgg gtatggcaat ggcaatgctt tctcaacctc actggagtat gctcgatgca 68640

atcgaccttt ataacgcgct gtcgctacag aaaatcaacg tcccaactcc gccgctcgtg 68700

ggccttcgga gtgctgacag gggcttcgct tcttgctgtc ttgttgatgg tactgacacc 68760

ctggactcca ttgacgcagc agagcacgtc gtcttcaaaa tggtcgctgc ccgagcaggg 68820

atcggctatc atcttgagag tagatcaatt gctgatccgg tgcgaaaagg cgcgttccca 68880

cactctggaa aactgccata ttatcgacac atcgaccgct ccgtaaaagc taacactcag 68940

cagtcccgtg gcggttctgc aaccgtttac actgcgttct tcgatccgga aatcattcag 69000

gtaatggaag ctaagagcaa ccgttcccct gatgaaaaga aaatcgataa gatggactac 69060

aacctgaagt ttaacagtat tctcctgaaa cgcttcctgc gtaaagagaa catcacactg 69120

atgagcttcc tgtacgctcc agaagtatac gcagcattcg actctggtga tgtagcagaa 69180

tttgaacgcc tgtacatcgc agccgaaaaa cgtctagcgg gcgttaccaa acgtggtttc 69240

aagggtgaag ttctccctgt agccccagtg attcctgccg cagaactgat tgagttctgg 69300

aaaactgtac gtatggaaac tggccgcctg tacactatgg acgctggtga agtgaaccgc 69360

aacagccgtt acaaagatcc ggtgcgtatg tccaaccttt gtgttgagat tgtacagcca 69420

acgttcccga tccctcacgt agtagatctg taccgtacag acgaagaact ggataaaatg 69480

gatgtttcag agtatgggga agtatctctg tgcaacttag gcgggttcgc cctaggtcgt 69540

atcaaaactc tggaagagtg ggagaagatc tcttacatcc tgttgaagtt cgttgatacc 69600

atcatcgaga ttcagcacta tccgttccca gctatgaagt acacggcatt acgccgccgt 69660

aacgtaggta ttgggctgat gaacgccgca ggagcgatgg ccgctgaagg cctggcattc 69720

gaaggcgaag aagcccgtaa ctggattcac cgtgaagcag agaaggcatc attcttcctt 69780

cataaagcgt ctgtacgtct ggcaaaagag atcggcccat gtgaatggtt ccatcgtact 69840

cacacttctg atggtacact gttaatcgat acttacaaga agactgtgga tgacctggtt 69900

tccgtaggtc tggaaatgga ctgggagagc ctccgtgaag agatcaaaac tcacggtatg 69960

cgcaactctg ttctgacggc aagtatgccg ggagagtcca gctctgttct gattggtgtt 70020

accaacgcag tagagcctcc tcgcagtgcg gtaactatca agacttcggg cgttaacaaa 70080

gtaattactg tagctccggg tctagacgat tgggacacca tgcagtccta taagtatgcg 70140

ttcgatattg accgtactga gcacattaag tggttagcag ttctgcagaa gttcacggat 70200

caggctatta gtgccaacct gtactacgac tttaacaaat atcctggagg tattattccg 70260

ggtactgaga ttatcaaaga tctccttaac tccactaaat atgggattaa gaacctctac 70320

tacgcaaact ttgacgtaga taccggaggc tctgcagcag agcagggttg ttccagtggc 70380

ggttgtactc tgtaattaag ctcgatccaa ccgaaagcaa aattttattt gcaagtaggt 70440

tggatttttt gttataatat tcgtatatta aatgagagag gaaattaaac aatggcaaca 70500

gtatttaacc gcgaatggga tcacactgag tctaaactat tcctgggcca agacctggga 70560

atcgccgact atgtaaacgt tcgctatcct cgtttagagg aacttgcatt actgcaacgc 70620

tcgcagttct gggttgagac tgagatctcc ctggaagccg ataagaaaca atggcctaat 70680

ctgccacaac atattaaaaa caaaaccctg ctgaacttag cctggcaaac ccaagccgac 70740

tccattatca cccgtgctcc ggaagatgcc attctgaaac tggtatctcg ccctgaactg 70800

gaaggtatgc ttattcagtg gagctacttt gagaatattc atagccgtgc gtattccaac 70860

attattcgta acgttctccc taatccgggt gagttcattg caaccgtaca ggctaacgac 70920

gaagcattcg cacgtctagc actgccggtt tctgttattg atgagttggc cgaaattgcc 70980

gacatttggc tggacgctag agccaatctg gaaatcgctg agaaggaagg tactctggaa 71040

tacaccgaag aggcagactt cttagcactt actgaacaag tacagcagaa gattctggag 71100

ttctactacg ctgtatacgc tctagaagcc attatgttct acgcgtcgtt tgcgtgcacc 71160

tttgctctgg cagaaaacga tatcctaacc ggtattgcaa agaacttaca gctgatcgct 71220

aaagatgagg cactccatac cgttatggct atggaagttc tccgtattct tcaaaatggg 71280

gaaattcccc cacatgtagt ggcagcagct caggctaacg ccccgaagat cctgcgcagt 71340

attctggaga cagaaattaa ctgggcgcat tatattttcc cggaaggcga agatattcca 71400

ggcctgaacg ccgatttgct ggtagagtac ctgtactaca acgcacgcct ggcatttatg 71460

gcgatcaaca ttccgtggcc ggaagatctc ccggtaatta tggaagaccc gattggctgg 71520

atgaaaggtt ggctgaacac caagaaccag caagtagctc cgcaagaagc acagattacc 71580

aactatcgtg ttggtgcaac ctctcaggct aacccggacg atctgtctga tgaatttgga 71640

gagttcctgt aatgattaca gctttatacg caatgcgagt tgacgccgcc ttcgggattt 71700

ttaatccggc tacaatggat gcctacgggg aacttccctg gggctccatt cccgaggagc 71760

tagaacagtt ctacagaatc ctggatacct atcaggttgt tatagtgggc cataatacct 71820

acgaaacagc ccctccacga ctgaaaaagg cactggagaa gaaatccatg gtgtacgtag 71880

taggttctaa ggctccagtt ctgataaaaa accctccccg taatgtgcgg tttattaccc 71940

acttgggttc caaaattcgg gacttctgta atgaagttga ggtagtctgc ataggaggga 72000

aagctctgct agaaacccta gcaactatgg gctgtctgga tgcgatttat cgctccacca 72060

tttatcctaa ggccggtaca gtaccaagcc tagaccacat catgtatctg gaacacccga 72120

tacttacgtc cactcctccg gatgctgtag taactcatat agcttctggg gaaaatgagc 72180

gctatcgttt tgttatggaa ggagtctatc tgtgattcac tatattaatg aaggcaaacg 72240

cattcttgaa gaaggtgtat ggctggagaa ccctcgaacg ggggttcgtt gtttaaccgt 72300

aatagggtca aactttgaat atgatgtact cggaaagaaa ttcccactta tcacaactcg 72360

taaagcgtat gctcttcagg ccatcatgga gcttatcgga tatctgcgag gatatgattc 72420

cgcagagcaa ttccgtgcta tcggctgcaa tacgtggaac gctaacgcca acgaaaacga 72480

ggcgtggttg gtcaacccta acagaaaggg aaccgacgat atgggtagag tctatggagt 72540

acagggcaga acgtggcttc gaccggatgg ttcccacttt gaccaactct ataagatcta 72600

tgagaattta cgacgaggca ttgatgaccg cggagagatt ctcaccttct ggaaccctgg 72660

cgaatttgat caaggatgct tacgaccgtg catgcatacc caccagttct cgctgctcaa 72720

tggaaatctg tatctcgact ccttccagag atccaatgac ttcctattgg gacaagcctt 72780

taacatggtc caatgctaca cgtttcttgc gcttatggcc cagatcacag ggaaccgggc 72840

aatcagagca aaccaacgta tagtaaatat gcacatctac gagaatcagt acaaggttct 72900

catggaacat gggcaatttg accgcaaacc tttcccggct cctcgtctag agatcaaccc 72960

ggagataaaa accctagagg acgtactcac ctgggtttct aaggacgact ttaaaatcgt 73020

ggggtataag tctcatgacc ctattgcata tccgttcact gcgtgaggac ttatgggatt 73080

atttaacaga cgccccaaaa taaccttctc cgaaagggag gagtctcagc tgaagtttct 73140

ggttcaatcc tcgggattac acatagatgt tatcctaggg atggtaaagt acaagggcat 73200

ggacgcacta atgcgtcagt ttgcccctaa accacctaaa gaaaaccctc cagccaagcg 73260

ggactataac agtaatttac tggttcctcc agctaaatta ctataactaa ggtggccttc 73320

gggccactta tattaaaaat tcatttgcaa accacgtgaa tttctaatat aatagattca 73380

taaatttgag agaggaaata aatatgtctt ttactgatgc aaaagcaatg gcagctaaag 73440

ccaaaaggtc taacgatatg gcagttatag cagctcgcag atctattata tcaaatattg 73500

atggatcagc ttcttcaggt aaaacagaag tagattctta cgcattgaat ggcctgccta 73560

tcgccgcacg gtctcagatt atggaagacc taaaggacgc gggctatgaa gtaaaagtaa 73620

atcatccgtt tgaccaacgc gatactgaat caattaccat ttcctggggg cacgcataat 73680

gtttcatgtt tatactgatg gtggttgccg cggtaatacc cgtggggtag acaacgttgg 73740

tgcttgggct atggtagttt acaactccag cgaagagcaa atcggcacca agtctgctcc 73800

caaacgcaac acaactaaca acgagatgga gcttcaagca gtcctagagg ctctgctatg 73860

gtctaacaaa aaccctggcc gaccaatgac aatctatctg gactcaacct acgttaagaa 73920

tggttgtgag tcctgggttt ggggctggga acgtaaaggc tggaagaagg cagatggtga 73980

tacacctctg aacttagacc agtggaagtg gattatcgac gaactcaaga agtatcgtct 74040

aaaccacaat gagatcccaa ctttcgttaa ggttaagggc cactctggtg tagaaggtaa 74100

tgaggccgca gataacctgc taaatgttcg aatgaccgaa ctggaaatgg aggatatgtg 74160

atgttggaga atttacgccg cctagttagt gaaatgaaat atgaagtgct cctgatggag 74220

cctggtgtgg atcgagtagt aatgaaattg cgaatcgcac gtatggaagc ccaaatcttt 74280

gaagcggagt ggaaagctct gaggggtgga gatgaattat aatggcacca gatttgaggg 74340

atttgttccc aaacgtacca cagtaccagc tcgatctcta cgccgcgttt ctggaagcgt 74400

caaaatcggg gaaccctcta cgcgtctacc gccaagaccg caggcacggg aaatcctgga 74460

tcctgagatg gctgaaagag aacgagccgc tcttaaagaa attgagcgaa agaaactctg 74520

tacagcaccg gcatacaaca aaggtgggta ccagtacatc agctcagaag agcaggcaaa 74580

acatatcggg cggtaacaga tacgagttca tcatcttcga tgatcttgta gatgaaaatg 74640

aaaaaacgca gttgctaaac gctaaaaatt aacgtataat agattcataa attaacgaaa 74700

ccaatcaaaa caaaggaaat aaatcatggc taagcagacc tctaaaaaag cagtagaaac 74760

caaagttgca acttttccca aaactgaagc gaatcgcaaa gcacgtctgg agcgtcatct 74820

gcgtaaacat ccggctgata ctcaagcagc atcagctgta ggcaaaccgg ccccgcgtcg 74880

taagaaaccg gtaactaagg gttctacctc cggctacgtc tccaagatcg tcggttggag 74940

tacgccggat aaggcagaca ccaaagaagt cctgcgcaag acccagggcc gtttcggtag 75000

cgtcaagccg aatatcttcg gttgcgaata cagccgtgag aatgttcgcg ctctgtgcta 75060

cggcgtaggt attaaattta cgggcaaggc aaataagccc cgtaatcaaa aacgcaaacc 75120

agctaagaag gcataatgcg aaattttgta gctaaaaacg atttcaatcg tgcagcgaca 75180

cataagtcgg ccctagatta ttctagggtc aactcccggg aactgatgga ttcgtgctac 75240

gaagaactcg aagattgggc ggctgactgg ccgtcgatgg aagaaaactg ggatgtgtcc 75300

gaagatatga ctaagccacc accggaggtg gcttctaaat gtgataacac atctagaagc 75360

aactttaata acaaaggaaa caatatgcaa aacttacaag accgctggat ctctgtttgt 75420

gatatcgaat ccctgggaac tccgggagat tgcaagagca cctttatcgc tatgccgttt 75480

ttcgctttcg tactgatgaa agatctatcg ttagatccgt atatcgttct aggcactcct 75540

aacgttgccc agcagttggc cctcggtgct aaagtctccg ccggaactat tgcattctgg 75600

atgaatgagg ctcgtgctgg tagtgctccg tcgctgtcca ttattgaagc tctgaacgct 75660

aaagacggtg agtctactgt tctggtctgc aatccgactc atgaatcacc ggtatccaag 75720

catacgttca tggatctgat ctgcccgttc gtagaggcaa aacaggtaat cgaaggcatt 75780

atcgatgagc aaggtatcga cactcgttcc ctgcgccact acggtaatgg cccgcagttc 75840

gatatgtcta tttacgaaac agtggcggct caggctaatg tcttctctcc gtctgatcct 75900

gcaatcgttc cgtggaaatt ctgggatatc tccagcgccc gtaacccgcg tgactatttc 75960

gaggctctcg gaggagactg gaaagcattg gtacgttgtg ctgaaatcta cgcacacgac 76020

gtaatcgagc gttacaacct gattcctgag ggggtctatc cgtcgaaaca tgatccggtg 76080

tttgacgccc tggtagaagc gtactgtatt aaaactatcg aatcgaaatt gaaaatttga 76140

tttgactaaa tggctgattt cttgatatac tattattctt gaatcaaaga gtaaaggaga 76200

aataatgaaa gcagccattc taatgatctc catcctcact agcttccatg cgcaggcaaa 76260

gattgatgcg catgagatag agtgcatagc taaaaatgcg tactttgaag ctagagggga 76320

aggagttaaa ggaatgaccg cagttgcaca agtaacgaaa aatcgtgtta actatggaaa 76380

attcccgtcc acatattgta aagtagtcta tcaaccaggg cagttcagct gggttggtaa 76440

gaagaaacat aaactcgatc gtaaagacga agagtggaaa caagctaaag agatagctag 76500

actagtttac tatatggatc ttccagtaga tccgacgaag ggagctttgt actttcacag 76560

taaagatact aaaccttact ggacaaaaga caaggacttc aaaagaacaa gtaaaattgg 76620

caaccatgtg ttctataaat taaaatctca gttgcctaat gcttaaaaag ttgatataat 76680

agtttcataa attagagaga acagcgggcc gattacgctg aacttgtttt aatgtaagac 76740

tcgtcgagca ttaagattcg ttgaatagaa tcggtgagtt aagagtgatc acctgacaaa 76800

gttcgtgcat ccagtccgga taccggccag ggagcgtatt ggacgggcgt aggttagaga 76860

tctcttgtaa aactcgggag ctgtcccgga gtctcgtaaa ctcttctcct gatttataga 76920

aaatggtgga atctcacttt aacctgttcg accagaatga agcatggtgc gtggcctgcc 76980

ggagaggtgg ggagctgagc ctgagaaact cgtatagctc ccacactgac ctgcctaggc 77040

cgcaaattgg agacatgtgt atagcgtctg gtgctagtta ttgccaccat agtggggtgt 77100

cgaaatcact tatgtagcaa cactgccgtc ctaagttaat tggtagactt ctgcacgcgg 77160

gggagctatc cccagatgcg gaaagtgcag gttcgaatcc tgcggtcgga aagagttaga 77220

taactgatgg ttctattggc gaaccactcg ctgctggagt acctcctccc ctcccaggga 77280

aagacttggg agactcgcgg gaacgaaaca gctaaaccac gaaggactag gatgctgatt 77340

tggctaccct tacctgatat atgcccaaat caaaagaaga actttaggcg gtagcctaga 77400

tagtgaagtt tttcctccac gaggagtcgt ttttcaagct atcaaaactt cacatcgaaa 77460

attcggaggt gtgattttaa cagaccgcgt ggaggatggc tctccagaag tgccaaagtt 77520

agtccttaaa tacggcatga tgatcgtatg aactttggcg aggtgggatc tcgcctgatt 77580

ctaagtggga aagagtattc ggatagccgt tcgtacaaac ggtggctccg agacctaagt 77640

gggacacggt tgagtataca gctccgcgga agctcgtata ccctgtgtaa gcatgtgaca 77700

atggagtcat gaccggagtc accccgagcg aaagcataac cactatttat agcaccctta 77760

cacaggctag aagtgcccct gtttggagtg tgccctcgcc tagaccgcat tagccgacgg 77820

atatccgttg gccgggatct ggcaaggtat attagtcacc ttgactataa ctggaagata 77880

cgtctgacag aagggccgca tagcttaaac aggggaaggc ccctacctac tggcggtatc 77940

tttaagagct ttcacgagag ttcttaaaga tactaattga cgaggtctat atgaacgatt 78000

taagtatgtt aactaagata cgctctgata ttgagtctat ggtctctcgt cgtagtgagc 78060

tgactaaggc taaacagatc atcagcggtg gtacacagaa acgcttcaca ttgcaagccg 78120

gggatattaa gtttgaccta tgtggcagcc agactcgaga ttacactttc gaaatgaaac 78180

cgtgttacga tatggtgaag ctggggctta tcaaagctct agacaaacaa atagatcagt 78240

gtacggacgc aatcaaaacc ctaaacgtcc agttcgccgc tgaatgcgat cgtctcaaaa 78300

actctatcaa ggtataataa tggtggcatc tgtgcatact cctccgtatg aacgtccagc 78360

acctaatctg acacctgaac agaaacagct aatcgccagg cgcactctag agtttaaaga 78420

gtcgctgcat aagagcgttg gccggtattc tgaacaggtt catgatctgg ttgtcaaaac 78480

acttaaactt tattaatgct tccttagctc agaggataga gcaacggtct tctaaaccgt 78540

gggtcacagg ttcgaatcct gtagggagta ccactttaat cgctgcccac acgtaatatt 78600

cagtgggcag cggcagaaag cccgcagggc gcagattaag attgattcta caaaattttt 78660

cttgcaattt tgtcagaaat tttgtataat agttctttaa atcaaagaga aagtagagga 78720

taaaatggct tacaaaattg aatatttaaa gaaaggggtt ctcactgagc tggttatcga 78780

tgcgaacatg gctcgcaacg agggcactaa atccgtattc tataaagacg gtagcgtagc 78840

tcgtatgatc aataccgaag acattcagga tctgtacgtg atctccgacg aagaagcagg 78900

tttcgtaaaa gatcctgagc cggctgaaga tactccaact gaagacactc cggtagcgga 78960

taccactact gaagaacctc cggtggaagg cactccggaa gatgaagcag cagtataaat 79020

aactaagggc tagaaatagc ccttctcctt gggccggtag cttaaagtta aagcagtggc 79080

ctcataagcc aacgagtggg agttagagtc tcccctggcc caccaatttc ataacaggag 79140

actaaaatgt ctactaaaaa cgcaatcgta tccttcgtgg atgacagtgg tatcgtccta 79200

gagtccacag taacagatat cagtcctaaa cgtctgctcc atcgtgatgg ggatatcctg 79260

gaaatcctta ataaacggtc tgagactatg ctggtcattc ctgtaaatcg tcttctctcg 79320

attaaaatcg tgtgggagga ctaatggacg ctcaattaca aacccagtac tatatgcttt 79380

taggcatgtt agaggatgct ggcccgacag tcagagggca ctatgagcgt cacaaagcag 79440

cttttgaagc cctactaaaa gaagttaatg agaacgaagg tggtaaaggc tctgactcct 79500

atgccgcatt cattatcgcg ctacaagttt tcctaatcaa tcaactcaag taataggcta 79560

aatatgctga atattaaacg taaaggtttt ttctacaagt ggcttaattt ctcttccgcg 79620

tctttcacct accggctgaa cgacaacaga gtcaccttgt gtagcctatt ttggcactca 79680

gtgtggtatt tcctgctaca gattggcgta actgctattg ctgtactctt ctccttgggg 79740

atgggaagta tcttatctac gttcttgggt ctcacctttg agctgggaat tactccctgg 79800

tacatgcttg tagggttaag tctagcagga ctatctacga taatagcgat tctgctggcg 79860

atagctggga tcggctgggc ctgcgctaag ataggggatc ggatccagga atggaacgcg 79920

agtaaatcct ttgaaagggc acagaaagag tataatgctc gcgatgaaga gctccgcttc 79980

ggtaatatct accagaagat gcgaatctat aagaaggaca aactttgtcc gctcattcgt 80040

gtagaccacg gcgagtagtt tgcatagtga cctgcgttgc cgggtcacta ccaaaatact 80100

tgaaaaattc aattgctaaa tgctctagaa tttgagataa tatttatatt gaaagggaat 80160

agccaagtgg ttacggcatc ggcctttgac tccgagatcg gtaggttcaa ctcctccttc 80220

ccttgccaaa tttaaaatgc tcctgtcgtc taagctggtt aggacaccac tctttcacag 80280

tgggaacacg ggttcgaacc ccgttgggag taccaaattt actgaaaaat tcagttgcta 80340

aatgcttaac aaattgatat aatatttata tagtttgtta aggaattaat ctgatactga 80400

gccggaacca aaaaacacgc ttgcagcttg ctcggtcatt gtactgaggg ttcgcaagaa 80460

tagcggagtg gctctccgaa acgcctggta agcgtagagt gtatcgtatt tgtgaagagc 80520

gggtatcctc gcatggctaa ttgcttaggg tattacgcgc accggattaa ttgccttaac 80580

aaattattgg gggatgggtc tgctgggagt ggacaccgca cttgcaatgc gggaatcaga 80640

acggttcaaa tccgttatcc tccaccaaac aaatggggat gtggcgaaat tggcagccgc 80700

gctagattta ggttctagtg gtgaaatatc cgtgtgggtt cgacccccctc catccctacc 80760

aaataacggg agttcgtgat gaacatagaa atcatgcagt tggatcgtaa gaaaaatgag 80820

ttccgtaagg tccatacctt tccgagtaaa gaagctctag agtttcatat taagtgtatg 80880

ggactggtgc taccggaaag cgagatcttc gacttagcat gtgctaacgg agttctgtac 80940

gtctgggaaa tcacgtatca tgctgatcct gatgaactcc gtaaagaagt agagcaaata 81000

ctaactggag agtagtgctc atgggagcaa gctgacttga aatcagtcgc catcggaaac 81060

ggtgagggtt cgattccttt attctccgcc aaacaacagg aaagctggtg aaatggtagc 81120

cacgcatcac tgctaatgat gagtccgcaa gggcatgaag gttcaagtcc ttcgctttcc 81180

gccaaacaat ggcccgacga gtaacggttg ccccctttcta gagaattttc tgggcgaaaa 81240

tccagaagta atcaactagt tgtaagtggg aagagtttct tagggccgcc aaatttgagt 81300

atcattggta ttgtaggagt cgtacgctgg gactacgtag tacactgagt gtcctatgcc 81360

cagtacgcgg tctaaccaaa tacggtgtgc gatgtgcatt ttatttgtgg aggtctgatc 81420

agccctcgat ggtactcaaa tttgggatat tatcataact ggataatgac ctcgattgtg 81480

gatcgagtct atcttggttc gaatccaaga tatccctcca gattactgca ccattagttt 81540

aatggataga atatagagct acgaactcta tggttgaggt tcgattcctc gatggtgtac 81600

cataaaatct ctgctgagag tgacgaggtt agccctctgg gtcacatccc tcttctagcc 81660

gcctcccata aatgcaagca tttatgttct ggccctagac acaacgttgt actcagcaga 81720

gtgcgcataa ttggggtata gctcagtagg tagagcggag gtctctgaag ccttaggtca 81780

caagttcgat tcttgttgcc cctgccaatt gcaccgtaga ggagaggccg tcctcgccag 81840

tctcataagc tggagatcgc aagttcgaat cttgccggag catccaattc taggagaaga 81900

tgatgagaat ctctttcaca gaacgagtac taggtactgg agtaatgcta atcacttcct 81960

gggatggaga tagctggtgt aacgtgacag gcttacgtaa gtcagaacaa acacccgaga 82020

atatcgctaa aatcaagaaa cgaatggcag aagctgctag tcgtcctgga gcacctcgta 82080

atggtaaacg ttgaggtaac tatgactcgc tatcaaggta tgctaattaa tacccacaca 82140

aaagagattg tattcttggc accggctttt cacgacacct acaatgaagc cgaggaagac 82200

gctaggatcg ctaaaataca cccggacgag gaaatctgcg tccgtcagca agaacaataa 82260

tgcttcaata gctcagttgg tagagcaaac gaccgataat cgttaggtca ctggttcgag 82320

tccagttcgg agtaccaatt tttgccccct ataggatatt tcatcggaat atcctccagc 82380

gatggtacgt agtatagtac ttacctgtta agcctagaca aagttacttt gtgggcaaaa 82440

taggtataga taggagaaga atagtagcgt aagattcttg aggcaaattc tttaggtcag 82500

ttggcagaga tggtttatgc actcgcttca tacgtgagac tacagtggtt cgagtccact 82560

attgaccacc aaatacttgc ttagctcaat cgggagagca tcgtctttac acggcgaggg 82620

tagctggttc gaaaccagca gcaagtacca atttacagtg agacttcggt cagggccgtc 82680

aaacgtccga gaagctgtaa tttctgatgg ggatgatccc agattcgtaa gaatacccca 82740

tccttacctt cacaggtttt agcgcaatgc tgagtaaaag tctagggaat cgactccatg 82800

ccatccagga gtataaatgg cgaatctagg gacttagacg gtcattgccc tagcgcgttg 82860

atgccgtgcc ggaatcggta tacggggctt cctaaagggc gtaagcagaa catccactct 82920

gcataagata cccgaaaacg aggctgagat aaatggtcta tcttgtgaag gttcgatccc 82980

ttccggggtt agcgtgtagt ggggctaatc aatccccacg ttaaacgttc aagttaagat 83040

ttgttagttg cagaagcggg gaggctatca accttcagtc cctgaaagct ctcagcgctt 83100

ggaactcttt cgtccgtaag gaatagatcc cctttcgctt tgactcgcaa acttcaaacc 83160

aagtgtaact aacagctgca agcctggatt accgctctcc ggagcggata attcaaaaat 83220

ttatttgcta aacgctctta tttactgtat aatagttaca taaattaatg agaggagtta 83280

gcaaatggaa aagattactg caactggtat tgaatctgca ctggtggttg attgggccgg 83340

atgggacgga gatcacgaat ggatggtctt ttatagctgt acgcttcagc cagaactatg 83400

gactaggctt accgatgagc atgctatgcc ctacggtatc atagatgtag aaattgagat 83460

taacaaactg gttggcacca ttatggtgca tcgagccgaa ggcgatcaca aggaaatctt 83520

ccgtaaaagc attaaactgg tagtttctac cggtgacttt atttaacaat taactgagga 83580

aatactatgt acacacgtcc tactaatgga aattctgctg tagtccgcct gatgattgtt 83640

caggacaacc tgtccaacaa catcgagtct ctagaccgtc gtattgagga gtatcgcact 83700

gagatgctgt ctctgatgcg cgaacgtgag gccaagatcg aagagcagct agaggtttgc 83760

gaagctatcg accgcctggt tgacggaacc gcagtattta tggcggaagc tcccgcagag 83820

cctaccttca ccccggtagc accagctgac atgcagtatg ctattctgcc tttccatctg 83880

gaagaagaag atggcgaagg cccgtcgctg gaagacgttg ttcgcttcct gcttgcctcc 83940

ggtttcccga acggaggtcg ttaatggatt ttatcgttgt ttgcggagcg aatactgact 84000

gcttcgagct gttaaacgac gccctagaca aggttgatga acacatgcag gaaggcagaa 84060

ctcctacatt cattgacctg tctcaaggta aaacttactt ctacccgtct cttgacgtag 84120

agcctacagt tctacctatc ttcatgcact ccctctcgtg ggacgaagaa gacgattaat 84180

gaaaaaattc atttgcctag tactctgaaa tttagtataa tatttatatt gaaacgaaag 84240

aggaaaagca aatggaagat gaagttaaat tgtacatttg ttcagattgc ggtgagttaa 84300

gtgaatgtca ttgggagtgt ccgacttgtg agtcagacga cttaatggaa tacgaaccgg 84360

aataacaaat taagcggcta tggtgttcag cggtcaacat accggcctgt cacgtcggag 84420

ccacgggttc gaatcccgtt agccgcgcca aattctctct gggctaagag atatgaccgt 84480

ctagaggtat cctcggacac aagggtcagc cctagacaca ataagttagc aaatatctcg 84540

tttcgacgag gtatttgaag aggttcttac gagagcttct tcaaatacgg gggaatattc 84600

tgtaagtggt agcagagcgg tctgtaaaat cgttgccatt gcggctcggg tggttcgact 84660

ccatcttccc ccaccaattt tgacaatcaa agagatccgg gttcgaatcc cgcgtacgca 84720

acaggcggca taaaggcctt gtagcttaaa tggacaaaag cgctttggtt gttaaatcta 84780

tttgggagag aagcagtaag tggtataggc ggtcgcctgt taagcgaatg acagtgagtt 84840

cgaatctcac ctctcccgcc aattttactg aaaaggttat ttaattaacc taggcacgcg 84900

taggaatact gccaccgcaa ttgaaagatg tggcccggtt tggagaggta tgccgctaca 84960

cgctacggtg ctaactccgt ctaggtgaaa atcctagtca gtaatacagt attagggtaa 85020

gaacagcgac ttaggttgca gtgaagcgtt agcaatcggt ggaactccgg tgcgccctaa 85080

ttaaacaatg catcattggc cgagtgacta ggcagaggct tgcaaaccct cgaagcatgg 85140

ttaaaatcca tgatggtgct ccaattacca gaggtactca tgattaagta taaggcgttt 85200

gtaacaagag agtcccaaac aggagattca agtattaaat tcgaaggtac aacgttacat 85260

gatacatttg aagccgcttt aacagaggcg gaaacccata tagtatcgaa aagctgctat 85320

gctcatgtat gggaagtaaa cactatttta gatcgctagc tcaatggtta gagcactcgc 85380

cttttaagcg ataggttccg ggttcgagtc ccgggcggtc taccacatta tgggacttca 85440

gctaatcggc taagcatcat agatagcggg gaatcccggt ctgtgagggg agtaacacgt 85500

agtctcccaa gttccaccaa acatcagagc agcgtgatgt actgcaaaga cccaaagacc 85560

ggggtggact tcttgattca aaggagcagg cacgaattac gcaactgtag ctcagcgagg 85620

tgagagcact ggtttgaaag tccaggggtc gttcgttcaa atcgaaccgg ttgcaccaaa 85680

ttaatagtat caatagctta tggagctgaa tagtcctaaa gctcacggta aagcagctgg 85740

ccgttagtga gcagacttgg aaacgtctgg tgatctctag gttagccggt gcgttggttc 85800

gaatccaact gatacttcca aatcccaagt agcccgttac aggctctctg attaaactca 85860

gacaagcagg taatgggtga caggataaaa taagccactg atttccggcc gtttgacgtg 85920

gtaaagtcct ccagtcaaga agaatttctg cgtgcagaaa tcactgaaag caatggggca 85980

gacaacttga gatagattgc ctataacgtc tcaagtagtg gcattgactt agggtggcat 86040

tttcccgaaa gttcgaaaaa ttcatttgct aaacgctctt atttataata taatatttat 86100

ataaattaat gagagggctt acctaatgaa tcaaaaaatt cttatgcgat ataatccacg 86160

agctttatgg ttccgctggg aagtgattgt atcgtaccag atacgagtgc gtaacggtga 86220

tcctgagaac aacattatcg tgctggagac attctctaat agagatgcgg cagttaagtt 86280

cctgaacacc atcgacaata ctttaatcaa ggtatattaa taatggatat ctttactact 86340

cctgctatca acttggtcgg tgtcggccta ttccaggcaa cggtctatcg tattgatgat 86400

agcactgacg ttgtaacgtt cattgtaccg gagttcttcc ttgagaagtt ctttgaagag 86460

tttgagcaat tccgtgaaga gcatgatgct tactccaata tggaagatct agcagcgatg 86520

ttcccaactg tatacggcta catctttgaa ggcaatgatc tgcttttgga taagtcagag 86580

ctggtggaac tcaactgggg cattagcttt gaagtgggct ctccgttccc gcggtatttc 86640

caaggtctgg agattcgata atgggcggct actctaattt catcgagaat tacattaatt 86700

ccgtagattc ctggaatcag gaaactctag tggtagtgct taaagagaga ttcaatatct 86760

ctactctgga agccctagag gctatagaag cctacttgga taacgattaa cacccacttg 86820

gtccaatctg gtagaggcat gaggcttaag acttcagggt tcccggttcg agtccgggag 86880

tgggtaccaa attatggggc acgactgatg gggaagtcgg cctggctagg gttgagatac 86940

ggttcgattc cgtaggcaaa tggtctcgta attccgcaca ggtgatggaa ggttcgagtc 87000

cttctcccat aactatacaa attcccctta gctcagtctg gcagagcggg cgctttggga 87060

gcgtcaggtc aagtgttcaa atcacttagg ggagaccaat cttgcctcaa tagctcagcc 87120

gggagagcaa ccgccttgta agcggtaggt cgtgggttcg attcctactt ggggcaccat 87180

tttcgctggt tatggttaca gtgtgattaa gtttacattg tcattaaatt ccggttcaat 87240

tccggaagcc agcaacccta aaaggtaagc atatgaggat tctttccata gaagatgtta 87300

tgtgtgacag atgctacggc tccatattct ctggtggctg tagttgtaag taatctatct 87360

aatgaccttc tgtagatgta aaataaatat gaagggtcga tgctcgcggc taccgacaga 87420

tcgtaatgat caagtagtag tctgaggtga agagactagc ccattaattc cgcgactaac 87480

tgtacgggtt acagcgtccg ccttccaagc ggtactgagt ggggttcgat tccccctagt 87540

cgctccaaat tcggtaaaat gaccgtcccc tgacgttacg gggaattaaa caaggaactg 87600

ggagccggta aggccatttt atcgatacta cttgagaggt acaacaatga aagcctttga 87660

tgcagaacta gtgttctcac tcttagctga gatggaagcc tgcgtagatc gtgtacgtgc 87720

gctgcgtctt agtatgttta gctcttaaat tatttgctgt tctagagcca atgtagtccg 87780

gggtgccgac gtctgcctgg aactcgactc taggatagtc aggacgtcac ttaacagcca 87840

gagatggcaa actataggag aagcaaatgt taacagttaa ggtaatgtca cctaacggtg 87900

gcgaagaaat tcacgatggt tcaagcgttg ggtttaatcc taagcagaag agcatctcta 87960

ttgctggtct tgatcagcat atcttcctga aagaagatga ggtagcctac gttatgaatc 88020

agaatggtaa gacagtatcc gtctaccacg gtagctaatt ttattccccg agtgttactg 88080

gacagcacgc cggtctccaa aaccgtgcag taggagttcg agtctcctgg ggtttgccag 88140

tttaaaggag tgatcatgat cacttatagc accaatttta tggggccagt ctccaacaat 88200

tggtacatcc gtatgggtat tccgtatacg gaagtaaccg agccgaatcg ttttgcagat 88260

ggcgggcaac taactcgaaa agtatttgcc aaacgatatg ccggtggtcg cattgacgtt 88320

cgtggtactg atgactattt cggccaggaa atcggtgttc cgattatgga ggccgagtct 88380

tggaatgaac tacagcagtt tctctggaca ttctcgtccg ataaggttct gacattggag 88440

caaattgtac aggctctaga ggacgagaca ggttttcgca ttgtttggtt taaggagcca 88500

gcatgtacat agatcgtaac caactgttca agttcctaga gcttgacctt cgttggcctc 88560

tatcagtcaa tccgggacga gctactggca agacgttcga ggctattaat acagcctatg 88620

agtttgcagt atttaaaggt attcaagcag tatacgtagc atccggtgtc cgtgaaatgg 88680

cacgcctaga gaagaagtat aacgagcttc aacctcatgt taaaattaca acgtatagca 88740

tgttagaacc ctaccgtata ggtcgtcgat tcagctgcat catgtttgac gaacctagct 88800

tggctattaa gtacggcgta aacgcttacg tggttcgtat agccagagaa aaccagtgtc 88860

ctgtaattat ttttggagag taaagtggaa caagaatttc aagtcttcgt agacgcctct 88920

aagagagttt tattcataca agccaccgat gaaggtcatg gcctgcaact ttccttcgac 88980

tctctggagc aaataaacca gattgttctg agggcacaaa aatcattaga aaagaacact 89040

gaggcacctc ctgacctcta aacaaaagcc ccttgtctct ttgagcgagg ggctttttct 89100

ttataaattc acttgcaaaa atgccaattt tgccgtataa tagatttata aattgatgag 89160

agagatttcc aagatgaaag taacaatgga aaacacagaa gagtttattg ctatctgtac 89220

tgcgtatgca gatacgcttc cacctgaggg tatggacgac catacaatgc agttagtggc 89280

ggatatctac agattagcag agttagctaa agaacaacac aacaggctgg tgtacgtcaa 89340

agaacgcctc gaaatgatgg ataaggagta atcaatgaac gaactcaatg aactgaatga 89400

attgcattac gctgaacgtg ctattgacga gctggatttc gctggtggtt attatacccg 89460

acacgtcaac gcaatgaccg ccgaagggct taatagtaag tctgcgattg ctgcggagtt 89520

agcagttcgg gactttgtta ttgatagtct ccagaagact attagcaact tgagcgaaaa 89580

caacaaagct gctctggaag ccctggataa gctgtccaac catcttctcg cattggggat 89640

caaataatga ataagcaatc tctacgtggt atccgagtat ttcgctctag ccttgttgat 89700

tccttctata tctggggcaa ggcaactcga cgcactgttg agcaagcact agacggtacg 89760

ttctatgatt ggcgagaaaa agagcgaaac cccgtattca gccgcccagg gctgtatcac 89820

gatcgtgtat ctaagacagc gtggtacgaa attgaagtaa ctcctggcgt tatcagagcg 89880

ttctatacgg attgggagca cgaaaagtgg gtttgggaca atcagattgc tcccggtgat 89940

cgtattatga actatgccga atataaagaa atgaagcgca tgttcgagct atacgatgtt 90000

cctaggctgt ctcgcccggc tatcttcatt gctagccaag agtactggca tactgttcgt 90060

atgaagcgtg attttaacaa gcatcacctg cgctatgaga aagaacacgg cacactgcgg 90120

gaacgtgtgg ccaagagaaa agccgaactg cgtgaaaaac gcctggagaa gaaatatggt 90180

gaaagctagt ctcttacgct tcactcctgg agttggcctc cagtataaaa ttgttggggg 90240

ccacaagttc caatacttca ccccgggtaa gctctacttc gtcgagctac acgatagtag 90300

agcaggctac aaattacgaa gcgacgcaaa tgagggcatt tgggtgagct tcacacaagt 90360

taaacgctgg tttacagttg aaggatataa tgattatgag taaagttgta tatttcgtaa 90420

aatgctgccg tgacacctta gagttggtcg accacaaaat gcagacctgt aaatgtggtg 90480

cttcctccat agatggtgta gccggagcct acgtccgttt tctaggcgac aaaagtaact 90540

tcatgcgtct gaatgagttc cagctcgaag ttgaaaagaa tcgaccggct ctagaggcag 90600

aggctgagcg tctcaaagat ttcgatggga acatcgtagc atataacatg gtaagcggta 90660

aagacttctg gtctgaactg gctgaaaaac ttaacatgcc gcggcaggcg gctaaggctt 90720

tatatcatgg cttcaactac tcgccacgtt ggaattaagt tttccaacag taacagaact 90780

tacgtttacc gagtacctag ttattggaaa tactccccgg agataggtga tgtagtagtc 90840

ataccgggga atgttatgtt taataatcct cgtcgcgcca aagtagtaga agtgcatggt 90900

atgtatggta agccagagta taaagaaaga aagaacatct cttatgtaga gctgcatgat 90960

tacttaccga aggaggaacg taatggacga taaaattgct cgggaagcaa tagaacttgt 91020

tcgtaaacga ctggaagaac gtaatgtcga ggtgccgaaa ataatgctta ttggctacgg 91080

cggcatcggc ggatttccca gcttcactga cctagaaaga atggaacgag agtcccaagc 91140

cagctttcta gagttagaat cctacgctcg ggaaatggaa cacgaacatc cgattggtaa 91200

taactttatg ccacgtagct cccgccagga ggttactcac ggcaagacta attcctggcc 91260

cactccgaaa cgcagaggta gaaaatgatt actacaggat ttggatattc tcacgaagaa 91320

ttgtgcaaaa tggttgaaag cgctccgttt attaagaagt tagtcgaaga gcaacgaccg 91380

gtgtgtttac atgctgcctg taccaagtgt cacggtactg gtgttgataa aaacggcaag 91440

atgtgcgtac atgcactgtc ctgcccgtgt cctaaatgta gctggagctg ttaatatgga 91500

tctaggatat tgtgtagtac atgaattcat ggagcagggg ttgccggatc gtatttgcgt 91560

tgtaacctct cgtaatctgg aagcagccca atcactagtg gagcgactct ctggctacta 91620

tcgtgaccat gaacgttacc agcagaaagt atttgacctg acaaaactgt accatcaaaa 91680

agctctggat atgccaactc cacagctgga cgatctcaag cagtttagtc ctgaggcctg 91740

gtatagcgtc aaagacgcca gtccggtaga ctataccgta caggtattct cgcattatgg 91800

tactcgtcac tggataaacc gtaaatggga ttccatggtt gactacctta attcggaact 91860

cgaaaagggg gctgccgaat acaaaagaaa gcgtgccgaa gccaaagtat tgaaaaattc 91920

agttgcattg taggcgattt ttcgatataa tagttacata aattgatagg gagagcttca 91980

tgagcaaact aagtattgaa agcattatcc gcccgttaat gcacgggtat gtacaaggtt 92040

cctgtgtaag cgaaactgaa gctctcaatg ttatcgaaga agagctggtg gctaacgggt 92100

ataatcttca cgaaggtgtt atcgaggatc tcttctggca gaccgcggaa gatatggaga 92160

tctttcggtg cgtgaattgc gggtggtggt gtcctgcttt tgaaagggcg gagaaccaaa 92220

tagaggaaat ctgccgggac tgcgagccag acctcgaagg tgaagtggat gaacaagata 92280

acgaaggtga agactatgag taagcgttca attgcagcaa tcatcgcatt cagtatgatg 92340

tactctggag tatctctggc cgcagagcgt aacaaagtag agatctctga taacgggcgg 92400

gttcgtgtaa caacgaatgg gattactaaa ggagctggta agtttcgtaa atctgaaacc 92460

cgttttgggg aaactaagat ctacacgaac aaaacctatg gcaagcccgc tgtgacactg 92520

gaccgctatg gtcgtcaggt agaagacgag gatgatagcg atgagtaatc ttcaccccaa 92580

acttcaagag accctagact ggattaatga agagtgtgct tttgaggaag ctccttactg 92640

tgtctgggca agagctggtg cagccccctc ggagtggtgt actgtgtttg ataatcgcta 92700

ccggataaca gttgaactaa gcctaaaaga ggacaaagta tacgctaaag cctctatgac 92760

cgcgctagga ttatccgggt tcgtggagat gcaagagctc tgtatgccta acactcacct 92820

tcgggttcag atcgagcagt tggcaacaat tcgtttgatg ttgccggaag ataacatcaa 92880

tgaccatttc cataaggtta ttgaaaatga atacaaacta cggcggcaac gtcgcaaagc 92940

acgacgggaa gtagagaaga ctcggatgat gtgtaacatg aatccacacg tataacggta 93000

gggccgttat aggagtcacc ttcctgttcc tatccggagt cgtgcccgcg atgaacgaag 93060

tggtgagttg gtcgccgacc actaactaat tcaaagacaa actgaggaag caaaatgttt 93120

actttattta tactggcagt atcggcgtgg atggcagttg gtatcaatca tggtctggac 93180

tctgctaagc tgctgtcagc taaagccttc gagttcctgg ctaagtttgc cacccgtaaa 93240

gatatcgagg ccatcatcgc aaaaggcggt gccaaagatg catcgagtgt cctgaagtcc 93300

ttcgataaga tcctagagct tcgtaacggt aagcatgccg cagagctacg ctgtatgagt 93360

cgcaagacca taggcagact gtgtaaggcc atcttcatcg tacaggggggc gttgaaaggc 93420

ccattcgcta agtataaacc ggatagtatc aagcgagcca agatctttaa cgattactgt 93480

gtggaacacc acccgttaaa tcgctaacta cccaagccca gcatcgaaag gtgttgggct 93540

tttctttttt aaaaattact tgcgctctcg cttaaaatgt tgtataatag ttttataaat 93600

gagaggagaa ctaacatgcg tattatctct aaattaaagg acgtatatga tctacaaggt 93660

actatgtatg atgcagaaag agcatggtat cgcgaagaag tgaaagaggt tgtaaacgta 93720

tccgctgatt tcgaacaaat tattttctac gctgaaatct tgcgtaaccg cacttcctct 93780

ggatatgggg gtgttaatat gggaactctg gaagttcgtc cagtattgat ttgtggtaca 93840

ctacgctggc tgtacggtta tcacactggc ctaggagcag atgctgtgca tatccagact 93900

ttcgatccag ttaaggtaaa agaggtactg gaagaacaag gatactacct gcggatgggt 93960

tgggacatga atacgattga gaagatcgac gctcatgttc gtaacgcaac cgccacggct 94020

tctgcgttcc tggagacttt caacaagccc attgcgatgg catgggatgc cgcaaagtct 94080

aagacagacc caacggttaa tattaccgtt aaaactgatt tcaacttcca tgcggaagat 94140

ttcccgtggc aggaaattga tccaaacctg tatcgctggc accagacctt agaatcatat 94200

atcttcggtg tgctgggtca aggggaacca aagaccgagt ctacgtctga tcgtgatcgg 94260

ttaattgcta agggcttcga tgctaaagtt tctttcagga atatggagcg gtaagactgg 94320

agcaattctg tttctggcaa ttgcagcagg caccttcggg ggtgcctact acattaccaa 94380

taagctaaca gatatgtcca gttctttaca gtccctatca aaccgtaatg aacaactaga 94440

aaagacagtt ggtaatctcc aaacagagat tcgaaatcga gatcgcaata ccactaccta 94500

cataaccaac ctagctaaga accaggaaga tctggatggg cgtattaata aactggatgc 94560

agctagagcc aaagagggcg tggttgccgc taaacctaaa cttgctacca aagtggcaaa 94620

agacaaagtt aatgagttcc aggagagact ttcatgcgta actggaaata tggactcctg 94680

ctctcggctg caattatcgc atccgggtgt gcagaacggc cagacccaag tagcacagta 94740

acgggggttg agccacagca cctaccgtgg ccagcaagcc tacagacttg cccgtttaat 94800

tttgagttca taaacgaaga agggaaagtg tatgttcgca taccttacca agattggatc 94860

acgatgggca agtgtaatga gcaggtctac acctacattg ccaatctgac tgcattaacg 94920

tgtacctatc gcgtgtcact taatgaatat cgttgcaaac cgttcaataa ggaaacaaaa 94980

tgaaatacgt tttaggatta attggtgatg ccggcgcagg caaagacacc tttgctgaca 95040

tggctaaggt ttgggcctgg gaagtcctcg gtccggagta ttctatcagt aaatttagtt 95100

ttgcagctcc agtttacgaa ctcgcggctg taatccttgg agtcacgcca gaaaagctgg 95160

cagagcgcag gacaaaagag attaagcagt ggttttgggt gactcaggaa gcccttgagc 95220

gtactgctaa cgtctggaag cgttttggga tcgacaagta cgccgatttc tcttacgttt 95280

ggcctcagtt tgaagcgtca gcactatatc cgttgattgc taagactgcc ccagactttt 95340

atcaaggtcg tgagaccccg ttgtacccat tatacacgtc ccctcgtaaa atgctagaat 95400

ttgttggcac ggagttagga cgcgctctgg tggatgagaa cttgtggttg aatattgtgg 95460

tagatcgtat cactgctacc aaagctgaca ttagtattat ttctgatgtt cgttttgata 95520

atgaagccgc gctagttcgg aacttccccg gtgcgcagaa ctctagtatt cttaaagttc 95580

acgcccctaa caacatccac gctatccaat ctactcatgc ctccgctaga ggtgttgcac 95640

ctgagtttat tgatgatgtg gtaacaaata actttgacgg actggaaaat ttccgtaaaa 95700

atgtaaacgc attttgcgac gagaggattc tctttatata aggtaacaat atgggacaaa 95760

ttaataacgt agagcagaaa ggtggcaata agactcctaa ttacttcgcc tccctagtgg 95820

cgactaaggc agagtataat atttaccact atcatctcga tgggccgata gtcgatgtag 95880

actactaccg cgacctatca gtcactctgg caactatgca agagggagac actcttaatc 95940

tttatattaa tagtcccggc gggtacgttg atacagcagt tcagttgtgc aaccttatca 96000

tgaactgcca gggaaccgta attgggcacc tggttgggcc atcagcatca gctgcctgct 96060

caatcttcct agcatgtcat ggttggctgg tgcaccctta cgttatgttg atgggtcata 96120

cctatcgtgg tgcgcactat ggtaagggca aaaatgagat ccagcactat gctgatcagt 96180

ttaactcgtt cttcgaggat atgatgctag acctgtacta cccgttcttc tctctagaag 96240

agatcactga gatgatagaa ggtggtaagg atatttggct gacctccaaa gaaatcaacg 96300

aacgtgtaga tcgtatggct gcgcaccgag aacaagaagc tcgtaaggct gcgggtcaat 96360

aaaactaagt aggccagggc tttttagctc tggccttttt ctttatctaa attctacttg 96420

acatttgtct caaagtatga tccgagcaat aactataaat ttttattgca acttcctcca 96480

ataaagggta taattataaa tggttagagg aggttcttaa tggataaatt tatacagttg 96540

atatcgctgt tactacaaga agcgaaggat ccagcttctc ttcttaaacg tttgctaacc 96600

ttactggttg gtctagttat ctacctcttt atagctaata cgagtgaagt catgtcgtac 96660

ttaaagactt tctctacttc ggcggtccta caagatgtta aagtacaacg cacactagag 96720

tttccaaatg tggcacgaga gaaggcaatg atcctattct cacagactcg agctgatgcc 96780

gtcttcgtgg ttaaatacaa gcctgaggct ataaatgatt accaaactat catagcttgg 96840

gaaagcaacg ttcagttgga taaatccgat gtatccgaca aagcagttga caagacgtct 96900

atgctctacc gagcgcattt agacggtctg aactttgcaa ttgatgcaag ggaaaaacga 96960

ggtttatcga agtggtctgg aacgggtttg ccaccgttca agagtgcaaa tttcgagtat 97020

gtgtacacgt gcccatattt taaccttaat aacatctact ctggatatgt tgccgtcgcg 97080

tgggagaagt atcccctaca agacgaagac atgggtatgt ttaatgacta tatggcaaaa 97140

atctgcgcat cgccgcagag atcattaggg agatcaatat gagtttcaga tttggaaacc 97200

gtagtctcca gcagctcgat actgtagatc ctaaactcaa ggctctagct attcgtgctc 97260

tggaactctc accgcacgat tttaccatca ttcagggcaa acgtaccgta caacagagtg 97320

cccagaacat tgctaatggt acttcatttt tgaaagaccc tagcaagtct aaacacgtta 97380

cgggcaaagc cattgacttc gccccatata tcaatggtaa gattgactgg aatgacttag 97440

aagcattctg ggctatcgtc ggtgcattta aaaaggccgc aaatgagatg aacattgccg 97500

ttcgtttcgg agcggattgg aataactctg gcgactaccg tgatgaaatc caacgtggta 97560

cttatgacgg cggacacgta gagttactgt aacattaagg ggagctttta ggctcccctt 97620

ctttgtatgg agcaagcaaa taggaggtgg ttatgtttgc aagtttagta actataatgc 97680

tactcaagat atttcaattc ggtatagtat tcttttccgc aacatggatt ttaatacgcg 97740

gtgccattta ttttcgcaga acacgcttag ctagggttgc tagatggctt ctacacttcg 97800

tatttggtat tttcggtgtg ttccgctgcc catgtgagaa aaagagggga acagggttct 97860

gctggctctg gttaggtcta gagaattgct tctcattgtc cttagcgcta ctatttggta 97920

tgatagtcct agctataacg ctagcattta taccactaat gtacgcaggt ggggtgacgt 97980

ctatcctaac ccttacttct cctgtgttga tgtactcagt ataccccatt acactatttt 98040

tcgtaagacg aggcaagcac tgcaattaat gaaaaattca attgactttc cgctcgattt 98100

agcgtataat atatttataa attcgagaga ggagatacaa aatgtcagac agattctaca 98160

ctcaaatgtg cgagcatttt aaagtatctc cctacgagtt aaatatagct ttgtgggatc 98220

gtgaatcacc ggagtttaag aaaattgcta agaaatcgga gggtgttatg tccaacggta 98280

agaaaatgac ccgaattgac cttaacaatg cgctaaccaa actgctcggc gttaacattg 98340

agggccagaa gctctctatg ccaactttga ctactatttt ggagaaagtc aaggctggag 98400

atgttaaaaa agtagcagtg cctgagggtc gtctgaaaaa gccgtatcag gaggctataa 98460

ttgaggcttt cggagaaaag ctagacctgg ataccgcaac cgtaaaaaca atgaaagcac 98520

tactggagag tattaataat gtctaagaaa attgtattcc ttaaaggttc tagctgcgtt 98580

ccttgcaagc aatttgaacc agtttttgat aaactcaccg ctgagttcaa cctgcccgtt 98640

gaaaaacgca cggacgacgt agattcccta cgtaagttcg gccttcgcac tgtacccgca 98700

gtagtcctgg tggatgtgga gaacggacgt gaagaagcac atcacattct tagtggtgcc 98760

acgcttcgct ctgcagtagt tagtaaagct atccaagact ttatcgacta cgtagaagaa 98820

taatacctaa ccccggctca atacgagacc ggggtttttt attatttgct aaacgcttaa 98880

aattttgata taatatttat attgaattga gagaggatta cacaatgact aagcaagcat 98940

atcttatcct gaataatggt tttgcagttg gtactacctt cgttgatctg gggtatacaa 99000

aagaagagtg gcaagctctc gatgctgccc agaagaatca gcttgttaat gaagccgcct 99060

gggagtatgc agaggcttac gtggaggcgg tagatgacga gttagttatt gtcgtttccc 99120

ttggtgccgt aggttgtgat gctcatgtac atacagactt ccagagcgaa gaagagtggg 99180

atgagttaga tctaacccac caaaatgctc tgattaacga agcgttctgg gaagttgtag 99240

actgctacgt tgcgttctgt aaggacgatg atgaagctaa cacctgcact aactatggct 99300

atgaacacga cgatgtggag tgtgcataat gcaaaaattc tctagagact ggtcttctga 99360

tatggcccgt aaaaatcgag ctgctgccta ctataataag aaaatacagc tcgataagtt 99420

aataaagggt atcacctaca atgtagagag gggcttttct ggtataaaag tagatgctag 99480

gagcctggac tactcgtgca tactgtgggc taagcagaat gggtacgcgt ttaaacgaat 99540

aggcaatgag atactgattg cctgggaacc cgaaggtcta gtgcaatacg taatatacga 99600

cccttatcga ggggaatatg taagagatca caggcagcag cccacagact tctcgctgcc 99660

aaaacgttac tatttagaga cgaggtatta atgaacgtac atgaaacagt taccgtgccc 99720

gacaatgcta atatcttctt cattggggat attcatggcg agtacgacat gatgatgggt 99780

gccctgaaac ttgcagggta cgaggaaggt cgtgactacg tgttctgtgt aggggatctt 99840

atcgaccgtg gcccgaaaaa cttacaggtt ctagcgaagt tcctgtacaa cccgaaattc 99900

cgctctgttc gcgggaatca tgacgaattc atgatccaag acgactacgc taactggatg 99960

tataatggcg gtagctggac tatcacggaa ggtttcgata cggataccat gaaaggtatc 100020

gcggaagaca tggacagcaa gatgccatac attatgaccg ttgaacaccg tggcaagcgt 100080

tacggggtag ttcatgctgg tatccctctg cgctaccagg ctcaaggtat gggtgtaact 100140

gtaccggtgt gggacgacat tgtgcacgaa cacgaatcta caccagattt acgtcgtttg 100200

ggtgtactgc tgtgggatcg tgatgtaatc caagaagttg ggtttaatct gtatcgtagt 100260

ggggagaagc atccgtactt cgatcgctac gccagcttct ccgaggagtg cgcagtcgat 100320

gtgcctgaaa tcgtgggagt agactacacg tttcatggcc atactggtgt cccgttcccc 100380

attcgctgga agaaccgtgt ctatttggac acaggtggca cctttaacgg tcgtatgacc 100440

gtggcgtcgc cggttctagg tcaattatac acattcacca cagatcgtga tgatccttgt 100500

ggttccgctg acattattta ataggtgaaa catgaaactt ttcaaagatc tggaagaagg 100560

tgaagtattc gtagttgctg gtggcttcga gttgcagaaa tgtgtagcaa tgctggacaa 100620

cggaaactcc gtgtttacag acgacgcgaa tatctcggtt actattgccc cggacactga 100680

aacctggaaa cccaaagaat tctgggagat ccataaagat cgtccattgg acgacctact 100740

ggacgacatt ctattcacag cctgaggtaa atcatgaaac tcgaatctcg ttatattgta 100800

tttaagcagt cagatgccgc taagtatcta accagcactg ctattcggga gataaacgac 100860

agcttatccc tgatctataa aggccgagag gctgacggca aggtaggatt cccgaactat 100920

atcgttctag aagaggattg gccggagtat cctatcgcta aagaagctct agaaggacgt 100980

atcgtgctgg aagagtttaa taaaagggcg gagaagaaac gtggggctaa ggctgcagaa 101040

gatcactata agcagcacca gtctacggaa ctactccggg gtatttctcc attctgtgca 101100

gggtggaacg actacatgag aagactggta atcgaggagt aaccatgtat actggaatgg 101160

gaaatgatat ggccaagatg tttattggcc tcttaatcct ggctgcgtta gtcggtgcag 101220

caattgtagg cggaatctgg gcgctcgtag catttgtatt ttaaattcag ttgcttccga 101280

gccaattttt ctgtataata gctgtataaa ttgatgagga agcaaatatg aaaaacgcaa 101340

tgatcgaact gaatgcaaat atggaatccc ttcgccacgc agttaacacc gcccgtgctt 101400

cttttaacct gctgatgcgc gatgagagca taccgctgtc cgctcgtgtc aaggcatttg 101460

aggagttcgc cgatgagctt cttcatatgg gagactatct cagcgactcc ccgtttaatg 101520

aagatcgccg ggattatcaa cacgcctact gcaatcgtgg ggaaatagtt tacctgaccg 101580

atgttctgga gagtgtgctg gagtatgcga actctttcat gcgaactcct gacgaatggg 101640

aagacgcttc gaacgactat gttctagacg agattcaaaa gaactggcca gaaattaaga 101700

aactggtaga agaacacatt cattctgaag tttacgctta ccggatcgat tggtaaaaag 101760

tttaaaaatt cacttgctaa gtagttagaa tttcggtata atatacgcat aaattaacga 101820

aacggacgga aatcattatg gctaagaaca ctatctctta caccactggt aaaactgctg 101880

acgaacaagc taacaccctg accaaagacg aaatggttgc ggtactggta atcctgctgg 101940

atatgagtgg gttcgaaggt cagcttgcta aactgtctct cccggcactt cgtgctctgt 102000

acgaaggcac taacaaaaat gctgcggcct acaacctcgc taaaaatgaa gcgcgctggg 102060

ccaaggaaca ccagcaggtt gctgaacgtc gtgctgagag tttcgaacgt gacctgaaac 102120

gtgaaaaggc gaagaaaaag taatggtact agaaattctc tccgggctgt taatagcagc 102180

cctagtaact ggaacgggtc tggcggtttg ggtatcgata ctgcgggaaa ataaccggag 102240

aatgagatta accaacaacg ggctacacga gaagttgatg gatcaagtac aagatgctga 102300

tgaattctct gctgcggctg agcgactttt agttcgcctg gcgaagattg aagagattat 102360

cggccaagat tccacaatgt cgaagacaac caaaatgcgg ttgatcacgg agattaagaa 102420

atgatctcac caattgtagc ggcactttac ttagtagttg ttggctacct gtccgggaag 102480

taccacggct tcggtttaaa aggtactatt aaggcagcaa tgctggttcc tctgtatcct 102540

ctggcaattc tgttaaccgg gtactacgcc tgtgttttaa gaatctttgg ccggggcaaa 102600

gttaactacg ataactgcac agcgttgctg gacgatattg aaaacaccat taagaaggaa 102660

gaaaaatgaa ccttaactcc aaagaacgcc aagtgttagt agatgctctg cgtcaggtag 102720

tagaccacga tttgctttgt gatgaagata tcgttgagtc aattgcccta atcgccaaga 102780

ttgagcttgc tgagaaggac tcatggcgtc ctttgagtga gcttcctcct ctaggcttgg 102840

caatcgtagt acaacgtgct gatggcgctc cgtttaacac tgtgatggtt cgcagagatc 102900

tggcaaagtc ctactccccg gatatcatca cgttgcacac taagatcacc aacgaacctt 102960

tcgagtttaa tactcgtcac tattactgga gactgaccaa tgcttaatca gcttcgaatc 103020

tataatttcc tggattgcaa cttccaggtc tggcgagaac tccccagccg tttcctaggc 103080

tgggcattat tcctctccat ggtggtttca gtcttccata acgtcccagc gacgttctat 103140

atggaagcaa ttcaaccagt cactgtattc atttacgaga tgtacctcgt agcaattaac 103200

gggtggaaag atggccgcat caactgaagt tttaaatcaa tattttaatc gtgagcacca 103260

agagttcagc gatctgttca tccagatgtt cgtcaacgct aataacgctc tggactatcg 103320

tttcttcaac gagttccatg agaccacgtt cagccatcag gatattaact ccgctctgaa 103380

agaactcatt ggctctaaag tgataccatt ccgacagact gcaaatgcag agacactaga 103440

gcttagtgtc gtttggggct tgttcaagaa agcatatgag tttggcaagt atcagaacgc 103500

acgtcactgg atttacgagg tgtatctaaa cactgaagtc attctacctc gccaaatgat 103560

gttgggctgg attgcaaaac aacgtcctga acgcaatgca aaatcattcg caccaattaa 103620

cgacgggaac ttataccatg caagtgaaaa atttgatgct ccaaaatccg tggcttgatc 103680

gcctggcgca agtagagaag atgcttctgg ttgaaggtct gaccgaagaa gacatttgtc 103740

tgaactcctt ctacaactgc aaaactcatg taatgcaggc gctagacgaa gaacgtgttg 103800

aactgagtaa gtttatggtg aacatcgcca cagctcaagt tcactggcaa acccagggct 103860

tatccgccga cgatatcctg aaacataccc tgaacgctat tgcagagtat gggaaagctc 103920

gtggtgaagc tctcttggct tcaaagaaag agtttgataa atcggagtca atgctgaaaa 103980

tggcaatcga tatccatatg gaaggcatcg acggtactat tcactaagag ggtgacaaat 104040

ggctaagaaa cgcgttgtgg taaacttcct agaggaagat tctggggact gcgagtacgg 104100

ttgctggaat actggctacg gtgttgaggt tatggtggat ggcaaatgcg tccaccgtca 104160

ggaagcctgg gcaagctgca ctaacaacag cagcgtagac tttgacgtat tggcccatgt 104220

tcttcagggc atcaagacga aagaaggcta cccggtcaaa gcagatcaca tcgactttgg 104280

agatccttcc gattatccag aggagtttct ggatctgttc acctaacaaa gaggccaggg 104340

ctaattgctc tggcctttcg tggtttaagg atattaaatg aaatctatag acaactattt 104400

gcgcggggaa aaccctgtag atcaagcagc agttactgtt gaaaaggtca ggaaagagtg 104460

ttttatactt actcaacgtg gaggtggtaa tcggcctaat cgagtgtatc ttaattggac 104520

tcagtccaaa gacctgtatg agaggttgaa aagggaattt gagtagtgga agaattaaga 104580

cagaagataa atcaagagct agtatgggaa gctaaatcct tccccattaa tcaattcctt 104640

aaacgtgacg gttcgatcaa ccataataag ataaagcaac ttaggccaga tttcaggcaa 104700

gatgctaaga acctcatctt tattaaccgt gctctagacg ctcatggagt attcttcgga 104760

tatgagaagc tagtgttcca cagcctaaat cagctggtgg aaatatggtg tcccgaccat 104820

caagattact ttatgcaaac tgctagaagc caccttgagg gtaacggttg ccaaaaatgc 104880

aggcaccgca tggttaccag agttacggat tatggaagtt acaccgtgcc agcatactat 104940

cacaaatttt caattgacgg agactccatt atttggtata ataactccag taaattgata 105000

aaacctttgg aggttaaaga tgaaatacga ttccctgaat aatccgagca ccaactatct 105060

gactgaccag tcagtttctg agatcaagtt ccatccgaac tactccccgg actctagcaa 105120

gccgagtgta gcagctatct ccttccgctt ccgcaatctg cgctttacgt tcgttggaga 105180

ggaagacaag atgatctcta taattgacaa ggttaaagca gtaagcgagc tgtccggtag 105240

cgataccgtt aagttcgaag cattaacctc gttgctgctg actagtgggg ctaccgttgg 105300

taagttcgaa cttattcagc cgcatgtttc tgcactgacc aataccagaa acttctggga 105360

tcaagccaat gtcgagagtc tcataaaatg ggatagtgct actgagttct acaacaagta 105420

agagggctag gatatgttat tctgtacagt tgattttgaa gaagctaacg aaacgtatat 105480

tgtctacggt atgtctgaaa gcaaagtacg tatcctctgg aatcagttcc aattagaagt 105540

accggacgac atatccaaga ctccgaaaga cttctttcat ttaatagata ttaaggcagt 105600

aaaagctcgt aagaagctaa ctccttatgt gttcccaggt gcagtattcg tccatgagtt 105660

aacagcgtat actaacgtgg ttctcaaaaa gtctcgacag cacccaggct atctcacgat 105720

gttgacgtac aaagttggag ctattcacga cggtgagctg gtggttcggg tagatgcacg 105780

cttgcagcaa gaagtcgaag aaatgattag gcagtgccaa aataaagcag aattaaaaca 105840

aagagcacgc ctattcgaca tggcagcacc tagcgaggca gttgccgcat atcacggctt 105900

ttataaagaa atagctgaat ccgatgaaga tttctttatg taagaggata acacaatgaa 105960

cgagaaatat gaagtatgga ctccggttgg ggagaattgt agctatcttc ttcgtaccct 106020

gtgtactcgg gaagatggca catctttctc agaatacttg agtgaatgcc acgctaaggc 106080

ccagcaggac aacccgctat ttaagatcag aggagaggat atcctcaaag ttaacggcgt 106140

gccgtacacg ccagtggaca gtttcgccgc tcttcaggtg tttaaggaac acagagagcg 106200

ggagcaccgg aggatgattg aacgcttgac aggtagagag ccgttttcac atcctaggtg 106260

gaatgaggag acataatgag cagagttgaa aagctacaac atatctataa cctggttaag 106320

aaagctgacc aaaagaaact ctcagagctg agtgaagaag agtatcaagc agtcctcttc 106380

tgttgttcgg caatgccagc gaagctcgat ggagtactgg caaagtcaga catccacaac 106440

ggtaaggaaa caactttcca gccgccgtat aaatggctag cgtccaacat ccagcaaatg 106500

gtgggtaaag ttacgggatt ctcaaataga aagacgccta acatctttat tgacattact 106560

cctagaaccc ctgagtttac gaaggactgg agagacgcat tggattcatt tccgtcatgg 106620

aaagtctttt ataaacctga cgatgaaacg tatgcacatc ttccctttt gaagcaccca 106680

ggctacacag ttgaagaccc aagttctggg gttaatttca aagacttcaa gtgtactgac 106740

gagaacattg cttacggact catgagaaca tccgtgagga ttgcaatgga tcatgaacta 106800

gacaaacaag atctagcagt cattgcactt tgtaaggatc gttatattaa agttaagagg 106860

atcgcagaga aactttccgt actttcttgc tttgaaacaa tccgagattg tgaaccagag 106920

ggtgaatatc ctaaaggttc cctctactgg aaagatgtta aacatctagg actatcagaa 106980

gaagccgtat tcctaggctt agtagttacg ggaagattcc tgaggctaca ggagaaataa 107040

tttgtacttc gtctatattt tcgctaatga agatcagcgg cttatcccta ggcggaccaa 107100

ggtgggttac tcgcgtgacc cattttatcg tctaaattcg cttcaacttc acagactacc 107160

tcatcgtgga ttacaggata tcgttattca ttctgtctat ataatagatg acgccagcga 107220

gttctcagca aagttgctag agaaggccgc gcataaaaag tttaagccta tgcgagttaa 107280

tttcggtgac aagtttgatg ggcatacaga atggtttgat gttgaacctc acgttattga 107340

gaagttcttc ctgtcagttg gggcaaaaca agtacctatt gacaaactca tagcccaaga 107400

acaaaagatt cgtaaatcca cgaaaaagta gttgaaaaaa aataaaacgc atgttataat 107460

aatctcatag attacataca atttgaaaaa tttatgaagc taggcggatt atgaaccaga 107520

atcctggact cggggcgacc aagcctacga tgtcacagag actttctggt ctcacataat 107580

ccgcatgcct agcgcttcgt aatctcacat gaacgatgga gaacctataa ctataataaa 107640

actaaggaga aaatagggaa acgtgggaat gaactcacga ttactcacgt ttaaaagtag 107700

gtaatcctta cacaccatcg tttcgcggct ctagggttga actctagtca tctttctata 107760

cagggcggtt ctttctacac acctaagggg agggcggtta ttttccaacc ctaaaaatcc 107820

ataaccattt tctggaattg cacaaatttt cacaccgtct cacatatccc acgaagccct 107880

cacacatctc acgcaatccc tctagtacgc ccaagttcta agcgtcactc cacaaagtcc 107940

tcacgaagtc cccacacaaa cccacgtcat tcacccaagt tctaagcgtc aaacattatc 108000

ggatttgcac attgctccta gatattaaag aagccaagca tttctagatt tctagcaatt 108060

gtcggatttg cacatgacaa aacgattgtc ggaaatgcac attaactctg aatccaaaaa 108120

cacggtcgaa tttgcacata taaaaactac tatcggattt gcacatactc aaacgcttgt 108180

cggaaatgca cattattact gaagtacggt agctgtggat caaaatcttc gattctgcga 108240

atataaaata tctcctgaaa tttcaagcct ttttacacgg tgtgtcaccg tgagttcgct 108300

tgtttttag agccacagga atttttctg tgtcaacccc tttaccccca tttaactcat 108360

aatattttcc cttatctgcc ccctgccccc atcatccccg aattgcccca attaaccccc 108420

tttatccctc ccccaaaaat acccatcgga tttgcacata ctcacccaaa ctcgcgccca 108480

ccgctgcgct gcagcaaact gcgcgccttc cccctaaaaa ttattatcgg ttttgcacat 108540

attagtatcg gatttgcaca tgcccctagg gcggtaaaaa taaattttca tcggatttgc 108600

acatacccta gcagcctcac gtaatatttt gcttgacaca ttgtcggatt cgcacataag 108660

cgcaggaagg gccgggggtc ggaaatgcaa atacgaatga gagtgattcg catttgagaa 108720

gttgaatgcg aatgataatt attctcgttt gataagctga atacgaatga gaatgattcg 108780

cattccggaa aggaagtgag aaacactatc atttaagtta tcaccagagt tatacaaaat 108840

tgtaaattag cttgacgctt gagaaggtcg cagacgagtt atccacagac ttattaacag 108900

gttatcctac tggttattta tacagtagtt cccggcaaca ctttctgcta atgtcgattt 108960

taagcgccct aggaagcgtt ctaagcgatt taaatttcgt gggggtattt tagtaagggg 109020

tcacgcggtg gaggagggcg gcgacactct tacatatcgc cgtggaaaca ctcaggccaa 109080

aagtgattta caactgaaac tattagcagg gtaatgattg cgctaataac tatcatgccc 109140

aaaaacatta ggccgctcat tattggcagc tctgcaaaaa gactagggtc ataataataa 109200

ccatgatgac acgaaaaccc cactcaccgc cgccaccgtc accgcctttc ttctgaccgt 109260

cacgaataac gttcaattgg taagtattgt ggctacggct tttgggacta ccaccgcgta 109320

aagttcgcat taaaaagcct ccttattaaa caaggtatca tagagggcat agccgcaaaa 109380

agcgataaaa cccaaaacca tcatagaacc aactaaaccg agcgccaaca ttgaaaaagc 109440

cattttcga tctcctatat gggtgagtca taataataac ataactctag cgggaagcaa 109500

ctactatttt tagtagtaga caagcaaatc cgatttccct atagtttgat ctcccggcaa 109560

gcatagaaaa attttgcttg ctaaaaagcg gagaatcttg ctataataga ttctcagcca 109620

aacaaaggag taacagaaga tgttacagaa atttaccccc gttgcaaatt tgcctatggt 109680

tcgcggtggc gctcgcaacc tgttagatgg tagtaaatgc gcctctatcg gtcatatttt 109740

aggcgtttac cgctcgaata tggaaagtag aaccagccgc gcttttgaac atagccgcga 109800

ctacgttcta gccaaccccg gcgctgcgat tgttattttt cacgacgatc aatatttagt 109860

tgacagccag cctattgatc tgatagtatc taccactacg gacgcttatt tgtataaggc 109920

atccgaaggt aagcaagcgt caagacgttt ttgctaccat gaaagcgaac tgctcgcttt 109980

caccgatgcc cgcgcatgga ttaaaaacct gtgcgatcat ctggaactac caccagcacg 110040

aatttctagc gaaatgatga tttttgtgct tgacaaagac ggaagcatcc tgctaccatg 110100

tgacccttac gatattgata tcgaagaagg ggcaaggact ggaaattatc gttatgatgg 110160

cgagctagaa gaagtcgccc cggctgttac tgaaaatgta gttaacccta ataattttga 110220

gactggagca ttacaaatga atactatcaa atctaccgct accgctatcg ttgccgctaa 110280

caaaaacgct gctgtaaacg ctgctaaact ggaagccggt tctatcgtcc tgaaaaaagt 110340

ttccggcatc gccgccagca aagcgccgtt tatggttcgc ggttatgttg acacggcggt 110400

aggtcgtgtg gtaattgcta acctgctgaa tttcgcggtt agccagtatg cgccgaacaa 110460

ccgcaaagcg gtgattgcgg ctgacgctgc aatgcaagcc gccatgttgg aactggtaca 110520

aagtttcaat gtaggcgaaa tgattgacga agtattgaaa ggcgtcaatc tttctagcct 110580

gattgaaagc gacgtagcag aataattata tctagcgcct ctataatggg gcgctataat 110640

aattaccctg ctaactaact ggagacaaaa aatggaacgg ctaaccgcta ctttcgaagg 110700

cgaaaagatg acgatcgcta atgtatggca gcgcctgcgc cagaatggcg atcgtggcaa 110760

ttttgctatt ttcatcgagc caaaaaactt ggataatctg gctcgccaga ttgaccgccg 110820

ggactgctac ccggatacag atgatatgct gggaatcccc ttgcggatta tcggggtata 110880

tggttacggc tttgatatct gtattggtga tagtagcttt gaaatcgact gcgaatccgg 110940

cgctaccgaa atcgaagtat tcctaattaa tttaggctcg ctaacgtttt tggatacgcc 111000

accagcggaa ccggaaccgg aaaagctgga ggtgaaaacg tccgttattg ttagttcgct 111060

aactatggat gagctggcgg atatcgtgtc aacgtatgac gaaattcacg ccgacgcgat 111120

taaagagcta aacaaccggc ttgatacttt ccgcgataag ctgtaaaatc cctcccggcg 111180

gctaaatctc tagccgcccc cattattgga gaaaaccatg tttcatgtga aatcttgcgt 111240

accgggcatt aattatacgg tagaagcgga agaaggttta tatttagagg gcgggcgaat 111300

tgagtctcag gaagtcgccg ccgtcctcaa atgtgacact aacgtttgcg gtacgtcctg 111360

gactgacctt catttttag gtcgtggaat tgacgtcgat tccctttcct gggaaaaggc 111420

ttgcgaacat gctgaaagta tgctaaacga ggatgattgg gatgatgacg acagcgacga 111480

aaaatacgcg aatgctgggg tagaagggtc gttttatatg tactggcccg gtcattcctg 111540

caacctcgtt aatggtggtt cgcccctcca ttccgttcta gagcgggcaa tctatttggg 111600

ctatatccag atagttgacg gaaaggcagt cattaatctg cgcgaattga aaacgtttat 111660

ctatatcccg gatgctgaaa ctatccttca tattgaggaa ggtttaaaat ccggttggaa 111720

ggttagcggg gtcgtatacc tatgatttac atctatgtca acaaatattt tctggcgcac 111780

tataaaacga tggaatctgt gatccagtac gttagccgcc agaatgcaag gcatattgat 111840

gaagtggcta ccctcaaaat cggattgcgg ggcgatgcta tcaatattag ctggcctttg 111900

ctaattctga tttgccgtga tcttgtagcg ggtaaacctg tttccgtttc cgcgctgggg 111960

gaatcttacc cgctttccga tgatctggat ctctatgatc tgctaaccaa atataaaact 112020

gaacgcctgt tttatcgtgg cgggtcggta tgctctagcg gcgaaacaat agaaacggta 112080

ttccgctaat agttagctaa ctaatgataa gcctgcttat aatgagcggg ctttttattt 112140

ttctgcgccc ctctagcaat ggcctttaat atggcctcta aatttaaagc gcttagaatg 112200

cgttatagag cgttctagag gcatattaga gtattaccgc tgccggaata tactgtataa 112260

atatacagta ggataacctg tggataagtc tggggatatc tcgttatacc gcttctcagc 112320

ttgtcaagtc aaaacgtgct gtggataact tgcccggaaa acaggagtgc agcataaaat 112380

aaacgcaagc attattttgc gttttcataa aaataatcgt ttgtctagtg gataactaat 112440

taaatttcat ttttgctttt tgtataagtt attaacaggg tctaaaacgc cctagaatcg 112500

attctaagcg gttttagata aaagccgatg aatcataccg ggtatgaggc gatctcctca 112560

cctcgtgtga aatagatttt gtcaacccct tttgaagaaa aatagtaaaa atattcgttg 112620

actttcttta aatattgtgt cacgtgcgcg cgcttcctat ctatcgtggg cctgttttct 112680

ctttacgctt ctttacaatt ctccgcttgc ggctaaacgc cattgtgtta ttatttatct 112740

cgtagggcgg caagacgaaa cggaaacacg aaagcgtttc actagtagtt aggtatctgg 112800

aggcggcaac attgccccga ctaccgcgaa aggaaaggcc gaaacgatat agtctgcccc 112860

cgccctacac tgctctttaa aaatttggga ttctataaaa agcgttatcg gctttcttta 112920

cttaataagg gaaccgaaaa catgttaaaa gaaaacgtaa tgagtagcga gattgtaaac 112980

gagtttacag tagcagacgc cgaacatttt atagagactt atttaaatgt gtacgacgta 113040

gatttagcct tcattcataa agacggccaa atc 113073

<210> 2
<211> 31078
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 2
aaacccggag caaggccaag cagcagccgc agaaagtacg ccagcagatc cggcggctaa 60

tgtttcacgt gaaacgaagc ccgaagattt aataaaaaac gacgtggccc cggctgaatt 120

aaccccggct ttttatgtgg tggctgaagg tcgcgcgatt acgtcaaaac gtggcatttt 180

ggccgctggt gaagcagtag aggcccgcga ctttgtaggc ggtgaagaaa cgctaaacag 240

ccttttagag cgtggtttag ttgaatgaat atccgagatt tagcggccca agatttcctt 300

aatatcgtga atgataaaaa tagcggtttt ggcgttcccg tggtgttaat tgccccggat 360

ggtaacgcgc agccgttaag cggattaacc acggatatat cgagctatat tgatccggaa 420

acgggcgttt tagttgcggg ccgtgttgca tcggtcacat tcgcaaacaa ggcaatccgt 480

gccgctggat tcgcagaaat gcccgtagcg gtggccgatt caaataaacg cccgtgggtg 540

gtgtgctttc gtgatcctga aggcatcccg tatttgttca aagtggttaa ggctatgccg 600

gatcgcgcga ttagtggcat agttttagaa ttggaagttt ataagcgttc tatttacttc 660

aatggggctt ataaatttga tgggacgacg ttatacgatg gagttttaga cttgttatga 720

atatagaagg ctttaaaaaa ctgcaaagcc cgattaacaa gctagatagt tttgaaatag 780

tccgcgacca gatcgcggct attttatttc ttgagcttga aaatcaaaaa gccattgctg 840

ggcgcgcgca gattgacccc gctagatttg atatgaaagt ttataaagag cgttctaatc 900

cgtgggatct attcgacgat ggcgaaaata agcccattat taacgtgtgg tttagtaata 960

gcgatttcga ttacaccaat agcagcacag tcgataagca gaaaaccacg gctattttta 1020

atattgattg catagcgacg gctataagcc aagaaacagc gaccgggcaa acgctgggcg 1080

atgaaatggc atctttagag gtgcagcgcg tggctaaagt gatccgaaat attttaatgt 1140

cagatacaaa tacatatttg caattgcgcg ggcttgtttg gtcgcgccgt gtgctgtcat 1200

taaacatatt tcagcccagc gcagaaaatg gaatgatgca aaatctatgc gcggcccggc 1260

ttgtacttca ggcgacgttt agcgagtttt cgccgcagta tgaaccccaa gagctagaga 1320

ttttgtccgt aactgtccat aattgcgatg gacaaatttt atttaacaag gagattgcta 1380

agaatggcaa ttagtaccgc tgttgatata agcgcggtgg cccgcgtttt aggtatcaaa 1440

acaaatttta aaaatttgcg ggatggtcgt gtggtgattt tgccgcagcg gatcgcctta 1500

attggtcaag gttccacggg gatggtgttt gcaacgtcaa aacgacaagt aacaagcgcc 1560

aatgaggtgg gttcgctata tggttatggt tcaccgcttc acttagcagc taaacaacta 1620

tttccgaata atggcgacgg agtggggacg atcccggtaa cggtttaccc gttaagtgat 1680

gcggacggat cgcaagcggc gaccggatca attgagcttc tagggacgca attagaatcc 1740

ggggcttata gagttgttgt gaacggtatc cgttcggaac aattttcaat tttgattaat 1800

gaggccgggc aaactgttct aaatcgagtt gcggcggcta ttaactccgt tttagatatg 1860

ccagtacgtg cgacggcaga ttcggaactt caaaaagtaa cgcttgtttc aaaatggaag 1920

ggtttaagcg ctaatgctat ttctgtccaa gttgatgggg atttagggca aggtatcgaa 1980

tttgcagtaa cgcagccagc gggcgggctt attaatccga gtgtttccgg tgcgctttcg 2040

cagtttggca acgtatggga aacaatggtt ttaaactgtc ttaatattca ggataccgaa 2100

gcattaagcg cttattctga ttttggggaa gggcgctggg gtgcgttggt gcgtaaaccg 2160

cttattgtat ttacggggaa tactgaagcc gacgtaaata gcgccgtttc agtcccggac 2220

gcgcgaaaac gtgatcggac aaatgttcaa cttgtggccc cggattctat cgatttgccg 2280

ttcgttgttg cgtcccgtca attggcccgt attgtaaaaa ttgcaaacga aaacccggct 2340

tgtgattacg gcagccaagt agccgacggc attaaccccg gcgaagatgg gaaacaatgg 2400

ctttataacg tgcgtgatat ggccgttaaa aaaggcagtt caactattga aattcgggac 2460

aatcaagtat ttatcgggga cgttgtaacc ttctatcatc ctgaaggtga agaaaatccg 2520

ccgtatcgtt acgtttgcga tattgtgaag ctgcaaaaca ttatttttaa cttaaatcta 2580

atttttgccg tgccggaatg ggacggagcg ccgttaattc caaacgatca gccgaccaca 2640

aacccacgcg ccaaaaagcc ttctatggcc gttgccgcta ttgccagcct tgtggatagc 2700

ttgggcctaa atgccattat tagcgatgcg gcatttacca agaaaaacac gtttgcacaa 2760

attaatgaac aaaatccgaa gcgtttagac gtttcgacga ctgtaaaact tagcggaaat 2820

acaaacattt taagtgtgga tcttaatttt ggtttctatt tcggtaattc ggtaattgtg 2880

gggtaaataa cttatgtcag ttggtggcag cattgagagc ttaactttag acggccgaac 2940

cttcagcgta gcagcggacg cggattcaac gcgcaattta ggcggcacgg ataacgaagt 3000

agaaatgaac ggggatggta cttatcgaat tgtaaaaacg cgcgtaccgt caaaactaga 3060

cggtatcacg gttgcaattg atgacgtgcg cggggatgca gaatacttgc aagagctaaa 3120

agatcgaaaa gagggctttc cctattcgat tacatacgcc agcggtgtga tttatcaagg 3180

tacggggaca atcgtaggag aaacgggaat ttctagccaa aacgcgaccg cttcgattac 3240

tatttcggga tcggctttaa ctaagcagta atttacagcg cggccataag attggccgcc 3300

ctttcttaat catttagggg gtttcacgtg gaacatatcg aaaatactga aaatcaaact 3360

ttgtggggct tgcctgttaa ggttgcgcgt gaagttgcgg aggctgaatt tatccgcttt 3420

tgtgatgcta tggacgtgga ttacaacacg gatcgaatga cggacgaaga tgcaaaagac 3480

tttaacgaaa gtaaagggct tttgcttgat gcgctgcaaa ttggcgtttt ggaaattgat 3540

agcgacggca tggccgttgt ttacccgaaa aaaggcgata ttaagcaaat taaatttaat 3600

gagctttgcg gggcggatta cgtggcaatg gacaataaaa aggatacgca aagtttcgct 3660

aaaatgttcg caatgatggg atctattacc aagttaccgc ccgcgacttt ctcaaaactt 3720

aaaaagtttg atgcaaaagt ttgtttgtcg attgctaaac ttttttggt ctagtcgata 3780

ccgttttaat cataaagggg ggcgaggttc gcctatcccc ttcgagagat tcggatggta 3840

tcgagcgcgg gaataatacg agatttcaag tttattcaac gatgcttatg cagatcctaa 3900

gagattataa cttgccgaat tttagaacct taacaagttc agaaattcgg ttttttatga 3960

cggattgcgg gccgagttga aagaaacaac aaaaccgagg aattaatgag ccgttacagc 4020

gtagaaacaa tatttagggc cgtggatcgc atgacggccc ccatatcccg gatgcaatcg 4080

ggaattagtc gatttactcg ccgggctgaa agcggactta ggcgcgtttc agatatgacg 4140

tggaatatat ccaaagtatc aggcgcagca gccgcggcca ttggtggcgc atttatggcg 4200

gccgctggtg gtattgccct ctttgtcgca gaaacaaacc gggccaattc agaaataaat 4260

gaaatgtcca aagctatggg ggtttccgcg ttatccgcaa gggccgcaga ttccttgctt 4320

acaccgcttg ggatgaattg ggaaaattac acggatctta ttgaagaatt gggaaataag 4380

atgggtgaat taaaaaacac gggggaaatg aaaacatttc aagaggctat tggacttact 4440

aatattaaaa tgaaggaatt aaaagcctta aagccggagc agcaatttac aagaattatg 4500

gattctttgg caaaaatgga ggatcagcaa aaagcccaat ttattgcaga tgaaattttc 4560

gggggtgagg gtaataaatt cgtttcagcg ttaaaggcgc gcggcttgac tatgacgagc 4620

ttgattgaaa attataaaaa gtacaatttt tataatgagc aaggcgaaaa agcaacggcc 4680

gcttttaatg cagctttaac cccgctaacc acgacggcaa attcggcaaa atcgcagatc 4740

gcggccttaa ctggtggcgc gatggttcca tatattcaaa aggcgacgga atgggctgcg 4800

gcaaataagg aattaattaa tagcaaaatc gaagtattcg ccaaaggctt ggcggattcg 4860

cttgtttggg tggtggttaa tttttccgag attgtgacgt gggttaaacg tgtcgctatt 4920

ggtatcggca tattcttagc gcttacagcc gttttaaaaa ctttcgtttt gattatgacg 4980

gccgttaatt tagtaatgat gatgaacccg atagggctaa tcattatcgc cgtggtcgcg 5040

cttattgctg tcattgcgta tctgattaat aagtttttg ggttgcaagg tgtcattgcc 5100

gcggctaatg gtgtgcttat ggggattggg gccgctattt tggtggcgat ggggccaata 5160

ggctggctaa ttggggccgc tgtcttgatt tggaaaaatt ggggcgtttt aagtggtttc 5220

tttagtggtt tatgggcggg tatcgtttca gtttttcagg gcgcgcaaaa tattattatg 5280

gggatcatta acgggattat gggcgcaatt gataacgtga ttaataaagc ggtttcgatg 5340

ggttcggctg ttaagggctt ttttagcttt ggcggcggtg gtggtgatca aaagcaagca 5400

gcagcagcgg gcggacgtgt ggcaagccca caagagcgaa ccgcaaaaag cgtaacggaa 5460

aataatagcc attcaacggt aacgatccaa gacaaaaccg gacgcgcgaa aatgtcaggt 5520

aaaccgggga atggggttcg attggttaaa acggggacta tgtaaacaat gagttgggaa 5580

gatcgtttaa aggaggcggc ttacaccgcc cccggaggta cacgggccac gttcttagtt 5640

gaggacgttt cccgtagttt tgataaaaaa acaaatggtt tcacgttccc ggatgcgtcc 5700

gggacttatg ttcaagattc aggcgtaagc gggtttaaat atccgctgac tatctatttt 5760

agtgggccgg attgcgatgt ggaggccgaa gcgtttgaag cgcttttgag agaaacggga 5820

atagggcgtt tagagcatcc gctttatggc gttattaacg tggttccgtt cggtacgatt 5880

acccgtaccg atgcaattaa aaccgaggca aaccaaacaa aaatagagct ggaattttgg 5940

gaaacaaacc ttttaattta cccattaccg caagccgacc aattaagcgc cgtatttgag 6000

gctatttccg acgttaaggc ggctttaagc ggtgatgtgc tagatagtat cgacgtaacc 6060

gacgcgagcg ccctagcgcg atttaaaaac aaaataacgg gggctttaag caaggtaaaa 6120

accgctttag ggaaaattaa gaatttagcg gacttgccgg ggcaattaat ggacaaggta 6180

aacggcttaa tttcgcccgg ccttgagttt atttccgatg ttaaagccca gcttggcgat 6240

gtggttaatt catttttga gcttgccacg ttgcccgaac aaattgtcga ttcattcaaa 6300

gagaaaatag cggtctataa ggatctcttt agcgaattaa cttcattcga gggcatattc 6360

cccagcaatg aagaatacga ggcagcttgt accggggtaa cggtgacttt atccggctta 6420

gtagtggatt tggttgaatc tgaatttaat acacaaagcg aagcattgga ggcggccgag 6480

gatctattag ccatttttga tgatgtaacg ggatggattg aagaaaaggc gcaaggcttg 6540

ggccgtaccg attcaaacgc ggtttatcag cgcttacata gcgccgtgat gaccgcggcc 6600

agctatttgg ttcagcaatc ttttacctta aaaaaagagc gtaaattggt tttaaaccgt 6660

agccgtacaa ttattgattt atgcgcggag ttatacgggg aagtcgatag cgctttagat 6720

ttctttatta cgtcgaatga tttaagcggg gctgaaatat tggaaattcc gaaagggcgc 6780

gaggtttttt attatgtctg acgtttctat gatgatccac gggacgcgct ttcatttttg 6840

gagtggtgta aggatctctt taaatattga cgcggtggca acgattagtt ttaacgcccc 6900

gtttgaccat gaggcccccg gatttaagcg caatttcgcg ccgtttggat tttccccggt 6960

tgctatcgac gtggacgatc agcgcttatt taccggaacc atgttggacg tttccccggt 7020

gattagtgaa gatggtaaaa aagagatttc cgtaaatgct tatgcaaaat gcggagtgct 7080

tcaggattgc accgccccgc ctgaatccat gccattagag ttcaataaat taaacctgtt 7140

ggatattgct agaaaaatgg cctcttattt tggggtgggt gtggtattta atgcagatcc 7200

gggaccggct tttgatcgcg tggcgtgtga cccggataag aaagttttag aatttttagc 7260

ggatctcgca aaacaacgcg gctttgtgat cggtagcgat gaaaacggca atttactttt 7320

ttctaaaagt tcaatcggcg gcattgttgc taagttggag caaggcgtat ccccgctttt 7380

aagtgtatcc cctactttta acccgcagga atattattcg catattacgg ggctatcccc 7440

tgtcgaagtg gcaaagcccg cggccaaaag cacggccaaa gtaaaaaagg acgctgcaac 7500

gcctgaaaaa gcagggcagg ggagcgaaaa ggcgaccgat aaggcgggcc aagccgaaat 7560

taaaaaggaa ccaaaaaaag aggaaaaaac caaaaaggaa aagcaaaaac caaagcccac 7620

gacttataaa aagtttacag ctatcgacga ggcccccgta tatcggccat tggtttttaa 7680

aattgatgat gcagaaggcg cgaccgatgt agaaacggcc acaaaagcaa aaatggcccg 7740

aatgcttggc aatatgtgta cttatgcaat tacggtttcg acgtggttcg atgcgtccgg 7800

ggatttatgg cggcccaata ctaaaattaa actcaaggcc ccggattcaa tgatttatga 7860

ttttttcgag tttgatatta aaagcgtgga attgtcggcc gatgaaaaca gccaacaagc 7920

aaatttaact ttatgtttac cgggttcgtt tacgggcgaa cccccggaga ttttcccgtg 7980

ggaattgtag cgactgtatt aagtaatgat ggtaaggatt taaaagtaga tcggggcaac 8040

ggggacaacg taacggccca gcagttcggc ccgtccggtg atgatgctcc cccgcttaaa 8100

aatgattatt cggttttagg atcggccaaa ggttcaggca atgccagcgc cgtggcctat 8160

cgtgaccaaa aggccgaaaa ctacatagcc aaagcagggg aaaaacggat ttattcgcgg 8220

gatgaatcgg gggcggtaaa agctgaagtt tatttaaaag cggacggaac cgcggagatt 8280

aaaaacgcca gcgggctttt tgttatggag ccgggcggtg atgtggtaat aaatggggtt 8340

agaattacta aagccggagt tattcaaacg ccgggcgggg cttcaatgag ttctgatttc 8400

acaaacgcgg gcggaataac tttgggcgac catgcggccg atacaagttt acataagcca 8460

taaggggaa tagtttttaa tgtctttttt tgatgtgcat ttatttgatt cagtcgatgg 8520

cggcaatgta acggatgatt tagaaacgcg ggacggccta gaaacggctg tttatctaag 8580

tctttttggc ggtaatgcct tagatgatgg aaggccccaa aacctttcga cgtggtgggg 8640

gaatattggg gagaatgaag cggcaaagca atataaaagc gaagccgctt ttttgcttcg 8700

cacggttccg ccgaatacag ccaatttaaa gcgaatcgaa gcggctgcat cgcgggatct 8760

tgcttggttg attcctgaat atgtgaataa gattcaagtt aaggcgttta tgcctaaatt 8820

gaatgcggtt aatttaacgg tttctttgga tggtttagat ccgttgcaat tccgtacaaa 8880

ttggggcgaa aaggttaaag agcctgttta tagactattg ccgcctaaag tttcccgaaa 8940

taatggggtt aatttagaag gcacagcaga aacaaaaact aaactaattc ttatccgtgc 9000

cgatggatca agattaagta cgctggttga tggttcaggg aattggaaat ttgattttta 9060

ccctttatat ggtggtgaac gtgcccggat gtatgttgag ggtgtagggg gtaaaatatc 9120

cgctattgtt acagttatcg gggttttacc gcttcgctat gatgggatgg caatttatga 9180

cggtacgcac aaatataacg gagttagatt aaattaatga gtacgccaac gactaaagaa 9240

atatcgaacc gtattttatc caagttagaa acgacattcg ggcaaagttt gcctaagtct 9300

tttacacgtg ttttatccac ggttttgggg ggtgtgtttg taattttata taaatacggt 9360

ggttttattg ctttgcaaat gtttgtttca acggccagcg ctaaagatac ggactttaac 9420

ggcaaaacaa ttaacccatt acgcgaatgg ggccgcctca ttggggcggg tgatcctaat 9480

ccagccgtta atgccattat tttaacgcgg attgtagtag aaaagccggg cgagatattg 9540

cccgcaggga cgcagctagt aaacagcggc aacggtgtta catacattac ccaagaagat 9600

attgagctag tcgaaggggc gcaagatatt gaagttttag cggcttcgga tacttcggga 9660

aattcaggcg caggcaaagc gggcaattta aatgcggggg atgttttgac ttttgcgaac 9720

ccgcttggat cggttggccg ttattcgact gtggtaacta caattcggga aggcctggac 9780

gctgaagcta tcgaaacata tcgcgcccgt gttgtttcac gtttccaatt gcgcgctcaa 9840

ggcggggcaa tggtggatta taagatttgg ggcgaatctg tttccggggt tagtcgaatt 9900

tatccttata cgtccgattt gccgggccaa gtggatattt atgtagatgt tttggagggc 9960

gtagcaagtc aagcgatttt aaatcaggtt aaaaacgccg tcgaatttga tgcaaataac 10020

gggcttgcac aaaaccgccc tttaaatgcg ctggtaaatt atttaccgat ggagtttgta 10080

gaatttaacg taacgattag cggtttaagt gttgagggcg cgctatctgt tagggctgaa 10140

attagagcag ctttagaaca ttattttaat atccgtgcgc cgtatattgt gggcctttct 10200

actgattcgc gcgcggaccg aatcacattg gcggccgcgt ccggtgttgt ggacgatgtt 10260

gttaataaag ctgggggcat ttttaacgat atgcagttat ttaaggggca aacgccaatt 10320

tctttttata tgttggggat tggtgaaaag gcgactttgg taaacgtcga gtatctataa 10380

tatgaatatg tttaagcact tgttacccag cggccgcgct tggaacctaa ccgcggaaaa 10440

gccactaaag gctttttttcc gttgcttgga tgttttgaga acggacgcag taaattattt 10500

taatttgctt tttttagata taaacccaaa aacaacgcgc ttacttgatc aatgggagca 10560

gcaattcggc attaaccgag gatttttaac cgaggcccag cgccgggaac gtgtcgcggc 10620

cgcttggcgt gatgtgggcg gacaatcccc ggcctacatt caagaagttt taagaaataa 10680

tggctttgat gtttatattc acgaatggtt cgatccggca gatcgcgggg aagtaggtga 10740

aaaacagcct ataacgccac gtaacccgct gtcgattatg tcggcccaat atgccgaggt 10800

tttgcccgtt gtggattgtg gcgaaccgct ggcgctatgt ggtgaagaat ttgcacatgc 10860

cggaaattat ttgggccttg ttgggtatcc gcttgttaat aagttcgttt atgacgcgga 10920

taaatacggc tacactgtcc ccgttgatcc ggcttattgg tatcactttt tttatgtttg 10980

tggccctaat tttggcgatg tggcccaagt tgaagcaacg cgacgcgctg aatttgaagc 11040

gctaattttg agaattaaac ccgcgcactt atgggcgggc gttattgtga gatacgttta 11100

atatgtcttt agtgtttaat gagaaatttc ccggaaaaac ggcaggggct acacaaaatt 11160

acccgtatgg cgaagcgcgt aacgtatcag gccccggaaa tggtgacggt acgccgtggg 11220

atgcggccct agtgaatgat atttttggat tacttcaagg gcttttagtt cgtgccaata 11280

ttcagccgaa cggccagtcg gacacggctt taaactcgca atatttacaa gccttgcttg 11340

ccctgtttat gccgaaacaa acgccaattt ccggaaagtt agagcaaaac ggatatttaa 11400

ctatcccttt ccctgttgta ataaacggcc aaacggtaga gcgtgaattt acaattcaat 11460

ggggttctaa ggattggtct agttatccgg gtgaaattca agattctatt gtttttgaaa 11520

agccttttaa aacagcctgt tttggtgttt ttccaatccg aaaaatgtcg cagcattccg 11580

cttatggtga tggtggtgtt aagcctattt ctgtttctaa aaccgggttt acagtttctt 11640

tgcaagccta cgggggttct gtgggccact tgttgggtta ttattggttc gctgttggtg 11700

tttaagttag ttctgatttt atggggtaaa tgatgaatct atttatacaa ggcatttatt 11760

tactatggaa ccaatttcaa cgggtggcac agccgctttt ttaaaggttt atggggtgtg 11820

gttggcggtt gttaccgctt tggtgtttgt tgctactgtc gttttaatga tgcgtttacc 11880

acgtagccca caagagttcc ttgtgggcat tattacgact gtcgtttcaa gtctaatggg 11940

cggatctttt ttaattcttt attttgattt acagatttgg gccaattcag cttatggcct 12000

tatggtaatt ggtgggcttt actttgtggc gggtattccc ggctgggctt tggttcgctg 12060

ggtgtttaat tttattgatg cgcgggaagg ttccacacta ttggacattt tccgcgaatt 12120

taatgaagaa tttagaggcg ggaaaaaatg agtaaaatta ttgcgatttg cgcggggcat 12180

agtgataaag atccgggcgc ggtaaatggt aaacgtaccg aggcggccat tgttttagat 12240

atgcgtaaga tggttgccag ttatttggaa aaagcgggcg tgaaatattt aacagacggc 12300

aaaggcgggg ttaatcagcc attggccgaa gctatcaaag tggcaaaaca agccagtatt 12360

gctgttgaat ttcactgtaa tgccgctaca tcgaaaaaag cgaccggggt ggaggtttta 12420

tccgctgaaa aaaataaggc cctagcgaag caaatagcgg ccaaaattaa cggggtttta 12480

aatattccgt tacgtgggga aagtggttgg aagtctgaag gatcagggca gcatagccgc 12540

ttaggtttta ttagttccgg gggcggttta attgttgaat tgttctttat ttccaatgat 12600

gacgatttag cgaaatggga cgcgaaaaaa tggcttgttg ccaaagaagt ggcggccgta 12660

ttgattgaac aagtaaaaaa ggcggaggcg gcataaatgg cagcattaac gatatttaac 12720

gcgatttcag aagttacaag ttttgcaggg gtggcccgtg agattttcga cacagcagcc 12780

aatgcaatgg acgcggccca aaatgagaaa aaaggcggag gaaataaaaa agtttgggta 12840

atggcttaca tggaatcatt tattaatgat ttgggcgaaa attgggaacg atgggccaaa 12900

gctatttttt cttttattga ttttgccaag tcgattttta atagtaagcg ctaataaaaa 12960

agccccgtat taattcgggg ctttttatg gttccacgtg gaacggttta gcttttcttt 13020

ttgcttgccg ggtttcttaa taaacgatct tttttgatct cgcttacaat cccgtcgatt 13080

aaaaattcca tgcttgttcc tttggttggt gggttggttc agatgattta attcgagttc 13140

ttagggccgc ttttacaatc ttatccgcca tgcgccctat ttgcgccttg tggcagttat 13200

tacacgcgca tccggcctta tatccccgaa cggttccgca gcctttaacg ggcttatatg 13260

cgtcccctgt cgtttcttca ataaaatcta tggttgattt gtccgccgtg tttcgcatcc 13320

tttaccccta agccgcagcg ggagcaacgg ccatttttaa ataaggtgaa tgtttggcaa 13380

ataaaacaaa agttagtcat ttttgccgtt tgccttagcg attcgcatta cattaagggc 13440

cttttgcttt agatccgcgt atagctcatt agtaaggtaa ctttgtgcta catcgtgaaa 13500

agtagataaa aaatgcgtgt cttgttttac cttgctttgt ttaagttccg cttggtttac 13560

ctgaattaag ccaatagctt tgtttgcctt tttgattaag ttattcacgt cgcttaattg 13620

cgcgtttatt ttggcctctt tttcgccttt tatgtgtgct ggggccttat ccatcaaaag 13680

ggcttcacgt tggccgttta ggtgggtttt taggcccgtt aattcctcta ttgagaattg 13740

ccccgccact tgcaaagtgg ttaatgctga aaattcaatg attgcggttt taagttctgt 13800

tttagtcatg ggtagcactt catttaaaaa gtattaagcc cagcagcagc cgggcaatgg 13860

tgggttagat ttcggttaag ccgtgttttt tcattttctt aataacggtt aatcggttaa 13920

tgcctaatat tcgggatact tcggcaatat tatattttga atatttaagc gctttttcca 13980

aaacgcactt ttcaatagga tctaatgcag ccgctagagc ttggccggaa ttttcataaa 14040

aaaaattcgc gtccaaagca tccgggttaa ataaattagt ggtttcgctc attcggatat 14100

tccttaaatt gcgcgttata ttcagcgaca aattccgctt gtttgtcgat ttcatcggct 14160

tgtttgataa tgaacatata agacaaagcc gcaagcataa aacagaaaaa caacgtgctt 14220

aaaatctctt ttatttttgc gccgtggttc gctgtttctt gtgaaaaatt gcttaattgt 14280

tgacgctgaa taactggctg tttcataata atcggactcc atgaaattag aaaaaagccc 14340

cgtagccgtc caaagttccg gggctttttg ctgtctatgt gttgcataat atacaatata 14400

aataaaaagt aaatagagaa attatagata ataaataaaa taaataaaat agataaaaag 14460

tattagtttt aattgtggca tgaatatttg ataagtgtta aaatttgttc taagcaatca 14520

tgctgaaaat aaaaaacccg ccggacgggg cgggttttag tttgtcttga gggtataaga 14580

cgtgaaaaag tttaacacga aatttaagca aaatcttgat gatgcaaata acaacgcatt 14640

tattccgaac agctttcaaa ttacaaatgc tttcgttgat aacatcatgg ataaaatttc 14700

ggatgcagca gtaaagatct atttaattac agtgcgtaaa acaacgggct ggggtaagca 14760

gatagattcg atttctttaa gccaatatga agcgtatagc ggcaagtcgc gccctactgt 14820

tgttaagtgt ttaaaagagt tggttaaggt gggtttattg gtagagcata ccgggacacg 14880

gtacggtaat tcgtattcgg tggcgcttgt aaatagcatc ggtttcgagc ttttatctgc 14940

tagtaaaaaa attttactag taaaaagttt taactacact agtaaaaaat ctttactgcc 15000

actagttaaa atttttaaca cacaaaaaca actatcaaaa aacactaatc aaaaacaaat 15060

aaataagcgc gattggtttt ctttaaaaac tttaaaagat gaattgttta aaaccgggtt 15120

gcaaattgag gctgaagatc taacagcggc taaatggttc gatagagaga aaacagcctt 15180

tgaaaactat gcacctaatc aaaacctttc agatccgcaa aaaatgtatt acttcgttga 15240

ttggctttta aaagcaaagc gcaagtacga cgcagcagag cgccagcaag cagctaaggc 15300

aaaagcggaa ggcaaaaacc aaaatcaaaa ccctgaagat acaaaaacag aaaacgaccc 15360

ttttaaactt tctactaaac aaatttcatt ctttgctagt cagttagccc atttaccatc 15420

atttgcaaaa tattgcactg gtaacaaagg ctttaaagaa tttgaaatgt ggattgcttc 15480

aatgttgaac aatcctgaaa atgttaaaaa gtggaataaa tatttaaatg aattgggtta 15540

tttgatcggg taatcagggg gattaaaaac aatgaagatt tcaaactttc attttcaaat 15600

gcaaatttta cttttgattt ctaaaaacac ggttttagat tttgagggat taaaagagaa 15660

gttagcgccg tcgattacag acaacgcatt aacggaatgt ttagaagaat tattgatgtg 15720

gggatgggta caagtacaaa agggccttta catggtttca ggcgttgctt atcagatcat 15780

gggggatatt tgccaatgct gatagacaaa tatttctatt aatcggcttc gatacggatg 15840

caatggaaaa atacaagtat tcagaatcaa acgccgtatt aagcccgcat ttaaattgcg 15900

gcctaacttc agttagtcgc gttggatctt caggccaagc aaagcataaa ccgcataagc 15960

gaagtgaaat agcagatcag gcagaaaaag agatttgcaa gaattgggcg ttaagacaac 16020

aagcattttt aaataacagc gtaagcaacg cggtactagg gggctaatat gaacaagttt 16080

attcacattg agggcaaacc aacggcccag caagtacgcg aagcgctggc aatgtatgca 16140

aaagacatta aacgcccgga attttcttta attgttcagc gtgagcttat cgaatcattc 16200

cgcaacgata cggcccacgc ccttaaatcc gcagttgcct tttattttaa aaatcgtgtg 16260

atccaacgcc ccggccttgt gttggcaagt ggtaaagatc aagcgcttat tgttgagagt 16320

tgcgaaaata aggcattaaa gcgccacttg gtcgcggtgt cggggtattc atcgcaattt 16380

ctgcaaatgg tgatagatca taaaacgcca ctttcagccg ttgccgcgcg ggatctaaag 16440

caggcattac caaaagcgga aaaactctat aaggccgaat gcaaggaaaa agatgcaaaa 16500

ttaaaaaaga atatttgcgg ttttgtcgct tgctatagaa atggctgtca ttgcacaaaa 16560

tgcaccacgg catataagaa atatcgctaa aagcaagcct atcttttaaa gagaaaaagc 16620

gcagttcgcg ccgtggccgc ttagtgtttc acgtggaacc aaacaacgcc ccggattaaa 16680

cgtccgggga tctaaaaaag agtaaggaaa aggaataaaa atgggtgttt cgattattaa 16740

tttagtttta ttggttggtg tttgcttatt gctaacaaat atcgccttaa attgtttgtt 16800

tcataccgaa aataaaacat atctagtcta tgcgtgtggt tttagtgcgg cttcggtggc 16860

gggtgccatt gctggcgtta ttggttgttt ggcttatggg gtaacagtgt aatgaaaaat 16920

aaatcaattc ttatgggcct attcgttgcg gccgctggtg tggtgtttta tatgggggcg 16980

gatagtgctt gcaatcaaaa ggctgttata gatccgggcg cgcttatgtc gcttggtggt 17040

atcactgttg aaaataaaaa agcctcattg gttcgcgtat gtgatacgcc agtaaaagaa 17100

aaccttgtga gctttgtttt gattaaagac ggcttgcgcg tgggtggtgt ggtcgataaa 17160

agccatgttg cgctcatagg tgaataaatg agtttaggaa aacgccccgc aggtgcgacg 17220

catatagaga gcgacggcac atattggaaa aatgaggacg cggattggta tttttggcgt 17280

gacttgtggg gctggtgtca atatgtcggg ccaaagaata gaaatttttt aaataagttt 17340

tcggtgttgg ggtgatggat ttatatattg gtcagattgt cgggcatagt tcgcccactt 17400

gggttgttca gggaaaattg aagataacca aaattaacga gggtaagcga agcggtttaa 17460

agattattac ggctacagat gaatcgggta aggaatttac cgcagtttat ggcgtgtttt 17520

ttagtgttga tagatattaa ttaaaatttt ggggtaatac gtgagaaacg aaaactttga 17580

agattattta aaacaaacgg atgattacgc cgtattactg aataattacg gatctagtct 17640

atttatccat gaaaatggcg tttatcgcgc tttgcctgtc cgggtggctt atgccgcttg 17700

ggtatcgggc ggggatcgct ggggagaggt gcagcacttg aaaggcaaaa ttaagaaaat 17760

ggccgaacgt gcagcagaaa cagcggattt ttaccatacc aaaatagaaa aattggaaag 17820

tagcacggtt aaaaaggcgg gtttattgga tatggccgaa caatgggacg gtttagagtt 17880

gcgcggacgt gatttggaat taaaccgggt gcaagaatca atttataagc gttgtgctta 17940

tttgttgcgg gtggctgtta atgggtaatc ggtggacgtt aagcggaaag gtaaaagggt 18000

taaaagattt gcccgaaagt ataaccgcgg cacaattcag ggaaatgata gaacgggggc 18060

aagtcaaaaa cacgccacaa gccccaaaaa agcgccgtag cggaaaagta agtagtccgg 18120

gggaggctac attagcccaa gccttaaaag cgcttaaaat cgaatttgtg caagagtatc 18180

gcttttgtga atatcgcaaa tggcgcgcag atttccatat accggggaca aacctttaa 18240

ttgaggtaga agggggcgta agatccggcg gccgccacgt gcgaccacaa ggctatataa 18300

acgacacgga aaaatataat gaggcggcta agttgggctt tgttgtattg cgctttgata 18360

cggaaacggt ttcacgtgga accgcaataa acgaaataga aagttattta gaaaggcgcg 18420

gatatttcca aaataagggg cttacttgtg aagaaagtta aaaagtttaa atacgattgg 18480

cgcgccgtgc cggatcatat taattggctt gcaacgtatg aaggcgggga aatggcctgg 18540

gggtatgtga ataaaccata tagaaaagaa aacgcgggga tatggtacga aacgggcgga 18600

gagtggcggc atcgtgtacc tgttgcccca tatcgcggcc attggacgca atcattagaa 18660

aaacgaccta gcaaggccca gctagtcgag tgggttttaa atggggctgt agtggtttaa 18720

tattcacgaa ccctcataga gtgttttata acattctgtt ttacaagcct cattgcctat 18780

agtgaggctt ttttttgctt tgcggtttga ttggattttt aattgttctg tgaattttgg 18840

gctaatatta gaaaaccgca taggcggcaa cgattgataa attagagagt aaataatggc 18900

tgaaaatagt tttattcaac caattgcaag aaaggacgcg attgccctta ttggccgtga 18960

tgagcttgtg gaaggtgggc cggaaggggc agcgaataaa caagcaattg cacttgcaaa 19020

taatattaag tatttaatgg gcttaattcc tgaaaattgg ggggtggaaa aaaccgaata 19080

tggtttagat gaagttgtaa ggctttcaaa tggtgacgtt gttaaatctg ttattgatga 19140

aaatatcaat aatccgaacg agaatttgtc gggttggtct tttgttacaa gtaattcagt 19200

aaatactatt tctgatttat taagtattaa aaatccgaaa aatggaatga aagtttatgt 19260

tcttggatac cataaaccgg ataattttgc tcttttaagc ccgtatgaag ggggcgggct 19320

tttcatatat agcgggaata aggcagcgga aaatgatggc ggcgtggttt taaatggctg 19380

gattcgtcaa tatgttggcg atgtggatat ttcttggttc ggagcaaaac aaggtcaaga 19440

cgcttcgccg tttattgaag cagctttaaa agtgaaaatg tcaattgtga ttcgtggaga 19500

atacaagtta gaaacaattt gcggcatacc aagacaaaat aactatgcgg caaaagttat 19560

tagaattaag ggggaaaatc aggcttcgct tactgtaaat tgcccggatg gtgctgtttt 19620

tacttcgtta gatgcaaaag caaaccctac aagtttatcc aatattttta ccgcaaaaat 19680

tgacgtattc gggattaact ttgtaggtac aacggttgca aattctgttc tgtttaatgg 19740

tgatcgttta tacaatatta atattcatca caataatttc aaaacaaata ttacaattgt 19800

taaagcgtat ttaaagcgcg aggcatcaag acaatatacg caaagcgttt ctattaatca 19860

taatcactta gcggaaattc accgggttat tgagtcggac aagtcttata acttcgattt 19920

tgcatacaat atgtgtgaag cgtgtaaagg tggcatgtat atcggtgttg atgcgcctta 19980

tgatccttca ggtatttcta taacaattca tcgaaattta tgggaagcca gcggggtttt 20040

attaaaaaca aatggcggga ttattgctgg tagtgtttca aaaaactatt ttgaagctaa 20100

cgtatatcaa gatgcagcaa ttgataaatg cttaatatat atcaaccgaa gcggaacggg 20160

ggcgggttat tccggtggtt taacttttga aaataattta ttttcaggga cttcgtcgat 20220

tccggattat gttgatgtgc gcgttttggg tcaaagtaca gaaacatcgg gaaattcaaa 20280

atctgctact acgcgaccgc ctgtatttat tggtaactgg tcaaatagtt acatgctaac 20340

aaatatggcc caagctattt tgatcggtaa taagtgttct aaccgcgaaa aaatgctgaa 20400

tgcttacagc ccgcaagaag cgcgcgttac ttactattcc ggctatttta ctaagcaatt 20460

ggctaatatt ttaaccgata aaaagttaaa tttattaaag gtgaatactt cagcagttca 20520

tgctattggt tcctctcaag ctaactttaa aactacatta gacgttattg tattctttaa 20580

aacatccggc gcagttggaa cagcaatggc gacttttaaa ttagatttat ttgtttacga 20640

atcagtcgga cttggcgctg gcaatgttcc aaaagcaaac ttaaaagccg tgatgtataa 20700

ttttatgcaa tccaccgcag acgacaaaat tacaccaacg gttaatatgt tttcggctat 20760

ttctgatccg ttaattaatg ttgttgataa ctcagacgga acgtatagca ttgagctttc 20820

gagttttact aataaatcat cgccaaactg ggggtttgtt tctgaattgc atattgaata 20880

cacggcccaa gcgacgctta tagcttcgca tacatccagt tattcagcgg ctaacttatt 20940

aaccatttca taaacttaat taatagctaa ctaaggggga gcgccaattt tgtttttaag 21000

attggcgctt tttttattgg ggttttatgt ttgatataga tacaaagcaa ttgcacggcc 21060

tggagaggcg tttagagcga ttaaaccgcc gtggcttgcc ttatgccact aggcaaacaa 21120

tgaacgatct agcgtttgaa tctcgcgccg tggcccgtgc cgagttacca acgcgcatgg 21180

ttttaagaaa taaacacgcg attaatagca ttcaagtaac taaagcaaca tcgctaaaca 21240

tttcccagca agccgcgcat gttggatcta cagccgacta tatggcaacg caagaaacgg 21300

gaggcattaa aaccaaacaa ggcggggccg ccgtgtctat tccgaccacg acggcagcag 21360

ggcagggcag aaacgcaaag ccccgaaccc gtttaccacg tgcagcgctc aaaatgggcg 21420

ctattcacct aaagcgtata gcggcaagcc gtaacgctaa gaatcgtaaa caacgcaatg 21480

ccattgctat ggctacatcg gataaatatg tatttctcga tttgggccgc cgtaaaggta 21540

tttttagaaa ggacaagggg ggaggggtaa caatgttgca tgatcttaca cgcgcatcgg 21600

tgcagatccc taagaatgaa tggctgaagc ccgcgaccga ggcagccgaa cggaagttac 21660

cgggattcta tggccgtgct ttagagttcc aattaaggcg cttttaatta accaaaaact 21720

taacttcggg cggttcgggc gggtagccgc ccgcggttaa gttaaagaat ttttcgcaca 21780

aaaagccacg gttcgcgccg tggtttttat ttgtctttat cattcacgtg atgaatggat 21840

ttatttttaa aatcaatagt ctgaaataaa aaaaggtact gtgccgaccc cccacccccc 21900

tgccgttttg attgcgacgc gcgggccgcg cacaaattca gaatttttaa cttgtcttaa 21960

cttcgggcgg gttaaatgtt aaatttcgca tcatggttaa aaagttaatt tctcgcagcg 22020

attttgctgc taaggcgggg gttagcgggg cggcaatcag taaggcatgt aaagggccgt 22080

tattagatgc tgttgagggt aaattcatcg acttaaacca taagtcggct atcgcttact 22140

tagaatcaaa gaaaaacggc aagacaacgc cagcacttga ggggattgat tcgctatatg 22200

aggaagcatt agaagtttgc agagaagcgg gccgatgctc gcaaacattg ttgcgtgaca 22260

aattaatgat aggcagcgac cgggctagaa agttggtcgc tttaattcaa aacgcaaata 22320

tccaagattt tgaaaaacca gcagccgaaa aggtaaaaag agaggagaaa gcgcgcccgc 22380

atacccgcgg gacggctgca aaaaaacagc aagcaattca agaggacgac gaagaattat 22440

ttgagctgtt agatcggaac gtagcgcaat atgcagatat gacgctaagg gacattgtta 22500

ggaaattcgg gacggcaacg cgatttgcgg aatatcttag agcaatgaaa gaaatatcaa 22560

tgattgaaga tcgggaaatt aaaatagccc aaacaaaggg cgagctagtc catagggatc 22620

tagttagtca attgatcatt gagccgatag attcggccca tgtaaaactt atgcgggacg 22680

gatctaaaac aatagccgtg cgaatggcag caatgcacgg cagcggggcg gacattaacg 22740

aaatgcagtt agtcacatca gaattaattg caagtttcat taaacccgta aaagccaaag 22800

taaataaaat cgcaacggaa ttaaaacgag gggctgaagc gtgaatatga attttatagg 22860

tatggattgg ctttgcgata aagtcgagaa tctaaccgag tatattaagc acgtaacgcc 22920

cagccaattt aatgaagaaa atagatattt gcccgaatct gtgaccagta ttccgggctt 22980

tatccgttac gacgtaaacc cgtttatgcg tgaaattgtc gattgctttg atattaattc 23040

acctgtccgg gaagtgaatt taaaaaaggg cgtacaaatt acatattcca cggttttaga 23100

atccggggct ttgtactata tgggccacgt taaaaccttg cccattatgt atatgacggc 23160

cgacaaggaa ttagcaaagg cccgtattga aaacaacttt atcccaatgc tggcacagtc 23220

ggacatggcc cacattgtcc gatcaagcga cgaaggtaac agcagaaaaa cgggtaaaac 23280

cgataatcat atccaatttg agggcggcgg ctatttggtt ccattcgggg ccattaatgc 23340

aaataaaatg cgttcgtttt ctattgctgt catgctcaag gatgagattg acgcgtggcc 23400

ggatcgcgtc ggaaaagatg gcgacccgga taagttgagt gatgaccgtt gtagcgccta 23460

ttgggaacgt cgaaagattt tccgaggttc cacgccctta atcaaaggat cttcaaaaat 23520

tgaaaaagca tacttgcgcg gggatcaaag aaaatatcac gtactttgta aaaaatgcag 23580

tttcccgcag gaattgcgat ggagtacgcc ggacggtgta ggcggtttta aatgggacac 23640

ggacgaggac ggaattttaa aacttgattc ggtgcgctac tgttgccagc aatgcgggga 23700

gccacatttc gagcatgaca aagagcgcct atttagtgag aaattcgggg caaaatggat 23760

accaacggcc cgccctgttg agccggggat tcgttcctat catttacccg cgttatattc 23820

gccgtttggg atgcaaccgt ggtacaagtg cgtgattgct tatttagacg cattcgaccc 23880

ggtagagcgc aaagtaaaag acatagagct ttaccaagta ttttataaca acgtattggc 23940

ggaaccgttc gagattcaag gtgctaaggt tcgctttgaa acggtttcgc atcatcgccg 24000

cacagtgtac cgattgggcc atattccgaa ccgttacgcg gttcaatatg ctggatcgcc 24060

tatcctattt ctaacctgtc aagtggacgt acataaatca ttcttagccg tttccgtgat 24120

gggttgggcc aaagatgcta aatgttttgt tattgattat ttgcggatcg agggcgagga 24180

cttttccgat agcgcggaac cgggttgggg taaattgcgc gagctaatcg aagaaaagca 24240

atatattgcc gatgacggta aaaaataccg cgttgctttg accttcatag attcgggtta 24300

tgctaacgat accgtcgtta aattttgttc tgaatattcg agttcagtct atccaatttt 24360

gggccgtgac cgaccaagta aaaaccaagc aattaaagaa tttgccgact ttaaaacgca 24420

agaagggaca acgggcttta gaattattgt cgatcattat aaggatcgtt tggccccggt 24480

gttgcgtcgt gaatgggacg agatgggcgg aggtttacag cctgtttatc attttaatgc 24540

gcctgtcgat ttgtctgata agtcattaaa agaattgacc gtagaaacgc gcaaggagaa 24600

aaccgacgca agcggcaata cttcatattt ttggcatcgc cccggcaatg cacgaaatga 24660

gctttgggat ttgctttgct atggacatgc agccgtcgag attttcgcgt ggtcgctatg 24720

cgttaaaaat atggaacaaa aggaagtgga ttgggcttgg ttttgggaat ttttggaaac 24780

agaagccccg tattttgagc aaggcgaacc cgtcgccagt gagtaacaaa aagcccgcta 24840

aattagcggg ctttgtttca cgtggaacct tataaaacgg ctataaaatc gaaatgcttt 24900

aggtttaagt gatccggggt aaaccaagtt ttaacccaca taatgcgatt gaaggttagc 24960

aagcggcctt tttgttcagc ctccttaaaa taggcgattc gatccccttt tactgcgacg 25020

atggtcgcgc cttcgggttt atttcccttc agcttttcta aattattttc atattgcatt 25080

ttgttagatc cttaaaaaat gtttaaacct tgattattaa aattaggcgt ttggcattgc 25140

ggcatatttt tagcgatgct gttgtaagtg ttttgcgtca tgtaaatttt accgtcaaaa 25200

gcaatcgtgt tttgatcggt gatttgcacc gggtagccgt gttgctggat cgttgcgcca 25260

gcttgtacga tttcgatttt atggccgcgc caattgttaa aagattggtt attcatgagt 25320

ttggttcctt aaattaattt gttgctggta ggttatattt accgtttgtt tgtgggccta 25380

atttaataag attgtgattc tcattaagcc cataaggtaa atgggttcgc gggtttaatt 25440

cggttttatc agtaataaaa atacattcat gcggattcac gttgtaaaga taggcgacca 25500

tgcgcggggc tacataatgg gattgcttat catgttttga gcgaacccag ccgccgaaaa 25560

ctaaatattt tttatctatc atttttggga aacagcctca ttttttaagt gttggttaag 25620

cagatcccgg acaagatcgc ccacgtttgg cactgtttca atgtattcga ttaaatgctt 25680

atcgcgttcc ttgagtagag aaaaattttt aattacgcgc tttttctcat aatcgctttt 25740

ttgcttttgc cttgcttcgc tttggcccat tatttacacc gttttacagc ttggttatat 25800

tgatttcttg caatgttgga gagcgttgta gttttggaat tattccgacc cgcttggcgt 25860

gatgaaccaa gcgggctttt ttttacattt cttcagccat aaacacggtt aagaagccac 25920

ccatatcatt ggcaaaaagg ccgatagatt caataatgcg ctttgcttcg tttagatttt 25980

taccttcaac cataagccaa acatcgcgtt tcactttata ttcagggcct agaatttttt 26040

taagtggctt ggtcaattcg cgtggtgttt ttacttgagt gtttccgatc attaacattt 26100

tgcaaaactc ttatttatct atttgatgtg tcaattatgt cgtattacga caagcaaggc 26160

aatagggaat gtataaaaaa tatatatttt ttaaaatggt tccacgtgga accgtggcgg 26220

gcgtttatgt tgcgctttcg ctttattgat atactaaaaa caacatagcg ggagtattta 26280

aaaaattgga tcaagcattt ttaaaagaaa ggatcgaagc gacaaagcgg caaattgtgg 26340

cctatgagga tgcagtaaac cagctttcaa gcggtgcggt tcaatcgtac tcattaaaca 26400

cggggcagac gacgcaaaac gtgacgcgct ttgatgttgc gcgcctaaat ggggatattg 26460

acgggcttta taatcgcttg gcgacgcttg aggcgcgttt aaatggttcg ggttctactt 26520

tggttcgtcc gggatggtaa tagatgaatt atgattttag ccgtgggctg gtaaaggttc 26580

cgacggtggg tttaaaaacc gagtttaaat attcaggggc tacaattgca ccgccgccaa 26640

tgcagggcgc aaaatccgac gctatcgaaa taaacgcgct gggcggtggg ttcaatcatt 26700

ccgcttttac cggggaaaaa tttataggcg gtttcgggcc tacaagttta tttactatgg 26760

attattggac gttacgcaaa agatccgagc agctatttag cgaaaactta tacgcggccg 26820

gattaatcga gcgtttagta acaaatgaaa taaacacagg attaaccccg gaggcttgtc 26880

ccgatgaacg gattttggga ttaaagccgg gtgatttaga agattggacg gaattagtag 26940

aaaaccgatt ttctatttgg gccaatagtt cggaatattg cgacttttac ggacaaaaca 27000

gcttagggga aattcagcgg atcgcaagac gcgaagccct tatttgtggt gatgtgctgg 27060

tggtgttacg ccaaaaccaa agtaccaaaa tgccgcaagt tcagcttgta agcggatctt 27120

taatccgaac cccgccggat atcccgcgca aaggccacaa aattaaacac ggtgtcgaat 27180

tagatacgca aggccgccag tgtgcttatt gggttttaca agacgatgga acctataagc 27240

gtttgcccgc gtttggtgaa aaatcaaagc gccgcattgc gtggatggtg tacggagcgc 27300

aaagacgttt aggcgaattg cgcggccagc cgcttttaag tatcgttttg cagagcttaa 27360

aagaaattga ccgataccgc gacgcggccc agcgtaaagc cgttgtaaat tctattttgg 27420

caatgtttat tgaaaaaacg caggataaaa tgtccacgtt gccaattacc gggggcgcaa 27480

tccgacgtga taaggttacg gataattcaa acaccgcggc cccgcgtagc tttgaaatag 27540

cttcgcaagt tccgggcgtg gtattgcaag aattacaagc gggagaaaag cccgtaggtt 27600

tccatagtca aggcacagat attaactttc ccgcgtttga ggaggccgtg attagtgcgg 27660

ttgcttggtg caagcagatc ccgccggaga ttctaaaact gtcgtttagt tctaattatt 27720

cggcaagtca ggcagccatt aacgaattta aaatttattt aaatatggtc tggaatgaat 27780

ggggcgctaa cttttgccag ccgatctata ccgagttttt aattagtgag gcgcttttag 27840

ggaaaattga cgcgccgggc tttttggacg catggcgcga cccggtaaaa atggatattt 27900

ttggggcttg gttgtggtgc gactggttcg gcagtattaa accgagtaca gacatgcgta 27960

aaatggggca aggcttggcg cttgccgtgg aacaaggttg gacgaccaac gcccaagcat 28020

cgcggcaaat gttcgggact aagttcacta aaaacattgc aagacaacgc cgcgaacgtg 28080

aattacaagc cagcctttta aggccaatgc ttgagctgca aaaagaatac ggcataagcg 28140

cggagcattt agtaaatgta gcccatgcga ttggcgggac aatttcggca caaactgaag 28200

aaacagagga aatttaatgg attggttttt aacgcctgaa gccctaaaag aaattcagga 28260

attacacgcc cgcggcttgg ttttgaccgc ggagcaaatg acggaattta acgcgcttta 28320

ttcggatgat ttccccggat cgcgtatttt tcaaaaagtg gggacggttg cacaagtaaa 28380

cattgccgga gttctaacaa aggaacctaa ttggatgtat cgctattacg gtggcggtaa 28440

tacagcatat agcgaaatta tttccgcgat taatgaggcg gagcgcgacc cagccattaa 28500

agaaattatt ttggcgattg atagccccgg cggacaaaca aacgggcttt gttcagcgat 28560

ggacgcaatt aaaaacacga aaaaaaccgt tttggccgtg gtggaaggtc aggcagcaag 28620

cgccgcttat ggccttgcat cgcaagcaaa taagattatt gccgcggatc gcggttgcat 28680

ggtcggaagt gtaggcgcgg ccgcttcgat tgttgttagc gaaaatgttg tcgatattgc 28740

cagtaccaac gcgccaaaga aacgcccgga cgtgaccaca gacgcgggta aagcggtaat 28800

acgtgaaaca ttagatcaaa ttgaaagtat ttttattgct gatattgccg ccgggcgcaa 28860

ggtaacggcc gataaagtta aacttgagtt tggtcagggt ggtatgtatg ttgcggccca 28920

tgcccttgag cgtggtatga ttgacgaaat taaaacggct gattctagcg ctacaacaaa 28980

cgcgaaaagt tcagcaactt acacagcaag cgaggaaaat tcaacaatgg atgcagcaac 29040

tttaaaggcg caattcccag cagtttacac agcaatttat aacgaaggca aaaccgcaga 29100

aaatgagcgc gtatccgcgc atttaacgct gggcgaggct tcaggcgata tgcaaacggc 29160

tatttctgca attaacgacg gttcagaatt aaccgcaagc attcaagcca agtatatggc 29220

ggcaaatatg aagcgcggcc aagttgctgg gcgtgaaaca gacgacacgg ccgcggctaa 29280

tgctttggat ggtgttaaac cgggcgcgac tgctacagat gcgaatgcag ttacaaacat 29340

ggttgctaaa aatttgggcg ttgcataagc ccaaaccgta aagacatttt agaaataaag 29400

gggtaacagt tgcatgatgc aggtaacgca gcacacaaac agttcaatta attggggtga 29460

agtagcttgt caggatgaca cgctaacttt aggcgcaaac gcaacgctaa aagaaggcac 29520

aattttagcc cgtgcagcaa cgggaaaact tatcccgttt gttaagggtg gcgcagatgg 29580

ggcgggggtt cctgttgcta ttgctatgca cgaaattaaa accgtggccg ctggtgatgt 29640

ttcagtacgt gcgggcattt ccggccaagt gcgtaaaaat aacttagtga tccatgccga 29700

tggaaacgcg accaatatcg acggagcagt aacagacgct ttgcgtagtt atggcattgt 29760

cgctttcaca gtaaacagca caaacaaacc ggataaccaa taaggaattt ttgatttatg 29820

actactagca caattgccgg ggtatataca caagttgcac caaagccgct atttttatcg 29880

ggctttttca aagcaccgcc acagaatcat tttaatactg aatctgtcga gctggacatt 29940

gagcgcgatt cgcagcaagt ggccgcggtt gttcaatcgc ttggcagcga ctacaacaaa 30000

aacgaaacgg gtgaatttac caataagaaa tttacgccgc cagtttataa agaaggcttt 30060

tcgcttaatg cgttcgattt gcttaaacgt gaagcgggcc aaagcggttt taatacgcct 30120

agcgaacaga tccgcggcaa tttgattacc cgctttatta aaggcgcgcg aaaagttgaa 30180

gcaaagattt tacgcggtat tgagttgcaa gcatcgcaaa ttttgcaaac gggtaatttg 30240

ttgctgaagg atcaagaagg caaagacgct tttaaaattg attacaagcc aaaagcaacg 30300

cattttgtga atgttgcgaa tgtttggacg ggtgcgaatg ccgacccgat gaaagatctt 30360

gaatcattgt ccgaagtaat ccaaaccgac ggccttgtaa ttcccgatat tatcattatg 30420

ggcgcttcag cactggcagc ggctaagggt aacgagaagt ttattaaaaa ctttgattct 30480

cgcaatattt cgggcaatgt tttagctgat atgcaaatta cggcccgcgg tggtatctat 30540

caagggacgt tgcgcgtagg taatgccgtt tgtgagcttt acacttatgg cgtgggttat 30600

caggcttcat cttcagcagt tgcaacgccg tttttaaata ccaataaagt gcttatgctt 30660

agttctgaat cgcaattaga cgcgcttttt ggtgcggttc caaacattgc ggacattttg 30720

ggcgtgagct tgcgcgaaca gcttttaccg gaattgccga cgcgctttga ttcaaacagt 30780

accgatttat ttacaaatgt gtatttgtcg gcaagtggtg agcagcttat gggcggggtt 30840

gctagtcgcc ctattcttgt cccgacggct attgattcat tcggctgttt aactgttgca 30900

taaaaattaa aatgaacccc cttcaatggg ggtttttttct tttaaatttg gagatattcg 30960

acgtgactaa aaccgattta attaacgcaa ttaaagccat tgattcaaac gcgaaaacgt 31020

ccggccttga taaagacgaa ttacaagccc ttttaacaga attacaagcc aaagcgac 31078

<210> 3
<211> 167285
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 3
tctgaacgac ctgccatttt atccatgtct ccaccgtcaa ttattcttgc ttctttttca 60

tcttttgcta cagtgtaagg atttgctgat aaagcatatc taactaataa accgatagat 120

ggctgcaaac tttctgggtc aactacaact ttaaatgcac ctacatgttc agggtcatct 180

aagtcaagac cttctgtata cggagcatag aaaattgatc caacaatttc tttttcaccg 240

atattttcta ctacaccaac gattacataa tctaatgggc tgttagtatc gcaataaagc 300

ggtaaaccat tagctaagaa cccataggca ttttgtgaaa gatatttatc atcttctggt 360

ttatgtttta accaacctga tgcagcaaga atcgcagcag cacgagctga agcaacacag 420

aacgttgctg tataagttga ttctttttgg atatgcgaaa ccatttcaca taccattcgg 480

tataatgaac gaccagcttc aggtgcagat gcataactca aatcgatgaa tccagtatca 540

gtaattcctg taactttata gcgttttgac actgtaatca aagactgcag aatatcttta 600

ttgatttcat ctgccatttc agttgcaagc aaatcttcca agaaattagg agcatcgaat 660

ccatttgctt ctaaatcttg tgctaattca actgtgatac cagttttaag tttacgagat 720

ttaactgcgg tttgccattt attaatctgg aatctagcat ccgcaatttc actatcagag 780

ctttcaaatt tgcttgttga cgctgcgtca gaaaatagac gaacctttaa aagaacaatt 840

gcaatctgaa gagctaattc taaatcgctt tcttcaatat cagcaaatgg tgtatcttct 900

aatactttat aaacgatatt attatatttg aataaatcgc ccttattgag agttaattta 960

gactcttctg ttaattctgt gatttgttct cggtctacat atccagcttc gccggcgtaa 1020

gtagcaccag ttttaaatgt aaattcgtta tccgggttaa ggtatttgat accataaaaa 1080

gcagcaacag gttgattagt tctttgcgtt gctacaatgt cagaatatat taatttagtg 1140

gtagcgcgag tcaaagcaac gagatttggg cgaccgattg agttgctatt cgttgtggtt 1200

gattcgcgca gaagttcgtt gattttagcc attgcgcttt cctttcagtt tatatgattt 1260

atttatacca taaaaacaac taaagggacc cgaaggtccc ttaaatcgtc aaagattaga 1320

tacctttaac atatacacgg cggaagtaag cgtttttacc aaggctattc agaatagaag 1380

gcataccgct ctggatgcga gaagccggag cctgagcagc ggattctgca aatgggttga 1440

taccgatacc gtaacgagtt ttgaatccca ttaccggttg gaagttcttc ggatcagaac 1500

cacgcagcgg agtcagagct acatatggag catagtaaat accagcatcc atttcgttcg 1560

gacctttata acctacggtg aaataatcct gtttagcata ctggtcgata tatacacggt 1620

atttaccacc cagaacacca gcaaatactg acttggtagt atcagtgtta aagccagtag 1680

ccagaccttg tgcagcataa gaaatgccgg tatcaactga agccagaacg ttaactacgt 1740

tacgggaagc gataatgaag ttaccttcgc cgcgaccagt ctgacgagca atttcaactg 1800

cttctttgtc aatctggaac aacagagctt taaaggattc acctgcccag cgagcaccac 1860

gaatatcgat tgggtcctgg aagtcaaata caccagcttt agaacccgga gtcagggtca 1920

taccagattt accaacctga gcggagtagt taatccaatc aacaacttcg cggttgattt 1980

ccagcataat ttcggtagcc agaataccag acagttcagc atcagcatcc ataccgtgaa 2040

cagcgcgaag gtcttgtgct aattcaatag agtaagcagc tttcagctga cgagatttag 2100

cttcgataac ttgtttatcg atacggaagc ccatttcatt ccatgggtta tcggtagaac 2160

cgttgaaacc ttcctgaagt tcagcgatag aagtagccat accttcagcg atttctacca 2220

gtacaccagc ttccatttgt ttcttaattt cagcatctaa tttgtctgcg tcagatgcgc 2280

ctgaatcaat ttgtttagct gctgtagctt gcagatatac tgtaccagtt tcctggaaga 2340

agtgagtgta aatagttccg acttcaagag tatcacttgc tttcaaagca gcgaatttct 2400

tagcagcacc ctgaccagag aacattgcat ctggaccata cattgggtgg aatgcttctt 2460

tagcgccgga agcgattgga tctttaccat atactgcgcg cagcgcgaat acctggccag 2520

tcgggctgtt cattggctga acaccacaaa tatcgaaagc aatcaggtta ggaatagcac 2580

gacgtaccat acccataaca gctgggccaa tctgagttac tgcgccagaa gtctgacctg 2640

cggcgatgtt ggtagcattg taaccgtggt caccaccgat ttcagcttct gttaagaaag 2700

aaccgaatgc ctgagcaatt ttttcgtctt tatattccgg agctgtctgg aaatcttttt 2760

cctggttttc aaagatttta gcgataatcg cttgtttgct attagcaatt tccggtaaac 2820

cttcaccttc cagtaatggc ttccatttgt tcaaaagttc agctttagtt ttgatagtca 2880

tttgtgttaa cctttaaaat tagaaacgag atgcgacttt cgcatataca cttacaatat 2940

cttctgcacc ttgtgcagat ttatcttcta cagcttcagt gacgaaattc agtccggctg 3000

cttcagtatc aggagtattt atactctcag taatagtgct ttcatcttta ttagatttct 3060

tcaccatttc tacgattgca ctcaatttac ttgagaatgc atctgaataa tccatacctt 3120

cgaccagagc agagactttt tctttttgag actcagtcag atctttagta ctttcgctca 3180

atgccacttc acgctgcaca taattgatat atgcgtcacg cttattgagt tcttcgaaca 3240

gacgagctga ttcttcttta tgttcttgca gttcttcttc catttcagct acaacatcaa 3300

ctgattcttc tggaacaaca acgttgtgtt caacgaagag ctctttcaat ccaccaagca 3360

tggattcaaa cagttcggct ttgatacctt tatctactgc taatttattt tcagtgagcc 3420

attcttttgc aagatggtca aggaatttag aagcttgctc agcgattttc ttctcagctt 3480

tttcttctgc ttcttcttta ttttttttcta cttcttcttc tgctttttca gcaattttag 3540

cgatatgaga ttcagctaat ttaacggcgt gctgcttgac ggtagcttcg aatacagtgc 3600

cgaaagtttc ttttgcttcc ggagaaatat taactgattc gaaaatacta tcaagagcaa 3660

cggaagcatc aattttctgc gcttcggcaa tcagttgttc tttaagcatt ttgtagtcct 3720

gttgtttaga taataatatt tataacgctt ttttcatggc ctctgcgaga gccatatagg 3780

cgtcatcggc acttgtatcg gcttccgccg tctgtgattc ggtaatttcc ttaggagtta 3840

cccatgcatc tggagcactt ggaccccata ctgcatcaac acctacagtt aatttgaatc 3900

cttcgtttac gatacgataa cctttatttg tgtcagtcaa tgaacctaat ccacgagaag 3960

aaactcctgg aatccatccg gcacgaatat tagctgctaa tttatctcca ggaccgtggt 4020

caccttcaat aacacgagct cgtccgtata cgtcatttcc tttccaccac atatcttcta 4080

taatgatagc ggcttgcatc gggtcaacat tagcgcgtgg aggatgattt aattctccga 4140

gagcttgttt agttaaaact tgctcattaa tatagtcttt taccgctttt tctaatatac 4200

gttttggata aagacgttta tttctattga cgacttccgc ttgcatgaat attccttcga 4260

tgtataaacc cggttttaaa cctaagtctt ttccatcatg agattcaagc attggtacgc 4320

catcaataat ttcgccaggt tgaccccaag tttcaattag taattggggt tcattcatta 4380

gcttaatcct aatgctttac ggcgtttaag agcttttta cgcttacgct gagcacgaga 4440

ttgacctgct ggattggcaa tcttcgtttt ggtagcttta cgagcaattt gtctacgttt 4500

tgctttagac aacccggtag tttgaaatgc attacgttcg cgggttttgc gatctttagt 4560

gcgagtaatt tcaccacggg cagaaacatg tttaacgata aattcattta acggcatatt 4620

ttcattaata gaagctaatg caaccgctaa atcagtttca tcatcaagca tattctcgac 4680

aattgtattt atatcgtctt tatttaaagc agaagacaat tcgtcaaagc gaccctgtgc 4740

ttcaggaata agtgcttcga cattctcgag aactaattca tgagtttcag ggatcagaag 4800

cattattcat catcctcgtc ttcgtcagag tctttgtctt ttttgtcgtc tttatcatca 4860

ctatcttcgt cttcgtcatc atcctcgtca tcaggttctt caccttcgat taagaaatta 4920

cgagcgatag cgatttttc ttctttaatt aaatcagtcg ttcttgcagc catggcttca 4980

gcaaataatt tacgagcggc tacgaggtcg tttgatttaa tagcttcaat taaaccttcc 5040

attaaaaatc ctcttgttct tggtcggggt cttggaaacg agcctcttta gactcttctt 5100

caatttgctt ggcttcttgt tctatttctt catcagtcat ctgcaaaata tctttcatag 5160

cagttctgtg agaaatatat ttaccaataa atggttctgc catggttagc atattaattc 5220

ttcgttccaa aatttctgct tctttgagct cagcaaagta gctatcccga tgaaattcta 5280

tcttaatatt atttatttca tcattccact catcttctgt gattatacct ttaagcaaaa 5340

gatttgtttt aagtggatct aggaaaactt cttcaaactt gtgctgtaac tcacgaataa 5400

atttagcaaa cgttaattca tcacgtgtaa tgctagttcc agaatcaaac atcacaccgc 5460

cttgttggtc ttgtggaatg cgtgaaagag gaacacgtaa tgccatgtaa agagcttgtc 5520

taaaccaacg aatatcttcc atattgccag tattatcagc accaggaaga gtatcaactt 5580

ctgtcacagc tttaccatca cggcgctgca accaatagtc ttcggtcata gacatattat 5640

gttgttgatt ttttatttta cctgttgatg catcatatac tacacggttt ttcatcgtgt 5700

tcataacatg ttgcatgtgc tcagcagctt tacgagcagg catattacct gtgtctacat 5760

accaaacacg acggtcagga gcacgagtaa tgcgataaat gactacagca tcttctaata 5820

attttaattg gttagcaggt ttaacagcac gatgtaaata cccgatgata tttttgccac 5880

agcaatcgac taatccagaa tgggcataaa caacagcagc ttttggaatt tttatttttg 5940

tgccagcttc atacattcta ccatcacatg catatgactc atgggcagta tcatatataa 6000

aatattcttt gtaaccttta actatttttg tgccagcttc agtttctgtt ataatttcgc 6060

gaacatactg aacttggcga gggtctaatc tacgtaattc ttttatgcct tcttttggac 6120

gttttggatc aatgatttta tgaaagaaaa ttcttgaatc aacataccaa cgtctaaaat 6180

gatcagaacc ttttcgttga aacgatagat gatttaatac atcactaaat tcatctaaca 6240

tcatattttt aatttttgga ctaaatttag atttatccaa atttaacgct acgacttcag 6300

tatcatcttc gtagacgata gcatctgaaa cgatttctga aactgcatta tctacttcat 6360

agttattcat gagattacga tatgtatcaa taagctcacg agtagttttc attcctggtt 6420

catatgaacc aaaaattgtt tggaatgcag cattataagg agaagcagct tcattcgagc 6480

ttacttcaaa ttctcttgct ccatcatcaa gctttggggc tgtaatggaa acaagatctt 6540

ctttttcttg gtctttaaaa tttcgttcgt ccattttagc ccatggagca aacaaactta 6600

atacattaaa tttcattgta ttctccaaat gggaattata gttatattta taatggactt 6660

ctctgcttta agcaggatgg ggatttctcc ccattcattt tattcccaat aatcgagagc 6720

aagagttact tcaaaggttt ggatttcatt gtttgaatcc caatctaatt gaagttcacc 6780

cacgttagta ggccacagac ctttaatttc aatttctttt gttactgttt tagcatcacg 6840

agcatattga cgaacaatag cgctcttttt atactctgca ggttttccac cagtaatttc 6900

gtttccttga ccagcagcaa tgctttgcca atcaacaaac ttctggcgag catcatgagc 6960

ttcatcgttc attactgtaa cagtccagtc atcgaatgta cgatcgcctg ctacgttaat 7020

tttacggttc ataaatccga ctggaatttt ttctacaata ccagctggta aagcagtggc 7080

tttacattgg aatgtaaaat tttgtccaag ataagaaatt tctacttgga ataagttagg 7140

tcgagcaaaa tcaccagatt caaacgctcg tgttacatca tctacaaaca tattagcctc 7200

tgtagtattt atatccctat gtttaaccta gggcatatag aattaaagaa ttaaggatat 7260

agtgtattta tatggcctgc cgaaacaggc ctttagaatg caccgtatta accagcaaga 7320

ccagttaact catcgaaatc tgcaccagta gcagttgcta cgaagttcaa ggtaatgtag 7380

ttaatgcttc tagccggttg aatgtagaat gttgcaacaa actcatttct atcaattact 7440

gacggagtgt tatttgttgt atcgcaaact acacgatatt cataaattcc accgagagct 7500

ttaattccct gtaagtattg ggcagtttct gtgcggaatg atgaacgagt aaacgcgttg 7560

tttaattcga acaaacgata ttttgaacta cgtccgatat tcgttttcaa catattaaac 7620

agacgacgaa cgttaatacg atcaaatgga gaaggaacag aagtagctgt tttatcacca 7680

tacaatacgt aaccatcgcc acctgtacca gttactggat taatagcttc ttggtataaa 7740

cggtcgcgct gagcttggcg agtttcaata gcaagtttaa taacgttaag aatctggcca 7800

cgattataac cagctggaga catccaagtc tgagatacgt tatcagttct tgcgcataaa 7860

ccagcaatat cagctgctaa tggaacccaa cgattcacat cattatattt gtcatactga 7920

tatttgtagt taccatcaat tgctgcgtag gttgaactga tattaaagtt attatcagtg 7980

tatgaacctg ctgcagttct ccagttaact aaattatcta ctgcacgagt tacaggaatt 8040

ccaactacag tttcacgcgg aggtgagcac aatactaagc aatcttgacg agcatcacca 8100

attgaaacaa catgtttttg gacagtagat gctgtttcaa gagattcacc ggcacaagaa 8160

cccgcaataa acaactgaac gtcaacagat tcgcggtcag caaagaagtc ccaagcttcc 8220

atcaaatctc ctgctgttac ttcagcattt gatgataatc caccagacag agttaaaatt 8280

ccagagaagc cttctggcca gttttgcgca gttgcgaaaa tatattctga accacctttt 8340

gcgaaaaagt catcaatata gatgttacta tcgtaaatat ctttttcacc acgcttagtt 8400

gaaagaacaa cgctttgaac aatagcatca tttcgacgaa ctataatagc gtactgtgag 8460

tcagtctgcg gcccatatcc aaatactgcc ttggcagtag atgcacgagt accaccacct 8520

ggataaattg gcagtaatgc agaagcgcct ttcgcatagt cagctttaga tacgatttca 8580

atttcaattt tatcgcctaa ttcgcctgga tagagagcta ctactcctgg aattccatat 8640

ttttcaagat ttgcctgaaa atcaactgct gtcatagcag tttcagcgct ctcgatttca 8700

gctaataaaa taccggaatc agtaataatt tttccaagag ttattactgc agctaaaccg 8760

gaagaagatg aagaaatttc tgcagtccag ttagaaccta atgttgggta ttcgccaact 8820

tctttagctt tagcaataat ttttgcagta ggaatattaa ttttcttaat ttttccatca 8880

gcatctactt cggtaatttt accttctgtt tcaacatctt ctgaaacata tttgaccgtg 8940

attttatctc caaccgcgta gttactacct ggggtagaaa ttgtgtattc aatattacca 9000

gcaatcggag atgagttttt agcggtatct ctatcgacag cgcgcacaac tcgcaaatca 9060

tttccatatt gtaagaaatt cattgcagac ataaaatagt cagcagtttc agctgtaggt 9120

tgaccaaaag tattaactaa atctacttcg tttgtaacct gtttaatctg aaaagcagga 9180

ccccactgga atttaccggc caaagctgct gtaccagtag agttattaac cacggtgctt 9240

tgaaccgtag tttctttgag ctcaatgccc ggagataata aagtcatttt taatcctctt 9300

taatatgctt taatatattt ataccattga cataccatga gatactggaa catactcagc 9360

agaatgaacc gaatcaacaa atataactgg agcgtattca tcccccatat cttgaagctc 9420

ttttgaaaac acttcagatg ctaatcgcat gtcatctttg tcggcataat caataaattt 9480

tgattgtgtt gataaccatc caaaaattac taaagacatt actaaatcgt catgataacc 9540

ttcttcagcc gcccaagaca cgccttttc actaaacgtt ctaaattctt gaatagttgc 9600

acggtgatga ataataagct tatcttttc aataaggtct tttaatgtag agcatcctac 9660

tgctttcgtt cgtttagttt gcttcattcc taaatcagta tatgaatcgc aaataacgcc 9720

ttcgtattct aaatccatgt aaagtgattt cgcaactgac acaccagtac tatttaattc 9780

aatataaact gggcattcat tatattctac taaataacgc ataacgatgt caggcagaat 9840

taaatgagaa atggtatttg aatgtaaaac accaacctgt tcccacacat catcggtaac 9900

atcaataata tgtaaagcgt ggtaatcttg cccacgacct tctgaacagt ctaaagttgc 9960

aatgtatttt ctatctggtt caggtccttt aaatcgatga aaaccatgat catctggagt 10020

tacttcaatg aaatccataa cagccaattt cattcctgaa attaatgtac cagaagtccc 10080

ttcaaacgct gcggtatgtt cttgacggaa ttgtgctaaa gtagaaccat taatggtttg 10140

tatgctccat tgccatccat cgtcaaaaat atcttcatca ttataaagac gttctttaac 10200

tgaattccaa atagcagtgt atggttcaaa tcctgattta ccttcaacag cagcagtcca 10260

aatatcataa aaatgattta atccattagg agtcgtagta ataataattt ttgaacgacg 10320

accagatgaa attactggtt gaatagcaag ccaggaatca tggaagtttg gaataaatgc 10380

acattcgtca atataaatca ttgcgaatga gttaccacga actgcgtcag gagaggaagc 10440

ataagcgcca attgaagaac cattatctag ttcaatagac cctttattcc attcaactat 10500

accaggctgt aaaaagtcag gaagcagttc aattgcttgc ttagtacggt ctaaaacttc 10560

cgcagacatt gagcctttgt gcgcaagaat acctacagct ttatccttgt taaaacatac 10620

aaagtgtgca agaaaaatag ctactacagt tgttttacca agctgacgtg atagattaca 10680

aacagtcata cgtttagatg acattatttt gagcatatca cgctgatagt cacgtaattg 10740

aacctttatg acaccatagt cgatatgagt aatggcgcag tatgtttctg caaaatatac 10800

aatatcatct cggcattttt tccattcctc aaccatttca cgagtccatt gtgttttaat 10860

attagctcgt tttaagttag gaagacccat ataccgagat cttttattat tcttatcttt 10920

ataagtttga aataattcag gcttatcaga attatttggg atttttacta ttttgtgtaa 10980

acgaagataa tcactgaatt tttcaggata ccattttcca tcccactgtg attttatcca 11040

atgaattcca tcttcatctt ttctttctgc taagcttggg tgttttatta aaatttttcc 11100

agcttcattt aatggatgga aatcatttaa tgcattaatc ggttgttcca tttatcacct 11160

tctcacgagc ttcttgagcc tcgtaagcat caccaatttc gtccattaat tctgttggtg 11220

aacccatgaa tactgtcgcg ttctgaatat tcatttgacc tgtaggaaca gcgcctttag 11280

tgccaacctg ctcagatgta atatctttca tatctttatg aagcttcagt atttctctgt 11340

tcgtcgtagt catttgcccc ataagagttg caaatacttc catgtgacga ggagaatcag 11400

cattctttgc cgtctcaaga aaaatcttgg ctgcgtccat tagcatttgt tgttgaaaat 11460

gcatatttcg acgaactact ccataatcat cttctaagtc aggagtacgg ttttgaggat 11520

tgcttttaac ttctactaat tgtagaggtt catatacttt aatttcctcc ccgtcgattc 11580

cggggaggtc agaaatatct aaaagtttgt ttatatcaag accttccata ataacctcta 11640

tgttcttggg ccaggaggtt ctggcggtgt tggtctattt acattgctag tgaaagtttg 11700

ttttactgtt ccatcccagt cctctgggtt aatatctcga ggaacaactt cgctatcaac 11760

agattcaaaa acaccttcgc catcaggcaa atctcttgta ttggcgtgaa aatctgtata 11820

agtagtacga attaatcctt ctgcatcatc tactggagga tacatccatc cgtttacttc 11880

aaatgttagt gaccattcga ttctacgacg agataaatta tctccatcta tagcttcatc 11940

tatagcagca gacatcagta caattttaat atccctttta aatggaatat catttccaaa 12000

ctgttcgtac atagttgtat taaaatgagg ttgaaaatat ggaagaatct gttcaactat 12060

ttgaaacata tcgtcttcgt aacgagtaaa gatactcaat tcataaatca ttttaatagg 12120

agatggatta tactgcgata ctacagaagt tgtacctttt tgcagtaaat tctgatttaa 12180

aatgtttgtt ttaaatggag cgttatagct aaaatcaact aaatgcaaat ttatacgagg 12240

tagaatagtt tcaaccttgg ccacatcttc ttgtgaattt atcgatgtcc atttattcaa 12300

tttcatcata aagtgttcct ttgatgcata cgtaatagga acacgtataa acttatcacc 12360

agattctaac tgacgtttga tttggatatt tgaaaacaaa tcgcccatca aggtagcata 12420

tcgtctaaaa gacgaattat aaaaataacc aaacatgatt tctcctaatc tgggctttaa 12480

ttagtttata atatttatta atccatgaaa tcattatcaa atgggctaga ttcaaaagat 12540

ttgcctctgt tattgacaac aacataaggt tcaacatatt ctttagcttc agaattaatt 12600

tgatctactt cagcatattg atcaatatta atatcatgaa taccgttaag attgcgaaca 12660

ggatttagtt ctaattcact aaattctgga atgttaattc cttcattttt ctgtagaact 12720

ggattaattt cttctccaga ataaatgaat ttacctgctg taattttacg aatagcgttt 12780

tgacctaatt gataaaatgg atcatatggt tcaacccagt taatttcaaa taagctgtta 12840

tccataggaa aatatatcaa atcgccttct ttcggttctt ttccattaac ttggtgttta 12900

aacaagtttg gattaatgga caaagtaact tcatcctgta cttgcatacc aaagttacta 12960

aagaacgatt tagctccttc atatccttca aatgaattta aatatgcagc gaatttccaa 13020

gctttagtaa atttattttt taagtcttcg ccaaatatca aatcagggga aacatactct 13080

cttggaacat aatagcattc tacacctcgc atttgaatgc tttcagctac taatacatca 13140

gctaatattt gactgttttt ataatgattg aaatttacat aaggatttag tatttcagtt 13200

tcattggtct gagaataacc agtgcggttt tccaatttag caaaaagatt tttatcataa 13260

gtagccatat taacctacca aaattccaaa tggaggatcg agcaagtata attcttcacg 13320

taatgcttct ttttctaatc gagcttcttc tattaagcgt tgtccatcaa tcgtaacacc 13380

gccaggaagc atcatacctt ggtggcgtgc taaaatttga ccattcaatt ctttagctaa 13440

agcagtagca tagtctttca cccaacgatt attataagca ccctgtttaa catttgggtc 13500

ttgaccaaca acacgaccaa ctaaattgtg gtctgggtta ttatatcgtt cagataatga 13560

ccagctatct tgtggaccga ctgttccata tcctactgta tttccaacca ttttattagt 13620

atcaatgtat gatttagtcc agctttctac gataattaaa tcatattttt ggaagtttcc 13680

catgactttg agctgttcat ttgctgaatt aaaccaaaag tctggaatag gagagagcat 13740

atcttgcatc attcccatgt aactggtaag ctgggtaaaa tatcctaaat cagctccaaa 13800

ggcatttggt ccataaaatc tattacaaga agtccccata ccgccattaa taccagccat 13860

tcctaaaaga aaatcagtaa accatggata tgtagcgttt ccgtccattg acgttattga 13920

tccaatattt gttcgcaaaa tgcgagttac tgcgaataca tttgaacctc ttaaatcgaa 13980

gactccagtt ttatattttt cttcgtcatc tcctacataa aatacatgaa aacctttgtt 14040

aagtccatca aaatggtatt caccgtataa ttctagggca cgctggatac aatcataaat 14100

ttgatcgggt gttaactcaa cattaataat tggagcccct aaacgtctta gaatgacatc 14160

tttgagttcc tttggattct gagaattata tcctgacatt taaaatcctt tggggccttg 14220

cggccccatg ttatgctggt gataaaaagg tagaaagtag tacccattcg ccgtctttac 14280

gaacgtaagc ttggccatct tttggagctt caggaatata acccgcttct tgtagagctt 14340

gaacgctgct ctgtaaagag gatatattgt ctttagctgt atttacttca tgcgtgactg 14400

ccgcaatgtt agtttcattc gtttttatag aattagttaa tcctcgttct tcaacagttg 14460

atccgtcagg attatttcca tttataagtg aagtaagttc aataacttga cctttaattc 14520

ctgttctatt atttcctatt tcaacttgta tattttgaac attattgttt aaaactgaaa 14580

cttctccttc aagcactgaa actttattta atagagatcc agaaggagac ggttgtcctc 14640

cgctggagtc agttccaaca atttgattta accacgaaac attcgctctt aaaccagacg 14700

aagtgttttc accaacaatt ccgtttaaag actcaataga agttgtgtga tttttaattt 14760

ttcctttaat actagaagga atatcatctg aacctataga agtttcaata gccgttaagc 14820

gctgtttaac accttcactc tgatttaatt cattattaat agattcaatg ctacttttgt 14880

tattattaat ttctgttatt atagaaacat tttctgggta tccaatagaa gatttaattt 14940

ctgctatatc agaatttatt aaagtttgtt tatcatctat agtgtttaat ctattataaa 15000

tatttggtcc aaaatctact ggtttattac caagttcatc gcgtaattta ccaacttcaa 15060

ccgtcaatga tcctacgtca gattcagtaa atttattttc taattcactt aaacgaatgc 15120

cttgtgaaga taataatgta ctatttgtta ttattctatg tttcattcct gtgctagcat 15180

taccaacaac aggaagaccg ttaatgtctt ggccagaata ttgccctagt tcttgtttaa 15240

tccacaataa atcatttcta attgttctat aaacagagtt ttcttcatca ttaaatggac 15300

ctatatcagc aataattttg tcaactgtat tattagttcc agttaatata tcagtgtgtt 15360

cattagtaag tgtctttaaa tttgatatgt cattttttatt aacactgatc tgcgatagtg 15420

cttctatatc tcctgataca tctaaaactc cttgaattgt tttaatatct ttctgcgatg 15480

tttcaatggc agttttaaga attcctatat tttcgtcaag aacctcaaca tttttaaaca 15540

cggaaacaat tggtctattc attgatccat cgtttccata cttagtgcta gctcctagta 15600

tttcttcacc atttttaatc catgaaatac gttcctgacc ttcatcagga acgctatcaa 15660

caaaaggtaa atcttttaat tcaatcattt gtaatcctta gtaatgaact ttaataatat 15720

agtttaatga tatattccat ggtctagttt cataaccaat taatccttca cgattaagtg 15780

taccaagggc atctctcggt ccgcctaatt caaatccatc attagtgaag tatgaagcat 15840

tatcccagtc ggcatatttt ctagttccaa gatatccttg ataaacagac gcgccaaatg 15900

ggccttcact tctgttatat tccccccaac caccggcgtg tttatggtat gacatttgtt 15960

gtgcttgaac accaccaaca tgcattccgt cacatcctac gccaagtcta tcctttccat 16020

aaccatcttg tcctcgttga tttaaaatat gaccgcctgt gccagctcct ctgacgaaaa 16080

gaccccgcat atcaggaacg ccaggattat tccaatcgcc accaaatctt gttccaacta 16140

cgtttctata atcaggaaat tggtcacctg acacggttcc accatgacac ataatccaac 16200

ctggaggtgc tgaatcaccc gcaaacatca taatagttcc aaccggaact cgttcggacg 16260

catatctttc agtggcaaca ggttgatcgc catttttcca cattccaccg cgtgaccaaa 16320

ttccatttgc tgtaagatgg tctaaattta aagaaccatt aatagtttgt ccaccacgcg 16380

tattaattac atctgcgttc cacgctaatg ctccagaact atcaccttca ggggcaatac 16440

cggcttgcgt cgttaattta actactccac gcatagaacc agtagctcct cgaccattta 16500

gtgtttcacc tgttactgca acatctccta aattactgtt aatttccgat tgtgttccta 16560

aacgtataac acccttatat tcttgtgttg caacagaatt cataaaggta tacggagaaa 16620

ttgcatatcc ttcgcggaga gttccttgac gagtttgcgc aacagttgat aattgaacca 16680

cacctctcac agattctgat gcagtatctt cggaaggagc tatttgtgaa attaatttta 16740

ttgcgagttt ttgggttttt agcggagtca tcgccgtagt atcatcaaca ccagccaaag 16800

ccgcaggcgt agatgatatt ttaataaccc cgtttgatga ctcagatgaa tatctatttc 16860

ggaacacatc atcagtatgg tatttcagtt tttgcggcgt tattgatgaa ttattatctg 16920

agccttctaa tgtttcttca tttgttgaat agcgcgttaa accatattta gtttcagtag 16980

catttggata caataatctt gttgctaatg tagctggtgt aacgatttta gaattatttg 17040

ttccatctaa aacctcttgc tctgatgcaa tcattgctat tcctttaact tccatagttg 17100

catcaggaat accatttacg ccgatattac ttatttttga taatgcagac tgtactgtcg 17160

taacagtgcc aggaaaattc gatcctactg gatcgaattt aacatatttt gattcatttg 17220

atacgtgctg atatgtattg ttactcatgc tattctctca aaataataaa atactgtagg 17280

ttgtgtgtga ctatctagcg taacagtttg cgcacctaat aattgccaag ttccataccc 17340

gggtttagaa ggagaaatta tttcttgttt gaaagtaatt cctttatcag agtattgttc 17400

taagatatgt tcttggttat ctaaatactt aacttgtatt ttattcccta tggtaggatg 17460

gtcttcaaat gaatcaattg caataaattt tacaaccatt tcctgtagag ctgttctaac 17520

agcactagta aattcaattg aagtcattcc attagtagct ttaactggaa taccaaacat 17580

gttaacaata actgggtcac ctggtttggc tgaagtatca gtaacagttc cttcaaatga 17640

ccaatagtcg gtttgttgca cgccagtagg agatacgccg cttatattaa ttaatacagc 17700

tccaacctgt tgctctgcca tatttctaac atcattgata gcagattcta catttgagtc 17760

ataaaaacct tttgctattt gtgaaattgt tacagcgcct accggctgat tattcataac 17820

cgaaatatca tttttcttag ttctaaaacc aagaaaatct gctaagcggg aaataactcc 17880

cgctttatta ttaagtaaac tcattatgca atccttatcc aacggtatac agtaatagac 17940

ggttgaatat tactaatatt agtaggagga gtatgtgaag agtttgttgt tgcgtagtct 18000

tcacgatatt ttgtatatat aggaccagtt tcgtctgggt catattgaca tcctccaata 18060

ataactgatc cattttcgtc ttcaattaaa actctttcat cagttttagt cgcaggaaga 18120

tttgcgtttt caagcgttac tgatgttgta ccaactgttc caccggcagt atgtgaagga 18180

tttccgctag aatctaaatc attattgttt aaagcaaagt ttggatccgt aacatcatca 18240

ttccatccta ctaaaacttg tcctttacca aataatttcc atgaaccaaa tcccatataa 18300

gtcaccggat tatttgggtt tatagcattt tcataaattg aaccaacagg ataaatgctg 18360

tcgaaaatag atgatattga attatacgtt ctagtataag aatcaacttt ttcaacattt 18420

ggccaaccga ttttatcaaa atctgttaag gctacatccc cagtaacttc agtagatgat 18480

cctttactaa cataacggtc atcagttaat tcaataatgt catcttttttc taaaagagtt 18540

cctaaatcat tattaaacca tgttataacg attatatcac ctgattcaaa ttttctatca 18600

aataaaagac tgacaggttt tccatcttca tattctatag aataatctgt gtttgattct 18660

ttccattcgc caccaagaga tatacatcct tcttgcgtat ctgaattagc gccttcgcac 18720

aaaaacagag gatacccagc tgttccagcc tgttgctgta aaattccatt aaaacgaacc 18780

tcaagagaat taggattaat gggttcgcca ggaattaatc caaaagctga aaatggaatt 18840

gatttcatcg ccgataaatc agtaacataa atgcttcctt ctaaagaagt ctttgatgtt 18900

agttttgaat ctagcacttt tatttggcgt cttgtatatg aacttctcca ttgtgataca 18960

ccatccataa acgtttcaat ttgaacagtg tcgccaatat tacaaggctg tcttaaccta 19020

atattaaatc catcaagagg aattaattct ccttcatttt cccccggaga gccaaagtca 19080

ctgttttcac taaatacatc gccgtaatat aattcgttac cgcggtgttt tactctgatg 19140

ttattgacat tataactagt tccatggaaa acatctaaaa agtcagtttg tccttgaact 19200

tctactaaaa attctttgcg agctacatta ctaatatctg aactaataat tttatcaatt 19260

tgtttgtttt tgacatattc ccaacgtcct ggagcacaat aaactaactc taaatcgcta 19320

aattgaacat taatttcaac tgatgacgat gatcctttaa tagtatcacc agaagcggct 19380

actagagtaa ctggattaac attccatgtt gcaaatacat ccctagcttt aattacttta 19440

ttataatcat taacggttcc tttaggaagt tgtagagtta ctcttccaga tgaagtgtta 19500

atagcatatg attttcccca ttctgctgtt aatgtttgtc ctgatgaagc attataagtt 19560

ttccaggcac cggctgaata tggaacatct ccatcaccaa gctcgtaata aagctcatca 19620

aagttttcat ttatttttat accaccttta cgcaggtagt caccggtacc atcatctaca 19680

acattaccga tattaatatt ttgtttcatt attgagccac cccgattttc tgcgtagcga 19740

taactttaac tgctgctctc ataccgacag ttgaagaact tatagtcgct gttacataat 19800

ttgttttaat actaaatgca atattagcga tttcgtcttc ttcagtttca ttcccaactc 19860

gcatgacagc atattcagaa gaaatgactt ctgaattaac agcatctaca agaatattta 19920

tttctgccgt tttaattttt cttccatcta ccgattggca cgtaactaac aatttagcca 19980

tattgtattc agtgcgatga aatagtggaa tatcaactga tccggatgta gaaatattcc 20040

atgtaccttc agctggtgat tccttttgtc caaacatact ttcaatagaa taattccaaa 20100

ccgatgtaga attatcagat gaaatacagc gtaaagttac tttactatat gggctagtta 20160

ctactaaatt acctgaaaca cctttaattg aatcaatagc ttgaattgtt aaaggattag 20220

taactgatat tgatccatta gagttaatga attcaacaca atcgccgagt tcgcctcttt 20280

caataataac tttaacacct acagtagagg tatcaatatc atgtctagtg ccaactttca 20340

ctggagttgc gtactctgta atagagtgtt tttgataata cccagtagca tggataattt 20400

gaccatctgc tccagtgcca tttgctactg ccattttacg ctgatcgcca aacgcattat 20460

aaattgcgtt aaaatcacta ttaattttat taccaccgtc gaataagata tcaccagtag 20520

aagcgttacc aatttcgccg gtatcaatca atttctttgg ttcttgaatg aacatagcgg 20580

tttccttatg agtttatagt atttataaag aaaaagggag cccatgggct cccttaattt 20640

aaaatgtaaa cagaatattg atttcttctg tttgatccat tgccataata ataggtggcc 20700

tattttccat ataaatcatt tcgcccgaat gcctcattaa atcttctggg tcataataat 20760

ccttttcagc tttaacgttt gggtcatttg gatgagcttt agcttcaaga ggattcgtga 20820

ttattgatat ttgtctaaat cctttatttc ctggcaatgc agcatcagga aaataaactg 20880

aatctaaata tgctttaaaa cggatagtat ttgccttaac ccggtaaatt aatccaaaat 20940

catcttgttg ccaagtgaga ttatcttcat atccccatct agtcgggtct tcttttaatt 21000

cctcaggcca aggaaccaca atatattcat tcgtgcatct atttatagat acatcgggtg 21060

gaatctcaaa aagatattcc catacatacc cgtccccagg ttcaattgtt ccttcagcat 21120

ctcctcgacc ttcaggagga gtcattgacc taacagaagg tgtccatttt ccgcctaatt 21180

taaggcattc atccttatca gttaaagatg caattgaaca cattccagta tcaggaacat 21240

ctaaacaacg atatactaac cagcctgcgc ctgattcagt agcgttgtaa ggagctgagt 21300

tacacactac aatatcgtta attctaaatg tgtatggatc cggatatcta gtatctcccc 21360

aatctcgacg aggaataact gcgtcaagca ttgatggaag aacctttact gttcccatca 21420

tatgcgtcca catgtcagtt acgcctaata cagaatcggt tggataaggt ggggcaaagc 21480

ccacctcatt ttcatttgat gaccacggtt ctgatcttcc aaatgtgata aagatagtgt 21540

ttttatccgg accacttcca attgaattat aaaaattcaa catttttct gttctaaatt 21600

ttgaagtaac tatcgcacga tagataacac ttgaatcatt catctatttt aacctgtgtt 21660

ggattttcag ggtctcttgg atttcctata ttatctttta gacgtttatt aactaaatct 21720

ctaaattgcg caaatgttgt tccagatgca tcaaataaag gactcattaa tttacgtcgt 21780

tcagacggca attgaccttg aaatattgaa ttattatttt cagcattata gtcatcagga 21840

agaggatatt ctacaccagc cattgggcca ggctcataaa ttgcttcgcc tgttactgaa 21900

tcatgctcaa tttcaccggt tggagttaat ttagctactc tatcagcata ttcagtaggc 21960

aatccagaat cccatttata gtttttatat ttattaatta ttgtctctgt gtgtttaaga 22020

gttaaaccaa cattaataaa catcgttaaa agggtaattg ctataaatcc aaatcctact 22080

ggatgaacaa aacgaataac gtcagatttc cagcgggaag aaggtaaatt ggatttaatt 22140

ttcattacat agtatgatct acttctatta atatagtcta tattgttttg aagcaaatcc 22200

tttcctttaa ctccacgaat aatttcgcct tcaaaactag ggagtctttc tgctttaact 22260

tcttgaccag caattaatct tcccaaaaga ttatgaatag ttacggtcca ttgcaattta 22320

ccattagaat aacttctttc tatataagta acattacatc ttcctgttgc cgtataaatc 22380

gtttgtccta ctaaatcttc agtcaaagaa tcagattgaa cgattatgtc atattcagta 22440

ccggccccag attcaatttc aatttcaact tcttcattat aaagaacttt aaaaagaaac 22500

ttgtatgatg cttcaattcc tttagtagaa taaaaatcat agctacgtga ttcaaagaat 22560

ctcgcaacag catcacgttt atcagcattt aaataaatgt ttcttttata tatctctgac 22620

cacaaatatt cccacgcatg ctcttctcgt ggatattggt tacgaattaa atttcgtaaa 22680

ttgttatact gagttccata tccatcagaa agatactgaa tatatgcttc gcaaaatgcc 22740

tcaaaattcg aatcctgcaa caaataagaa tcaggcatca ttgtgccaat taatggtctt 22800

aaatcaggat cagctaatcc atgctcttct tctggtgacc aaggagtctc atgctcttgg 22860

ttttgtaaaa atgcttttaa aaatactcca gtcggcttcc aaataatttc tactgtatct 22920

ctcacacgat agttaaaatc atagtaagaa attatttcac cagaagattt ataaaaaagc 22980

atcccagacg catatttttt aaatcccgtg aatttaacat ttggcattac tatcgtacaa 23040

tcaccatcat cccagtattc atgaactaat ctatctggtg atgtttccgg aatattttct 23100

ataactttag tgtattttaa atcagcataa actactacag ctctattaga gttgtttatc 23160

caacagcgtg tgttagattt tttagaccaa ttaaagaacg gttctgcgta gtatttcatt 23220

ggttgaggag taaaagtctc ccaatcagat ttttcatccg ctataaatgc catcatatga 23280

taatgcttat cagctaacca ttcacgggga aattcatatt taacagcacc gattaactga 23340

tatttcacca tagtttcagg gtcattaaca acattatcac ttaaaaattt aaaattactc 23400

gaagacagag aaactaattt accgtcagtt gacatgtttg cgtatccagg ttgaatacgt 23460

cttctttctt cttcggtatt accgaaaact cttttccatg ttttttcgtc atgatttaaa 23520

acatatattc ctttatcagc agaatcaatt atttttgaag ttctcggatt ggcatttaat 23580

gtttcaactt caccaataat aagagcaaaa actttatcac cgatagaatc cattttatag 23640

catactgctt taggatttcc agttatagtc attgtatcag gttcaaaaag tctttccgag 23700

tatgttggtg ataacgggtc agaatctata ggtgcattac tcgtttttat atatctaact 23760

ttatctctgg caacaacata gatataatca tccgtacaag taatggcttc agctatacga 23820

tatacattcg ctggtaaagt cgcataagta ccaaagattt ctacatcaaa tcctaaatgt 23880

aactggtcgc caagtttagc aaatgttata tcctgcgaac tgaatctgac atcatctgct 23940

gaccatctaa cgtcagtcga tttacggcca tagaaaatct tgtcgtatcc tagaacgtat 24000

gttgtgttcg cagattggta atatactgtc ttagataaag gatatcctac acggtcattg 24060

aagagcttca cagctttcca ggtttgtcct ttatcattag atactttaac cacgggttga 24120

taacgctcaa aaagatatag aatcccttct gattccatca aataaactcg gttaatatcc 24180

ttacatactt gctgaatgga accttgtatt tcatgatact cattttcacc aataataaaa 24240

ttactgattg atgaaacatc aacatatgat gggctgaatt ggaacgattc attcatcaat 24300

gcagccatta tagtgtcatt attaaaattg acataattag aattgttaag agtaaatttt 24360

tcctgaatga atttattggc taattgcatt tcaatcatgt tttgaaatgt gtaagcattc 24420

gtagcaaaag tttcaaactc ttccgtataa acccaatcag attgctcaaa atcttgtgca 24480

gctgtagcta ctctaatgat gtatgatgtt agtggatcag catcatcaaa aaagaaacta 24540

ttgtttgctg tatatcctaa attaatccaa cgatattgat cactcgggag attttccccc 24600

gagtctgttt ttgtctcagc gatttctaca aaatagtaga aattagcacc aacgtcatcc 24660

cagcgtactt gcacctgatt tgcggataac ttggaaattc tgagactagt gactgaaggt 24720

gcttttactg tcattgtgat ataggctcca aatcgatagt taagtattgc ggacgtaaat 24780

cattttcaaa tacaatcagt gaaccatcac gggtaaagat aacatcatcg gttgggtcag 24840

aatataattc aatagtctga acctcaaatt tttcagatgt taaattaatt ttagcgatat 24900

tccaataaat catgtcagcc ggataattta tttcaccgat aacatagtat ttgtcgcgtc 24960

catcagaatt tgctaattta ttaaaatcat tgcctgtata tggctgaatg ttttcatttt 25020

ctgtaacatc gccagaagca aatggaccaa taataacttt accaattcct ttagaatctc 25080

ggtctgttga tactatacga acatcatata atacatcttc ttctaaacca gtatcaggat 25140

ttacaacctt tcgtccagaa ttaaatgaaa acgtattaga ttccatagaa cgatctttta 25200

tttgattatt gtatttaata cctgcttcag gtgttttata gaagttttgt acttcacgaa 25260

ccatttgaat agtcgctgat gaaccaatga cagaatgatc tgcatcatct acataagtta 25320

acatcttaga tttagcgaaa gacgagttaa aaatttctac atcttcggta taatagcgat 25380

caattttatc aattatttga ccttcaagcc actgctcgga ttcttgtagt ttatttaaag 25440

catatgtgac ttttaaatta gtcttaataa aaagataatt aggagaaata attgatggcg 25500

taataggagc taaattatag tctttgagat aatttttaat atcttcacgc tgtacagtag 25560

ttaaatacag acctgattta ggtttagcag caataaatgc atacccaggt ttagtagaat 25620

cagtgaaagt ctgaactgcc tgaataatag aaccaaatct ctctgaaacg aatgtatcgt 25680

agtcagtcgc agttacgcat cgttgctggg tttcgcgttt aatagtaccc aattcgcgaa 25740

tacgctcaat atcttctgga tcaccgcctc catctgcccc aacaaaatct gggtcaccgt 25800

ttggattttc attaatattg atgatagtta tatttgttaa tgtatctgcg tatgaaaatc 25860

cgactgctcc gttcgcgtca gcaccattag tactaatgta ctcaataaca atcgtagagt 25920

tctgagtagg tttgagacct ccgatataat tagcggtcaa agctccttca gaagcattaa 25980

cagaaatttc accttcacca aaatagaatt cagtgtttcc atcaatagtt tcacgcatgt 26040

agtaaattgt tgatgtagaa ccagcatgaa ccattgactt tcttgtccag ttaatccatt 26100

ccgctccatc aacgtataat ttaacctggt ttctatcaat atttttatca taaatgataa 26160

taggtgtcaa tttatcataa atgatttcag ttcttactat acgtccttgg gccaatttta 26220

atcgtggaaa atattggtta tttttatcac gaatagcaat aacatcttcg gtagatacaa 26280

agttatatgg attaacagaa gtatcttttg catatgctaa aaagcgagtt ccgcgaggaa 26340

ttgtaatgta attcctattc aatgcgtcgg tgcatgttaa cataatttcg gtctgcgcag 26400

cggattttga agtaggtaaa tatccgttat cttgtgcagc ttgaacaact gaacttcgta 26460

agttagcagt acgcataaag ctttcataca cagcagcatt accaaactgc tgaatgtaca 26520

atgtattata agccaaaagg tcacacagaa cgtttaatct tgagccttca aaatcataat 26580

ccaaaaattc attttggcca ttaagccatt caatgaggtt ttgttttatt tcagcaaacg 26640

taccccgac gaatatctcg ggaatagcat ttgctgttct tgttaattga taatttacag 26700

gggtatttgc cattttaaat cctatttaat gaatacttta gatgatgcct gagccacagt 26760

atcaccgcat gatattggat cagccatttg aacagctttc tttccagtga catatacctt 26820

agaagttctg ggttgtgtca ctccgccatg tgtttcatat ggctttttaa tttctgtatg 26880

ttctgtaatt ggatcacctg ctacgagaac agcaattcct ccagtgaata ctttactttg 26940

tgtggcattc acaactgttg gaggccatgc ttcatggcca gcagtaacac acttatcata 27000

acttaatcct gacatctatg acctctcata cacatagctt cttaatttat tagcccaacg 27060

actccaattt ccaactatag tttttgtgta atttttaact agagtttttc ttactggagc 27120

aggaggatcc gtcggttcag tagtatcaga ggatgaccta gaattactgc cagaacctcc 27180

agattcactt tgttcttggt agtcatatat taatgttact tcgtaagtga atgtcttctg 27240

gaggttttga ggagctttcc ataaatacaa ctgagtatca gaatcagtag gaagttcttc 27300

ccatgaagca gcagttttaa attcatcgcc taaacgatat ttcaacgcgt catttccaaa 27360

tccaaacaca gattcatatg ttccgtataa gcgattttct tctactaaaa ccccaggagt 27420

ttcttcgtaa ctagttatat ttatagatac taacgtttca cctgtttcta attgagcggt 27480

aaaggtgacg tcgatagaag aaccttccat ggattctcct aaatcagcgc tcattggaag 27540

tatattagcc aatgtcaatc ctcgatccat caattgtgta ttgaccagat gaaatagaac 27600

tcatagatgc catttttct gtccaatcac caccaacgtc ccaatcaact gtcccagcaa 27660

ctttccaaga aagatttcca tttactgtgt tagtttgatt tccttcaact aaagtggtag 27720

catctccttt aactgtaatg tcagcattac cttcaactac aatagtaaca ttacctttaa 27780

ctaggatagt tccattgcct tcaactgtct tagtttcatc gccacgtaca aatattgtat 27840

tgcttccatc tatttggtga agacgattat ccatgttgta ataaatttct gatccaccga 27900

cgttagtctt tttatcaccg gctaccaaaa aattaccatc agcgttggtt atatcataca 27960

aattatcgac agtttttctt gttcttcttc ctgacggtga tacttcttca taagttccag 28020

tcggatgaac taatctgtat cgttcttgcc caggagtatc atcaaattcc tgaatatgtc 28080

cgctttcagt ttccattgta tgcacataag gatattcacc tttatatgaa gaaactggtt 28140

ctttgaataa aattctcgag tcatttggaa taggagggtc agccgggtca gaagatttag 28200

ctacagtagc agccattgct gatagagacc tagctggggt tttcacttca acaccatatg 28260

attccaaatt ccccgtaaga ataatcatgg taacacggga tgcacggcct tttgtttgtt 28320

gataccacaa tgaatcacga ccggctttat atgctttttc ccaatctccg gctaacatag 28380

cagttaacat tgtgttaaat ttagctacac cgccaacacc catttgaaat gccatatttt 28440

ctaacgccat ttgacgagaa cggttgacag cttgccagac tggtcctact ttagaatgtg 28500

atttaatgtc ccgttgcata tcagccaaat cacgttcaaa taaagtcgtc gcctcttcca 28560

tcgtaataga acctgggttt ccagtaattt cacgaccaac ttgttttgat aaaactttat 28620

taatttgagc catatcacga actggctgct tcatgataag atgaccaata ccaattgtcg 28680

gatatccttc agtatcccaa taaactttta gtcttaatcc ttcatcacgg cgaagcatgt 28740

cagccattga catatttgga ttatcatcgg ttggaatctc tgatagtggt ctatcatcgg 28800

gatttattgc agtgtctaag ttactatctt ggataatgtt agaagacgaa tcatatccta 28860

cttctccgcc ttggtttaat acattagtat catttcctaa acgtctagga tattgcccag 28920

ttgggtcaga aaatccttca agtctattcg gtttttcgcg aactattcca ccatacgtgc 28980

caaggacaat tccgttagtt ttccatttgt ctaaaaaatg accataaact ctagttcctt 29040

ctaccggtcc agtaacagaa cctccaattc cagacattgc tgcagaagtt ataggttgaa 29100

taactgacat ccatggtaat ttttcagttg gaatacccat tacatcgcct tgtgctcttt 29160

gaggtggatg cagaccaacc acacgaacac gaacacgacc taattttaat gggtccattc 29220

tatcttcaac aacaccaaca aaccaattaa ggttattact tatcatttcc ataagatttc 29280

tccattatac gtataaggtc gttcataaat gaattaatgt ctgattttgc tattattttt 29340

atttgacgaa gtttttcatt ttcaagaaca gcatcttcat acgtattaac agcagcaagt 29400

gctccttcat attgaggata ttttctagct ttatcacctt tatcatacca aacatatgga 29460

ttatcatcgt atgatattaa attataaaat ttttcaccgt tctcattcac atgatatact 29520

atttggtctc cacctacatt tttgtatttt tgtatagatg cttgataagc tgcttcttgt 29580

gaagtaatcc atccataata cgggtcataa ttatcattac acatcaataa aacccaatac 29640

aactgtggat ttccatatat agtatttgct aattcttccg ggcgtggtga acctttgata 29700

taataagtac gtaagcggta tcccgcaaga gcgcgtttaa aatagtcttt atagtttcta 29760

aaaatatctg tcataggaat agtcggcgcg tttttattca ccgttttggc cgcatattca 29820

atcggatcaa aaaatgtaaa gagcatgggc cctcctgttt ataaatatat tatctattta 29880

taaggagaat ccaatggcat attctggaaa atgggttcct aaaaatatat caaagtatag 29940

aggtgaccct aaaaaaatta cgtatagatc aaattgggaa aaattctttt ttgaatggtt 30000

agataaaaat ccagaaatta ttgcatgggg tagtgaaaca gcagtaattc cttatttttg 30060

taatgcagaa gggaaaaaac gtagatactt catggatatt tggatgaaag attcttctgg 30120

acaagaattt tttattgaaa taaaacctaa aaaagaaaca caaccaccag ttaaaccagc 30180

acatctaaca actgcagcga agaaaagatt tatgaatgaa atttatacat attccgttaa 30240

tactgacaaa tggaaagcag ctcaagcttt agctgaaaag cgtggaataa aatttagaat 30300

tttaacagaa gatggattac gagctcttgg ctttaagggg gcataatggc tatttttcaa 30360

ataattaatg aaagcactcc ccaagttcca aaggttaagc aatcattaaa cgaaaagaaa 30420

tggattcaga taggtcttga atataaaaag gccaaagcaa aaggaatgac cggaaagcaa 30480

tttgctgaag aaagaggaat caaatactct acgtttactt cagcaatgtc aaaatatgct 30540

tcaggaatta aaacggctga aaagattcaa aagcttgaat caaaaccaat gaataaactc 30600

aataagcaag aaagacaact gcttatgata aattcattca gacaaacatt gcgcgataaa 30660

attcgtaatg aaggcgcagc aattaataat aaaaccagaa agtggtttgc tgaaactatt 30720

aagcaagtaa aaggacataa agttgttcgc ccgcagccgg gacgaatata tgcttttgct 30780

tatgatgcta aacacaagga aactcttcct tactgggata aatttccttt gataatttac 30840

cttggtttag gtaagcataa tttaatgtac ggattgaact tgcactatat tccacctaaa 30900

gctcgtcaac agtttctaga agagctttta aagcaatatg caaatacacc tactattact 30960

aataaaacga aattaaaaat tgattggagt caagtgaaag gatttagggg tgcagaccaa 31020

atgattaagg catatatacc tggtaatatt atgggtagcc ttgttgaaat cgccccgaaa 31080

gactgggcga acgttgtgtt aatgccactt cagcagttcg tttcaaaagg aaaacgtttc 31140

tctgcaaaca aagtctggtc aaatatctaa ttctattatc ttccattctt ttctgttgtt 31200

tgttctaaat ggaattgaat ggaagggact tagacccatt ataccaccaa cagttataaa 31260

gcattatgag gaatatatgt cgcaagcact gcaacaaatt tttaaccaag caaatacaac 31320

taactttgta gtatcaatac cacatagtaa tactacatct gcttttactt taaatgctca 31380

gtcagttcct attccaggaa ttagaatacc tgttactgat accgtgactg ggccgtttgg 31440

actgggccga gcacaacgtc caggtgctac atttgagtac gatccactca tcgtgagatt 31500

tatagttgat gaagaactta agtcatggat aggaatgtat gaatggatgc taggaactag 31560

caactatctt acaggtgaaa atactgccca aaaaacaggt cctgaataca ttacgcttta 31620

cattttagat aatagcaaaa ctgaaatcgt gatgtcaata aatttttata agccttgggt 31680

ttctgacctg tctgaagtag aatttagcta cacagaagat tcagacccgg ctttagtatg 31740

tacagcaacg attccttata cgtattttca agtagaaaaa gatggaaaaa ttatagcgga 31800

agtttaatgc ttcagtttca tgtgttataa tcttaactaa atttgaggag aaacatatga 31860

aactaatctt tttaagcggt gtaaagcgta gtggaaaaga tactactgct gattttatca 31920

tgagcaatta ttctgcagtt aaataccaac ttgctggtcc tattaaggat gcattggctt 31980

atgcatgggg agtatttgca gcaaataccg actatccttg cttaactcgt aaagagtttg 32040

aaggaattga ctatgatcgt gagactaatt taaatctaac taaattagaa gtaatcacga 32100

ttatggaaca agcattttgc tatcttaatg gtaaaagccc aattaaaggt gtgtttgttt 32160

ttgatgacga aggacaagaa tcagttaatt ccgtagcatt taacaagatt attgacgtta 32220

taaataatat tgaagatcaa tggtcagtcc gtcgtctgat gcaagcccta ggtacggatt 32280

tgattgttaa taacttcgac cgcatgtact gggtaaaatt atttgcttta gattatcttg 32340

ataaatttaa ctcaggttat gattattata tcgttcctga tacccgtcaa gatcatgaaa 32400

tggatgcggc tagggcgatg ggtgctacag taattcatgt agttcgtcct ggtcaaaaat 32460

ccaatgatac acatattaca gaagctggat tgccaattcg tgatggcgat ttagtaatta 32520

caaacgatgg ttctcttgaa gaacttttt ctaaaattaa aaatacacta aaggtactat 32580

aatgtctgaa caaactattg aacaaaaact gtctgctgaa atcgtaactc tgaaatctcg 32640

tattcttgat acgcaggacc aagcggctcg tctgatggaa gaatccaaaa ttctgcaagg 32700

aactttggct gaaattgctc atgcagtagg tatcactggc gatactatta aagttgaaga 32760

aatcgttgaa gctgtcaaga atcttactgc tgaatctgca gatgaagaat gatggaattt 32820

aaagactttt caacgggtct ttatgtagca gctaagtttt cagaattaac acttgacgcg 32880

ctggaagaac tccagcgctc tttacgtgtt cctaatccag ttcctagaga aaaaattcat 32940

tcgactatat gttattcaag agtaaatgtt ccatatgttc catcgagtgg aagttttgaa 33000

gtagcttctt ctggacattt agaagtgtgg aaaacacaag atggatcgac tcttgtactt 33060

gtgctagatt ctgaatatct gcgctgtcga cacatgtatg cgcgggcact aggtgctaca 33120

cacgattttg atgattacac accgcatata acattgtctt ataatgttgg gcccttatca 33180

tttagcggtg atgtacaaat tccggttgta cttgaccgtg aatacaaaga gcctcttaaa 33240

ctcgattggg cagatgattt aaaataattt cacaaagttg tttacatact gatgaggtag 33300

tgatactatt acctcatcaa aattaattag gaaaataaaa atgaaaactt tcaaagagtt 33360

tgctacaaaa actactatca ctgaatcttc ccacggtatg gaagtaaagc ttggaatggc 33420

tttagctgaa gctgagcgtc ttttctctcg tattaaagaa cttgctgctg cggtcgatcc 33480

ttcatctttt aaaggagacc aaactaaagt taaagcactt ttagcattat gctccgatgc 33540

aggagaaatt gctaaaaatg gttctaagat gaagaaacga ttagaagatt taaaataatt 33600

tcacaaagtt gtttacatag ggttttagtt gtgatactat taccctatca aaacaaaacc 33660

aaatggaaat caaaatgaaa acttaccaag aatttattgc tgaaactgct gatgtaaaag 33720

ttgagtttat ttacactggc aagaaagata aaatgggtga aatgcctcat ggagttcttc 33780

gtgatgcatt agataatttc ggtcaactcg ccgcagaaga ttacggtgat aaaattgttg 33840

ttactggtcc tgctgcagtt attgaaaaat gggcagcaga aaataaatca atttttcgta 33900

aaaaataagt ttacttttag atagggtagt gatactatta ccctatctac tactgaggag 33960

aataaaatga aacgttgtga attaattcga aatgttgcta ttgcaatttc tgcttccgct 34020

ttcagttttt caatgtttgt tggatttata tgcggattat tgactacggc agaaaatgtt 34080

ttttcacttg tagtagcatt tttaattggt ttaattgcta ttgttatgga taaaatttct 34140

aaaggtgaat aatgaacgtt gaatattatg tatatgcgga ttacgaaaat aatccgtcta 34200

aagatgaaga taatcgttta ggtgtagatg ctttcgattc ccctgcggcg gcatggcaat 34260

gggttgaaag aaccgatatt ccttaccgtt atattgaagt ggttgaccac gcaggaaaca 34320

agtatcctaa ggaagcatat gttgcttccg ggaaggtaaa tttccttttg tttgcaggtg 34380

ataattatta tccccgtggt gggtataccg atttaattgc taaagcattc tctgaagatg 34440

aactccgtga cattatcaaa gaaaatgaaa acaaaccgat ggattctaat cgctttgatt 34500

ggtggcaaat cgtaaatgct aatactcaca ctattgttga tgaaggctga taatgattct 34560

ttatgcgaaa gtatcatcca ttgaaaatgg atataaatat gatcaagacg cggctaaagc 34620

tttgattgat gattatggca ttttaacatg ttttgaagtt gaaaaggttt acattgaccg 34680

ttcatcttct caagttaaat tagtgaagga agaacgtaaa tttaatacag taaattttga 34740

tttctttatt gaaacagaaa aaggtcctct tgaatatgat attttcaaga atcctttggg 34800

tcttgaatgc atcgtaaata tgtattatta taaatggtaa atatgcttta agaattattt 34860

gttattatta actcatatcg cactgattaa taccctctat catcaagggt tcttgcttaa 34920

gagcctttgt taataattgg gaattagcca agttggtaag gcactggatt ttgattccag 34980

gatgcaaagg ttcgagtcct ttattcccag cgcgagaatg gccaaattgg taaaggcaca 35040

gcacttaaaa tgctgcggaa tgatttcctt gtgggttcga gtcccacttc tcgcaccaaa 35100

tttgcggata tcgtataatg gtattacctc agacttccaa tctgatgatg tgagttcgat 35160

tctcattatc cgctccaatt taatttactc cgtgtagctc agtttggtag agcgtctgct 35220

ttgggagcag aatgtcgtag gttcaaatcc tgccacggag actggaggcg tggcagagtg 35280

gtttaatgca ccggtcttga aaaccggcag tcgctccggc gactcatagg ttcaaatcct 35340

atcgcctccg ccagttttgc tgatttagct cagtaggtag agcaactcac ttgtaatgag 35400

aaggtcggcg gttcgattcc gtcaatcagc accaaggccc tgtagctgga aggttcaagc 35460

aagcgactca taatcgccag atggtggttc aattccaccc agggccacca aattaatttg 35520

gggagttatc ccgtagaggt agcggtgtgg actgtaaatc cattgtcatt gcgactcggg 35580

tggttcgact ccaccactcc ccaccaattt ggatgtgtag ctcaatggca gagcgatcgc 35640

ctgttaagcg attggttata ggttcgaatc ctatcacgtc cgccaaattt gtgacaactg 35700

tcacattaat atctacttga cgcgattata ggggttgaac tgatcactct tctcttaatt 35760

tcgtgtgaag acatcttgat tgttggagta ggtattaatg tggccgtagt tcagttggta 35820

gaactcgaga ttgtgattct cgtagtcatg ggttcgactc ccatcggtca ccccaattac 35880

ggggcatagc tcagaaggaa gagcaaggac cttctaagtc ctaggtcgta ggttcgatcc 35940

ctactgcctc gaccaattat aagtgaggaa aatatgaaag gtaatgttta tttagtagtt 36000

catgatttaa cattctattt taatcataat gatactgtta tttctgaacg tgtaattaat 36060

ttgctttatc agcatgcaga ttatgtttat gtcgaaaacg aatatggtca ttggcaattt 36120

ctcaaaaatc gttcatttgg tttagatggt tacgaatatt ttgatcgtaa agacctttta 36180

gatacaattc cgttatctac acaatatcaa aatcataagt ctttacataa atgccggcta 36240

attcgaaatg ctgaatccgc gtatgaagca attgatttgt ggcgtaaacg ccgtgaatat 36300

attgattctt taaaagaata ttaagaaacc gggtcgctac cggtaagtcg tcggactgat 36360

gttccctgga gtatagtttc ctcccacagt tttactgtgt tctggctctt tactatcaca 36420

gcagaaacgg cgcaccgaat tatcgattcg aggaaatatc tttgccgtaa gccgagtagc 36480

gtttttgacg gaacgttcgg atatggtcga gatatggcct tttaaaaata ttgagtagcg 36540

tcaactactt aataaccggg ttcgaatccc ggcgtttcgt acaaacactt gccttagcag 36600

gtggaacccc gacaaggttg ccgcaaggct tagccccgac cgaaaggttg gggctttttg 36660

gtataaatat tagtatatta aatctacaaa ttaaaacagg aaataagatg aaatcatata 36720

ctcaattttt aaatgaagcg gtgttaaatg aagcatctag caccgaaatt caagctgttg 36780

caaaagctgc cattgccgcg ggtaaatatt cctataaaga tgcttctgat gaatcgcgat 36840

tccagtttgc acgcgacatg aaagcggaag gatttacggg aaatgcagtt agtatggcct 36900

ggaaaagttt agttgctact ggcgctgctt ttgcaaaggc ttcgggtaaa cctgctccta 36960

aagcagatcc taaagcggca caagaaaaaa atatcgttaa aggaattatc gctaaatatg 37020

aagctatcct taaagagctt ttagtaatca aaaccgaagg ccaaaagtta gcccgtgctt 37080

atagtttcaa agataatcca catgttcact ctcttgagta tgttgaagac atccaaaaaa 37140

ttattaaaga ccgcatttgg tctgctaaac aaatcaaatg acattcttag ccccgaccga 37200

aaggttgggg ctttttagtt tgaatcactc ggataacgct gttacggata gtaacaaagt 37260

aataaataat taataaccaa ccgataaatt atttcaagga ttttaaatga aaacctatgc 37320

cgaattttta accgaagcag caaaattacc atctgaagca gatcttacta aagtattctt 37380

ccaattggac ccaaaagacc gcggcgattt tcttaagtgg aaagctaaag ctattgaaat 37440

gtacaacatc gataatagtt cttttacaat gagtcaagaa aataaattca ataaagcatt 37500

tttcaaaatt tctaagaaat tggcatctgg cgctcaggtt cctaaatctg tgttagctac 37560

tcctgaacgc gcacctgtta aaatttctaa gaatatgttc gacactaaaa aatacgttaa 37620

tgctttgaat aaagctcttg atgcattgga tgatgcaaag aaggcagccc gcgatcttca 37680

agacgtgtac accgattttg accgcaaaac taaaggttct atttcaaata gcgaacgcaa 37740

tagtgtaagt gtttattctg atagccttga tgttcttggc gatgcgtata ctgaaattaa 37800

aaatcgtatt aacactgcat ctaagctaaa agctgctgca gaagctataa taagtaaact 37860

aggtaaataa ttttaaatcc ctatctaaat gatagggctt tttggtatct aggcctttct 37920

ggacctctct aggcatcatt tagtttatac cctttataat atattatcct atcctttaat 37980

tgcccatccc tgccctagaa ttccctaaaa atttttttcac aaaactgttt acatctctgt 38040

tcttccatgg tactatacaa ctatcaacta ctgatacaga aaacaacttg gagaatgaaa 38100

tggataatta cggcgaactg ttcaacttct ttatgaaatg cgtttcagaa gatttcggtc 38160

gtacagtgaa tgatattaaa gttatcggtc ctgatcatcc gatgtttgaa acttacgcag 38220

taatgggtaa tgaagacggt cagtggtata ctgtaaaagt tgtgattaat atgttcacag 38280

cagaaggtta tgttaaactg tcttctaaag tttaccatga taacgacgaa atcgcggaag 38340

aatatttcaa taatatgaaa taagtttacg caggctcatg attgagatat tatgagccta 38400

taatttgacg atagagtatt atactcctac ggattttaaa tctcaattaa cctaaggaaa 38460

tactatgaac acactgaaga aaattgttga gtttattcgc actaaacttg gttctgctat 38520

ggctaaaaat ctatctgtcg aagaacagta tactgctgca gcagcaaaac tacttgataa 38580

aattaaagat ctaaaaactg cttctgttaa atctattaac gaagaaaaac gtattcgtga 38640

acttgttatc gaaaagaatc gacaggccga atcaaaagag cgtgaaattc gtaaacttct 38700

ttccgaaggc caagatgtaa caatgcatgc taaactcggt ttactatatc gtcgaacagc 38760

tgagcagttg actactaagg ctgacggtta tgctgaaatg cgaattgaaa tcgccaagaa 38820

agtagttgag ttagatgatg ctcgtcaaga acttgcggtt aaattggaat atatccgtga 38880

aactcgtgca gcaaatgccc ttggaattag tactgctgat gatgtagttg aaattgcagc 38940

actgactaag gttgatattg aagataccct tgctcgagtt gaaaccttta acggtaatat 39000

ttctggggtt gaaactacct ctgccgatgt tcaggaatac attaattctc tgaaataatg 39060

ataaggggct tcggcccctt atacttggag taaataggaa tgaaaatgaa aatgcaaagt 39120

gatttcaatt caatgtttga agagttccaa agacaggttg atgttccaga ccaattacta 39180

aatgctctta aacgcatggc agaaggacgt aattactatt gggggtcttc atatgaaact 39240

gatgaaagcc tttccggaag attttctaga ggtaaaaagt ctttaatacg tcctggaata 39300

ctcattaaca gtattgaatc aattcattca ttgacgtgtg attttgatgt tgaatttact 39360

gatttcattt ctcctgaatg gacggtttgt tatttaaacg acgattttga ttatctcggt 39420

gtttatagtt taagtgacgc atggtttaaa cgtaatttac aaaagtcaaa tttatttttat 39480

attgatacta ctgtaaaatt tcagggcaag aaatatttct ttactcttat agttgattct 39540

gaaacgaagc atgaaaataa acgtattctt agtaaaaaga atatcttaac tattgttgat 39600

gatctttttg ataaatttgt agaaaatccc aattttgaaa gtgatttatt actagaaaaa 39660

tttgttaagg aatgtagaga atatgtcaaa accatcacta taccttccaa gtaaacctgt 39720

gaagtatgaa ccaaagcgtc agataatttc tactgatgtg ttaataggtc ctgttatact 39780

catatcattt gtaattctat tgattattgg aggtgtttta gatgttatga ctgatattga 39840

ttctggcgaa atacttgtgt taatgctaat tcttccatta atagttccac ttttattagt 39900

acccgtaaat tgggtaggat actggtatca aggaagacat tatcgtaaac gtgtacgtga 39960

ttggaaagct cagtgtaaaa agattaaaaa ggaacaccag cttaagctag atatgtatga 40020

atttgatgaa attatgaaat ttgttaagga atcacgatgc aaaagccaaa actaaataaa 40080

gtcaaatatt cgtttcctga ggcactatta attcttgctg tatcagtatt tacagctctt 40140

gcgggtagtc ttattggatt gttaattgac tgttttattt taaatatcga cggcacagta 40200

attataacag aggtttggag tgaacttcgt tttactatag cgatttcatt attttcattc 40260

tttggtacca tgttatattt tcattatgat aattttaaaa taaattggca aagaaaaaag 40320

gattacaaaa tacaattaaa ggaatataat agctatatgt cttatattga aaaagaatca 40380

atggaagagt ttgtgagtga ttgtaggaaa attaaatgat tttaaaaact cgctggtatg 40440

atttagatga tggggacgat ggcatttcag ttgatagagt tgactggagc ggctgttctg 40500

aagatacaaa gaaacgatta attagggagt ttagaatggg atatcaagca gttaagccat 40560

ctactgtaac agatgataaa ttcgtgtgta ttcataatgg tcgtgctaag ttaacgaatg 40620

ctgaatggtt cacagataag attatgattc tgtggtatat cattagtctt cctgtgtcat 40680

cattcgtatt ttacttttt ataaaaaatc caatggacag aataggagat tggattcttt 40740

taaccatact tgttaatatt tttacagcat caatattatc tgggatatgg tacacgttca 40800

ttgaaatgcc atggcggcta cgcagacaac aaaagatttt tgatgaaaag aaatatactc 40860

aaaatttaaa taactttatc actgaatgca ggaaattaaa atgaaaacat tatcagctgg 40920

tattatcttc atgacagaag ataaagattt atttatgggt cgggttactg gttctcgtaa 40980

gcctggaatg atggcacatc gctgggatat tccaaaggga cgtgtagaaa gttctgattt 41040

gaatgcactg gaagctgcaa aaagagaatg cttagaagag accggtttta gcaattataa 41100

tccagacctt ctagaagacc taggtgtatt taaatattct agtaataaag acttacagtt 41160

attttattat acgattccag tagagcatga gatgtttaga aattgccatt gcgagtctta 41220

ttttgaaaat aaagatggcg ttatgattcc agagatggat gcttttgctc ttattcctcg 41280

tactcagtgg caatatgtga tgggtccttc actttaccga ataatgaaca gcctctttta 41340

atttataaat accttctata aatacttagg aggtattatg aatatatttg aaatgttacg 41400

tatagatgaa ggtcttagac tcaaaatcta taaagacaca gaaggctatt acactattgg 41460

catcggtcat ttgcttacta aaagtccatc actaagtgtt gctaaatctg aattagataa 41520

agctattggg cgtaattgta atggtgtaat tacaaaagat gaggccgaaa aactctttaa 41580

tcaggatgtt gatgctgctg ttcgcggaat tctgagaaat gctaaattaa aaccagttta 41640

tgattctctt gatgctgttc gccgctgtgc attgattaac atggtcttcc aaatggggga 41700

aaccggcgta gcaggattta ctaattcttt acgcatgctc cagcaaaaac gctgggatga 41760

agcagcagtt aacttagcta aaagtagatg gtataatcaa acacctaatc gcgcaaaacg 41820

agtcattgca acgtttagaa ctggcacttg ggacgcgtat aaaaatctat aaagttgttt 41880

actttctcct agaattgtga tagtatattc acagttactt ggagggataa aatgactcgt 41940

attaatttga ctttagtatc tgaacttgct gatcaacatt taatcgcaga ataccgtgaa 42000

ttgccgcgtg tttttggtat agttcgtaag catgtggcaa acggtaagcg cgttaaagat 42060

tttaaaatat cttctaaatt tattttaggt tctggtcatg ttactttctt ttacgataag 42120

ttagaatttt tgcgaaagcg tcaatcggac attataacgg aatgcttaaa acgcgggttc 42180

agtataaaag atactgaagt tcctgacatc agcgatattc cagtagaatg gaaaaatgat 42240

tataatccat gcaaatcagc tattaagttg agtcaacaac gactcgatga aaaaatttta 42300

atgaagccac actggtataa gtattacggc aaaaatattt acatttaaat aacatgggaa 42360

taacctggac ctcatgattc tgtgagggat tcccgccaac ctgtaataag gtcgagccca 42420

agtgcggtaa tgggtaaata cagaaatgga caattcatgc gccatggaat ggcccaaacc 42480

tagagagaac aaaatgagaa catttttaac tggtccttat ctatccctga tgaatgcttt 42540

tacacaccat tctgatgcta gagtagaaga aatttgtaaa aacgaatata tcccgccatt 42600

tgaagactta cttaaacagt attgtacact tcgactagat ggtgggcgtc aatctggtaa 42660

atcaactgca gtaactaatt ttgccgctaa ttggttgtat gacggtggaa cagttattgt 42720

tctttctaat acttcagctt acgctaaaat ttccgcagat aatattaaaa aggaatttc 42780

gcgttattct aatgatgata tacgttttcg tttatttact gattctgtgc gcagttttat 42840

tggtaataaa ggaagcaagt tcagaggttt atcgctttcg cgaattttgt atataattga 42900

tgagcctgtc aaatctcctg atatggataa gatttatagt gtccatattg acactgtaca 42960

ctgctgctgt aatattaaat gttgcattgg tggtattact cgtccacagt ttttcgtaat 43020

cggaatgcaa tgatgacaga cactcagctt ttcgaatatc tttatttttc gccaaaaact 43080

attaaaaata aattggtgaa tcattttgaa attttggcaa aaaataacat tttgagcgaa 43140

ttttatccca agcaatacaa attacaaaaa ggcgtattca aaggatgcag agttttgtgc 43200

acggctccta atgcacggct aatgaataaa attccatatt ttaccatgga atttattgat 43260

gggcctttta aaggactaat cacacagagt ttaatggcat atgattctga gccattttta 43320

attaaagaac aatcttggat aaatttattt tttaattgag gttatatgaa agcatatcaa 43380

attcttgaag gcacacataa aggtactatt tattttgaag atggtattca agcacgaatt 43440

attgtctcta aaacctttaa agaggactct tttgtagacc cagaaatttt ctatggtttg 43500

catgcccgtg aaattgaaat tgagcaacag cctacagtta aaattgaagg tggtcaacac 43560

ctgaacgtta acgttctgcg tcgtgaaact ctggaagatg cagttaagca tccggaaaaa 43620

tatccgcagc tgaccatccg tgtatccggt tatgcagttc gctttaactc tctgactccg 43680

gaacagcagc gcgacgttat cgctcgtacc ttcaccgaga gtttgtaatg gcaaagataa 43740

ttattgaagg ttctgaagat gtgctaaatg ctttcgccga gtggtttagt aattcaggcg 43800

aacagcaatt taacgaagca tggaacatgg gtgatattaa tggaatttat cctacgacag 43860

aaatttctgt tcaaggatat ggcattcatg aacctattcg tttagttgaa tatgatttgg 43920

gaacaggtga ggaagtaaaa tatgattgaa gacattaaag gttataaacc acatactgac 43980

gataaaatca gtaaagtgaa tgctatcaaa gatgctgaag ttcgtttagg gcttatcttt 44040

gatgctttat atgatgaatt ctgggaagca tttgatagct gtgaagatga tgaactcgcg 44100

aagaattacg ccgaaagcct cgatcagtta actattgcta aaatgaaact caaagaagcc 44160

agtatgtggg cttgtcgcgc agtgttccaa ccagaggaaa aatactaatg gctcaattaa 44220

gcgcagggtt tggttatgag tattatactg cccctcgtcg tgtatctgtt gctcctaaga 44280

aaattcaaag tcttgatgac ttccaggaag tagttcgtaa cgctttccag gactatgcac 44340

gttatcttaa agaagattca caggactgtc tcgaagaaga tgaaattgct tactatgagc 44400

agcgtcttga acagctcaaa aatctacatg aggttcgtgc agaagtttca aagtctatga 44460

ataaattgat tagatttaaa gaataactgt ttacttttcc tcttgactgt ggtataattt 44520

ttctatcagt taagaggaga ataacatgac tatcaataca gaagttttta tccgtcgaaa 44580

taagcttcgt cgtcactttg agtcggagtt tcgtcaaatt aacaatgaga ttcgtgaggc 44640

atcaaaagca gcaggagtct catcgtttca tctaaaatat tctcaacatc ttcttgatcg 44700

tgcaattcaa cgggagattg atgagacata tgtttttgaa ttattccata aaataaaaga 44760

ccatgtttta gaagttaatg aattcctgag tatgcctccg cgtcctgaca ttgacgagga 44820

ttttattgat ggggttgaat atcgtcctgg acgtttagaa atcacagatg gaaatctttg 44880

gcttggattt acagtttgta aacctaacgc gaagttcaaa gacccgtcac ttcaatgtag 44940

gatggcaatt atcaacagtc gtcgtttacc aggaaaggct tctaaagcag taattaaaac 45000

tcaatgaggt aagcatgaga aaagcactac tcgctggtct attggccatt tcaatgatgg 45060

cacatagctc cgagcatact ttcagtaatg tccaactcga taacatgcgt tacgcgtatc 45120

aattcgggga acaattttct aaggatggaa aatataaaac acacaaaaac atccataaga 45180

gcggattggg tcatataatg gctgctattt tgtggcaaga aagctctgcc ggagttaatt 45240

taaaatctaa accaaagcat catgcctatg gaatgttcca aaattatttg cctactatgc 45300

gagcgagagt caaggaactt ggttataata tgaccgatgc tgaaataaaa agaatgttga 45360

ataaacggtc caattcagct tcctgggcgt acattgaact ttcttattgg ttaaatatac 45420

ataagggtga tataagaaaa gcaatatcat cttataattc gggatggaat gttaaagcag 45480

gttctaaata tgcttctgaa gtcctagaaa aggctaatta ccttaaaaat aataaacttt 45540

tggaaatagt aaatgactaa aattttggtt ttatgtatag gattaatttc attttctgtg 45600

ttagcagata catcatatac tgaaattaga gagtatgtaa accgtactgc agcggattat 45660

tgcgggaaaa ataaagcatg ccaagctgaa tttgcgcaga aattaatata tgcatataaa 45720

gacggagaaa gagataaatc aagcagatac aaaaatgata cattgttaaa acgatatgct 45780

aaaaagtgga ataccttaga atgttcagtt gcggaggaga aagataaagc cgcttgtcat 45840

tcaatggttg accgtttagt agattcttat aatcgaggat tgagtactag atgattgtaa 45900

aatatatcaa gggcgatatt gtcgccctat ttcttcaagg taatattatt gcgcacgggt 45960

gcaattgctt ccacacaatg ggctctggcg tagcgggtca attagcaaga gcctatccca 46020

aaattttaga aatagataaa accactaccg agtacggttc tcgtgataaa ttaggcgata 46080

tgtctattgt ttttaaacat agtcctacgg gatttggtat atgctataac ctgtatacac 46140

aatacgaacc gggtcctaat cttgattatg gtgctttagt aaactgcatg atagaattaa 46200

atctacaggc agaaaccctt ttgtttaaac cagtaattta cattccacgc ataggttgcg 46260

gtattgctgg cggcgattgg gataaggttt ctaaattaat cgacatgttt actcctgata 46320

ttgatttaat agtggtggat tatgaaagta cattacccgc atccgtttga tcctaaaaac 46380

aaagtggaaa ttattcgtca atgggaacgc atttgccgta ctaaatgccc aattaatagt 46440

ccacatgatg tagataaaga ctatattgga acattcgttg aatatacctt tattgatagg 46500

aaaggtcgta aacaacatgt agaagaatat tgtttaaagg ttacatggtt atgagccaaa 46560

ctagtattct taaaaatgcc cactgcgaaa agtgtgaatg gccagttgtt tttgctttat 46620

gtaatgatga aatggcttgt gatttcgatt attggtgcta ttgttctaat aaaggatgca 46680

tcaatcataa aggtgaagga ttttattcag gattttatcc ttatcctgat ttcgttaaag 46740

aaggtaaacc gaaatgaata gttttgagtt acagtatgaa gtgttacgtg agcttgataa 46800

tttaattgaa ctcgctgtca ataaaggttt tgccattgga atcggtcaaa aagatactgg 46860

tcatttaact atggaaatat ttaagcaaaa gcgaattatt ttaaaactcc tggaaattaa 46920

tatatgagtc tgagtaaaga acaaaaagat aaattgtttg agcttatcca tgaacttcta 46980

gatgagcata cagaagcaaa caccttttat gatgaatacg gcccgctatc tcccgaacag 47040

caagaagaat ttgctgatcg gtttgataag aaagaaaacg aattaatagc ttatgtgaat 47100

atgctttaag aaggtgatat ggcgagttta atttttactt acgcagcaat gaatgctgga 47160

aaatctgctt ctcttttgac tgctgcacat aattataaag aacgcggaat gggtgtatta 47220

gttcttaagc ctgctattga tactcgcgat tctgtctgtg aagtcgtttc tcgcattgga 47280

attaagcagg aagcgaatat tattacggat gatatggata tttttgagtt ctataaatgg 47340

gctgaagcac aaaaagatat tcattgtgta tttgtagatg aagctcagtt tttaaaaact 47400

gaacaggtgc atcaattaag tcgaattgtt gatacatata atgttcctgt tatggcttat 47460

gggctaagga ctgatttcgc tggaaaatta tttgaaggtt ctaaagaact tttggcgatt 47520

gcagataaac ttattgaact aaaggcagtt tgtcattgtg gtaaaaaagc tattatgaca 47580

gctcgattaa tggaagatgg aacaccagtt aaagaaggta atcaaatctg tattggtgat 47640

gaaatttatg tttctttgtg tagaaaacat tggaacgaat taactaaaaa gctcggttag 47700

tgcaaaagtt ataaataggt ttatctaact aaaggggtat atatgctaca attaactgaa 47760

aagcaacttc gcaatcttac tgttcttcaa ttagatgaaa ttcgtaggga agttggaaat 47820

atcatttcag ctttgcgtcg agaagtatca ctcaaccaat ctccggcaga ctatactaga 47880

ttgcgaaatt ttgaaaaata ccttgataaa gttaaggccg tgcatcggca taaagtaaat 47940

acaggacaaa aatgatagga ggcctttatg gccttaaaag caacggcact atttgccatg 48000

ctaggattag cgtttgcttt atctccacca attgaagcga atgtcgatcc tcattttgat 48060

aaatttatgg aatctggtat tagacacgtt tatatgcttt ttgaaaataa aagcgtagaa 48120

tcatctgaac agttctatag ttttatgcga acgacttata aaaatgaccc gtgctcttcc 48180

gattttgaat gtatagagcg aggcgcggag atggcacaat catacgctag aattatgaac 48240

attaaattgg agactgaatg aaattcagcg acttttcaca aagtggaaaa ccttcaaagg 48300

cagatgaata cttaggttta ttaatggctg cacaagctta ttttcattct gcgcattttg 48360

aaactaaaag ttatgctaga cacaaagcat acgattttat tttctctgag ttgccagatt 48420

tgattgataa atttggtgag caatatttgg ggtattctgg tagaaaatac acgccttcta 48480

ttccagatgc cagtaaactt cctaccgaca caattaaaat gattgatcgc atactagacc 48540

aatctaacag catttataaa gaaatgcctc cagccattca aagcacgata gatgatatta 48600

ctgggatgtt ttaccagagt aaatatcttc tttccctcga ataacattag tctccttcgg 48660

gagacttttt tcattttacc ggtttacttt ccatttgagc tgtgatacta tacaactatc 48720

ggataaagag gagaacatca tgaaaattga agcacttaat caagaaggaa atatctacgt 48780

catcattaat ggtgattttt tcgtcgacat ggatgaagtt actagtgaag aacttgtaga 48840

acttcttaag aaacgttatg atatgtgtga tgaagctgca actcatatgg cgtgtgcaat 48900

attctctctt tcatatgtgg tggaataatg actagaattg aacaagcaga taaaattaaa 48960

gaattggtag ctttaattcg caaagcagat gaggaactta gtgactttgc ttggttttcg 49020

gcaggcattg caaataaagg tattgaaaaa tttgaagcta aagttgataa tgctttagaa 49080

gcgttagata tgtttcttga tgaaattatc gatcataata cgagagtgta agtatgctaa 49140

cacgcgaaca gtttgaaaaa atcattaaat tagcacgtga tattgaaata gattcatatc 49200

aattagcagt tgagcattgt gaaggatatt catacgatgg tatagaagca gctaaaaagg 49260

atttggataa atctaaagct aagttagttc aatatcttga aatgattagg tggaataatg 49320

aaaactgaaa agcagatgtt tttaatgaag ctaattgaag aatatgctaa tgcagtttct 49380

gactatgaat gttcttctcg tgaaagaggt acagctttcg ctaaagaaga attgaaaatc 49440

atggttgatg ctcatacaaa gcttcagaat tttattgaaa acgtcattta atggtttaca 49500

agttggcaag gttatggtat agtaatcttg tcaactgcca aggagaagag aatgaaagtt 49560

ttgtttgttg tgtatgtgat gattcaatat aattacccaa tgtttactta taatctggtg 49620

aacaacatta ttgatattat tcaaaggagt atgtaatgac aagtgagcag gcttttaaat 49680

taaaagaatt aattgaaaca tatagcaaag ctgttcatac agcaacagtt attgatgaat 49740

cagctttctc cggacatgct aacaagatta aatacaaaac tcttatggaa gaagctaaag 49800

taaatcttga ttcttatatt gaaactttaa ttggtgaata acatgggctt tcctaaatta 49860

gaagtaggtg atttagtttt aacaaaatta tggaatggtg ttcaatcagt agaaatctgc 49920

caatatcgtg gagcaacagg taatttgatg tacacgattt ataatccaga aattttgtta 49980

gagtgtcatt tggaacgctt tataaaagac accgatagta tgccttatag tgtatcaatt 50040

gtacgtaaat ctgatacaaa ggaatattct aaaattttag aacaaattcg tgccaataaa 50100

aaggattaat atgaaacgat tagtattaga agttagtccg ctttttggtg aattggctat 50160

agaaaaagta aataacatgt atcgtttgac gcaagaagac gatatgctat attttacgcc 50220

tagtgaaatc attcatttaa cccaaattga atatccttat actgataaaa tagtaagcat 50280

caatgatgag cacaaaattc atttttattc ttcatgccca ggatttaata ttaaaagtga 50340

gtcaatgtgt ttatcagtta tccattggga tagttttata gataagatta aatattttta 50400

ttattctaat gaaagaaaac atagtttaaa atggctcaaa aattgcaatg ctattattac 50460

taacgcttgc aatcagaatg atgaaactct tttaaatgta tcaaaatgtt atgaagaggg 50520

agatgtctta actattcgcc aaattgacga ttttcgatca catattgtca catttaccaa 50580

agacgaagct attgcgttaa agacttatct tgattctgtc attccaacta tgatttcaaa 50640

gtgaggaaat atgtttattt caagtggaag cggtttaatt cgtgttgaat ttaaaaatga 50700

catctttctt agtcaaggag atgatattat taaaatgagt tatgacgaaa tcaagaaaat 50760

ttgtcatgct cttgaaagtc atggaaagga aaatgctact atcgatatag gtgatttatg 50820

ggtgacactt tatgaagtat ccgaaggatt taacattgaa gatgaaaaca acattttagc 50880

tattgataaa agaagtgatt tgtttgatgt attaaaagtt tatgaacagt caaatggtgg 50940

aagaaaagct gtattagttt atcaaaaacc acattcatgt ggaactgctt caatcatttc 51000

aaatattgaa gatgaaactg atacttatat gtgtgtttta aaagctggtg gtgaccgtca 51060

tccggatttt atttctattc gtcaaaataa tggagaaatt tcattatcaa aatcagaagc 51120

tgaagctatg attaagtatt taacaactgt tacaccttca atgaaaggat aattatgatt 51180

attaatgaaa actcttggca ttataaatta ttcaaaatgt ttaacgacga atggaaacga 51240

cctaagacac tttgtgcata tttttggtct attgttatcc ctacattttt cgtttctttt 51300

ttcggatgta ctatactcgc aggtctaact attatctgtg cagaaatcat acagaaatgg 51360

cttatttttg gtagtttatg gactcttatt ccatcagcat ttatacttgc cattttgctt 51420

gttttactta ttatcggttc atttgttatt cctgcacaac tacatgaaaa atataaagat 51480

tataaatgga aaaaggatta tgctttacat gtagaaaata ttgatagggc gtataaaggt 51540

ttacctccta ttcaacccaa gaaatctatt atcgtcgaat ttttaaaagc gcgtaaagct 51600

aaagtatgtc ctgttattga atataaggct gaatgatgaa aacagtaatg aaaagctatt 51660

ttggtagtca tctttatgga acttctactc cagaatctga tgtagatttt aaagaaatct 51720

ttgttcctcc tgctcgcgat attcttatcg gaaatgttaa agagcatatg agtaaaaaca 51780

ctaacaacac atcatctaaa aacactaaag atgatattga ccatgaacta tacagtctta 51840

aatatttctt taaattagca gcagatggtg aaactgtagc gttagatatg cttcacactc 51900

cacctgagtt agtggttaaa tctgatttgc ctgatgtgtg gaagtttatt caagacaacc 51960

gttctcgttt ttatacgact aacatgaaat cctatttagg atatgtccgt aagcaagctt 52020

ctaaatacgg cgttaagggt tctcgtttgg ctgcattacg tgatgtattg aaagtagtta 52080

atcaaatccc tgagcagtgg gttgattacc aagaagatgg ttctattaag cagcgtcgta 52140

ctaaagttga agatattaag catcgtcttc cagaaaacga attctgtgaa tgggtgttcc 52200

ataatcatga gaaaacaggc ccacagacgt tctacacagt gttgggtcgt aaatatcaga 52260

caacgctttc tcttattgag cttaagcagt cactgaacaa attagatgct gaatatggtg 52320

aacgcgctcg taaggccgaa gccaatgaag gtattgactg gaaagctctg agtcatgctt 52380

gccgtggtgg actccaacta ttggaaattt acaaaactgg tgacttggtt tatccactcc 52440

aagatgctcc atttattctc gacgtgaagt tgggtaaaca tccatttaaa acggttcaag 52500

agtttttgga agatgtggtc gatcaagtag aagcagcatc tactgaagct tctaagaacg 52560

gtatgcagca aaaagtagac atgagtttct gggatgactt ccttgagaag gtctatcttg 52620

aaaaccatcg aagttattat aaatgatagg gagccttcgg gctccctttt ttattttaaa 52680

aatttttca caaaactgtt tacaagcata aagctttatg gtactataca actatcaaaa 52740

caaacactta aacggaaaac aaaatgaaaa ttacaccaat tgaagtaaaa aagttgattg 52800

atacagaaga aatttcagag tgttttgaaa gtttcttaga agacgcaact gaagataacg 52860

cggtttatct cgcccagaaa attatcgaaa cttatttgga gaagaatcaa tgacagttta 52920

cgtagatgtt ttaatgaatc atggatggaa acttcgcggt catccaacta aaaattgtca 52980

tatgttcact gatggagata ttgaagagct tcatgaaatg gcagaagcaa taggaatgaa 53040

acgttcttgg tttcaagata aacgcattaa acattatgac ttacacgctc gccgacgcca 53100

aaaagctgta gaacttggag ctgtagaagt atctcgccgt gaagcagtaa aaatttggcg 53160

aacgttaaaa taaattgttt acagaagggt agtagtgtga tactattacc ctatcaaaac 53220

aaatgtgaga ttggagaata aaatgaaaac tgtaactatc aataagggta tctacttcgg 53280

taaagaaatc tctggaactt ttgagctctt aggtgaatgg ttcccagata atgctccggt 53340

agatgcacaa ggagatggta aagtttttgt tgaaattgac ggtaagcgtc gcggtgtttg 53400

ggtttacaaa tcagacattt catatgatgg tgtaaaagtt gaagaagtta aagaatcata 53460

tgaagatatg aaaacccgca ttaataaaag atttaatgtt atgggaatga tgacgaatgg 53520

tattattaac ggaaacattc gttcattaat tatctctggt gcggcgggta ttggtaaaac 53580

gtattcttta gataaagctt tgaataaagc aaatgataat ggatacattg aatataaaag 53640

cattaacggt aaaatctccg gtatcggtct ttatgaacaa ctttggaata atcgtgaaga 53700

gaattctgtc cttttgattg atgatgtgga tgttttctct gatatggaca ttcttaatct 53760

tctgaaagct gctctggaca ctggagagac ccgtaaagtc tgctggagca ccgcatcttc 53820

ttacttagaa gaaaaaggca ttgagcgtga gtttgaattt aaaggaacga ttgtttttat 53880

cacaaacgtt gacattgacc gcgaattaga ccgtggtact aaacttgctc cacatttaca 53940

agcattagtg tcccgctcgg tttatttgga tttgggtgtt cacactaatg aagaaattat 54000

ggtcagggtt gaagatgtta ttctttcaac tgacatgatg caaaagcgcg gtctttctga 54060

tgaagaaact tataaagcat tatcatggat gaaagttaat gttaatcgtt tacgcaatgt 54120

ttcactgcgt actgctcttt atcttgctga ctttattatg accgacaaaa acggttggga 54180

agaaattgct gaggttactc ttctgaaata attcataaga ggacttctat gacaaaaagg 54240

cagttcagaa atagattata tggactgcca ttaaaaagat gactagaatt aaactggtga 54300

atggaggtaa tgatgttata ctcaaaggct cgtgaaattt acgaaactaa aattaaagaa 54360

gcagtattta agttcgcaac gacaatgcga tggacaaatg actgggagta ttcaaaaaat 54420

cataagaagc ccatggtgac aagaaaggct catatgttag tgttaataga ccgtgagcag 54480

attaaagccc gagaagccct ccagaatcat aaaaaggctg cctttgaatg gtttatggat 54540

aacactgctc ctgagactaa gaaagcggta agcgcatggt tcagtggaaa aaattgtgaa 54600

agaagtttct tttagtggtt tacaagactg ttcctctgtg gtactataca actatcaact 54660

acggaggaac acaaaatgaa cgctaaagat attttcaacc tggtaaatta caacgatggt 54720

aaatttaaat ctgaagcaca aagtaagttc tttaatgaca tctcaatcgg aggtgaaatc 54780

acggttgacg gaggacaaat ttacaaatct cgttggaatt ggatcgttat tatcgatgag 54840

attggtattg tagaaattta caagaatacg aataaaaatc gtacattaca ctggtctcgt 54900

gatactaacg aacagtacaa aaaggataaa gcatctaaat tatctcgtgt aactcaagaa 54960

gatattgagt tcatcaagaa agatattttg atgtatgata acttaattgc tgaagagcaa 55020

gctgttattg ataaatttga tgagattaaa gcttctcgtg aaattcctga ttttatgaaa 55080

gaatcagtaa atgaacgata cactctcatt tcagagcgta ttgaaactta caaaaagcaa 55140

agagctgaac gccagaatac tcttcggaag tttgaagaac ggttaaagac ggtactcgca 55200

taaccgcttt ataccaagga tggtataatg gttctaagcc cttttaattg agattattat 55260

gaaacagttg ataattaaaa gattgaattt attgatatgt tgtttatgta tagcaattgc 55320

atatggttat tacgcaatta atgattatat gcattataaa gattatgatg ttactgtagt 55380

taataccatt acaggaacac aaggaaaagg gtctagttta tcgtttattg ccgtatatga 55440

actcaaagat ggttatagat ttagtgaata tatttcccca gagatgtatt catcaataga 55500

aaaaggtgat aatattactg taagtttacg tcctttcgac gtaaaacaga cattgtttga 55560

taatattgtt tggttctttg gaatggtatt agttcaatct gtgtgtggtg cttatatagt 55620

ctgttccatc ttattctgta tatttagtaa aattgaaatt gagtgaggaa aatatgtcag 55680

tagtaattaa taatgtcaat gcagtaatta aatctttagt taataaaaaa ttaaatgaat 55740

ggactgtact tcgtcgtgga gagccagata aatttttca tagatttaac ccaactttgg 55800

atttgaatgt tattgacaga gatgttcatg ctgaaatttt agataaattt aaagttgata 55860

ttgggtttgg gttagataaa catttgcaac gaacaaacgg atctggaatg ggtttatcta 55920

atcgcatcat gaaagccctt aataaaattg gagcgttgtc tcgtattaat gcgagtgaaa 55980

tccttcgcaa ttataataaa ggatatgacc tttatggtcg actaatgccg aaattatcat 56040

ttgaccaaat gattgcggat ttgtgggaaa atcaacgacg attattagca ttaggcgctc 56100

gattagctaa aggtctagat aaacaaatga tttttaagac caataataca gaagacctta 56160

aatgctttaa atttagtact cgtggagatg attattacat cagagctcgc tctacagatt 56220

atgttaatat ggggcatcat ctctgtttag cttttgaagt tttaaaagaa gccggaacat 56280

tagaatatgt gtctggtgct aaatgtccga ttggttcaaa ttgcatttta atttatcgcc 56340

cagatgaatc cagttcaact aaattaccta caaaacctgt accagttcgc agtaatgaaa 56400

aacattctga acaaattgct tattttaata agcagattga agagctaaat atttctattc 56460

agcaatatga tgatgaaatt ttcagactat ctggattgag tagtaaagct aaatctgagc 56520

gtgaaaaatt aattaaaatc gttgatttac ttaaatctta aggaacacca tgaaaactcg 56580

ttctcaaatt gaagatatgg ttcgtaatgc cagctatact cgtgatgtta tgacattttt 56640

gtgtgaaaat aatttagacc ctgataaagt taatcgtgtt attcatcact ttaagtatac 56700

gaatagcagt gaatgggtgc gtaattttag taaagcaggg tatattacac aaatgactgc 56760

tcgtgaacag ctcaccgatt tctgtaaaac tattgattat aaaaatcctt tgattgttca 56820

aggcgttggt caaagtaagg tcgatttatc atctggattt ttcaatccaa atcattatcg 56880

tattgaatgg agatttattg ctctattccg taaacaatta aagcaaattt tgtctactgc 56940

tagtcgatta aaaggctctg atattaactt aaagaacctg aaatttgatg gttatactct 57000

tcagatggaa gtaagaccgt taaaagaaaa taatagaact gcacgaatta gctttaagcc 57060

taatactaaa aattctcttt caatttgtga atgtcttaaa tcacagctga cagaagcatt 57120

taagtatatg gatgttgttg ctgctgttca atctaagatt ttacctcgtt ttgagcgaaa 57180

ttgggaacat acaacaacat atgaacttga tatgatcgtt tcatttaaat atgaattttt 57240

gagaaaggat gaaattgttc aagagaaaaa gcaggaagtg caagatacct taaatttaaa 57300

tttatccaat tacttatcaa acgatcctaa attttggatg tatagctcaa gcaatataga 57360

tgcatgtaaa cttaataaag tgagttttct tcctactgaa aattcaaatt ttaaacctgt 57420

agaaaaatgg cacgctgacg cgattgagaa gtctcttaag gcagtagatg atgaactcgt 57480

taaagcgacc aatgaagtgc tagaagctga aaaggcgtta gaacaagctc agtcaagggt 57540

tcaaaatctg acaaagcaac gttctaaact gaacaatgca ctaaatgcac tgaactagtt 57600

tactttgcca caaggatgtg gtataatgtt tttactttct actgaggaga ttattatgac 57660

tcgtaacgaa tatatcaaat cattcaatag cgttattgat gataaagcta taccgatgtt 57720

tggccaaaat agcgttcttt ctattatcaa tcaatggctc aatagtgttg atgcaagtat 57780

tgtttcttct actaaattta ttcatgaaat tcgtaaaatt tctagccgtg tagataaaga 57840

tgttatcaag aaaaccttta aagagtctcg tcttctttca tatttggtta atcgggatat 57900

tcttggtaat tttgggaaag aaattaaacg aactaaagat gtagtaggat acaattggtt 57960

cggtgatgtt aattcttatc atcttaatat taaagaagac cctgagaata tttttactcg 58020

tcgttggatc agtaatttca gacttttaa gaaacaaatt ctaaaatcag cttctaaatt 58080

atgttatggc gattatcgtc aaattcatcc tttggcttct gatatgatta tcataaaaga 58140

atatgaactt gataaaaata aagtatctat ttttgtgaat tatggatttt ttacaccaga 58200

aactaaccaa aagaatatta ataaattttt ctcaattgct agcactataa ctcgtcaatt 58260

agagaccgca ttactttgta tggaaacagt agaaaatatt catacatatc cttttaagaa 58320

tatatgcggt tgggaaggat ataaactcgt aattagcctt cgtgaagtga aatgtgctta 58380

ttcacctact gataaagaaa tttaccaaca aaaatgtgat gaaattgtga atactcctaa 58440

agaagaaact acccttgagg aactaatgga atgtcttgat gattcacctg aaccgataga 58500

aattcgtcca gaagttattg cactagaaaa agcttataaa gaagttctag aaatttctaa 58560

taaagcgcag aaagaatatg agcaggctaa aaggatttgg gaagaatctg ttaatcgtct 58620

tgatcgtctg gaacaagctt tacagttaat taagtaattt aaagccaagg atggctcgga 58680

gtataaatca ttaaccaagt gagaagaaca tgaaaactcg taaacattat attgattatt 58740

ttgacagtct tattactaaa catcgtaatt atcagatagg acacagagca gtaatcaata 58800

atattcttcg tgatttttta gactatattg gatgggaaaa ccatatttgt aaagatacac 58860

aaaatgcgta ttcacattct cttggttctt tgctcgagtg gttcaaacgt tcccgattac 58920

tatcttctgt gatagctgtt aataatgtta aaaaatttat gtatccaagc tacattgaga 58980

ctaatgtatc aaatgctagt gttgttacat ttaatattat taacgacgtg aaaagaactt 59040

atttagaaga atggttttct aaagatagta aagaaaaatt tgctagtgaa ttttcacacg 59100

aattcaataa taacgtgaat atgcttttta agcattctcg tagactgttt tgtcatggtg 59160

ataaccgtac tattaatgtg aatgtaaaag actgggttac ggctaaattc actccatcgt 59220

cccagaatgg gcaatttgaa ttgtcaatta tcatttgtgc tccgcacgag atatataaaa 59280

accttccgta tatgaaacca cgcgaagcta ataaacacaa tgaaactatt agttctttgg 59340

cttataattt acgcgtgtta ttatctgata tggatgtagt caaatccttt gatgataata 59400

cgaattatgg tctttcgctg tttgaaacta aatttgttat taaattaaag gaccctagtg 59460

aatttaaacc tacaccaaaa tccaatcatg gaaatgatac tatgaaagaa gaacgcgaat 59520

atctcagtgc ccgtttgatt gaagttgaaa aacagattga agagcatact aaagttctta 59580

aggctttaac cgccaaagca aatggtttac gtaatgctat tgaggtattg aaatgaaaaa 59640

gcgtttatta gaagacattg cagcttcaag taattccagt ttaattaaaa ttattatggc 59700

tggtgaggaa gatgatatgg aaatgcgtgg aaagattcac ggctgcgacg atttagattt 59760

taaacctcca gcatgggatg ctattatggc tatggttgaa cgacgtgaaa gagcttctaa 59820

aaacgttcct aattgccctg aatgcggtac tgaacaagtt caattgatta actggcgtaa 59880

accagagctt gaatataaat gccgtcaatg taaacataaa ttcagtaagc atgctccgga 59940

aatggttaaa ttgcctgact ctactgagtt ctttaaagaa cttgtgagtg ttcaaccaat 60000

gcctaataat attttggatt aaaaatgacc aagcgtaaag aatatatgga ggctgctgaa 60060

aaggcagtcc gtgaattagc aatagcttat tataatgaac atggtaaatt tcctgataga 60120

tacagcgtgc ttaaatctgc tttaactcgt tcatataaaa atatgctatc agaagtaagt 60180

gatattatat acaaacataa agaacaaacg ggccaaagtc ttgattacga cgagactttt 60240

aaacaagtac taggaattaa ggaataatat gtttaaagta tatggttatg atagcaacat 60300

tcataaatgt gtgtattgcg ataatgcaaa acgtcttttg accgtgaaga aacagccgtt 60360

tgaatttatc aacattatgc cggaaaaagg tgtttttgat gatgagaaaa ttgctgagct 60420

tctgactaaa ctaggtcgtg atactcaaat cggcttgaca atgccccagg tatttgctcc 60480

tgatggaagt catattggtg gatttgacca actgcgagaa tattttaaat gatgctcgaa 60540

ggaactgact atattcatga ttaccgcgga agcgcggtat atgtaggtga tgaagttgca 60600

gtttattatg ggtatggaac tttgatgaca gccaaggtta ttcaaattaa aaataatcgt 60660

gctaaactcg aagtttatta ttctaatggt gaaaagtcta tttctaagtg gaaatacggc 60720

gattgtatgg ttaaattggg gtaaatatga tttacgatat taatgtatca agaactccgt 60780

caatggttac tattccagcc gaagaactag atcgtcttca gaaaattgaa gagcttcttt 60840

gggaaattga atctgatttg ccatcaggat tagaatcctg gattgattat gaagaactta 60900

ataagcttcg gggttaaacc ttggtgggcg gctagatggg aaactgtaga gccagagccg 60960

gaagaaccgg tttacattga tgaagaaaca gtatataatg aaccaacgat aaatgactta 61020

attgatatgg agatgggaca tgattacagt agataagtgg tttagaatta atcgtgttga 61080

tacagggcta tgtaattact ggccggaact tagtgcaggt actgtcttta aagttcgtga 61140

acttgcaaaa gaatgcgaag atgatataga acctgatact ggaattattg aaattgaact 61200

ttccgacgga aagattatta acatctatga taagccaatt acatactggt gtttgtggaa 61260

tactgaatcc gttgaaaatg gcgaaattga agaagttgta gagagaacta gccaagatgt 61320

tcagaagcct aaagccgctt ttcaaggtga acgtatttca tacgcattag ctaaattagc 61380

tgcgcaagaa aataacgatg gctatgaagg taacctgatg caagctgccg cagagtacat 61440

tgaatggctt gaaactcaaa tttctttttc tgaccaaaag attcggcaat ataagcgatt 61500

gcatcaaatg ttttacaata cttgaaaaaa ctcaaaattc tttttctgac aggacatttt 61560

aatgaaaacc gaattggttt atactgaaaa gttaaatggc ggtaaggttt ggaaactttt 61620

tattaaagga cattctacgg accctcatat gaccacttgc gtaggaacct attctcgtcc 61680

tactaaaaag atgattcgac agtataaacg attgcatcga atgttttaca atacttaaaa 61740

ataataaata cccttatcta tttaaggtaa gggtatttat tatgttattg actggcaaat 61800

tatacaaaga agaaaaacaa aaattttatg atgcacaaaa tggtaaatgc ttaatttgcc 61860

aacgagaact aaatcctgac gttcaagcta atcatcttga tcatgaccat gaattaaatg 61920

gaccaaaagc aggaaaggta cgtggattgc tttgtaatct ctgcaatgct gcagaaggtc 61980

aaatgaagca caaatttaat cgttctggct taaagggaca aggtgttgat tatcttgaat 62040

ggttagaaaa tttacttact tatttaaaat ccgattacac ccaaaataat attcatccta 62100

actttgttgg agataaatca aaggaatttt ctcgtttagg aaaagaggaa atgatggccg 62160

agatgcttca aagaggattt gaatataatg aatctgacac caaaacacaa ttaatagctt 62220

catttaagaa gcagcttaga aagagtttaa aatgacaatt gaaaaagaaa ttgaaggatt 62280

gattcataaa actaataaag acctttaaa cgagaatgct aataaagatt ctcgtgtttt 62340

tccaactcaa cgggacctta tggctggtat tgtgtctaaa cacattgcca aaaatatggt 62400

cccgtctttt attatgaaag cgcatgaaag cggaattatt catttccatg atattgatta 62460

ttcccctgct cttccattta ctaattgttg tttagtagat ttaaaaggaa tgcttgaaaa 62520

cggatttaag cttggtaatg cacagattga aactcctaaa tcaattggcg ttgctactgc 62580

aattatggcg caaattactg cacaggttgc ttctcaccaa tacggcggaa cgacttttgc 62640

taatgtagat aaagtacttt ctccttatgt taaacgcacc tatgcaaaac atattgagga 62700

tgcagaaaaa tggcaaatcg ctgatgcgtt aaattatgct caatctaaaa cagaaaaaga 62760

tgtatacgat gcattccaag cttatgaata tgaagtaaat actctcttta gttcaaacgg 62820

acagactcct tttgtaacaa ttacatttgg tacgggaact gactggactg aacgaatgat 62880

tcagaaagca attctgaaaa atcgtattaa aggtctcggt cgtgatggga taactcctat 62940

tttccctaag cttgttatgt tcgttgaaga aggcgttaat ctttataaag acgatccgaa 63000

ctatgatatt aagcagcttg ctttagagtg tgcaagcaaa aggatgtatc ctgatattat 63060

ttcagctaag aacaataaag ctatcaccgg ctcatctatt cctgtttctc caatgggttg 63120

ccgcagtttc ttgagcgcgt ggaaagattc aaccggtaat gaaattcttg atggacgtaa 63180

taatcttggt gttgtaacac tgaatcttcc tcgtattgcg ttggattctt atattggaac 63240

acagttcaat gaacagaaat ttactgaatt gttcaatgag cgaatggatt tatgttttga 63300

agctttgatg tgtagaatta gttccttaaa aggagttaaa gcgactgttg ctcctattct 63360

ttaccaagaa ggtgcattcg gggttcgtct taaacctgat gacgacataa ttgagttatt 63420

taaaaacggt agaagttcag tgtctttagg atacattggt attcatgaat tgaatattct 63480

tgtcggtcgt gatattggac aagaaatttt aactaaaatg aatgctcgtc ttaaacagtg 63540

ggctgaaaga actgggtttg cttttagttt gtattcgact cctgctgaaa acctttgtta 63600

tcgcttctgt aaacttgata cagaaaaata tggaagtgta aaagatgtta ccgataaagg 63660

atggtacact aacagtttcc atgtttcagt agaagaaaat attactccgt ttgaaaagat 63720

ttctcgcgaa gccccatatc atttcattgc gacaggtggt cacatttctt atgttgaact 63780

tcctgatatg aaaaataacc taaaaggtct tgaggctgtc tgggattatg ctgcacaaca 63840

tttagattat tttggtgtta atatgccagt agataagtgt tttacatgcg gaagtaccca 63900

tgaaatgact cctactgaaa acggatttgt ttgttctatt tgtggagaaa ctgatcctaa 63960

aaagatgaac acaataagaa gaacatgtgg ttatttggga aatccgaacg aacgcggatt 64020

taatctcggc aaaaataaag aaatcatgca tagggttaag caccaatgaa ttatgataga 64080

ttttatcctt gcgattttgt taatggtcct ggctgcagga ccgttctttt cgttacaggt 64140

tgtttgcata aatgtgaagg gtgttataat aaatcaacat ggaatgctag aaatggtatt 64200

ccattcactg gtgaaacact agaacaatta attgaatgtt tgaataatga ttatatagaa 64260

ggattaacta taaccggagg tgaccctctt tatcctgata acagagacgt gattcattgc 64320

atcgttcaaa cagtaaaaaa tctttatccc aataaaagca tttggttgtg gacaggatat 64380

aagtttgaag atattaaaca actagaaatg cttaaatatg ttgatgttat tattgatggg 64440

aagtatgaga aaaatcttcc gactaaaaag ctgtggcgag gatcagataa tcagcgactt 64500

tggtcaaata ccgatggggt gtggaaacat gattaaattg aattatatta tggatactat 64560

aaatgatatg atttttcatt ttggtccaga attttattcc caatatagtt tagtgcttat 64620

caatgcttgg ttaattaatt aagggtaaaa tatgtataaa tttcgtaaag gtttagctga 64680

ttttcttaca actgtaacat tctttctgtt tatggcagtt ggagctattt tccttattcc 64740

ttttattgct atatttttcg tgattagttt aatttctcca gaaaagggct tatcttctag 64800

tgagtttaat gagcgtctgg ataaaattac taacaagctg aatgctgttc ttgataaaaa 64860

ggcttaatta tgattagttt tgagcggtat gtagtagaga gttggaatgg ttttgatatg 64920

ttcggtaatg actattattt ctatgaatgt agtctgaacc caagcttctg ggctggacgt 64980

gaacaagacc tcgaagaaat caacgctcgt gccgatttgt taggtgaact gcctactact 65040

tatttcacct ttgatgaatc cggcttcgtt atccaggttt attttcctga agaaaactct 65100

ggtgaggatt ctgttaatcc tccttattgg gcttaccaag gaattatttc tcgtggaaca 65160

aaactcgaac ttaaagaata agattgaagt ctatggaatt ccagatgaag taggtcgttg 65220

tcctggatgt caatcagtta caaaacttct aaaggagctc aatgctcctt ttactttcta 65280

taaagttctt acaaataatg gtaagattga gtatgatcgt ccactgattg tatctcttgc 65340

taaacgcgct ggattcacat ctcttaacat tcgttatcca gtcattttca ttaatgattc 65400

tagacaaaag aacattaaac acttcaaaga aactctcatt tcacttggat atgatagaga 65460

tatcatagaa gactaagacg ggccctctgg gcctttcttt ctcacattct gtatattacc 65520

attctaagct atcgttccct tcttatcatt ccctaaaata atttcacaaa gttgtttaca 65580

acaagttcaa actgtggtat tattaacata tgaattgcct ttgaggattt gatatggttg 65640

tggttgataa agagattaaa aagggacaat attattttat taatggtaat gttgttcgtg 65700

ttacttatgt aaacggtttt gaagtttatt atcttatact caagttacat aaacagatga 65760

tttgtgatcg tgctgtattt agttcagttg ctaaggaaat taaactccat gggtaaaacg 65820

tatcgtcgta aagatttaaa agtacgtgat tatgactatt tcggaaagcg taaagctcct 65880

gatggtgtaa gtcataaaga tatggttgaa aacatttttc gctctgataa atggcgtaga 65940

atgaaaggca ttgattcaga agttaaagat gagctaaatc gtcaattacg tagtgaagta 66000

agaaagttga aaaaatcagt ttacattgac gatgattttg attacaatac ttctcaacga 66060

gttgctaagc gcaaatcaaa cgagtgttat cgttatagct gaggaaaata tgaatatcaa 66120

acgcatgctt tttaagcaag ggctatatac tttaaatgct actccaaaag gcgatacaac 66180

taagtggtca gtaaatgact ggattaaatt tattgatgaa aacggtaatt gggaaattta 66240

aatgaatcct gaatctaaat tatcgcagcg aattgctgaa gaacgcgcca aatttttcca 66300

gaacatgaaa cacaatggta ttgaggatga agtttttcta aattggttct ggaataataa 66360

gtatgcagca tgcgaaggag ccttgtcatt gtcagtcgca atgatgtacg aaggctggaa 66420

gggtgccaaa aagtttagct aagggcttcg gccctttttg gataataaaa ttttaatgca 66480

attgaggata atgtatgact attcaaatta aaaacgccat caattcttac gcatatgata 66540

aagtagtttc tctgctagaa aaaggcgata ttgtaactcc tcaaattttg gataaatggg 66600

aaaaagagct tcatcagacg atgaaacaga atgatcagaa gattggacgc aatactgtcc 66660

gtgaattgtt ggttcaatat atcttgtcag aatttgatgt taaagctttt ggtgtagaat 66720

ctaaagctta tcaaaagcat gaaatttccg ataaaactat tcgtcgtatg aaaaatcaac 66780

gcaagaaaaa atttgcagac ctgaaaatta ctaaggtata attatgaacg aagctcttat 66840

taacgatttg cgtcttgccg gatatgaagt aaatacaaat ggcattggtt taactcaaat 66900

tgaaggaaac ggattcatcc ttgagtatga atttagccaa tggtggttat atgccaatta 66960

cggcgaattg attgaatatg ttgaccaatt tgattcacta gatgcagctc ttgaagcggc 67020

taagttgatg aatgtatgaa attaattaat atttctattg ctattgaaaa ttttggtatt 67080

ttctatgttg accaatacat gaaaatttca tttttcccaa ataaaactgg tgttggatat 67140

tgggaaagcc atgtttctga attaaatgaa agtgaatatg ttagtacaca taaaaagttt 67200

ttagactttt tatatcgcgc tgatattaat gatcattaca tagatattca tgaatttaaa 67260

aagatgatgg agaaagtgtt ccaagcatac tgcttactta gataactgat atcctctatg 67320

ctttaagata gatcttcaaa tattatgata taatagatct atgaattgag ctaagaggtg 67380

aaaatgtcag aaactaagcc taagtataat tacgtaaaca ataaagagct tttacaagct 67440

attattgatt ggaaaacaga attagcaaat aataaagacc caaataaagt agttcgtcag 67500

aatgatacta tcggattagc cattatgctt attgcagaag gcttatctaa acgtttcaac 67560

ttttcaggat acacccagtc ttggaaacaa gaaatgattg cagatggtat agaagcttct 67620

attaaggggc ttcacaattt tgatgaaacg aaatataaaa acccacatgc gtatataact 67680

caagcttgtt ttaatgcatt tgtccaacgt attaaaaaag aacgtaagga agttgcaaag 67740

aaatatagtt acttcgttca caatgtctat gacagtcgtg acgacgatat ggttgcgtta 67800

gtagatgaaa cttttattca agacatctac gataaaatga cgcattacga agaatcaacc 67860

tatagaacac cgggggctga aaagaaaagt gttgtagacg attctcctag tttggatttt 67920

ttatatgagg ctaacgatta acctctccgg attcttggaa gaaatacctg aagttgaagc 67980

tattccctat ttacttaaaa tgtatctcag ggaagtttta gctcttgaca ttgatattga 68040

tccagaaaat ccgtatgata ccgcttttaa atctaatggt gtagaattaa actatcggta 68100

tcatttaaca gatgatgatt tttattttat attagagaaa taatatgact gataaacccg 68160

aaattaatga tgaagtggaa aagcttattt cttctattga agaaaagaac cgtcttgaag 68220

cagaaagaaa agcaaataag ttattgtcta aaaacaaacg cgaactgaat cgtctttata 68280

agcacgctca gatcgcagct gaaaacaata attttgctca atacgaatat gctatcaaga 68340

aaagtcggga tattctgaaa cagccatata acgatgaact catcagtatt ctttggaaga 68400

ctactagatc gcagattgag gatatgattg atgcttacac acgtaaaatt caagcgtctt 68460

aaaattaatg caggatttac tgaatctttg aatggtcatc tttgtgtgaa aatttctgaa 68520

aaagaatacc atgatagttc aattaaagaa gttaatcctc ctattgtaag agcagacccc 68580

aatatgaaag tgtgggttga ttcttatcaa gtcaaaaaat ggtggcagtt atgaaagatg 68640

aacacccaga cttctgaaat agattataat aaaattcgtt cctctaaaga ggaaatgatg 68700

agacgcttta aagagtctca tgataaagct aaagcagaag gaactataaa atataagcgc 68760

ataaaattta aaagttctaa cgagcctctg tatggcgtat tatgtggata ggagcttcgg 68820

ctcctatatt gctttataaa tttttggtaa aataaaccaa aacaaagagg atattaaatg 68880

aaagtatgta tttttatggc tcgaggtctt gaaggttgcg gtgtaactaa attttctctt 68940

gagcagcgtg attggtttat taaaaatggt catgaagtaa ctttggttta tgctaaagat 69000

aaatcattta ctcgtaattg tgcgcatgat tataaatcat tttcaattcc ggttttatta 69060

gcaaaagaat acgataaaac acttaagctg gtaaatgatt gtgatattct aattatcaat 69120

tcagttcctg ctacttcggt tgaagaagac actattaata actataaaaa aattattgat 69180

aacattaaac cttctgttcg tgttgtagtt tatcaacatg accattcttc tctttctttg 69240

cgccgaaatt tgggattaga agaaactatt cgtcgagctg atgttatttt tagccattct 69300

gataatggtg attttaataa agttctgatg aaagaatggt atcctgaaac agtttctctg 69360

tttgatgata ttgaagaagc accgacagta tataactttc agcctcctat ggatattgcg 69420

aaggttcggt caacctactg gaaagatgtt tctgaaatta acatgaatat caaccgttgg 69480

attggtcgta cgactacatg gaaaggtttt tatcagatgt ttgattttca tgaaaaacat 69540

cttaaacctg caggactaag tactattatg gaaggtctgg aacgttctcc agcgttcatt 69600

cctattaaag aaaaaggaat tccatacgag tattatcgtc ttcatcaagt agaccaaatt 69660

aaaattgctc ctaatttgcc aacgcaaatt cttgaccgtt atgtaaatag cgaaatgctt 69720

gaacgcatga gtaaatccgg atttggttat cagctgagta agttggacaa aaaatatcta 69780

caacgttctt tagaatatac tcatctcgag cttggtgcat gtggaacaat tccggtattt 69840

tggaaatcta ctggcgaaaa tttaaaattc cgtgttgata atactccttt gacctcgcat 69900

gatagcggta tcatttggtt tgatgaaaat gacatggaat caacatttga acgtattaaa 69960

gaactgtcat ctgaccgaac tctttatgac cgtgaacgcg aaaaagctta tgaatttttg 70020

tatcagcatc aagattcaag cttctgcttt aaagaacagt ttgacattat tacaaaataa 70080

agggcttcgg ccctttagct ttatacggag tttgatataa tgatatttct tggatatgtg 70140

atacttttc ttgcatttta tctattcact agagcatgtt ggattgggtt ctttagcacg 70200

ccagatgggt ttatttcaat aattttattt tgcatttcaa tgacggttct tgatatatga 70260

aaattttaaa tttaggtgat tggcatttag gcgttaaagc cgatgatgag tgggttcaat 70320

ccattcagtt ggatggaatt aaacaagcaa tagaatattc taagaaaaat ggaattacta 70380

cctggattca atacggtgat atttttgatg tgcgaaaagc aatcacacac aaaactatgg 70440

agttcgcccg tgaaatagtt caaatgcttg atgatgctgg tattacccta catactattg 70500

taggaaacca tgatatgcac tttaaaaata ctttaactcc aaatgcctct actgagcttt 70560

tggctaaata tcctaatgtt aaagtatatg ataagcctac tacagtagat tttgacggat 70620

gtttaattga tttaattcct tggatgtgtg aagaaaatac tggtgaaatt cttgagcata 70680

tcaaaacttc atctgcttct ttttgtgttg gtcactggga actgaatgga ttttatttt 70740

ataaaggaat gaaatctcac ggtcttgaac ctgatttcct taagacttat aaagaggtgt 70800

ggtctggtca cttccatact atctctgagg ctgctaacgt cagatatatt gggacaccat 70860

ggacactaac tgcaggtgac gagaatgacc ctcgtgggtt ctggatgttt gatacagaaa 70920

cagaacgaat ggaatttatt ccaaacaata ctacctggca tcgtagaatt cattatccat 70980

ttaaaggaaa aattgactat aaagatttta caaatctatc agtacgtgtt atagtaactg 71040

aagtagacaa aaatctgacg aagttcgaat ctgaactaga aaaagttgtg cattcattac 71100

gagttgtgtc aaagattgat aactctgtcg agtcagatga cagtgaagaa gttgaagttc 71160

aatctcttca gacgttgatg gaagaataca ttaatgcaat tccagacatc actgattctg 71220

accgtgaagc acttattcaa tatgcaaatc agttatatgt agaggcaaca caatgacttt 71280

tgatgaattt aaaaatgtta tgatgagtca gcattttgaa tgcgaagtaa aagatgatat 71340

tggtcataaa gaaattattg aatattggtt tgaaccgcta gaggttgaag ataattgtat 71400

taaaaaagtt acggtctgta cagattgggc tgtatctttt aacttcaaca ttttagataa 71460

tgacacacct aaatcattgc gagatatggc cgtatcttgt attaaggatg catactgtga 71520

agttttcgac atttgacatt aatgatgaat tcatagcaaa cattgattat accgaagaag 71580

attctagata tgttggaata atttatatta catcaaaaac agcacaaggt gttgtttgca 71640

tggctgaatt tgatgaatac tttttagatt atgatgatat gatagaatgg tctaaaagat 71700

acattaaaag gaatcttttg tgaagaattt taaactaaac cgagttaggt accaaaatat 71760

aatgtcagta ggtggaaatc ctattgacat tcaattagat aaggttcaaa aaactcttat 71820

tactggacga aatggtggtg gtaagtctac tatgttagaa gccatcacat ttgggctttt 71880

tggcaagcca tttcgtgatg taaagaaagg tcaattaata aacagcacaa ataagaaaga 71940

acttttagtt gaactgtgga tggaatatga tgagaaaaag tactatatca aaagaggaca 72000

aaaaccgaac gttttcgaaa tcaccgttaa cggtacacgt cttaatgaat ctgccagcag 72060

taaagatttc caagcagaat ttgaacagct tatcggaatg tcatatgcca gtttcaagca 72120

gattgttgtc cttggtacag cagggtatac ccctttcatg ggtttgtcga cccctgcgcg 72180

aagaaagctt gtggaagact tgcttgaggt aggaacatta gctgaaatgg ataagcttaa 72240

taaagcacta atacgcgaat taaattcaca aaaccaagtg cttgatgtta aaaaagatag 72300

tattatccaa caaattaaaa tatataatga taacgttgaa cgccagaaaa aattaacggg 72360

tgacaacctt actcgtctgc aaaatatgta tgatgatttg gcaaaagaag ctagaacgct 72420

aaaatcggaa atagaagaag ctaatgaaag attagttaat attgttttag acgaagaccc 72480

gactgatgca tttaataaaa tcggtcaaga agcagtttta attaaatcaa aaattgactc 72540

gtataataaa gtcattaata tgtatcacga aggtggatta tgcccaacct gtttgtcaca 72600

attaagttcc ggtgataaag ttgtttctaa aattaaagat aaagtttctg aatgcacaca 72660

ttcatttgaa cagctttcaa cgcatcgtga taatttaaaa gttcttgttg atgaataccg 72720

agataatatt aaaacccaac agtcgttggc aaatgatatc cgcaataaaa agcaatctct 72780

aatcacgacg gtagataaag ctaaaaaagt taaagcggct atagaaaaag catcttctga 72840

gtttattgac catgctgatg aaatagcact gcttcaagaa gaacttgata aaattgttaa 72900

gacaaaaact aatttagtaa tggaaaaata ccaccgagga attttgactg atatgctcaa 72960

agattctggt attaaaggtg ctattattaa aaagtacatt ccattattta ataagcagat 73020

taaccattat cttaaaataa tggaagcgga ttatgtgttt acattagatg aagaatttaa 73080

tgagacaatt aaatcccgtg gtcgtgaaga ttttagttat gcttcattca gtcaaggtga 73140

aaaagcacga attgatattg ctcttttatt tacttggcgt gatattgctg aaaaagtttc 73200

aggtgttaaa ataaacacac taattcttga tgaagttttt gattcagcga ccgacgttga 73260

aggtgtaaaa gctatttcaa ctattttaga tagtttaaaa aatactaacg tttttgttat 73320

ttcgcataga gaccatgacc cgcaagcata cggtcagcat cttcaaatga agaaagttgg 73380

tcgatttact gtaatggttt aatttataag agattatgct ttaatttatt agagtataat 73440

ctctatggag gaaaaacatg gaatattcaa ccggacagca tctattaact attcctgaaa 73500

taaaacgata tattctgaga aataattttt ctaatgaaga gcatatagtt actgaatcta 73560

tgcttaggaa tgcatttaaa gcagaatata caaaaataat gtccaataga aatgaagctt 73620

ggactgttac tgattattat gactaaaggt gtattatgac taaaattact gtgaattata 73680

ctgttgatgt aaaagatatt cagccaaaac acgtgcgttc tgaatcaaat ccacaaaacc 73740

aaaataaaat tcgtcgagca tgggttttgt ctctttctga taacgcaatg gaagttattc 73800

agaacaaaat taaatctgca cctgctcgtc atgcgtatta tgaagctatc gatcgtgaag 73860

taagtaataa atggattgaa ctaatgcgca aacatactac agaatcccta aacgctggtg 73920

ctaaatttat tatgacttca tgtggtgaac gccttgaaga tgaatattgt ggcaatgcag 73980

atgaacgtct gattgttgcc gctcaaattg ttgccgaaac aatcgcagct gattttaatc 74040

gttaattgct ttattaaatt agttataaaa ttaaatctca tttgaattga aggaaattac 74100

atgaaactgt ctaaagatac tactgctctg cttaaaaatt tcgctactat taactctggt 74160

attatgctta aatccggtca atttattatg actcgcgcag ttaatggtac aacttatgcg 74220

gaagcaaata tttctgacgt tattgatttt gatgtagcaa tttacgattt gaacggtttt 74280

ctcggtattc tgtctctagt taatgatgat gcagaaattt cccagtcaga agatggaaat 74340

attaaaattg ctgatgcccg ctcaacaatt ttttggccag cagccgatcc gagtacagta 74400

gttgctccta ataaaccaat tccattcccg gtagcatctg ttgttactga aattaaagct 74460

gaagaccttc aacaactgtt gcgtgtatct cgtggtctgc aaattgatac aattgctatc 74520

acggtaaaag aaggtaaaat cgtaattaac ggttttaata aagtagaaga ttctgctttg 74580

actcgtgtta aatattcttt gactcttggt gattatgatg gtgaaaacac atttaatttc 74640

attatcaata tggcaaatat gaaaatgcaa ccaggaaatt ataaacttct gctttgggca 74700

aaaggtaaac aaggcgctgc taaatttgaa ggtgaacatg cgaattatgt agtagctctt 74760

gaagctgatt ctacccatga tttttaatag agggcttcgg ccctttataa tttacactaa 74820

aacttgaatg aggaaattat gattaccgta aatgaaaaag aacacattct tgaacagaaa 74880

tatcgtccat ctactatcga tgaatgtatt cttcccgcct ttgataaaga aacctttaaa 74940

tctattacaa gtaaaggtaa gattccacat attattcttc attctccttc tccaggaaca 75000

ggtaaaacaa ctgtagcaaa agcattgtgt catgatgtaa atgctgatat gatgtttgtg 75060

aatggatcag actgtaaaat tgatttcgtt cgtggtcctt tgactaattt tgctagtgca 75120

gcttcatttg atggtcgtca aaaagtaatc gttattgatg aatttgaccg ttcaggttta 75180

gcagaatctc agcgacatct tcgttccttt atggaagctt atagttcaaa ctgtagtatt 75240

attattactg ctaacaatat tgatggtatt attaaaccac ttcagtcacg ctgccgagtt 75300

attacgttcg gtcaaccgac cgatgaagat aaaattgaaa tgatgaagca gatgattcgt 75360

cgattgactg aaatctgtaa gcatgaagga attgctatag ctgatatgaa agttgtagca 75420

gctttggtta aaaagaattt tcctgatttt cgtaaaacta ttggcgagct cgatagttat 75480

tcatctaaag gtgttttgga tgctggtatt ttatcactgg ttactaacga tcgtggtgct 75540

attgatgatg ttcttgagtc tctcaaaaat aaagatgtta aacaactcag agctttagca 75600

ccaaaatatg cagccgatta ttcgtggttc gtgggtaaac ttgccgaaga aatctattca 75660

cgtgtaactc cacagagtat tattcgtatg tacgaaattg tcggcgaaaa taatcagtat 75720

catggtattg cagctaatac tgaattgcat ctagcttatc ttttcattca gttagcatgt 75780

gaaatgcagt ggaagtgata tgagcttatt tgaagatgat attcaattaa acgagcatca 75840

agttgcttgg tattcaaaag attggacagc cgtccaatcc gctgctgatt cttttaaaga 75900

aaaagctgaa aatgagtttt ttgaaataat tggagctatt aataataaaa ctaaatgctc 75960

tattgctcaa aaagattatt caaaattcat ggttgaaaat gcattatcac aatttccaga 76020

gtgcatgcca gctgtatatg caatgaattt aatcggttct ggattaagtg atgaagctca 76080

ttttaattat ctaatggctg ctgttcctcg tggtaaaaga tatggtaaat gggcaaaact 76140

ggttgaagat tccaccgaag tattgattat taagttactt gctaagcggt atcaagttaa 76200

tacaaatgat gcaattaact ataaatcaat tcttactaaa aatggaaaac ttcctttagt 76260

attaaaagaa ctaaaaggtt tagtcacgga tgatttttg aaagaagtga ctaagaacgt 76320

aaaagaacag aaacaactca aaaaactagc attggaatgg taaaatgatt gaaattactc 76380

ttaaaaaacc tgaagatttt ctgaaagtaa aagaaacttt gactcgtatg ggaattgcta 76440

ataataaaga taaagttctg tatcagtcct gtcatattct tcagaaaaaa ggactatact 76500

atatcgttca ttttaaagaa atgcttcgta tggatggccg tcaagttgaa atgacagaag 76560

aagatgaagt tcgtcgtgat tcgattgcat ggctgttaga agattggggg ctgattgaaa 76620

tcgttcctgg tcaaagaact tttatgaaag atttaactaa taacttccga gttatttctt 76680

ttaaacaaaa acatgaatgg aaactcgttc ctaaatatac gattggtaat taatatgact 76740

gctataactc cacaagaata catggcgtct cttaaagaaa aatataatct ttctgcaaca 76800

gaaacacttt ttgatttacc agaaaacctc caattaaaat ttcaggtaga atttcaaaaa 76860

ttagttcacc cagaacaaaa acattttact gcagtcgtta agtcaattaa tgcagatgga 76920

atgataattt tcacccggca aatagtacta atttaagcaa ggggcttcgg ccccttattt 76980

ggagtataat atatcaagag cctaataact cgggctataa actaaggaat atctatgaaa 77040

gaattttata tctctattga aacagtcgga aataacattg ttgaacgtta tattgatgaa 77100

aacggaaagg aacgtactcg tgaagtagaa tatcttccaa ctatgtttag gcattgtaag 77160

gaagagtcaa agtacaaaga catctatggt aaaaactgcg ctcctcaaaa atttccatca 77220

atgaaagatg ctcgagattg gatgaaacga atggaagaca tcggtctcga agctctcggt 77280

atgaacgatt ttaaactcgc ttatatcagt gatacatatg gttcagaaat tgtttatgac 77340

cgaaaatttg ttcgtgtagc taactgtgac attgaggtta ctggtgataa atttcctgac 77400

ccaatgaaag ctgaatatga aattgatgct atcactcatt acgattcaat tgatgatcgt 77460

ttttatgttt tcgacctttt gaattcaatg tacggttcag tatcaaaatg ggatgcaaag 77520

ttagctgcta agcttgactg tgaaggtggt gatgaagttc ctcaagaaat tcttgaccga 77580

gtaatttata tgccattcga taatgagcgc gatatgctca tggaatatat caatctttgg 77640

gaacagaaac gacctgctat ttttactggt tggaatattg agggatttga cgttccgtat 77700

atcatgaatc gcgttaaaat ggttctcggt gaacgcagta tgaaacgttt ctctccaatc 77760

ggtcgagtaa aatctaaact tatccaaaat atgtacggta gcaaagaaat ttattctatt 77820

gatggcgtat ctattcttga ttatttagat ttgtataaga aattcgcatt tactaatttg 77880

ccgtcattct ctttggaatc agttgctcaa catgaaacca aaaaaggtaa attaccatac 77940

gacggtccta ttaataaact tcgtgagact aatcatcaac gatacattag ttataacatc 78000

attgacgtag aatcagttca agcaattgat aaaattcgtg ggtttatcga tctagtttta 78060

agtatgtctt attacgccaa aatgcctttt tctggtgtaa tgagtcctat taaaacttgg 78120

gatgctatta tttttaactc attgaaaggt gaacacaagg ttattcctca acaaggttcg 78180

cacgttaaac aaagttttcc gggtgcattt gtatttgaac ctaaaccaat tgctcgtcga 78240

tatattatga gttttgactt gacgtctctg tatccgagca ttattcgtca ggttaacatt 78300

agtcctgaga ctattcgtgg gcaatttaaa gttcatccaa ttcatgaata tatcgcagga 78360

acagctccta agccaagtga agaatattct tgttctccga atggatggat gtatgataag 78420

catcaagaag gtatcattcc aaaggaaatc gctaaagtat ttttccagcg taaagactgg 78480

aaaaagaaaa tgttcgctga agaaatgaat gccgaagcta ttaaaaagat tattatgaaa 78540

ggcgcagggt cttgttcaac taaaccagaa gttgaacgat atgttaagtt cagtgatgat 78600

ttcttaaatg aactatcgaa ttatactgaa tctgttctca atagtctgat tgaagaatgt 78660

gaaaaagctg ctacacttgc taatacaaat cagctgaacc gtaaaattct cattaacagt 78720

ctttatggcg ctcttggtaa tattcatttc cgttactatg atttgcgaaa tgctactgct 78780

atcacaattt tcggccaagt tggtattcag tggattgctc gtaaaattaa tgaatatctg 78840

aataaagtat gcggaactaa tggtgaagat ttcatcgcag caggtgatac tgattcggta 78900

tatgtttgtg tagataaagt tattgaaaaa gttggtcttg accgattcaa agagcagaac 78960

gatttagttg aattcatgaa tcagttcggt aagaaaaaga tggaacctat gattgatgtt 79020

gcatatcgtg agttatgtga ttatatgaat aaccgcgagc atctgatgca tatggaccgt 79080

gaagctattt cttgccctcc acttggttca aagggtgttg gtggattttg gaaagcgaaa 79140

aagcgttatg ctctgaacgt ttatgatatg gaagataaac gatttgctga accgcatcta 79200

aaaatcatgg gtatggaaac tcagcagagt tcaacaccaa aagcagtgca agaagctctc 79260

gaagaaagta ttcgtcgtat tcttcaagaa ggtgaagagt ctgtccaaga atactacaag 79320

aacttcgaga aagaatatcg tcaacttgac tataaagtta ttgctgaagt aaaaaccgcg 79380

aacgatatag cgaaatatga tgataaaggt tggccagggt ttaaatgccc gttccatatt 79440

cgcggtgtgc taacttatcg tcgagctgtt agtggtctgg gtgtagctcc aattttggat 79500

ggaaataagg taatggttct tccattacgt gaaggaaatc catttggtga caagtgtatt 79560

gcttggccgt cgggcacaga acttccaaaa gaaattcgtt ctgacgtact gtcttggatt 79620

gactactcaa ctttgttcca aaaatcgttt gttaaaccgc ttgcgggtat gtgtgaatcg 79680

gctggtatgg actatgaaga aaaagcttcg ttagacttcc tgtttggctg atagaataaa 79740

tctagggacc tccgggtccc tttttcatac aagtaatata aatctatact tatgaaaaac 79800

agatgattct ggacctttag aattccctaa aaaatttttc acaaaactgt ttacaagact 79860

gttcctctgt ggtactatac aactatcaac taatacggat ttggagaatg aaatgaaaat 79920

cgctattttg gttattgcat taggtcttac tggttgtgta gctcaaggac cggtagtaaa 79980

tcagtctgat gtaggaaaaa ttgtaaactg ttcaagcaaa ttttataatc ctaatgtcaa 80040

gtgttataaa gaagctccaa agcaaacagt agaacaaatg caggcgaatt ttgacgaagc 80100

tattcgtcca gatgaatctg ctcaagcata tcgtaattct gatgtaatta cacgcgaaga 80160

aaaaattgaa aactactgcg cagagctttg ggcaaattgg gctaataatt accaatggcg 80220

tactggtaaa aatgctccga tggagtatgt agtgaattct tataattcat gcgtaaaaaa 80280

tttgactaag tgaggaaaag atggaaactt tagtagcagg ttcaattttt atggttttag 80340

tttcaggcgt gttggctatt attatataca tgcttccatg gttcatcgcc ttgatgcgtg 80400

ggtcaaaatc gacagtagga atctttttca cgtctttact gtttaactgg tcaattattg 80460

gttggtttat tacatttatt tggtcaattg cgggtgaaac taaaaagtct gcacaaccaa 80520

accaggtaat tatcatcaga gagaaggaat gaaaagcaaa attataacag tgttgctttt 80580

aatcttgatg attataataa gtatatacta tagtgtaacg gttcctctta tgattccaac 80640

tattatttta ggttggggtt tattactgtt acaagttaaa tatgaatgta tcaattgagg 80700

tttaaatgat tagtgactct atgacagttg aagaaatccg tcttcatttg gggcttgcat 80760

taaaagaaaa agatttcgta gttgataaaa ctggtgttaa aactattgaa attattggcg 80820

catcatttgt agcagatgaa ccgtttattt ttggcgctct taatgatgaa tacattcagc 80880

gtgaacttga atggtataaa tctaagagct tgtttgttaa agatattcca ggtgaaacac 80940

caaagatttg gcagcaggta gcatcttcta aaggcgaaat taactcgaat tatggttggg 81000

ctatttggtc agaagataac tatgcccagt atgatatgtg tttagctgaa cttggtcaaa 81060

atcctgattc tcggcgtggt atcatgattt atactcgtcc atccatgcaa tttgactaca 81120

ataaagatgg tatgtcagat ttcatgtgta ctaatacagt acagtacctg attcgtgata 81180

agaaagtcaa tgcggttgtt agcatgagaa gcaatgattg ctgggcaggc tatcgtaatg 81240

attatgcttg gcaaaaatac gtactagata aattagtatc tgatttgaat gcaggcgacc 81300

catcgcggca atataaagca ggttctatta tatggaacgt tggaagtctt catgtgtacg 81360

aaaatcagtt ttatttagtt gaccattggt ggaacaccgg tgagactcat attgctaaaa 81420

aggattatac tggaaaatgg aagtaaatgt gccgcatgtt tataagtata aacatcctaa 81480

aactaaaaag tggtatatag gaagtcatga tggtcacaac ccgaattatg atggttcggg 81540

tgtagtttgg caacatgtta aaaagaaata tggaataaaa tcctttaata aagaaatatt 81600

atatgaagga ccaatgttta gacaggttga agaaattatt ttaacttgtt tagatgctgc 81660

taattgtccg gattcatata atttaaagaa tgaagcatgg ggaggaagtt ttccaggcaa 81720

attaaatgga atgtacggta aaaaactatc tccagaagaa agatataagt gcggaaatgc 81780

ctttcgtgga atcaagcgtc ctgatcattc taaaagaatg aaaggcgaag gtaatccaat 81840

gtatggtaaa aatgagcagg catatggaat tataaatcga gccaaggaaa attctggtaa 81900

aacttatgaa gaaatttttg gcgtagaaaa agctaaaata attaaagaaa cgatgtctaa 81960

aaatcgtaaa ggaaaacctc ataatttgat agaaaaaata tgtccgcatt gcggactaaa 82020

aggacgtggg ccaaatatga caagatacca ttttgataaa tgtaaggcac ttaaatgatt 82080

caattcgtaa ttccgagcta tcaacgtgta ggggcagttt ctgcccttga tatgtttccg 82140

actgattatg aacctcatat cgtagtacgt gaacatgaag aaaaagctta ttatgatgcc 82200

tatgggtcta aagctaaaat tgtaactatt cctgatgatg ttaatggaat tgccggtact 82260

cgtaaagcaa ttactgatat gtatgcaggt caacgaatct ggatgattga cgatgatact 82320

actattcgta tgagttcaat gcgaaaaaga gatgatcgtc gttgtgtgga taaagtcaat 82380

caattgactc gtgaacagtt ctatgaattg attcaatacg tcgaagatgc catggattgt 82440

gggtattatc acggtcatgc tcgcctacca atttttaaaa ttacttcatc ttggggtaat 82500

tatcgtgaaa attcatatgg attcacgaat acatggtatg accttggaaa acttacgaca 82560

gaacaaattg ggtatggaaa aattgatttg tgcgaagata tgtatgcatt tctcaattta 82620

attaatcaag gttatccgca tttggccttg ttcaaatatc tggttgtatc tggaaaagca 82680

caagctcctg gagggtgcag ttcaattcgt agtaattcta aacataatag agcgcttgag 82740

caaatcaata gagagtttcc agagcaagct cgttggaaaa cttctaatat tgaaaaacga 82800

aaatcgttgg gtgaagaaga cgagccatta aaggttcttc gcatgtgcgt ttcgcgtaaa 82860

gaaaaatcag aagcatttca taagtttaat gctattcatc caatagcagt tgattaatgc 82920

ctaaatttat tgtgttataa ttactctatc tttaaccagt gaggaaaata taatgatgcc 82980

tatggaaaaa aatgaatgtc tattgcagat ttaaaatccc gtttgattaa agcttccact 83040

tctaaaatga ctgctgaact gactacatct aaattcttta atgaaaagga tgtaattcgt 83100

acaaaaattc caatgcttaa tattgctatt tctggtgcga ttgatggcgg tatgcagtct 83160

ggtttaacta ttttcgcagg gccttctaaa cactttaaat caaatatgtc tttgactatg 83220

gttgcggcat atttgaacaa atatcctgac gcggtttgtc tattctatga tagtgaattt 83280

ggtattactc cagcttattt gcgatccatg ggagttgacc cggaacgagt aattcatacg 83340

ccaatccagt cagttgaaca gctgaaaatt gatatggtga atcagcttga agctattgag 83400

cgtggtgaaa aagttattgt attcatcgac tcaatcggta atatggcttc taagaaagaa 83460

acggaagatg ccttgaatga aaaatctgtg gcagatatga ctcgtgctaa atcactgaag 83520

tcattattcc gtattgttac tccttacttt agcattaaaa atattccatg tgttgcggtt 83580

aaccatacaa ttgaaacaat tgaaatgttt agtaaaaccg tgatgacagg tggtacaggc 83640

gtaatgtatt cggctgatac tgtattcatt atcggtaagc gtcagattaa agatggttct 83700

gatcttcagg ggtatcaatt tgttctaaat gtagaaaaat ctcgtaccgt taaagaaaaa 83760

agtaaattct ttattgatgt taaatttgac ggtggtattg atccttattc tggattgtta 83820

gatatggctc tagaattagg atttgtagta aaacctaaaa atggttggta tgctcgtgaa 83880

tttcttgatg aagaaaccgg cgagatgatt cgcgaagaaa aatcttggcg tgcaaaagat 83940

accaactgca ctacattctg gggtccttta tttaagcatc aaccattccg agatgctatt 84000

aaacgtgctt atcagttagg tgctattgat agtaatgaaa ttgttgaagc tgaagttgat 84060

gaattgatta actcaaaggt tgaaaaattt aaatctccag aaagtaaaag taaatcagca 84120

gctgatttag aaactgacct cgagcagtta agtgatatgg aagaatttaa tgagtaaaga 84180

tgatttagat ttagaaatta tcgatgaatc cccctcttcg gaggggggaag aagaaagaaa 84240

agaacgtctt tttaatgagt ctcttaagat aattaaatcc gctatggaaa atgttatcca 84300

ggagattgtc attaaactag aagatggttc tacacacatt gtgtatgtga caaaattaga 84360

ttgggttgat ggaaaagtcg taatggactt tgctgttctt gaccaagaaa gaaaagctga 84420

gttagctcct catgtagaaa aatgtattac aatgcaacta caagatgcat ttaataaaag 84480

gtcaaagaaa aaatttaaat tcttttaagg agtaagtgtg gtagaaatta ttctttccca 84540

tctcatattt gatcaagctt atttttcaaa agtttggcca tatatggatt cagaatattt 84600

tgaaagtggt ccagctaaaa atacattcaa attaattaaa tctcatgtta atgagtacca 84660

tagcgttcca tctattaatg cgttaaatgt tgcattagaa aatagttcat ttactgaaac 84720

agaatattct ggtgtaaaaa cacttatttc aaaactagcc gattctccgg aagaccacag 84780

ctggttagta aaagaaacag aaaaatatgt tcagcaaagg gcgatgttta atgctacgtc 84840

taaaataatt gaaattcaaa ctaatgctga gcttcctccg gaaaaacgaa ataagaaaat 84900

gccagatgta ggtgctattc ctgacatcat gcgccaagca ttatcaattt catttgatag 84960

ttacgttggt catgattgga tggatgacta cgaagcacgt tggctatctt atatgaataa 85020

agctcgtaag gttccattta aactcaaaat tctaaataaa attactaaag gcggagctga 85080

gactggaaca ctgaacgttt taatggctgg tgttaacgtt ggtaagtcat taggattgtg 85140

ttcattggca gcagattatt tacagctcgg tcataatgtt ctttacattt ccatggaaat 85200

ggcagaagaa gtctgtgcta aacgtattga cgctaatatg cttgatgttt ctcttgatga 85260

cattgatgat gggcatattt cttacgctga gtataaagga aaaatggaaa aatggcgtga 85320

gaaatctact ctcggtcgtt taatcgttaa gcaatatcct actggtggag cagacgctaa 85380

tacatttcga tctcttttaa acgaattgaa gctcaagaag aattttgttc caacaatcat 85440

tattgttgac tatctgggta tttgtaaatc ttgccgcatc agagtttatt cggaaaatag 85500

ttacacaact gttaaagcta tcgcagaaga attgcgtgct ctggctgttg aaactgaaac 85560

tgttctttgg actgcagcac aggttggtaa gcaagcttgg gattcttctg atgttaacat 85620

gagcgatatt gcggaatctg ccggtcttcc agcaacagcc gattttatgc ttgcggtcat 85680

tgaaaccgag gagttagcag ctgctgaaca acaactcatt aagcaaatca aatcacgata 85740

tggtgataag aataaatgga ataagttttt gatgggtgtt caaaaaggaa atcagaaatg 85800

ggtagaaatt gaacaagatt ctactccaac tgaagtgaac gaagtagcag gttcacaaca 85860

gatacaagct gaacagaacc gctatcaaag aaacgaatcc actcgagctc agttagatgc 85920

tttggcgaat gaattaaaat tttagtttac aagctgacaa gactatggta tagtagtctt 85980

gttggttaaa tgaggagatt gttatggaat tggtaaaggt agttttatg gggtggttta 86040

agaatgaaag catgtttact aaagaaatca caatgatgaa agatgacgtt caatgggcta 86100

ctactcaata tgctgaagtt aataaagcgc tagttaaagc tttcattgat gacaagaaag 86160

tatgtgaagt ggattgccga ggataatatg cacattgttt tatttaaacc tactccgtat 86220

aatgtcagga aaaatactca attcaaagca cttatcgcag atacgtggga attggtgtta 86280

gatattccag cagaagaaag tcctccattt ggtcgagtgg aatttattaa gtttgctgtg 86340

cgccctacga agcgacagat tcgccaatgc aaaagatact ttcgtaaaat cgtcaagtta 86400

gagaaacagt tattgatgct agtaaaatag tagtttacaa gctgatagag ttgtgttata 86460

gtaattctat cagctaatcg cggagaaaag aaaatgatgc tagttaatag agaatatcag 86520

tttaaatcag aagaagattt ggaaaaattc gcgagtggtt gtgaactgaa tagacgcaca 86580

gctaaagtca taggattaaa acccttaca gttctagatt gtgaagtttc taaattccgc 86640

agagggtgtt ctattagcgg tcatgctctg gttgatggaa acacattttt ctttgttttt 86700

agcgtcagag aacttttatt gattaacgaa cttgaggaaa taaaatagtt tacttttgtt 86760

ttaaacatgt tattatagac ctatcaaaac aaacgagtaa atggagaaca aaatgtctaa 86820

agtatcaggt tatcaattat taacacaaga acaacgttca gagatggatt ctttacaaga 86880

acggtgtcag catagaaata acgcacttga ttcattttta ttagttgaat atgaaaactt 86940

gtgctctaga cttgaaaaag aatatgttca tcaacatgaa ggaggagaag aatgaaactg 87000

aaatcaccaa ttattgcaat ttgtctgttt gcttctacta gtgtttactt ttgttgaaaa 87060

ttgagatact ataaacataa actactgagg agattatcat gaaaaaattt atctttgctg 87120

caatttttgc tttatcttct tgcgctgctc agcctgctat ggcgggttat gacaaagatt 87180

tgtgtgagtg gtctatgact gcagatcaga ctgaagttga aactcaaatt gaagcggata 87240

ttatgaatat cgttgagcgt gatcgtcctg aaatgaaagc tgaagtgcaa aaacagctca 87300

agtctggtgg tgtaatgcag tataattacg ttctgtattg tgataaaaac ttcaataata 87360

aaaatatcat cgctgaagtg gtaggtgagt aattagaggt taatatgtat agttctgaat 87420

tttcatattt aaaaatggaa aaaaatttca tacgatttta tagatgaaaa ggtttattac 87480

agtttccatg aaccacgttt taatagtgag gttgggttta ttgcagtaaa agacaatttc 87540

attttaaaaa tatattcggc attaaaggat tttcactacg aaaatattaa cctaaaattt 87600

gataaagaaa acgttcgtaa ttgcgcagta acaattacag gaaataaagg tacatgcgtt 87660

atgctatctg atgaaattaa tgatttgcta aatgatgccg aaaaggttgc tattccatcg 87720

attgatgacc aaatttttaa tgcttttatg aatagaggtt aatatgaaaa cgtttaaaga 87780

atttatcaaa gaagatatgg tcgctggaga ttcaggtggt aatcctgaaa atatctctac 87840

tggaacaacg tcaggcgctg tagtaaataa aggtcctgaa cagattccta aaaagaaaaa 87900

agaggaatct aaagaaaaag aagagtaaaa atgtcatcga taccttggat tgataatgag 87960

tttgcatatc gtgcattagc tcatttacct aaattcacac aagtaaataa tagttcaact 88020

tttaaattgc ggtttagatg ccctgtttgt ggagattcaa aaaccgacca aaataaagcc 88080

cgtggatggt attatggtga taataatgaa ggaaatattc attgttataa ctgtaactat 88140

catgcaccaa tcggaatata tttaaaggag tttgaacctg atttatatcg tgagtatatc 88200

tttgaaataa gaaaagaaaa aggtaaaagt cgtccagtag aaaaacctaa agaacttcct 88260

aaacaacctg agaagaaaat aattaaatct cttccgtcat gcattagatt agataaattg 88320

gcggaagacc atccaattat aaaatacgta aaagctcgct gtattccaaa ggataaatgg 88380

aaatatcttt ggtttacaac tgaatggcct aaattagtta atagcatagc accaggaaca 88440

tataaaaagg aaatacctga gcctcgtctt gttattccaa tttataatgc taatggaaaa 88500

gctgagtctt ttcaagggcg tgcattaaag aaagatgctc cccaaaaata tatcaccatc 88560

aaagcttatc ctgaggcaac aaaaatctat ggtgttgaac gggttaaaga tggtgatgta 88620

tatgttctag aaggacctat agattcgctt tttattgaaa atggtatagc tattacgggt 88680

ggtcaattag acctagaaat tgttccattt aaagatagac gtgtatgggt tttagataat 88740

gaacctcgtc accctgacac tattaaacga atgactaaat tagttgatgc aggagaaagg 88800

gttatgtttt gggataaatc tccctggaaa tcaaaagatg tcaatgatat gattagaaag 88860

gaaggtgcaa cccctgaaca aattatggaa tatatgaaaa ataatattgc ccaagggttg 88920

atggctaaaa tgcggctatc taaatatgct aagatttaaa ttaacccaac caaagcaaat 88980

gctaaatcta cgaatgtatc aagagtaatt actggaatac taacgccatg agcaatagca 89040

actggcgata aaacaaaatt ccaaagtaaa attcctatca tagcagaaat agtaaaagct 89100

atacgttttt tattaccttt gatggcatta acaagtgcca ttaatttttg taccatatgt 89160

cctccttatt gctttatata tttattgtat aattaatcta ctaatccatg aattgaaagg 89220

aaaaataatg gcatacttta atgaatgcgc tcatttgatc gaaggtgttg ataaagcaaa 89280

tcgtgcatat gctgagaata ttatgcacaa tattgacccg ctgcaggtta tgcttgatat 89340

gcagcggcat ttacaaattc gtttggctaa cgataaacca gaaacaaatc gtcatcccga 89400

ttcacttgaa actgcgggag aagttcttgc ttggctgcga aaccaagacg attatatcgc 89460

agacgaaact cgcgagctat atacttctct tggtggtatg agtaatggtg aaaaagaagc 89520

ttctgctgta tggaaacctt ggaagaaacg ttattctgaa atgcaatcca agaaaattca 89580

agatttatct cctgaagatc agcttgaaat taaatttgaa ctgattgatc aatttcactt 89640

tttcatgaat aaatttattg ctcttggaat gtcagctgaa gaaatcttta aactttatta 89700

tctgaaaaat gctgaaaatt tcgctcgtca agatcgaggt tattaatggc tcgtttaaat 89760

aaacgccagc ttaagaaagc ccacaagaaa cgtattgacc agctatttaa aaattatgac 89820

aaagagctcg tgtgtgagct cttatctaat cagcttcgtg cggttgattg ggttgtagaa 89880

gaaggtcctg atgaaatttt tgtcagcgaa gaagccttaa aattaattat agagcattca 89940

aaatgaaaat atccaaagaa gaatttatta gacgacaaaa agctttaatt aatttacacg 90000

agtggtatgc ttaccagctt aaagtagata gctctaatat aaatgctgta atggctttat 90060

ataaacaaat tcaagatgaa cacgaattcc tggcacaagt tttcattgaa gactgatata 90120

aatacacctg taattaaaca ataaaggagt ttattatggg tggtttcgtt aacatcaaga 90180

cctttactca tccagcgggt gaaggcaaag aagttaaagg tatggaagtt tctgttccgt 90240

ttgaaattta ttctaacgag catcgtatcg cagattctca ttatcagatc tttccgtcag 90300

aaaaggcagc atattctact gtagtttctg atgcagctga ttggaaaact aagaatgctg 90360

caatgtttac gcctacacaa ataggtggtt aataattcaa ggactcctcc gggagtcctt 90420

ttttcatttt actggtttac tttccaaaat gagtatggta taataaaatt atcttataga 90480

ggagagcact atgttaaatc gttggattaa accaaatgaa gatttagata ttatcatttc 90540

acggcatgta atgaagaaat atgaactgca gccatggtct acagaagttg ttgtgcattc 90600

atttatgatg tacgcagatg gttctgtcga atttaatgca gaaattcgat atgattatgg 90660

cgagaagcaa gtcgaattca agagaggctt tttgtaatgt ttatctttaa ttggtttaaa 90720

agcttcttta cagatttttt ctctacaact cctggagaag gtgtagttcc tatttcaaat 90780

gactaccttc ctttaactgt agttgaatat gtttatatgg gagatggaac agtagaagca 90840

gttactatga cttatgaaga agcccaagaa tattataaaa atccttggcg ctggtcaaca 90900

cctattacat catctaatac acagaataca cagtctagtt ctgattcata tgacactaat 90960

gttcctgttc atgtatggac gggcgattcg tgtggaagtt cttgtgattc tagttgttca 91020

tctacatctt gtgattgagg aaaattatgg aagcgatttt gtttgaaatg tatattagca 91080

gtaatagtat gtcgtttgct aaagacgttc caattaccgt agcagtaatg attgataagg 91140

gttattgtga cccaatgtat ctcgtagaaa atttcgtttc aatgccagtt ccagaagatg 91200

ctgaaataaa acttaaaaag attggtatta ttgaaactgt accaaatatt ccgtttagag 91260

caattgaagc atttactaaa tccgaataca ttaatgttag cgcagaacaa tataatgata 91320

aacctatatc tttctattcg tatgattcag tatatagttg gaaaatagat aaaggaaata 91380

aatttataat tgtgagtgaa gatgctttat catactttat ttcttctata tggaatagtt 91440

tacatccaaa tttgctaaaa attcatgaat tcgatgatgc tcctactgtt gttttaggta 91500

aaacaaatga aagttctgaa gaaaatgttt gaatggttca gtagaccaaa ctcaatgtac 91560

attgatgatg gttgggttga acaagcaaat aaagaaatgc agaacgaatc agaagaatgg 91620

atgaaatcaa tgattagcgt tgagaaagaa aagaaattag aacgctcagc gcttaaattg 91680

atgagagaca tttatgggga taaatcgtga acagagatat gacgctagaa gaggctaaag 91740

ctaaagcaaa tgaagcttta gatttgcttc ttaaaattgg cagtaaaatg atggaagaaa 91800

atgagaaata tatccaggaa aacaaaattc ctgatggtcc attagtaggc aaaaggaaat 91860

cgcatgattg aagtagcaaa acattattca atagaattta tgtctaaaga aggtaaatca 91920

gtaaatacac ttgataaaaa gtgctcatta attattcctt tagcagaaaa tccggatatt 91980

ttaattaaag atataaaaga aagaaaatat ccagaaaatg ttattctaat tataaagcat 92040

actgaagata ttttgcagaa tactgattca ccgttttctt cttctgaagc tttaactatt 92100

aaaggctata aaagagctca tgaatatggt ctttttgacc tgtttgaaga cgataaagtt 92160

aaattagcac ttaatttagc aggtcaatct tctaaaagta aaacattcat tattgaagat 92220

attaaagata taaatgcatt tgttaagatg gtctgggctc attttgacgt tggactacgc 92280

tggagaatgt ccgaagaaga aagaaaaatt attgaagcta atcgttattt tggtttttat 92340

cgctaggaat taatatggat ttatttgaga tgttagaaga taatcattct acgaatatcc 92400

agaatgattc tagtgattat aagaaagagt accgtatagt attacagaat tatggaattg 92460

aagccccaga tgctcttcta gaagaactag cttcatacca tcttgaccct ccgccctggg 92520

ctccctgggc aaaataattc aaaaagttgt ttactttcct tcctaacaat gatatgatag 92580

cttctgaagt atatggaggc tatcatgatt attaatcttg cagatgttga acagttatct 92640

ataaaagctg aaagcgttga ttttcaatat gatatgtata aaaaagtctg tgaaaaattt 92700

actgactttg aacaatcagt tctttggcaa tgtatggaag ccaaaaagaa taaagctctt 92760

catcggcagt tgaataaaat cattaaaaag catttaacta aatcacctta tcagctatat 92820

cgtggtatat caaaatcgac aaaagaactc attaaagatt tacaagttgg agaagtgttt 92880

tcaacgaaca gagtagattc atttactact agtttgcaca cagcgtgcgg tttttcttat 92940

gttgagtatt tcactgaaat aatatttcgc ttaaaaactg ataaagcttt taattattct 93000

gaccatatca gcgatattat actttcttct cctaatactg agtttaagta tacatatgaa 93060

gatactgatg gattagattc agaacgtact gataacttaa tgatgattgt gcgtgaacaa 93120

gaatggatga ttccaattgg aaagtataaa ataacttcta tttcaaaaga aaaattacac 93180

gattcatttg gaacatttaa agtgtatgat attgaggtag ttgaatgaaa tattcagcaa 93240

tgcaattaaa agattttaaa atcaaatcaa tggatgcatc ggtgcgtgct tctattcgtg 93300

aagaattact ttctgaagga tttaatttat ctgaaattga acttttaatt cattgtatta 93360

ctaataagcc agacgatcat tcttggttaa atgaaataat caaatctcgt ttggttccaa 93420

acgataaacc tctttggaga ggtgttccag ttgagactaa gcaggtgtta aatcaaggaa 93480

ttgatattat tacatttgat aaagtagtat cagcttcata tgataaaaat gtagagctac 93540

attttgcttc tggattagaa tacaacacgc aagttatttt tgaattcaaa gctcctatgg 93600

tatttaattt ccaggagtat gctataaaag ctctacgttg taaagaatat agtccgagtt 93660

ttaagtttcc agatagccat cgttatcgta atatggaatt agtttcagat gaacaagaag 93720

taatgatacc agctggaagt gtatttagaa ttgcggatag atacgagtat aaaaagcatt 93780

caacatacac tatctatact cttgactttg aaggatttaa tctataatgg aaggacttag 93840

attcattata ccatgaaagt tttaaagcat ttttcataaa gttgtttaca agctgaagta 93900

aaaatgttat agtataagta gttaaccgtc cgtgagaaaa atatgaaact gtctaaaaat 93960

caaattcgta aaattacacg tcgtttagag catactcagg catctgctaa aagacgttct 94020

aaagatttta acttagactt caattacatt aagaacattt tagatcagaa agtttgcgct 94080

tactcgggag aacctttga taatcgtatt gaaggagaga aattatcatt agaacgtttt 94140

gataataacg ttggatacat taaagggaat gttattgcag taaagaaaaa gtataataca 94200

tttcgttctg attatacttt agaagagttg attgaaaagc gtgatttatt tgctttgcga 94260

attggtcgtt catctgcgaa aaaagttcat aaactaaatt tagatgaaaa gaaatgggct 94320

aaaatcaaaa agacttataa tcaaattaaa gctatacaga aaaaacgtga aaaccgaatt 94380

gagcacattt ctcagctttc taaatcaaaa caaacttctg acgttaagct aacgattata 94440

gcacttaaag ctcgtattga tggttctcgt atagcagaag gcgctgaagt tgttaaattg 94500

aacgttcttc ttaaaggctc ggattggaaa actgtgaaaa agctgtcaga agcagaaatg 94560

caatatgata tgtgtgataa aattattcaa ggtgtagagc ggtatcaaaa cttgtctttt 94620

attgataaac ttaaactgaa aagaggatac ccgctaaatt gttcaatttt taaacttatc 94680

cgaggataat atgttttatg tatatgcgat agtgtataga gataaagatg gatttgcggt 94740

gcctgttcct cttgatgaac atcgccctgc tgtatttttt gaaagggaga ttgctgataa 94800

agtatttaca actcttaaag agcagtatca actagcttta ggtatgggaa ttccgagatt 94860

agttgagact ccacgcaagt tttggtttaa taaaatagaa gttaaacatg ttaagcctga 94920

tgtagacacg caaagattat atcggcgaat tttagatact gggcgtattg ttagtatacc 94980

aattgcaggg aatttacgat gacatttgat gatttgacag aaggccagaa aaatgccttt 95040

aacatcgtta tgagggctat caaagaaaag aaacatcatg taactattaa tggacctgcc 95100

ggtactggta aaactactct tactaagttc atcattgaag ctttaatatc tacgggcgaa 95160

actggcatta ttttagcagc tcctacacat gcagctaaaa agattctttc aaaactgtca 95220

gggaaagaag cgagtactat tcatagtatt cttaaaatta accccgtaac atacgaagaa 95280

aacgttcttt ttgaacaaaa agaagtaccg gatttagcca aatgtagagt attaatctgc 95340

gacgaagtgt caatgtatga tagaaagcta tttaaaattc tgctttcaac tatcccgcca 95400

tggtgtacta taattggaat aggcgataat aagcaaatta gacctgttga cccaggggaa 95460

aacactgctt atatcagtcc attctttaca cataaagatt tttatcagtg tgaactcact 95520

gaagttaaac gcagtaatgc tcctattatt gatgtagcta ctgatgttcg caacggtaag 95580

tggatttatg ataaagttgt tgacggacat ggagtacgtg gatttactgg tgataccgct 95640

ttacgcgatt ttatggtaaa ttatttttca atcgttaaat cactagatga tttgtttgaa 95700

aatcgcgtaa tggcatttac gaataaatct gttgataagt taaatagcat tattcgtaaa 95760

aagatttttg aaactgataa agattttatt gtcggtgaaa ttattgtaat gcaggaaccg 95820

ttaattaaaa catataaaat tgatggaaag cctgtgtcag aaattatttt taataacgga 95880

caattagttc gtattataga agcagaatat acatcaacat ttgttaaagc tcgtggcgtt 95940

cctggagaat atctaattcg tcattgggat ttaacagtag aaacttacgg cgatgatgaa 96000

tattatcgtg aaaagattaa aataatttca tctgatgaag agctgtataa gtttaactta 96060

tttttaggta aaacagcaga aacttataaa aactggaata agggtggaaa agctccatgg 96120

agtgattttt gggatgctaa atcacagttt agtaaagtga aagcacttcc tgcatcaaca 96180

ttccataaag cgcagggtat gtctgtagac cgtgctttca tctatacacc ttgtattcat 96240

tatgcagatg ctgaattggc tcaacaactt ctttatgttg gtgttacccg tggtcgttat 96300

gacgtatttt atgtgtgagg atatatgatt aacatcaatt caaaatattt aaatcgtcta 96360

atagatggta taaggaagca tactaataag caagataatc tcgatgttat ggtaacagga 96420

gctgagctcc ttcataagct ttatcttata agtgatacta tattagcaat taaacgaatt 96480

gaaaaacaat catatcacag taatacagat acggtaatta cactagatga aagtgtctgt 96540

aaattactaa ttaaatttga ggaagctatt cgtggaaata actaaagacc agttttatct 96600

gcttcaagat aaagtgagcg aaatttatga aatagcttat agtaaaaatc gtgaaactgt 96660

aaaaattgaa tctagtaagt tgatgcttca attagaagaa attgaacgag atttaattgc 96720

gttagaattc ttttgtggtg aagtgaaaac tgtcacaatc agtgattatg ttttaggtga 96780

aattagctat ctttataagg cgattattaa tgattgaatt aagttggtgt cagtttaaat 96840

ctcttatgac aaatgttaaa gctgtcattg agaaaaattc tggtcctgaa aatattacta 96900

ttcgcgaaaa agctttaaag ataatataca gtcttgaaga gatgcaaaaa gatattgaat 96960

ctatggcaaa atttattgat gaacctatta ataaagttta tattcaagac tatactgtag 97020

gccaaattcg cgatttagcg aggaaaattt aatgtttgat tttattatag attttgaaac 97080

aatgggaagt ggtgaaaaag cagctgttat tgatttagct gtaattgctt ttgaccctaa 97140

cccagaagta gttgaaacat ttgatgaatt agtttcacgc ggcattaaaa tcaaatttga 97200

tttaaaaagc caaaaaggac atcgtctttt tactaaaagc actatcgaat ggtggaaaaa 97260

tcagtctcct gaagctcgaa aaaatattgc accgtccgat gaagatgtaa gcactatcga 97320

cggtattgcg aaatttaatg attacatcaa tgcacataat atcgatcctt ggaaatctca 97380

aggctggtgc cgtggaatgt cgtttgattt tccaatttta gtcgatctca ttcgtgatat 97440

tcaacgtctt aatggtgttt ctgagaatga acttgacaca tttaagttag aaccatgtaa 97500

attctggaat cagcgtgata ttcgtaccag aattgaagca cttctgcttg ttcgtgatat 97560

gaccacgtgt cctcttccaa aaggaacttt agatggattc gttgcgcatg attctattca 97620

tgactgcgcg aaagacatcc tgatgatgaa gtacgctttg cgatatgcta tgggtcttga 97680

agatgctcca tcagaggaag attgcgatcc tctatctctt ccaacaaaac gataaaaagt 97740

tgtttacttc ctcggttagt tgtggtatta taacaccata gctactgagg ataataaaat 97800

gaaaatttat cgtgttgaat catcgtttag tattcttgat tatgaagatg ctataacaat 97860

acgtcgaaat ctttgtgttc aaataacgcc gtacaggagt ataatagatt catggagcga 97920

agagtggcta ttacacgtag gttatgacag acctaatttt atgcatcata gcgataataa 97980

taaaagaatt cctttaccac acgaagataa actattagtt aaaaacgcta atatagtaat 98040

taatactaag ttcaagaaag attatgttgg agtagaatat catattccag gatggtttat 98100

agctctttat cattttgctt tcgctagcga atatgatatg atgagatggt tcacacgaga 98160

agagcgtgaa gaattagctt cgaaaggatt ttatcttgct gtatacgaag taccagatga 98220

ccaagttatc gttggcgggc atcaagtaat gttccgtaaa tcccatgctg aacttgtaga 98280

ttttattgaa atgagataat tatgaaattt aattataatc ctgaatacac accgaatccg 98340

gcagctaaac tgattgattt tgacgttgta agtacttatg tatgccctgt taaaccactg 98400

gaaattaagg aacctactat gactaccgct attgaaatcg gcaaaaccta caaactggtt 98460

gaacctaaaa ttaaaactaa tgccttgatt tctggtcata aaactctgac tgatgttttt 98520

ggcgaaggcg aatttattgt tgaagaattt gccaaaagtg agtggtttga caaatcttac 98580

gtcatccacg gtcgccggtt agataataac aaaataaaga aaaacctggt ttatgaagat 98640

gagttcatcc tgttccaaga agttgaagaa caagacccta cagacctgtt gtgtgctgct 98700

gtgtctatcc gtcgtccttt tgataatcct atctgtggtt gggtaacaga ccagtggatt 98760

gaagatggtg ttgagcttct gaacgttgtc catgcaggag attttagtgt agtacctcgt 98820

agtgcggtgg tagctatttt gaattaatag tttacaaact cttgggacca gagtataatg 98880

gtcctgtgga gtataaaatc tttttaacaa gtgagagata actatgatta ttaatattgg 98940

tgaaattgct cgtgtatctg ataaatcccg ttctaaagca gcaggaaaat tggtcgaagt 99000

tgtaagcatt cagcttaaac acggtgttaa agatgaagat tctgaagtaa aagtacgtat 99060

cattgctaaa gatggaatgt ctaagcccca gtttggttat gttcgatgga aatttcttga 99120

gcctgcgttt ttgaaagctg ttcctgctaa aggaattgaa acgattgata cttcgcatgt 99180

aggtgtagac tttaagtgga aactcggtca agctatcaag ttcattgctc cttgtgaatt 99240

taaatttatc aaagatgatg gaaaggctgt ttatactcgc gctatgtgtg gatacattac 99300

cgatcaatgg gtagaagatg gcgttaagtt gtacaacgtg gtatttttag gaacatataa 99360

agtcattcct gaaagttgga ttaaacacta cagcaatgct ctctatgcat aaagtttaaa 99420

atttttttcat aaaactatat acatcagtag ttgattatgg tactatatca atatcaacta 99480

ctgatacaga aaacaacttg gagaataaaa tggataattc gttaaaggtg cgctgatact 99540

cttctgaaac gcatcgctcc aatgttcaat taatgaggaa attatgatga aacgtaaaat 99600

tgttcagaat tgcactaatg atgaatttga agatgtatta ttcgatccag atttggtagt 99660

agttcaaaag gaacacacta tcaagtttac tcacttgact tcggtttatg tgtatgaaaa 99720

ggttggggat aaacaaccaa tttacggtgt atttcgtgaa atcactgaag atggtacaac 99780

ttactggaag gaaatttatt aatggctatt aaatttgaag ttaataaatg gtatcaattt 99840

aaaaataaac aagctcaaga aaattttatt aaagaccata ctgataacgg aatctatgca 99900

cgccgtttag gtatgcatcc ttttaaaatt ttagatgtgg atgctcttgg gcgtcctatt 99960

aaaattatgt catttgctgg aaatttagta ctatcttctg gtaaagatat tttggatgaa 100020

gattttattt ggctttcatc gaatgaagct gaattcttta atgaagttga aaatccatac 100080

caggcagctg aagagcagga agaatctgca ccgataactg atcaatctaa attccctgta 100140

atgaaagtta ctattgaaaa tgatgaacag gcatggtcct tgtatcagat gttgaaagct 100200

cactttaagg aataattatg ccgctttatg attataaatg tcaatcaaaa gactgcgcaa 100260

aagaatacga aaaaatcaag aaaatttctg aaagagatac tgatgtatgt cctgattgtc 100320

atcggattgc tattcggtta gtctctgccc ctaagcatgt gaatggcgga ttttacgact 100380

tacttaaagg gtaattatgt ttaaaatcgg taagaaatat cgcattcgcg aaggtgaaga 100440

aaagaaatat ctattttctg ctatttatag gaatggttct attaatgctg taatatctac 100500

aagcgaattt atcgttgaag atatgaaagg taataatgtt acaatgatta gtacagcatc 100560

tggaaatgac ggaaaaattc ttcacagttt tcagagtaat gttctaattt atgatgaaga 100620

atttgacttc ttcgaagaag ttcccgaagg ttttgctttt gaatgcacta tcactatgaa 100680

atctggtgac cctctttctt ttacagttaa agatgaagga agtcgcttga gaattattag 100740

tcttcttcaa gccattaaat ttaagtgaaa attatgaaat atattaatcg ttctatcgcg 100800

gcattagtat tagcagtgtc tttagtagga tgtactgatg ctgataatgc aaccaaagtt 100860

ttgtcttcaa gcggttttac taatattgaa atcactggat ataactggtt cggttgttct 100920

gaaaatgatt tccaacatac tggatttcgt gctattggac ctactgggca gaaagtagaa 100980

ggaacagtat gttctgggct gttctttaag gattcaacta ttcgttttaa ataaaaggcc 101040

ttcgggcctt tagctttatg attaccggag tataatattc ccgaaaccaa acgaggataa 101100

gtgatgatta agaatgaaat taaaattctg agcgatattg aacatatcaa aaagcgtagc 101160

ggcatgtata ttggctcttc tgctaatgaa atgcatgagc gctttctgtt tggtaaatgg 101220

gaaagtgttc agtatgtacc tggtcttgtt aagcttattg atgaaattat cgataactca 101280

gtagatgaag gtattcgtac taagtttaaa ttcgcaaata aaattaatgt tactattaaa 101340

aacaatcaag taacagttga agataacggt cgcggtattc cacaagcgat ggttaaaaca 101400

cctactggtg aagaaattcc tggtccagtt gctgcgtgga ctattccaaa agcaggtggt 101460

aactttggtg atgataaaga acgcgtcacc ggtggtatga atggtgttgg ttctagttta 101520

actaacattt tttctgtgat gtttgtcggt gaaactggcg atggtcaaaa taatattgta 101580

gttcgttgtt caaatggcat ggaaaataaa tcatgggaaa ctattcctgg aaaatggaaa 101640

ggaactcgtg ttactttcat tccagatttt atgtcatttg aaactaatga attatctcaa 101700

gtttatcttg acattacatt agatcgtctc cagacacttg ctgttgttta tcctgatatt 101760

caatttacct ttaatggtaa aaaggttcag ggcaatttta agaaatatgc acgccaatat 101820

gatgagcatg ctatcgttca agaacaagaa aactgttcta ttgcagttgg tcgttcaccg 101880

gatggttttc gtcaattaac atacgttaat aacattcata ctaagaatgg tggccatcac 101940

attgactgtg ttatggatga tatttgtgaa gaccttattc cacaaatcaa acgtaagttc 102000

aaaattgatg tgactaaagc acgcgttaaa gaatgtttga caatcgttat gtttgttcgt 102060

gatatgaaaa acatgcgatt tgattctcaa actaaagagc gtttgacttc tccatttggt 102120

gaaatccgta gtcatattca gcttgatgct aaaaagattt cacgtgctat tttgaataat 102180

gaagcaattc tgatgccaat tattgaagct gctttggctc gtaaattggc ggcagaaaaa 102240

gcagcagaaa ctaaagcagc taaaaaggca tctaaagcta aggttcataa acatatcaaa 102300

gcgaatcttt gtggtaaaga tgctgatact acattgttct tgactgaggg tgattctgct 102360

atcggatatc ttattgatgt tcgtaataaa gaacttcatg gtggttatcc attacgtggt 102420

aaagttctca acagttgggg tatgtcatat gctgacatgc ttaaaaacaa agaactgttt 102480

gatatttgcg caatcactgg attagttctc ggtgaaaaag ctgaaaactt gaattatcat 102540

aatattgcta ttatgactga tgctgaccat gatggtctag gaagcattta tccttctctg 102600

cttggatttt ttagtaattg gccagaactg tttgagcaag gaagaattcg cttcgtcaaa 102660

actcctgtaa tcatcgctca ggtcggtaaa aaacaagaat ggttttatac agtcgctgaa 102720

tatgagagtg ccaaagatgc tctacctaaa catagcatcc gttatattaa aggacttggc 102780

tctttggaaa aatctgaata tcgtgagatg attcaaaacc cagtatatga tgttgttaaa 102840

cttcctgaga actggaaaga gctttttgaa atgctcatgg gagataatgc tgaccttcgt 102900

aaagaatgga tgagccagta gtttacttta ccacaaggat gtggtataat taattgggca 102960

aatgaggata ttgaaatgaa atcatataaa gtaaatttag aacttttga taaagcagtt 103020

catcgagaat atagaatcat tcaacgcttt ttcgatatgg gagaagctga agagtttaaa 103080

aaccgcttta aggatattag agataaaatt caatccgaca ccgcaactaa agatgaacta 103140

ctagaagttg ctgaagttat taaacgcaat atgaattaat gaggaaatta tgattatcac 103200

cactgaaaaa gaaacaattc ttggtaatgg ttctaaatca aaagcattta gcatcacagc 103260

atctcctaaa gtatttaaaa ttctatcatc tgatttgtac acaaacaaga ttcgcgcagt 103320

agtccgtgaa ttgattacca acatgattga tgcccatgct ctcaatggaa atcctgaaaa 103380

atttatcatt caagttcctg gacgtttaga cccacgattt gtttgtcgag attttggtcc 103440

gggtatgagt gattttgata ttcagggtga tgataattct cctgggttgt ataattcata 103500

cttcagttca tctaaagctg aatctaatga ctttattggc ggatttggtt taggttctaa 103560

atctccgttt agttatactg atacgtttag tattacttcg tatcataaag gtgaaattcg 103620

tggttatgta gcttacatgg atggtgatgg cccacagatt aaacctacat tcgtaaaaga 103680

aatgggtcca gatgataaaa ctggtattga aatcgtagtt ccagttgaag aaaaagactt 103740

tagaaacttt gcttatgaag tttcttatat catgcgacca ttcaaagatt tggctatcat 103800

taatggtctt gaccgcgaaa ttgattattt tccggatttt gatgattatt acggcataaa 103860

tccagaaaga tactggcctg atcgtggtgg attatatgct atctatggcg gtattgttta 103920

tcctatcgat ggtgttatta aagaccgtaa ctggctaagc attcgtaatg aagtgaatta 103980

cattaagttt ccaatgggtt cgcttgatat tgctccatca cgcgaagctc tttcactaga 104040

tgatcgtact cgtaaaaata ttattgaacg agttaaagaa ctcagtgaga aagcatttaa 104100

tgaagatgta aaacgattta aagaatctac atctcctcgt cacacatatc gtgaattgat 104160

gaagatggga tattctgctc gagattatat gattagtaat tcagtcaaat tcacgactaa 104220

aaatctgtca tataaaaaga tgcagagcat gtttgaacct gacaataagt tatgtaatgc 104280

aggagttgtg tatgaagtaa atcttgatcc tcgactgaag cgcattaagc aaagtcatga 104340

aacttcagcc gttgcatcaa gttatcgtct gtttggtatt aatacaacaa aaattaatat 104400

cgttattgat aatattaaaa atcgtgttaa tattgttcgt ggattagcac gagcgttaga 104460

tgatagtgaa tttaataaca ctttgaatat tcatcataat gagcgtcttc tgtttattaa 104520

tccagaagta gaatcgcaga ttgatttgct tcctgatatt atggcgatgt ttgaaagtga 104580

tgaagttaac attcattatt tgtcagaaat tgaagcttta gttaaaagct atattccaaa 104640

ggtagttaaa agtaaagctc ctcgtcctaa agctgctaca gcatttaagt ttgaaattaa 104700

agacgggcgc tgggaaaaag aggaattatt tacgctcaca tcagaagcag atgaaattac 104760

tgggtatgta gcgtatatgc atcgttctga tattttctct atggatggta ctacatctct 104820

ttgtcatcca tctatgaata ttttgattcg tatggctaat cttattggca ttaatgagtt 104880

ttatgttatt cgtccgcttt tgcagaaaaa ggtaaaagaa ctcggtcagt gccaatgtat 104940

ttttgaaact ctgcgtgatt tatatgtaga tgcttttgat gatgtagatt atgataagta 105000

tgtaggttat tcaagttcag ctaaacgata tattgataaa attattaagt atcctgaact 105060

agattttatg atgaagtact tcagtgtaga tgaagtttct gaagaatata cacgactcgc 105120

taatatggtt agttcattac agggtgtata tttcaacggt ggaaaagata ccatcggtca 105180

tgacatctgg acagtaacta atctttttga tgaattatca cgtaatgctt caaaaaacag 105240

tgataaaatg gttgctgagt ttaccaagaa attccgtatt gtttccgact tcatcggata 105300

tcgcaactct ttaagtgatg atgaagtttc ccaaatcgct aaaactatga aggcccttgc 105360

ggcctaataa ggaaaattat gtacaatatt aaatgcctga ccaaaaacga acaagctgaa 105420

attgttaaac tgtattcaag tggtaattac acccagcagg aattggctga ttggcaaggt 105480

gtatcggttg acacaatccg tcgtgttttg aaaaatgctg aagaagcaga acgctctaaa 105540

gttactatta gcggtgacat tacagttaaa gttaatagcg atgcagttat tgctccagtt 105600

gctaaatctg acattatttg gaatgcatct aaaaaattca tttcaattac tgttgacggt 105660

gtaacttata acgcaactcc taatactcat tcaaacttcc aggaaattct taatctgctt 105720

gtagcggata agttggaaga agcggcacaa aaaattaatg ttcgtcgcgc tgttgaaaaa 105780

tatatttccg gcgatgttcg aattgaaggt ggaagcttat tctatcaaaa tattgaattg 105840

cggtctggtt tggttgatcg tattcttgat tcgatggaaa aaggcgaaaa ctttgaattt 105900

tattttccgt tcttggaaaa tctgctggaa aacccaagcc agaaagcggt atctcgactc 105960

tttgatttct tggtagcaaa cgatattgaa attacagaag atggttactt ctatgcttgg 106020

aaagtagttc gtagcaatta ctttgattgt cactcaaaca cttttgataa cagtcctggt 106080

aaagtagtta aaatgccgcg tactcgtgtg aatgacgatg atacgcaaac ttgttcccgc 106140

ggtttgcatg tatgttctaa atcttatatt cgtcactttg gcagttcaac cagccgagtc 106200

gtaaaagtta aagtacatcc gcgtgatgta gtatcaattc cgattgatta caacgatgct 106260

aaaatgcgta cctgccaata cgaagtagtt gaagacgtta ctgaacaatt taaataaggg 106320

cttcggccct taactaagga aaattatgtt aggttatcaa gcacgagtaa aagaagaata 106380

cgatcaatta atgctcaaaa ttaatgcact tagcaatttt ttagaaagca caaagtttct 106440

aacggttagt gcagttgagc aagaattgct actttcgcag tttatctcaa tgaaatctta 106500

cgcagattgt ttagaaaaaa gaattgcaca attcaaataa aataagggct tcggcccttt 106560

tgttttaagg gaaattatga ttccgacata aaggaaagtt taaatgcaga aaacgaatcc 106620

gggtttgcag agactatttc agattccgtc atttacccta tcgaacagtg acttgactag 106680

tgaaatgaag gtcaaaattg ctgatactgc aagatactct ttaaaacaaa acccgaacca 106740

ggataaagca gaagttatcg aaagatgtcg tatcgctgtg tacgcagagt tttttgtggc 106800

agattggcta agagggtatg ttaacaaagg ccaagaggat gttaatgacc cgtatacata 106860

cgcatgggat gtactggcgc atccaaaata ctgcgggctt cgtgtagaag ttaagacaca 106920

tcaaactgac tcacgttgga tttcggtaac aacaggatgc agcggagagt atccatatgg 106980

ttctggaata aatctagggc ccattctaaa tcatcaagtc gctgactgta taattatatt 107040

caacactaaa gaaattcatc caggtgtcat ccagtacact ccgaagttca tcggtgacag 107100

agaagacctt cgtaaggttg taagaaaaag caactacaat ggatggtatc tttccattta 107160

aaaattttca caaaacggtt tacataccac aaggactgtg gtactataca actatcagct 107220

acggaggagt aaaaatgaaa tttaaatttt attacgctaa acataaaatt accggtgaat 107280

ttattgcatt tacgacttca actacagatg aaggagatat ttttactgca gtatttttat 107340

caaaatggga atcagatcaa ccttacttat catcacgtga agatctccaa cgattagtta 107400

atggagaata taatgattca tggtcatatt tagtccatga ttgtgttaaa aaggcaataa 107460

aacaaaaaca cttggaaatc gttgagattg aactatgagt tcattatggt ggtgtttcgt 107520

ttggttaatt agtattccat taatttgttt aacatttact tttgtgatga ggttattatg 107580

aaaattttga attctgtgct tattgcttgt gcgtggtggg ttgcgcaagt ttcagcagta 107640

gtagttggta ttcacattta ttacgaatat ttttaaaaaa gttgtttaca agactgttct 107700

tccgtggtat tattacccta tcaactacgg aggaacagaa aatgaaaaag attgttaaag 107760

ctatatggaa tgtagttata atactaatag ttttgagtat attcccaatc gttttaatga 107820

ttgatgtatt aaacgcttac tttggattta tgtgaggaaa atatgaagcg taaacgcagt 107880

gcttttacat ttattgaatg gtttttcgat aatatttttc cggctttatt cattttcatg 107940

ctgatttttg ctttaggttc agttgtagtt ggaatctatt tgatgacagt agtcggaatt 108000

gatattcatc aaaatggttt aaaatccgta gttgaaacaa tttggaacgg tgtaaaatga 108060

tgaatttgct gagcggttgg ttttatattc ttatgtttta cattggcgca aattttccat 108120

attggatggg atggtcaaca actgcgtttg gattttatac tccttgaggt gaattatgaa 108180

aatctttaaa gatgtaaaag ttggtgaaat tttctgttta gataacggtg atcagttaat 108240

tcgtatttca cctcttaaga gcactagcga gaaaccgaca gttaacgcta ctttagcaaa 108300

caatagtaat gaacgtttct gtattgaaaa tgatactgaa acttataccg tagaagagtt 108360

ttgggaattg agcgtcgact gcgacgatta atttaatggc cgtgtgtatt catgcggcct 108420

tggagtagaa aataatttag aggaaattaa tatgaaatac atgactgtta ctgatctgaa 108480

taatgcaggc gctaccgtta ttggtacaat caagaacggt gaatggtttt tgggagttcc 108540

acataaagat attttatcta aacctggatt ttacttttta gtaagtaaat tagatggtcg 108600

tccatttagt aatccatgtg tgtctgcacg attttatgta ggtaatcagc gttctaagca 108660

aggatttagt gcggttctaa gtcatattcg tcaacgtcgg tctcagcttg cgcgtactat 108720

tgcaaataac aatgttccat acacagtatt ttatctgcct gcttctaaga tgaaacctct 108780

gactacggga tttggaaaag gtcagttagc tttggcgttt attcgtaatc atcattctga 108840

gtatcaaaca cttgaagaaa tgaaccgtat gttggctgat aactttaaat tcgttttgca 108900

ggcatattaa tgagtaattt ccacaacgaa catgtgatgc agttctatcg taataatttt 108960

aaaactaaag gcgtcttcgg acgccagtga ggaaaatatg aatattgcaa aattattagg 109020

agttatttca tttatttgtt ggatagtagc atgtgtttta actatctgta ttgatgtcag 109080

cagtgtgttt tcgcaagctt tagctcaggg tatgtgtgca tatttaacat ttgtgttgtt 109140

atctactaat gattaagaaa atcttgggct attcattagc ccttgctatt ttattgatag 109200

cattatatta cggaataatg ttcggattaa ttcaagtcgt gcttttcatt tctgatgtta 109260

ttatggcact acattcacta gtatggtaaa tttatgcaac tgaataatcg tgatttaaaa 109320

agtatcattg ataatgaagc attggcttat gctatgtaca cggttgaaaa tcgtgccatt 109380

ccaaatatga ttgacggatt taagccagtt caacgatttg ttattgctcg agctcttgat 109440

ttggcacgag gaaataaaga taagtttcac aaactcgctt ctatcgcagg cggtgtagcg 109500

gaccttggat atcatcatgg tgaaaactct gcgcaagacg caggtgcttt gatggctaac 109560

acttggaata ataactttcc tctgttagac ggtcaaggaa actttggttc tcgtactgtc 109620

caaaaggcag cagcaagtcg ttatattttt gctcgtgtaa gtaaaaattt ctataacgta 109680

tataaagata ctgaatatgc tccagtacat caagataaag aacacattcc gcctgctttc 109740

tatttgccta ttattcctac tgttcttctt aatggcgttt ccggtattgc aactggttat 109800

gcaacttaca ttcttcctca tagtgtttct tctgtcaaga aagctgtact gcaagctctt 109860

caaggaaaga aagtaactaa accgaaggta gaattcccag aatttcgtgg tgaagtcgtt 109920

gaaattgatg ggcaatatga aattcgtgga acatataagt ttacttcacg aactcaaatg 109980

catatcactg agattccata taagtatgat cgtgaaactt atgtgagtaa aatcttagac 110040

ccgcttgaag ataaaggctt cattacatgg gatgatgctt gtggtgagca tggctttggc 110100

ttcaaagtta aattccgaaa agaatactct ttgagcgata atgaagaaga acgccatgca 110160

aaaattatga aagacttcgg gttgattgag cgtcgttccc agaatattac cgtcattaat 110220

gagaaaggaa agctgcaagt ttacgataat gtagttgatt taatcaaaga cttcgttgaa 110280

gttcgtaaaa cttatgtcca aaaacgaatt gataacaaaa tcaaagaaac tgaatcagca 110340

tttcgtttag cttttgccaa ggcacatttc attaagaaag taatttcagg tgaaattgtt 110400

gtacaaggta aaactcgcaa agaactgacc gaagaacttt ctaaaattga tatgtattct 110460

tcttatgttg ataaactagt tggaatgaac atttttcata tgacttccga cgaagcaaag 110520

aaacttgctg aagaagctaa agccaaaaaa gaagaaaacg aatattggaa aactactgat 110580

gtagttacag aatacaccaa agatttagag gaaatcaaat gagtccattc attggtatca 110640

caagcgctgc attagtatct ggtggcattt tactggcggg tttaggtgtt gttcctgccg 110700

tagcaggagg tcttcttgcg ttcggaattc aacgtgttat catgacagtt atcacagtca 110760

tgcagtaatt ttagggagag cctcggctct ccctttttat ttcaaaaatt ttttcacaaa 110820

acggtttaca accaaagcat actgtggtac tatacaacta tcaaataaat gaactgaaac 110880

aaacaacccg gagatacaaa aaatgaaatt taaaatcgaa aacgaaatcg ttaaagctaa 110940

aaatgctctg actgctaaca aactggttgt agatggtatt gaatatgata tctgtggagt 111000

tcgtgaagaa aaacctggtg ttctgacttt cttcacaatg atttttaaat ttaaaggtga 111060

cacagaattc aaacagtttg attttgccca tgaagacgaa atcgaagttc gtaatctgaa 111120

cattaagtaa gtactttatt agagctcttg aaaaagagtg caaaaaagtg tttacttctg 111180

ctttaaacat gatactatag acctatcaaa taaatgaact gaaacggaga ttaaaatgtc 111240

taaagtaact tacatcatca aagcttctaa cgatgttctg aatgaaaaaa ctgctgcgat 111300

tttaattacc attgctaaga aagatttcat tacagccgca gaagttcgtg aggtgcatcc 111360

agatttaggt aacgcagtag ttaatagtaa tattggggta ttgattaaaa aaggcctggt 111420

ggagaaatct ggtgatggat taatcattac tggtgaagct caagatatta tttcaaacgc 111480

agcaacttta tacgcgcagg aaaatgctcc ggaactactg aaaaaacgtg ctactcgtaa 111540

agctcgtgag attacttctg atatggaaga agataaagac ctcatgttaa aacttttaga 111600

tgaaaatgga tttgttctta aaaaggttga aacttatcgt agtaattatc ttgccatttt 111660

agaaaaacgc actcacggaa ttcgtaattt tgaaattaac aataatggaa atatgcgaat 111720

ttttggatac aaaatgatgg aacatcatat tcagaaattt actgatatcg gaatgtcatg 111780

taaaatcgct aaaaacggta atgtgtatct tgacattaaa cgctcggcag aaaacattga 111840

agctgtaatc actgtagcat ctgaactgtg aggaataaat aatgaacaag ttagaaattg 111900

tcaatgaact tcgtcgttgt gtagaaccta ctcaagaggg ttgggacatc tggtaccatg 111960

gagcttatct tggaactatc gtaaagatta agactggtaa atacatgatt attcgtgaaa 112020

gtaaagatgc tccagtaggt attcgcaata attttatggc agcgataagt tcatttacag 112080

atgcagctta cgaaatttac cttgccgatt ataaagaatt ccaggaatct caaccggtta 112140

ttcgttcaat tggtgttaac aaagctcagc agaaaacttt gtggcagcgt attaaaggat 112200

ggtttaaatg aacccattta ttaatcgttt aaaaatgctg aatgttcctt tatctcgtga 112260

aactccagaa agtcttgttg aaaaatttaa agcgcatggt tataaatgca cagaagaaga 112320

tattctgaaa gaagttcctg aaatctgttg gcagactgcg tactgggatg aaaaccaaaa 112380

gtatcaacga cgaattgtct gcgcagctaa tcgttttaaa ttaaaagatg gacgaactct 112440

tattattcca ggtgctcgtc attattctaa agatatggca gaagttttag atgtagttaa 112500

acctcaatta gttactcaac aagtttgtga tgatgaccaa ggatttattg accaatatag 112560

taattattgg acacgtgaag aagcaatgat tattgcaact tacgccggac aagtacgtat 112620

tgaacgtggt ggtagtgaaa aagaacttta ctctgaggac ctttactaat gaatattaaa 112680

aagtttcaaa ttgatggaat tacgaatcaa attaaggcat tggaatatgc caataaaatg 112740

atgtcaacta attggggaat ttatgcgaat gagccagcat ttaaattttg tgatatggaa 112800

tttaccaaaa agcttgtagg aaaagatcat gtatgcccat ttagttctcc ggtaaatgga 112860

atgctaaaac ctgctttacg cgatctttat attgcgatga acgaagaaat gataaaagag 112920

ctaaaacgtc aactgaaggt gattcaattt ggccagggaa attaattcaa aatcagatta 112980

ttttaactct ctcaatgata aagataaaaa tctaatacgg cattttattg ttgagatggg 113040

atataccgat acacacgatt taagagaaca tatatttgaa tgtggtgtag ctaaaaagtt 113100

ttcattcacg tgcaaatgtt taagagaggt aattcaacac tatgaacaat ttagtcgcaa 113160

aacataattt taataaagct tctgtccata aagataagaa gaaagcgttt aaagaatcta 113220

atcgcaaaca gaaacataag gggaaggtct atgattattg attctcaatc tgtagttcaa 113280

tatacaatca aaattgatat tctagaaaag ctatataagt ttctaccaaa tttataccac 113340

tcaattgtta atgaattagt tgaagaactg catcttggga ataatgattt cttgattgga 113400

acttataaag acctctcaaa agcaggatat ttttacataa ttccagctcc aggaaaaagt 113460

attgatgatg tattaaaaac tataatgatt tatgtccatg attatgaaat tgaagattat 113520

ttcgaatgag tcataatctt gaaaaagtaa tcgagcataa tgtagctcag gaacgtaagt 113580

cgttcaagga attcgtagaa aaaatttttg aagaaaatac cacagaccag tttacaaatc 113640

aagcgtctga tgatattata acaaagtcaa ctaattgagt ggtatagtta atgaataaaa 113700

atattgatac agttcgtgaa attattactg ttgcgtctat tttgattaaa ttttccagag 113760

aagatattgt tgagaatcgc gctaatttta ttgcatttct gaatgagatt ggagtaacgc 113820

atgaaggtag aaagttaaat cagaattcat tccgtaaaat tgtttctgaa ttaactcaag 113880

aagataagaa aaccctcatc gacgaattca acgagggttt tgagggtgta tatcgatatc 113940

tagagatgta tacgaacaaa taattattta gcccttccta atattctggc cgcctgagca 114000

catattgatt caaggcggtc attacttata tgatcatttc tataccagta catggttatt 114060

gttccagcat agatattatc caaattaaaa tatggacaac tgtacatgta gtttatttcg 114120

ggagtaggct ttttagttgg taaaaaagca aattttgagt cggaataata atgacgtcca 114180

tttaaatgaa ctgtatattc atccatagtt ttatcaacag gatatcctcc aagtgatttt 114240

tcacttattg ttgaaggtaa ttttccttca tatgctataa tatcaacaaa atagtttaag 114300

tttttagggc ggaaagaata caccgcacta aagtctgcct cagatgatat atgaactatc 114360

tggagttgtt ccagggcgac agattcaaag cgtgcatttc tttccttttc aataatttca 114420

ctgtatgttt catactttga ttgcttatag tactcaaaga aactatctcc cctataccaa 114480

acaatcgcca tcataaataa aagaattacg acagctaccc gggaagcaag aactttcccg 114540

gtagcgttat ctttgaacaa gcgatctaga acaccaaaca gaatatcaga gggcgaaaat 114600

gatattctag gtgctgccat agaccctcct tttaagggta tttattcaca ttatactctt 114660

ggaccatata ttgctccaac attttgccat gttggagcgg accctatgac agcataacca 114720

gcagcgccgc cattatattc agatccttga ccgcgaatat tgcatctacc tcccgcggaa 114780

cctacttcac caccgtttcc accattatag ataccattca cggatcctga gccaggtgca 114840

gaaatagtac cgccagtcgc gcctgattgc atatcaatag atcctcctgg cgcaccaaaa 114900

ggacgaccgc caccaccacc aaaggtcaat ctcatttgtg aaaaaggaga ataatatccg 114960

ccgccgccac cgccgccacc gcctgcaata gctccgccat tattaattct tagtctccca 115020

ccaatatcgt tttgaataca atgacctcca gctgagccag gactattgct accgccatta 115080

cctccacgac catacatcgt tacgccatgt atatttaact gaacatattc atttggtgta 115140

tctccgtaca tgaagaataa aggaacatct ttagaataag aaacgatatc accaacaata 115200

ttgaatacaa taggtgcacc gccagcttca aagcatctat cacggaacca ctgaccatta 115260

aaattgtggt ttgctcctac agtatgaata atttctcgtg agcgacctgc aaattgactc 115320

atccagcaag gaacacccaa tcttaattga ccagctgctt gactcatcca gcgctgtcct 115380

gtttcatttg cggctgaact tccaatccaa ccaggaacac caactactgc cataatttat 115440

actccaaagg gggcatttcc cccttgttgt tagaatttaa aatatttact aattttgcga 115500

gcaattttag taaagagagg cgttttcaat tctttaattt cttcactcat ttcctgaata 115560

gccttaatta aaagagcatt cacagcagag ttagaaattg tcagaacatc agatccatca 115620

acttcaactt tagatacagc ttccggtaat tccttttcaa ggtcctgagc aataatacca 115680

acttcacgtt taataacact acggtcttta atagacttaa ctttatcgta aatataaact 115740

ttcagtcggc aaacttttttc gactgctcca tattctaatt cttctttatt aatcttgaga 115800

cgggagtcag aacgaatata cacatcgcta aagctaccat ttcctggtgt ataaaagaat 115860

ccatcatgat ggaattcaaa cacagcttgt gggtgtccag catcaggaga agcctccgtg 115920

gatccgacac gaatgattgc ttgcccccac tgtgatggaa tacgacgcat accaaagtca 115980

acagcggtgc tatatccttg attggttata acgcttcttg ctttaagaat aggataataa 116040

ctatcttgac caacataacc atgatcaacg aataatggag cttctactcg ccattggttg 116100

ccccaatcac ccggttgtct agcaatccat ccagaaccgt taatgtgtac acggtcacgg 116160

ttaacgttaa ccattgcggt attttgcggg tttaacgcaa tctcaccatt gtttgtgata 116220

tgtactgccg cctgagaagc atagctataa aatgctagcg aattatcagc accacccttg 116280

ccaatatacc agttaccagt cccgtctatg tcaccgcgaa tatgcaaaga attactagca 116340

gttgttgata atacaataga atcattaggt gcattgattg ttaaccgacc tgtcatcgta 116400

tcaccgcctt tacctaggcg agtattcaag gcagcatcta aattggttgc atcgttgtat 116460

ttcttccaga ttgaaccagc aatgttacca tcagtgttca agaatgctgc gccagcataa 116520

actcggcttt gtgacatgaa tcggccagac ggcaagaaac gccatgtagc taattcagtg 116580

gctgtagttc cagtagcgga taaatcaccc tgagcaacga tacgatattc tgaactagca 116640

atatccatac cagaagccat agtaatattt gttacagtgt ttttctgttt aacaattggc 116700

gcaaactggt ttttatttga atcgtcaata gcctgatata atggcgcaat ggtagtattc 116760

tgatttgcgt aagtattaga accagaaccg ctagcagggg cttgaatata tgctcctgga 116820

gcaagtgaaa ttttctgatt agcaccaaga ttaacagcag cagtgatatt cagcaatccc 116880

ctaaagtttt gttgagcagt ccaagtatgt gatccgtctt caagaacaac acgacgacaa 116940

gtattagtcc tacttcctgg attaccagcg atacgaacaa cgaaataacg atagttcgcc 117000

tgagatacag taccgcgcca cacttgaaca gttcgacccg ttccggtatg ttcgctagga 117060

ccgacagaaa acataaccag gtttccatca atcgtgcccc aatccatatt tgctggcata 117120

ttctttattt tgttcaaagg aacactaaac atactaccag ggacaaaatc aaaggtttgc 117180

caatctaact ccgctaattg agctttaata ccacccatac ccaaagtaat tggcagagaa 117240

taagatgtat atacttcgtt ccatgcaccc cacgcaccac cagtatatgc acgctcaaaa 117300

atacgatcgc gagtagttgc acccgttcct gcggtagtga aacgttggaa aatagcaccg 117360

ccagaagcac gctgtttaac ttccagcaaa ccaacaataa cagtcggcaa accttcacct 117420

gtaggacagt taataacggc atcagtgcct aaaatattat ataacccggg agttttaaaa 117480

tcattcagat ctccatcata gaaagtcgct ggtgtgccat gaccaacctg cttccattcc 117540

tcccacttag gtgcactagc atcccatgca gcagcgagac aacgagtata aaccataccc 117600

atgcgggtag tataacgctg agttctcgtg tataaaccac cttcaaatat ttctaaaaat 117660

ccttgtgcgg ctgatccttc ttctggataa tggcgatcaa atgatgcgat tgcgcttgaa 117720

ctgtttcgcc ataagccaca atgttctaat tctcccaagc tatcaaggtc aatcgtttgt 117780

gaaagtggac gagttgacgc ttgaacatta cgccacacac cccatggacc atcgacgcca 117840

ttccatttag cagataagga acgaatatag acgttaccag atcttacagt ataacgctga 117900

gtgccagcaa attggccggc cacaaacact tctagtacac ctacggcatt ttcttctggg 117960

aatttatttg ctggttgcgc atttgttgaa gtagatttcg accaaacacc aagatattct 118020

tcaatgggcc catacgtatc taaattagca tcagtaggta attcgccatt atttttata 118080

aatgttgtgc tattgacatt tatgtcagat ggagttaagg taatgtcctt tgacccatca 118140

aaagatatac cattaatttt cctaggtgtt tgcaatttag tagctgtgct agaatttcca 118200

attaaagttc cagttatatt ttctgtaacc tctaaagacc catttatagt tcctccatat 118260

tttaaaccta attctataac actacctgag tcatcttttg tgaaaattgt tttatctttt 118320

aagtttatag ccaattcacc ttcggctaat actgaagcag caggacgttg acctgcagtt 118380

ttgcttcttt taaattgtat ttgttttaaa gtagccataa gtcctcttaa taatagccga 118440

aatcttgaac agaatcctta attacgattt ggtcaaatcg tggaacgtgt gaaggttgag 118500

atgcaggatt ctgtgaaaaa aggtttggcg cagttaaatt tcctgtcata gtgtctccag 118560

agcgtaatac cctagagttt gcatttgctg taacagtatt tattgctcca tcaacataat 118620

ctttgcgagt aacatcagat gctgcggaag gagtagatgt aacagttacc gatggagccg 118680

ttacagccct ggtaaatgtt gtcaaacctt ctggcgtaat agtaatttgt ccagtagtga 118740

tttcactacc tgcaggtcta aaactaatac caccggaaga gccgccaact acaagagtat 118800

taccagtgcc gccaccagaa cgaattcgga taggggtttc attattactt aattgaagat 118860

aactatttac cccgtaatta atagtaattg gaccggcgta agtaccacca ttagctttag 118920

aaacgaaatc gttatcagct gcctgcggtt tattatattc tgaatatatt ttaaatgatt 118980

tgtagagtac atcgtcaccg gctgaattca atggaaaatt tccttgatgc caaatgacag 119040

atccacccac agttgaacct acttttaaat cagccattat atgccccttt attttaatat 119100

tatttataaa gaaaaaggga acccgaaggc tccctcagtt taaacttctc taaattcctg 119160

tccaaacact ttgccagttt tagaagaggc ttgtgtagga agtaccatta tatctggagg 119220

tgaagccgat tcacagacat aattaacgcg aataccgttg acgccaaatt cggcaggttt 119280

tgaaatgccg ccatttcttg atacttcaga aaaacttaaa tttctcatgc cgccttgacc 119340

tgcttgagca gttctttgtg catatatcgt aaatcctacg gcgttttctg gaacaactac 119400

atagtcttct tttaattccc aagacccagc ttgcccagta aactcagctt gggtcgagga 119460

aatatatcca tttgatgcat cataaaaacg aatggatatg tttgtagttc caagatcaag 119520

taaatcagca tcagcatata actgtgcttt aagataaaga acatcaccag gaattaaatt 119580

atagtcagaa agtttactta tagcagctga agttggcaat cgcgcaattt cgttattagt 119640

tccaccaact gctgacatga attgctctac actttcataa gttctttttg gaaatcctgt 119700

cgctccgacg tcttctaaac tatcaaatac aacatctaaa atagtttgat aatcatctgt 119760

gctttttcta ttacttagtt taacatgctc taatgcaata gctcttttag aagaagtata 119820

aaaagcagca tatgatacgt caaatcttga caatactgaa tctgatggaa aaactgaagt 119880

tcctgctccc cttaaccaag ataccacttc aggaggaaaa ttaacctttc cgctagttaa 119940

tatagcaaca agtctattgt ttgacaaaga attcatgaaa ctgacaaaag cggcagatgt 120000

tgtattgttt gaagcagaaa aagcatatga cttgctatca actaatgctc ccgtagaagg 120060

gtcaaaaact cttaaatgaa gacctgcact aaatgtttga tttccaacgg gattatcctg 120120

aaatttaaca tatggccccg cagtagaaag cgggcaagaa cccgctatgc ttattttgta 120180

tcttactgaa ttactttccg ataaaaatgg cgtttggacg tatccttgtc caaactctgc 120240

cataaatttt tccataatac ctcttattca acccattcaa atttaacagt tttattcact 120300

gggtcaggaa taatgcgaac attaccaatt cgtaagaaat cacgaatagt aagattacct 120360

attattccat tatcagatgg gattgctcct atatccgaag gttgaggagg gttacctcca 120420

tcaaatacct gaacaaaact tgaccaagaa tttttagttt tctgccatgt acgcgtccag 120480

cgagtggtac gtgcttctgg ggtcgttgga taagtaatcc aatcttggta aagcgaatca 120540

agtgtgttac caaactgagt caatgtacca ggagatttaa cttcttcgcc acgttctaag 120600

tatggaagcc cagtcacttc attagttttt tcaaccattt taaaataacc cgggaactgg 120660

ttataagtgg ctgaatcgtt aatatcaatt gaccagaatc ctacagtatc agatgttgga 120720

gcgcgggtgt ataaatcaga tgttttagtg ccctgagaac gaattctcga gttaacagtc 120780

aaaccgcctg aatttatagt agcacctttg gcaatgatta agctttcacc aatcgttact 120840

tggccagatg cattattaat agctaaagga cgtaatccat taaatccacc agtctgatca 120900

cccgatgcag taagcataaa attcgttact gatccatcat tgcgaacaat gaaaccataa 120960

tttccgttaa tagcacggaa agcatttgcg cttcgagaaa taatttcacc agttgcagtg 121020

actgaattac caaatgttgc tacaccattt gcattcaatg ttcctgaagc attaacattt 121080

atcggtgtta ctgtaccgtt gatattaaat gttatatttc cagctttatt acgctgagaa 121140

taaaaatgac tagacgtttc atcactaact tcaaatacgg tagaacgtgt tgtgtctgat 121200

tccccgctaa attgatttcc ccacactctg actgtcatcg tttgagccgg gtttgttcca 121260

gtttgaggtc ctttctcaaa aatcagacga gttgccgttc cagtattaga aatagttaat 121320

gtactatttg ctgaaactga tccaccgaat gtagcagtac tagatgatac aagaggggca 121380

cccagattcg tttgttgggt taaggttagt gaaccattaa ctgtttgtgc aatgtcccta 121440

cgaatgaact ggagcgaatc tagaccatct aataaattac tatctacagc ttttgctttt 121500

aatggcaaat aatttgctaa tacgcgattt aattcatatg gtgatactgc ataaccattt 121560

ttctcatatg attctaatgg ctgtgttgaa cctaccgtat cattaccaac aaacgttaat 121620

gaaccagaag aagttttaac aaaccctctt atcagagtag ttgctgccca agttggttca 121680

ctctgcacaa tccattttaa atttttgga gatacagcag tatttgctga cgttccagtc 121740

acagtttcag actgagttgc aactttaata acaccttctt gcgattcggt agatttagta 121800

cctaaaagct ttttaggagt tattaaaaca ttatctaatg ttcctgcagc agcttcaact 121860

tgtgtagcta cacgaagtgt accacgctgt gtctcatttg cttcaagaat attaagggta 121920

taatggtccc agagagttcc tgattcaact aatccagata gagcaacaac agaagtacga 121980

tcagtactat taaatctggt tttaattttt aatggtgtag agatacgagt atcgtcgacg 122040

cctgcgtcga attcaacttg cgtagcaatt tcagctatac cacttaaact ttcagttgct 122100

ctacggtcat ttaaagtttt aggagtgact gcgcgagtat aatcagttcc tgtattaact 122160

tcgctttgcg tagcaatttc aattaaacca attcttccat cagttgatgt ctttttatgt 122220

aacgtttctg gtgttacaac cgcatttgcc catccttctt ggctttgtcc agcaattact 122280

tcactttcaa ctgctaaaat tactgcgcct tgttgcgttg gagtagcttt atactgatcc 122340

aaagctttag gtgaaacaac taaattatta gtgtttttat tataaacatt cgtaccattt 122400

aattcacgac tagaagctgg agtagctcct gcggtagata caaaagttac aataccagat 122460

aatgattcag aaccttgacg agcttgaagc tttttaggag tgatgattgt agtatcatca 122520

gtacctgtat tagtttcctg ctgcgtagca atttcagcga cacctctacg agtttctgta 122580

gcagttcttt cattcagctt tttaggagtg atgataaggt catctgcaaa agagaatgtg 122640

gtgttctgat ttacttgagc agtagttgct attcttgcaa tacctctgcg agtttcagta 122700

gcagtacgat tagctaacgt ttctggagta attgccaatt ctttttgcgg agaattttct 122760

aaatcagcat ttgcttgagc ttgtgtagct aaagcaatta cgcctaatct tgctctagta 122820

gaagcattta aagagtctac tctttctaca gttggaacgt tttgctgtac aacccagtat 122880

tttccatcag aatcttctat ataagcaagt tgtaaaactg gaacataatt agtttcaccg 122940

ttaaaaacta attcttgaac tgttacccat tcagcttcag gcggatattc tgaacgtttt 123000

gggaattgca gcaattgaac tgaagaagca attttatctt caccagcagc tttgatttta 123060

actgtttgtc cttttctcat gtaattcatg gaaattttaa cagtatcacc aacagaaata 123120

tcagtcggaa gctgaagttc aattgtttgg gttgttccat tattcgcgcc aaataccatg 123180

acttcttcat ttggacgaat atttgaatta gttgttataa tgcgtaaacg tgctttacta 123240

tccccgtcaa acaatctcca caatttctca ttatcgtcaa acatcaagaa accgtcaatc 123300

gatgtacggc cttcaatgga atgagttcca acttcttgta ctgaagtcgt ttcatcgtat 123360

gtagtaacaa ttgtatgata aagtggattc agtttatcta aatcaacgaa attaataata 123420

tcgccatgat tagcaaatct cggaagttta acattaattg gtgcagcaga agtaaatcta 123480

cgtacgataa aatcattaga ttgtgcttga tacgcagtcg atggagtaac aatcgcagct 123540

tctctgctat aatcagcaac atacatttgc cacaaacgat tattaaaaat gaatatcatc 123600

tgtgactttg gatgagtcat taaaactgaa cgtacttgtt cacctctaaa attgacaata 123660

ctctgatttg aagaatttat tttaacctga tttatgccag gttttccacc gatatcttga 123720

attattacgg tttctccatc aagcggagaa ggtggtaaag taaactcaat gtcattgcca 123780

actgatgtat ctactgaaat tgcttctccg gattttaatt gatatggtcc agatgataca 123840

gttgtatata cagcatcagt acgtaatgct ttccaacgaa ttctattaaa atttccagca 123900

ggttttggaa tattatccgt tgctgcccaa aaacgattat tataaatgat tacaaaatct 123960

tttaaatatc cacgagttgg atcatattgc tgaactgtgt tttcttgaat taagtaatca 124020

acgttaacac cgtcagttcc tacggtacga tcagctaaag ctacgttgat tattttatcg 124080

ccacctgcgt ccagaccatc ttctgctctg aactttcttt taatctcggc cattctcccg 124140

ggctcctatt gtgttttcaa taataagtat ttatacctgt ttactttaag atttagatag 124200

tatataatag aaatctcact aattgaacga ggttcatatg gatttagaaa tgatgctgga 124260

tgaagattac aaagaaggaa tttgctttat tgactttagt caaattgctc tttcaactgc 124320

tctggtaaac ttcccagata aagaaaaaat taatttatcg atggttcgtc atttgatatt 124380

gaactcaatt aagtttaatg tcaaaaaagc aaaaacgctt ggatacacta aaattgtgct 124440

gtgtattgat aacgcgaaat ctggatactg gcgtcgtgat tttgcttact attacaagaa 124500

aaaccgtgga aaagcacgag aagaatctac ttgggactgg gaaggttatt ttgaatccag 124560

tcataaagtt atagatgaat tgaaagctta tatgccatac attgttatgg atattgataa 124620

gtatgaagca gatgaccaca ttgctgttct tgttaaaaag ttctctttag aaggacataa 124680

gattttaatc atttcatcgg acggtgactt tacacagctt cacaaatatc caaatgttaa 124740

gcaatggtca ccgatgcata agaaatgggt taaaattaaa agcggttctg ctgaaattga 124800

ctgtatgact aaaatcctta aaggcgacaa aaaggataac gttgcttcag ttaaagtacg 124860

atctgacttt tggtttacca gagttgaagg tgaacgaacc ccttcaatga aaacttcaat 124920

cgttgaagct attgctaatg accgtgagca agctaaggtg cttctcacag aatctgaata 124980

taatcgttat aaagaaaatt tagttctaat tgattttgat tatattcctg ataatattgc 125040

ttcaaacatt gtgaattact ataattcata taaattacca ccgcgtggca aaatttattc 125100

atattttgta aaagcgggtc tttctaaatt aactaatagc attaatgaat tttgaggtga 125160

ataatggcta aaaaagaaat ggttgaattt gatgaagcta tccatggcga agacttggct 125220

aaatttatta aagaagcatc tgatcataaa ctgaaaattt ccggttataa tgaactgatt 125280

aaagatattc gaattcgtgc taaagatgaa cttggcgttg atggtaagat gtttaatcgt 125340

ctattagctt tgtatcataa agataaccgt gatgtgtttg aagctgaaac tgaagaggta 125400

gttgaacttt atgacacagt tttctctaaa tgatattcgc ccggtcgatg agaccggtct 125460

ttcagaaaaa gaactttcaa ttaagaaaga aaaggatgaa attgcaaagc ttcttgaccg 125520

ccaagaaaat ggatttatta ttgaaaaaat ggtagaagaa tttggaatga gttatcttga 125580

agctacgaca gcattcttgg aagaaaactc tattcctgaa actcaatttg ctaaatttat 125640

tccttcgggt ataattgaaa aaattcagtc agaagccatt gacgaaaatc ttttacgtcc 125700

ttctgttgtt cgttgtgaaa aaactaatac attagatttt ctgctatgat taaactccgc 125760

atgcctgctg gtggtgaaag atacattgat ggtaaatcag tttataaatt atacttaatg 125820

ataaaacagc atatgaatgg aaagtatgat gtaattaagt ataattggtg catgcgggtg 125880

tctgatgccg cttatcaaaa gcgaagggat aagtattttt tccagaagtt atcagaaaaa 125940

tataaattaa aggaacttgc tttaattttt ataagtaatt tggttgctaa ccaagatgct 126000

tggattggtg acatctctga cgctgatgca cttgtgtttt atcgtgaata tatcggacgc 126060

ttaaagcaaa ttaaatttaa gtttgaagaa gatattcgca atatttacta ttttagtaaa 126120

aaagttgaag tttctgcttt taaagaaatc tttgagtata atccaaaagt tcaatcaagt 126180

tatattttta aactacttca atcgaatata atttcgtttg aaacgtttat cttgcttgat 126240

tcgtttttaa atataattga taaacatgat gaacagactg ataatttagt ctggaataat 126300

tattctataa agttaaaggc ttatagaaaa attttaaata ttgattcaca gaaagctaaa 126360

aatgttttca ttgaaactgt gaaatcttgc aagtattaat tgcttattat aaataagatt 126420

ataattatct cactgaccag ctatgaggtc atacatcgtc atagcaccaa ctgttaatta 126480

aattaaaaag gaaataaaaa tgtttaaacg taaatctact gctgaactcg ctgcgcaaat 126540

ggctaaactg gctggaaata aaggtggttt ttcttctgaa gataaaggcg agtggaaact 126600

gaaactcgac aatgcgggta acggccaagc agtaattcgt tttcttccgt ctaaaaatga 126660

tgaacaagca ccattcgcac ttcttgtaaa tcacggtttc aagaaaaatg gtaaatggta 126720

tatcgaaaca tgctcatcta cctacggtga ttacgattct tgtccagtat gtcagtacat 126780

cagtaaaaat gatttgtaca acactgacaa taaagagtac agtcttgtta aacgtaaaac 126840

ttcttactgg gctaacattc ttgttgtaaa agacccagct gctccagaaa acgaaggtaa 126900

agtatttaaa tatcgtttcg gtaagaaaat ctgggataaa atcaatgcaa tgattgcagt 126960

tgatgttgaa atgggtgaaa ctccggttga tgtaacttgt ccgtgggaag gtgctaactt 127020

tgtactgaaa gttaaacaag tttctggttt tagtaactac gacgaatcta aattcctgaa 127080

tcaatctgcg attccaaaca ttgacgatga atctttccag aaagaactgt tcgaacaaat 127140

ggttgacctt tctgaaatga cttctaaaga taaattcaaa tcatttgaag aactgagcac 127200

taagttcagt caagttatgg gaactgctgc aatgggtggt gccgctgcaa ctgccgctaa 127260

gaaagctgat aaagttgctg atgatttgga tgcattcaat gttgatgact tcaaaacaaa 127320

aactgaagat gattttatga gctcaagctc tggcagttca tctagtgctg atgacacgga 127380

tctagatgac cttttgaatg acctttaaca gattatatta ctaattaatt ggggacccta 127440

gaggtcccct ttttatttca aaaatttttt cacaaaactg tttacatcct tgtccttcca 127500

tggtactata caactatcgg caatactgct gataattaaa gaggaaaata atatggctaa 127560

agttgatatt gacatcgttg attttgaata tattgaagaa attattcgta atcgttatcc 127620

tgaacttagt atcacaagta ttcacgatga tcccaattat tgcaattttt ctattgtcat 127680

tgaaggtcct cttgaagacc tcacccgctt tatggctaat gaatattgtg atggtatgga 127740

ttctgaagac gcagaatttt acatgggatt gattgaacaa taattatcaa ggggctatta 127800

caagccccgt taaaatgagg aaaacgtaat gtatattggc aaaaagtatg agcttgttcc 127860

aagacttatt gatacattta ttaattatcg cccacgttct aattcatcga tagttaaaat 127920

tattcaagaa aatggtggat ggtttgaagt taaagaagct ttctttgttg atggatttag 127980

agtaataaaa cacattgaat gcgcaaatgg aaagcatttt tactttaacg tttgtgaaga 128040

cgaatttcat tgttttcgtg agtataaaga accgacttct gaagaagatg gagccgaaga 128100

catagtttct ggcgtaacaa aaattcactg cattgttgac gaaaataatg tagatgaaat 128160

cattgaactt ttgcgaaaaa ctttcaaaaa gtagtttaca acagggtagt agtgtgatac 128220

tattacccta tcaaaactaa tggagaaaag aaaatgttcg caccttatat tatggcagca 128280

gttatgttgg tctgtttata tcttttgatt aaagcttgct aaggagaata aaatgagatt 128340

acaacgccag agcatcaaag attcagaagt tagaggtaaa tggtatttta atatcatcgg 128400

taaagattct gaacttgttg aaaaagctga acatctttta cgtgacatgg gatgggaaga 128460

tgaatgtgat ggatgtcctc tttatgaaga cggagaaagc gcaggattct ggatttatca 128520

ttctgatgtt gatcagttta aagctgattg gaaaattgtg aaaaagtctg tttgaggaaa 128580

ataatatgtc tggcattcat gtaactggaa ttgctcaagt aaacatccgc tgccaattta 128640

aaactgtacc tggggtgact catattactt tatcacacga cccatattct cgtggaagac 128700

agttaactgg cgtaattaag tttttcggcg gaattggcgg aagcgaattt actataggag 128760

atgacgaaat tgttggctgt aaattaaaag ttcagaaggg cgtgttagaa ctttttagtg 128820

atgaagtttt tgatgaaatc tcacgagcag ttaacaaagg aatgttaacg ttaattaaaa 128880

tgattaaagc tagcggatat gttactgatc ctttttaata ggaggcaata tgatttttgt 128940

atttgaattt atgaatgatg aattcgatta tgcaattttt aacgcattgc ataatcctga 129000

tttaagtgaa tttaatgaaa tgttttctga cgctttgagt atgtcagaag aatactgtgg 129060

agaatgtcaa cgtgtttgtg tgacagtctt tgaaaacaaa gaaaagacct atgaagaatt 129120

attctttgat gctaataaag ccactgaatg gtttgttgaa agaggttttg cgtaatgatt 129180

aaattggtat tcgcttattc tccaactaaa acggtcgaag gctttaatga attagcattc 129240

ggtttaggtg atggtttacc atggggacga attaaaaagg acctccagaa ttttaaagct 129300

cgtacagaag gtacaatttt gattatgggt gctaaaacgt tccagtcatt atctacatta 129360

cttcccggtc gtagccatat tgtggtgtgt gaccttgcgc gtgattatcc tgtaactaaa 129420

gacggcgatt tagcacattt ctatattact tgggaacagt acataactta catttctggc 129480

ggcgaaattc aagtttcaag tcctaatgca ccattcgaga ctatgcttgg tcagaattcc 129540

aaagtaagtg taattggcgg gcctgctctg ttatatgctg cgttacctta tgcggatgaa 129600

gtagttgttt ctcgcatcgt taaaaggcat cgtgttaatt caacggttca attagacgca 129660

agttttcttg atgatataag caagcgtgaa atggttgaaa cgcattggta taaaatagat 129720

gaagtaacaa cccttacgga atcagtatat aaatgagcaa taaattaaaa gttaaggatg 129780

ttcctaatgc tatggccctt tttatttgta ggcagatgca tcaagggcct atgacaccaa 129840

aacaatatct taaaggtgag cgttctttag gatttactcg caaagcaaaa caaatggtta 129900

aattaggata taagcctaac tttgccaaat atccttctac atattcttgg atgaactaat 129960

gaaacaatac caatttttaa ttaaagatat cctggaaaat ggctacgaaa ccgatgaccg 130020

aacaggcaca ggaacaattg ctttgttcgg tactaaatta cgctgggatt taactaaagg 130080

ttttcctgca gtaacaacta agaagctcgc ctggaatgca tgtatttctg agttattgtg 130140

gttcttatca ggaagtacta acgtaaatga tttgcgatta attcaacata attcattaat 130200

tcaaggcaaa acagtttggg atgaaaatta cgaaaatcaa gcaaaagatt taggatacca 130260

tagcggtgaa cttggtccaa tttatggaaa acagtggcgt gattttggtg gtgtagacca 130320

aattatagaa gttattgatc gtattaaaaa attgccaaat gataggcgtc aaattgtttc 130380

agcatggaat ccagctgaac tcaagcagat ggcattaccg ccttgtcata tgttctatca 130440

gtttaatgtg cgtaatggct atttggattt gcagtggtat caacgatcag tagatgtttt 130500

cttgggttaa ttgaggcctg agtataaggt gacttatact tgtaatctat ctaaacgggg 130560

aacctctcta gtagacaatc ccgtgctaaa ttgtaggact gccctttaat aaatacttct 130620

atatttaaag aggtatttat gaaaagcgga atttatcaga ttaaaaatac tttaaacaat 130680

aaagtatatg taggaagtgc taaagatttt gaaaagagat ggaagaggca ttttaaagat 130740

ttagaaaaag gatgccattc ttctataaag cttcagaggt cttttaacaa acatggtaat 130800

gtgtttgaat gttctatttt ggaagaaatt ccatatgaga aagatttgat tattgaacga 130860

gaaaattttt ggattaaaga gcttaattct aaaattaatg gatacaatat tgctgatgca 130920

acgtttggtg atacatgttc tacgcatcca ttaaaagaag aaattattaa gaaacgttct 130980

gaaactgtta aagctaagat gcttaaactt ggacctgatg gtcggaaagc tctttacagt 131040

aaacccggaa gtaaaaacgg gcgttggaat ccagaaaccc ataagttttg taagtgcggt 131100

gttcgcatac aaacttctgc ttatacttgt agtaaatgca gaaatcgttc aggtgaaaat 131160

aattcattct ttaatcataa gcattcagac ataactaaat ctaaaatatc agaaaagatg 131220

aaaggtaaaa agcctagtaa tattaaaaag atttcatgtg atggggttat ttttgattgt 131280

gcagcagatg cagctagaca ttttaaaatt tcgtctggat tagttactta tcgtgtaaaa 131340

tctgataaat ggaattggtt ctacataaat gcctaacgac tatccctttg gggagtaggg 131400

tcaagtgact cgaaacgata gacaacttgc tttaacaagt tggagatata gtctgctctg 131460

catggtgaca tgtagctgga tataattccg gggtaagatt aacgacctta tctgaacata 131520

atgctaccgt ttaatattgc atcatatgct acgttagttc atattgtagc taagatgtgt 131580

aatcttatcc caggagattt gatattttct ggtggtaata ctcatatcta tatgaatcac 131640

gtagaacaat gtaaagaaat tttgcgtcgt gaacctaaag agctttgtga actggtaata 131700

ggcggattgc cttataaatt ccgctatctt tctactaaag aacaattgga atacattctt 131760

aaactcaggc ctaaagattt cgttctcaaa gattatcagt cccacggcgt cttgaaagga 131820

aaaatggcgg tgtaatttca atttaattgc gaggatatat gattttacga tttaaagata 131880

cttctggtgc agttcttttt acacttccta atccaagtga gctagaagtt ccaggaccaa 131940

atcagcctat tatcatttat ggcaaaaaat attatactca taaaatgact cgtgagtatt 132000

ttgataataa aatttctaca gttaaaactt cttctgattg ttactatgat attactgttt 132060

taacggaaaa acaatatgac gaattatcac cgcgcgggcc gtctatgcca ggtagtgaat 132120

aaatataaat ccgactttga tgtcaatatt caccgcggta cattttgggg aaattacgtc 132180

ggtaaagatg ctggcagccg ggaggctgcc attgaattat tcaaaaaaga ttttatacgt 132240

cgaattaaat ccggagaaat aactaaagca catttagagc ctttacgtgg aatgaggcta 132300

ggatgcacat gtaaaccaaa gccgtgtcat ggtgatataa tagctcatat agttaaccga 132360

ttgtttaaag acgattttca agttgaggac ttatgcaatt aattaatgtt atcaaaagta 132420

gtggtgtttc tcagagcttt gacccacaaa aaattattaa agttttatct tgggcagctg 132480

aaggaacatc agtagatcct tatgaattat atgaaaatat taaatcatat ctccgtgatg 132540

gaatgacaac tgatgatatt cagactattg tcattaaggc cgctgcgaat tctatttcgg 132600

ttgaagaacc tgattatcaa tatgtagctg cacgttgttt aatgtttgct cttcgtaagc 132660

atgtttacgg gcagtatgaa ccgcgttcat ttattgacca tatttcttac tgtgtaaatg 132720

aaggtaaata tgaccctgaa ttgttgtcaa aatattcagc agaagaaatt acatttttag 132780

aatcaaaaat taagcacgag cgggatatgg aatttactta ttccggggcg atgcaattaa 132840

aagaaaaata tctcgttaaa gataaaacca ctggtcaaat ttatgaaact ccgcagtttg 132900

catttatgac tattggaatg gcattgcatc aagatgaacc tgttgataga ttaaaacatg 132960

ttattcgttt ttatgaagca gtatctactc gacagatttc attaccaact cctattatgg 133020

ctggttgtcg tactccgact cgacagttta gttcatgtgt tgttattgag gcaggtgatt 133080

cgctgaagtc tatcaataag gcttccgctt cgattgttga atatatctct aaacgcgctg 133140

gaattggtat taacgttggt atgattcgtg ccgaaggttc taagattggc atgggtgaag 133200

tacgccatac tggtgttatt ccttttgga aacattttca gactgcagtt aaatcatgtt 133260

cacagggtgg aattcgtggc ggcgctgcta ctgcttatta tcctatttgg catttggaag 133320

ttgaaaatct tctcgttttg aaaaataaca aaggcgtaga agaaaaccgc attcgtcata 133380

tggattatgg tgttcaactg aatgatttga tgatggaacg attcggaaag aacgattaca 133440

ttactttgtt cagtccgcat gaaatgggtg gagagcttta ttattcttat tttaaagacc 133500

aagaccgttt ccgtgaatta tacgaagcag cagaaaaaga ccctaatatt cgtaaaaagc 133560

gtattaaagc ccgtgaacta tttgaattgc tcatgactga acgttcagga acagcaagaa 133620

tttatgtaca gttcattgat aatacgaata actatactcc gtttattcgt gaaaaggcac 133680

ctattcgtca gagtaacttg tgctgtgaaa ttgctattcc aacaaatgat gtgaatagtc 133740

ctgatgctga aattggattg tgtactctct ctgcattcgt actagataat tttgactggc 133800

aagaccaaga taaaattaat gaattggcag aagttcaagt tcgtgctctt gataatcttt 133860

tggattacca aggatatcca gttcctgaag cagaaaaagc taaaaagcgt cgtaacctcg 133920

gtgtaggtgt taccaactat gcagcttggc tggcaagtaa ctttgcttct tatgaagatg 133980

ctaacgattt aacacatgaa ctatttgaga gattacagta tggactcatt aaagcatcca 134040

ttaagctcgc caaagaaaaa ggaccttgcg aatattattc agacactcgt tggtctcgag 134100

gcgaattacc tatcgactgg tacaataaaa agattgacca aatcgcagct ccaaaatacg 134160

tttgtgactg gtcgtcgctg cgggaagacc ttaagctctt tggcatccgt aatagcacac 134220

tatcagcact tatgccatgt gagtcatctt cccaagtttc taacagtaca aacggtatcg 134280

agcctccacg tggaccagtc tctgttaaag aatcaaaaga gggttccttt aatcaagtcg 134340

tgcccaatat tgaacataac atagacctat atgattatac atggaaatta gctaagaaag 134400

gtaataaacc ttatcttacg caagtagcta ttatgctgaa atgggtatgt caatcagctt 134460

cagcgaatac atactatgac ccgcagattt ttccaaaagg aaaggttcca atgtcaataa 134520

tgattgatga ccttttgtat ttttggtatt ttggcggaaa aaatttctat tatcataata 134580

cccgtgatgg ttctggtact gatgattatg aaatagaaac tccaaaagct gaagattgtt 134640

catcctgtaa attatgatat aatttgactc acggacgagt caccaactat taactaagcg 134700

gaaaatttat gagcacagtt tttaatacaa atccagttga tgttttaaaa gaacctatgt 134760

tttttggttc aggtcttggt attgcgcgtt atgatattca acgccataaa gtttttgaag 134820

atttgaccga aaagcaatta tcatttttct ggcgtcctga agaagtaaac ttaatgatgg 134880

atgctgcaca gtttaataag cttcctcaat atcagcagaa tatttttact aataatctga 134940

agtatcaatc acttctagat agcattcagg gtcgtgcacc gtctgctgta cttatgtcat 135000

tgatttcaga cccaagcctt gatacatggg ttgctacatg gacttttagt gaaactattc 135060

acagtcgttc atatactcat atcatgcgaa atctttatac tgatccatcg aaggtatttg 135120

atgaaattgt attagatgaa gctattatga aacgtgctga atctattgga cgttattatg 135180

atgatgttct gattaaaact cgttattggg aaaacgctaa agctgatatc gaataccaaa 135240

aagaaattaa tgcagacgaa gacgttattg aagatgctat tgagcatgag acatattgga 135300

agcgtgagct aatgaaatct ctttacctct gtttgcatgt aatcaacgca ttggaagcta 135360

ttcgttttta tgtatctttt gcatgtacct ttaacttcca taagaacatg gaaatcatgg 135420

aaggtaatgc caagattatg aagttcattg cacgtgatga gcagcttcac cttaaaggca 135480

cccaatatat tattcgtcaa cttcaacttg gcactgatgg cgatgaatgg gttaaaattg 135540

ctcaagagtg tgaacaagaa gcagttgata ttttcatgga agttaaccgc caagaaaaag 135600

attgggcagt tcatttattt aaagatggtg atgttcctgg attaaataca aatagcatgt 135660

ggagctttat tgattactta actgtatctc gtatgaagca gtgtggtctt ccatgcccaa 135720

ttaccgatgc tccggttaaa catccatatc cttggattcg tgaatatctt aattctgata 135780

atgttcaatc tgcgccacaa gaagtagaat tgtcatctta ccttgttgca cagattgata 135840

atgatgttga tgataaagtt atgatgagtt ttaaaaaata cttttaagga gtgggccgca 135900

aggcccattt tattatgaaa gaaattgcaa cagaatattc atttattaaa tatactgagc 135960

tagaattaga ctacaacgga agtataaaac aattatctat tccaaacaag tataacgtaa 136020

tttatgctat tgctataaat gatgaacttg tttatattgg aaaaactaaa aatttacgca 136080

aaagaataaa ctattataga actgctatta accgtaaaga caaaacgtct gattctacta 136140

aatctgcatt aattcatgct gcgctaaagg aaggaagcaa agttgaattt tacgcccgcc 136200

aatgttttaa tctttctatg acaaatgagt taggtacaat gacaatcgcg acgattgacc 136260

tagaggaacc actattcatt aagctgttta acccgccttg gaatattcaa cataagaaaa 136320

aatgatgctt ccacatggag tgtggtacta tattcaaaac acaaaagagg atacacaatg 136380

caagaacttt ttaacaattt aatggaacta tgcaaggatt cacagcgtaa gttttttac 136440

tcggatgatg taagtgcgtc tggaagaact tacagaattt tctcatataa ttatgcatct 136500

tattctgatt ggttacttcc agacgcattg gaatgtcgtg gaatcatgtt tgaaatggat 136560

ggagaaaaac cagtaagaat tgcttctcgt cctatggaaa agtttttaa cttgaatgaa 136620

aatccattca cgatgaatat cgatttaaat gatgttgatt acattctaac aaaagaagat 136680

gggtctttgg tatcaactta tttagacggt gatgaaattc tgttcaaatc aaagggttca 136740

atcaaatccg aacaggcttt aatggctaat ggtattttga tgaatattaa tcaccatcgg 136800

ttgcgtgata gacttaaaga attagctgaa gatggattta ctgctaactt cgaattcgtt 136860

gctccgacga atagaatcgt tcttgcttac caagaaatga aaattatttt actgaatgtt 136920

cgtgaaaacg aaacgggtga atacatttca tatgatgata tttataaaga tgctgctctt 136980

cgtccatatc tagttgaacg atacgaaatc gatagcccta aatgggtaga agaagctaaa 137040

aatgcggaaa acatcgaagg ctatgttgct gtgatgaaag atggttctca ttttaaaatt 137100

aagtctgact ggtatgtgtc tcttcatagc acaaaaagtt cattagataa tccagaaaaa 137160

ttgtttaaga ctattattga tggtgcatca gatgatctta aagcaatgta tgctgacgat 137220

gaatattcat acagaaaaat tgaagcattt gaaacgactt atctgaagta cttagaccga 137280

gctctgtttt tagttcttga ctgtcataat aagcattgtg gtaaggatag aaagacttat 137340

gcgatggaag cgcaaggtgt tgctaaaggt gctggaatgg atcacttgtt cggtatcatc 137400

atgagcttat accaggggta tgatagtcaa gagaaggtta tgtgtgaaat cgaacagaat 137460

tttttgaaaa attataaaaa atttatccca gaaggatact aagctgttta caagtccctc 137520

gtgttgtgtt acagtagtct tactgacata acatgaggac tttatgatgg atttgcagct 137580

cattactact gaaatggtcg ttgaagcata cggtgatact acagatggga tttctgtatt 137640

taaaggaaac cgtcgagttg gatatatcac cgatcttaag aaagatttag ctaagcaagt 137700

caagcggaaa acgaccatta aagaatatcg aaatcgtcgt cttgagcaag cccgtgatat 137760

gcttcctgat gcggttgaag agatgaaagt ctttttagaa aatcagcttg cgaaatatga 137820

ttgtgatgta tttattaatc agactcaacc taatgttcat atcaatagtt gtaaatgcta 137880

tatcatcgtt aatcctttga ctggaaagca tcgtcttgga attagtaatc caaatcgtag 137940

tgcatcggat atggcagaag atgttgaggc atgctttaaa atttctaaat ctccagctga 138000

acatcatatt ttaattaacg gtctttctca agacgatatt atagaggtta ttaaaacttt 138060

atgcatgtaa gtaattttac agctggattg ctattacttg taatagcatt tggcggaaca 138120

tctattattt taaaaaataa ggtagaaaga ttagaaacat cagttactga aattacaaaa 138180

acagccaatg aaaacgcctt agcattaaat aatttgcgaa ttcagtataa ttatattgat 138240

gcgatgaata ataaaaatcg tgaggcaatt gctgctattg agcgtgaaaa tgaaaaactg 138300

cgcaaagacg caaagaaggc ggatgtggtg gctcataagc caggattggt tgaaaaacaa 138360

atcaacaact ccttcaacaa gttcgcagaa gacatccagg acctttctaa atgattaaac 138420

tatcagcagt aatattatct attggtcttc tagttggttg ttcgacaaag cctctagaag 138480

taaagaaaga aacagttcat cctaattggc ctgtgcaaat aaagtcatat gacgaagcta 138540

aactatcttg gcaagttaaa gttattgatg gtaaagcttg ggtaggtatg ccatttgaag 138600

attctcagga atttcgtatt tggcttaatg atgtaaaacg atatgtacat gaccagaaaa 138660

ctatgatatg ttattatcgt caagagctaa aagaggataa atgtaaatga tttcatggta 138720

tcaatttgaa catctaaaag gattaattta tgaatccgag atggctgcaa tgatttatgg 138780

acgacagatt caacgattag aatctttacc tccaactaat gatgttttat tagctcaatc 138840

acgtgctaat ctcaaaaatg aatatcaaaa taagtggggt aaagcatcta aagacttgca 138900

tgattatatt caatcattag ttgagaaaaa taaatgaaaa ctctgctaga acgttatatt 138960

gaatgctcgg accgttacat tgatgtatgc catgacaatg catcaagcat tagcgaagac 139020

attgaacatg ctaaagcttt agatgatgct ggtaaagccc tacgaaaaga agcaaaagct 139080

cgtgggtttg atatgtatca gcttaaaaat cacatgataa aatttatttc atctaatgtt 139140

cagagcaaat cggtgaatca atcaacagct gaattatata aagggcggcg tgagcataat 139200

attcgtattc ttgaagtttt cttaggaatt aaatgatgaa aaagattatt ttgactattg 139260

gctgtcctgg ttctggtaag agtacttggg ctcgtgaatt tattgctaaa aatccagggt 139320

tttataatat caatcgtgat gactatcgcc aatctattat ggcacatgaa gaacgcgatg 139380

agtacaagta taccaaaaat aaagaaggta tcgtaactta catgcagcat gatgttgcta 139440

acatgattct ctgccaagac gcaacgaagg gtgtaattgt ttcagatact aatctgaatc 139500

ctgaacgacg taaggtttgg gaagagtttg ccaaagagct tgggcatcaa attgaatata 139560

aagtgtttga tgttccttgg actgaattgg ttaaacgtaa ctcaaaacgc ggaactaaag 139620

cagtaccaat tgatgtttta cgctcaatgt ataaaagcat gcgagagtat ctcggtcttc 139680

cggtatataa agggactcct ggtaaaccaa aagcagttat ttttgatgtt gatggcacgt 139740

tagcaaaaat gaatggtcgt ggtccttatg accttgaaaa atgcgatatc gatattatta 139800

atccaatggt cgttgaacta tccaagatgt atgctcttat gggttatcaa atcgtagtcg 139860

tttcaggccg tgaaagtgga accgaagaag atccaacgaa atattatcgt atgacccgta 139920

aatgggttga ggacattgct ggtgttccat tagtcatgca gtgtcaacgc gaacaaggcg 139980

atacccgtaa agatgatgta gttaaagaag aaatttttctg gaaacacatc gcaccacatt 140040

ttgatgtgaa attagctatt gatgaccgaa ctcaagtagt tgaaatgtgg cgccgcatcg 140100

gtgttgaatg ctggcaagtc gcttcgggag atttttaatg gcttggcacc atgaaacttg 140160

ggctttgtta ttgtaaatag cggtttagtt ggtactagta atgggcaatt ttgtgtattt 140220

actagtgaaa atagagcatg ggaggaatgc cttaaattaa gagaaaagaa tcctgatgtt 140280

gaactagtag taaagaaaac taaactgcct ttaccatgga aaacgtatga ataacctaga 140340

aaagatttat cgtctttgtg ataaaattga aaaagaaaag aaatatctat tttgtctatg 140400

gcctattgtt gacggaagag taggcctaga tgttcttgat tatgaaacag aagacaaagt 140460

agatggcgca acttttgata acgctttgga tgttattgat tggctcgaag aaaattatgt 140520

gaggtaaata tgtttccgac ttactctaaa atcgtagaag tagtgtttag ccaaattatc 140580

gctaataaca tgtttgaaaa gcttgataat gcagctgaac ttcgaatcca cgctcaagtg 140640

actcatgtat tgaacgcttt gcttccagac caggtggatt ctattgccat tacgttgtat 140700

ccaggttccg cgcatatcat tgttgtattt ggtcttgatg ctgagctagt tatcaaaggc 140760

gacattcgct ttgaatcaca gacatcagaa ttcaaagcaa tttaatagtt tactttacgg 140820

tagagttgtg atattatagc tctaccaaaa caaatgagga aattgaaatg agcgaatggt 140880

ttgaagaaga taaggtttat cgctttaaag ctggatataa agatattttt aatgaaactt 140940

gcggggctaa taaacgaatt gcccagttta ttggggaaaa ttcatttaaa gtaaaaatag 141000

atcctgcgaa aaatgttatt agcattaaac gtgaaattga tgattgttgg tataaagctg 141060

ttgatgtaat gggtgaatcc tataaagtta gcccgttatt ttcaattgct tatatgttag 141120

aatattcttt tttcgaagaa gttcaaaaag atgattctgt aagtaaattt gaaattaaaa 141180

ctgataaaga aattaagtgg aaagtagtag gtattactgg ttgtatgttc tatatctatg 141240

ctcaaactga tacgaaggaa gaagctaaaa agaaagctct agaatatctt gaagagcatg 141300

aagaaggtcc ggtaatgatt acccaagatg ctgaattagt ttctgtcaaa ttagttaaaa 141360

atgttgaaag taaggagcta ggatcaacat gctaagcgaa aaaccaatta ctgttaaaga 141420

attccaagaa aaagttaaac tatttgctca agaattggta aataaggttt ctgaacgatt 141480

tcctgaaacg tcggttcgtg ttattaccga aactcctcgt tcagtattag taattgtgaa 141540

tccaggtgat ggcgatcaaa tatcgcatct taaactggat tttgatggat tagttgaagc 141600

acaaagggtg tatggcgtac tatgatgaat ttaactgata taattgataa ttgtcttgaa 141660

aatgatactg gcgatcatag agcgcttgat tctgaaacag cacagttcat tagaataact 141720

ttaatgaatg atactctggt gaatagtatt catccttctg tgtatgatgc tattattgtg 141780

acgaagtatc cggttgagct tcacaaaaag atgactggcg cagtttttat tgataagaaa 141840

aaccgcttta aagatgggca gaatataact agttctgtta ttaaaagtat aactaaactt 141900

cgtcacgaaa tttatcgtgt tgaaactgct aaatctgctt atctggtgat tatgaaatga 141960

aagcgagtac agtacttcaa attgcatatt tagtatcaca ggaatcaaaa tgttgctcct 142020

ggaaggtagg agcagtaatt gaaaagaatg gacgtattat ttctactggg tataatggtt 142080

cacccgcagg cggtgtgaac tgttgtgatt atgctgctga gcaaggttgg ttgctgaata 142140

agcctaaaca cactatcatt caaggccata agcctgaatg cgtatcattt ggttcaactg 142200

atcgctttgt cttggcgaaa gaacatcgta gtgctcactc ggaatggtca tctaaaaatg 142260

aaattcatgc tgaactaaat gcaattttgt ttgctgcacg aaatggttct tctattgaag 142320

gcgctactat gtatgtaaca ctttctcctt gtccggattg cgcaaaagcg atagctcaat 142380

ctggtattaa aaagctggtt tattgtgaaa catacgataa aaataaacct ggctgggatg 142440

atattctgcg aaatgcaggt attgaagtgt ttaatgttcc taagaaaaac ttgaataagt 142500

taaactggga aaatatcaac gaattctgtg gtgaataatg aaatttcgtt tggtaaagct 142560

cacagcaatt agttcttatt ctaacgagaa catctcattt gctgtagagt ataagaaata 142620

ttttttctct aaatggaaac agtattataa aactgattgg actagtattg ataggccata 142680

tagttggaaa tctgatttag aaaaatgcca aaaattactt tccactctta aagaacgtgg 142740

aacaactcat attaaaactg taataggtaa atgaatgaaa ctgacgactg aacagaaagt 142800

agcaattcgt gaaattttga aaactaaatt gtccatgggt atttcaaacg tagttttga 142860

aaagtctgat ggtactattc gtattatgaa atgtactcgt gatgcagact ttatgccaac 142920

catgcaaact ggtaaattga ctgaatctac tcggaaagaa tctactgata tgattccagt 142980

atttgatgtt gaacttggtg cgtggcgagg tttttctatt gacaaattga tttccgttaa 143040

tggtatgaaa gttgagcatt tgctccaatt tattggtaaa taaatgcttt aagaattatt 143100

tgttattatt aattcatctg ttaacaaaaa ggaaaaacga tgtctgaagt acaacagtta 143160

ccaattcgtg ctgtcggtga atatgttatt ttagtttctg aacctgcaca agccggtgat 143220

gaagaagtta cagaatcagg acttattatt ggtaaacgta tccaaggcga agttcctgaa 143280

ctgtgtgtag ttcactctgt cggtcctgat gttcctgaag gtttctgcga agttggtgat 143340

ttgacttctc ttccagttgg tcaaattcga aatgttccgc atccttttgt agctctgggt 143400

cttaagcagc caaaagaaat taaacaaaaa tttgttacct gtcactataa agctattccg 143460

tgtctttata agtgatataa ataataatat gaattgggtg tcggaataat aagttaaccg 143520

aacaattcta tgtggtagtc tacaactgag agatctgtcg aaagaagatg aaattcagaa 143580

gaacgtgact accgagtttt aatctctaac gagaattttt aaatgattaa acaattacaa 143640

cacgctcttg aactgcaacg aaacgcatgg aataatggtc acgaaaacta tggcgcatct 143700

attgatgttg aagccgaagc tcttgaaatc ctgcgttatt tcaaacatct gaatcctgct 143760

caaactgcat tagctgctga gcttcaggaa aaagatgaac ttaaatatgc taagcctctg 143820

gcttctgctg cacgaaaagc agttcgtcat tttgtggtaa cactgaagta atttattgga 143880

gattcactgc cttagtgtga gctaaatcga ggagccgtcg aactgtctga ttaatgattt 143940

gcgaatcatt atagttttaa gaccccggca gttttacggt gtacctcttg aatgttattt 144000

tatagcggca agtgcatgct accccgaggt gatggccaat cgggagtacg cctcaaggcc 144060

tatatatcca tcagtatata tcttatcctc gagtaatcgg acccggaacc tttaagctaa 144120

cggtgtgcaa cagataagag ctataaggta tgttgacgag gtttatggtt atcctgtcgg 144180

taaatattca aaacctaagt acccctttga gggattgcgc aggcaatgcc aataagtcct 144240

gcattttcat ttaaaagaga atttataatg gcaaaacaag ttaaagcaaa gaaagcagtt 144300

gaaaagaaag ttggtgattc taaacgcgct ggctacaagc gtgggtcgaa ctctcgtatc 144360

aatcaaactg ttgagaagat catgcgccga gcacgtgcgg ttcttcgaga tgatgcttct 144420

cgttttggta agcagaaagc ataagttgag gactccttcg ggagtccttt tttattttcc 144480

aaagattgca caaagttgtt tacagtacgg ttcctttgtg atagtattat cttacacaaa 144540

caaaggagaa taaaatgaac tacatcaact ttgaacgtaa atatgtttct aatggtattg 144600

caggttctat tgatactatt tgtctctgga aacatcaaaa cggatcagta tgcgaaatcg 144660

atcagtatat gactcctaat tacgtttata tgcgatttga aaatggcatc acggtttcaa 144720

tcactaagga aggttccaac tttaaaatcg ctctagatga tgatttccgt gaacgcgatt 144780

tagggactca tccttgttgg aatggcgttc atcgcaagct tctgattaaa acttggattc 144840

gtcatattct gagtaacaaa gctaaacctg agcatcttga agcaatcttt gatgtagttc 144900

ttaacgaatt tgatatttaa gcttcggccc cttactgagg aaaatattat gtttatgact 144960

acttattttg atacccgcaa aaatttctgt gaagttgttt tctcaaaggc gcctaaagac 145020

cttcctgcac atttgcaacc taccagtgaa tcgattaaaa actacgttaa tgtagtctgc 145080

cctttagagt tccgtactgt aaatgggcgc gatactttag ctatcactaa actcaatcgc 145140

gaaattgaca ttgatccctc aattgcacgt gaaattaata gttctgatat taatggcggt 145200

aatgttaaat cgcacggttt tcagatgagg ttttaatgaa attcttttta ggtcaaactg 145260

ttgaattaaa gggagttggt atacctggat taatttctaa ggttctacct ccgtttaaat 145320

ggagtggtat tcaaataaaa gaggcttata ttgtttcttg ggtagatgga aatgaagacc 145380

ttcgtatggg cgatgaatta tctcctatct acggattaaa ggaattagta tgaatataat 145440

taataagatt tttggaattc agtacattaa ggtcacatat aaagtaacag ataaaaatcc 145500

gtatactgat gaacacgaag aaccgcaagt taagtctatt atattagaaa aaggcagtga 145560

ctggccagtt gaatttcgtc taccaaacta tggtcattgg gctgatgttg aaattataag 145620

cattgaaaat gtctgagtta gagattagaa gcaattttaa atggccatca tgtgcattaa 145680

gtaatttcgc ccaatggcct ttcgttatgg atggtattca atttggaggt cttgaaggat 145740

tcctccaagg atgcaaggtg aaaaatgttg aacaacaacg tcgtatattt gggttatccg 145800

ggcttgccgc ccaacaagct ggaaggtctt atgctagagc tcaggaccgt gggaccctct 145860

tctggcttgg agttccgttt tcaagatact ccccagcatg gaaagaatta tacacaaatg 145920

catattttga agcagcgatc caaaacaagg gctttcgtga tgcattacac gcctcgaaag 145980

gaaaagtttt gaagcacagc atggctagtg gtctaacaaa agatgataca atattaaccg 146040

aagctgaatt tattgatgtg ttaaacctat taagagactc tctatgaagc ctactatttt 146100

aactgatatt gatggagtat gtttaagctg gcaatcaggc cttccttatt ttgctcagaa 146160

atataatctt ccgttagaac atattttaaa aatgatccaa gatgagaaat ttatttctcc 146220

aggtaaactc tttaattgtg acgaagaact tggcgtcaag ttaattgaaa aatacaatcg 146280

ttcagatttt attcgttact tgtctccata taaagatgct ctgtgtgtaa ttaacaaatt 146340

aaaagaagat tataattttg tagctgttac agcattgggt gattctattg acgctctgct 146400

gaatcgtcaa tttaatttga acgctctttt tcctggtgcc ttctcagaag tactgatgtg 146460

tggtcatgat tcttcaaaag aagagttgtt taaaaaggca aaagagaaat ataacgtgat 146520

ttgttatatt gacgatctcg ctcaccattg cgatcatgcg agtgaaatat taaatgttcc 146580

tgtttattgg atggctcgag gggaacgtga cagtattcca aaaactgcac agcgagttta 146640

tacatggaat gatgtagaaa ataagctttt ttcaccaaag gaaaataaag aaagttttga 146700

tagtgaaaaa gctataaaag atgtaattga gaagatgatc aaaaacgatt cttttccttg 146760

gaacactacc tggagaactc ctggatttaa tccttataat catctatatc atccatatca 146820

gacacatccg tttcagacat ggaactatat taaacctggt ggcatagagt atttgtataa 146880

tagacctact agtggtgata atattttcca aggagcattc taatgtttgt tgttcatact 146940

atttatgaaa atgaaggtaa tactacacgt gattacggtc acgtaaatca atttttaga 147000

tgcaatccag aattccgagc tcaaaaagac gaacgaattt ttaaaaaatg tgtagagcaa 147060

ggtttcattt acgtcaagca ctggatgcaa ggaaataaag ttagaaccac gtaccacagg 147120

tctttgactg agcttaatga tgaattgatt tataatagag ctgtaaacca aactctaaag 147180

gatgaacaat gattcttaaa attctgaacg aaatagcatc tattggttca actaagcaga 147240

agcaagcaat tcttgaaaag aataaagata atgaattgct taaacgagta tatcgtctga 147300

cttattctcg tgggttacag tattatatca agaaatggcc taaaccgggt attgctaccc 147360

agagttttgg aatgttgact cttaccgata tgcttgactt cattgaattc acgttagcta 147420

ctcggaaatt gactggaaat gcggcaattg aggaattaac tggatatatt actgacggta 147480

aaaaagatga tgttgaagtt ttgcgtcggg tgatgatgcg agaccttgaa tgcggtgctt 147540

cagtatctat tgcaaacaaa gtttggccag gtttaattcc tgaacaacct caaatgcttg 147600

caagttctta tgatgaaaaa ggcattaata agaatatcaa atttccagcc tttgcccagt 147660

taaaagctga tggagctcgg tgttttgctg aagtcagagg tgatgaatta gatgatgttc 147720

gtcttttatc acgagctggt aatgaatatc taggattaga tcttcttaag gaagagttaa 147780

tcaaaatgac tacagaagct cgccagattc atccagaagg tgtgttaatt gatggcgaat 147840

tggtatacca tgagcaagtt gaaaaggaac cagaaggcct agattttctt tttgatgctt 147900

atcctgaaat tagtaaagct aaagaattcg ccgaagtagc tgaatcacgt actgcatcta 147960

atggcatcgc caataaatct ttaaagggaa ccatttctga aaaagaagct caatgcatga 148020

agtttcaggt ctgggattat gtcccgttgg tagaaatata cggtcttcct gcatttcgtt 148080

tgaaatatga tgtacgtttt tctaaactag aacaaatgac atcaggttat gataaagtaa 148140

ttttaattga aaaccaggta gtaaataacc tagatgaagc taaggtaatt tataaaaagt 148200

atattgacca aggtcttgaa ggtattattc tcaaaaatac cgatggattg tgggaaaatg 148260

ctcgttcaaa aaatctctat aaatttaaag aagtaattga tgttgattta aaaattgtag 148320

gaatttatcc tcaccgtaaa gaccctacta aagcgggtgg atttattctt gaatcagagt 148380

gtggaaaaat taaggtaaat gctggttcag gcttaaaaga taaagccagt gtaaaatcgc 148440

atgaacttga ccgtactcgc attatggaaa accaaaatta ttatattgga aaaattctag 148500

agtgcgaatg caacggttgg ttaaaatctg atggccgcac tgattacgtt aaattatttc 148560

ttccgattgc gattcgttta cgtgaagata aaactaaagc taatacattc gaggatgtat 148620

ttggtgattt tcatgaggta actggtttat gaaagcttac ttagaaacaa ttgtcgtggc 148680

tcaaaaagaa ggtggagatg tttctacttc tgtatcacaa gtcattctcg aatttgtaga 148740

tgcatacgct tataataaat ttacagaaac atttgatgcc tatgaaaaag gaccaaagtt 148800

tgaaatatat cgtactctct taccactaga ttactaaagg ccttcgggcc tttaatttta 148860

taaatagaat aaacactaga gaggctatga tggaacttat tacagaatta tttgacgaag 148920

atactactct tccgattaca aacttaaatc caaagaagaa aataccgcaa atttttcag 148980

ttcatgttga tgatgcaatt gaacagccag gctttcgttt atgtacatat acatctggag 149040

gtgatactaa tcgcgattta aaaatgggcg ataaaatgat gcatattgtt ccttttacat 149100

taactgctaa aggttcaatt gctaaattaa aaggtcttgg tccaagccca attaattata 149160

tcaattcagt ttttactgtt gcaatgcaaa caatgcgcca gtataaaatt gatgcttgta 149220

tgcttcgtat tcttaagtct aaaaccgctg gtcaagctcg acaaattcaa gttattgctg 149280

atagacttat ccgtagccgt tcaggtggca gatacgtcct tcttaaggaa ctctgggatt 149340

atgataaaaa gtatgcatat attcttatac atcgcaaaaa tgtatcacta gaagacattc 149400

caggagttcc ggaaattagt accgagctct ttactaaagt tgaatcgaaa gtcggcgatg 149460

tttacatcaa taaagatact ggagctcaag taactaaaaa tgaggcaatt gcagcatcta 149520

ttgcacaaga aaatgataaa cgttctgacc aagctgtaat cgttaaagtt aaaatttccc 149580

gtagagcaat tgcgcaaagt caatcattgg aatcttctag atttgaaagt gaattattcc 149640

agaagtatga atctacagca gctaatttta ataaaccagc tactgcacct ttaattcccg 149700

aagcagaaga aatgaaaatt ggaattaatt cattagcttc taaaacaaag gcagcaaaaa 149760

ttattgctga aggaacggca gatgaacttc actatgatta taaattcttt ccaatgagtc 149820

aagtcggtga agtttcagaa aaaattaaag aagtaatttt taatgcaatt aaaaatgaac 149880

caactacttc aataaaatgt ttagagaaat acgcagcagc tgctaatcaa ctctttgaag 149940

aatataaaga taattggctt gataaacata ataaaactcg taaagggcag ccagatgaag 150000

tctgggaaga aatgactaaa aattcctgga acgcagcaaa aactaaattc ctcaaaagaa 150060

tgatttatag tttttctgga attggtgcag gtccaatgat tgatattact attgcccgtg 150120

atggttctaa atatactcca tcacaaaagc gcggcattag agagtattgt ggttcagggt 150180

atactgacat caataatctt cttttgggtc gttatgatcc agaacgttat gaagtaatga 150240

gtgaaaaaga aattgaagct gctataacta atttagattc tgcttttgaa aatggtgatc 150300

gtataccaga aggcattaca gtttatcgtg ctcaaagtat gactgctcct atatacgaag 150360

cactagttaa aaataaagta ttctatttca gaaattttgt atctacttct ttaactccta 150420

tcatttttgg acgttttgga attacacatg ctggtattgg tcttttagaa ccagaagctc 150480

gcaatgaatt aacagttgat aaaaatgaag aaggaataac tattaatcca aacgaaataa 150540

gagcgtataa agaaaatcct gaatacgtta aagttcaaat aggatgggca attgatggag 150600

ctcataaagt taatgttgta tatccaggaa gtctcggaat agcaacagaa gctgaagtta 150660

ttctaccgcg tggattgatg gtcaaagtta ataaaataac tgatgcttct aataatgacg 150720

gaacaacatc taataataca aaactcattc aagctgaagt tatgaccacg gaagagctca 150780

ccgaatcggt aatctatgat ggagaccatt taatggaaac tggtgaattg gttgcaatga 150840

caggtgatat tgaaatagaa gacagagttg actttgcatc atttgtttca tcaaacgtta 150900

aacagaaagt agaatcatct cttggaatta ttgcgtcttg catagatatt acaaacatgc 150960

cttacaagtt cgttcaagga taaatcatgg aacttattac agaattattt gacggcgctt 151020

cggcgccggt tgttaactta aatcctaagc ataaaatacc tcaaattttt gctattcaag 151080

ccggtgaaga aagcgtgctt cctggattta gattttgtac atacacctct ggcggtgata 151140

caaataaaaa cgttaagccg ggcgataaaa tgatgcatat cgtaatgata ggtgtcaacg 151200

agaaattatc gttagtcaag cttagaaact tgggtggaaa tccaattggc gtcattaatg 151260

ctgtttttga tactgctctt caaacaatga aacagtataa aatcgacgca tgcctattcc 151320

gcgtactaaa aagtaaaaca aatggcgcag ctcgtcaaat gcaagttatt gctgaccgtt 151380

tagtacgtac taaaggagca ggtcgatatg ttcttttaaa ggaaatctgg ggctatgata 151440

agaaatatgc atatattatg gtttaccgta aaaatgccaa tttagaagac attccaggtg 151500

tacctcctat ttcaactgag ttattcacaa aagttgaatc aaaggttggt gatgtttatg 151560

tagacgttaa aacaggtaat gctgttccta aagctgtcgc tgttgctgct tctattgctt 151620

tagaaaatga taagcgcacg gatcaagctg ttattcagaa aactaaaatt agtcgtcgat 151680

tagcagcaca agctcaatat tctactgttg atgcttcact tcagggtgat agcttcgctg 151740

ctaagaaata tcaagagttt gaatctaaag ttccggtata taaagcagaa ggtccgatga 151800

actctggcgt tattcagatt ggttcaaact ttagcaaagg agctatcggt ggtatgagaa 151860

gtgcttctcg ttttaaatct aacgattatg aactagaaag tttccgaaat catattgcat 151920

tagcccatgc acgtttacgt gatccatcta tcaagttgca gagcgatata acatatcaag 151980

gttctcaaga atatttaaag aataaagaat tctttgatta taaaactgat aaaattttaa 152040

gcgatcttgc tgacattaat atttctaata gctttgatgt tattaagaaa attatcaatg 152100

atttagttaa aggttctaaa gctacaccag atgaaaagac agctattatt caatttgtca 152160

tgaatggcat ttataaattg attaatgaat ctgccgctca ggcatatgaa tacgcaagca 152220

ctgaagtaac tccaaaagga ttaactcagg ctgagtctga tgtaattgaa gattattgtg 152280

cagattcata tgttgaaatg aactcgttcc ttttaggtaa acctgattct acccgtgaag 152340

aatatatgga acgagctatt aaacacatcg agacgttgga ttctgcattt gctaaaggtt 152400

cagttcttcc tccaggaact actctttatc gtgggcaaga agttaccttt aaaactttgc 152460

gtcataacat tgaaaataaa atgttctatt tcaagaactt cgtatccaca tcgcttaaac 152520

caaatatctt cggtgagcat ggtaaaaact atatggctct agatgattct ggcgcagtat 152580

tttctggtga aggagaaggt tccattgatg cagaagattt gatgcatatg ggtagtcatt 152640

ctacatatgt taatgaagat gctgaaacta gcgtgggtat ggtaattaaa ggagctgagc 152700

gaatcaaagt tatcgttcca ggtcatttat caggatttcc atcagaagct gaagttattc 152760

taccacgtgg aattttactg aagattaata aagtaagtac ttactttatg aaagaaactg 152820

cttataacaa gtatctaatc gaaggtacaa tcgttcctcc ttctgaacaa ttagaggaat 152880

cagtatatga tggcgatcat ttgatggaaa ctggtgaagt tcgtccaatg actggattta 152940

atcaattcct tgtagaagaa tcaaaagaag aggaaaacga agtttctcaa atcttagctt 153000

ctttggttaa catcaacgga atgtctaaaa agttcaaaat gtagtttaca agtccctcat 153060

gttgtgttat agtagtctta ctgacataac atgaggaaca caaaatgaaa tcttctttgc 153120

gctttttggg tcaagaactt gtagttgaag gcgttattcc tgctgataat gcttttaatg 153180

aagcagttta caatgaattt atcaaaattt ttggaacaga taaaaagttc ggaatttttc 153240

cttctgaaaa tttttcaaag ccagaacaga ctgaaagtat tttccaaggt gtagtaacag 153300

gtaaatttga gtcagaagct ccggtaaaaa ttgaggttta tattgaagac agtttagttg 153360

cttcagttgc tgcttttatt tcattccgta aataaaaata tggggaccga aaggtcccca 153420

ttgttatatt gctcctaata ttttactttg cgaattgaca attcctgtca tagtattaat 153480

gtttgaaatg cttcctgcag ttccccctaa tctactgagt cgtgaaagcg aattagatag 153540

tccagtaaca cctccactat ttccgagaac gctttgaata ccatttatag cagcagattc 153600

aagccattca agcgcagctt gcctatcaac tgctccagcc tgcatcactc tatacgcaaa 153660

agtaacgtca aatgtagtta tttggttatc tccatcatat gataactcag gagcgctcac 153720

tgatattgga atgcatccag tgaacatcac cgcagtatga ggcaatccat tacgagaatg 153780

aagattaacc tgaatatctg cctcgacatc ctgtggcaaa gcacgcagtc cagttactgg 153840

gtcttgaacg gagttaaccc agtcttgcat tgcacgatag ttacaagctt ctgaatccat 153900

tctaaatgaa ataaccaaag ggtctaattc tctcccagtt atacgaatat taggagaatt 153960

atagttccag tcagtttcat aggataatct attctctggc atttttacag agtatatcat 154020

caatccagat gagttatatg ccatgttaaa gaagtcaatt aaatatgtac caactgtaaa 154080

tgagcctaat aaactttgaa ctgtacgttg actcatggca ccaataagat atttactaac 154140

ccctgatttt cttatcagtt tttgtgtgcc agcagtaatt agcgtggtaa ttccctgatt 154200

aatatcacct tgagtcaatc ctaaccaatc tgaatttagg cccaagttat tataagaaaa 154260

gttgctaatt gaacttatca acgaagagct tttagttgat ggagttgttg caaaaacgca 154320

gctaaacata ttattacgtt ggaaatctgc gtttattgct tgattattaa attcctctaa 154380

agaatacatt aaaaagtccc cgcatataaa gaagcacggt ttaacgtgat aatttctctc 154440

atagtaatct cgagagtaaa tgtactaggg aggtttggag caatagctaa tccgttaaag 154500

ttaccattag gtgttttgtc aaatctgata ctctggattt gacatggacc gaatatttcc 154560

gtttttccat caaacttaga tgttgcacca aagtttttca ccatccaaat tgtcgggttt 154620

gaaactacaa gaacgttagt taaactcgat gtcattttct caaataacgt cttatttta 154680

actgcatctt ctggagttaa cggctcaata aaagtagaac ggtaccactc atctaaatat 154740

ccttttattt cagcagcata ttgagattta ccagtttcac cgtaagaaaa atagttaaaa 154800

tactgataga tattaataat agccattaaa tcttctgttg agcgcggagt caaatcccaa 154860

gtgaacactt tagttctatt ttcagcaccg ccgtacatgc ttctggctgt cgtataaatc 154920

tgttcattat tatcagccat tataccttgt gttatacttt ccagcgctcc aaatactgcg 154980

gttgaagcca tattgcttag cacaccagta gcagtacctc cacctttgt aataagacta 155040

tcttgaacat cattaaatct atgtgatgac gtatcgacgt cagatttaga tctaggtaaa 155100

agaatatttg caacaggaac tttacttatt gttcctgaat tattatctga tattagtcca 155160

tttgatagtt ttgatactgt attactgata gtgtttctgg ctgtacgtaa aatactcgaa 155220

gatgaagaag agtagttaga tctcatcgtt ctaagacttc cagaatccct agatgacata 155280

ttgtatgcag taaataataa tccattctta tatagatctg ttacctggaa gtcccctgta 155340

gtgtcattac cactagcacg cccagttgga aactgggcag tgtatgtttt agttgctact 155400

tctgatttag tactctgtcc ggctgaaatt ttctcaccgg acttttaat taaatcagca 155460

gttatttctt taacaattgc catattattc cttaattaac tccagtcgca tcaaatacac 155520

caggagcagt cgtgctcgtt acgggtgtca tattatgaac gacagtattt ttcttaataa 155580

cattattagt attattgatt gaaggagatg cttgttgaat aggagcttgc tgtgctttgt 155640

tcttttctat tacctggact tgttttgctt ctggcgattt agcagaagtt tgaggtttgg 155700

cattaggctg atttttcttg agctcttgat aagtagcatc aattttagaa aatctagcag 155760

caagttcttt tttaactgcc ggtgaattat ttaaatccgg gtcatccatt cgtttttaa 155820

ggtcttcata ggcagcttca actgatttaa ccgttgagtc tttactcata tcagctgaat 155880

tagcgtattc atcaaaacga ttcatagcag cacgagcttc attagctttc attaaagcaa 155940

ttttagcttc ctccggagaa agttgcttta atttttcttc ttcctctgct ctctcttcat 156000

cagtcgttag tgcttcttta ttatcaacac cacgaatcca gttagatgca cgagttttcc 156060

agttcgcaat tttgtctagc ccttttgcta ttggaccaag atcgtcattc attcttttat 156120

attgataatt tgcaactttt tcttggtctt ctttgctaag agaagcattt gtagtatttt 156180

ggaaattttc tagtgctctt ccttctactt catcagcagt atccttcata ccaggaataa 156240

ctcgaagaat tgccgcagat aatttagcca ttccaagttg aataagctct cctaaattaa 156300

aaagaacctt tccaagtcct tcgacaatag ctactgtcaa tccgccccag tctccagctt 156360

cccacagctt cttaatttta tcaatagaac caaagatgct ctgtaataaa ggaccccacg 156420

ttccggtttc gctagagaat ttggtaaagt ttgtactaaa caaatcccat gcctgcgaaa 156480

atttatctga ccaatatttg aagtgaacca tcaacagatc tattccaaca acaacagcca 156540

atatcattgc agtcatttta gcagcttcaa tagcagcact aacggtatac ttaaataaca 156600

tgcttgatat tttatcacta attgaaatag atttcttaaa tccaaaatca acagtctttg 156660

ttaatttatc taaagcttga gataatttta agttaaatgc ttctttttc tgtttttctt 156720

ctggcgattc ttgtttaggt tcaactggct gaggggtagg gaaaaaatca gcatcaggat 156780

cattattaac tgcttcagga gctggtaata aaggacccac ggattcagct gtatcgtcct 156840

caacaacttt aacaggaata gcgctttcaa ccgtagctaa actagttcct gtttgttgaa 156900

ttccggctgt ctggattttt tgctcgagta aactcgttaa tttatctaat ttacttccga 156960

gcgattcacc gatttcttta ttaatattat tgccaatttc gacagtttca gcaattaact 157020

cagaaccagc agtagtatca ctcactgcgc tttctacatt gtcaattgct ccaattattt 157080

cattcgattt ttcttcaaca gtttgagcaa ttaattcaga agcagcttga gcatcatcca 157140

atttcgtaga tatatcgtta agtccagata aagtgttaga agcggattta gccgcttcct 157200

gtgttggttt attatctgaa ataacttttc tacgcatcgt ttgcatttct tgtggctttt 157260

tcattcaaat aatccaataa tattgccaat tccggttatt ggaccattag ggccaggaat 157320

tgctaaagtt gtaaaaatat catttgccca ttttaaaacg aatgctggca tctcaagaaa 157380

attaatttct ttaacttcat cattgacctt aagcaagcat ttggataaca tatcgctcac 157440

cgttaaaaat tgttcaaatt ttccaggagg tctaaaataa aatgtatttc cttggtattg 157500

aaattctaat ctttggcaca cataaacatc attaatgtca taagtataac catctatttc 157560

tttacgagat ttaatctttc cattaaattc caataaatga atggaaacga aatcaacttc 157620

tgccggtgat aaatttggac aaatagaatc aataagaagc tttaaatttt catcaggacc 157680

tttaacatct tttaaaatgt tataatgttt aagacccatc ttaggaatag aaacttcttt 157740

attacttatc ggaagaacta ctttcttcag tggtagtatc agttttaaat tcatttttaa 157800

ccttaactgg gtcgattgtt tccagtttcg ttgcattagt gaacatatat agatgagtta 157860

cggaattatt atttgataat tcgtgaataa cttcatcaac gtaaaattct gttttaaatt 157920

ggtttttact atcattaaaa ataattttaa cgccaggagt caagttaaaa ttaccgacag 157980

tagaacattt agcatagccg tcatattgcg ccatagtctg aagacgaata gcttcttcat 158040

atccatttct ataagtcatt tcagaataag cacctgacct tgacactaca atagagtttt 158100

caccctttcc tgtagtaatc attggtaatg aagaatctaa aaatgaatga gcatagatag 158160

tagcattttt cattggatca cgtttatgcg ggtttgattt agtcaaccaa acaaaatcat 158220

atgctaatgg atatttcaat tcttggacga attgacctat taaagttggc tcacctacaa 158280

tcattggata tggttcttga tttatcatca tatcatagtc catcatgtta actcccatga 158340

tgtcttgcca tacaaatacg aacttatcgc ttcctaccgc tagagcaact tctcttacat 158400

atgacaaata gttttcaaat gtgctagtcc atggaatatc aggaacataa gcattaatag 158460

catttatcgc tggagttaat aatgtacgat cttgataaat tacgccaagc atttccttta 158520

tagattcacc ggcatcaggg aaaaatggtc taccaaattt aagattttct atagaatgaa 158580

tagttcccaa ttcaatagca atgatgttat caccttttga atctacagat acagaaaaat 158640

gcttacatcc ataaattctt gttttaacat tattaatatc gtttgcatta gctacagaaa 158700

tctgaattat ttcatttcca tccatttttg tatggatatt tttagaatca taaaattgta 158760

gcattccttc atttcgacca taaagagaat cccgcatagt taatgtggta atagtagcag 158820

ctaattcaac aaatctatta ttactccaag cgtcataact ctcaaataat ttaacgctga 158880

gatttggata tccaggacgt tgtaacatac tcattgatgt ttatccttct caatcagttt 158940

taatacgaat ccgcgctcgg caggaatcat tttcattatt gaatttaagc tataattact 159000

ttttacaagc gtgtgattaa tttgataaaa agtaaatatc tcatctggat taactaatag 159060

cttaaacaca tctactatat cagtgtattt tttaatgtac ttatcacaac acgacatgtg 159120

caatgttaaa ttaataggat tcattgcatc gagaattttt tctaatgttt ctatctcgat 159180

ggcgtcaact agttctattt gactggactc gctaatttcc ttccaatcat accatatttc 159240

atctacttga acagaatgaa tattttcagt aatcatcttt gctttatttt cataaaactc 159300

agaaggaaac tttaatttaa ttttaacatt agctacatca aaaacaggtt cctttaattc 159360

tttttgatat atttcaaatg gaactgtctt ttctttttta cattttggac atacaaatgt 159420

gactggtact ttagttttac ctattgaacc tacaaatacc tgcaaaaata taaatggttg 159480

ccaagtcttc ggatagtctc caaaataatc atcaattaaa tcagtaatta tttctttttg 159540

ttcttgtggt gaccgatgtt ctatatcgtt tcgaactaac aaaaaatctc gataatcttc 159600

taccgtaaat ggtttaaaac gatgaacacc atctggtaat ttacaacgaa taatgtttgc 159660

catagatgct ccttttattc tatttataaa tatgataaat aaaggagcta aatatgtatg 159720

aatacaaatt tgatgtgaga gttggttcta aaataatcaa ctgtcgcgca tttactctta 159780

aagaatatct agaacttatt actgccaaaa ataatggttc tgtagaagta attgttaaaa 159840

agctaatcaa agactgtaca aatgcaaaag atttaaaccg ccaagaatca gaactattac 159900

tgattcattt atgggcgcat tctcttggtg aagttaatca cgaaaactct tggaagtgca 159960

cctgtggaac tgaaatacca acccatataa atctattaca tacacaaata gatgcaccag 160020

aagacctctg gtatacactg ggtgacatta aaattaaatt ccgataccct aaaatttttg 160080

atgataaaaa tatagcccac atgatagtat catgcataga aacgattcat gctaacgggg 160140

aaagcattcc agttgaagac ttaaatgaaa aggaactaga agatttatat tctatcatca 160200

cagagtcaga tattgtagct ataaaagata tgcttttaaa acctaccgtt tatttggctg 160260

ttccaattaa gtgtccagag tgtggaaaaa cccatgctca tgtaataaga ggcctcaaag 160320

agttctttga gttactataa tggcaaatat taataagctt tattctgaca ttgacccaga 160380

aatgaaaatg gattggaaca aagatgtttc cagatcgctt ggattaaggt caattaaaaa 160440

cagtcttttg ggaattatta caacaagaaa aggttcaaga ccgtttgacc ctgaatttgg 160500

atgtgattta tcagaccagc tttttgaaaa tatgactcct cttactgctg atactgttga 160560

gcgtaatatc gaaagcgcag taagaaacta tgagccacgt attgataaat tagcagttaa 160620

tgtaataccg gtttatgatg attatacttt gatagtagaa atacgctttt cagtcatcga 160680

taaccctgat gatattgagc agataaaact acaactggct tccagtaata gagtataatg 160740

cttcacgtat aaacgtggta taatgaatct aagtccatcc aataacaatt gaatagagaa 160800

caatatgaga ttagaagatc ttcaagaaga attgaagaaa gatgtgttta tagattcgac 160860

taaattacag tatgaagcag ctaataatgt gatgttatat agtaaatggc ttaataagca 160920

ttcaagtatt aaaaaggaaa tgcttagaat tgaagcacag aaaaaagttg ctcttaaagc 160980

taaattagac tactactcgg gacgaggaga tggtgatgaa tttagtatgg atcgttacga 161040

gaaatcagaa atgaagacag ttctatcagc tgataaggat gttttaaagg ttgatacctc 161100

gttacagtat tgggggattt tattagattt ctgtagcgga gctcttgatg ctattaaatc 161160

acgtggattt gctattaagc atattcaaga catgcgagca tttgaggctg gaaaataatg 161220

agatataaca ttgatgatgc ttttaattat gaagaagaat ttgaaacgga aattcaattc 161280

ttaatgaaaa agcataatct taagcgtcag gatattcgta tcctggccga ccacccgtgc 161340

ggtgaagatg ttctttatat taaaggaaaa tttgccggat atcttgatga atatttttat 161400

tctaaagata tgggcattga tatgcatatg agagttgtat aaatagatat ataattcaga 161460

ggagacaatc atgtcagata agatttgtgt tgtctgtaaa actccaatcg attctgcatt 161520

ggttgttgaa acagacaaag gtcctgtaca tcctgggcct tgctataatt acattaaaga 161580

actaccagtt tcagaaagtt cggaagaaca attaaatgaa acgcaacttt tgctatagtg 161640

tgacctttag tctatagttt tggcccttcc tttttggttg ggccttttt aatttaaaag 161700

ctttcttcta cttcatcgtc tgaatcttct aattcagctc tttttcctgc caaagcatct 161760

ctgactgaga tgtcatcagt atcttttaat tcagtttctt taactctttt cttataataa 161820

gcttcaagtt cttctaaacc ttctaatgtt tgacaagagg caattttacc cataaattca 161880

tcaatagaag cttcataaag aaattgttta aattctagta acatcttttt ctccaaaggg 161940

ccgaagccct tataaattaa ctgttttcat tacgtaatta aatttttcat ctgcgtagcg 162000

ctgaatacga tcaatgccgt gttttaaaag atagttcaag tgaacatatt tctttttagt 162060

attagcagat tttggcttga caccacagtc atctatgagg tcccagactg ttgcgattgt 162120

tttagaacca tgcttacgta atacacgacc gattgtttgt aatacaatga tttttgattt 162180

aacaccgtgc gctaaaacaa cgtgatgcag atttttaact gaaataccag tagaaaatac 162240

accataacta gctactataa ttattccttt accattttca gctaaggttt tcattatatt 162300

gcgggtttcg gtatcaactt cccctgatac gtaataaact ttatcgtatt cattttaat 162360

taaatcgaaa atagctttac catgtgatac atgtttaaac atgacaaaag cgttttcatc 162420

tttttgtgca agcttaatag ccaatttagc gatccattta tttcttttac taagccccgt 162480

aataattttt atttcttctt gataagtttt tccctttaat ttagtagtga actcatcggg 162540

atagcgaaga aaaatactat taatttttag ctcagttact tgtccatctt ccattaactt 162600

agaagtcgtt actggcttaa atatttcacc aaacattcca acatactgca tgatattggc 162660

tttgccatca cgtaatgaac cagatagacc aaatttgaac atgcagttat ttaaacctga 162720

tatgatagat gaaatacttt ttcctgtagc aagatggcat tcatcattca tcatcattcc 162780

aaactgtgag aaccattctt tcggttgttt tactacagtt tgccatgtac caacaacgac 162840

tggtgcatca tttttatatt tatcatcttt tgatgctccg ccaccaattt tctttatcat 162900

tgcatgactg aataaacgat agtcaacgaa gtcatcagcc atctgagttg ttagagcagt 162960

tgttggaaca atgataagaa ttttaccttc ataattttcc aaataatatc gcgcaagcaa 163020

agcttgaatt aacgatttac cagcggatgt tggaagatta agaattctac gacgattaac 163080

taatccttcg aacactgcat ctttttgata ccaatgcggt tcaattcttt tatttcctga 163140

atagatttct aatttagaaa gccattcatc aaaatctttt cttgataatt cttctttttc 163200

gttaatctgt gggtcaatcc aggctttata gccaaagtta tcgcagaact ttttaatttg 163260

cccgactaaa ccgaatggaa gaaggcgatt ataatctaaa agacgaattc gtccatccca 163320

gtggccatat ttgtacttcg gattaaaacg atacccatca gcttcaaagc taaagaaatc 163380

acggagttca tgaaatgtac tttcttcgca atcaattctc acgtgactaa aatcataaaa 163440

atgtacttta atgtcagtca tgtctaaata ccatgtaata aatatatcta tatttatact 163500

gaggaaatat tatgatagat aaagattata ttgcagagct gaaggctctt gatgataata 163560

aagaagctaa agctaaatta gctgaatatg ctgaacagtt tggtataaag gtcaaaaaga 163620

ataaatcttt tgataatatc gttaatgata ttgaagaagc tctccagaag ctcgctagtg 163680

aacctatgcc ggagactgat gggttatcta ttaaagactt aattgatgct gctgatgctg 163740

cagaggggtt aaaatatgac gatgaagaag tcaatccaga agcagcactt ttgattgatt 163800

ctccggttaa atctgacatt aaaattgaag tagtagaaac agataaaatt cctgaaaata 163860

ccgatgtttt gattgaagat actccatttg ttgaagaaaa atttgaacag gctgtagctg 163920

agattattga atctgaaaag ccgtctgtat ttactcttcc ggaaaacttt agcccgaatc 163980

ttcagttgat tggaaaaaat ccaggattct gtactgttcc ttggtggatt tatcaatgga 164040

ttgctgaaac tcctgattgg aaatctcacc caactagttt tgaacatgcg tcagcacacc 164100

aaactttatt tagcttaatt tattatatta accgtgacgg atcagttcta attcgtgaaa 164160

cacgcaactc ttctttcgta acattaaaat aaggataact tatgactttt acagttgata 164220

taactcctaa aacaccgaca ggggttattg atgaaactaa gcagtttact gctacaccca 164280

gtggtgaaac tggaggcgga actattacat atgcttggac tgtagacgac gctccacagg 164340

aagaaacgtc agcaactttt agttatgtac taaaaggacc tgccggtcaa aagactatta 164400

aagtagttgc aaccaatcaa gttgcagaat ctgaacctga aacagctgaa attagtacaa 164460

ctatcacagt tcaaaataag acacaaacaa ctactttggc agtaactcct ggtagccctg 164520

atgctggagt gattggaact ccaattgaat ttaccgctgc cttagcttca cagccatcag 164580

gtgcaaacgc tacgtatcaa tggtacgttg acggttctcc tgtgggcgaa gcaactagca 164640

ctacattcaa ttacactcct gacgcaagcg gagttaaaac aattaagtgc gtagctcaag 164700

taaccgcgac agattatgat acaaaggaag ttacttccaa tgaagtgtca ctgactgtta 164760

ataaaaagac gcagacaact actttggcag taactcctga tagtcctcca gcgggagtaa 164820

tcggaacccc agttcaattt actgctgcct tagcttctca acctgatgga gcgtctgcta 164880

cgtatcagtg gtatgtagat gattcacaag ttggtggaga aactaactct acatttagct 164940

atactccaac tacaagtgga gtaaaaagaa ttaaatgcgt agcccaagta actgctgaaa 165000

attacaatga aaaggaagtt acttctaatg aagtatcatt gacagttaat aagaagacaa 165060

tgaatccaca ggttacattg actcctcctt ctattaatgt tcagcaagat gcttcggcta 165120

catttacggc taatgttacg ggtgctccag aagaagcaca aattacttac tcatggaaga 165180

aagattcttc tcctgtagaa gggtcaacta acgtatatac tgtcgatacc tcatctgttg 165240

gaagtcaaac tattgaagtt actgctgtcg ttactgcaac tgattacgat agcaaaacta 165300

ttacagcaga aggtcaagtt caggtaactg ataaagttgc tccagaacca gaaggtgaac 165360

taccttatgt tcatcctctt ccacatcgta cttcagctta tatctggtgc ggttggtggg 165420

ttatggatga aatccaaaaa atgaccgaag aaggtaaaga ttggaaaact gacgacccag 165480

atagtaaata ttacctacat cgttacactc ttcagaagat gatgaaagac tatccagaag 165540

ttgatgttca agaatcgcgt aatggataca tcattcataa aactgcttta gaaactggta 165600

tcatctatac ctatccataa tcataagggg cttcggcccc tttcttcatt ttgaaagcac 165660

acaaaacaca atcagaaaat gatgtatata atggcaccaa ctcgataaca tgagattgat 165720

tatgagaact gaggttgtgg tgtttactct tcatgagtct ggaaagtcat tcattgaaat 165780

tgctcgtgaa ttaaacttac aggcaaaaga agtggctgta ttatgggctc gagctatgac 165840

tgctaaaaat aaatttgaaa ctcgagaaaa agtcgtctat agaaaaagac atatcaataa 165900

aaaggtgaaa aatggaacag tatgatcttt atgaaaatga atcttttgct aatcaattgc 165960

gcgaaaaagc acttaaaagt aaacagttta agctagagtg ttttattaaa gatttttcgg 166020

aacttgctaa taaagcagct gaacaaggta aaacacattt tagttattat tgtattgctc 166080

gtgataaatt gattactgaa gaaattggtg attggctgag aaaagaagga ttcagcttta 166140

aagtcaatag tgatcagcgt gatggtgatt ggttagaaat tacattttga ggattaatta 166200

tgtttaaaaa gtatagcagt cttgaaaatc attacaactc taaatttatt gaaaaacttt 166260

atagcttggg attgactggt ggggagtggg tagctcgtga aaagattcac ggcacaaatt 166320

tctcattgat tattgagcgt gataaagtaa cttgcgctaa acgtactgga ccgattcttc 166380

ctgctgaaga tttctttggg tatgaaatta ttctaaagaa ttacgaagat tctattaaag 166440

cagtacaaga tattatggaa acctcagcgg ttgtatctta tcaagtcttt ggcgaattcg 166500

ctggacctgg cattcagaag aatgtcgatt atggcgataa agatttttat gtatttgaca 166560

ttattgtcac tacagaaagt ggtgatgtga cttatgtcga tgattatatg atggaatcat 166620

tttgtaatac atttaaattt aaaatggctc cacttttagg tcgcggtaaa tttgaagagc 166680

ttattaaatt gccaaatgat ttagattctg tcgtccaaga ttataatttt acagtagacc 166740

atgctggatt agttgacgct aacaaatgtg tttggaaagc tgaagccaaa ggcgaagtat 166800

ttaccgctga aggatatgta ttgaaacctt gttatccttc ttggcttcat aatggaaatc 166860

gtgtagccat caaatgcaag aattccaaat ttagtgaaaa gaaaaagtct gataagccta 166920

ttaaagctaa agttgaacta tcagaagctg ataacaaatt ggtgggaatt ttagcttgct 166980

acgttacact gaaccgagta aataacgtta tttctaaaat tggtgaaatt ggtccgaagg 167040

attttggaaa ggtgatggga ctaactgttc aagatatttt ggaagaaact tctcgtgaag 167100

gtattactct aactcaagca gataatcctt ctttggttaa aaaggaatta gttaaaatgg 167160

tacaagatgt acttcgtccg gcttggattg aattggtaag ttaaataaaa agggaccgaa 167220

aggtcccttt gttttattca tcaacgataa tttttggtag cttaacacct aataaaacag 167280

acaaa 167285

<210> 4
<211> 43313
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 4
cctactcaac gaggccgtgg ctagcaaggt gctaaactcc cgcctgggct ggtccgcagt 60

cggcgagtat gtcgaactgt tcaaccgcac gcaatcccgc gtggccgggt tgattcccga 120

gtagctcaag ccgagtacct gcatagtcgg gtgctccact ggaactactg gaatttttat 180

tgagattggc tggaggttgg ctgtctgtgg ctgggggggg tagttactcc gggtctaatt 240

ttggtatcgt cgtgtgagaa ccctcccgac tctgatcagc ccacccttcc cccgtaggcc 300

ctccgcctgg tgggccatcc ctcgcattgc ctgggtgttg cttcctagcc tcctgggagc 360

ttccagctcc gctgggtggc gtgggcttcc ctgccctgtc gccgaccatt ctacgcatcc 420

tgtcgggagt gtcaaccctt gggctggccg tagtgcctgg agcgctccag cgcttccctg 480

tgcttggtca gcgctaccgc gtactcctgg gatgcctggc gcttccgcca cggtgctgcg 540

tagtgccggt ggtcctgcgc tgcccacgtc gctatctgcc tctgccatgc tgcgtcctgc 600

tggtgccagg ctcgctcgcc tctgtcctgt ctgctcagca tcctgtgcct cctgtggcct 660

ctgctggtcc tgtcgggtgg tggtgcggga gtggctggcc ttgcctcttg tggtattgcc 720

tcctggctgt acctggcgtt gcctgggtgg tcccggctct gcctggggcc tacctggcca 780

ctccctctag gccacgtact ctacccgcct gcctctgcct tgtctagtcc ctcctggctg 840

gtgcctgggt gctggtctgt ctcaccctgg ctcactctgt ctctacctgt gccctgcctg 900

gctctgtcct ggctaccgct ggtcctgctg tcttgcctcg ccgctccctc gcatgctcgg 960

tcgcacctgc ggcgctgatg gactcctgtt tgtccattgt gtgtgacata accgcagccc 1020

tagtgccacg cgggttccag ggcggtgggt cgggtgcctg ggtggcggct gtcgctccct 1080

ggtaacgcaa atcctggcta gctagactaa gcctcgcacg tgggtctcta tacgtgtggg 1140

aaggctccag ggagcgccct gggagggttg acacgtgggc agtaggtctg tagagttcgc 1200

cctgtcttca cgcaacaacg cctctacagg cagcctggag acggggttga cacactgcca 1260

gggcatcggt agagtacgca gccagaacga cgggagattg caaccttcca agcgcggcac 1320

aagccatagg cgcaagggac acggcaaact cttagggcag gaaccgcagt gtgtaaggcc 1380

ggcaggcatc actgagggga ttgacacggt gcaggacacg cggtacagtt cgcaccacct 1440

gatggccact cagcaaaagg gcctatgcca gagaactgga cgaactaatc cccgacagag 1500

gattgacaag acaagcgcaa gtctctaaca tgcgcagcaa gacgaaagga tggttcagcc 1560

atctggcggt agaggttcga agcttcacca gcggtacatg gactggtgcg gtaggttgac 1620

cgaagctgca actggttagg cagggtccca gggaatacct gtcgggtgct gaagactcac 1680

ccaaaagagt ctgagcggga agcctccccg tccacggtta agcaaaggca cgttagtgcc 1740

ggtgggaacg aacagagtgt cagtgggatc gagaactaga aacctcggtt aatcgcgact 1800

gacagtatgc tgggtagtat cggcgggccg attgaacaag gccaggcaga tagcgcaaag 1860

ggtacggggg atgagtgctg acgatcccga agagtatgcg caggacaagc cagaaccgct 1920

gatactacag ggactatgcc aatgccaagg tttgtccctt gaggcccttc caccgagggg 1980

attcaagaga cagacctagt gaggattgcc gatggcacac ttcaaggcta aggctcccaa 2040

gtcgcccttt gctgctcagg tagcgtactg gcgggactgg gaagccaaac gtactaagct 2100

catcgcacag gataacgtcg aagggcgtaa agagcttcgc aagatgcgtg acgtgcgcta 2160

cgccaccgac ccggagccag cgccaggacg ctaccataac cctgaacaga aggctttcgt 2220

gaagggtagc gaaggcaagg cgcggaacat cctgaaggga tggaacgcta agaagtcgca 2280

agggaagggt ttgtaatgcc acgtgtgaat gaactgacgc cgcgtcaacg caaggccgcc 2340

aaggctcgcc gcgacaaggc tcgccggatt gatctagcgc acaggatgcc gaaaggtgcc 2400

gactgcccga tcttccgcaa ggctgagcag gcgcaagcta agcagccacg agtcgatacc 2460

ctgaccactc cccgcagtgc tggctacctg gccgccgctg cttacctgaa caaatccatc 2520

tgaggtacat accatgacca acgcaatctc caaaaccgta atcgcattcc gtggcaccga 2580

agagatcaac cgcgctatcg acgccatccg tgtccgtggc aaggaactcg acgaagccat 2640

ccaactgacc ggcctgtcga tcatccacca catcgaccag tgcggcgacg tgaccgtagt 2700

caaggcgctg tatgaagcca tgccgaaggg cagccgccgc aatgcgctgg tcgagtggct 2760

ggtgctgcac ggcaaggtac aggttaacac tgacaagaaa tcgaacaagg acctgccctt 2820

cctgtacaac aagttcggca agaccgatct cgtcggcgcc accaacagcc cgtggtacag 2880

cttcaagcct gagaaagcgc tggaccagga gttcaacctg gctgctgccc tggccacgat 2940

caaaaagcag gtgctccagg ctcagaccaa gggcaaggtg atcgtcggta tggaactgct 3000

gggtgacttg gaagcgctgg ccgccaaggc tgcacccatc gccgagcaga gcaagcgcgc 3060

tgccgcccat tgactcaagt cgaacgcctg ctaagcgggc gttccgctgg aatcaatgac 3120

aactggagaa acacgatgag cttcaaacaa cgcctgcaac gtcaaatcgc cctggcacag 3180

tacagccgcc cggctcagtt cccgtatggc gagcaagccg tccaggcgaa gggggagtga 3240

ccatggactt ctggatcgcc cttcccttcc tcgaactcgg cctcaacctc ggcgaggatg 3300

aactgcgcat gttgtggttc agcggcctga cgatattctt catccacctc ctgaagcggt 3360

gactcaagtc atggccctgg cgggcgaccc tcgcctactc cggggccatc gctggactca 3420

tcacaagcga gaactaaacc atgcaagctt tgaataccct gttgattgca atccccaagg 3480

acccgaccgc aggcatgcac gccgccgaca aggtgctgtg cgcccacgga ttccgcatgg 3540

gtgacctgaa taccgcgcac gtcctgaccc caggcgggtt cgtggtagtg ggcgccggcg 3600

tgactgtgaa ccgctatgac gaagcgtatc gtatgagccg gaacctcgac tccgaaggct 3660

tcgacgtgct gctggtccag ggcagcccgc tgtccgggcg tgtcacctgc caggcgtacg 3720

gatggatcaa cgccgagtac cacaagggct gtgcgaatgg ccgtcccatc ttcgacatcg 3780

caggaacctc gtaccatgtc atcgcgtgac ccgtaccgca tcggccaccg cgttgggctg 3840

gtgaactaca gcgaccgcta cctgggtgcc gacgcggcag gcaccaaggg catcatcgag 3900

gccataaccc gaccgtcgcg ctgtatgacg gtctaccacg ttcgctgcga gcggaccctg 3960

cgcctgatcg aggcagaggc ccgcaacgtg cgattcatcc gacagcgggc ggagcggtga 4020

gctggcgcat cgtggtagtg acgccaggca acgggtgcgc cttcgtgtgg acccgtcgca 4080

agcgcgtccg gcctctgaga ttctactccc gcaaggccgc taaacgctgg ctccgtaggc 4140

accgccgccc ggcgatcctc ggtagccagt acctgatcgt gaactggagc aaacgtatat 4200

gaccctcgtg gccaccgtag tagacagcgc gcacaacctg gaagtcgacg acctcaccgc 4260

cggcaacctg tatgccgcca gctcgcccag cgggaacatg ttcatcgtgg tagtgggtaa 4320

tcacaatggg cgcaggcttc ccgtagtcct gtcatccacc gatacccgca ccatcgggga 4380

cgtgataagc aacactgggt tccggtacag tgagatcgcc gggttctccg taaacctggc 4440

acagggagat tatgactgat ggtcacccgt actgtatacg tcacgcctga agacccgacg 4500

ccgccgatct tgtccgtggg ccgactggct ccgggagaac tctacaaggt ggtggcaccc 4560

agctcggcgg aaggtatcat tgtgctggcg accaagcaga cgccggcgct agcccaagca 4620

gccgtcgtac tgcacagcat gaaccctgcg cagtatcccg caggttcggc tatcctcaac 4680

acggcctgga agtgccgccg cctgggagtg ggcgagtacg tcaagctcgt ccaaggggag 4740

gaggactgat ggccgtggca atactcatcc tggccgtgtg gttgatcggc ggcgccctgc 4800

tattcctgcc gttcgacctt gtggtctcac cgcgcttgcc gctatcagac gaggccctca 4860

accgaaccgc actgtacacc gtgctttggc cggtaaccct acctaccctg atcgccataa 4920

ccgtggttgt catgctgcat tccgcgtaca ggggcgccat cgaactctac caggagatga 4980

aatcatgatc cgtacccata cccacaacgt cgagcgcaca ccgcaccgac tgtaccggca 5040

cactgagctg gcgtctggcg agctgtaccg tgtagtgcag cccgactcca agcgcggcac 5100

gttggtggtc ggcgtagcgg cctgggacag ccagggccgg cccgcagtgc tgcccgtggt 5160

catccatgac gatggtgacg ccaaggtgac ctgcgcacgt cctaccgtac tgcgcaacga 5220

cgggtggcgc atggtcctcg ccgacaaggg gacccaggtg acactcaccg ccgagtgacc 5280

aaggcgaagg ctggtgcgcc agccttccac cgtggccatt ccctgccgcg aaccaactca 5340

actgaggagc tacaacatga ccaacgtcaa caccaccacc gaaaccacca ccgctgctgt 5400

cctgggtgcc aagctgatca agaagccggc caccgtcgag gacttccgca acaacgtggt 5460

cttccaccat agcgccctga ccaaactgac cgaggtctac aacgaagcgg tcgccgccct 5520

gcaaaccgcc gagcgcctgt ccagcctcgt cgccggtgac gtgatcacct tcgaccacgg 5580

caagggcgag aaagccgaag tgctgagcgg cgaagtcatc agcgtggtcg ccggcgtcta 5640

tcaggtgctg gtccgcttca gcgacagcgc accggccaag ctgctggacg tgaaggccag 5700

cgccatccgc gccgtccagt cgtcggcagc ccaggctgca accctcgacg aagccatcgc 5760

ccagggcgag taaggcccgc acgtaatagg cccggccctc cgggcctatt gcgagctagc 5820

cataccatag gaggaatcac catgagcaag cgcaaccccg aacacatcaa cggcaccgtt 5880

cgtagcgtca gcgtccagaa gttggcggcc acccaggaac tggaggatcg tctggaggct 5940

gccctggccg tgtgccagca gcgggcagag gacatcgacc tgctgagccg ccgtctccag 6000

gccgccgagc gcgcccgtcg ctgggagatc gacgagattc gcaaccacca ggcgaccatc 6060

cgcctgttgc aaaacgatct gaacgctgcg catgatgccc acgaggcaca agagcgccgc 6120

gctcgcaagg caaccatcat ggcctgggta tgcctgctga ccgcaggttt ggccgtcacc 6180

ctgaagctgg caggagtctg accatgcagt gcaaagacct ttacacgaac ctcgcgtcgg 6240

gcatgttcaa cgtgccgtgc tcccaggtga ccccggagat gcgacgggta gccaagagcc 6300

gggcattcgc ccacgcctat acgcccaaga aacaggcttc gggcgggact tacaccgccc 6360

gtgtgagcgg cgtcacctgt gacggtggta aggtggaggt gcgcctggat aacgtggagc 6420

gcgtcagcac cttcgactat gccgagctgg agacgcgggt agcggccagt ctgtgccagg 6480

ccgacgcgaa gcgcgccgct gaatacgaaa agctactgct gaaagcgttc ccgtcggtat 6540

ccccgaagga tggcccgctg tccgccaagg acttcgaatt gcgcctgcat gatctgtgct 6600

caaccaagct ggtagtgctt cgtgccttgc gtgatgccgg gatagagatg gacggtccgc 6660

tgcgcagccg ggtacggaag ctggcggatc ggaataacgt gatgggtgct gagttgttca 6720

gcctcaagca ggagttggca caactggtcg cggtcggcca aaaggctgga ctgaattggg 6780

acggggcgga gactcagcgc ctgctgacgg tggccccgac caaggctctc tgtcgactca 6840

tcagcgcgct gaccggcgtg cggtataccc accacaccgt cgtagccaag gccgaggctg 6900

aggcgcgcga gcgggcaaag gccgaggcca aggattcatt gcaggcggca accttcgcag 6960

ccgccatcgc tggtggcgtc gtcggcagcg ccctgatgtt cctgctcggc tagggcgacc 7020

agggcctact ccggggtcaa atccgagggc gttcctagag cgccctctcg tgtgagtctg 7080

gaggatcacg aacatgcaat accacttcac gcattacaac ggataccgct tcggcgtcga 7140

gctggaggac gaggctgtct tcccgtgcat cgacggtaag cgggcgacct gggacaaggt 7200

ggcggcatgt gccggtagcc ttgtgcatta catggcgcag gacctgatcg actttggcca 7260

gcgcaagtta agggagtttg aagatgagca agacgagcct gtatccgctg aacctgcatc 7320

ccggcctgat tcaaatcagg acgattcacg tattcagcat ccaagccccg agcaacgccg 7380

agaactggtg gcagtggttc ctctggcagc ggaagtacca cccgctccgg gaaagcctga 7440

gtccagccgg ggagctgagt gcgagtatcg ccgagtgtgt gctccacctc cgccggaatg 7500

gctggcaaga tagcgacatc tggcgcaaga agggaggcgt gctggccctc ggtgccttcg 7560

acctgtccgg cctgatggta ggttcctgcc tcgtagtagg tggtgagctg aaggccctgt 7620

gcgttgatga ccggcacagc aggcagggta tcggcgctga gctggtgcgg gccgctgagc 7680

tggctggtgc cgagtatctg acctgcttcg agttcctgga gccgttctac gccgacttgg 7740

gctggagcac cacccaccgc gaggcgaact ggacagcagg agagccggac gtgctgcaca 7800

tgagggcacc cggtcatgac gtatgaggtg atgacatggc ttatcgagaa caaaccgctg 7860

gtcatcggag tcgccttcag tctggtggcc ctgggcgtgc tgctcacaca gaacaacggc 7920

ggcccgccta cggcgcccgc atgacctggc acctccagga catgttcgag gcccgaggcg 7980

ggctgcggcc tttgtgggag gaatggtacc aatggcactg cgccgtgact cctggctaaa 8040

gcaagcgcaa tccctggcgg tcggtcaggc gggtcgattc cgccacgtcc tgggatgcca 8100

gagcatgagc cggggcggga ccaacatgac ctgcaagaac cttcctgacc gctgggtggc 8160

ttactgctac tcctgtcagg agggtggcgt ggtcgagaaa acgcatgtgc ggagggtaca 8220

atgcgcggat caagaacgct tcatgccctg gcccgaggat gcctcggact ggacgcaagc 8280

cgactgctat caatcgcttt atggtttgct gctgtccaag ggcatagact acaacgtgat 8340

gacgccaggg ctgccgctgc tgtacagcga aaggcagcat cggcttatct tccctaccga 8400

cgcgggctgg attgggcgcg ctactgccga ccaaaatccc aagtgggtgg gttacgggta 8460

tcctgccccg gattaccatg gatggcccca ggaattatca atgggcaggc catgggtgct 8520

gacggaagac tacttgtcgg cgctgaaggt gcggtgggcc tgtcccgaag tctttgctgt 8580

cggtctgaac ggtacaaggc tgcgcgacag gctggcggcg atcatgttgc agcagacctg 8640

caagcgcgcc ttcatcttct tggatggcga ccgggcaggt gtccgtggta gtgcaggcgt 8700

gatgcgccgg ctccggtccc tgcttatcga aggccaagtc ataccaacgc cggacgggtt 8760

cgaccccaag gacctgaccc gcgagcagat aaggagccta gtaattggac gtattgacgc 8820

ttcacgcact gagtgaccgg gaccgcttcc gcacattgcg gagtgtggtg cccgaaggaa 8880

tgatggggcc ggagacgtgc ttcgtcatcg actggatcga gcagtattgg aaggtctacc 8940

cggcgcatca gaaggtagac ccgcaggcac tgcgcgaact gatcaagctg cgaggtggct 9000

accagccgga gcaactggcg gtggtcctga acctcgtcaa ccaactggac aagccggtgg 9060

acccggactc gctacagggc gtcgtgtccc agctcaacga actggatttc tcagggcggg 9120

tggatgccct cctggcgcag tacaaccagg gcgaggacat cgacctggcg tatgagctgc 9180

gccggctgag cgacgaggcc ctgcgccgcg gaggggtcag cacgccgacc gactacgtga 9240

cggacgacgt gtttgatatc ctcgcggagg agcagggtga ccacggcatc aagctgccgg 9300

ggctggtgct accggcgtac atgaagggcc tccacgccgg ggcctcggtg ctggtggcag 9360

cgccgccgga tgcgggcaag acctcgttca tggcctggat cgctgtccat atcgcgccgc 9420

agctcaagcg gtacttcgac cccggacgac ccatcctgtg gctgaacaac gagggcaagg 9480

gccggcggat caagccgcgc ctgtactcgg cagccttggg catgaccgtg ggcgagattc 9540

ttgccctgga cccggaggaa gttcgcagga tgtacgccga gaaaatcggc ggcgactctg 9600

agctgatccg catcaaggac ttccacggcg ggtccctggc ccaggccgag caggtcattg 9660

acgcgatgaa gccgtcggtg gtgttttggg acatgatggc tcacgtcaag ggtggacagc 9720

gcaaggacca gaaccgcacc gacgagatgg agtacaaggt ggccgaggtc cgcgagatgg 9780

cggtgcgcca cgacttcatc agcttcatga cgtggcagat tagcaacgac ggccacgacc 9840

agttgttccc accgcagtcc tgcctcaagg attcgaagac agcagtgcag ggtgcggtag 9900

atgtgcaaat ccacctgggc cgtctcaacg gtgcggatca acaggtcatg cgtggcctgt 9960

ccctgccgaa gaacaagttc cagatggacg ggaagccttc gaacgtggag gctatgatta 10020

acttcgacgc cgcacggtgt cgattcttcg agagtgtaga ccatgcaagc taagcatagc 10080

cgggtgctcg aaggcaccaa agaaattccg ctgggtagca tcgagccgtt actgggcagc 10140

gtcgcgggcc tgctgttgtg cctgtactcc gacgcaactc acgaggaggg cgtcgccttg 10200

gccggtgggt tccctcgcga cttgatgcac ggcgccactc ccaaggacgt ggatgtggcc 10260

ctgtatagca tgacctgggg gcgggcagag cacctgatcc agaaggcact cccggtcctg 10320

aaccccatct tcgtccggga tggtgggtgg cgctcggact acgctgatgg tggtgacggt 10380

ggtatcttca agggcgtgat gtccctcgtg ggctgccgtg ggttgaatgg catggacttg 10440

gactttaact actacgacgc cgacagcctc ggtcgagtga tggagtcgtt cgacttcacc 10500

atcaaccagg taggcatcgc gtacaactgg cccgaccccg agggtgggcc gcgcctgggt 10560

gcgtacctgc acaaggacgt tacctggggc gtgaacaagg aagtcggtgc cggctcacgt 10620

ctgccggaac gatgcgagaa aatgcgagcc aaggccgcgt actacggatg ggagaacgtg 10680

tgatgagcaa gcgcgacgtg gtactggata tcgagaaagg catctggcgt ggtgttgacc 10740

agaacgacaa ggccgtcgag gccatcatca agaagaacgg gtacgtgatc gtcgagccta 10800

agatcgacgg gtgccgtgcc atcgtcggtg cgcatggcgt ggtgtcccgc agtgggcgcc 10860

gcttcccggc cctggatggc ttggaagacc gcatcatcga gcgactggcc cgaccggggc 10920

tggactccgg cctggtgctg gactgcgaga tgtacctggc cggcatgccc ttcagcgagg 10980

cgactggccg catgtcgagt aagaccccgc tgaccgagga agagctggag tgcctgcact 11040

tcgcggtatt cgacgccacc catatcgacg tgctccgaaa ggcgcgcacc tcacacctgg 11100

tatacgaaga gcgccgagcc atggccagca gcctcctggc agcctgtcgg ctcagcgaca 11160

ctccgacgtt cttccaggtg gggttcaccg tctgccggag aatgtctgac gtttaccgcc 11220

agtacaagtt caaccgggag gtgggctacg agggatcaat ggagaaagac cccagcctgg 11280

tctaccgcaa cggcaaggtc gccggctgct acaagcgcaa gccgggcatc accgtagatg 11340

gccgcatcgt cgggtacgtg atgggcaaga ctggcaagaa cgtgggccgc gtcgtgggct 11400

accgcgtgga gctggaagat ggttccggca ccgtggccgc caccggcctg agcgaggagc 11460

acatccagct cctgacctac gcccacctca acgcccacat cgacgaggcc atgccgaact 11520

acggtcgtat cgtcgaggtc tccgcgatgg agcgctcagc caacaccctc cgccatccca 11580

gcttcagtcg cttccgcgac ctggccagta atccaggagt caaggtatga agattcgaaa 11640

gtcccgtaac cgcaactacc cggaagatat ggtgtaccac gccaccaacc gggattcact 11700

gctgtatccg aagtacgtca tgggttccgt gttcatcagc caggacggaa cattccgcat 11760

ctgcgtcatg gcagggacct gggaccacgt tgggtccgaa gttctgcatc atgcacggga 11820

catccaatcc cttggcgccg gtcgccgtaa gttgcaccgg gtcatgcgac ggctgcgccg 11880

caatctgcaa caggtaggag tcaaggtatg agaatgccaa ccgaagaaga acgcacgatc 11940

cgctgcctgc tggcagatat ccacgaaccc ttgaacctgc tgttccccgg tatccgtgta 12000

aaggccgaga caatgccctt gggctgggga gatagtatct gtgccctggt actccgggtg 12060

agctacgaac atctcacgct ggggcgcctg gagtacatgc acgaggtccc catcctgcac 12120

ctgtcgcagt ggggccggga cggcctgcta cagcacctga tgaacgagat tccccgtcgg 12180

gtgctggatg gcatgctacg tcaggcacag aaatacagcc agagtaactg gtacagcaaa 12240

tgacgactat ccgaatcctc gacctcgaaa ccgagagcta cgagcacaaa gggcgcaagg 12300

cgtcgccctt tgacccccgc aactatatcg tcatggccgg ctggcgtgac gatgttgacg 12360

gcaaggtcgg ccagaaggtg gagcatcgct tccgcagccg ggccgaagcc gaagacccga 12420

acaaccgctg gttcaacctc gacggcgtgg acgtgatcgt agcgcacaac gccatgttcg 12480

aatcgaactg gttcttcacc cgctaccggg acgagtacct ggccttcctg cgacgtggtg 12540

gccgggtctg gtgtacccag caggccgagt atctgctgag tcatcagacg tggctgtacc 12600

cggcgctcga cgagctggcc ccgaagtacg gcggcaccca caaggtggac ggcatcaaga 12660

tgctgtggga ccagggtgtg ctcacctcgg agatggacca ggacctgctg agcgaatacc 12720

tgtctggccc gtgcggcgac atcgagaata ccgccctcgt attctacggt cagttgatga 12780

agctccaggc ccgtggcatg tgggctggtt acctggagcg ctgcgaggcc ctgatcggtt 12840

tctcggcgat ggagtgcgcc ggcctgaagg tggacctcga agtcgccaag gtgaaccacg 12900

ccaagcaact ggaagaggtg gccgggatcg aggccgagct gaagaagctg atgcccgact 12960

tcccggaata cttcgagttc aagtatacca gcctctacca tatgagcgca tggctatacg 13020

gtggcgaggt gcggtacaag ggccgggtgc cctacgaaga tggccggatg gagaaagccg 13080

acttcgtgcg cttcggcaca gccaagcggg ggactcctat cgagagtacc tcggtacggg 13140

tcccgatcca cgaagtgacc gaccagggtg aatggcactg gcccaccatc accgagctgg 13200

cgaccaagca cggtccggtc atcacgttct ccgccggcaa gaacaagggc agcgtcaaag 13260

tgttccgtga ggatacggac atcccggcga ccaagtggga cgatgaccag cgattccggt 13320

tccccggcct gatcaacctg accaacctgc cggaagtagt gcgtgagaaa ttcctgggca 13380

agcgcccgga gttccagtgc gccctcaccc tggcggatgg atcgcccgtg ttcagcacca 13440

gcggcgacgc cctcaaggct ctggagaaac agggcttcga ggcggccaag ctgttgatgc 13500

gcctggccga gctgcacaag gacaactcct cgttctacat cacccacacc tacaacaagg 13560

atgggacgat taaggacacg aaggggatgc ttcagtacgt ggacgatgat ggtatcatcc 13620

accactcgct gaatacgacg gcgacggcga caacgcgtct gtcgtccagc cgcccgaacc 13680

tccagcagct cccgtcgaag gacgaggacg acccggaagc cggcagccgc gtgaaggaga 13740

tgttcgtgtc tcgcttcggc gcagacggga tgatcggcga gaccgactat accgccctgg 13800

aggtggtgat gttggcggcc ctgtcgaagg accggaacct cctggcgaaa ctgatggccg 13860

gcactgacat gcacttgtac cgcctggcag ggaagcacaa caactggaac gggttcgact 13920

acgaccagct cgtggccatc aagaaggacc ccaaccaccc gtggcacggt cgcatgatgc 13980

aggctcgaaa gaacatcaag cccaaggcat tctcggcgca gtacggcgcg agtgcggctg 14040

gtatcgcatt caacaccggc tgtaccgtgg aagaggccca ggaattcctg gacaacgagg 14100

cggccctgtt cccagagtcc atcgcattcc ggcagatcgt ccgagacagt gcagaggcca 14160

ccagcctcgt catgtacaag gccgaggacc agatgccggc aggcgccttc agcgagatgg 14220

ggccggatgg caactggcgc cagtaccgcc ggggattctg gcaagcgccg ggtggcacct 14280

gctacagctt ccgccaacag gagcgctggg acaaggaaca gcgcaagacg gtcatggact 14340

tcaaggacac gcagatcgcc aactactgga accagggcga ggctgggttc atgatgaccg 14400

tgagcgtagg gcgcatcttc cgttggatgc tgcatcgccc aggattcatg gtcaccgagt 14460

tcctgatcaa caacgtacac gatgccgtgt acaccgactg ccacaaggac accgccgccg 14520

aggtcaacaa gggcgtgcgc gacatcatgg ccgacgctgc ccgctacatg agcgagcgcc 14580

tgggctacga catcgccgac gttccgttcc cagcagtggc tgagatgggg ccgaacatgt 14640

tcaatatgga ggtgatccag tgaaagaact gcacccgctg cacacgcctg agttcgtcaa 14700

gacattcctg gaccagaccg ggtgcctgcc gggagtacgc cgtacgggtc gcaccaccgg 14760

cattgctcta caggccattg gcatggcgct gtcccatccg agggaaaccc tgacgttcgt 14820

ggaccacccg gacggcagcg cggcagcact ggtggccagc attgaaacca tactggcgac 14880

cctgggctac aagaacgtcc tcgttcgacc cacaacccgt gcggatgggc gcagcgtgag 14940

catcgtcttc aagacgctgc cgaacgcctg acgacccttc cctactccgg ccttaaatct 15000

tcatccgaca cgagagagac cacgcatgac tcaacaactc aacgctctgc aagccgccct 15060

cgccctggcc aacaaggctg ccgagaccgc aaccatcgac atgtccgaaa cctccaccgg 15120

cggtggcggc ggtcgcatct tcccggcggg caccgccatg ggccgcttct gcatctacat 15180

cgagctgggt gaccacgcca aggaattcca gggcaagctc aagaacccgg cgcctcaaat 15240

ccgcctgggc ttcgcactgt ggggcgacgt gaacccgcag gccggtaacc cgcagagccg 15300

cccggacgac ctgttccaca cttacgaggc cgacggctcg atcaagcccg gcctgttccg 15360

taccttcgag atgaccctcg gcaacaacga aaagtccaag accaagctgg ccttcgacaa 15420

gatgaactgg agcgggcagc atacccactt cgctcagatg ctcggccagg cgttcatcat 15480

cccgatcaag cgcaccaaga tcaccaaggg caacaacgcc ggcaaggaac gcaacgacat 15540

cgattggggc ggcatcatga agccctacaa cccggtcgat ggcagcccgt acaacgtgcc 15600

ggaactgccg atggacctgt tgcagtattt cttcttcgac gcgccgacca aggagacctg 15660

ggacgccctg tatatcgagg gcacctcgga caacggcaag tccaagaact tcctgcaaga 15720

gaccattcgc tcggccacca acttccccgg ctcggccctg cacatcatgt tgggcggcgg 15780

cgacgatctg atcatcaagc caacgagcca ggccgcaggc agcaacctgc cggcagtgcc 15840

caacgtggcc gccgatgcag gcgtagcagc agcccctgcc gtcccggcag tcccgcaggc 15900

agtggctcag acggccccca gcgtgcccca ggtggcgaat gtggctgccc ctgtggtagg 15960

tactgccgag gcgcagaacg tgctgcctga cgtgccccag gtggctcaga cggcggctcc 16020

ggcagcggtc gaagtcccgg cggtcccggt agtgccggca gtaccgcagg tctaatgcgc 16080

ctgccatcgg aagagttcct ggcaggacta tccgcgcagt tcgaccgcag catggcaggc 16140

gggacgttgg tgtgtgacgc cgatggaccc gcctacgtgg ctgcggccac tgctaagacc 16200

ctggacactg cactccgaag attctggaag ctcattttgg agcagcagtt cctagcgcac 16260

tgcacaggga cacgggttca cctcacggca gcaggtgggg cgaaggcgta ccgcgacacg 16320

tatccgacca tgaaaccgta ccagggccag cgcaagggca aggcaaagcc cgcgctgctg 16380

gagccactgc ggcgggccgt ggcggacgtg catgagcgag gcggggcgcc ggaggggatc 16440

gatgtcatcc tgcacacgtt cttcgaggcg gacgacggca tgatgatgga cgcctacgcc 16500

atgcaggaca aggccatcat ccggtccgac gacaaagacc tgcggatgac gatctacccg 16560

tattgggaga tcgatacggc gtgtgtgagc aggatcgaag gcggcttcgg ctacctcaag 16620

gaagcgtaca cgccttccgg ccagttcaag ctcaagggcc atggacggaa gttcttcttg 16680

gcgcagtggc tcggcggcga caccgctgac aacatccgag ggatcgatcg attcaacggt 16740

aagctctgcg gtatgaagac ggccttcgac atcctccatc cgatcacgga tgaggacgag 16800

gccatcgaca tgatcctgga ggcgtacgcc aagatcaagc aaaacccgct ggcagaggcc 16860

gaggtgctgt ggatgcgccg aacgcctacc gacaacgcag cgcagtacct gttaagccgc 16920

gaccttcgtc cggccttccg ccagtggatc atcgagctgg acgcctacca cgaggcgctg 16980

ctccagaagc ggagggagag cgattatgac gagtgagccg aaggtctacc agataccgcg 17040

cagtcaacag cgcaccttca ccctgaagct atgggccgag cagaacaagc tgtgcccgct 17100

ctgcggcaag cccatcgata tcagcgtgaa gggcgaagcg gtgatggacc acgaccacga 17160

aacggggctg gtgcggggcg tcctgcaccg gtcctgtaac accgcagaag gcaagataac 17220

gaatgcggca ggttcctggg gatgcaagtc gatgaagtat tcagacatca tcccctacct 17280

tcgtgccctc ctgacgtatc tggaggggcc gaagcatccg ctgatctacc ccctgcacaa 17340

gaccgacgag gagaaacacg aagcgaagct ggccaagcgc cggcaggcag ccgccaaacg 17400

caaggcggcg atggccgtcg caaagcacaa cgcgaggaac gtatgagcaa actccgcaag 17460

caattcacca atgagtacct gcgaaacgtc tatgtcgagc tgggcctcaa gaagggtgcc 17520

gagcacctga ccgagcattc gcgcttcggt gaggtgagcc gccagtgctt ccgcaactgg 17580

tgcatcaagc tgggcttcca cgacagcagg acgcgcggca tgtacgccaa gaagggcgcg 17640

atgcactggc tgggccgcaa ggctgccgag gtagtgcgca agttccctgg cgccgtgggc 17700

aacgtggtag gccagggtcc gaaggtgctg agcctggaca tcgagacctc gcctatcgag 17760

ggctgggtct ggtcgctctg gaagcagaac gtgggcctca accagatcaa gcgggactgg 17820

accatcctgt cgttctgtgc gaagtggatg cacagcgacg aggtgatcta catggactgc 17880

cagggtgatc ccttggacga catgcacctg ctggtcgcgc tgcacaagct gttggacgag 17940

gccgacatca tcatcgtcca gaacggcaag cgcttcgacg tgcccaagat caacgcccgg 18000

ttcttcctga acaagatgcc gccgccgcga ccgttcaagg tgatcgacac cttgatcatc 18060

gccaagcagc aattcgcgtt caccagccgc aagctggagt acatgaccca caaggcatgc 18120

accatcaaga agcgactgca cggcaagttc cccggattcg acctgtgggc ggcctgcctc 18180

caggacaacc cggaggcgtg ggaagagatg cgcctgtaca acatcgacga cgtacggtcg 18240

atggaagagc tgtacatcct gatgcgtcca tggttcgtcg gccaccccaa cgtggccgtg 18300

tacttcaatg acgccgaacc gaccatccgc tgcccgaagt gcggcgacac ggatgttaag 18360

caagaaggct gggtgcatac gcagaccggc aagtacgagc actatcactg cggtggctgc 18420

ggtggctgga gccgagggcg gtacacccgc aacacctcgg aacagcgcaa agccctgctg 18480

agcaactaag gaggtagcat gagcctagca ttcccggact cttacgagtc gacgatcacg 18540

actgaaccgt accgcaaagg tgcgagtctg gaagaacgca aggtcggcaa gcttcccatg 18600

cacctggtag tcgaggggtt cccgctgctg aagcgggagc ttgctcgaat gatgcaatgg 18660

gctgccgagg tcaaggggta tctgccgcac gactggaaga agatgacggt gggcgagttc 18720

aagtccgccc aacacaggca cgagtccaag cggctgatcg acgggccgct ggatgacgag 18780

tccaacctga tgcacctggt gcatgaggca ttcaacgcaa tggccgccgc cgaggtggcc 18840

ctgatggacc gggagaaagg caatgagtaa aatctgttgg tgtacccgac cgcacgagac 18900

cgatgaaggt gttcgggtca tctgggcctt caacgagcgg ggcatcgggg tcaactacgt 18960

cacagcgtac atcacgccgg cgatggtcag ccatcgggac tggagcgatg tcatactccc 19020

ggacattctc cgggagatgg cggagcgcct ggagcgggaa gtgaagctgg tggaactgcg 19080

ctggttccgc gctgagattc tgagctgcgg ggaatggcgt gactaccgag cgatgacgct 19140

ggaggggcg gttagcctgg ccgaggccga gtggggtccc gaggatatcg ggcgcgtaat 19200

cgaaagacga taggagatgg aatggacctg atacagcagc agatcgccca cgaagaggcc 19260

ctggtcgggg cggcgcagaa tgacgcccgc attgccttgg aaaaggcgat tgcccaaggg 19320

tccatcgacc gcatcccgag ggcgcgcatc atgttgatgc ggatgctccc catcgtgacc 19380

gaagcgatct tcgcccacca ggaagcgaag gcggcggggc cggcagcgaa gcttcggcac 19440

ctgctgcgga tcatcgacgc ccaggacctc gcggtcatgg cgctgcgggc tgggctgtcg 19500

atgctcatca actacccaac gatcacagcg acgaagtatt acacccacat gggtaagata 19560

ctctgtcgag agatcgaagt gcggttggcc ttcaaggtca accaacccta ttacgaccgg 19620

acgctggact acctcaagac cagcaggact cgcagcgtcc ggcacatcca gaagacgatg 19680

gacgctcttc tggacgcggt actaccggaa gaggcacgta tcgacctgcc ggatggcgac 19740

tacctgcgcc tcggcaagtt catcggtgat ccgctgatac agtgcggcct gttcgagccg 19800

aaccgcttca caggtcgtgg aggtactagc gtccacctgg agccgtcgcc ggaagccaag 19860

gagttcctgc aagacccttc ggcggcgatg acctggggag gcccaggccg tagcgtgatg 19920

ctggcaccgc cgcgaccatg gaacgactgg tgcgatggcg gttactacag cgctaaggcg 19980

cagaaacacc atgtgctagt gcgccgtacc aagcaccaga ccaagcgggc gcgccagatg 20040

cagctacgcc acctgggccg ggacaagatg cccagggtgt atgaggcggt caacgcgctg 20100

caatcagtgg cctacgagat caaccacgac gtgtacgaga tcatcgagcg cgtcttcact 20160

tccggcggcg gtgtgctggg catccctcag cgcacctacc cggacaaacc tgagttcccg 20220

ctcggcgacg agtgggccaa ggagaacgcc agtgaacaag agctggaagc cttcaaccgc 20280

tggaagcgat ccgtccaccg atggtacacc ggcgagcggg agcataccgc caagcttcgc 20340

gagtttgctg cactctaccg agttgttcga gagcatcatg gcaaggcagt gtacttcccg 20400

atgcacgttg actcccgtgg ccgcatgtac tattggggca caccgaatcc ccaggggtcc 20460

gacatcgcca aggcatgtct gcgattccac gaaaagcgtg ccctcggtaa gcgcggactg 20520

tactggctca aggtccacgt cgccaactcc ctcggatgcg acaaggtgta cttcgacgac 20580

cgagcagcct gggtcgatga gcgctgggac gacttccagc gagcgctcga cgaagggccg 20640

gagaactatc cgaatctctt ccccgaagac gagtccccac tgtgcgccat cgcaggtctg 20700

ctggagttgc gggcggccta cgcttccggc aatcccgagg gctacgccag tggtttcatc 20760

gtccacatgg acgccacctg ctccggcctc caacactact cggctattct ccgcgacgag 20820

atcggcgggg cctacgtcaa cctgctgcca cctggacttg caaaagctga tatctactcc 20880

cgagtgctcg gactcgttaa tgagtctctg gagagagacc gagcggaagg cgcggatggc 20940

gaggcgcggg gttatgccat tctatgggat aaagctggtc tgacgcggag cctgaccaag 21000

aagccctgca tgacgctggt gtacggcacc acgttcaagg gcgtcgtgga ccactgcctg 21060

gactacctcg acgagtccgg tgtggagatt cccgagggtg tgccgtcata ccgcctagga 21120

agctacatgg cgacgctcat actggacgca atccgcgaga cagtaccatc ggcagtcttc 21180

gccatggagt ggctccagcg gcttgctagg gcccttcctg acgcatccaa ggatttgcac 21240

tggaccacgc cgctcggcat gcaggtcttc cagtcctacc cgaagaccga ggaggtgcga 21300

gtacggctgc gcgccgaggc tgtcgagtac gtcaccctgt acgaggccaa ggacgagctg 21360

gacccggtac gcaacgccaa cggcatcgct ccgaacttcg tccacgggct ggacagcagc 21420

cacctgggcc tgacggcctt ggcatgcgcg gcagagggaa tcccgatcca ggccatccac 21480

gacagcatgg gcacttatgc ggcagacgtg gaccggatgc acgttcacat cagggagcag 21540

ttcatcgcca tgtacagtgg cccctgtgtg ctcgtagagc tggcaaagca gcttggtata 21600

gaggctaccc cgccccggag aggatcgttg aatctggagg ctgtacggga ctcctgggcg 21660

ttcttctgct gaggcggatt atgtcaccca cataggagca agtgcatccg tccaaggccc 21720

tcgtagaggg agcgggggag aggagaggtc agggaagacc tggtagagga gaggtgaaga 21780

tgagaatgga tgactacgaa ggattctaga tagaatagac taaccagcat aggagatatg 21840

atagatggct actatgaaga cccaccgccc tacggttatg tcacccacag tggaaggatc 21900

gagaacaggc aagggtacgg cccgtcctgt cacgttcacc tctcagcaga tcgagtggtt 21960

agaacagacc ttccccgaac atcagatcgg tcctggaacc acgatggaag acatccagtt 22020

ccaggccggt aggcgagacg tggtgcgagc agtacgcctg cgccgacgcg atgccatcgc 22080

agtggagctg aagtgatgaa caagtccatc tggcgagtcc acgcaaaggc cggcactccc 22140

tcggaactcc agggcctgtg ctggctggcg atacaggagt tggaggagtt caccctcttc 22200

cgctcgaaag acgacgccct gaatgcgatg ctggacagta tcgagggcaa tgatcgaacc 22260

gagctgttgg tattccgcga tggccagttg gctggcggtg cctgcattgt gttcgaggac 22320

gatccccacg tcggcccgtg cgtcacagca cagtggcagt acgtcctacc gcgctaccgc 22380

aatacaggcg tggtccggga gttcatccgc gaactccacc gtcaggccgg ctggggtcaa 22440

atccccctcg tgtgctggag ccatcgtgaa agcgatagcc ggtacacgat ccactaccgg 22500

agagccaagc cttatgggca agaaagtaaa gaaggtgctg ggcaagacca tcatcggcaa 22560

actcgctgat ggcctgctgg gcaccgacct gagcggcgca caatccgatg cccgcaagat 22620

ggaagagcag aaccgcctaa tgcagcagca ggcggaccag ctcgcacgaa accagcaggt 22680

tgacctcacc gccgagaacg tggcgcaggt tgacctagga gcgatggccg atgccactgg 22740

caccggcacg cgacggcgcc ggaatcaggc gggcacaggc gtatcgcaaa ccctcggtat 22800

caactactga cgaggtacgc catgaaaacc accgcagcta tgctgtggga gaaacttcgg 22860

gatgggagcg tggagagtcg agccatcgag ttcgccaaga ccacgcttcc ctacctgatg 22920

gtcgatccca tgtccggcag ccggggagtc gtagagcatg acttccagtc cgccggtgcc 22980

ctcctggtga acaacctcgc cgccaagctg gcgagatcgc tgttccccac ggggattccg 23040

ttcttccgat ccgaactcac tgatgcgatc cgccgcgagg ccgacagccg ggacacagac 23100

attaccgaag tgaccgctgc cttggctcgg gtggatcgca aagcaacaca gcgcctgttc 23160

cagaacgcct ccctggcggt cctgacgcag gtgatcaagc tactgatcgt gactggcaat 23220

gctctgctgt accgagacag cgccgccgct acggtggtcg catggtcgct ccgctcctat 23280

gcggtgcgtc gagatgcgac tggccgctgg atggatatcg tcctaaagca gcgctacaag 23340

tccaaggacc tggatgaaga gtacaagcag gacctgatgc gcgcaggccg caacctatcc 23400

ggttcgggca gcgtggacct gtacacccac gtacagcgca agaagggcac ggcgatggaa 23460

tacgccgagc tgtaccacga gatcgacggc gtgcgtgtgg gcaaggaggg ccgctggcct 23520

atccacctgt gcccgtacat cgtgccgacc tggaacctcg cacctggcga gcactacggt 23580

cgaggccacg tcgaggacta catcggcgac ttcgccaagc tgtccctgct gagcgagaaa 23640

ctcggcctgt acgagctgga gtcgctggag gtcctgaacc tcgtggacga ggccaagggt 23700

gcggtggtcg atgactacca agacgccgag atgggtgact acgtgccagg tggcgcggag 23760

gccgtccgtg cttacgagcg tggcgactac aacaagatgg ctgctataca gcagagcttg 23820

caagccgtag tcgtccgcct gaaccaggcg ttcatgtatg gtgccaacca gcgcgacgcc 23880

gagcgcgtta ctgccgagga agtccgcatc actgcggagg aggcagagaa cacgctgggt 23940

ggtacatact cgctcttggc tgagaacctc cagtcgcccc tggcctacgt ctgcctatcc 24000

gaggtggatg acgcgctact ccagggcttg atcaccaagc agcacaagcc ggctatcgag 24060

acgggcctcc cagctctgtc ccgctccgcc gctgtgcaga gcatgctcaa cgcttcccaa 24120

gtcatcgctg gcttggcccc gattgctcag ctcgatcccc gcatctcgct accgaagatg 24180

atggacacga tttgggcagc cttcagtgtc gatacgtcgc agttctacaa gagcgccgac 24240

gaactggaag ccgaggcaga acagcagcgc cagcaggccg cacaggccca ggcagcgcag 24300

gagaccttgc tggaaggcgc ttccgacatg accaatgcac tcgcaggagt ctgatagatg 24360

acccaaccga acgatcagca actgccaccg ggcctcgcta acctggttgc caacgtaccg 24420

cccgccgccg cgccgacccc gagtcatgtg caggtgttgc cgaacccggt gatccagccg 24480

caggctccgg tccagcccgg ccaggtaggt gcgccgcagc aactggccat cccgacccag 24540

cagccgcaac ccgttccgac cagcgccatg acgccccact accagccggt agcggtgccc 24600

gtcgccggtc aacccgttgt tccgcaagca cccgctcagc cggccccggt agctccgccg 24660

gctgcgggtg cagttcttcc cgagaacctg gaagtcccgc cgcctccggc cttcactccc 24720

aacggggaga tcgtaggcac cctggcaggg aacctcgaag gcgacccgca gttggcgccc 24780

tctatcagct atctggaagc attctctgac aagctggata ccgtccgtgc cttcggcaag 24840

gccgccgaga accgcgatcc gcgattcatc gacgagcact atctgaagga agtcctgggt 24900

ccggcccagg cacagcacgt catcaacgtg gccaagggcg tcctgaccta tgtcgatgcg 24960

cagaccaagg ccgtcctgaa tcagacctat gccgccgtcg gcggtgaggc cgtcctgaag 25020

caggctgccg gagtcttcaa ccagcacgct gacccggcca ccaaggccgc catcggtcgg 25080

ctgatggact cgggcgatgc ccaggccatg cagtacgcag cgaagcaaat tgtggccttc 25140

gcacaaggct cgggtgccgt ggtacaggct accggccaac ccctgggtgc tgcggcacct 25200

gcactggcag ctctgagcgc tgagcagtac cgcttggaag tatctaagct gccgctgaac 25260

gcatccgaag ccgagatggc tgcgctgcgc gagcgtcgta aggcaggcat ggcgcagggt 25320

atctaacgac cctgccctac tccggcctta aacccacatc caaaagagag agaatcgcat 25380

gagctttctg aacgacctga ctcgtccgaa ctacgctggc aagaacgcgg acgttgacat 25440

ccacctggaa gagcacctcg gcatcgtcga taagcacttc gcctacacct ccaagttcgc 25500

accgctgatg aacatccgcg acctgcgtgg ctcgaacgtg gtccgcctgg atcgcctggg 25560

taacgtcgag gccaagggtc gccgcgccgg tgaagagctg gagcgcagcc gagtcgtgaa 25620

cgacaagtgg aacctgaccg tcgacaccct gctgtacctc cgccaccagt tcgaccacca 25680

ggacgagtgg acccaatcct tcgacatgcg caaggaagtc gccgagctgg acggccagga 25740

actggctcgc aagttcgacc aagcctgcct gatccaggtg atcaaggctg ccgcgatgga 25800

cgcgccggtg gacctggaag atgcgttctc gccgggcgtg ctggagaaac tggacctgac 25860

cggcctgacc gccaagcagg ctgccgacaa gatcgtccgc atgcaccgcc gcgtagtcga 25920

gaccttcatc gaccgcgacc tgggcgatgc ggtttactcc gagggcctga ccccgatgtc 25980

gccgcgtgtg ttcagcctgc tgctggagca cgacaagctg atgaacgtcg agtaccaggc 26040

aaccggcgcg accaacgact acgtgaagtc ccgcgtggcc atcctcaacg gcgtcaaggt 26100

gctggagact ccgcgcttcg ccaccaaggc aatcgcagcc cacccgctgg gccgtcactt 26160

caacgtgagc gccgaggagt ccgagcgcca gatcgccctg ttcctcccga gcaagaccct 26220

gatcaccgcc caagtggcgc cggtccaggc caagctgtgg gaagacaacg agaaattctc 26280

gtgggtcctg gataccttcc agatgtacaa catcggtgcc cgtcgtccgg acaccgctgg 26340

tgccatcgaa ctgaagggta tcggcgcctt cgacatcacc gcgtgatgcc acgaaacccc 26400

gcacttcggt gtggggtttc ttcaaagcct aacgacccgc gcagattccc tgcgtgggtt 26460

tttgcgcttt aggagaaacc ctatgctact actcgacgca gtgaatgtca tcctgcgcaa 26520

gatcggcgag ctgccgattc cgagcatgga tgagacgtat cccaccatgg ccattgccct 26580

cccggagttg gaggaccagc gcatccagtt gctgacgcaa ggctggtggt tcaacacctg 26640

gtggaagcac aagctgacac ctgacccgca gggtcgcatc aacctgccca aggatacctt 26700

ggcattctac cccgactccc cggacctcca gtgggacggc ctgggagtac gggatgccaa 26760

caccggcgac gaccgtatcg gcaagtcggt cgagggtcgg ctggtgctgt cccgcgagtg 26820

ggaccgtatc ccggagattg cgcagcgcgt cattgcgcac caagccgccc ttgcggtata 26880

cacccacgag attggcccgg acgagaccgc ccaggtcatc gcccaggaat tgcaggcgta 26940

tcagaacgaa ctgtctcgca tgcacactcg atcccgtccg ctgaacaccc aggccaagcg 27000

tagcttcagc cggtggcggc gtagcttgag gacctgagca tgagctacaa gcaatccgcg 27060

tatcccaatc tgctgatggg cgtgagccaa caggtgccct tcgagcgcct gcccggccag 27120

ctcagcgagc agatcaacat ggtatccgac cccgtgtcgg gactgcggcg gcgcagtggt 27180

atcgagctga tggctcacct gctgcatacc gaccagccct ggccgaggcc gttcctctac 27240

cacacgaacc taggtggccg cagcattgcg atgctggtgg cccaacaccg tggcgagctg 27300

tacctgttcg acgagcggga tggacgcctg ctgatgggcc agccgctggc ccacgactac 27360

ctcaaggccg acgactatcg gcagctacgg gccgctacgg tggcagatga cctgttcatc 27420

gccaacctga gcgtgaagcc cgaggccgac cgcaccgatg tcaagggtgt agaccccaac 27480

aaagcgggct ggctgtacat caaggccggg cagtattcga aggcattctc tatgaccatc 27540

aaggtcaagg acaacgccac gggcaccacc tacagccata ccgccactta cgtgacgccg 27600

gacaacgcca gcacgaaccc caacctcgct gaggcgccat tccaaacgag cgtaggctac 27660

atcgcgtggc agctctacgg caagttcttt ggtgcgccgg agtacactct gcccaactcg 27720

acgaagaagt acccgaaggt ggacccggac gccaacgcgg caaccatagc cggctacctc 27780

aaccaacggg gcgtgcagga cgggtacatc gcgttccgtg gtgatgccga tatcgtggtc 27840

gaagtgtcca cggacatggg caacaactac ggcatagcct ccggcggtat gagcctcaac 27900

gccacggcag acctgccagc cttactgccg ggcgcgggtg ctcctggcgt gggtgtgcag 27960

ttcatgggcg gcgctgtcat ggccaccggc tccaccaagg ccccggtata cttcgagtgg 28020

gattccgcta accgccgctg ggcagagcgg gccgcctacg gcaccgattg ggtcctgaag 28080

aagatgccac tggccctgcg ctgggatgag gctaccgaca cctacagctt gaacgagctg 28140

gagtatgatc gacgtggctc cggcgacgag gatacgaacc ccacgttcaa cttcgtcacc 28200

cgaggcatca ccggcatgac gaccttccag ggtcgcctcg tcctcctgtc gcaggagtac 28260

gtctgcatgt cggccagtaa caatccgcac cgctggttca agaagtcggc agccgcgctg 28320

aacgacgatg atcctatcga gatcgcagcc caggggagcc tgactgaacc gtacgagcac 28380

gcggtcacct tcaacaagga cttgatcgtc ttcgccaaga agtatcaggc cgtggtcccc 28440

ggtggcggca ttgtaactcc ccgcacggcg gttatcagca tcaccacgca gtacgacctc 28500

gataccaggg cggcacctgc cgtgactggc cgcagtgtgt acttcgctgc ggagcgtgcc 28560

ctgggtttca tgggcctgca tgagatggcc ccgtctccgt ccacggacag ccactacgtc 28620

gccgaagacg ttaccagcca catcccgagc tacatgccgg ggcctgctga gtacatccag 28680

gcggcggcct ccagcggcta cctggtgttc ggcaccagca cggcggacga gatgatctgc 28740

caccagtacc tctggcaggg caacgagaaa gtgcagaacg cgtttcatcg ctggacgttg 28800

cggcatcaga tcatcggcgc ctacttcact ggcgacaacc tgatggttct gattcagaag 28860

ggccaggaga tcgccctggg acggatgcac ctgaacagcc tgccagcccg tgagggtctg 28920

caatacccta aatacgacta ctggcggcgt atcgaggcga ccgtcgatgg tgagctggaa 28980

ctgaccaagc agcattggga cctgatcaag gatgcctctg ccgtgtacca gctacagcct 29040

gtggccggcg cctacatgga gcgtacccat ctaggcgtga agcgcgagac gaatacgaag 29100

gtgttcctcg acgtgcccga ggccgtggtc ggggcggtgt atgtggtcgg ctgcgagttc 29160

tggtcgaagg tggagttcac tccgccggtt ctccgggacc acaatggcct gcccatgacc 29220

tcgacccgtg cagtgcttca tcggtacaac gtaaacttcg gctggaccgg cgagttcctg 29280

tggcgcatca gcgacacggc tcgacccaac cagccgtggt acgacacgac gccccttcgg 29340

ttgttcagcc ggcaactcaa tgccggggag cctctggtgg atagcgctgt ggtgccgctg 29400

ccggcacggg tcgatatggc cacgtccaag ttcgagctga gctgtcacag tccgtacgac 29460

atgaacgttc gggctgtcga gtacaacttc aagtccaacc aaacctacag gagggtgtga 29520

tggctttctg gctaccacta ttggccgctg gcggcatgtc cgcccttcaa cagggattgg 29580

ccaacaagga agagcgcaac aagatcaagg ccgagaacaa ggctcgactg aagacggacc 29640

tcgacaacct gggcgccgct gcccgcgaca tcgccaacct cggagtcatg gctgctagct 29700

accgcaagca agccgtggcc tcgcaggtgg aggccaagcg ccaggggatg ctagccggcg 29760

gaagcgccga ggctcaggcc ggggcgttcg gcgtcaaggg tgcatccgtc gatgcggtgg 29820

ccctggatat cgagcgggag gtcggcgagg ccctgatcca gattgacgac aacctggaca 29880

atcagatgtg gaacctcgcc gagcaggcgc actccatcca ggctcaggct aaggccggcc 29940

tgctgggtca gaagagtacc acggcggggc aacggtcccc gctggtggcc ggtctgatgt 30000

cggcgggttc cctgtacgca agtcaatact tcaagttcgg cgccacgcct aaaggaggca 30060

actgatggcg gaatcgcaac gtgcttccca agagcttggg atcaacgtcg gacagacgca 30120

actccagccg ggccagagtg ctcggcgcgg agtgcgcgac tccgaggtca actacagcgg 30180

tccgagcgta ggctcgcaga ttctcgacgg catcctgggt gccggtcagc agatcgctgg 30240

caaatggttc gagcacaacg tgcagcagga agttctgcgc ggtgagcgtg cccgtatggc 30300

cggcgaggcg gaggaggcag tagacagcaa cgtactggcc aaaccattcg tgaagggtgg 30360

ttggcgtaag caggactacc gtatcgccca ggcggacttc agcctgaaga tgcagcgatt 30420

catcgccaac aagggccggg agatgactcc cgaggagttc cgcaagtacc tgtcccagga 30480

ggctacgcac gtcctggact cgaccgaggg catgaacccc aacgatgcct tacaggcgct 30540

ggcgcagcag cagaaggccg aggaacagct cttcggcatg caggctaagg cgtacatgga 30600

ctggtccatc gaccaggccg cccgtggctt ccgtacccag ggtaacagta tcctggccaa 30660

ggctgtgcag gctcaggcca ccggcgacga actgtcccgg cagctcagcc tggaagaggc 30720

cggcctgttc tataccaaca tcatgacctc cgaggatatc ccgctggagg tgcgcgacaa 30780

ggtaggcatg cagttcctgg cggccagcct ggacatgaac cagcggggca tctatgaggg 30840

cctgcgcgat gccgggttcc tggacagtat gtcctttgac gaccggcgtg cgctcaacgg 30900

cctctatgaa aaatcgaagg cacagacccg tgccaaggaa tcgatggcta ccctgcgggc 30960

cgacgcggac ttccagcagc gggtggccaa cggcgccatc acagaccttg ccgaggttga 31020

agcgtactca cgaggcatgg tcgaggaggg ccgctggagc gacgctcagg ccatctcatt 31080

catgaccaag gccatgaccg gtctgggcaa tgcccaacgc atgcagggca tcatggcggc 31140

cctggaagcg ggggacatca acgccctaca cacgctgggg acgaacgtta ctgaggccct 31200

ggagcagtgg gacaagatgc aggccgccaa cggctcaagc ctgactgacc gtctcgtgca 31260

gggcacacag ctcggcctgc gcctggggac cttccccaag acctacggcg agtccgtggg 31320

cagcgcggtg cgcatgatcc aggccgccaa agaaggcgag gcaaacccgg agctggtcaa 31380

cacgctgaac agcatcttcg agcaggtggc ctcggcccag gagatcaacc cctccgccgg 31440

caacgtgatg ctatccggca tcccggaagc cgagcaaggt gccgtggcct gggcactcaa 31500

gcagatgaag atgggcatcg caccagctca agctctgcgc gagttcagcg ccaacgccga 31560

agtcgtgaaa cagatggacg agttcgagaa aggccagaac accaaggcat tcaaggacaa 31620

cctcggcaag caggtcaacg acaagttcgt gaacaacatc ttcggtcggg cctggaacat 31680

gctgaccggt gaaagcgacc tgagtaacaa cgaggccgtt ctcagcatgt accgtcgagc 31740

aaccatcgac gaggcgaact ggctggccag cgaccgcaag catgcgggtc tgctcaccag 31800

tgacacgggc cgcgaggccc tgctggagat cgccgccgcc aacgtgcgta accgcaccat 31860

ccaggtaggc gaaggtcgga atctgaagga aggggaccta ttcagccgcc gcgatagcgc 31920

gccgctgatc ctgccgcgtg gcaccaccgc cgagcagcta ttcgggacca acgacaccga 31980

gaccatcgga accgtcctgg ccgagcagca caagccgcat gtcgaaggac tcctcggcta 32040

caagtcggta gtcgccttcg agtacgaccg caccaggggc agcctcctcg ccgtcgagta 32100

cgacgagaac ggtgtggccc tggaccgcac gcgggttgat ccccaggcag tcggtaacga 32160

ggtgctcaag cgcaacgcgg ataagctgaa tgcgatgcgg ggcgccgagt acggtgccaa 32220

cgtcaaggtc agcggcacgg acattcgcat gaacgggggt aacagtgccg gcatgctgaa 32280

gcaggacgtg ttcaactggc ggaaggaact ggctcagttc gaggcttacc gaggggaggc 32340

gtataaggat gccgatggtt atagtgtggg cctggggcat tacctgggca gtggcaatgc 32400

tggggcaggc actacagtca cgcctgagca agccgcgcag tggttcgccg aggacaccga 32460

ccgcgcactc gaccagggtg tgaggttggc cgacgagctg ggcgttacga acaatgcctc 32520

tatcctggga ttggccggta tggccttcca gatgggcgaa ggacgtgccc ggcagttccg 32580

taacaccttc caggcgatca aggatcgcaa caaggaagcc ttcgaggctg gtgtacgaaa 32640

cagcaagtgg tacacgcaga cgcccaaccg ggccgaggca ttcatcaagc gcatggcgcc 32700

ccacttcgat acaccgagtc aaatcggtgt cgattggtac agcgccgcaa cagcggagta 32760

agacatggca aagcaattca agggccgcat gacgcccaag tatccccttg accaagtaca 32820

gctcgacgag gcccaagtac agggccaact cgacgcggtg cctaccgtgg ggttcgacgc 32880

cctgacgggt ggtgagatcg gagaacggaa cgtggcagcg ggccaacgag ccaatgcgcg 32940

ggaactggaa cgcatcgtag cggaccagga actgccggcc cttgaccgtg cttccgcact 33000

ctggaaccag tccaccctcg tcggacgctg ggtcgatgcg ctccagctcg acgcagacct 33060

tgcggcgaac agtaccggcg aggtggaccc taacttcgac gctgggacct atggggtcca 33120

ggcgctccag gcggcaggta tccagccgac tgataactac cttcagatca tggcccgtgc 33180

cggcaatgcc gaggacgcgg cctacctcct atcgaggatt caacggtatg agcaggacga 33240

acaaatcgtg cgggacaacc catactggaa cttcgcggtt ggtatgctgg acccggcagc 33300

cctggcagtt gatgcggtta ctttcggcgc tggccgtgct ctgcggctcg gtcgtgctgg 33360

catggctgct gctggcggcg ctgggcaagt cgggtatgtt gctgggctgg atgccgcagg 33420

ggccgatgtg gatgctggaa cctacatcgt ggcgggtgct cttggcgctg gcgtgggtgc 33480

tctgctgggg tctggtgcgg gacgcattgc cgcagaggcc ccaacgcaac cgcatgtgcc 33540

cgaagtatcg gcgcctactg tcgggctgcc agaagtagcc atgaccgccg aggaggccgc 33600

agcacgcggc ttcaaggcag gtgacgtggt agacctgctg gacgagggca ctgtgctatc 33660

ccgtgtcagt gcccgcgtgg agcaggctga gataccggct attccgcgac gtgacactgc 33720

cttcggcgac gagctgcata gcctgtcggg ccggaagctg tctgaggtcc tggaccacat 33780

caagacccac gcagaggtgc ccaagccgct ccagggcatc gccgccaagg tggctgacac 33840

tatcaggacc ctggagggcc tggggcagcg taccgcgttc cgtgtggtgc agggcggtga 33900

cactgccagc tctgccttcc tcaaaccggg tacggcgggg attcactcca cccagggcct 33960

cgacaccctg gtccaggtac gcggcagcac cgcacctggt cgagttggca ccaacccggt 34020

gaccgtgctc cacgaggcgg ttcacgctgc caccgtgggc gtgatgaacg ccgccctgcg 34080

caaccccggt gcgatgagtc cgaaggtggc tcaggccatg cagaccctgg agaatgtccg 34140

gggtaacgtg ctcaacgccc tgaagcagga ccgcgccgcc ggtcggcaac tgtccgagtt 34200

cgaagagaca ctgctggccg gtaactccaa caccctggcc aacgtcaagg aactggtagc 34260

ctggggcctg acggataccc gcttccagcg gaccctgaat cgcctccgct acagcgacgg 34320

cgggccgggc ctgtggtccc gcttcgtgga gggcatccgc accctgctgg gtctgcggtc 34380

cgatgctgac acggccctga gccgcgtcct ggccgcctct gagacgatta tggaggccat 34440

gcccggttac actaaggcac aggccaagtg ggccaacaag ggcgctccgg taaccgagga 34500

ggccagcctg gagaccatcg tccggtccac cagggagcgc gcccgcgagg gtgccggctt 34560

cgtgaacagg ttcttcagcg aggcagacct cctggcacag cccggagagg gcgcacggcg 34620

actcctgagc cgtcttattg acgacccggt acgtcgggat gggttcagca cgaacgacaa 34680

cgcagcgagc tatctccgcc gctatcggaa cgagttcgag ggctacgtga agtcctacga 34740

cgagatgatg gccaaggcaa tggctgagca gggtgtgggc ctgacggcac gtgcgctgaa 34800

ctcccgccgc gccatggcag tccgggacca gctcaacgag caggtcaccc gcgagctgct 34860

gcgccgggac cgggagtgga ccgcctacgg cagcgtccgc gtggacccta acctacctcc 34920

gaccatcaag gccctggccg accgctcaga cgagattcat ggtctgatgg gccagcgtgc 34980

cagggaagct ggggtgcgcg ggttcgagaa cttcgcaccg cgaccgggat acttccaccg 35040

ctcgtggaac tggtcgaaga tggcgcagat ggacgaggcc gcccctggcc tggcccgccg 35100

tgccatcagt gaggccgtgt tccgtggcat ccctgggctg gagcgcgccg acgccgatac 35160

catcgcacag gccattgtgc agcgggcgcg ggatcgggcc accggaatcc gctccgagtt 35220

catgggcgcg atgggcgtgg cggacacggc attcatccgg caggcgctgg aggaggccaa 35280

cgtgtcccag gccaagttcg acagcatcat ggccaagatc gagcagaagc agtccgacca 35340

gggcaccgtc aagtacggca agggccggct gtcgctggac atgaccgccg agatcaacca 35400

caacggcacc gtgtatcgtg tgcaagacct gatcgaccgg gacctcgacc ggctgatgga 35460

gaactacgcc ggcagtatgt cgggccgctc agcattggcc cgcgcaggca tgccggggga 35520

ctcggagatc gaagccttca tccgggagta ccagcgagag gcagcccacc tgggcaccga 35580

taaggtgcag gagctgacgg ggcaactgcg gggagtcttc ggggacttca ccggcaacgt 35640

gccgagggag catcagctcg gcccggttgc tcagcgggcc agcggcctaa ccagcgccac 35700

catgctggga ttctccggcg tgtaccagct cgccgaactg gccacgatgg cgcaccgtca 35760

aggcgtcttc aacgtcatga aggccatgct gaactcccgc ctgggagact tcgtgggcgc 35820

catgcgtcgc gacccggacc tcgctgacga gatgcagacc gtcctcggcc tgaacctcgc 35880

caacgatatc cggatgaagc cctggaagcg gcagttcgac accttcctgg tcagccaaga 35940

caccttcatg gatcgcttcc tccacgcagg taagcaggct gtcccagtgc tcaacggcat 36000

gaagttcatc cacaactggc aatcccgtat gaacgccaac ctcaccttga acaaggtggc 36060

gcgggcggcg caggggatg aagcagccct tcgcgtgctc cagcagtacg ggaaggacgt 36120

ggactggacg ccagtcctgg cgcgggttcg cggttatgtc acatacagag gaaggaacgc 36180

ccgatccatg aattggggcg cctggagcca agcagacgtg aacactgtca tgaacaccgc 36240

actgcggatc atggacgact cactcctgta cggtagggtc ggtcagaact cgggcttcgc 36300

tcggtctccg gtcggtcaaa tcctgggcca gttccgcagc tttgtggcct tcgcacacaa 36360

caagctcctc cggggaacct atgagaactc cggcgtgctt ggcgtggcct cgctcctcgc 36420

attccagtat ccgctcaccg cgctgatgat gggtgccaag gcagcgatca acggcaagtt 36480

cgacacctct gatgaaggca tccgcaagat ggccatcgac ggcatcggtt acactgccgg 36540

cctcggcttc accgccgaca tgtggggtgt gatcaccggg cactcccgga tgtccgcacc 36600

ggtctttggc ctggcggagc actccaacga ggtgttccgc ggcgtcaagg acctagtaac 36660

cggcgacgac cccgcagccg ccaccggcga tatcgtcaac ggcgccgcag gggcactgcc 36720

tttcgtcaac gtattcccgg cgaccaagtt gctgctggaa tccatcaaag gggaataacg 36780

tggctcggtt caagaatccc gagaccatcc acgtcgcaga tggggtcgag gctgtcttca 36840

gtctcgactt cccgttcctg cggcgtgagg acgtattcgt ccaggtcgat aagatactcg 36900

tcaccgacta tacgtgggta gacgacacca acattcaatt ggccgtggtg ccgaagaagg 36960

atcaagaggt ccgcatcttc cgcgacacac ccgcccaggt cccggacact cagttcagcc 37020

agggcatccc gttcctgcct cgatacatcg acgcgaacaa caagcagctc ctgtacgctg 37080

tgcaggaagg catcaacacc gcgaacctcg ctctcgacgg cgtactcgac gcgatccgca 37140

tcgccgagga agctcgtcgc ctggcacagg aagcactcga cgccgccaat gaggcgctgc 37200

gccgtgccct aggcttcgcc gagattcgca ccgtgaccga ggactcggac atcgatccga 37260

gctggcgtgg ttactggaac cgctgcatca cctccgagca gtccctgact ctgaccatgc 37320

agatggagga cccggacgag ccttggatcg agttcagcga ggtccacttc gaacaggcgg 37380

gcattcgcga cctcaacatc gtggccggcc ctggcgtgac catcaaccgc ttgcagaaca 37440

ccaccatgca gctctatggc gagaacggtg tgtgtaccct gaagcgcctc ggccctaacc 37500

actggatcat cttcggggcg atggaggacg actaatgcgt ggcattatcg caggtgtggt 37560

ggcgtcgcag attcgccggc ccaagccggt gctgaccacc atcacctacc cgcagtcttc 37620

ctcggatcgt gggggtatga cgtttcatgc catcgccggg atcatccaag ataccgtgaa 37680

gttcgcggat agtaaggacc tgggtagtta tgagatgctt gtgcgggacg ctaccctgaa 37740

gagcatggtc attacactca ctgaggttaa ggacagtagc gtctggagta tgggtgtgct 37800

gagtgcggca atcaaatccg tagttcagtt cttgacacca gtcgaggaga aatcctcgtt 37860

ggatatgagc atcatccacg gcgagcacaa gcaatcggtc attccatact cccgctgggc 37920

tgaggctggg tccctgtcca tgggtatcac agagggtaaa gtttatgtac catagcagca 37980

ccattcgagg tgagttcgat ctggagattg tacgtcctga cggtacagtc cgccagcacc 38040

tgcacttcaa gaacctgatc accgacttgg cccttgaggc catgagttcc aagggcgtcc 38100

cgagtggcgg ctggacgaac atgttcgccg gcactggcaa ccgtaccccg gtccccgctg 38160

acgtgtccct cgtggcgcct gtggctaatg ccagtgcctc gctgaactac ggcaaccgcg 38220

cagtgtggga ttccaccact ggcgagaaag tgcatactgg cacggggacc ttccgcgcag 38280

gttccttcca aggccagtcc ctggccgagg taggaatcgg tcgggtagtc tctgagctgt 38340

actcccgatc cctgatcaag gacgccaacg gcgatcctac cacgatcacg gtgctggtgg 38400

atgaggaact gcgtgtgacc tacactctgc ggattgctcc gccggcgtcc agtgaagtca 38460

agatcacgat gaagggtatc gagtacaccc tgagcatgcg ggaccgccgt accttccggg 38520

acttatcgcc cgagcctgcg gctgagtttg gcactcgcgg cagtctgtcg tggagcgcta 38580

tcagtgcgcc ggacagtaac ggccagacca agaccgccaa cttgagcggc gacgccggga 38640

ccgggattat ccaggttcct gcacagtctg cacagatcat gcgtatccag cccgccgatg 38700

ccaactggac ggaaggtatt cagtacctcc gctgggagac tccggcagga cgtgagctgg 38760

agatcaagct ggacccgcct ctggtcaaga acagcttgga gcgcgtggac atcaccgtaa 38820

cccacatctt caatcgggta tgattcagtt caagttcggt gactaccgga cccgtgtgcc 38880

cttccagggt gcgcgggacc ggcgggatat caacgaccgc agcgactacg tggacggtgg 38940

cgtcgccatc caagacccta gtcaaggtct gttgtatcag gagtggcacg ccgagctact 39000

cgaagacggc atctacctga cacctgagaa agagcgagtg actacccgca tcggaccagg 39060

tatcaatgaa ggcgtggcta gtatggcggt cacgttcgac cagaacatga actatgtcct 39120

ggtgtatacc aagcaaggcg aaggcttcat cgacttcttc gattccgcta ccgaagagcg 39180

caatgtgatg aaccttgggc cggtggacta tatcaagaca gacctagacg atcggcggcc 39240

agagggcagc gcctgggcgc aggttctggt ctgctacaca cggcagggaa acttctacgt 39300

ccgagccagc tcaactcgct ttactgaaga ggagcttatc gtcggtacgg gcaaagtgac 39360

ccggcctatc gtcaaatgcg gaatggcagc gaactggaga ttccaggtcc tgttccgagg 39420

gagaatgtaa tgagcaagaa gcagaccgcg agtgctgagc ggctgggcct gctacatgag 39480

ctggtctgca ccgccatcga gcgtaacttc aagtggtaca tggacaacga catcccgatc 39540

cccgcatcgg atatcgctgc cgccaccaag ttcctcaagg acaacgagat cacctgcgat 39600

ccgtccgaca ccatcaacat cgaccgcctc cgcgaggaga tgcggcaggc gcaggcggag 39660

aatcgccgta tcgcgctgga gggcttcatc gccggtgaga cggacgatga gatggaacgc 39720

ctgtacaccc actaaggagg cagcatgacg ccgcaagaac gattccagat agcccacgag 39780

gtgcgggaca tgtacccgcg cttccgggac ttctgcctgg acgccatgct gttcctcggc 39840

ttcaagatga cgtggatgca gctcgacatc gccgacttca tgcaggactc gcccaacaag 39900

gcgatggtcg ctgcacagcg cggcgaagct aagtccacca tcgcctgtat ctatgtggtg 39960

tggtgcataa cgcagaaccc ggctacccgc gccatgctgg tatccggttc cggtgacaag 40020

gccgaggaga acggccagtt gatcacgaag ctgatcatgc attgggacct gctggcgtac 40080

ctgcgccccg aggcccgcat gggtgaccgt acctcggcca ccagcttcga cgtgaactgg 40140

gcgttgaagg gtgtcgagaa atcggcctct atcaactgca tcgggatcac cgctgccctc 40200

cagggctacc gggctgacat cctgatccct gacgacatcg agaccacgaa gaacggcctc 40260

accgccaccg agcgggccaa gctgacgcgg cagtcgcagg agttcacctc tatctgtacc 40320

cacggtaaga ttctctacct gggcacgccg cagtcccgtg agtcgatcta caacggtctg 40380

ccggcgcggg gcttcctgat gcgcatctgg ccgggccgct tcccgaccct ggatgagcag 40440

gaacgctacg gtgactggct cgcaccttcc atcctagcgc gcattgcccg cctggaggag 40500

aaaggccaca acccgcgtac tggcaagggc ctggatggca ctcgtggctg ggcggctgat 40560

ccgcagcgct acaacgaaga ggacctgctc gacaaggagc ttgaccaagg ccccgagggc 40620

ttccagcttc agtacatgct ggacaccagc ctcgccgacg agcagcgtat gcagctcaag 40680

ctgcgcgacc tgctgttcat cgacgccacg catgagagcg tgccggagca agtggcctgg 40740

gctgccgacg agcgcttcaa gctcaagttc gacgcccacc gattcccggt catcaagcct 40800

gagctgtacc tgccggcgct gatggctggc ggctgggcac cactccagca aatgacgatg 40860

ttcgtggacc ctgccggcga cggtggcgac gagctgtcgt atgccgtggg cgggactctt 40920

ggcccgtaca tccacgtcgt gagcatcggc ggctggaagg gtggctttgc tgaggagaac 40980

ctggagaaat gtattgccct agctgcgcgt tatggcgtca aggtgatcta tgtcgagaaa 41040

aacctcggcg ctggtgcagt tggccagctc ttccgcaacc acatgcgatc catcgacccg 41100

gacaccaaca agccccgcta tgaggggatc ggcgtagaag accgccagaa gtccggacag 41160

aaagagcgtc gtatcatcga caccctgcgg cccatcatgc agcggcaccg tctgatcttc 41220

cacgtatcgg cgatggattc cgaccacgtg gcctgccagc agtacccagc ggacaagcgc 41280

aatgagcgct ccgtgttcca ccagattcac aacatcacca ccgaccgagg ctcactgccg 41340

aaggacgacc ggatcgatgc ccttgagggc cttgtccgcg agctagcacc cacgctcgta 41400

aaggacgacg aagccgcaac ccgcgctcgt gaagaggctg ccaagaagga atggctgaac 41460

aacccgatgg gttacactaa gtctgtcctt cggtctctcg gcatgggccg ggagcgtcgc 41520

aagggccgcc caaaaggacg aagactatga tgctcgatac cgccaccgag gcgggcaaag 41580

gcaccctcgc cgtcactggc gtggggatcg ccgtttactc gccctatgag atcgccagcc 41640

tctgtgctgc ggtactcacc gcgctctatg tgggcgccca gctcatcacc ctgctcccga 41700

agatgctcga tagcatcgcg gagcttcgcc ggaggttcaa gaagtgaaca agcccctgcg 41760

cggcgcagcc cttgcggctg ccctcgccgg ccttgtcgcc ctggaaggta gtgagaccac 41820

tgcctaccgg gacatcgccg gcgtgcccac catctgttct ggcaccactg ccggggtcaa 41880

gatgggtgac aaagccacac cggagcagtg ctaccagatg acgctcaagg actaccagcg 41940

cttcgagcgc atcgtcctgg acgccatcaa ggtgccgctg aacgtcaacg agcagaccgc 42000

cctgacgttc ttctgctaca acgtgggtcc agtctgtaca accagcacag cgttcaagcg 42060

cttcaaccaa ggccgcgcca ctgagggctg ccaagccctg gccatgtgga acaaggtcac 42120

gatcaacggc cagaaggtcg tatccaaggg cctcgtgaat cgccgcaacg cggagatcaa 42180

gcaatgcctc gaaccatcgt cgcaatactc gtccttgctg tggtagccct gggagcctca 42240

tacggcttcg tccagagcta ccgggccttg ggtatcgccc aggaggagat caagcggcag 42300

acggcccgtg cggaggccct ggaggtgcgt tatgccacct tgcagcgcca cgtcaaggag 42360

gtcgctgcca ggaccaacac ccagcgccag gaggtggacc gtgccctgga ccagaaccgc 42420

ccgtgggctg accggcctgt tcctgctgct gtcgttgaca gcctgtgcaa ccgccccggc 42480

gcccgctgtg ctgtgcgaac acccactgat tgaccctacc acccaggctg gcctgatccg 42540

cgctgtagcg gcctatcagg acgccctgga cctatgcaac gccttgaatc aaggagactg 42600

acatggcgaa cacccgtgag caatacctcg ctggccgtaa caccggcctg accttctacc 42660

aggtctgcca gcccggcacc gacaaccgca tcgccctgca cgacatggac gaggccgatg 42720

tcaaggccaa ggccaccgcc gtaatcgcag cagccaccgc cctgggcggc gaaggtggcg 42780

ctactccacc ggacccgctc accgcctaca aggtgaagaa cggtgacacc ctgcccgtgg 42840

acggcggtgg ttccgtgaag gtgaccgtag ccaacggtgc tatcaccaag gtcgtgtaca 42900

ccgcaccggc gggctgagct acagcccgtc ccacctgact ccatccctaa cacaaggaac 42960

tgaaccatgg caaccttcgc cgctgcaact cagaaagacc tccgcgcctt cgccggcgct 43020

atcgagaacc tgatccgccc tctggaagaa gcggccttgg gttccggctt caccgaggtg 43080

atcaccatca ccaagggcac cgatggcaac gagactcgca cctccgagcg taaggtacgt 43140

cccgagctgg tcgctaacct cgacgccctg atggccgctg tcgagaccgc caaagccgcc 43200

gtctacaagt aaggggacac catgagcaaa gccaaactac gagtcatcgc cgacaccccg 43260

gagctggagt cagtgctaaa agcattgctg accgccacct acgctatcga gga 43313

<210> 5
<211> 62
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 5
Met Lys Arg Phe Val Ile Ser Ser Lys Pro Ala Ala Lys Leu Asn Lys
1 5 10 15

Met Ala Ser Ser Glu Leu Val Lys Met Gln Arg Asp Met Ala Arg Arg
            20   25   30

Tyr Arg Ser Tyr Gln Arg Gly Gly Gln Gln Gly Leu Pro Met Ile Trp
        35   40   45

Asp Asn Met Met Arg Tyr Leu Lys Ser Leu Gln Asn Asn Val
    50   55   60

<210> 6
<211> 86
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 6
Met Gln Asn Val Lys Thr Pro Met Ile Gly Asp Ser Val Phe Ile Pro
1   5   10   15

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

Tyr Ile Lys Gly Ala Ala Met Ile Pro Phe Asp Lys Ile Asn Ala Val
        35   40   45

Tyr Ala Glu Thr Glu Lys Ala Lys Asn Ser Asp Ala Lys Ile Tyr Ser
    50   55   60

Val Arg Val Asp Ser Gly Asp Val Val Lys Val Ile Arg Lys Asp Asp
65   70   75   80

Lys Trp Leu Ala Val Ala
                85

<210> 7
<211> 134
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 7
Met Thr Ala Thr Lys Thr Glu Lys Phe Ala Trp Asn Glu Thr Asn Ala
1   5   10   15

Ala Thr Ala Val Glu Met Tyr Glu Lys Ile Ile Ala Ser Asp Gly Leu
            20   25   30

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

Ala Glu Ser His Val Lys Val Arg Ser Lys Leu Val Ser Ala Lys Val
50 55 60

Tyr Gln Lys Ser Asp Lys Pro Arg Lys Val Gly Gly Gly Ser Ser Leu
65 70 75 80

Arg Lys Ala His Tyr Val Arg Val Leu Thr Gln His Ala Ile Ala Asp
85 90 95

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

Leu Asp Gln Leu Asp Val Ile Ala Arg Met Val Gly Val Gln Asp Glu
115 120 125

Val Lys Glu Ser Ala Glu
130

<210> 8
<211> 89
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 8
Met Ala Leu Ile Lys Gly Ser Val Ile Lys Leu Thr Gly Thr Val Val
1 5 10 15

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

Pro Ser Val Lys Val Pro Glu Tyr Ile Val Leu Trp Val Asn Pro Asp
35 40 45

Ala Asp Thr Phe Gly Met Ala Ile Asn Arg Glu Val Phe Lys Pro Glu
50 55 60

Met Leu Glu Leu Ser Ser Arg Glu Ile Tyr Leu Leu Asn Tyr Ala Phe
65 70 75 80

Ser Val Glu Glu Lys Glu Val Val Lys
85

<210> 9
<211> 75
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 9
Met Ile Phe Phe Pro Thr Glu Ser Leu Ile Leu Ile Ala Gly Phe Phe
1 5 10 15

Ala Ala Ala Cys Leu Tyr Gly Tyr Tyr Asn Phe Met Glu Ile Gly Ser
            20   25   30

Glu Gln Thr Asp Leu Leu Arg Arg Asp Phe Trp Phe Lys Lys Ala Ser
        35   40   45

Ile Cys Arg Arg Trp Ser Ile Ile Phe Ile Ile Leu Ala Val Thr Phe
    50   55   60

Gly Ile Ser Ala Ser Ile Ile Pro Ala Ile Val
65   70   75

<210> 10
<211> 558
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 10
Met Ile Ile Ala Ile Glu Lys Gln Lys Ala Ile Leu Thr Ala Ala Asn
1   5   10   15

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

Cys Asp Glu Leu Ser Lys Glu His Tyr Gly Thr Ala Lys His Ser Ser
        35   40   45

Glu Ile Cys Asp Trp Leu Asp Ser Asn Lys Pro Val Lys Pro Ala Ala
    50   55   60

Glu Lys Arg Ala Gln Arg Val Ala Val Glu Asp Ser Arg Pro Val Ala
65   70   75   80

Ala Gly Gln Leu Asn Ser Ser Val Glu Ser Trp Lys Val Ile Pro Gly
                85   90   95

Arg Arg Phe Leu Leu Thr Ser Ile Gln Asn Asn Thr Phe Pro His Ala
            100   105   110

Asn Phe Trp Lys Thr Leu Gln Glu Ala Ala Lys Tyr Leu Gly Ala Thr
        115   120   125

Leu Leu Val Ser Lys Tyr Ala Tyr Asn Lys Lys Gly Phe Gln Asn Gly
    130   135   140

Gln Gly Asn Asp Glu Leu Lys Tyr Asp Asp Ala Phe Ser Asp Phe Ile
145   150   155   160

Cys Asp Glu Asn Val Phe Leu Gly Asn Arg Glu Thr Gly Phe Ala Phe

```
                165                 170                 175

Met Ala Glu Ile Asn Ile Leu Pro Thr Ala Asp Phe Pro Leu Ser Gly
            180                 185                 190

Phe Gly Glu Thr Ala Thr Ala Tyr Gly Leu Lys Gly Leu Ala Ile Gly
        195                 200                 205

His Ala Lys Ile Thr Ala Glu Ser Val Pro Ala Met Lys Gly Asp Thr
    210                 215                 220

Val Arg Arg Met Tyr Ser Thr Gly Thr Ala Thr Leu Lys Asn Tyr Ile
225                 230                 235                 240

Gln Gln Lys Ala Gly Gln Lys Ala Glu Ala Leu His Asn Tyr Gly Ala
                245                 250                 255

Leu Leu Val Glu Ile Asp Asp Asn Gly Asn Phe Phe Ala Arg Gln Ile
            260                 265                 270

Glu Thr Met Asp Glu Ser Gly Met Phe Tyr Asp Leu Asn His Lys Phe
        275                 280                 285

Thr Val Asn Gly Gly Glu Glu Val Thr Gly His Val Ala Ala Leu Gln
    290                 295                 300

Tyr Gly Asp Ile His Ala Glu Lys Leu Asp His Ala Val Ala Phe Ala
305                 310                 315                 320

Ser Trp Gly Pro Cys Asp Asp Ser Leu Val Asn Val Leu Arg Pro Arg
                325                 330                 335

Tyr Gln Ile Val His Asp Val His Asp Phe Thr Ser Arg Asn His His
            340                 345                 350

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

Asp Lys Val Ile Asp Asp Leu Ile Asp Thr Gly Arg Val Leu Glu Ala
    370                 375                 380

Met Glu Arg Glu Phe Ser Gln Thr Val Ile Val Glu Ser Asn His Asp
385                 390                 395                 400

Leu Ala Leu Ser Arg Trp Leu Asp Asp Ser Lys Ala Asn Ile Gln Gln
                405                 410                 415

Asp Pro Ala Asn Ala His Leu Tyr Tyr Arg Leu Asn Ala Ala Ile Tyr
            420                 425                 430

Glu Ala Ile Glu Asn Lys Asp Asp Thr Phe Asn Val Leu Asp Tyr Ala
```

435 440 445

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

Asp Glu Ser Met Lys Ile Ala Gly Ile Glu Cys Gly Ser His Gly His
465 470 475 480

Asn Gly Ile Asn Gly Ala Arg Gly Asn Pro Lys Gly Phe Arg Lys Leu
485 490 495

Gly Lys Met Asn Thr Gly His Thr His Thr Pro Ser Ile Tyr Gly Gly
500 505 510

Val Tyr Thr Ala Gly Val Ala Gly Ser Leu Asp Met Gly Tyr Asn Ile
515 520 525

Gly Ala Ser Ser Trp Ser Gln Thr His Leu Ile Thr Tyr Glu Asn Gly
530 535 540

Gln Arg Thr Leu Ile Asp Phe Lys Asp Gly Val Phe Phe Ala
545 550 555

<210> 11
<211> 150
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 11
Met Lys Leu Thr Phe Ile Tyr Asn Asn Arg Lys Ser Phe Thr Ala Ser
1 5 10 15

Asn Val Val Glu Asn Ser Leu Val Ile Ser Arg Asp Ser Glu Gly Arg
20 25 30

Pro His Val Ser Tyr Gln Lys Val Asn Thr Val Asp Gly Asp Thr Val
35 40 45

Leu Lys Ala Leu Ala Ala Ile Leu Pro Arg Pro Ala Glu Phe Lys Glu
50 55 60

Ser Gly Ile Val Ser Gln Leu Val Ala Ala Asp Ser Ile Leu Tyr Glu
65 70 75 80

Ala Asp Ile Cys Glu Ile Val Glu Ile Asp Ala Ala Ala Ala Gly Leu
85 90 95

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

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

Ile Val Pro Val Met Ala Thr Arg Ile Lys Pro Ala Glu Leu Ala Asp
    130   135   140

Ala Leu Thr Leu Phe Phe
145   150

<210> 12
<211> 238
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 12
Met Ala Phe Asn Lys Leu Ala Ile Lys Ala Ile Lys Leu Trp Asp Leu
1   5   10   15

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

Asp Lys Gly Asn Leu Asp Leu Asn Met Tyr Arg Glu Lys Ala Cys Val
        35   40   45

His Asp Ala Ile Met Thr Asp Thr Leu Leu Pro Leu Val Glu Tyr Met
    50   55   60

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

Arg Tyr Met Gly Lys Ser Asp Tyr Tyr Phe Leu Arg Lys Gln Arg Ile
                85   90   95

Arg Ala Gly Arg Gly Gly Asn Ile Gln Ile Leu Ser Arg Asp Val Leu
            100   105   110

His Arg Tyr Ile Gly Asp Ala Asp Tyr Lys Glu Val Tyr Tyr Ser Lys
        115   120   125

Asp Gly Ile Tyr Lys Thr His Tyr Phe Glu Met Leu Lys Ala Glu Tyr
    130   135   140

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

Ala Ala Ala Ala Ala Gly Leu Gln Thr Met Asp Ala Thr Ala Ile Asn
                165   170   175

Asp Ile Leu Ser Ile Gly Val Arg Leu Ala Gly Glu Ser Phe Ile Asp
            180   185   190

Glu Ala Leu Asp Asp Asp Asn Asp Tyr Gln Tyr Leu Cys Glu Arg Leu
195 200 205

Ala His Cys Trp Glu Gly Met Thr Glu Glu Glu Arg Ser Asp Tyr Gly
210 215 220

Ile Lys Pro Gln Gln Phe Ile Gln Ser Leu Ala Ile Ala Ser
225 230 235

<210> 13
<211> 153
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 13
Met Thr Ile Val Leu Ile Phe Thr Thr Phe Phe Phe Leu Ala Ala Val
1 5 10 15

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

Asp Leu Arg Asn Lys Ser Leu His Gln Glu Ile Leu Gln Thr Arg Ala
35 40 45

Glu Arg Gln Val Ala Ile Ser Lys His Gln Arg Val Met Asn Asp Leu
50 55 60

Arg Asn Asp Pro Ser Asn Pro Tyr Tyr Ile Pro Pro Val Thr Pro Gln
65 70 75 80

Val Ala Lys Arg Lys Gln Lys Arg Ala Gly Ser Asp Asn Ser Arg Lys
85 90 95

Val Ser Gly Ser Pro Ser Ser Asn Ser Gly Ser Ser Arg Ser Asp Asp
100 105 110

Gly Ser Thr Ala Ala Ile Ile Ala Thr Thr Ala Ala Val Ala Thr Tyr
115 120 125

Ser Gly Tyr Asp Ser Gly Ser Ser Tyr Cys Asp Ser Gly Ser Ser Ser
130 135 140

Ser Ser Phe Asp Ser Gly Cys Ser Phe
145 150

<210> 14
<211> 74
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F391/08

<400> 14
Met Glu Val Val Ile Gly Ala Leu Val Leu Leu Ser Ile Val Leu Phe
1   5   10   15

Val Ile Thr Val Lys Gln Gly Lys Ala Ile Lys Gln Leu Glu Arg Thr
            20   25   30

Asn Gly Val Leu Gln Lys Ser Tyr Asp Asn Gln Thr Arg Leu Leu His
        35   40   45

Lys Ala Gln Leu Asn Leu Ser Glu Cys Lys Ala Glu Leu Glu Ser Ala
    50   55   60

Asn Lys Ile Tyr Ile Thr Lys Gly Met Val
65   70

<210> 15
<211> 658
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 15
Met Gly Phe Tyr Ala Gly Arg Ile Gly Asp Lys Lys Val Leu Ser Leu
1   5   10   15

Thr Ser Gly Asn Asn Lys Asp Val Asn Asn His Thr Asn Pro Gly Trp
            20   25   30

Asp Thr Ile Phe His Ser Asp Met Pro His Val Val Val Leu Glu Thr
        35   40   45

His Glu Arg Asp Leu Trp Asp Gly Gly Asp Trp Tyr Arg Cys Thr Arg
    50   55   60

Met Pro Asp Arg Ile Ile Gln Val Leu Ser Ala Asp Tyr Asp Arg Val
65   70   75   80

Val Leu Thr Glu Val Glu Phe Glu Asp Gly Thr Arg Arg Phe Ile Tyr
                85   90   95

Gly Thr Ser Leu Gly Val Gly Ala Lys Ala Tyr Asn Ala Tyr Phe Ser
            100   105   110

Asn Thr Val Gly Ser Gln Ala Ser Ala Gly Thr Met Ala Ser Met Lys
        115   120   125

Thr Asn Val Cys Ala Ser Ala Asp Leu His Met Asp Ile Ser Phe Tyr
    130   135   140

```
Phe Glu Glu Thr Pro Gly Thr Ile Asn Glu Lys Leu Arg Asp Gly Thr
145                 150                 155                 160

Gly Cys Met Tyr Thr Trp Gly Val Asn Ser Glu Trp Gly Asp Arg Gly
                165                 170                 175

Pro Gly Pro Pro Val Gly Ala Pro Ile Arg Pro Asn Phe Glu Thr Ile
            180                 185                 190

Ile Lys Ala Gly Trp Val Leu Tyr Arg Gly Ala Phe Ser Gly Asn Ile
        195                 200                 205

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

Ala Met Arg His Pro Trp Met Arg Thr Thr Gly Val Asn Ser Ile Cys
225                 230                 235                 240

Leu Arg Gly Glu Thr Leu Asn Arg Asn Met Tyr Gly His Met Gly Pro
                245                 250                 255

Arg Tyr Gly Gln Ser Ser Asn Pro Val Gly Gly Pro Tyr Ala His Asn
            260                 265                 270

Ile Gln Thr Glu Ser Tyr Gln Glu Val Gln Tyr Lys Ala Gly Phe Phe
        275                 280                 285

Arg Gly Pro Pro Asn Asn Phe Met Gly Trp Glu Asn Thr Asp Asn Asn
    290                 295                 300

Asn Ala Gly Ser Gly Trp Gly Asn Asn Ala Ile Tyr Arg Asp Asn Asn
305                 310                 315                 320

Phe Arg Val Pro Lys Arg Val Arg Trp Tyr Ile Thr Asn Met Lys Tyr
                325                 330                 335

Asn Gly Gln Gly Phe Tyr Ala Glu Asn Val Phe Gly Ser Arg Asn Gln
            340                 345                 350

Glu Ile Lys Ile Ser Pro Arg Glu Phe Ile Val Asn Gly Ile Asn Leu
        355                 360                 365

Met Asn Thr Gly Trp Lys Phe Ile Asn Gln Asn Asp Ile Asn Tyr Ser
    370                 375                 380

Pro Gly Asn Arg Pro Asp Ile Arg Val Ile Ala Thr Asn Val Ala Arg
385                 390                 395                 400

Phe Ser Gly Asn Pro Thr Val Gly Asn Asn Gly Tyr Val His Phe Asn
                405                 410                 415
```

```
Gln Pro Leu Thr Arg Pro Asp Asn Gly Ala Glu Phe Gly Gln Gly Asn
            420                 425                 430

Val Ser Glu Met His Val Thr Thr Val Gly Val Tyr Asn Phe Arg Ser
        435                 440                 445

Asp Ala Gln Trp Tyr Val Lys Ser Asn Pro Pro Glu Ile Gly Asn Gln
    450                 455                 460

Trp Gly Pro Val Trp Ser Glu Ser Thr Arg Pro Leu Arg Leu Val Gly
465                 470                 475                 480

Gly Thr Gly Ser Ala Asp Ile Gly Gly Asn Leu Arg Thr Ser Gly Asn
                485                 490                 495

Ala Ser His His Leu Ala Thr Leu Trp Leu Gly Val Asn Asn Ser Arg
            500                 505                 510

Asn Gly Ala Cys Val Val Thr Leu Asp Trp Lys Asn Asp Glu Trp Ile
        515                 520                 525

Ala Ala Ala Gly Ile Gly Cys Tyr Asn Pro Leu Glu Asp Leu Thr Gln
    530                 535                 540

Trp Ser Glu Val Asp Ser Arg Leu Arg Ile Phe Gly Asn His Phe Gln
545                 550                 555                 560

Lys Arg Val His Gln Ile Met Cys Leu Pro Val Asn Met Cys Val Pro
                565                 570                 575

Phe His Phe Ile Arg Gly Thr Val Thr Gln Cys Gly Val Ile Pro Gly
            580                 585                 590

Asn Asn Ala Met Gln Met Lys Ala Met Trp Ala Pro Thr Thr Thr Asn
        595                 600                 605

Ser Ala Thr Gln Gly Asp Tyr Ala Ile Ile Tyr Trp Leu Ile Ala Arg
    610                 615                 620

Ala Asp Gly Ser Val Glu Val Trp Val Asn Val Glu Met Ser Asn Ile
625                 630                 635                 640

Met Asn Met Arg Val Ile Leu Pro Glu Val Arg Ile Ala Val Gln Arg
                645                 650                 655

Leu Ala
```

<210> 16
<211> 157
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 16
Met Ser Asn Asp Leu Ile Val Pro Asp Thr Met Ser Pro Glu Gly Met
1   5   10   15

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

Ala Leu Ala Val Gly Met Glu Glu Pro Lys Phe Arg Glu Ile Met Arg
        35   40   45

Lys Pro Glu Val Lys Ala Tyr Leu Thr Asp Ile Phe Met Glu Ser Gly
    50   55   60

Phe Arg Asn Arg Asp Lys Phe Phe Gly Ile Leu Asp Thr Val Leu Thr
65   70   75   80

Met Lys Met Glu Glu Leu Asp Glu Thr Gly Met Gly Ser Glu Met Asp
                85   90   95

Ile Met Asp Ile Leu Lys Leu Met His Lys Met Lys Met Asp Glu Met
            100   105   110

Lys Met Gln Ile Glu Tyr Glu Lys Val Lys Gln Ala Lys Ala Pro Ile
        115   120   125

His Gln Asn Asn Thr Gln Ile Asn Leu Ala Gly Gly His Asp Ser Asn
    130   135   140

Tyr Thr Asp Leu Leu Ser Arg Ile Val Gly Ala Gly Lys
145   150   155

<210> 17
<211> 438
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 17
Met Glu Ile Ser Arg Ser Tyr Ile Asn Thr Thr Asp Val Val Asp Phe
1   5   10   15

Gly Val Asp Lys Arg Phe Phe Lys Phe Pro Val Ser Gly Leu Leu Ala
            20   25   30

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

Leu Glu Asp Pro Arg His Arg Phe Val Thr Ala Cys Val Ser Arg Arg
    50   55   60

```
Val Gly Lys Ser Phe Ile Ala Tyr Thr Leu Gly Phe Leu Lys Leu Leu
65                  70                  75                  80

Glu Pro Asn Val Lys Val Leu Val Val Ala Pro Asn Tyr Ser Leu Ala
                85                  90                  95

Asn Ile Gly Trp Ala Gln Ile Lys Gly Leu Ile Lys Lys Tyr Gly Leu
            100                 105                 110

Gln Thr Glu Arg Glu Asn Ala Lys Asp Lys Glu Ile Glu Leu Ala Asn
        115                 120                 125

Gly Ser Leu Phe Lys Leu Ala Ser Ala Ala Gln Ala Asp Ser Ala Val
    130                 135                 140

Gly Arg Ser Tyr Asp Phe Ile Ile Phe Asp Glu Ala Ala Ile Ser Asp
145                 150                 155                 160

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

Pro Asn Ser Lys Ala Leu Phe Ile Ser Thr Pro Arg Gly Gly Asn Trp
            180                 185                 190

Phe Lys Arg Phe Tyr Glu Gln Gly Phe Arg Glu Asp Leu Pro Gln Trp
        195                 200                 205

Val Ser Ile His Gly Thr Tyr Arg Asp Asn Pro Arg Val Ser Leu Ala
    210                 215                 220

Asp Ile Glu Glu Ala Arg Lys Thr Val Ser Lys Asn Tyr Phe Lys Gln
225                 230                 235                 240

Glu Tyr Glu Ala Asp Phe Ser Val Phe Glu Gly Gln Ile Tyr Asp Thr
                245                 250                 255

Phe Ser Val Ser Glu His Val Gln Asp Leu Ala Gly Met Gly His Phe
            260                 265                 270

Phe Ala Ala Asp His Glu Phe Glu Thr Ile Leu Gly Ile Asp Val Gly
        275                 280                 285

Tyr Arg Asp Pro Thr Ala Val Leu Thr Ile Lys Tyr His Tyr Asp Gln
    290                 295                 300

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

Ala Gln His Ala Met Tyr Ile Gln His Cys Ile Asp Arg Tyr Asn Val
                325                 330                 335
```

```
Asp Arg Ile Phe Val Asp Ser Ala Ala Ala Gln Phe Arg Gln Asp Leu
            340                 345                 350

Ala Tyr Glu His Glu Ile Ser Ser Ala Pro Ala Lys Lys Ser Val Leu
        355                 360                 365

Asp Gly Leu Ala Cys Leu Ala Ala Leu Phe Gln Gln Gly Lys Ile Ile
    370                 375                 380

Val Asp Ala Ser Cys Thr Ala Leu Ile His Ala Leu Gln Asn Tyr Lys
385                 390                 395                 400

Trp Asp Phe Gln Glu Gly Glu Glu Lys Leu Ser Arg Glu Lys Pro Arg
                405                 410                 415

His Asp Ala Asn Ser His Leu Cys Asp Ala Leu Arg Tyr Gly Ile Tyr
            420                 425                 430

Ser Ile Ser Arg Gly Lys
        435


<210> 18
<211> 160
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 18
Leu Ala Ser Asn Val Lys Tyr Lys Arg Asp Ala Ile Ser Ile Met Arg
1               5                   10                  15

Asp Gly Ile Lys Ala Gln Tyr Lys Arg Gly Asn Cys Cys Ala Ile Cys
            20                  25                  30

Asp Ser Gln Glu Asn Leu Glu Leu His His Tyr Ser Thr Val Ala Leu
        35                  40                  45

Leu Val Lys Asn Phe Ala Lys Glu Phe Gln Leu Asp Phe Thr Asp Ser
    50                  55                  60

Glu Val Val Leu Ser Asn Arg Asp Lys Phe Tyr Lys His Tyr Trp His
65                  70                  75                  80

Glu Leu Val Glu Asp Thr Val Thr Leu Cys Val Phe His His Gln Thr
                85                  90                  95

Leu His Lys Val Tyr Thr Lys Glu Pro Pro Leu Phe Ser Ala Asn Lys
            100                 105                 110

Gln Lys Ile Trp Val Glu Lys Gln Arg Glu Arg Cys Met Asn Pro Glu
```

115 120 125

Ala Pro Arg Thr Ser Asn Thr Gly Glu Arg Ser Gly Phe Ala Lys Trp
130 135 140

Leu Pro Thr Asp Val Lys Thr Glu Lys Ser Gly Phe Ala Arg Phe Leu
145 150 155 160

<210> 19
<211> 403
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 19
Met Ala Ile Arg Asp Trp Leu Val Thr Lys Leu Asn Arg Gly Gln Arg
1 5 10 15

Ile Ile Arg Asp Leu Glu Asp Val Ser His Arg Thr Asn Val Lys Pro
20 25 30

Phe Thr Thr Gly Lys Ala Tyr Ser Ser Ile Glu Ile Leu Asn Arg Ser
35 40 45

Ala Asn Met Val Ile Asp Ser Ala Ala Glu Cys Ser Tyr Thr Val Gly
50 55 60

Glu Gln Tyr Lys Thr Ile Thr Thr Tyr Gly Thr Ile Arg Ser Lys Thr
65 70 75 80

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

Thr Phe Arg Arg Leu Ile Val Ser Asp Leu Leu Phe Glu Gly Cys Ala
100 105 110

Tyr Ile His Trp Asp Gly Ser Ser Leu Tyr His Leu Pro Ala Ala Leu
115 120 125

Met Glu Val Lys Ala Asp Asp Lys Lys Phe Val Asn Lys Phe Val Phe
130 135 140

Asn Asn Met Ile Asp Tyr Arg Val Asp Glu Ile Ile Phe Ile Lys Asp
145 150 155 160

Asn Gly Gln Asn Gly Gly Ile Asn Ser Gln Ile Thr Gly Gln Ser Arg
165 170 175

Val Ala Thr Val Ile Asn Ser Leu Thr Lys Arg Glu Lys Met Leu Glu
180 185 190

```
Phe Lys Glu Lys Phe Leu Asp Asn Gly Thr Val Ile Gly Leu Ile Leu
        195                 200                 205

Glu Thr Asp Glu Ile Leu Asn Lys Lys Leu Arg Glu Arg Lys Gln Glu
    210                 215                 220

Glu Leu Gln Leu Asp Tyr Asn Pro Ser Thr Gly Gln Ser Thr Val Leu
225                 230                 235                 240

Ile Leu Asp Gly Gly Met Lys Ala Lys Pro Tyr Ser Gln Ile Ser Ser
                245                 250                 255

Phe Lys Asp Leu Asp Phe Glu Asn Asp Ile Ala Arg Phe Asn Lys Asp
            260                 265                 270

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

Asn Ala Asn Ile Arg Pro Asn Ile Glu Leu Phe Tyr Tyr Met Thr Ile
    290                 295                 300

Val Pro Met Leu Asn Lys Val Cys Ser Ser Leu Thr Phe Phe Phe Gly
305                 310                 315                 320

Phe Lys Val Thr Pro Asn Thr Lys Asp Val Val Ala Leu Thr Pro Asp
                325                 330                 335

Lys Glu Lys Glu Ala Lys Phe Val Thr Ala Leu Val Asn Asn Gly Ile
            340                 345                 350

Leu Thr Gly Asn Glu Gly Arg Ile Glu Leu Gly Tyr Glu Glu Leu Ala
        355                 360                 365

Asp Glu Gln Met Lys Lys Ile Arg Ile Pro Ala Asn Val Ala Gly Ser
    370                 375                 380

Ala Thr Gly Val Ser Gly Gln Glu Gly Gly Ala Pro Asn Lys Asp Glu
385                 390                 395                 400

Glu Lys Gln
```

<210> 20
<211> 239
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 20

```
Met Ile Asp Tyr Lys Ala Leu Lys Ala Leu Phe Pro Asn Gly Leu Pro
1               5                   10                  15
```

```
Glu Ala His Asn Val Phe Ala Thr Val Lys Ala His Leu Thr Tyr Gln
            20                  25                  30

Ile Leu Arg Lys Glu Tyr Gly Tyr Ala Ala Thr Asn Ser Lys Thr Trp
        35                  40                  45

Asp Gln Phe Lys Glu Ala Tyr Ala Glu Ala Thr Lys Pro Val Pro Val
    50                  55                  60

Ala Ser Val Ser Ile Thr Gly Ala Pro Ala Ser Leu Asp Tyr Thr Lys
65                  70                  75                  80

Thr Val Gln Leu Ala Ala Thr Val Leu Pro Thr Asn Ala Asp Asn Lys
                85                  90                  95

Thr Val Thr Trp Lys Thr Ser Asp Ala Thr Leu Ala Thr Val Ser Ser
            100                 105                 110

Thr Gly Leu Val Thr Ala Leu Ser Lys Ala Gly Thr Val Lys Ile Thr
        115                 120                 125

Ala Thr Ala Gly Gly Lys Ser Ser Glu Val Ser Ile Gln Val Lys Ala
    130                 135                 140

Pro Val Val Ala Val Thr Gly Val Thr Met Ser Pro Lys Thr Ile Thr
145                 150                 155                 160

Ile Glu Ala Gly Lys Thr Gly Lys Leu Thr Gly Thr Val Ala Pro Ala
                165                 170                 175

Asn Ala Thr Asn Lys Ser Val Thr Tyr Thr Ser Ala Asp Thr Thr Lys
            180                 185                 190

Ala Thr Val Ala Ala Asp Gly Thr Val Thr Val Pro Ala Asn Leu Ala
        195                 200                 205

Ala Asp Ser Thr Val Val Ile Thr Val Lys Thr Ala Asp Gly Asn Lys
    210                 215                 220

Thr Asp Thr Ala Ile Val Thr Val Lys Val Pro Thr Ala Gly Val
225                 230                 235


<210> 21
<211> 198
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 21
Met Gln Asn Ile Asn Leu Asn Ala Glu Ile Lys Ser Val Lys Ala Val
1               5                   10                  15
```

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

Ile Thr Lys Asp Arg Ala Gly Asp Val Ile Leu Ser Glu Ala Trp Thr
        35                  40                  45

Thr Ser Asn Ala Leu Lys Asn Phe Met Lys Asn Pro Ile Met Leu Phe
    50                  55                  60

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

Thr Glu Ser Gly Leu Met Val Glu Gly Glu Val Ser Ala Ala Asp Leu
                85                  90                  95

Gln Ile Tyr Ser Leu Ile Arg Asp Glu Val Leu Lys Thr Phe Ser Val
            100                 105                 110

Gly Phe Tyr Ile Lys Asp Ala Glu Trp Asp Asp Met Thr Glu Thr Phe
        115                 120                 125

Ile Ile Lys Asp Leu Glu Leu Leu Glu Ile Ser Val Val Ser Val Pro
    130                 135                 140

Cys Asn Gln Asp Ser Thr Phe Ser Leu Ser Lys Ser Val Asn His Asn
145                 150                 155                 160

Asp Tyr Met Glu Leu Arg Lys Ser Phe Val Lys Ser Ser Gln Val Gln
                165                 170                 175

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

Ala Gly Tyr Ala Lys Gly
        195


<210> 22
<211> 460
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 22
Met Ser Tyr Asp Ile Ala Gln Leu Ser Lys Asp Leu Gly Leu Gly Asp
1               5                   10                  15

Ile Ala Glu Gln Leu Lys Gly Leu Thr Ala Ser Gln Lys Ala Glu Glu
            20                  25                  30

Ala Arg Lys Phe Ala Ala Glu Gln Glu Ala Lys Glu Leu Lys Arg Met
```

35 40 45

Glu Asp Leu Val Ala Lys Ala Thr Gly Glu Asp Arg Lys Asn Leu Ala
50 55 60

Glu Ala Leu Glu Leu Val Lys Asn Leu Asp Glu Lys Ser Lys Gln Ser
65 70 75 80

Ala Glu Ala Phe Val Lys Ala Met Asn Ser Gln Gln Glu Glu Ile Thr
85 90 95

Gly Leu Lys Glu Glu Ile Lys Ser Leu Leu Ala Ala Arg Glu Asn Gly
100 105 110

Arg Ser Phe Val Ala Asp Gly Val Ala Lys Ala Met Phe Gly Lys Gln
115 120 125

Glu Asp Phe Glu Asp Glu Val Glu Lys Leu Val Leu Leu Ser Tyr Val
130 135 140

Met Gln Lys Asp Val Phe Gly Thr Lys Arg Gly Glu Ala His Leu Lys
145 150 155 160

Ala Val Asn Gly Ser Ser Ser Ile Glu Val Ser Thr Glu Ala Tyr Glu
165 170 175

Thr Ile Phe Ser Leu Arg Ile Leu Arg Asp Ile Gln Ala Lys Leu Ile
180 185 190

Ile Gly Thr Met Phe Glu Glu Leu Pro Met Ser Ser Lys Leu Leu Thr
195 200 205

Met Met Val Glu Pro Glu Ala Gly Glu Ala Ser Trp Val Asp Ala Ser
210 215 220

Thr Tyr Gly Thr Pro Ala Thr Val Gly Ala Glu Asp Lys Thr Lys Leu
225 230 235 240

Ser Glu Ile Thr Phe Lys Thr Tyr Lys Leu Ala Ala Lys Ala Tyr Met
245 250 255

Thr Asp Glu Thr Glu Glu Asp Ala Ile Phe Thr Leu Leu Pro Ile Met
260 265 270

Arg Arg Arg Leu Ile Glu Ala His Ala Ile Ala Ile Glu Lys Ala Phe
275 280 285

Leu Thr Gly Thr Gly Ala Ala Gly Thr Pro Lys Gly Leu Ile Gln Phe
290 295 300

Ala Lys Asp Asp Gly Lys Val Val Ala Thr Thr Ala Lys Ala Asp Gly

305 310 315 320

Ser Val Lys Val Thr Ala Lys Glu Ile His Lys Leu Arg Arg Ser Leu
325 330 335

Gly Arg His Gly Leu Asp Leu Asn Lys Leu Ala Leu Val Val Ser Met
340 345 350

Asp Ala Tyr Tyr Asp Leu Ile Glu Asp Glu Glu Phe Gln Asp Val Ala
355 360 365

Gln Val Thr Ala Thr Thr Ala Ile Lys Leu Gln Gly Gln Val Gly Arg
370 375 380

Ile Tyr Gly Leu Pro Val Leu Val Ser Glu Phe Phe Pro Ala Lys Ala
385 390 395 400

Ala Ser Ala Glu Phe Cys Val Val Val Tyr Arg Asp Asn Phe Ile Val
405 410 415

Pro Arg Gln Arg Ala Ile Thr Val Glu Lys Glu Arg Gln Ala Glu Arg
420 425 430

Gln Arg Asp Ala Tyr Tyr Val Thr Gln Arg Leu Asn Leu Met Arg Phe
435 440 445

Phe Glu Asn Gly Val Val Ala Gly Ala Tyr Ala Ala
450 455 460

<210> 23
<211> 170
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 23
Met Gln Phe Met Thr Asp Ser Asp Trp Arg Thr Tyr Gly Gly Leu Lys
1 5 10 15

Arg Pro Asp Leu Glu Ser Asn Ile Pro Met Leu Ile Lys Ala Ala Asn
20 25 30

Ala Leu Ile Thr Gln Leu Leu Gly Ile Asp Asp Thr Ala Asn Val Val
35 40 45

Asp Val Leu Pro Thr Lys Pro Ala Arg Lys Lys Tyr Phe Leu Ser Ser
50 55 60

Pro Val Pro Ser Thr Ile Thr Lys Ile Thr Ile Asn Asp Gln Glu Ile
65 70 75 80

Asp Lys Ser Gln Tyr Lys Asn Tyr Pro Asp Gly Thr Leu Leu Leu Lys
85 90 95

Phe Ser Pro Pro Glu Gly Tyr Met Glu Val Glu Phe Thr Gln Thr Gly
100 105 110

Phe Thr Ser Ile Pro Asp Asp Leu Val Leu Ala Ala Cys Phe Leu Val
115 120 125

Asp His Trp Val Lys Lys Asp Tyr Arg Glu Ser Arg Thr Phe Gly Gly
130 135 140

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

Arg Thr Ile Ile Glu Val Tyr Arg Arg Leu
165 170

<210> 24
<211> 253
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 24
Val Ala Leu Gly Asp Leu Ala Arg Gln Ile Val Lys Glu Gln Leu Asp
1 5 10 15

Ile Met Ser Gly Gly Ser His Ser Thr Lys Asn Thr Val Ile Tyr Ser
20 25 30

Ala Glu Thr Met Asp Asn His Lys Asp Gly Thr Ile Gly Lys Val Ser
35 40 45

Phe Arg Phe Thr Lys Pro Val Ser Glu Asp Leu Leu Asn Val Arg Thr
50 55 60

Ser Ser Ile Leu Lys Ala Val Ser Ser Ser Leu Asn Leu Glu Gly Asp
65 70 75 80

Val Gly Val Ile Asp Asn Leu Leu Asn Ser Ile Thr Gly Lys Lys Ser
85 90 95

Lys Ile Gly Arg Lys Arg Ser Thr Gly Arg Val Glu Val Asn Phe Gly
100 105 110

Asp Pro Ser Asp Ala Asp Asn Gly Tyr Ala Gly Ala Ile Ser Gly Ala
115 120 125

Ser Gly Arg Phe Val Ser Asn Thr Asn Leu Arg Ala Leu Leu Glu Leu
130 135 140

```
Val Ala Lys Glu Tyr Leu Val Lys Asp Met Lys Lys Ala Gly Ala Pro
145                 150                 155                 160


Leu Lys Phe Arg Thr Gly Arg Phe Ala Asn Ser Leu Lys Ile Lys Asp
                165                 170                 175


Val Leu Leu Arg Glu Asp Ala Gly Ala Lys Thr Pro Asp Leu Asn Ile
            180                 185                 190


Thr Tyr Asn Tyr Met Leu Lys Pro Tyr Ser Val Phe Asn Pro Ala Val
        195                 200                 205


Ser Thr Tyr Arg Gly Leu Ser Leu Arg Pro Phe Pro Gly Ala Arg Asn
    210                 215                 220


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


Ile His Ser Arg Tyr Arg Ile Arg Val Asn Gln Gly Thr
                245                 250


<210> 25
<211> 161
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 25
Met Asn Tyr Arg Thr Ser Ile Ala Asp Ala Leu Val Glu Arg Leu Lys
1               5                   10                  15


Lys Asp Met Asp Gly Ser Asn Pro Thr Glu Phe Phe Thr Asn Met Tyr
            20                  25                  30


Gly Asn Val Ser Arg Gln Thr Tyr Ser Phe Glu Gln Ile Asn Glu Phe
        35                  40                  45


Pro Tyr Ile Ala Val His Val Gly Thr Glu Thr Gly Asn Tyr Leu Pro
    50                  55                  60


Ser Ala Gln Gln Trp Val Tyr Leu Glu Ile Pro Ile Leu Ile Tyr Asp
65                  70                  75                  80


Lys Glu Lys Asp Asp Ile Asn Met Gln Leu Glu Lys Leu Ile Ala Asp
                85                  90                  95


Val Lys Thr Ser Ile Asp Thr Gly Gly Asn Leu Gln Tyr Thr Ile Met
            100                 105                 110


Lys Pro Asp Gly Ser Thr Ile Asp Ser Glu Ala Thr Asp Met Gln Ile
        115                 120                 125
```

Thr Ser Val Ser Thr Asp Glu Gly Ile Leu Ser Pro Phe Gly Phe Ala
130 135 140

Gln Val Asn Val Thr Val Arg Tyr Met Pro Leu Arg Arg Ala Leu Asp
145 150 155 160

Arg

<210> 26
<211> 375
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 26
Met Ser Val Gln Leu Leu Arg Asn Thr Arg Ile Phe Val Ser Thr Val
1 5 10 15

Thr Thr Gly Phe Thr Lys Ala Asn Thr Gln Glu Ile Leu Val Gln Asp
20 25 30

Asp Val Ser Trp Ser Gln Asp Ser Asn Ser Thr Asp Ile Thr Leu Asn
35 40 45

Glu Ala Gly Pro Lys Pro Thr Arg Gly Ser Gln Arg Phe Asn Asp Ser
50 55 60

Leu Asn Ala Ala Glu Trp Ser Phe Ser Thr Tyr Ile Leu Pro Tyr Asp
65 70 75 80

Asp Ala Gly Lys Gln Ile Leu Pro Asp Tyr Leu Leu Trp His Gly Leu
85 90 95

Ala Thr Gly Ala Ala Val Asn Leu Ala Gly Thr Thr Gly Val Phe Gln
100 105 110

Asn Ala Thr Asn Leu Val Val Asn Phe Lys Asp Asn Gly Tyr His Glu
115 120 125

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

Ile Arg Asn Cys Gln Val Gly Gln Ala Glu Val Asn Val Asp Ile Asp
145 150 155 160

Asp Ile Gly Arg Val Thr Trp Ser Gly Asn Gly Thr Arg Leu Glu Thr
165 170 175

Leu Ala Ser Gln Pro Phe Asp Pro Lys Thr Ile Gly Ile Asp Asp Ala

180 185 190

Leu Tyr Ala Lys Ile Gln Ser Ser Tyr Ile Lys Asn Lys Leu Thr Ile
195 200 205

Leu Lys Leu Lys Asn Asn Ala Thr Gly Gly Lys Thr Tyr Asn Ile Pro
210 215 220

Ile Thr Gly Gly Ser Phe Thr Met Asn Asn Asn Val Thr Tyr Leu Thr
225 230 235 240

Pro Asn Ile Met Ser Arg Val Asp Val Pro Ile Gly Ser Phe Thr Gly
245 250 255

Ser Phe Glu Leu Thr Gly Ser Leu Thr Ala Tyr Met Asn Asp Ala Ala
260 265 270

Asn Gly Ser Ile Gln Leu Tyr Lys Asp Leu Val Ser Asp Leu Lys Ala
275 280 285

Val Asn Asp Phe Glu Val Ala Ile Ile Leu Gly Gly Glu Tyr Asp Thr
290 295 300

Ala Arg Pro Ala Ala Val Leu Val Ala Lys His Ala Asn Leu Asn Ile
305 310 315 320

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

Ala Ile Pro Thr Gln Met Asp Ala Gly Asp Glu Gly Tyr Leu Gly Phe
340 345 350

Ser Ser Lys Tyr Thr Lys Thr Ser Ile Ala Lys Leu Ile Ser Ser Gly
355 360 365

Asp Gly Asn Pro Val Thr Pro
370 375

<210> 27
<211> 295
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 27
Met Leu Tyr Ser Leu Met Arg Glu Ser Arg Val Val Ile Glu Tyr Asp
1 5 10 15

Gly Arg Ala Tyr Gly Phe Asp Ala Leu Ser Asp Tyr Thr Ala Gly Thr
20 25 30

```
Ser Tyr Glu Glu Phe Lys Ala Asn Arg Arg Thr Ile His Arg Arg Ser
        35                  40                  45

Asn Tyr Ala Tyr Ser Lys Ile Thr Ala Gln Ser Pro Ser Ser Ile Ser
    50                  55                  60

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

Leu Met Gly Phe Ile Glu Ile Asp Gly Met Tyr Gln Met Pro Leu Phe
                85                  90                  95

Ser Asn Asn Ile Glu Pro Lys Met Phe Ser Val Tyr Ile Ile Asn Lys
            100                 105                 110

Asn Thr Ser Leu Arg Phe Asp Asn Cys Phe Ala Thr Thr Cys Asp Phe
        115                 120                 125

Ser Leu Asp Lys Ser Val Pro Val Leu Asn Val Gly Ile Glu Ser Gly
    130                 135                 140

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

Gly Glu Val Leu Pro Phe Ser Leu Pro Gln Val Ser Ser Asn Gly Arg
                165                 170                 175

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

Glu Trp Arg Gly Asp Arg Ser Leu Phe Asp Ile Asn Lys Ile Tyr Asn
        195                 200                 205

Asn Arg Arg Ala Ile Val Asn Glu Leu Asn Ser Ser Ala Leu Ile Ser
    210                 215                 220

Met Tyr Tyr Ala Lys Ser Leu Gln Ile Asp Ser Thr His Asn Ile Lys
225                 230                 235                 240

Pro Asp Ile Gly Leu Pro Val Gln Ile Arg Asn Lys Tyr Ile Val Val
                245                 250                 255

Asp Phe Pro Ser Thr Arg Ile Thr Lys Arg Leu Asp Leu Thr Asp Val
            260                 265                 270

Tyr Lys Ile Asp Tyr Asp Val Ile Pro Thr Glu Gln Ser Asp Pro Val
        275                 280                 285

Arg Ile Lys Leu Ile Gly Glu
    290                 295
```

<210> 28
<211> 140
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 28
Met Ser Ile Asn Leu Lys Asp Ile Ala Leu Asp Thr Lys Gln Ile Thr
1   5   10   15

Ile Ala Tyr Pro Gly Leu Pro His Phe Lys Leu Lys Val Asn Tyr Val
            20   25   30

Ser Arg Lys Leu Ser Lys Lys Ile Leu Glu Ala Ala Gln Glu Asn Gln
        35   40   45

Phe Val Asn Gly Ile Ala Val Lys Val Gln Asn Asp Asp Lys Phe Ala
    50   55   60

Glu Glu Phe Val Lys Val Ala Ile Ala Gly Trp Glu Gly Leu Thr Val
65   70   75   80

Ala Asp Val Glu Lys Leu Met Leu Ile Glu Val Pro Glu Asp Arg Leu
                85   90   95

Glu Asp Lys Val Glu Phe Ser Ile Asp Asn Ala Met Met Leu Val Arg
            100   105   110

Asn Ser Ser Ala Phe Glu Thr Trp Met Asn Ser Thr Val Phe His Leu
        115   120   125

Asp Thr Phe Arg Gly Ser Lys Ser Glu Pro Thr Ala
    130   135   140

<210> 29
<211> 108
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 29
Met Cys Glu Ser Leu Gly Glu Glu Pro Asn Pro Glu Val Leu Lys Arg
1   5   10   15

Phe Val Glu Ile His Asp Phe Pro Glu Ile Ala Gln Thr Ala Leu Thr
            20   25   30

Ile Tyr Asn Asn Leu Ser Asp Asn Tyr Ile Pro Gly Asp Tyr Pro Thr
        35   40   45

Tyr Leu Gly Lys Asp Lys Ser Ala Leu Leu Val Phe Phe Asp Ile Tyr
    50   55   60

Gly Val Glu Asp Ala Asp Glu Lys Ser Leu Ile Leu Gln Ile Ile Asn
65 70 75 80

Ile Phe Asp Ser His Ala Val Ala Ala Ser Arg Lys Arg Val Glu Ala
85 90 95

Ala Ile Lys Lys Ser Lys Met Lys Ser Ser Ser Arg
100 105

<210> 30
<211> 1692
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 30
Met Thr Asp Arg Leu Ile Arg Glu Leu Leu Val Asp Ile Lys Gln Arg
1 5 10 15

Gly Gly Ser Lys Ala Ala Lys Gln Ile Arg Asp Val Glu Ala Ala Leu
20 25 30

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

Leu Pro Gly Ser Phe Thr Ala Leu Glu Arg Ser Val Ser Arg Thr Ala
50 55 60

Lys Ser Leu Glu Lys Leu Ser Ser Thr Thr Ser Ile Thr Ala Leu Ala
65 70 75 80

Ala Ser Ile Gly Met Leu Ser Gly Lys Phe Thr Ser Phe Glu Val Asp
85 90 95

Leu Ala Lys Ser Val Leu Lys Ile Asn Ala Asn Leu Asn Gly Val Thr
100 105 110

Ser Ala Ala Asn Lys Met Ala Ser Gly Phe Asp Thr Ala Ala Thr Ser
115 120 125

Ser Val Ala Asp Leu Asn Arg Val Asn Lys Ala Leu Gln Glu Leu Asp
130 135 140

Ala His Ala Ser Ser Val Ala Lys Val Leu Gln Thr Leu Lys Ala Gly
145 150 155 160

Ala Gly Leu Glu Ser Ile Ser Ser Ser Ala Ala Lys Ala Ser Thr Asp
165 170 175

Leu Ser His Leu Val Ser Gly Val Glu Lys Ile Gly Asn Gln Leu Ala

```
            180                 185                 190

Arg Met Ala Glu Gln Ala Val Leu Ala Gly Arg Ser Leu Gln Gly Leu
        195                 200                 205

Lys Ala Asp Ser Leu Gly Ala Ala Gly Glu His Leu Ser Lys Ala Ala
    210                 215                 220

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

Leu Asn Lys Leu Leu Leu Glu Leu Ala Val Lys Ala Asp Leu Ala Ser
                245                 250                 255

Lys Ser Ile Ala Asn Ile Ala Pro Gly Thr Lys Leu Asn Ser Leu Gly
            260                 265                 270

Thr Glu Ile Gln Lys Ile Asn Thr Ser Leu Ala Thr Ala Ala Asn Thr
        275                 280                 285

Ser Val Ala Glu Ile Ser Lys Ile Lys Ala Ala Leu Thr Ser Leu Val
    290                 295                 300

Ser Ser Thr Ala Thr Ala Ala Ala Ser Met Lys Thr Val Gly Thr Gly
305                 310                 315                 320

Ser Gly Leu Ser Lys Leu Ile Ser Glu Ile Ser Ala Ala Thr Ser Ala
                325                 330                 335

Ser Thr Ser Asp Ile Ser Lys Val Thr Ala Ala Leu Lys Gln Leu Asn
            340                 345                 350

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

Ala Asn Leu Ser Ser Val Pro Thr Val Val Gly Lys Ile Gly Thr Ser
    370                 375                 380

Met Thr Gln Leu Arg Ala Gln Leu Glu Gly Ser Val Thr Gly Ile Glu
385                 390                 395                 400

Lys Ser Leu Asn Asp Leu Ser Arg Ala Phe Ala Thr Met Gly Gly Thr
                405                 410                 415

Gly Asn Leu Asn Pro Leu Gly Asn Ser Ile Arg Gly Met Ile Pro Ser
            420                 425                 430

Leu Thr Gln Leu Ala Lys Ala Ala Val Gln Val Asn Ser Ala Leu Ser
        435                 440                 445

Lys Ile Gln Ala Gly Arg Gly Val Leu Gln Leu Pro Thr Gln Phe Lys
```

```
450                 455                 460

Ala Val Thr Ala Ser Leu Asn Ala Leu Glu Thr Lys Leu Ala Ser Thr
465                 470                 475                 480

Ser Gln Ile Leu Glu Arg Gly Phe Ser Lys Gly Phe Gln Asp Met Ala
                485                 490                 495

Ser Lys Ser Thr Ser Ser Ser Thr Arg Met Ile Asn Asn Phe Gln Lys
            500                 505                 510

Val Val Pro Glu Leu Asn Ala Ile Glu Ala Ala Ala Ile Arg Ser Ala
        515                 520                 525

Ala Ala Ile Asp Lys Leu Ile Ala Lys Arg Ile Arg Leu Gly Gln Ala
    530                 535                 540

Gly Gly Gly Gly Asn Pro Ala Ala Phe Asn Met Gly Ala Leu Val Ala
545                 550                 555                 560

Glu Met Asn Arg Ile Val Thr Ser Ile Glu Ala Met Gly Asn Lys Met
                565                 570                 575

Asn Thr Thr Met Ala Asp Met Ala Arg Ser Thr Asp Lys Val Ser Asp
            580                 585                 590

Lys Leu Thr Asp Leu Asn Ser Gly Val Arg Asp Val Asn Thr Gly Leu
        595                 600                 605

Gly Gly Leu Asn Ser Thr Leu Thr Gly Thr Gly Ser Ala Ala Asn Arg
    610                 615                 620

Ala Ser Arg Ala Leu Gly Asn Thr Ser Gly Ser Ala Arg Gly Ala Thr
625                 630                 635                 640

Arg Asn Phe Ala Ala Leu Ala Met Val Thr Gly Pro Met Pro Leu Ile
                645                 650                 655

Tyr Gly Ala Ile Ala Ser Asn Val Tyr Val Leu Lys Ala Ala Phe Asp
            660                 665                 670

Gln Leu Lys Leu Gly Asp Gln Leu Asn Arg Leu Glu Gln Phe Gly Ser
        675                 680                 685

Ile Val Gly Ala Lys Thr Gly Thr Pro Ile Gln Ser Leu Ala Val Ala
    690                 695                 700

Leu Gln Glu Ala Thr Gly His Ala Val Ser Phe Glu Glu Ala Met Arg
705                 710                 715                 720

Gln Ala Ser Thr Ala Ala Ala Tyr Gly Phe Asp Ala Lys Gln Ile Ser
```

725 730 735

Glu Phe Ala Leu Val Ala Arg Arg Ala Ala Ala Thr Leu Gly Val Asp
740 745 750

Met Thr Asp Ala Leu Asn Arg Val Ile Lys Gly Val Ser Lys Gln Glu
755 760 765

Ile Glu Leu Leu Asp Glu Leu Gly Val Thr Ile Arg Leu Asn Asp Ala
770 775 780

Tyr Ala Glu Tyr Val Lys Ile Leu Asn Ala Ala Asn Thr Gly Ile Thr
785 790 795 800

Tyr Asn Ile Gln Gly Leu Thr Ser Phe Gln Lys Gln Gln Ala Tyr Ala
805 810 815

Asn Ala Val Val Ala Glu Ser Thr Lys Arg Phe Gly Tyr Leu Asp Glu
820 825 830

Val Leu Arg Ala Thr Pro Trp Glu Gln Phe Ala Ala Asn Ala Asp Ser
835 840 845

Ala Leu Arg Lys Val Gln Gln Ala Ala Ala Lys Tyr Leu Gly Pro Val
850 855 860

Ile Ala Ser Ile Asn Ala Ala Phe Tyr Thr Ser Lys Ala Ser Val Ser
865 870 875 880

Ala Glu Ala Ala Thr Ala Gln Gln Glu Ser Ile Lys Gln Met Asp Gly
885 890 895

Lys Asp Ser Asn Ala Val Val Met Asn Leu Glu Ala Ser Gln Lys Gly
900 905 910

Leu Asp Asp Ala Val Lys Ala Lys Glu Glu Val Lys Asn Lys Leu Ala
915 920 925

Ala Leu Asn Lys Glu Ile Met Asp Arg Glu Ala Lys Met Asp Met Ser
930 935 940

Thr Ala Leu Ala Thr Ala Ala Asn Tyr Ser Gly Phe Gly Asn Leu Leu
945 950 955 960

Thr Leu Gly Ala Ser Lys Ala Asn Lys Glu Phe Thr Gln Gln Thr Ala
965 970 975

Asp Met Arg Arg Gln Ala Tyr Met Leu Gln Gln Glu Leu Ala Asp Ser
980 985 990

Ala Gly Ala Ile Gln Lys Trp Lys Asp Ala Arg Asp Ser Ala Leu Ser

```
995                 1000                1005

Lys Ala  Gln Lys Glu Asn Pro  Glu Leu Ala Gly Lys  Leu Asn Ile
    1010                1015                1020

Gly Gln  Asn Val Glu Ala Ser  Asn Gly Leu Tyr Thr  Phe Asp Asn
    1025                1030                1035

Ala Ala  Leu Asp Gly Ala Val  Ala Leu Arg Lys Glu  Phe Asn Asn
    1040                1045                1050

Ile Lys  Lys Thr Ser Gly Asp  Leu Ser Asn Asp Ile  Gln Asn Phe
    1055                1060                1065

Ala Gln  Asp Ser Asn Thr Ala  Ser Arg Ala Thr Ala  Ala Leu Gly
    1070                1075                1080

Asp Ala  Leu Lys Ala Val Glu  Ser Leu Ala Gly Gly  Ser Thr Glu
    1085                1090                1095

Lys Ala  Asn Gln Met Thr Lys  Asp Leu Asn Leu Gly  Tyr Ser Thr
    1100                1105                1110

Val Thr  Glu Met Asn Thr Ala  Tyr Lys Ala Met Ser  Asn Tyr Gln
    1115                1120                1125

Lys Ile  Val Asn Asp Glu Ala  Lys Ser Lys Leu Asp  Val Glu Lys
    1130                1135                1140

Arg Ile  Ala Glu Val Tyr Ala  Ala Thr Arg Asn Lys  Asp Lys Ala
    1145                1150                1155

Glu Glu  Ala Gly Arg Ala Leu  Glu Met Gln Gln Leu  Ser Ala Lys
    1160                1165                1170

Lys Glu  Ala Leu Lys Ala Val  Leu Ala Thr Asn Lys  Asp Asn Lys
    1175                1180                1185

Ala Ile  Gln Lys Glu Leu Thr  Leu Leu Glu Thr Glu  Glu Leu Lys
    1190                1195                1200

Val Lys  Asn Gln Gly Met Glu  Ala Thr Lys Lys Glu  Lys Phe Tyr
    1205                1210                1215

Lys Asp  Lys Ile Val Gly Ile  Asp Arg Glu Ile Ala  Leu Leu Asn
    1220                1225                1230

Asn Arg  Thr Met Thr Asp Ser  Gln Tyr Asn Val Ala  Asn Leu Lys
    1235                1240                1245

Leu Asn  Leu Gln Val Glu Lys  Asp Arg Leu Ala Leu  Leu Lys Thr
```

```
    1250                1255                1260

Gln Ala  Asp Lys Glu Lys Glu  Ala Glu Gln Ser Arg  Arg Asn Ile
    1265                1270                1275

Ala Ser  Ile Glu Arg Glu Ile  Trp Lys Glu Gln Leu  Asp Arg Asn
    1280                1285                1290

Ala Lys  Thr Ala Glu Met Arg  Lys Glu Glu Phe Glu  Arg Asn Gln
    1295                1300                1305

Ser Met  Lys Pro Leu Met Gly  Glu Ser Gln Lys Met  Gln Glu Gln
    1310                1315                1320

Leu Ala  Phe Tyr Gln Glu Met  Lys Glu Phe Thr Lys  Gly Asn Ala
    1325                1330                1335

Asp Glu  Gln Ala Arg Trp Ser  Lys Glu Ile Ala Asn  Thr Thr Ala
    1340                1345                1350

Gln Met  Ala Ala Leu Lys Ala  Gln Arg Thr Ala Gln  Met Met Asp
    1355                1360                1365

Arg Val  Gly Gln Ser Leu Gly  Ala Asp Tyr Thr Pro  Thr Thr Gly
    1370                1375                1380

Leu Glu  Gly Glu Asp Lys Lys  Phe Ala Asp Met Glu  Asn Gln Met
    1385                1390                1395

Ala Ser  Tyr Asp Thr Ala Ile  Gly Lys Leu Ser Gln  Leu Asn Ser
    1400                1405                1410

Glu Ala  Thr Ala Thr Ala Gln  Ser Met Gly Asn Leu  Ala Asn Ala
    1415                1420                1425

Met Ile  Gln Phe Ser Gln Gly  Ser Leu Asp Thr Thr  Ser Met Ile
    1430                1435                1440

Ala Ala  Gly Met Gln Thr Val  Ser Gln Met Ile Ser  Tyr Gly Thr
    1445                1450                1455

Asn Gln  Gln Ile Ser Ala Ile  Asp Ala Ala Ile Ala  Ala Glu Gln
    1460                1465                1470

Lys Arg  Asp Gly Lys Ser Glu  Gln Ser Lys Asn Lys  Ile Lys Lys
    1475                1480                1485

Met Glu  Ala Glu Lys Ile Lys  Leu Gln Gln Glu Ser  Ala Lys Lys
    1490                1495                1500

Gln Ile  Ile Ile Gln Thr Ala  Val Ala Val Met Gln  Ala Ala Thr
```

1505 1510 1515

Ala Val Pro Tyr Pro Phe Ser Ile Pro Leu Met Ile Ala Ala Gly
1520 1525 1530

Leu Ala Gly Ala Leu Ser Leu Ala Gln Ala Ser Ser Ala Thr Gly
1535 1540 1545

Met Thr Asp Ile Ala Gly Ser Gly Gly Glu Thr Ala Ser Tyr Leu
1550 1555 1560

Thr Leu Gly Glu Arg Gln Lys Asn Val Asp Val Ser Met Gly Ala
1565 1570 1575

Asn Ala Gly Glu Leu Ser Tyr Val Arg Gly Asp Lys Gly Ile Gly
1580 1585 1590

Ser Ala Asn Gly Phe Ile Pro Arg Ala Glu Gly Gly Asn Thr Tyr
1595 1600 1605

Pro Gly Val Ser Tyr Lys Met Gly Glu His Gly Thr Glu Val Ala
1610 1615 1620

Thr Pro Met Val Pro Thr Lys Val Thr Pro Ala Asp Lys Val Ala
1625 1630 1635

Ser Glu Thr Ser Ser Gly Gly Ala Arg Arg Pro Val Asn Leu Asn
1640 1645 1650

Ile Gln Ala Met Asp Ala Lys Ser Phe Met Glu Tyr Ala Leu Glu
1655 1660 1665

Asn Pro Ala Ala Phe Gln Ala Ala Val Glu Leu Ala Leu Asn Glu
1670 1675 1680

Gln Gly Leu Ser Leu Lys Asn Leu Asn
1685 1690

<210> 31
<211> 204
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 31
Met Arg Leu Pro Asp Pro Phe Thr His Pro Gln Tyr Asn Gly Leu Gly
1 5 10 15

Phe Asp Lys Ala Thr Leu Ile Asp Asn Asp Pro Val Ile Arg Asp Glu
20 25 30

Leu Pro Asn Gly Lys Val Asn Glu Val Lys Thr Ala Thr Gln Tyr Trp
35 40 45

Gly Leu Asn Ile Ser Tyr Pro Val Met Phe Pro Asp Glu Tyr Ala Val
50 55 60

Leu Ser Ser Ala Ile Leu Glu Tyr Lys Arg Thr Arg Gly Tyr Leu Asp
65 70 75 80

Val Ile Leu Pro His Tyr Glu Ser Tyr Arg Val Arg Gly Asp Ala Asn
85 90 95

Asn Cys Arg Ile Ala Ala Gly Gln Lys Gly Ser Thr Leu Val Ile Thr
100 105 110

Asn Thr Asn Ser Leu Ser Gly Glu Pro Lys Pro Gly Asp Leu Phe Gln
115 120 125

Leu Thr Thr His Pro Lys Val Tyr Lys Ile Thr Ser Phe Lys Asn Val
130 135 140

Ala Gly Val Trp Thr Leu Asn Leu Tyr Pro Asp Leu Leu Leu Thr Thr
145 150 155 160

Asn Gly Ser Glu Arg Pro Arg Phe Asn Gly Ile Leu Phe Gln Thr Lys
165 170 175

Leu Met Asn Gly Asp Ser Phe Ser Glu Glu Ile Thr Val Asp Gly Val
180 185 190

Tyr Asp Gly Val Asn Leu Val Leu Arg Glu Ser Leu
195 200

<210> 32
<211> 948
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 32
Met Arg Gln Ile Leu Pro Ser Ala Lys Ala Tyr Leu Ala Asn Asn Asp
1 5 10 15

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

Gly Asn Asn Ala Val Tyr Ala Tyr Met Thr Asp Tyr Met Arg Asp Ile
35 40 45

Asn Tyr Gly Gly Ile Leu Phe Gln Ser Gly Lys Ile Lys Thr Ile Ser
50 55 60

```
Ser His Lys Gln Asn Arg Thr Leu Thr Val Gly Ser Leu Ser Phe Ser
65                  70                  75                  80

Val Thr Gly Thr Asp Ala Asn Glu Val Ile Lys Leu Val Gln Ser Gly
                85                  90                  95

Val Ser Phe Leu Asp Arg Ser Ile Ser Ile Tyr Gln Ala Ile Ile Asp
            100                 105                 110

Asp Asn Gly Glu Ile Leu Pro Val Asp Pro Asp Thr Asn Gly Pro Leu
        115                 120                 125

Leu Phe Phe Arg Gly Lys Ile Val Gly Gly Gly Ile Lys Glu Ser Asn
    130                 135                 140

Thr Val Ser Gly Val Gly Thr Ser Val Ile Thr Trp Asn Cys Ser Asn
145                 150                 155                 160

Glu Phe Tyr Asp Phe Glu Arg Val Ala Gly Arg Phe Thr Asp Asp Ala
                165                 170                 175

Ser His Arg Gly Leu Glu Ile Val Asn Gly Glu Leu Leu Pro Ser His
            180                 185                 190

Gly Ala Lys Arg Pro Glu Tyr Gln Glu Asp Tyr Gly Phe Phe His Ala
        195                 200                 205

Asn Lys Ser Val Asn Phe Leu Ala Lys Tyr Gln Val Lys Glu Glu Arg
    210                 215                 220

Tyr Lys Leu Glu Ser Lys Lys Lys Leu Phe Gly Leu Ser Lys Ser Tyr
225                 230                 235                 240

Ser Leu Lys Lys Tyr Tyr Glu Thr Val Thr Lys Glu Val Asp Leu Asp
                245                 250                 255

Phe Asn Leu Ala Ala Lys Phe Ile Pro Val Val Tyr Gly Thr Gln Lys
            260                 265                 270

Val Pro Gly Ile Pro Val Phe Ala Asp Thr Glu Arg Asn Asn Pro Asn
        275                 280                 285

Val Val Tyr Val Val Tyr Ala Phe Cys Glu Gly Glu Ile Glu Gly Phe
    290                 295                 300

Leu Asp Phe Gln Phe Gly Asp Ala Pro Met Ile Cys Thr Asp Gln Thr
305                 310                 315                 320

Asp Ser Thr Ser Arg Thr Cys Phe Gly Gln Lys Arg Val Ser Gly Asp
                325                 330                 335
```

```
Thr Met Ala Arg Ile Ser Thr Gly Leu Pro Ser Thr Ser Leu Ser Thr
            340                 345                 350

His Gly Gln Glu Tyr Lys Tyr Asn Asp Gly Asn Gly Asp Ile Arg Ile
        355                 360                 365

Trp Thr Phe His Gly Lys Pro Asp Gln Thr Val Ala Thr Val Leu Arg
    370                 375                 380

Asp Ile Ala Ala Ala Asn Asn Phe Phe Leu Gln Gly Glu Asn Gly Asn
385                 390                 395                 400

Gly Pro Glu Tyr Trp Asp Ser Arg Tyr Lys Leu Leu Asp Thr Ala Tyr
                405                 410                 415

Ala Val Ile Arg Phe Thr Ile Thr Glu Asn Arg Thr Asp Ile Pro Glu
            420                 425                 430

Val Ser Ala Glu Leu Ser Gly Arg Lys Val Lys Val Tyr Gln Ala Asp
        435                 440                 445

Gly Ser Val Lys Met Asp Lys Thr Ser Gln Asn Gly Val Trp Gln Thr
    450                 455                 460

Phe Asp Tyr Leu Thr Ser Thr Thr Phe Gly Ala Ser Ile Pro Ile Asp
465                 470                 475                 480

Arg Met Val Ile Gly Asp Trp Arg Lys Glu Ala Asp Leu Leu Asn Ile
                485                 490                 495

Ile Asp Thr Ser Tyr Gln Thr Ser Trp Gln Pro Phe Trp Arg Tyr Val
            500                 505                 510

Gly Trp Glu Ser Trp Thr Ala Glu Asn Arg Gln Ile Met Gln Met Asn
        515                 520                 525

Thr Ile Leu Asp Asn Ser Asn Ser Val Phe Lys Asn Val Gln Glu Leu
    530                 535                 540

Leu Glu Ser Phe Gln Gly Ala Leu Asn Asn Leu Ser Gly Ile Phe Arg
545                 550                 555                 560

Ile Thr Val Glu Lys Asp Ser Lys Thr Pro Leu Glu Leu Asn Phe Leu
                565                 570                 575

Asp Thr Tyr Gly Asp Leu Asp Leu Ser Asp Thr Thr Gly Arg Asn Lys
            580                 585                 590

Tyr Asn Ser Val Gln Ala Ser Leu Ile Asp Pro Thr Leu Asn Trp Lys
        595                 600                 605
```

```
Thr Asn Ser Ile Thr Phe Tyr Asn Ser Lys Phe Lys Asn Glu Asp Arg
    610                 615                 620

Gly Val Asp Lys Lys Leu Gln Leu Ser Phe Ala Asn Ile Thr Asn Tyr
625                 630                 635                 640

Tyr Thr Ala Arg Ser Leu Ala Asp Arg Glu Leu Lys Lys Ser Arg Tyr
                645                 650                 655

Ser Arg Ser Leu Ser Phe Ser Leu Pro Tyr Lys Phe Leu Gly Ile Glu
            660                 665                 670

Pro Asn Asp Pro Val Val Phe Thr Tyr Asp Arg Tyr Gly Trp Asn Lys
        675                 680                 685

Lys Phe Phe Leu Val Asp Glu Val Glu Asn Thr Arg Asp Gly Lys Ile
    690                 695                 700

Asn Val Thr Leu Gln Glu Tyr Gly Glu Asp Val Phe Ile Asn Ser Thr
705                 710                 715                 720

Gln Val Asp Asn Ser Ser Glu Ala Val Pro Glu Ile Ser Asn Asn Val
                725                 730                 735

Leu Pro Pro Arg Asp Phe Lys Tyr Thr Pro Thr Pro Gly Gly Met Val
            740                 745                 750

Gly Asp Val Gly Lys Asn Gly Glu Leu Ser Trp Leu Pro Ser Leu Thr
        755                 760                 765

Pro Asn Val Val Tyr Tyr Ser Ile Arg Lys Ser Asp Arg Val Asp Pro
    770                 775                 780

Tyr Ile Val Gln Gln Thr Ala Phe Thr Pro Asn Val Arg Met Phe Gln
785                 790                 795                 800

Asp Ile Val Gly Glu Pro Ala Gly Leu Thr Ile Phe Glu Ile Arg Ala
                805                 810                 815

Val Asp Ile Asn Gly Arg Arg Ser Ser Pro Val Thr Ile Ser Val Asp
            820                 825                 830

Leu Asn Ser Ala Lys Asn Leu Ser Met Val Glu Asn Phe Arg Val Leu
        835                 840                 845

Asn Leu Ala Pro Asp Pro Ala Glu Trp Val Gly Pro Asp Leu Glu Leu
    850                 855                 860

Gly Trp Asp Lys Leu Gln Glu Glu Gly Leu Ile Ser Gly Ile Phe Tyr
865                 870                 875                 880
```

Thr Leu Glu Ile Arg Asp Asn Thr Asn Lys Leu Leu Arg Ser Ala Lys
885 890 895

Ile Thr Ser Leu Tyr Asn Tyr Ser Tyr Leu Leu Gly Tyr Asn Lys Leu
900 905 910

Asp Tyr Lys Ala Asn Asn Ser Asn Thr Leu Gly Ile Tyr Arg Ala Leu
915 920 925

Gln Pro Arg Ile Gln Ala Glu Gly Pro Lys Gly Glu Lys Ser Val Ala
930 935 940

Trp Ala Tyr Ile
945

<210> 33
<211> 3463
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 33
Met Ile Ser Asn Ile Ala Pro Ala Lys Met Val Leu Gln Asn Ile Val
1 5 10 15

Thr Gly Tyr Thr Ile Ala Ser Ile Gln His Ser Ile Phe Ser Asp Tyr
20 25 30

Asp Val Ile Gly Arg Thr Phe Trp Leu Thr Thr Gly Gly Val Thr Thr
35 40 45

Arg Arg Asp Phe Thr Gly Val Asp Thr Phe Ile Ala Thr Ile Asn Asn
50 55 60

Leu Ile Ala Gly Ala Thr Tyr Ser Ala Gln Gly Ala Phe Tyr Asp Ser
65 70 75 80

Met Val Asp Ala Glu Leu Met Ala Ala Lys Val Gly Met Asn Leu Ser
85 90 95

Ser Thr Ile Asn Phe Lys Met Lys Thr Ala Pro Lys Ile Thr Lys Val
100 105 110

Ser Ser Phe Ala Glu Ser Val Asp Val Gly Val Gly Ala Pro Met Val
115 120 125

Val Val Glu Leu Ser Gly Glu Ala Glu Tyr Val Thr Ile Glu Met Lys
130 135 140

Pro Glu Gly Ser Ser Thr Trp Thr Lys Tyr Tyr Arg Gly Pro Ile Thr
145 150 155 160

```
Glu Gln Ile Ile Phe Gly Gly Val Pro Val Gly Arg Tyr Asn Ile Arg
                165                 170                 175

Val Ser Gly Val Val Thr Met Pro Asp Gly Val Thr Val Asp Val Ser
            180                 185                 190

Gly Tyr Asp Thr Trp Pro Ser Leu Phe Asn Leu Thr Tyr Asn Phe Thr
        195                 200                 205

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

Asp Gly Met Glu Arg Phe Asp Val Arg Leu Glu Trp Asp Trp Thr Arg
225                 230                 235                 240

Gly Thr Gly Ala Asn Val Arg Glu Phe Ile Ile Gln Tyr Ile Ser Asn
                245                 250                 255

Asp Glu Phe Ala Lys Thr Gly Trp Thr Lys Ala Asn Lys Leu Asn Val
            260                 265                 270

Gly Ala Ala Lys Ala Gly Thr Ile Thr Ser Phe Pro Tyr Lys Ile Arg
        275                 280                 285

His Arg Phe Arg Val Leu Ser Val Ala Trp Gly Pro Asp Thr Gln Ser
    290                 295                 300

Ile Thr Asn Ser Asn Glu Val Thr Tyr Ile Ile Asp Glu Ser Thr Thr
305                 310                 315                 320

Phe Asp Asn Ala Phe Ile Asn Glu Thr Gly Val Glu Met Thr Tyr Ala
                325                 330                 335

Gly Ile Lys Gly Lys Leu Trp Asn Ser Asn Thr Lys Gln Trp Glu Gln
            340                 345                 350

Thr Phe Leu Val Asp Ala Ala Thr Gly Ala Val Val Leu Gly Thr Leu
        355                 360                 365

Asp Glu Asn Gly Lys Ala Pro Ile Ser Phe Asp Pro Val Asn Lys Ile
    370                 375                 380

Val Asn Val Asp Gly Lys Val Ile Thr Lys Asp Ile Asn Ala Ala Asn
385                 390                 395                 400

Val Ile Leu Thr Asn Leu Thr Gly Lys Asp Asn Pro Ala Ile Phe Thr
                405                 410                 415

Gln Gly Lys Lys Tyr Gly Asn Asn Ala Gly Gly Val Trp Met Gly Val
            420                 425                 430
```

```
Asp Asn Val Asp Gly Lys Ala Lys Phe Asp Leu Gly Asn Asn Thr Gln
        435                 440                 445

Tyr Val Arg Trp Asp Gly Asp Thr Leu Arg Ile Ser Gly Asn Val Val
    450                 455                 460

Ile Gly Thr Pro Gly Gly Asp Val Asp Leu Glu Thr Gly Met Gln Gly
465                 470                 475                 480

Lys Gln Thr Val Phe Ala Tyr Lys Leu Gly Thr Ser Leu Pro Ser Arg
                485                 490                 495

Pro Leu Asp Gln Val Tyr Pro Pro Ala Gly Trp Ser Ala Phe Pro Pro
            500                 505                 510

Asn Arg Thr Ala Gln Asn Gln Asn Val Tyr Val Val Gln Gly Thr Leu
        515                 520                 525

Asp Pro Lys Lys Ser Pro Pro Ala Leu Val Asp Gly Thr Asn Tyr Ser
    530                 535                 540

Ala Ala Ser Gln Trp Ser Gly Val Pro Gly Thr Gly Gly Thr Asp Gly
545                 550                 555                 560

Ser Asn Gly Asp Tyr Thr Val Gln Ile Tyr Gln Ile Ser Ala Ser Lys
                565                 570                 575

Pro Thr Lys Pro Gly Asn Ile Asn Asp Pro Ser Gly Trp Ser Arg Thr
            580                 585                 590

Pro Pro Thr Gly Thr Pro Leu Trp Met Cys Ser Gly Arg Phe Asn Gly
        595                 600                 605

Asp Thr Asn Ala Leu Thr Val Glu Gly Trp Ser Asp Pro Ile Arg Val
    610                 615                 620

Asp Gly Glu Lys Gly Ala Thr Gly Ala Thr Gly Ala Thr Gly Pro Gln
625                 630                 635                 640

Gly Pro Gln Gly Pro Ala Gly Gly Ser Val Glu Val Gln Trp Ser Lys
                645                 650                 655

Asp Gly Thr Thr Asn Trp His Ala Asn Phe Thr Thr Gly Asp Ile Tyr
            660                 665                 670

Met Arg Gln Arg Val Gly Thr Gly Gly Trp Ser Ser Ala Ile Arg Ala
        675                 680                 685

Val Gly Glu Asp Gly Thr Asn Gly Thr Pro Gly Ser Lys Gly Asn Tyr
    690                 695                 700
```

```
Ile Gly Met Arg Phe Arg Val Ala Ala Glu Lys Pro Ala Thr Pro Thr
705                 710                 715                 720

Gly Gln Thr Pro Ser Gly Trp Ser Asp Ala Pro Pro Gln Gly Asn Pro
                725                 730                 735

Leu Trp Met Val Lys Ala Glu Phe Asn Gly Gln Thr Asn Ala Leu Val
            740                 745                 750

Gly Thr Trp Ser Glu Pro Val Arg Ile Asp Gly Glu Gly Ile Gly Val
        755                 760                 765

Asn Leu Tyr Pro Val Lys Lys Thr Leu Asp Gln Trp Thr Gly Met Ser
    770                 775                 780

Asn Gly Thr Met Val Lys Asn Pro Asp Thr Leu Ser Phe Thr Ile Thr
785                 790                 795                 800

Asn Thr Glu Ser Thr Thr Ser Ser Thr Gly Pro Gly Ala His Pro Val
                805                 810                 815

Pro Phe Gln Gly Ser Gln Gly Pro Ile Val Glu Ile Pro Val Lys Pro
            820                 825                 830

Asn Thr Ala Tyr Ile Phe Thr Tyr Glu Val Ser Thr Asp Ser Thr Ser
        835                 840                 845

Phe Val Leu Arg Asp Leu Leu Leu Glu Phe Ser Ser Ile Thr Gly Ser
    850                 855                 860

Phe Thr Asn Phe Gln Glu Leu Leu Thr Gly Ala Lys Gly Lys Gln Glu
865                 870                 875                 880

Ala Lys Ile Val Thr Arg Ala Asp Thr Lys Phe Leu Ser Phe Arg Pro
                885                 890                 895

Gly Val Arg Thr Ala Gly Ala Thr Val Thr Tyr Ser Asn Leu Lys Leu
            900                 905                 910

Glu Glu Gly Ile Lys Ala Thr Ala Tyr Ser Val Glu Ala Ser Asp Ser
        915                 920                 925

Ile Gly Glu Lys Gly Asp Gln Gly Thr Gln Gly Pro Gln Gly Pro Gln
    930                 935                 940

Gly Asn Gln Gly Pro Gln Gly Asn Gln Gly Pro Gln Gly Ala Lys Gly
945                 950                 955                 960

Asp Asn Ala Lys Gly Phe Ser Leu Ser Ser Leu Gly Gln Thr Phe Thr
                965                 970                 975
```

```
Tyr Asp Ala Glu Gly Lys Leu Lys Ser Asp Ala Thr Ile Leu Phe Gln
            980                 985                 990

Ala Phe Arg Gln Asn Thr Thr Ala  Asn Val Thr Trp Ser  Ala Lys Asp
        995                 1000                1005

Glu Lys  Gly Gly Asn Ile Thr  Leu Thr Ser Thr Ser  Asn Thr Gly
    1010                1015                1020

Ala Thr  Leu Thr Ala Ala Asn  Phe Lys Thr Ser Lys  Ser Val Val
    1025                1030                1035

Val Thr  Ala Val Cys Asp Gly  Ile Thr Asp Gln Ile  Thr Ile Val
    1040                1045                1050

Arg Leu  Asp Asp Gly Ser Asn  Ala Leu Val Gly Leu  Leu Thr Asn
    1055                1060                1065

Glu Gly  Ser Thr Val Leu Ala  Asn Tyr Ala Gly Tyr  Val Gln Asn
    1070                1075                1080

Tyr Ser  Thr Gly Ser Gly Asp  Phe Lys Val Phe Tyr  Gly Ala Lys
    1085                1090                1095

Asp Ile  Thr Ser Glu Cys Thr  Phe Ser Thr Met Glu  Lys Asn Asn
    1100                1105                1110

Leu Asp  Ala Asp Ile Thr Ser  Ala Gly Lys Tyr Thr  Leu Lys Gly
    1115                1120                1125

Met Pro  Ala Gly Thr Asp Val  Ile Asn Gly Trp Val  Asp Leu Arg
    1130                1135                1140

Ala Val  His Pro Thr Tyr Gly  Ala Val Val Arg Arg  Val Ala Thr
    1145                1150                1155

Thr Lys  Ser Ile Leu Ala Lys  Gly Tyr Asp Arg Val  Ile Thr Thr
    1160                1165                1170

Ser Phe  Glu Asn Gly Asn Lys  Gly Thr Trp Ser Thr  Gly Ser Val
    1175                1180                1185

Gln Gly  Val Ser Gly Ala Thr  Ile Val Ala Ala Gly  Phe Ser Lys
    1190                1195                1200

Ala Leu  Val Ile Ser Ala Arg  Asp Cys Ile Glu Asp  Ala Asn Ala
    1205                1210                1215

Phe Pro  Val Val Ala Gly Gln  Lys Tyr Arg Leu Gly  Met Trp Ile
    1220                1225                1230
```

```
Met Ala  Ser Glu Ser Lys Val  Asn Ile Asn Met Gly  Met Arg Ile
    1235                 1240                 1245

Val Arg  Ala Ala Asp Gly Val  Val Asp Trp Gln Gly  Thr Leu Met
    1250                 1255                 1260

Ile Ala  Gln Gly Thr Val Val  Pro Gly Gly Trp Ser  Tyr Ile Glu
    1265                 1270                 1275

Lys Glu  Phe Thr Val Gly Ser  Ser Asn Thr Gly Ile  Ala Met Pro
    1280                 1285                 1290

Trp Ile  Gln Met Ala Gly Ser  Ser Gly Ser Asp Leu  Gly Lys Ala
    1295                 1300                 1305

Tyr Val  Thr Asp Ile His Ile  Phe Ala Leu Glu Met  Asp Gly Glu
    1310                 1315                 1320

Lys Gly  Asp Thr Gly Ala Thr  Gly Ala Thr Gly Ser  Gln Gly Pro
    1325                 1330                 1335

Gln Gly  Pro Gln Gly Asn Lys  Gly Asp Lys Gly Asp  Thr Gly Ala
    1340                 1345                 1350

Thr Gly  Ala Gln Gly Pro Ala  Gly Ser Ser Val Asn  Val Gln Trp
    1355                 1360                 1365

Ser Lys  Asp Gly Ser Thr Asn  Trp His Ala Gly Phe  Gln Pro Gly
    1370                 1375                 1380

Asp Ile  Phe Met Arg Gln Gln  Val Asn Gly Val Trp  Gly Ser Ala
    1385                 1390                 1395

Ile Arg  Ala Val Gly Glu Asp  Gly Lys Asn Gly Ala  Asp Gly Thr
    1400                 1405                 1410

Asp Gly  Asp Tyr Ile Ser Met  Lys Phe Ile Val Gln  Asp Thr Lys
    1415                 1420                 1425

Pro Gly  Thr Pro Thr Gly Asn  Asn Pro Gly Ser Trp  Ser Asp Ala
    1430                 1435                 1440

Pro Pro  Val Gly Ser Pro Leu  Trp Met Thr Lys Gly  Thr Met Asn
    1445                 1450                 1455

Ala Ser  Gly Gln Leu Gln Gly  Thr Trp Ser Asn Pro  Val Arg Leu
    1460                 1465                 1470

Asp Gly  Thr Ile Asn Pro Asn  Leu Phe Ala Val Arg  Lys Trp Met
    1475                 1480                 1485
```

```
Ala Gly  Met Thr Gly Thr Glu  Ala Gly Thr Ser Lys  Asn Asp Ile
    1490                 1495                 1500

Glu Lys  Leu Ala His Thr Leu  Thr Arg Thr Ser Gly  Thr Asp Asn
    1505                 1510                 1515

Thr Ala  Pro Gly Cys Tyr Ala  Thr Pro Tyr Leu Gly  Ser Gly Ala
    1520                 1525                 1530

Phe Ser  His Pro Val Thr Pro  Gly Lys Arg Tyr Thr  Leu Thr Tyr
    1535                 1540                 1545

Asn Ile  Asp Ala Ala Ser Glu  Val Gln Thr Arg Asp  Thr Ile Phe
    1550                 1555                 1560

Trp Gln  Ala Asn Pro Asp Ser  Gly Gln Ser Thr Tyr  Ile Glu Glu
    1565                 1570                 1575

Leu Asn  Thr Gly Thr Ser Ile  Lys Val Lys Arg Thr  Phe Val Val
    1580                 1585                 1590

Pro Thr  Gly Met Asn Tyr Leu  Thr Leu Arg Pro Ser  Ala Leu Thr
    1595                 1600                 1605

Leu Asn  Val Ala Thr Thr Trp  Ser Lys Ile Lys Leu  Glu Glu Gly
    1610                 1615                 1620

Gly Glu  Lys Thr Glu Tyr Gln  Val Glu Tyr Ser Asp  Ser Ile Gly
    1625                 1630                 1635

Ile Val  Gly Lys Ser Val Leu  Val Gln Trp Ser Lys  Asp Ser Ser
    1640                 1645                 1650

Ser Ser  Asn Trp His Asp Thr  Phe Gln Thr Gly Asp  Leu Phe Met
    1655                 1660                 1665

Arg Gln  Asn Val Asp Gly Val  Trp Gly Pro Ala Ile  Arg Ala Ile
    1670                 1675                 1680

Gly Glu  Lys Gly Glu Ile Gly  Pro Asp Gly Lys Lys  Gly Asn Tyr
    1685                 1690                 1695

Thr Asn  Ile Ile Phe Arg Ile  Ser Asp Thr Lys Pro  Ala Lys Pro
    1700                 1705                 1710

Thr Gly  Asn Lys Pro Thr Asp  Trp Phe Asp Ala Pro  Pro Asp Gly
    1715                 1720                 1725

Ser Pro  Leu Trp Met Ala Thr  Ala Thr Phe Asn Gly  Asp Thr Asn
    1730                 1735                 1740
```

```
Ala Ile  Ile Gly Ala Trp Ser  Asp Pro Val Arg Ile  Asp Ala Ser
    1745                1750                1755

Gly Val  Gly Glu Asn Phe Leu  Ala Phe Lys Glu Trp  Met Met Ser
    1760                1765                1770

Ile Gln  Arg Ala Glu Gly Thr  Gly Ser Ser Val Ser  Lys Asn Pro
    1775                1780                1785

Asp Gln  Met Arg Phe Arg Val  Thr Ala Gly Pro Ser  Arg Asn Asp
    1790                1795                1800

Ala Tyr  Thr Thr Pro Tyr Gln  Gly Thr Gly Thr His  Phe Ile Glu
    1805                1810                1815

Val Ser  Pro Asn Thr Val Tyr  Thr Leu Ser Phe Glu  Met Glu Thr
    1820                1825                1830

Ala Val  Ser Thr Arg Met Met  Leu Leu Gln Phe Asp  Asn Gly Asn
    1835                1840                1845

Gly Gly  Thr His Ala Arg Asn  Asn Gln Val Ile Ser  Thr Ser Thr
    1850                1855                1860

Gly Ile  Asn Ser Leu Thr Ile  Thr Thr Gly Ala Asn  Thr Thr His
    1865                1870                1875

Leu Ser  Met Arg Met Ser Ile  Ser Asn Met Gly Glu  Thr Asn Val
    1880                1885                1890

Leu Met  Lys Pro Lys Leu Glu  Leu Gly Ala Phe Pro  Thr Ala Tyr
    1895                1900                1905

Val Ala  His Pro Ser Asp Leu  Leu Gly Lys Asp Gly  Ala Thr Gly
    1910                1915                1920

Ala Thr  Gly Pro Gln Gly Pro  Gln Gly Asn Thr Gly  Ala Thr Gly
    1925                1930                1935

Ala Thr  Gly Pro Gln Gly Ser  Lys Gly Asp Thr Gly  Ala Thr Gly
    1940                1945                1950

Pro Gln  Gly Pro Gln Gly Pro  Lys Gly Asn Ala Gly  Glu Asn Ala
    1955                1960                1965

Lys Gly  Phe Ala Leu Thr Ser  Asp Tyr Gln Ser Phe  Val Tyr Asp
    1970                1975                1980

Thr Val  Gly Asp Ile Lys Ser  Ala Thr Thr Ile Leu  Phe Lys Gly
    1985                1990                1995
```

```
Leu Lys  Gln Asn Thr Thr Ala  Gly Ile Thr Trp Ser  Ala Val Asn
    2000                 2005                 2010

Asn Thr  Gly Ala Ala Val Thr  Leu Met Asn Ser Gly  Asp Asn Arg
    2015                 2020                 2025

Gln Leu  Thr Ala Ala Asn Phe  Gly Ala Ser Lys Trp  Val Thr Ile
    2030                 2035                 2040

Thr Ala  Thr Cys Asp Gly Leu  Ser Asp Gln Ile Thr  Val Val Arg
    2045                 2050                 2055

Leu Gln  Asp Gly Glu Asn Val  Leu Thr Ala Val Met  Thr Asn Glu
    2060                 2065                 2070

Ala Ala  Thr Val Leu Ala Asn  Tyr Ser Gly Tyr Cys  Gln Ser Tyr
    2075                 2080                 2085

Glu Asn  Ala Lys Gly Gln Met  Arg Val Trp Tyr Gly  Ser Thr Asp
    2090                 2095                 2100

Val Thr  Gly Gln Cys Thr Phe  Ser Glu Gly Gly Arg  Ser Asn Val
    2105                 2110                 2115

Thr Pro  Ser Ile Asn Ser Ala  Asn Gly Asn Tyr Ser  Val Thr Gly
    2120                 2125                 2130

Met Leu  Asp Gly Thr Asp Ile  Thr Glu Gly Trp Val  Asp Val Lys
    2135                 2140                 2145

Ala Thr  His Pro Lys Tyr Gly  Ala Ile Thr Lys Arg  Phe Ala Val
    2150                 2155                 2160

Thr Lys  Val Phe Leu Ala Lys  Ser Tyr Glu Met Val  Ile Thr Asn
    2165                 2170                 2175

Thr Phe  Glu Asn Gly Asn Lys  Gly Ser Trp Ala Gly  Ala Leu Gln
    2180                 2185                 2190

Ser Val  Ser Gly Pro Thr Asn  Gln Ser Ile Ser Lys  Ala Leu Arg
    2195                 2200                 2205

Ile Thr  Ala Arg Asp Asn Leu  Glu Gly Arg Asn Thr  Ile Pro Val
    2210                 2215                 2220

Ala Gly  Gly Gln Lys Val Arg  Ile Arg Phe Trp Tyr  Asn Pro Leu
    2225                 2230                 2235

Gly Leu  Glu Glu Ala Ile Phe  Arg Val Gly Phe Ile  Val His Arg
    2240                 2245                 2250
```

```
Lys Asp  Gly Gly Lys Gly Tyr  Pro Ser Arg Thr Val  Val Thr Gly
    2255                 2260                 2265

Pro Ala  Pro Asn Ser Ser Trp  Ala Tyr Phe Asp Gln  Glu Leu Thr
    2270                 2275                 2280

Leu Ser  Ala Asn Asp Glu Gly  Ile Ala Trp Pro Trp  Phe Gln Leu
    2285                 2290                 2295

Asp Asn  Lys Thr Ser Gly Ser  Ser Leu Gly Tyr Met  Leu Val Ala
    2300                 2305                 2310

Asp Ile  His Phe Glu Asp Leu  Ser Met Asp Gly Ala  Asp Gly Ala
    2315                 2320                 2325

Thr Gly  Pro Gln Gly Pro Gln  Gly Asn Thr Gly Ala  Thr Gly Pro
    2330                 2335                 2340

Gln Gly  Asn Lys Gly Asp Thr  Gly Pro Gln Gly Pro  Gln Gly Pro
    2345                 2350                 2355

Ala Gly  Ala Ser Val Gly Val  Gln Trp Ser Lys Thr  Gly Asn Ala
    2360                 2365                 2370

Ser Asp  Trp His Thr Asn Tyr  Ala Thr Gly Asp Ile  Tyr Met Arg
    2375                 2380                 2385

Gln Gln  Val Asn Gly Val Trp  Ser Ser Ala Ile Arg  Ala Val Gly
    2390                 2395                 2400

Glu Asp  Gly Arg Val Gly Ala  Asp Gly Lys Tyr Thr  Ser Leu Arg
    2405                 2410                 2415

Phe Gln  Val Ala Ala Thr Lys  Pro Ala Arg Pro Thr  Gly Asn Ser
    2420                 2425                 2430

Pro Ala  Asn Trp Ser Asp Ser  Pro Pro Glu Gly Ser  Pro Leu Trp
    2435                 2440                 2445

Met Val  Lys Gly Glu Phe Asp  Ser Ser Asn Gln Leu  Gln Gly Thr
    2450                 2455                 2460

Trp Ser  Asp Pro Val Arg Leu  Asp Gly Glu Thr Val  Asn Leu Asn
    2465                 2470                 2475

Leu Phe  Ala Asn Lys Ala Trp  Ile Ala Ser Ile Thr  Gly Ala Ser
    2480                 2485                 2490

Gly Ser  Gly Ser Val Val Ala  Lys Asn Pro Asp Glu  Leu Arg Leu
    2495                 2500                 2505
```

```
Arg Ile  Thr Ala Gly Ser Gly  Ala Thr Asp Ala Tyr  Thr Met Pro
    2510                 2515                 2520

Ser Gly  Gly Asp Gly Thr Phe  Phe Thr Lys Val Thr  Ala Gly Lys
    2525                 2530                 2535

Arg Tyr  Thr Met Ser Phe Asp  Thr Asp Ser Ala Leu  Glu Met Arg
    2540                 2545                 2550

Met His  Val Phe Phe Ile Gln  Ala Gly Ala Asn Thr  Thr Thr Ser
    2555                 2560                 2565

Ser Phe  Ser Trp Ile Ala Ser  Thr Thr Ala Gly Arg  Thr Ser Trp
    2570                 2575                 2580

Ser Phe  Thr Val Pro Ala Gly  Cys Asp Arg Val Ser  Val Arg Val
    2585                 2590                 2595

Ser Leu  Asn Asn Asn Pro Gly  Gly Thr Asn Val Val  Ser Asn Ile
    2600                 2605                 2610

Lys Leu  Glu Glu Gly Asp Phe  Ala Thr Ala Phe Ile  Arg Asn Glu
    2615                 2620                 2625

Leu Asp  Thr Ile Gly Ala Asp  Gly Ser Gln Gly Pro  Gln Gly Pro
    2630                 2635                 2640

Gln Gly  Ser Lys Gly Asp Lys  Gly Asp Thr Gly Ala  Thr Gly Pro
    2645                 2650                 2655

Gln Gly  Pro Gln Gly Pro Asn  Gly Thr Ser Ala Lys  Ala Phe Ala
    2660                 2665                 2670

Leu Thr  Ser Asp Ser Leu Ser  Phe Ser Phe Asp Thr  Ser Gly Asn
    2675                 2680                 2685

Leu Lys  Ser Asn Gly Thr Ile  Lys Ile Asp Ser Trp  Arg Gln Asn
    2690                 2695                 2700

Thr Thr  Ala Ala Ile Thr Trp  Thr Ala Lys Asn Gln  Ala Gly Ser
    2705                 2710                 2715

Asn Ile  Thr Leu Gly Gly Thr  Ala Thr Asn Lys Thr  Ile Thr Ser
    2720                 2725                 2730

Ala Gln  Phe Gly Ser Ser Glu  Tyr Val Thr Val Thr  Ala Thr Cys
    2735                 2740                 2745

Asp Gly  Ile Thr Asp Ser Ile  Thr Ile Val Arg Leu  Gln Asp Gly
    2750                 2755                 2760
```

```
Val Asn  Ser Leu Val Gly Tyr  Leu Thr Asn Glu Ala  Ala Asn Leu
    2765                 2770                 2775

Ser Cys  Asn Ser Tyr Gly Phe  Val Gln Asn Trp Asp  Gly Thr Thr
    2780                 2785                 2790

Gly Asn  Phe Lys Val Phe Tyr  Gly Thr Val Asp Val  Thr Ser Gln
    2795                 2800                 2805

Cys Thr  Phe Gly Val Glu Asp  Lys Ser Asn Leu Asn  Gly Asn Ile
    2810                 2815                 2820

Gly Ser  Ser Gly Tyr Tyr Ala  Pro Ser Ala Met Pro  Asn Gly Leu
    2825                 2830                 2835

Glu Ile  Thr Ser Gly Trp Val  Asp Tyr Lys Ala Thr  His Pro Lys
    2840                 2845                 2850

Tyr Gly  Thr Leu Ile Lys Arg  Phe Thr Leu Lys Lys  Ser Leu Pro
    2855                 2860                 2865

Gly Ile  Gly Tyr Asp Arg Val  Phe Thr Gly Ser Phe  Asp Ser Gly
    2870                 2875                 2880

Asn Asn  Gly Ser Trp Gly Arg  Thr Val Val Asp Ile  Ala Thr Gly
    2885                 2890                 2895

Ser Pro  Gly Gly His Thr Lys  Ala Ile Gln Cys Thr  Ser Arg Asp
    2900                 2905                 2910

Thr Met  Glu Ser Ser Asn Trp  Phe Pro Thr Arg Lys  Gly Met Arg
    2915                 2920                 2925

Tyr Arg  Val Thr Ala Trp Val  Asn Asn Ser Glu Gly  Glu Tyr Gln
    2930                 2935                 2940

Leu Arg  Leu Gly Leu His Thr  Gln Asn Ser Ser Gly  Ser Val Asn
    2945                 2950                 2955

Thr Gly  Tyr Pro Thr Met Leu  Ala Ala Ser Ala Lys  Asp Ser Glu
    2960                 2965                 2970

Gly Trp  Lys Leu Val Thr Gly  Ile Val Thr Val Gly  Asp Gly Ser
    2975                 2980                 2985

Thr Ala  Glu Thr Gly Arg Ala  Arg Pro Phe Ile Gln  Met Asn Gly
    2990                 2995                 3000

Ser Ala  Ser Pro Phe Gly Asn  Ala Tyr Val Ala Ala  Ile Ala Ile
    3005                 3010                 3015
```

```
Glu Asp  Leu Ser Met Asp Gly  Ala Asp Gly Ala Thr  Gly Pro Gln
    3020                 3025                 3030

Gly Pro  Gln Gly Asn Thr Gly  Ala Thr Gly Pro Gln  Gly Asp Lys
    3035                 3040                 3045

Gly Asp  Thr Gly Pro Gln Gly  Pro Gln Gly Pro Ala  Gly Asn Ser
    3050                 3055                 3060

Val Asn  Val Gln Trp Ser Lys  Asp Gly Ser Thr Asn  Trp His Ser
    3065                 3070                 3075

Thr Phe  Thr Ser Gly Asp Leu  Tyr Met Arg Gln Gln  Val Asn Gly
    3080                 3085                 3090

Ser Trp  Gly Pro Ala Ile Arg  Ala Val Gly Glu Asn  Gly Ala Asn
    3095                 3100                 3105

Gly Thr  Pro Gly Ser Lys Gly  Asn Tyr Val Ser Met  Lys Phe Ala
    3110                 3115                 3120

Val Met  Ala Ser Thr Pro Ser  Arg Pro Ser Gly Ser  Asn Pro Ala
    3125                 3130                 3135

Gly Trp  Ser Asp Ser Pro Pro  Pro Gly Asn Pro Leu  Trp Met Ile
    3140                 3145                 3150

Lys Ala  Glu Phe Asn Gly Glu  Thr Asn Ala Ile Ile  Gly Asn Trp
    3155                 3160                 3165

Ser Asp  Pro Ile Arg Leu Asp  Gly Asp Ser Ile Asn  Glu Asn Leu
    3170                 3175                 3180

Phe Tyr  Phe Lys Ala Trp Leu  Asp Ser Ile Thr Gly  Val Ala Gly
    3185                 3190                 3195

Asn Gly  Ser Ser Ile Gly Lys  Asn Tyr Glu Leu Leu  Arg Ala Arg
    3200                 3205                 3210

Ile Ile  Ala Gly Thr Gly Val  Thr Asp Ala Tyr Thr  Leu Pro Ser
    3215                 3220                 3225

Asp Gly  Ser Ala Ser Met Phe  Thr Tyr Leu Pro Pro  Ser Thr Thr
    3230                 3235                 3240

Tyr Thr  Met Ser Phe Glu Thr  Asp Asn Ala Val Glu  Val Arg Cys
    3245                 3250                 3255

His Val  Phe Trp Tyr Ala Lys  Gly Ser Asn Thr Thr  Gly Gly Val
    3260                 3265                 3270
```

```
Leu Lys  Thr Ile Ala Ser Thr  Thr Ala Gly Leu Ser  Ser Phe Thr
    3275                 3280                 3285

Phe Thr  Thr Pro Ala Asn Ser  Asp Arg Ile Ser Val  Arg Phe Ser
    3290                 3295                 3300

Val Asn  Glu Ser Gly Gly Asn  Asn Val Val Gly Arg  Cys Lys Ile
    3305                 3310                 3315

Glu Lys  Gly Ala Phe Val Thr  Ser Tyr Val Arg Asn  Gln Tyr Asp
    3320                 3325                 3330

Ala Val  Gly Asp Arg Gly Pro  Gly Phe Tyr Thr Gln  Ala Ile Thr
    3335                 3340                 3345

Asn Leu  Thr Gly Trp Asn Asp  Thr Gln Ala Ala Ser  Phe Phe Gln
    3350                 3355                 3360

Ser Thr  Phe Gly Gly Pro Pro  Val Lys Tyr Asp Val  Leu Thr Gln
    3365                 3370                 3375

Tyr Lys  Ser Gly Ser Pro Gln  Asn Ser Trp Thr Arg  Gln Trp Asn
    3380                 3385                 3390

Gly Ser  Ala Trp Thr Ala Pro  Ala Leu Thr Val His  Gly Asp Met
    3395                 3400                 3405

Ile Val  Ser Gly Ser Ile Thr  Ala Asp Lys Ile Ile  Ala Asn Asn
    3410                 3415                 3420

Ala Phe  Leu Ala Gln Ile Gly  Val Asp Ile Leu Tyr  Asn Arg Ala
    3425                 3430                 3435

Ala Ala  Leu Ser Ser Asn Pro  Glu Gly Thr Tyr Thr  Met Lys Ile
    3440                 3445                 3450

Asp Leu  Ala Asn Gly Tyr Ile  His Ile Arg
    3455                 3460


<210> 34
<211> 139
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 34
Met Ser Thr Glu Asn Arg Val Val Asp Ile Ile Leu Asp Gln Asn Val
1               5                  10                  15

Ser Tyr Gly Leu Met Leu Gln Phe Met Asp Ile Asp Asp Ser Ala Tyr
```

20 25 30

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

Ser Ile Lys Asp Ser Leu Glu Ser Thr Gly Val Lys Leu Ala Asp Phe
50 55 60

Val Val Thr Val Val Asn Ala Thr Gln Gly Gln Ala Ser Leu Gly Leu
65 70 75 80

Thr Ala Ala Thr Val Ala Thr Ile Val Ser Lys Ala Ser Lys Glu Arg
85 90 95

Asp Lys Tyr Asn Pro Arg Leu Arg Phe Ala Gly Tyr Tyr Asp Val Ile
100 105 110

Met Thr Lys Gly Thr Gly Ala Thr Ala Thr Ser Tyr Arg Val Met Glu
115 120 125

Gly Ser Val Tyr Val Ser Asp Gly Val Thr Ala
130 135

<210> 35
<211> 679
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 35
Met Ala Ile Thr Thr Arg Ile Ile Ala Gln Gln Val Thr Ala Leu Asp
1 5 10 15

Gly Ala Asn Ser Arg Val Ser Lys Tyr Pro Lys Phe Thr Val Gln Leu
20 25 30

Gly Tyr Ser Val Ser Ser Leu Ala Ala Thr Glu Leu Leu Asp Ala Ala
35 40 45

Thr Arg Ser Ala Ala Ser Ala Ala Ala Ala Lys Thr Ser Glu Thr Asn
50 55 60

Ala Lys Ala Ser Glu Thr Ala Ser Lys Asn Ser Gln Thr Ala Ala Lys
65 70 75 80

Thr Ser Glu Thr Asn Ala Ala Ala Ser Ala Gln Val Ala Gln Asn Leu
85 90 95

Ala Gly Lys Ala Ser Leu Val Thr Pro Leu Gly Val Met Thr Gly Ser
100 105 110

```
Ala Glu Ala Lys Ile Ala Ser Ile Thr Ile Ala Ala Asn Gln Ser Ser
        115                 120                 125

Ser Val His Val Leu Phe Ala Leu Tyr Ala Thr Gly Asn Gly Ala Asn
    130                 135                 140

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

Pro Val Thr Ser Val Thr Ala Asp Asn Ile Gly Ser Phe Leu Ser His
                165                 170                 175

Arg Val Ile Gly Pro Ala Asn Thr Asn Gly Phe Met Val Gly Leu Lys
            180                 185                 190

Ser Thr Ile Glu Gly Ser Asn Val Thr Tyr Asp Val Tyr Leu Lys Ser
        195                 200                 205

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

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

Trp Lys Thr Thr Gly Phe Asp Thr Asp Val Ile Tyr Val Asn Arg Ala
                245                 250                 255

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

Ile Thr Asn Gly Lys Thr Asp Ser Ser Ile Leu Leu Leu Ser Tyr Leu
        275                 280                 285

Asn Glu Thr Gly Ile Leu Ser Thr Asn Lys Lys Ser Ile Ser Leu Arg
    290                 295                 300

Pro Gly Gly Thr Ser Asp Ser Ser Ile Ala Ala Thr Glu Phe Leu Pro
305                 310                 315                 320

Asn Gly Asn Ile Ile Leu Pro Asn Gly Asp Thr Gly Asn Gln Thr Ile
                325                 330                 335

Ser Trp Leu Gly Gly Pro Arg Ile Arg Val Asn Ser Asn Gly Ser Phe
            340                 345                 350

Val Leu Ser Thr Asn Asn Pro Ser Asn Gln Thr Ser Gly Phe Ile Thr
        355                 360                 365

Phe Arg Pro Gln Gly Asp Gln Val Thr Ser Thr Glu Leu Gln Ile Arg
    370                 375                 380
```

```
Asp Asp Gly Asn Ile Lys Gln Thr Ala Pro Gln Ser Ser Ala Gly Asn
385                 390                 395                 400

Ala Leu Ile Arg Gln Asp Ala Ala Ile Gln His Ile Met Asp Lys Ala
                405                 410                 415

Pro Ala Ala Gly Ile Thr Ala Asn Pro Leu Ser Asp Leu Asn Val Ile
            420                 425                 430

Pro Thr Pro Glu Gly Thr Asp Pro Trp Gly Ala Asp Gly Val Arg Val
        435                 440                 445

Phe Gln Ser Gly Val Ser Thr Lys Asn Thr Pro Asp Gly Thr Thr Gly
    450                 455                 460

Arg Leu Gly Thr Ile Leu Asn Val Arg His Thr Gln Tyr Arg Ile Met
465                 470                 475                 480

Gln Phe Phe Met Gln Ser Asn Ala Thr Ala Pro Ile Leu His Ile Arg
                485                 490                 495

Ser Leu Arg Ala Asp Gln Gly Asn Thr Pro Pro Ala Trp Phe Lys Val
            500                 505                 510

Tyr Thr Glu Tyr Ser Lys Pro Asn Ile Gln Ser Asp Ile Ala Gly Ile
        515                 520                 525

Thr Ile Asp Gly Asn Gly Phe Val Lys Lys Ala Ser Pro Ile Ala Lys
    530                 535                 540

Leu Ile Ala Glu Ile Pro Ser Lys Glu Asp Ser Phe Phe Trp Thr Gly
545                 550                 555                 560

Val Glu Thr Val Gly Gly Tyr Val Gly Cys Asn Ala Glu Ala Gln Gly
                565                 570                 575

Val Phe Ala Val Lys Thr Gly Leu Gly Lys Tyr Thr Ile Lys Gly Ser
            580                 585                 590

Leu Gly Trp Asn Thr Glu Gly Trp Lys Phe Glu Leu Pro Arg Asp Asp
        595                 600                 605

Asn Gly Asn Met Leu Cys Phe Val Glu Ser Asp Trp Asn Glu Glu Glu
    610                 615                 620

Lys Glu Leu Asn Ile Gln Val Phe Thr Arg Lys Phe Asp Ile Asn Thr
625                 630                 635                 640

Gly Asn Ile Ile Ala Gly Glu Pro Met Glu Ile Pro Gln Gly Arg Trp
                645                 650                 655
```

Ile Asp Leu Arg Leu Glu Met Pro Lys Val Glu Ile Pro Glu Val Glu
660 665 670

Phe Pro Glu Asp Pro Glu Val
675

<210> 36
<211> 147
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 36
Met Arg Ile Lys Leu Ser His Pro Asp Cys Lys Pro His Val Gly Ser
1 5 10 15

Ser Glu Ala Ala Gly Met Asp Leu Arg Ala Tyr Phe Gly Asp Arg Ala
20 25 30

Ser Asp Leu Leu Arg Ala Ile Pro Pro Gly Glu Ser Leu Met Ile Asp
35 40 45

Thr Gly Val Ala Val Glu Ile Pro Glu Gly Trp Val Gly Ile Val Val
50 55 60

Pro Arg Ser Ser Leu Gly Lys Arg Arg Leu Met Ile Ala Asn Thr Thr
65 70 75 80

Gly Val Ile Asp Ser Asp Tyr Arg Gly Thr Ile Lys Met Asn Leu Leu
85 90 95

Asn Met Ser Asn Glu Thr Gln Pro Ile Asp Asn Phe Glu Arg Leu Cys
100 105 110

Gln Leu Val Ile Val Pro His Tyr Asn Pro Asn Asp Ile Glu Ile Val
115 120 125

Asp Ser Leu Thr Asp Thr Asp Arg Gly Glu Gly Gly Phe Gly Ser Ser
130 135 140

Gly Lys Met
145

<210> 37
<211> 292
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 37
Met Ser Lys Ser Trp Gly Thr Met Lys Arg Glu Ala Glu Gln Arg Leu
1 5 10 15

```
Ala Ser Arg Arg Asn Leu Met Ile Val Asp Gly Thr Asn Leu Gly Phe
            20                  25                  30

Arg Phe Lys Lys Asp Ser Gly Lys Pro Ile Ala Ala Ser Phe Ala Asn
        35                  40                  45

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

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

Tyr Lys Gly Asn Arg Asp Ala Lys Tyr Ala Asp Arg Ser Glu Ala Glu
                85                  90                  95

Val Glu Ala Asp Arg Gln Phe Phe Glu Tyr Leu Asp Asp Ala Phe Asp
            100                 105                 110

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

Asp Asp Met Ala Ala Phe Ile Ile Gln Leu Ile Gly His His Tyr Asp
    130                 135                 140

His Ile Trp Leu Ile Ser Thr Asp Gly Asp Trp Asp Thr Leu Leu Ala
145                 150                 155                 160

Pro Asn Ile Ser Arg Phe Ser Phe Thr Thr Arg Lys Glu Tyr His Glu
                165                 170                 175

Lys Asp Met Phe Asp Asn His Asn Val Asp Thr Val Asp Gln Phe Ile
            180                 185                 190

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

Glu Gly Ile Gly Glu Lys Arg Gly Tyr Asn Leu Ile Arg Glu His Gly
    210                 215                 220

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

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

Thr Leu Val Asp Leu Pro Ser Phe Cys Gly Glu Ala Val Ala Ala Ala
            260                 265                 270

Gly Gln Asp Ile Tyr Asp Gln Phe Val Lys Asp Ile Thr Ala Ile Ala
        275                 280                 285
```

Thr Gly Glu Val
290

<210> 38
<211> 160
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 38
Met Ala Val Asp Ser Arg Glu Lys Gly Lys Arg Ala Glu Tyr Gln Ile
1 5 10 15

Arg Asp Met Leu Arg Lys Tyr Thr Ser Leu Asp Trp Glu Arg Val Pro
20 25 30

Gly Ser Gly Ala Phe Gly Gln Ser His Ser Leu Lys Gly Asp Val Tyr
35 40 45

Leu Pro Pro Ser Val Gly Lys Met Ser Gln Tyr Cys Phe Glu Ile Lys
50 55 60

His Tyr Ala Asp Glu Lys Phe Asn Ser Asn Ile Leu Asn Val Gly Glu
65 70 75 80

Ser Gln Leu Glu Lys Trp Trp Ala Gln Ala Ala Arg Glu Gly Glu Gln
85 90 95

Met Asn Met Lys Pro Ala Leu Ile Phe Lys Lys Asp Arg Gly Gln Trp
100 105 110

Leu Ile Ala Leu Asp Ser Ser Asp Pro Met Ile Asp Asn Leu Met Ser
115 120 125

Arg Ala His Phe Ile Val Asn Lys Arg Gly Met Glu Ile Val Ile Gly
130 135 140

Leu Phe Glu Pro Trp Leu Asn Ala Cys Glu Ile Gly Asp Leu Val Lys
145 150 155 160

<210> 39
<211> 611
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 39
Met Ser Ile Val Ile Asn Lys Leu Thr Ile Ser His Phe Met Ser Tyr
1 5 10 15

```
Ala Glu Asn Val Val Ile Glu Phe Asp Asn His Arg Val Thr Gln Leu
            20                  25                  30

Ile Gly Arg Asn Gly Leu Gly Lys Ser Thr Ile Gly Thr Ala Leu Glu
        35                  40                  45

Glu Leu Leu Tyr Asn Lys Asn Ser Arg Gly Ile Lys Lys Asp Asp Leu
    50                  55                  60

Phe Asn Trp His Thr Gly Ser Lys Ala Tyr Thr Leu Glu Gly Gln Phe
65                  70                  75                  80

Thr Lys Asp Gly Asp Val Tyr Asn Val Lys Lys Val Val Lys Ser Thr
                85                  90                  95

Ala Lys Val Thr Leu Thr Lys Asn Gly Glu Asp Ile Ser Gly His Thr
            100                 105                 110

Ala Thr Gln Thr Tyr Lys Leu Ile Glu Glu Val Leu Ala Cys Asp Phe
        115                 120                 125

Thr Thr Phe Thr Lys Leu Val Tyr Gln Ser Val Gly Ser Ser Leu Asp
    130                 135                 140

Phe Leu Lys Thr Thr Asp Ala Gln Arg Lys Thr Phe Leu Val Asn Leu
145                 150                 155                 160

Phe Asp Gln Glu Gln Tyr Lys Glu Val Ser Glu Arg Val Lys Ala Gly
                165                 170                 175

Arg Lys Ala Val Ser Ala Lys Leu Ser Gly Leu Glu Gly Ser Leu Arg
            180                 185                 190

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

Ser Glu Ile Pro Ile Pro Val Phe Asp Glu Glu Pro Leu Val Glu Glu
    210                 215                 220

Leu Thr Glu Ala Lys Val Lys Val Ala Leu Ala Gln Lys Gln Lys Ala
225                 230                 235                 240

Ser Ile Ala Lys Arg Ser Ser Leu Asp Met Ala Val Gln Ala Ala Glu
                245                 250                 255

Lys Thr Phe Ala Pro Phe Glu Asn Leu Pro Ala Pro Thr Ser Lys Ser
            260                 265                 270

Glu Glu Leu Leu Ser Val Thr Arg Asn Leu Thr Val Val Ala Thr Arg
        275                 280                 285
```

```
Ala Asp Asp Leu Lys Lys Arg Tyr Tyr Asp Phe Lys Asn Ala Ala Gly
    290                 295                 300

Lys Thr Gln Cys Ser Ala Cys Gly Thr His Leu Asp Thr Ser Ala Ala
305                 310                 315                 320

Gln Glu Ala Met Arg Arg Thr Lys Glu Glu Tyr Asp Pro Leu Tyr Lys
                325                 330                 335

Glu Arg Gln Lys Leu Glu Ala Glu Val Glu Glu Leu Arg Lys Glu Asp
            340                 345                 350

Arg Ala Phe Lys Asp Tyr Ile Ser Lys Phe Asn Ala Leu Glu Gln Ala
        355                 360                 365

Arg Lys Asn Leu Lys Glu Phe Asp Glu Val Asn Gly Thr Gln Asp Glu
    370                 375                 380

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

Ser Ile Arg Gln Gly Arg Ser Ser Val Glu Leu Ala Arg Thr His Asn
                405                 410                 415

Glu Ser Val Val Arg Glu Asn Ala Lys Tyr Glu Ala Lys Arg Glu Gln
            420                 425                 430

Ile Gln Lys Ala Glu Gln Glu Phe Asp Lys Ile Gln Ala Glu Leu Ser
        435                 440                 445

Leu Val Ala Glu Glu Val Ala Asp Leu Asp Ile Leu Ile Thr Gly Leu
    450                 455                 460

Lys Asp Leu Val Gly Tyr Lys Leu Glu His Ser Val Lys Val Phe Glu
465                 470                 475                 480

Glu Met Ile Asn His Tyr Leu Ser Ile Met Thr Ser Gly Lys Phe Ala
                485                 490                 495

Leu Gly Phe Glu Leu Asp Glu Thr Lys Leu Gln Val Val Ile Tyr Asn
            500                 505                 510

Asp Gly Asn Arg Thr Ser Met Val Asn Cys Ser Thr Gly Gln Gln Ser
        515                 520                 525

Arg Ile Asn Ile Ser Thr Leu Leu Ala Ile Arg Met Leu Leu Ser Thr
    530                 535                 540

Ile Ser Lys Val Asn Ile Asn Leu Leu Phe Leu Asp Glu Val Val Ser
545                 550                 555                 560
```

Tyr Ile Asp Pro Asp Gly Ile Asn Thr Leu Val Glu Leu Leu Gln Glu
565 570 575

Glu Asp Gln Leu Asn Ser Ile Ile Val Ser His Gly His Thr His Pro
580 585 590

Tyr Ala His Lys Ile Glu Val Lys Gln Asp Glu Ala Gly Leu Ser Ile
595 600 605

Leu Glu Ala
610

<210> 40
<211> 330
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 40
Met Lys Ile Leu Phe Ser Ala Asp His His Ile Lys Leu Gly Ala Lys
1 5 10 15

Asn Val Pro Gln Glu Trp Gln Lys Asn Arg Phe Ile Leu Leu Gly Glu
20 25 30

Lys Leu Asp Glu Val Phe Gly Ala Thr Gly Cys Asp Leu His Ile Ile
35 40 45

Gly Gly Asp Ile Met Asp Val Ser Asp Pro Ser Ser Glu Glu Val Glu
50 55 60

Leu Leu Phe Ala Phe Leu Ala Thr Leu Gln His Pro Gly Ile Ile Tyr
65 70 75 80

Thr Gly Asn His Glu Met Lys Ser Lys Thr Ile Ser Cys Leu Asp His
85 90 95

Tyr Ala Ala Ala Ile Ser Asp Ala Thr Asp Gly Leu Trp Lys Val Val
100 105 110

Lys Asp Tyr Arg Ser Pro Glu Phe Asp Ile Ile Pro Tyr Ser Ser Leu
115 120 125

His Lys Ala Ser Trp Lys Pro Arg Val Ser Asp Ile Cys Phe Thr His
130 135 140

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

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

```
Ser Tyr Lys Asn Ser Gln Lys Ile Gly Asp Val Asp Leu Leu Tyr Pro
            180                 185                 190

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

Asn Gly Ala Phe Ile Ile Asp Thr Val Leu Pro Arg Asp His Glu His
    210                 215                 220

Tyr Leu Ser Trp Ile Glu Leu Gly Asp Leu Pro Gln Leu Ile Arg Lys
225                 230                 235                 240

Thr Ile Glu Val Gly Glu Pro Met Glu Ala Asp Ala Tyr Asp Arg Val
                245                 250                 255

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

Ser Glu Leu Leu Asp Lys Lys Ile Asn Asn Arg Val Thr Lys Asp Ala
        275                 280                 285

Lys Leu Asp Leu Asp Asp Met Ser Leu Leu Gln Glu Leu Asp Thr Tyr
    290                 295                 300

Phe Thr Asn Val Gln Lys Leu Asp Glu Ala Ser Arg Thr Arg Ile Leu
305                 310                 315                 320

Lys Arg Ala Ala Glu Tyr Val Asp Ser Asn
                325                 330


<210> 41
<211> 257
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 41
Met Ala Thr Lys Ser Trp Gly Ser Thr Thr Gly Gly Ser Asn Gly Asp
1               5                   10                  15

Lys Leu Asp Tyr Met Lys Phe Asn Asn Gly Lys Asn Val Val Arg Ile
            20                  25                  30

Val Ser Gly Val Leu Pro Arg Tyr Val Tyr Trp Ile Gln Asn Lys Glu
        35                  40                  45

Gly Lys Pro Ala Pro Phe Glu Cys Leu Arg Phe Asp Arg Glu Lys Glu
    50                  55                  60

Arg Phe Ile Arg Gly Ala Ser Asp Pro Val His Asp Met Gly Phe Lys
65                  70                  75                  80
```

```
Asp Pro Glu Lys Lys Asp Gly Lys Ala Gln Pro Leu Arg Pro Lys Lys
                85                  90                  95

Asn Tyr Leu Ala Val Val Ile Asp Arg Thr Asp Asn Lys Leu Lys Leu
            100                 105                 110

Met Glu Val Lys Ala Thr Ile Leu Thr Gly Ile His Ser Ile Met Ala
        115                 120                 125

Gln Leu Asn Leu Glu Asp Pro Gly Glu Ile Asp Ile Thr Ile Ser Lys
    130                 135                 140

Ser Gly Thr Gly Phe Asp Thr Lys Tyr Asp Val Gln Gln Ile Ala Ala
145                 150                 155                 160

Met Gln Phe Gln Met Ala Lys Asn Gln Pro Gly Ser Lys Glu Ala Ala
                165                 170                 175

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

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

Tyr Pro Val Pro Ser Tyr Asp Glu Gln Lys Lys Ala Ile Gln Ala Trp
    210                 215                 220

Leu Glu Gly Lys Lys Asp Glu Glu Gly Asp Glu Ser Lys Gly Asn Glu
225                 230                 235                 240

Gly Ser Ala Asn Ser Gly Asn Ile Asp His Glu Ala Ala Ser Asp Leu
                245                 250                 255

Asp
```

<210> 42
<211> 117
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 42

```
Met Leu Phe Tyr Asp Tyr Glu Lys Ile Tyr Ile Leu Ala Arg Gly Asn
1               5                   10                  15

Ser Ser Leu Ile Val Gln Ile Ile Arg Arg Met Val Glu Asp Pro Glu
            20                  25                  30

Ala His Val Met Leu Thr Gly Arg Ser Phe Ile Leu Asn Glu Asp Thr
```

35 40 45

Ile Val Tyr Asn Lys Arg Lys Leu Ser Asp Arg Gln Leu Ala Glu Tyr
50 55 60

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

Asp Thr Ser Leu Asp Met Gln Tyr Ile Pro Pro Trp Val Pro Arg Ala
85 90 95

Val Ile Glu His His Pro Leu Ile Ala Ile Asn Lys Ser Lys Leu Thr
100 105 110

Phe Ile Glu Glu Asn
115

<210> 43
<211> 452
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 43
Met Lys Ile Val Ile Ser Asn Lys Ile Tyr Cys Lys Pro Ser Asn Glu
1 5 10 15

Leu Trp Glu Tyr Leu Leu Lys His Thr Ser Tyr Gln Ile Phe Lys Pro
20 25 30

Gly Ala Lys Tyr Pro Leu Met Phe Gln Asn Ser Gly Ser Val Gly Lys
35 40 45

Glu Ile Lys Trp Phe Pro Val Thr Arg Leu Asp Leu Leu Glu Ser Phe
50 55 60

Gly Gln Lys Val Thr Glu Ile Val Asp Lys Arg Thr Leu Val Pro Met
65 70 75 80

Asp Ile Pro Lys Pro Ser Phe Thr Leu Arg Pro Gly Asp Gln Leu Pro
85 90 95

Ile Tyr Glu Asp Cys Asn Asp Thr Cys Ile Ile Asn Gly Lys Pro Gly
100 105 110

Phe Gly Lys Thr Ile Leu Ala Leu Ala Ile Ala His Lys Leu Gly Gln
115 120 125

Lys Thr Leu Val Ile Cys Thr Asn Thr Thr Ile Arg Ala Met Trp Glu
130 135 140

```
Lys Glu Val Arg Lys Phe Phe Gly Ile Glu Pro Gly Val Ile Gly Ser
145                 150                 155                 160

Gly Lys Phe Asn Ile Asp Ser Pro Ile Val Ile Ser Asn Ile Gln Thr
                165                 170                 175

Val Asn Lys His Gly Ala Ala Leu Ala Lys Glu Phe Gly Thr Val Ile
            180                 185                 190

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

Glu Gln Ser Ser Ala Arg Tyr Lys Ile Gly Leu Ser Gly Thr Leu Lys
    210                 215                 220

Arg Lys Asp Gly Leu Gln Val Met Phe Lys Asp Tyr Phe Gly Thr Lys
225                 230                 235                 240

Val Tyr Ser Pro Pro Val Asn Asn Thr Met Pro Pro Thr Ile His Arg
                245                 250                 255

Phe Ala Leu Lys Thr Gln Val Ser Gly Asn Met Asn Val Pro Trp Ala
            260                 265                 270

Ile Arg Ala Asn Asp Val Tyr Ser Gln Pro Glu Tyr Phe Gln Gln Val
        275                 280                 285

Val Asp Leu Cys Glu Leu Tyr Ser Met Ala Gly His Lys Val Leu Phe
    290                 295                 300

Val Ser Asp Arg Ile Asp Leu Ile Glu Arg Val Thr Asn Ala Leu Glu
305                 310                 315                 320

Leu Arg Gly Val Lys Thr Tyr Thr Ile Thr Gly Val Thr Ser Leu Asp
                325                 330                 335

Asp Arg Glu Gln Val Gln Ile Asp Val Thr Asn Asp Gly Pro Cys Val
            340                 345                 350

Leu Ala Ala Ser Gln Ser Ile Phe Ser Glu Gly Val Ser Leu Asn Ala
        355                 360                 365

Leu Ser Cys Leu Val Leu Gly Ser Leu Ile Asn Asn Glu Ser Leu Ile
    370                 375                 380

Glu Gln Leu Ala Gly Arg Val Gln Arg Met Ala Asp Asp Lys Leu Asp
385                 390                 395                 400

Pro Ile Leu Val Asp Leu Lys Leu Gly Gly Val Gly Phe Lys Gln Ala
                405                 410                 415
```

Ala Gly Arg Glu Ala Val Tyr Arg Leu Asn Gly Trp Glu Val Leu Asp
420 425 430

Phe Asn Glu Lys Asn Met Ala Asn Leu Asp Lys Ile Leu Phe Ala Lys
435 440 445

Asn Pro Lys Val
450

<210> 44
<211> 165
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 44
Val Leu Asn Phe Ser Leu Pro Val Tyr Ala Leu Arg Ala Tyr Asp Val
1 5 10 15

Leu Phe Gln Glu Gly Glu Tyr Ile Val Ile Gln Thr Arg Phe Thr Arg
20 25 30

Tyr Val Leu Asp Asn Pro Ser Leu Pro Gly Thr Phe Ser Gln Arg Arg
35 40 45

Leu Phe Leu Tyr Gly Glu Arg Glu Asn Leu Pro Tyr Lys Leu Tyr Pro
50 55 60

Leu Lys Lys Gln Phe Lys Tyr Leu Ser Gln Ile Ile Asn Ser Gly Leu
65 70 75 80

Lys His Phe Ile Asp Ser Thr Gly Lys Ile Val Thr Trp Lys Pro Thr
85 90 95

Thr Tyr Tyr Asn Ile Ile Thr Glu Arg Val Arg Gly Ser Thr Arg Ile
100 105 110

Phe Asn Gly Lys Tyr Gln Cys Tyr Val Lys Asn Val Pro Tyr Pro Phe
115 120 125

Leu Leu Ser Glu Pro Ala Asn Tyr Ile Ser Tyr Ala Leu Val Arg Gly
130 135 140

Ser Pro Val Ile Phe Asp Thr His Glu Glu Glu Pro Glu Thr Pro Arg
145 150 155 160

Leu Arg Val Lys Ile
165

<210> 45
<211> 856
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 45
Met Lys Ile Ala Val Val Asp Lys Ser Pro Asn Asn Val Arg Tyr Gln
1 5 10 15

Lys His Phe Glu Leu Phe Asp His Glu Val Glu Thr Phe Phe Met Ala
20 25 30

Ser Glu Lys Val Thr Gly Arg Leu Leu Lys Lys His Ile Thr Ile Gly
35 40 45

Thr Pro Glu Asn Pro Phe Asn Pro Glu Asp Phe Asp Tyr Val Ile Leu
50 55 60

Val Gly Ala Asp Pro Phe Leu Lys Phe Ala Ala Lys Lys Gly Ile Ser
65 70 75 80

Asp Tyr Ser Gly Lys Arg Val Glu His Asp Gly Tyr Ala Asn Trp Ile
85 90 95

Ala Ser Ile Ser Pro Ala Gln Leu His Phe Lys Pro Glu Met Lys Pro
100 105 110

Val Phe Glu Ala Thr Val Glu Ser Ile His Ala Ile Leu Asn Gly Arg
115 120 125

Glu Lys Arg Ser Lys Ala Gly Asp Tyr Arg Pro Ile Gln Cys Pro Asp
130 135 140

Glu Ala Glu Ala Tyr Val Lys Met Val Tyr Thr Met Cys Pro Gly Met
145 150 155 160

Ile Ala Tyr Asp Ser Glu Thr Ser Ala Leu Tyr Cys Arg Asp Gly Tyr
165 170 175

Met Leu Gly Ile Ser Ile Ser His Gln Glu Tyr Gln Gly Val Tyr Ile
180 185 190

Asp Ala Asp Val Ile Thr Glu Asn Thr Val Tyr Tyr Leu Gln Lys Leu
195 200 205

Phe Asp Ser Pro Glu His Gly Val Val Phe His Asn Leu Lys Phe Asp
210 215 220

Met His Phe Tyr Cys Tyr His Leu Gly Leu Ser Phe Asp Lys Ala Ala
225 230 235 240

Glu Glu Lys Arg Leu His Asp Thr Met Leu Met His Tyr Ala Leu Asp
245 250 255

```
Glu Arg Arg Gly Thr His Gly Leu Lys Ser Leu Ala Met Lys Tyr Thr
            260                 265                 270

Asp Met Gly Asp Tyr Asp Phe Glu Leu Asp Gln Phe Lys Glu Thr Tyr
        275                 280                 285

Cys Lys Thr His Lys Ile Lys Lys Glu Asp Phe Ser Tyr Asp Leu Ile
    290                 295                 300

Pro Phe Asp Ile Met Trp Pro Tyr Ala Ala Lys Asp Thr Asp Ala Thr
305                 310                 315                 320

Leu Arg Leu Ser Asn Phe Phe Leu Pro Lys Val Glu Ala Asn Pro Arg
                325                 330                 335

Leu Lys Ser Leu Tyr Tyr Asp Val Leu Met Pro Gly Cys Val Phe Leu
            340                 345                 350

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

Glu Ala Gln Val Gln Leu Met Thr Ala Leu Gln Leu Ala Lys Ala Lys
    370                 375                 380

Leu Tyr Glu Tyr Pro Glu Val Arg Lys Leu Glu Glu Asp Gln Gly Ser
385                 390                 395                 400

Val Phe Asn Ala Ala Ser Val Val Gln Leu Arg Lys Leu Leu Phe Asp
                405                 410                 415

Tyr Val Gly Leu Thr Pro Thr Gly Ile Met Thr Asp Thr Gly Ala Asp
            420                 425                 430

Ser Thr Gly Ala Asp Ala Leu Lys Glu Leu Ser Asp Gln His Pro Ile
        435                 440                 445

Ala Lys Thr Leu Leu Glu Ile Arg Lys Ile Ser Lys Leu Leu Ser Thr
    450                 455                 460

Tyr Ile Glu Lys Met Leu Ile Ser Ile Asp Ala Asp Gly Cys Ile Arg
465                 470                 475                 480

Thr Gly Phe His Ile His Met Thr Thr Ser Gly Arg Leu Ser Ser Ser
                485                 490                 495

Gly Lys Leu Asn Leu Gln Gln Leu Pro Arg Asp Glu Ser Val Ile Lys
            500                 505                 510

Gly Cys Ile Val Ala Pro Val Gly Tyr Arg Ile Ile Ala Trp Asp Leu
        515                 520                 525
```

```
Thr Thr Ala Glu Ile Tyr Tyr Ala Ala Val Leu Ser Gly Asp Ile Asn
    530                 535                 540

Met Gln Gln Val Phe Ile Asn Met Gln Asn Asp Pro Glu Asn Tyr Ser
545                 550                 555                 560

Asp Phe His Gly Ser Ile Ala His Met Val Phe Ala Leu Pro Cys Lys
                565                 570                 575

Pro Thr Glu Val Lys Lys Leu Tyr Pro Ala Leu Arg Gln Ala Ala Lys
            580                 585                 590

Ala Ile Ser Phe Gly Ile Leu Tyr Gly Ser Gly Pro Ala Lys Val Ala
        595                 600                 605

Ala Ser Val Asn Glu Ala Leu Leu Glu Glu His Met Lys Thr Gly Lys
    610                 615                 620

Pro Tyr Thr Glu Cys Thr Thr Gly Asp Ala Lys Glu Tyr Ile Glu Thr
625                 630                 635                 640

Tyr Phe Gly Arg Phe Pro Gln Leu Lys Lys Trp Ile Asp Lys Ser His
                645                 650                 655

Ala Gln Ile Gln Thr Asn Gly Phe Ile Tyr Ser His Phe Gly Arg Lys
            660                 665                 670

Arg Arg Leu His Asn Ile Asn Ser Glu Asp Arg Gly Val Gln Gly Glu
        675                 680                 685

Glu Leu Arg Ser Gly Phe Asn Ala Ile Ile Gln Ser Ala Ser Ser Asp
    690                 695                 700

Ser Leu Leu Leu Gly Ala Ile Asp Thr Asp Asn Glu Ile Arg Ser Leu
705                 710                 715                 720

Gly Leu Gln Asp Glu Met Lys Ile Ile Met Leu Val His Asp Ser Val
                725                 730                 735

Val Ala Ile Val Arg Glu Asp Leu Val Asp Gln Tyr Asn Glu Met Leu
            740                 745                 750

Ile Arg Asn Ile Gln Val Asp Arg Gly Ile Ser Ile Pro Gly Cys Pro
        755                 760                 765

Ile Gly Ile Asp Ser Asp Ser Glu Ala Gly Gly Ser Arg Asp Tyr Ser
    770                 775                 780

Cys Gly Lys Ile Lys Lys Gln Arg Pro Ser Val Ala Cys Ile Glu Asp
785                 790                 795                 800
```

Lys Glu Phe Glu Glu Lys Val Arg Ser Ile Ile Gly Met Glu Asp Phe
805 810 815

Asp Tyr Ala Ala Ile Ala Ala Asn Asp Glu Asn His Pro Asp His Asp
820 825 830

Lys Tyr Ala Asn Ile Lys Phe Leu Pro Glu Ile Ser Lys Asp Ile Val
835 840 845

Asn Val Arg Arg Val Leu Gly Ala
850 855

<210> 46
<211> 294
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 46
Met Ser Arg Ile Thr Glu Leu Leu Asp Leu Lys Gly Ile Glu Tyr Arg
1 5 10 15

Asp Thr Gly Gly Asp Ile Leu Ile Arg Cys Leu Asn Pro Asp His Glu
20 25 30

Asp Ala His Pro Ser Leu Arg Val Asp Pro Asp Ser Gly Val Phe His
35 40 45

Cys Leu Ser Cys Gly Phe Gly Arg Gly Ile Pro Ser Ile Phe His Tyr
50 55 60

Phe Asn Glu Glu Gln Tyr Arg Thr Ser Pro Arg Leu Leu Arg Val Arg
65 70 75 80

Arg Met Ile Ser Asp Leu Arg Thr Glu Gly Arg Ser Leu Glu Ile Pro
85 90 95

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

Thr Phe Lys Lys Tyr Phe Ala Phe Gln Gln Thr Glu Asp Trp Glu Gly
115 120 125

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

Leu Gly Arg Asn Met Asp Ser Ser Ala Pro Pro Lys Tyr Met Ile Arg
145 150 155 160

Pro Lys Lys Val Ser Pro Pro Ile Phe Pro Val Arg Tyr Asn Thr Pro

165 170 175

Ala Leu Ile Leu Val Glu Gly Ile Phe Asp Met Leu Asn Leu Glu Asp
180 185 190

Lys Gly Cys His Asn Val Ser Cys Cys Phe Gly Thr His Gln Phe Ser
195 200 205

Leu Asp Asn Ile Ala Asp Lys Phe Met Pro Phe Gln Ile Ala Gly Thr
210 215 220

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

Ala Lys Lys Leu Ala Lys Leu Ile Arg Asp Lys Thr Arg Ile Ile Pro
245 250 255

Ile Ile Gly Asn Phe Leu Leu Pro Glu Gly Lys Asp Pro Gly Asp Leu
260 265 270

Asp Ala Glu Glu Val Asp Gln Leu Ile Arg Asn Val Glu Ile Leu Ile
275 280 285

Ala Glu His Val Lys Ile
290

<210> 47
<211> 492
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 47
Met Tyr Asn Val Gln Ala Val Val Leu Lys Met Leu Leu Ala Ser Asp
1 5 10 15

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

Phe Asn Asp Ala Phe Thr Ala Ile Tyr Gln Ala Val Gln Asn Tyr Tyr
35 40 45

Lys Lys His Asn Gly Met Pro Ser Leu Asp Ala Leu Met Leu Glu Ser
50 55 60

Asn Arg Asn Ala Arg Leu Ser Gln Ala Leu Thr Val Leu Ala Asn Thr
65 70 75 80

Gln Ile Pro Asp Val Asp Ile Ser His Ala Ile His Val Leu Glu Ser
85 90 95

```
Glu Tyr Thr Gln Asp Leu Phe Leu Asn Leu Leu Glu Thr Asp Val Leu
            100                 105                 110

Gln Asp Ile Thr Ile Leu Asp Gln Gly Glu Leu Leu Asp Arg Val Ala
        115                 120                 125

Ala Leu His Met Lys Leu Glu Glu Arg Val Thr Thr Thr Gly Lys Val
    130                 135                 140

Phe Asn Ala Asp Thr Met Arg Val Phe Lys Arg Lys Glu Asp Ser Met
145                 150                 155                 160

Leu Asn Leu Ile Ser Leu Gly Ile Ser Asn Glu Phe Asp Ala Gln Leu
                165                 170                 175

Gly Gly Ile Ala Arg Lys Glu Thr Leu Leu Leu Gly Gly Trp Arg Gly
            180                 185                 190

Thr Gly Lys Ser Ile Ile Cys Ser Asn Ile Gln Val Ala Gln Tyr Tyr
        195                 200                 205

Asn Gly Asp Ile Ala Pro Tyr Phe Ser Ile Glu Met Pro Glu Asn Glu
    210                 215                 220

Val Phe Arg Arg Asn Leu Ala Ile Met Ala Gly Val Ser Ala Lys Ala
225                 230                 235                 240

Met Arg Asn Asp Ser Leu Gln Gly Ile Glu Leu Asn Lys Leu Ala Lys
                245                 250                 255

Thr Arg Ala Lys Met Phe Glu Gly Gly Leu Glu Val Tyr Asn Asp Phe
            260                 265                 270

Val Ser Arg Tyr Thr Leu Asn Glu Met Ser Asp Phe His Asp Met Glu
        275                 280                 285

Thr Met Leu Met Gln Glu Arg Pro Leu His Thr Pro Met Ile Ile Val
    290                 295                 300

Tyr Asp Pro Glu Leu Ser Thr Ala Thr Ile Asp Val Glu Leu Thr Lys
305                 310                 315                 320

Leu Thr Ser Lys Tyr Gly Asp Lys Val Thr Ile Ala Leu Leu Asp Tyr
                325                 330                 335

Ile Asn Gln Val Arg Leu Pro Asp Thr Lys Thr Leu Asp Met Tyr Asp
            340                 345                 350

Trp Lys Gln Gln Met Val Val Ser Ser Thr Phe Lys Ser Thr Cys Gln
        355                 360                 365
```

```
Lys His Asn Val Ala Gly Val Ala Pro Tyr Gln Ile Asp Gln Gln Gly
    370                 375                 380

Asn Ala Arg Met Ala Arg Gly Ile Leu Asp Ser Cys Asp Met Ala Ala
385                 390                 395                 400

Asn Leu Asn Ala Ala Lys Gln Asn Glu Gly His Asp Gly Ala Ile Lys
                405                 410                 415

Phe Asp Phe Val Lys Thr Arg Asn Ser Glu Gly Met Thr Phe Met Pro
            420                 425                 430

Lys Ile Asn Trp Asn Ser Leu Arg Met Asp Gln Thr Ser Asp Leu Lys
        435                 440                 445

Leu Glu Asp Ile Arg Gln Met Glu Ala Glu Phe Val Ile Pro Leu Glu
    450                 455                 460

Ser Asp Lys Pro Lys Asp Lys Pro Lys Arg Lys Lys Ala Ser Asp Glu
465                 470                 475                 480

Asp Thr Asn Pro Thr Gly Glu Ser Ser Arg Asp Leu
                485                 490


<210> 48
<211> 252
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 48
Met Ala Lys Leu Thr Trp Asn Glu Glu Ile Thr Ala Ser Leu Thr Ala
1               5                   10                  15

Lys Ala Asn Ala Leu Asn Ala Thr Val Ile Ser Gln Glu Ala Val Ala
            20                  25                  30

Asn Ile Ala Ala Glu Leu Ala Ala Glu Thr Gly Lys Glu Val Thr Ala
        35                  40                  45

Arg Ser Val Gly Ser Lys Leu Arg Lys Glu Gly Phe Glu Val Gln Lys
    50                  55                  60

Ala Ser Asp Val Thr Lys Ser Pro Trp Thr Pro Gly Gln Glu Asp Glu
65                  70                  75                  80

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

Ile Ala Ala Ala Val Val Gly Gly Ala Tyr Thr Ala Lys Gln Val Gln
            100                 105                 110
```

```
Gly Lys Ile Leu Ser Leu Glu Leu Thr Ala Ala Val Lys Pro Thr Glu
        115                 120                 125

Lys Ala Ala Ala Val Arg Ser Phe Ser Pro Asp Gln Glu Ala Ala Phe
    130                 135                 140

Ile Asn Ala Val Ala Ser Gly Ala Ser Val Glu Ala Ile Ala Ala Gln
145                 150                 155                 160

Phe Glu Arg Thr Val Lys Gln Ile Arg Gly Lys Ala Leu Ser Leu Leu
                165                 170                 175

Arg Glu Gly Arg Ile Glu Ala Met Pro Val Gln Glu Val Ser Asn Ala
            180                 185                 190

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

Val Ala Glu Ile Ala Glu Ala Thr Gly Lys Ser Glu Arg Gly Val Lys
    210                 215                 220

Ser Met Leu Ser Arg Arg Gly Ile Ser Ala Lys Asp His Asp Gly Val
225                 230                 235                 240

Ala Lys Arg Ala Lys Leu Asp Ala Lys Ser Ala Lys
                245                 250

<210> 49
<211> 249
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 49
Met Lys Ile Glu Ile Pro Leu Asn Cys His Ser Cys Gly Ser Lys Leu
1               5                   10                  15

Asp Leu Val Asn Asp Gln Leu Phe Cys Arg Asn Lys Ser Met Cys Pro
            20                  25                  30

Ala Gln Ser Ser Lys Leu Ile Glu Asn Phe Cys Ser Lys Met Lys Leu
        35                  40                  45

Lys Gly Phe Gly Pro Gln Thr Ile Ala Lys Leu Glu Ile Thr Lys Val
    50                  55                  60

Ser Glu Leu Phe Phe Leu Thr Lys Glu Asp Leu Val Arg Ala Val Gly
65                  70                  75                  80

Asp Lys Val Ala Thr Lys Leu Glu Leu Glu Leu Glu Thr Lys Leu Arg
                85                  90                  95
```

```
Gln Asp Val Asp Phe Gly Ser Val Leu Gly Ser Leu Ser Ile Pro Leu
            100                 105                 110

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

Gln Ser Val Lys Ala Glu Gly Lys Ala Gly Glu Asn Leu Ala Ser Trp
    130                 135                 140

Lys Asn Thr Pro Ala Gly Gln Asn Val Ile Asn Leu Pro Trp Lys Phe
145                 150                 155                 160

Ser Gly Ala Arg Glu Ala Gln Val Thr Pro Ala Thr Glu Ser Asn Gly
                165                 170                 175

Val Val Leu Cys Ile Thr Gly Lys Leu Asn Asp Phe Lys Asn Arg Ala
            180                 185                 190

Asp Ala Thr Lys Tyr Leu Glu Ser Leu Gly Tyr Thr Val Lys Thr Ser
        195                 200                 205

Val Thr Lys Ala Val Asn Tyr Leu Ile Cys Glu Asp Glu Thr Lys Ile
    210                 215                 220

Gly Ser Ser Ser Tyr Lys Lys Ala Gln Ser Leu Gly Ile Glu Val Leu
225                 230                 235                 240

Thr Ile Lys Ile Leu Leu Glu Asn Lys
                245
```

<210> 50
<211> 320
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 50

```
Met Gln His Val Lys Glu Phe Ile Lys Leu Cys Gln Asp Ala Tyr Tyr
1               5                   10                  15

Lys Gly Met Ser Ile Ile Ser Asp Glu Glu Tyr Asp Ala Leu Ile Arg
            20                  25                  30

Arg Phe Pro Leu Glu Glu Glu Ile Gly Pro Lys Gly Asp Val Pro His
        35                  40                  45

Leu Phe Arg Met Phe Ser Leu Gln Lys Val Tyr Pro Gly Arg Gly Glu
    50                  55                  60

Glu Val Pro Phe Gln Gly Ile Glu Thr Pro Lys Leu Asp Gly Cys Ala
```

65 70 75 80

Ile Ser Leu Leu Tyr Ile Asp Gly Lys Phe Val Ser Ala Leu Thr Arg
85 90 95

Gly Asn Gly Val Leu Gly Asn Asp Val Thr His Asn Val Lys Leu Leu
100 105 110

Asn Ile Pro Lys Arg Ile Ser Gln Lys Thr Pro Val Gln Ile Thr Gly
115 120 125

Glu Val His Ile Thr Lys Glu Val Glu Asn Met Arg Asn Phe Ala Ser
130 135 140

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

Glu Gly Gly Leu Met Phe Thr Ala Tyr Ser Ile Gln Cys Glu Thr Gly
165 170 175

Lys Val Gly Leu Thr Ala Thr Phe Cys Gly Asp Met His Ile Leu Gln
180 185 190

Gly Asp Gly Phe Val Thr Cys Leu Asp Ile Ser Ser Arg Val Asp Trp
195 200 205

Phe Pro Thr Asp Gly Val Val Val Arg Met Asp Gly Asn Asn Gln Phe
210 215 220

Asn Ala Ala Gly Trp Thr Asn Lys Phe Pro Arg Gly Ala Tyr Ala Ile
225 230 235 240

Lys Glu Asp Asp Glu Gly Glu Val Thr Thr Leu Glu Arg Val Glu Trp
245 250 255

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

Val Val Ile Asp Asp Ala Val Ile Ser Lys Ala Thr Leu Asn Asn Val
275 280 285

Gly Tyr Ile Thr Ala Leu Asp Leu Glu Ile Gly Cys Gln Ile Arg Val
290 295 300

Ile Arg Ser Gly Gly Val Ile Pro Arg Ile Val Glu Arg Val Tyr Glu
305 310 315 320

<210> 51
<211> 91
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 51
Met Gln Lys Ile Thr Leu Asn Ala Tyr Ser Ser Pro Pro Leu Gln Gly
1   5   10   15

Gln Glu Leu Val Leu Thr Trp Leu Glu Lys Glu Lys Gly Lys Pro Val
            20   25   30

Val Arg Thr Met Ser Gly Phe Gln Met Leu Gly Met Trp Tyr Glu Lys
        35   40   45

Asn Val Leu Val Cys Glu Leu Tyr Ser Pro Lys Ser Lys Arg Arg Val
    50   55   60

Met Ser Thr Phe Gln Ala Val Cys Glu Asn Phe Tyr Trp Glu Gly Lys
65   70   75   80

Thr Gln Met Leu Phe Asp Tyr Tyr Glu Ala Lys
                85   90

<210> 52
<211> 45
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 52
Met Lys Asp His Glu Ile Ala Gln Leu Val Asn Lys Leu Thr Glu Ala
1   5   10   15

Ala Lys Thr Tyr Ala His Thr Gln Gln Leu Arg Ala His Met Ser Arg
            20   25   30

Ile Val Asn Glu Ala Leu Lys Asn Ala Lys Asp Asn Ala
        35   40   45

<210> 53
<211> 102
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 53
Met Asn Gln Asn Ile Cys Gln Asp Tyr Glu Gly His Ile Asp Asp Gln
1   5   10   15

Ser His Val Ile Phe Glu Asp Glu Gly Arg Gln Ile Arg Met Thr Val
            20   25   30

Ser Glu Phe Arg Gly Asn Leu Tyr Phe Gly Phe Arg Leu Trp Leu Leu
        35   40   45

```
Asp Ile Glu Asp Asn Trp Phe Pro Thr Lys Ser Gly Phe Ser Phe Pro
    50                  55                  60

Tyr Thr Leu Glu Met Thr Ser Thr Leu Phe Arg Ala Phe Thr Lys Ile
65                  70                  75                  80

Leu Ser Asn Ser Glu Val Leu His Glu Val Tyr Arg Glu Ser Gln Lys
                85                  90                  95

Thr Gln Ala Ser Asp Asp
            100
```

<210> 54
<211> 98
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 54

```
Met Asn Lys Ala Gln Val Val Ala Ile Cys Glu Lys His Gly Glu Phe
1               5                   10                  15

Cys Met Gln Tyr Thr Lys Leu Arg Thr Lys Gly Val Thr Tyr Leu Tyr
            20                  25                  30

Gly Thr Thr Glu Phe Asp Pro Lys Gln Asp Lys Tyr Leu Ala Glu Arg
        35                  40                  45

Ile Val Arg Glu Gly Leu Glu Pro Ala Asp Lys Asp His Ile Leu Val
    50                  55                  60

Phe Ser Arg Ser Ser Asp Lys Phe Arg Tyr Ile Pro Ile Ala Asn Ile
65                  70                  75                  80

Lys Arg Ile Thr Ser Leu Asn Gln Glu Leu Asp Arg Ala Thr Pro Val
                85                  90                  95

Gly Arg
```

<210> 55
<211> 134
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 55

```
Met Ser Thr Pro Thr Gln Trp Ser Pro Glu Leu Glu Ala Glu Leu Thr
1               5                   10                  15
```

Ser Ala Tyr Val Ala Lys Ile Glu Leu Phe Pro Glu Asp Glu Arg Pro
20 25 30

Gly Val Ser Met Glu Ile Val Ala Glu Ile Ala Lys Glu His Gly Val
35 40 45

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

Lys Lys Glu Ala Gly Lys Ser Thr Ala Lys Thr Gly Gly Asp Ala Pro
65 70 75 80

Lys Ala Gly Gly Arg Thr Ser Lys Ser Asp Ala Gln Ala Glu Leu Arg
85 90 95

Ala Ala Phe Asn Asp Ala Gly Leu Glu Asp Gly Phe Leu Asp Glu Ser
100 105 110

Ile Val Asp Lys Leu Thr Gly Lys Ala Ala Ser His Leu Ala Glu Ala
115 120 125

Ile Arg Lys Ile Thr Lys
130

<210> 56
<211> 72
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 56
Val Ser Lys Tyr Gln Leu Leu Asn Leu Phe Gln Ile Tyr Ser Glu Gly
1 5 10 15

Ala Thr Ala Ile Arg Asp Leu His Tyr Ala Leu Pro Met Asp Glu Ala
20 25 30

Glu Asp Asn Gly Trp Leu Thr Lys Tyr Asp Arg Gly Leu Leu Lys Met
35 40 45

Tyr Arg Leu Ser Pro Asn Gly Leu Val Ala Val Asn Gln Ile Leu Glu
50 55 60

Asn Ser Val Cys Phe Ala Ala Gln
65 70

<210> 57
<211> 231
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 57
Met Ala Ile Arg Lys Lys Leu His Ala Asn Ser Ile Pro Asp Glu Lys
1   5   10   15

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

Ala Cys Glu Ile Leu Gly Val Ala Ser Asn Ser Thr Met Glu Arg Leu
        35   40   45

Ile Glu Glu Trp Lys Asp Asn Gln Arg Val Ser Ala Glu Met Arg Lys
    50   55   60

Lys Lys Arg Gly Thr Lys Ile Glu Gly Ala Glu Leu Ala Asn Val Ile
65   70   75   80

Asp Ser Tyr Leu Ser Gly Asp Ser Phe Glu Ala Ile Ala Glu Arg Phe
                85   90   95

Tyr Arg Ser Ala Asn Met Ile Arg Met Val Leu Ser Ala His Gly Ala
            100   105   110

Leu Leu Arg Val Asn Gly Glu Val Asp Pro Leu Phe Pro Pro Ala Ile
        115   120   125

Pro Glu Glu Ser Met Lys Glu Val Phe Glu Val Gly Glu His Val Trp
    130   135   140

Val Pro Gly Tyr Gln Cys Ile Gly Glu Val Lys Lys Ala Leu Asp Asn
145   150   155   160

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

Tyr Val Asn Tyr Met Tyr Trp Asp Leu Ala Ser Val Glu His Leu Val
            180   185   190

Ala Leu Gly Val Asp Ile Lys Ser Leu Gly Phe Lys Trp Gly Lys Glu
        195   200   205

Asp Val Ala Glu Leu Val Asn Asn Ala Val Lys Ala Ala Leu Lys Leu
    210   215   220

Glu Lys Arg Gly Lys Gly Glu
225   230

<210> 58
<211> 94
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F391/08

<400> 58
Met Ser Lys Arg Asp Ala Arg Trp Glu Thr Arg Lys Phe Pro Lys Arg
1   5   10   15

Asp Thr Lys Ala Arg Lys Ala Lys Glu Ile Glu Leu Cys Arg Val Ile
            20   25   30

Pro Ile Arg Leu Ala Gln Met Pro Asn Ile Tyr Asp Trp Leu Glu Ala
        35   40   45

Gln Arg Lys Thr Arg Leu Ser Ile Arg Ile Asn Met Glu Leu Asn Met
    50   55   60

Gly Tyr Lys Ser Leu Ser Glu Phe Met His Val Thr Phe Asp Pro Thr
65   70   75   80

Phe Tyr Glu Asn Arg Asp Cys Leu Glu Ala Lys Ser Val Leu
                85   90

<210> 59
<211> 929
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 59
Met Phe Ser Ile Leu Glu Gly His Ala Gly Phe Ser Arg Asp Pro Ala
1   5   10   15

Ser Gly Asn Trp Lys Glu Val Lys Thr Thr Asp Tyr Leu Phe Ala Lys
            20   25   30

Glu Phe Ser Asn Glu His Pro Glu Gly Lys Pro Ala Ser Met Pro Tyr
        35   40   45

Lys Phe Asn Val Val Asp Thr Val Asp Pro Lys Asn Leu Asn Glu Ala
    50   55   60

Tyr Glu Leu Met Val Gln Leu Thr Gln Asp Pro His Leu Val Ala Val
65   70   75   80

Arg Gly Thr Cys Leu Val Ala Glu Lys Ala Val Arg Arg Lys Arg Thr
                85   90   95

Asn Phe Lys Ile Asp His Lys Ser Asn Ile Ile Ala Met Asp Val Asp
            100   105   110

Gly Ile Ser Asp Thr Gly Gly Cys Asp Arg Phe Asp Ile Val Gly Met
        115   120   125

```
Gly Arg His Val Ile Lys Leu Leu Asn Ser Ile Ser Glu Asp Met Phe
    130                 135                 140

Pro Leu Asn Ala Gly Phe Ile Ala His Ala Ser Ser Ser Ala Gly Ile
145                 150                 155                 160

Lys Pro Gly Ile Arg Met His Met Leu Leu Glu Ser Asn Ile Pro Val
                165                 170                 175

Thr Gln Gly Gln Leu Lys Phe Leu Phe Thr Ser Leu Asn Asp Ser Ser
            180                 185                 190

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

Val Gln Leu His Tyr Phe Ala Asp Pro Ile Phe Arg Asp Gln Phe Thr
    210                 215                 220

Asp Pro Phe Lys Ala Glu Gly Lys Pro Arg Leu Val Lys Val Asn Gly
225                 230                 235                 240

Ala Arg Ile Glu Leu Pro Asn Thr Met Pro Asp Tyr Glu Ala Thr Arg
                245                 250                 255

Gly Glu Phe Lys Glu Glu Phe Leu Ser Leu Leu Asn Gln Ile Lys Gly
            260                 265                 270

Lys Arg Val Ala Ser Glu Lys Val Glu Gln Thr Ile Ala Glu Leu Glu
        275                 280                 285

Glu Ala Glu Asp Gly Val Tyr Leu Arg Ile Ile Pro Lys Leu Tyr His
    290                 295                 300

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

Thr Ser Ala Leu Ser Asp Tyr Ile Asn Thr Lys Asp Asn Ser Arg Ser
                325                 330                 335

Leu Gln Asp Tyr Phe Asn Asn Gly Arg Lys Gln Ala Leu Lys Ala Phe
            340                 345                 350

Val Asn Asn Ser Met Arg Asp Ile Pro Glu Ser Asn Val Lys Gly Val
        355                 360                 365

Pro Val His Lys Leu Thr Ser Asp Ser Pro Asp Gly Met Asn Tyr Leu
    370                 375                 380

Lys Ile Asn Arg Pro Pro Pro Glu Gly His Leu Thr Phe Ile Lys Ala
385                 390                 395                 400
```

```
Ser Leu Gly Thr Gly Lys Thr Thr Ala Val Thr Lys Trp Leu Glu Arg
                405                 410                 415

Asp Gln Leu Lys Gly Asn Phe Leu Ala Val Thr Asn Thr Arg Ala Leu
            420                 425                 430

Val Ser Ser Asn Ala Lys Lys Phe Glu Ala Gly Gln Tyr Asp Lys Ser
        435                 440                 445

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

Thr Ile His Ser Ile His Lys Phe Lys Asn Phe Val Gly Gln Ile Asp
465                 470                 475                 480

Val Ile Phe Ile Asp Glu Cys Asp Ala Val Met Asn Asp Leu Leu Phe
                485                 490                 495

Ala Pro Val Val Lys Gln Arg Arg Glu Cys Ile Ser Val Leu Arg Glu
            500                 505                 510

Ile Leu Leu Ser Ala Lys Val Val Ile Leu Ser Asp Gly Asp Ile Ser
        515                 520                 525

Ala Glu Thr Ile Glu Ala Tyr Gly Ser Leu Ile Asp Phe Asp Lys Pro
    530                 535                 540

Val Ser Tyr Tyr Lys His His Arg Lys Met Leu Ser Asp Ala Gln Ala
545                 550                 555                 560

Tyr Glu Phe Pro Asp Glu Ser Ser Ile Trp Val Ala Leu Gln Thr Ser
                565                 570                 575

Leu Glu Met Gly Glu Lys Ser Ile Leu Val Ser Asp Cys Gly Pro Asp
            580                 585                 590

Glu Leu Asn Glu Lys Gly Leu Thr Leu Arg Asn Asn Thr Gly Ala Ile
        595                 600                 605

Val Lys Glu Ile His Ser Asn Ser Thr Ser Asp Ile Asp Ile Arg Arg
    610                 615                 620

Ile Leu Asp Tyr Thr Thr Asn Glu Leu Ile Glu Gln Gln Ile Asp Cys
625                 630                 635                 640

Leu Leu Cys Ser Pro Ser Val Thr Ser Gly Val Asp Phe Asn Tyr Phe
                645                 650                 655

Asp Asn Val Phe Val Ile Thr Arg Thr Ala Asn Gln Ala Pro Asn Met
            660                 665                 670
```

```
Arg Phe Gln Ala Ile Arg Arg Asp Arg Gly Ala Lys Asn Ile Phe Tyr
        675                 680                 685

Phe Ile Asp Lys Ser Thr Ser Gly Phe Ser Ala Gly Ser Glu Gln Tyr
    690                 695                 700

Asn Ile Asp Glu Gly Trp Leu Glu Leu Ala Gln Gln Leu Tyr Val Lys
705                 710                 715                 720

Arg Arg Glu Leu Glu Ser Arg Asn Phe Ile Ser Thr Leu Arg Tyr Tyr
                725                 730                 735

Leu Leu Asp Gln Gly Ala Thr Ile Asp Ile Phe Ser Glu Ser Trp Gly
            740                 745                 750

Lys Ile Asp Ser Ser Ala Ala Glu Tyr Thr Ala Glu Arg Val Ser Ala
        755                 760                 765

Ile Leu Ser Ser Thr Pro Asp Trp Cys Ala Pro Arg His Ala Asp Ala
    770                 775                 780

Tyr Glu Ala Lys Leu Met Leu Val Lys Tyr Phe His Leu Asp Ser Ile
785                 790                 795                 800

Lys Ser Ile Thr Gln Glu His Ala Glu Met Trp Ile Ser Lys Lys Pro
                805                 810                 815

His Lys Arg Ala Glu Phe Phe His Lys Leu Gln Asp Ile Phe Trp Lys
            820                 825                 830

Asp Ile Lys Lys Cys Ser Asn Val Thr Ile Ser Pro Phe Ile Glu Ala
        835                 840                 845

Leu Lys Lys His Lys Lys Asp Phe Phe Ile Arg Thr Gly Gln Ser Ala
    850                 855                 860

Asn Pro Lys Tyr Ala Arg Met Tyr Leu Thr Gln Met Gly Ile Asn Lys
865                 870                 875                 880

Glu Met Glu Thr Glu Gln Ile Val Asp Trp Tyr Arg Thr Tyr Cys Ser
                885                 890                 895

Ile Glu Gly Ile Ser Val Pro Tyr Glu Phe Met Thr Asp Glu Glu Lys
            900                 905                 910

Ala Leu Ala Asp Glu Ala Gln Asn Glu Leu Gly Val Arg Asn Glu Gln
        915                 920                 925

Ala
```

<210> 60
<211> 131
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 60
Met Ser Ile Pro Lys Met Glu Arg Ile Ser Trp Ala Asp Ile Pro Lys
1   5   10   15

Glu Leu Ile Asp Val Ala Glu Asn Leu Leu Arg Ala Ala Leu Arg Asp
            20   25   30

Glu Glu Leu Cys Phe Ile Ile Gln His Asp Val Cys Val Gly Leu Ser
        35   40   45

Lys Gly Ser Leu Ala Gln Asp Tyr Glu Ile Leu Phe Asp Trp Asp Asp
    50   55   60

Leu Ser Asp Leu Gly Leu Met Val Leu Val Asn Asn Val Val Phe His
65   70   75   80

Pro Ser Asn Phe Ala Ala Phe Arg Glu Pro Gly Ala Gly Ile Ser Pro
                85   90   95

Gly Phe Leu Val Ala Asp Glu Pro Trp Thr Tyr Ala Pro Glu Val Leu
            100   105   110

Arg Glu Gly Lys Gln Asn Ala Ser Ser Asn Ser Ile Asn Ile Met Gly
        115   120   125

Trp Asn Ala
    130

<210> 61
<211> 133
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 61
Met Leu Val Asn Glu Lys Val Val Asn Gln Gly Val Gly Leu Val Pro
1   5   10   15

Trp Ala Glu Ile Pro Leu Asp Val Lys Glu Ser Leu Leu Asp His Leu
            20   25   30

Arg Val Trp Cys Asp Asn Met Glu Val Tyr Phe Asp Tyr Asp Asn Met
        35   40   45

His Leu Gly Leu Trp Val Pro Met Asp Glu Asp Gln Asp Glu Val Leu
    50   55   60

Asp Trp Gly Asp Leu Thr Glu Met Gly Leu Val Phe Ala Leu Gly Tyr
65 70 75 80

Val Cys Leu Leu Arg Glu Ser Tyr Ile Pro Val Gly Val Thr Gly Val
85 90 95

Ser Ala Gly Ile Trp Val Gly Arg Asn Glu Asp Tyr Tyr Ala Pro Glu
100 105 110

Asn Ile Asn Gly Trp Ile Gln Val Leu Arg Arg Phe Gly Phe Gln Val
115 120 125

Glu Gly Leu Thr Lys
130

<210> 62
<211> 54
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 62
Met Tyr His Pro Asp Asp Ile Leu Leu Trp Pro Asn Gly Ser Trp Cys
1 5 10 15

Tyr Arg Ser Asp Val Gln Asp Met Ser His Leu Ser Asp Asp Tyr Gln
20 25 30

Val Leu Arg Ala Asp Ser Glu Gln Trp His Glu Phe Ile Gln Met Gly
35 40 45

Glu Glu Tyr Ala Gly Gln
50

<210> 63
<211> 260
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 63
Val Pro Thr Phe Arg Lys Gly Ala Ile Thr Pro Leu Trp Asp Lys Tyr
1 5 10 15

Lys Leu Thr Glu Val Cys Asn Ile Gln Ala Phe Asp Lys Gly Phe His
20 25 30

Tyr Leu Asn Asp Pro Met Pro Pro Leu Glu Ala Leu Ser Glu Gly Ser
35 40 45

```
Asp Asp Glu Pro Ser Arg Asn Leu Tyr Glu Leu Thr His Glu Phe Tyr
    50                  55                  60

Asn Met Arg Arg Gln Glu Leu Gly Thr Val Glu Pro Asn Ile Ala His
65                  70                  75                  80

Leu Arg Ile Ala Glu Trp Tyr Glu Arg Phe Pro Gly Gln Val Val Asn
                85                  90                  95

Phe Thr Thr Asn Val Asp Asp Leu Leu Glu Arg Ala Gly Ile Pro His
            100                 105                 110

Asp Asp Val Ile His Ala His Gly Tyr Leu Thr Glu Ile Met Tyr Arg
        115                 120                 125

Arg Gly Lys Asp Val Ile Val Glu Asp Ile Gly Tyr Thr Ala Val Asp
    130                 135                 140

Tyr Arg Lys Tyr Glu Trp Val Lys Pro Ala Ile Thr Phe Phe Gly Glu
145                 150                 155                 160

Thr Ala Pro Trp Tyr Met Gly Gln Ile Asn Leu Phe Asp Thr Leu Thr
                165                 170                 175

Thr Gln Asp Leu Val Ile Val Val Gly Ala Ser Asn Gln Val Ile Asp
            180                 185                 190

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

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

Arg Gly Ile Pro Val Trp Tyr Asp Thr Ala Ala Asn Val Phe Ser Asn
225                 230                 235                 240

Lys His Phe Ile Gly Gln Val Glu Ala Trp Leu Glu Glu Lys Ile Tyr
                245                 250                 255

Val Pro Ser Arg
            260


<210> 64
<211> 70
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 64
Met Lys Ile His Lys Thr Asp Glu Lys Arg Ile Tyr Phe Met Met Asp
1               5                   10                  15
```

Ser Gly Ala Tyr Gly Ser Ile Ser Arg Glu Asp Val Val Lys Leu Leu
20 25 30

Arg Cys Arg Asn His Leu Trp Lys Asp Lys Val Asp Pro Arg Thr Ser
35 40 45

Glu Cys Leu Ser Glu Lys Ala Glu Gln Leu Arg Lys Glu Glu Met Arg
50 55 60

Asn Tyr Met Glu Phe Leu
65 70

<210> 65
<211> 609
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 65
Met Asn Glu Leu Asp Leu Ile Asp Asn Ile Tyr Ser Ile Leu Asp Asn
1 5 10 15

Glu Gly Glu Glu Asp Leu Met Phe Asn Asn Ala Asn Lys Ala Ser Glu
20 25 30

Gln Phe Pro Thr Gln Arg Asp Met Ile Ala Gly Glu Val Ser Lys Tyr
35 40 45

Val Val Ala Gln Glu Leu Pro Ala Tyr Leu Leu Ala Ala His Asn Arg
50 55 60

Gly Glu Ile His Ile His Asp Met Asp Tyr Arg Ala Gln Gly Tyr Thr
65 70 75 80

Asn Cys Cys Leu Val Asp Leu Ala Gly Met Phe Lys Asn Gly Thr Lys
85 90 95

Ile Gly Gly Ala Glu Ile Glu Thr Pro Lys Ser Ile Ser Thr Ala Ala
100 105 110

Ala Val Thr Ala Gln Val Ile Ala Gln Val Ser Ser Cys Gln Tyr Gly
115 120 125

Gly Thr Ser Ile Asp Arg Ile Asp Glu Val Phe Ala Pro Tyr Val Arg
130 135 140

Lys Ser Tyr Asp Lys His Leu Ala Ile Gly Gln Arg Trp Leu His Asp
145 150 155 160

Ser Lys Lys Ala Ala Val Tyr Ala Thr Glu Met Thr Glu Lys Glu Val
165 170 175

```
Tyr Asp Ala Cys Gln Gly Leu Glu Tyr Glu Val Asn Thr Leu Phe Asn
            180                 185                 190

Ser Asn Gly Gln Gln Pro Phe Val Thr Phe Gly Phe Gly Leu Gly Glu
        195                 200                 205

Ser Trp Glu Ala Arg Met Leu Gln Lys Ala Met Leu Glu Val Arg Ile
    210                 215                 220

Arg Gly Leu Gly Ala Ser Gly His Thr Ala Val Phe Pro Lys Leu Ile
225                 230                 235                 240

Phe Ala Val Lys Glu Gly Leu Asn Lys Ser Pro Ser Asp Pro Asn Tyr
                245                 250                 255

Asp Ile Lys Gln Leu Ala Leu Thr Cys Thr Ser Lys Arg Met Tyr Pro
            260                 265                 270

Asp Tyr Val Ser Tyr Glu Arg Val Thr Ala Val Thr Gly Asp Phe Lys
        275                 280                 285

Phe Pro Met Gly Cys Arg Ser Phe Leu Ser Ala Ile Glu Ser Gly Glu
    290                 295                 300

Thr Ala Gly Arg Asn Asn Leu Gly Val Val Ser Ile Asn Leu Pro Leu
305                 310                 315                 320

Val Ala Val Glu Ser Glu Gly Tyr Phe Asp Arg Phe Trp Lys Leu Leu
                325                 330                 335

Asp Glu Tyr Ile Asp Lys Ala Met Ala Ala His Asp Trp Ala Ile Glu
            340                 345                 350

Arg Leu Lys Arg Val Arg Ala Lys Gln Ala Pro Ile Leu Tyr Met His
        355                 360                 365

Gly Ala Phe Gly Val Arg Leu Lys Ala Asn Asp Leu Val Trp Pro Ile
    370                 375                 380

Phe Glu Gly Arg Ala Ser Val Ser Leu Gly Tyr Ile Gly Ile Asn Glu
385                 390                 395                 400

Leu Val Glu Val Met Phe Glu Asp Thr Asp Pro Met Ser Pro Pro Ala
                405                 410                 415

Ile Glu Phe Ala Val Gln Val Leu Asn His Met Lys Asp Arg Cys Asn
            420                 425                 430

Lys Lys Ala Glu Glu Thr Asn Leu Gly Phe Ser Leu Tyr Ala Thr Pro
        435                 440                 445
```

```
Ser Glu Ser Leu Cys Asn Arg Phe Asn Thr Lys Ile Ala Glu Gln Tyr
    450                 455                 460

Pro Glu Tyr Asp Trp Leu Thr Asp Lys Gly Tyr Leu Thr Asn Ser His
465                 470                 475                 480

His Leu Asp Val Arg Thr Lys Val Ala Pro Asn Val Lys Phe Asp Tyr
                485                 490                 495

Glu Ala Asn Phe Thr Thr Ile Ala Asn Gly Gly Asn Ile Ser Phe Val
            500                 505                 510

Glu Leu Pro Glu Met Arg Lys Phe Ile Pro Ala Leu Glu Trp Val Val
        515                 520                 525

Asp Tyr Gly Leu Ser Lys Ser His Tyr Ile Gly Val Asn Ile Pro Val
    530                 535                 540

Asp Glu Cys Glu Glu Cys Gly Tyr Leu Gly Glu Ser Val Ser Gly Glu
545                 550                 555                 560

His Gly Phe Val Cys Pro Gln Cys Gly Ser Gly Asn Ile Ser Val Thr
                565                 570                 575

Arg Arg Val Cys Gly Tyr Leu Gly Ser Pro Gly Ser Arg Pro Phe Asn
            580                 585                 590

Pro Gly Lys Gln Gln Glu Val Met Gln Arg Val Lys His Met Asn Leu
        595                 600                 605

Lys
```

<210> 66
<211> 249
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 66

```
Met Arg Lys Ala Ala Arg Arg Lys Glu Ser Arg Arg Asn Gly Ser Ala
1               5                   10                  15

Lys Arg Glu Arg His Glu Asn Val Ile Pro Val Asp Phe Glu Ala Arg
            20                  25                  30

Glu Arg Phe Gln Pro Thr Ala Lys Glu Leu Lys Pro Lys Asn Ala Glu
        35                  40                  45

Gln Lys His Tyr Ile Ser Thr Ile Arg Asn Phe Thr Val Thr Val Gly
```

50 55 60

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

Ala Gln Glu Leu Ala Thr Pro Gly Ser Val Tyr Glu Lys Phe Ile Leu
85 90 95

Val Arg Pro Asn Glu Pro Leu Gly Lys Ser Leu Gly Met Leu Pro Gly
100 105 110

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

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

Lys Ala Ile Gln Tyr Leu Ala Ile Glu His Ala Arg Gly Arg Thr Phe
145 150 155 160

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

Ala Met Lys Cys Ile Leu Thr Arg Val Gly Gln Asp Cys Lys Leu Val
180 185 190

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

Gln Leu Ile Met Asp Ile Tyr Asp Gln Tyr Glu His Val Pro Phe Ser
210 215 220

Leu Val Glu Leu His Asp Asn Val Arg Ser Ala Glu Ser Lys Ala Phe
225 230 235 240

Gln Ala Ile Phe Asn Asp Met Gly Ile
245

<210> 67
<211> 59
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 67
Met Ile Thr Cys Val Pro Leu Asn Pro Lys His Ser Arg Gln Ser Leu
1 5 10 15

Thr Ile Trp Glu Ser Asn Met Val Thr Glu Leu Ile Ile Gly Tyr Gly
20 25 30

Glu Gly Ile Thr Ser Glu Glu Asn Trp Gly Phe Val Gly Phe Gly Glu
        35   40   45

Gly Ile Thr Ser His Asp Glu Arg Pro Asp Leu
    50   55

<210> 68
<211> 69
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 68
Met Asn Asn Val Phe Thr Leu Asn Asn Phe Arg Thr Arg Lys Thr Lys
1   5   10   15

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

Pro Glu Asp Glu Arg Arg His His Ala Ala Phe Lys Ile Ala Asn Glu
        35   40   45

Phe Pro Asn Gln Pro Leu Gly Thr Lys Glu Leu Val Ser Arg Met Lys
    50   55   60

Lys Leu His Phe Tyr
65

<210> 69
<211> 774
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 69
Met Thr Gln Arg Ile Glu Tyr Val Ile Lys Arg Asp Gly Thr Lys Glu
1   5   10   15

Pro Phe Met Ala Gln Lys Leu Asn Asp Trp Ala Lys Tyr Ile Gly Ile
            20   25   30

Arg Ser Asp Val Pro Trp Ser Pro Val Ala Val Ala Ala Val Lys Asn
        35   40   45

Leu Pro Lys Gly Asp Val His Ser Asp Asp Leu Gln Thr Met Leu Ile
    50   55   60

Lys Ser Ala Glu Ser Met Ile Glu Arg Asp His Arg Tyr Asp Arg Phe
65   70   75   80

Ala Leu Glu Leu Arg Leu Ala Gln Leu Arg Lys Asn Leu Phe Asp Ser
                85   90   95

```
Tyr Thr Pro Pro Ser Leu Arg Phe Phe His Asp His Met Val Glu Leu
            100                 105                 110

Gly Ala Trp Glu Asp Met Ser Gly Trp Ile Ser Asp Asp Gln Phe Glu
        115                 120                 125

Ala Leu Asn Glu Val Ile Asp His Ser Arg Asp Glu Leu Phe Thr Asn
    130                 135                 140

Ala Gly Leu Lys Gln Phe Met Asp Lys Tyr Ser Arg Arg Asn Ile Tyr
145                 150                 155                 160

Thr Glu Glu Ile Tyr Glu Thr Pro Gln Phe Ala Tyr Met Gly Met Ala
                165                 170                 175

Met Ala Met Leu Ser Gln Pro His Trp Ser Met Leu Asp Ala Ile Asp
            180                 185                 190

Leu Tyr Asn Ala Leu Ser Leu Gln Lys Ile Asn Val Pro Thr Pro Pro
        195                 200                 205

Leu Val Gly Leu Arg Ser Ala Asp Arg Gly Phe Ala Ser Cys Cys Leu
    210                 215                 220

Val Asp Gly Thr Asp Thr Leu Asp Ser Ile Asp Ala Ala Glu His Val
225                 230                 235                 240

Val Phe Lys Met Val Ala Ala Arg Ala Gly Ile Gly Tyr His Leu Glu
                245                 250                 255

Ser Arg Ser Ile Ala Asp Pro Val Arg Lys Gly Ala Phe Pro His Ser
            260                 265                 270

Gly Lys Leu Pro Tyr Tyr Arg His Ile Asp Arg Ser Val Lys Ala Asn
        275                 280                 285

Thr Gln Gln Ser Arg Gly Gly Ser Ala Thr Val Tyr Thr Ala Phe Phe
    290                 295                 300

Asp Pro Glu Ile Ile Gln Val Met Glu Ala Lys Ser Asn Arg Ser Pro
305                 310                 315                 320

Asp Glu Lys Lys Ile Asp Lys Met Asp Tyr Asn Leu Lys Phe Asn Ser
                325                 330                 335

Ile Leu Leu Lys Arg Phe Leu Arg Lys Glu Asn Ile Thr Leu Met Ser
            340                 345                 350

Phe Leu Tyr Ala Pro Glu Val Tyr Ala Ala Phe Asp Ser Gly Asp Val
        355                 360                 365
```

```
Ala Glu Phe Glu Arg Leu Tyr Ile Ala Ala Glu Lys Arg Leu Ala Gly
    370                 375                 380

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

Ile Pro Ala Ala Glu Leu Ile Glu Phe Trp Lys Thr Val Arg Met Glu
                405                 410                 415

Thr Gly Arg Leu Tyr Thr Met Asp Ala Gly Glu Val Asn Arg Asn Ser
            420                 425                 430

Arg Tyr Lys Asp Pro Val Arg Met Ser Asn Leu Cys Val Glu Ile Val
        435                 440                 445

Gln Pro Thr Phe Pro Ile Pro His Val Val Asp Leu Tyr Arg Thr Asp
    450                 455                 460

Glu Glu Leu Asp Lys Met Asp Val Ser Glu Tyr Gly Glu Val Ser Leu
465                 470                 475                 480

Cys Asn Leu Gly Gly Phe Ala Leu Gly Arg Ile Lys Thr Leu Glu Glu
                485                 490                 495

Trp Glu Lys Ile Ser Tyr Ile Leu Leu Lys Phe Val Asp Thr Ile Ile
            500                 505                 510

Glu Ile Gln His Tyr Pro Phe Pro Ala Met Lys Tyr Thr Ala Leu Arg
        515                 520                 525

Arg Arg Asn Val Gly Ile Gly Leu Met Asn Ala Ala Gly Ala Met Ala
    530                 535                 540

Ala Glu Gly Leu Ala Phe Glu Gly Glu Glu Ala Arg Asn Trp Ile His
545                 550                 555                 560

Arg Glu Ala Glu Lys Ala Ser Phe Phe Leu His Lys Ala Ser Val Arg
                565                 570                 575

Leu Ala Lys Glu Ile Gly Pro Cys Glu Trp Phe His Arg Thr His Thr
            580                 585                 590

Ser Asp Gly Thr Leu Leu Ile Asp Thr Tyr Lys Lys Thr Val Asp Asp
        595                 600                 605

Leu Val Ser Val Gly Leu Glu Met Asp Trp Glu Ser Leu Arg Glu Glu
    610                 615                 620

Ile Lys Thr His Gly Met Arg Asn Ser Val Leu Thr Ala Ser Met Pro
625                 630                 635                 640
```

Gly Glu Ser Ser Ser Val Leu Ile Gly Val Thr Asn Ala Val Glu Pro
645 650 655

Pro Arg Ser Ala Val Thr Ile Lys Thr Ser Gly Val Asn Lys Val Ile
660 665 670

Thr Val Ala Pro Gly Leu Asp Asp Trp Asp Thr Met Gln Ser Tyr Lys
675 680 685

Tyr Ala Phe Asp Ile Asp Arg Thr Glu His Ile Lys Trp Leu Ala Val
690 695 700

Leu Gln Lys Phe Thr Asp Gln Ala Ile Ser Ala Asn Leu Tyr Tyr Asp
705 710 715 720

Phe Asn Lys Tyr Pro Gly Gly Ile Ile Pro Gly Thr Glu Ile Ile Lys
725 730 735

Asp Leu Leu Asn Ser Thr Lys Tyr Gly Ile Lys Asn Leu Tyr Tyr Ala
740 745 750

Asn Phe Asp Val Asp Thr Gly Gly Ser Ala Ala Glu Gln Gly Cys Ser
755 760 765

Ser Gly Gly Cys Thr Leu
770

<210> 70
<211> 386
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 70
Met Ala Thr Val Phe Asn Arg Glu Trp Asp His Thr Glu Ser Lys Leu
1 5 10 15

Phe Leu Gly Gln Asp Leu Gly Ile Ala Asp Tyr Val Asn Val Arg Tyr
20 25 30

Pro Arg Leu Glu Glu Leu Ala Leu Leu Gln Arg Ser Gln Phe Trp Val
35 40 45

Glu Thr Glu Ile Ser Leu Glu Ala Asp Lys Lys Gln Trp Pro Asn Leu
50 55 60

Pro Gln His Ile Lys Asn Lys Thr Leu Leu Asn Leu Ala Trp Gln Thr
65 70 75 80

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

85 90 95

Leu Val Ser Arg Pro Glu Leu Glu Gly Met Leu Ile Gln Trp Ser Tyr
100 105 110

Phe Glu Asn Ile His Ser Arg Ala Tyr Ser Asn Ile Ile Arg Asn Val
115 120 125

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

Ala Phe Ala Arg Leu Ala Leu Pro Val Ser Val Ile Asp Glu Leu Ala
145 150 155 160

Glu Ile Ala Asp Ile Trp Leu Asp Ala Arg Ala Asn Leu Glu Ile Ala
165 170 175

Glu Lys Glu Gly Thr Leu Glu Tyr Thr Glu Glu Ala Asp Phe Leu Ala
180 185 190

Leu Thr Glu Gln Val Gln Gln Lys Ile Leu Glu Phe Tyr Tyr Ala Val
195 200 205

Tyr Ala Leu Glu Ala Ile Met Phe Tyr Ala Ser Phe Ala Cys Thr Phe
210 215 220

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

Leu Ile Ala Lys Asp Glu Ala Leu His Thr Val Met Ala Met Glu Val
245 250 255

Leu Arg Ile Leu Gln Asn Gly Glu Ile Pro Pro His Val Val Ala Ala
260 265 270

Ala Gln Ala Asn Ala Pro Lys Ile Leu Arg Ser Ile Leu Glu Thr Glu
275 280 285

Ile Asn Trp Ala His Tyr Ile Phe Pro Glu Gly Glu Asp Ile Pro Gly
290 295 300

Leu Asn Ala Asp Leu Leu Val Glu Tyr Leu Tyr Tyr Asn Ala Arg Leu
305 310 315 320

Ala Phe Met Ala Ile Asn Ile Pro Trp Pro Glu Asp Leu Pro Val Ile
325 330 335

Met Glu Asp Pro Ile Gly Trp Met Lys Gly Trp Leu Asn Thr Lys Asn
340 345 350

Gln Gln Val Ala Pro Gln Glu Ala Gln Ile Thr Asn Tyr Arg Val Gly

355 360 365

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

Phe Leu
385

<210> 71
<211> 187
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 71
Met Ile Thr Ala Leu Tyr Ala Met Arg Val Asp Ala Ala Phe Gly Ile
1 5 10 15

Phe Asn Pro Ala Thr Met Asp Ala Tyr Gly Glu Leu Pro Trp Gly Ser
20 25 30

Ile Pro Glu Glu Leu Glu Gln Phe Tyr Arg Ile Leu Asp Thr Tyr Gln
35 40 45

Val Val Ile Val Gly His Asn Thr Tyr Glu Thr Ala Pro Pro Arg Leu
50 55 60

Lys Lys Ala Leu Glu Lys Lys Ser Met Val Tyr Val Val Gly Ser Lys
65 70 75 80

Ala Pro Val Leu Ile Lys Asn Pro Pro Arg Asn Val Arg Phe Ile Thr
85 90 95

His Leu Gly Ser Lys Ile Arg Asp Phe Cys Asn Glu Val Glu Val Val
100 105 110

Cys Ile Gly Gly Lys Ala Leu Leu Glu Thr Leu Ala Thr Met Gly Cys
115 120 125

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

Pro Ser Leu Asp His Ile Met Tyr Leu Glu His Pro Ile Leu Thr Ser
145 150 155 160

Thr Pro Pro Asp Ala Val Val Thr His Ile Ala Ser Gly Glu Asn Glu
165 170 175

Arg Tyr Arg Phe Val Met Glu Gly Val Tyr Leu
180 185

<210> 72
<211> 284
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 72
Val Ile His Tyr Ile Asn Glu Gly Lys Arg Ile Leu Glu Glu Gly Val
1   5   10   15

Trp Leu Glu Asn Pro Arg Thr Gly Val Arg Cys Leu Thr Val Ile Gly
            20   25   30

Ser Asn Phe Glu Tyr Asp Val Leu Gly Lys Lys Phe Pro Leu Ile Thr
        35   40   45

Thr Arg Lys Ala Tyr Ala Leu Gln Ala Ile Met Glu Leu Ile Gly Tyr
    50   55   60

Leu Arg Gly Tyr Asp Ser Ala Glu Gln Phe Arg Ala Ile Gly Cys Asn
65   70   75   80

Thr Trp Asn Ala Asn Ala Asn Glu Asn Glu Ala Trp Leu Val Asn Pro
                85   90   95

Asn Arg Lys Gly Thr Asp Asp Met Gly Arg Val Tyr Gly Val Gln Gly
            100   105   110

Arg Thr Trp Leu Arg Pro Asp Gly Ser His Phe Asp Gln Leu Tyr Lys
        115   120   125

Ile Tyr Glu Asn Leu Arg Arg Gly Ile Asp Asp Arg Gly Glu Ile Leu
    130   135   140

Thr Phe Trp Asn Pro Gly Glu Phe Asp Gln Gly Cys Leu Arg Pro Cys
145   150   155   160

Met His Thr His Gln Phe Ser Leu Leu Asn Gly Asn Leu Tyr Leu Asp
                165   170   175

Ser Phe Gln Arg Ser Asn Asp Phe Leu Leu Gly Gln Ala Phe Asn Met
            180   185   190

Val Gln Cys Tyr Thr Phe Leu Ala Leu Met Ala Gln Ile Thr Gly Asn
        195   200   205

Arg Ala Ile Arg Ala Asn Gln Arg Ile Val Asn Met His Ile Tyr Glu
    210   215   220

Asn Gln Tyr Lys Val Leu Met Glu His Gly Gln Phe Asp Arg Lys Pro
225   230   235   240

Phe Pro Ala Pro Arg Leu Glu Ile Asn Pro Glu Ile Lys Thr Leu Glu
245 250 255

Asp Val Leu Thr Trp Val Ser Lys Asp Asp Phe Lys Ile Val Gly Tyr
260 265 270

Lys Ser His Asp Pro Ile Ala Tyr Pro Phe Thr Ala
275 280

<210> 73
<211> 77
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 73
Met Gly Leu Phe Asn Arg Arg Pro Lys Ile Thr Phe Ser Glu Arg Glu
1 5 10 15

Glu Ser Gln Leu Lys Phe Leu Val Gln Ser Ser Gly Leu His Ile Asp
20 25 30

Val Ile Leu Gly Met Val Lys Tyr Lys Gly Met Asp Ala Leu Met Arg
35 40 45

Gln Phe Ala Pro Lys Pro Pro Lys Glu Asn Pro Pro Ala Lys Arg Asp
50 55 60

Tyr Asn Ser Asn Leu Leu Val Pro Pro Ala Lys Leu Leu
65 70 75

<210> 74
<211> 91
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 74
Met Ser Phe Thr Asp Ala Lys Ala Met Ala Ala Lys Ala Lys Arg Ser
1 5 10 15

Asn Asp Met Ala Val Ile Ala Ala Arg Arg Ser Ile Ile Ser Asn Ile
20 25 30

Asp Gly Ser Ala Ser Ser Gly Lys Thr Glu Val Asp Ser Tyr Ala Leu
35 40 45

Asn Gly Leu Pro Ile Ala Ala Arg Ser Gln Ile Met Glu Asp Leu Lys
50 55 60

Asp Ala Gly Tyr Glu Val Lys Val Asn His Pro Phe Asp Gln Arg Asp

65 70 75 80

Thr Glu Ser Ile Thr Ile Ser Trp Gly His Ala
85 90

<210> 75
<211> 160
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 75
Met Phe His Val Tyr Thr Asp Gly Gly Cys Arg Gly Asn Thr Arg Gly
1 5 10 15

Val Asp Asn Val Gly Ala Trp Ala Met Val Val Tyr Asn Ser Ser Glu
20 25 30

Glu Gln Ile Gly Thr Lys Ser Ala Pro Lys Arg Asn Thr Thr Asn Asn
35 40 45

Glu Met Glu Leu Gln Ala Val Leu Glu Ala Leu Leu Trp Ser Asn Lys
50 55 60

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

Asn Gly Cys Glu Ser Trp Val Trp Gly Trp Glu Arg Lys Gly Trp Lys
85 90 95

Lys Ala Asp Gly Asp Thr Pro Leu Asn Leu Asp Gln Trp Lys Trp Ile
100 105 110

Ile Asp Glu Leu Lys Lys Tyr Arg Leu Asn His Asn Glu Ile Pro Thr
115 120 125

Phe Val Lys Val Lys Gly His Ser Gly Val Glu Gly Asn Glu Ala Ala
130 135 140

Asp Asn Leu Leu Asn Val Arg Met Thr Glu Leu Glu Met Glu Asp Met
145 150 155 160

<210> 76
<211> 53
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 76
Met Leu Glu Asn Leu Arg Arg Leu Val Ser Glu Met Lys Tyr Glu Val
1 5 10 15

Leu Leu Met Glu Pro Gly Val Asp Arg Val Val Met Lys Leu Arg Ile
20 25 30

Ala Arg Met Glu Ala Gln Ile Phe Glu Ala Glu Trp Lys Ala Leu Arg
35 40 45

Gly Gly Asp Glu Leu
50

<210> 77
<211> 116
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 77
Met Ala Pro Asp Leu Arg Asp Leu Phe Pro Asn Val Pro Gln Tyr Gln
1 5 10 15

Leu Asp Leu Tyr Ala Ala Phe Leu Glu Ala Ser Lys Ser Gly Asn Pro
20 25 30

Leu Arg Val Tyr Arg Gln Asp Arg Arg His Gly Lys Ser Trp Ile Leu
35 40 45

Arg Trp Leu Lys Glu Asn Glu Pro Leu Leu Lys Lys Leu Ser Glu Arg
50 55 60

Asn Ser Val Gln His Arg His Thr Thr Lys Val Gly Thr Ser Thr Ser
65 70 75 80

Ala Gln Lys Ser Arg Gln Asn Ile Ser Gly Gly Asn Arg Tyr Glu Phe
85 90 95

Ile Ile Phe Asp Asp Leu Val Asp Glu Asn Glu Lys Thr Gln Leu Leu
100 105 110

Asn Ala Lys Asn
115

<210> 78
<211> 136
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 78
Met Ala Lys Gln Thr Ser Lys Lys Ala Val Glu Thr Lys Val Ala Thr
1 5 10 15

Phe Pro Lys Thr Glu Ala Asn Arg Lys Ala Arg Leu Glu Arg His Leu

20 25 30

Arg Lys His Pro Ala Asp Thr Gln Ala Ala Ser Ala Val Gly Lys Pro
35 40 45

Ala Pro Arg Arg Lys Lys Pro Val Thr Lys Gly Ser Thr Ser Gly Tyr
50 55 60

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

Glu Val Leu Arg Lys Thr Gln Gly Arg Phe Gly Ser Val Lys Pro Asn
85 90 95

Ile Phe Gly Cys Glu Tyr Ser Arg Glu Asn Val Arg Ala Leu Cys Tyr
100 105 110

Gly Val Gly Ile Lys Phe Thr Gly Lys Ala Asn Lys Pro Arg Asn Gln
115 120 125

Lys Arg Lys Pro Ala Lys Lys Ala
130 135

<210> 79
<211> 334
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 79
Met Arg Asn Phe Val Ala Lys Asn Asp Phe Asn Arg Ala Ala Thr His
1 5 10 15

Lys Ser Ala Leu Asp Tyr Ser Arg Val Asn Ser Arg Glu Leu Met Asp
20 25 30

Ser Cys Tyr Glu Glu Leu Glu Asp Trp Ala Ala Asp Trp Pro Ser Met
35 40 45

Glu Glu Asn Trp Asp Val Ser Glu Asp Met Thr Lys Pro Pro Pro Glu
50 55 60

Val Ala Ser Lys Cys Asp Asn Thr Ser Arg Ser Asn Phe Asn Asn Lys
65 70 75 80

Gly Asn Asn Met Gln Asn Leu Gln Asp Arg Trp Ile Ser Val Cys Asp
85 90 95

Ile Glu Ser Leu Gly Thr Pro Gly Asp Cys Lys Ser Thr Phe Ile Ala
100 105 110

```
Met Pro Phe Phe Ala Phe Val Leu Met Lys Asp Leu Ser Leu Asp Pro
        115                 120                 125

Tyr Ile Val Leu Gly Thr Pro Asn Val Ala Gln Gln Leu Ala Leu Gly
    130                 135                 140

Ala Lys Val Ser Ala Gly Thr Ile Ala Phe Trp Met Asn Glu Ala Arg
145                 150                 155                 160

Ala Gly Ser Ala Pro Ser Leu Ser Ile Ile Glu Ala Leu Asn Ala Lys
                165                 170                 175

Asp Gly Glu Ser Thr Val Leu Val Cys Asn Pro Thr His Glu Ser Pro
            180                 185                 190

Val Ser Lys His Thr Phe Met Asp Leu Ile Cys Pro Phe Val Glu Ala
        195                 200                 205

Lys Gln Val Ile Glu Gly Ile Ile Asp Glu Gln Gly Ile Asp Thr Arg
    210                 215                 220

Ser Leu Arg His Tyr Gly Asn Gly Pro Gln Phe Asp Met Ser Ile Tyr
225                 230                 235                 240

Glu Thr Val Ala Ala Gln Ala Asn Val Phe Ser Pro Ser Asp Pro Ala
                245                 250                 255

Ile Val Pro Trp Lys Phe Trp Asp Ile Ser Ser Ala Arg Asn Pro Arg
            260                 265                 270

Asp Tyr Phe Glu Ala Leu Gly Gly Asp Trp Lys Ala Leu Val Arg Cys
        275                 280                 285

Ala Glu Ile Tyr Ala His Asp Val Ile Glu Arg Tyr Asn Leu Ile Pro
    290                 295                 300

Glu Gly Val Tyr Pro Ser Lys His Asp Pro Val Phe Asp Ala Leu Val
305                 310                 315                 320

Glu Ala Tyr Cys Ile Lys Thr Ile Glu Ser Lys Leu Lys Ile
                325                 330
```

<210> 80
<211> 153
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 80

```
Met Lys Ala Ala Ile Leu Met Ile Ser Ile Leu Thr Ser Phe His Ala
1               5                   10                  15
```

```
Gln Ala Lys Ile Asp Ala His Glu Ile Glu Cys Ile Ala Lys Asn Ala
            20                  25                  30

Tyr Phe Glu Ala Arg Gly Glu Gly Val Lys Gly Met Thr Ala Val Ala
        35                  40                  45

Gln Val Thr Lys Asn Arg Val Asn Tyr Gly Lys Phe Pro Ser Thr Tyr
    50                  55                  60

Cys Lys Val Val Tyr Gln Pro Gly Gln Phe Ser Trp Val Gly Lys Lys
65                  70                  75                  80

Lys His Lys Leu Asp Arg Lys Asp Glu Glu Trp Lys Gln Ala Lys Glu
                85                  90                  95

Ile Ala Arg Leu Val Tyr Tyr Met Asp Leu Pro Val Asp Pro Thr Lys
            100                 105                 110

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

Asp Lys Asp Phe Lys Arg Thr Ser Lys Ile Gly Asn His Val Phe Tyr
    130                 135                 140

Lys Leu Lys Ser Gln Leu Pro Asn Ala
145                 150
```

<210> 81
<211> 108
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 81

```
Met Asn Asp Leu Ser Met Leu Thr Lys Ile Arg Ser Asp Ile Glu Ser
1               5                   10                  15

Met Val Ser Arg Arg Ser Glu Leu Thr Lys Ala Lys Gln Ile Ile Ser
            20                  25                  30

Gly Gly Thr Gln Lys Arg Phe Thr Leu Gln Ala Gly Asp Ile Lys Phe
        35                  40                  45

Asp Leu Cys Gly Ser Gln Thr Arg Asp Tyr Thr Phe Glu Met Lys Pro
    50                  55                  60

Cys Tyr Asp Met Val Lys Leu Gly Leu Ile Lys Ala Leu Asp Lys Gln
65                  70                  75                  80

Ile Asp Gln Cys Thr Asp Ala Ile Lys Thr Leu Asn Val Gln Phe Ala
                85                  90                  95
```

Ala Glu Cys Asp Arg Leu Lys Asn Ser Ile Lys Val
100 105

<210> 82
<211> 58
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 82
Met Val Ala Ser Val His Thr Pro Pro Tyr Glu Arg Pro Ala Pro Asn
1 5 10 15

Leu Thr Pro Glu Gln Lys Gln Leu Ile Ala Arg Arg Thr Leu Glu Phe
20 25 30

Lys Glu Ser Leu His Lys Ser Val Gly Arg Tyr Ser Glu Gln Val His
35 40 45

Asp Leu Val Val Lys Thr Leu Lys Leu Tyr
50 55

<210> 83
<211> 73
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 83
gcuuccuuag cucagaggau agagcaacgg ucuucuaaac cgugggucac agguucgaau 60

ccuguaggga gua 73

<210> 84
<211> 97
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 84
Met Ala Tyr Lys Ile Glu Tyr Leu Lys Lys Gly Val Leu Thr Glu Leu
1 5 10 15

Val Ile Asp Ala Asn Met Ala Arg Asn Glu Gly Thr Lys Ser Val Phe
20 25 30

Tyr Lys Asp Gly Ser Val Ala Arg Met Ile Asn Thr Glu Asp Ile Gln
35 40 45

Asp Leu Tyr Val Ile Ser Asp Glu Glu Ala Gly Phe Val Lys Asp Pro
50 55 60

Glu Pro Ala Glu Asp Thr Pro Thr Glu Asp Thr Pro Val Ala Asp Thr
65 70 75 80

Thr Thr Glu Glu Pro Pro Val Glu Gly Thr Pro Glu Asp Glu Ala Ala
85 90 95

Val

<210> 85
<211> 72
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 85
gggccgguag cuuaaaguua aagcaguggc cucauaagcc aacgaguggg aguuagaguc 60

uccccuggcc ca 72

<210> 86
<211> 65
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 86
Met Ser Thr Lys Asn Ala Ile Val Ser Phe Val Asp Asp Ser Gly Ile
1 5 10 15

Val Leu Glu Ser Thr Val Thr Asp Ile Ser Pro Lys Arg Leu Leu His
20 25 30

Arg Asp Gly Asp Ile Leu Glu Ile Leu Asn Lys Arg Ser Glu Thr Met
35 40 45

Leu Val Ile Pro Val Asn Arg Leu Leu Ser Ile Lys Ile Val Trp Glu
50 55 60

Asp
65

<210> 87
<211> 69
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 87
Met Asp Ala Gln Leu Gln Thr Gln Tyr Tyr Met Leu Leu Gly Met Leu
1 5 10 15

Glu Asp Ala Gly Pro Thr Val Arg Gly His Tyr Glu Arg His Lys Ala
            20   25   30

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

Gly Ser Asp Ser Tyr Ala Ala Phe Ile Ile Ala Leu Gln Val Phe Leu
    50   55   60

Ile Asn Gln Leu Lys
65

<210> 88
<211> 164
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 88
Met Leu Asn Ile Lys Arg Lys Gly Phe Phe Tyr Lys Trp Leu Asn Phe
1   5   10   15

Ser Ser Ala Ser Phe Thr Tyr Arg Leu Asn Asp Asn Arg Val Thr Leu
            20   25   30

Cys Ser Leu Phe Trp His Ser Val Trp Tyr Phe Leu Leu Gln Ile Gly
        35   40   45

Val Thr Ala Ile Ala Val Leu Phe Ser Leu Gly Met Gly Ser Ile Leu
    50   55   60

Ser Thr Phe Leu Gly Leu Thr Phe Glu Leu Gly Ile Thr Pro Trp Tyr
65   70   75   80

Met Leu Val Gly Leu Ser Leu Ala Gly Leu Ser Thr Ile Ile Ala Ile
                85   90   95

Leu Leu Ala Ile Ala Gly Ile Gly Trp Ala Cys Ala Lys Ile Gly Asp
            100   105   110

Arg Ile Gln Glu Trp Asn Ala Ser Lys Ser Phe Glu Arg Ala Gln Lys
        115   120   125

Glu Tyr Asn Ala Arg Asp Glu Glu Leu Arg Phe Gly Asn Ile Tyr Gln
    130   135   140

Lys Met Arg Ile Tyr Lys Lys Asp Lys Leu Cys Pro Leu Ile Arg Val
145   150   155   160

Asp His Gly Glu

<210> 89
<211> 73
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 89
aagggaauag ccaagugguu acggcaucgg ccuuugacuc cgagaucggu agguucaacu 60

ccuccuuccc uug 73

<210> 90
<211> 77
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 90
gcuccugucg ucuaagcugg uuaggacacc acucuuucac agugggaaca cggguucgaa 60

ccccguuggg aguacca 77

<210> 91
<211> 79
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 91
gggggauggg ucugcuggga guggacaccg cacuugcaau gcgggaauca gaacgguuca 60

aauccguuau ccuccacca 79

<210> 92
<211> 87
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 92
ggggaugugg cgaaauuggc agccgcgcua gauuuagguu cuagugguga aauauccgug 60

uggguucgac ccccuccauc ccuacca 87

<210> 93
<211> 78
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 93

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

Lys Val His Thr Phe Pro Ser Lys Glu Ala Leu Glu Phe His Ile Lys
20 25 30

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

Ala Asn Gly Val Leu Tyr Val Trp Glu Ile Thr Tyr His Ala Asp Pro
50 55 60

Asp Glu Leu Arg Lys Glu Val Glu Gln Ile Leu Thr Gly Glu
65 70 75

<210> 94
<211> 85
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 94
ggagaguagu gcucauggga gcaagcugac uugaaaucag ucgccaucgg aaacggugag 60

gguucgauuc cuuuauucuc cgcca 85

<210> 95
<211> 86
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 95
ggaaagcugg ugaaauggua gccacgcauc acugcuaaug augaguccgc aagggcauga 60

agguucaagu ccuucgcuuu ccgcca 86

<210> 96
<211> 77
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 96
gggauauuau cauaacugga uaaugaccuc gauuguggau cgagucuauc uugguucgaa 60

uccaagauau cccucca 77

<210> 97
<211> 75
<212> RNA
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F391/08

<400> 97
gcaccauuag uuuaauggau agaauauaga gcuacgaacu cuaugguuga gguucgauuc 60

cucgauggug uacca 75

<210> 98
<211> 75
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 98
uggggguauag cucaguaggu agagcggagg ucucugaagc cuaggucaca aguucgauuc 60

uuguugcccc ugcca 75

<210> 99
<211> 77
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 99
ugcaccguag aggagaggcc guccucgcca gucucauaag cuggagaucg caaguucgaa 60

ucuugccgga gcaucca 77

<210> 100
<211> 64
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 100
Met Met Arg Ile Ser Phe Thr Glu Arg Val Leu Gly Thr Gly Val Met
1 5 10 15

Leu Ile Thr Ser Trp Asp Gly Asp Ser Trp Cys Asn Val Thr Gly Leu
20 25 30

Arg Lys Ser Glu Gln Thr Pro Glu Asn Ile Ala Lys Ile Lys Lys Arg
35 40 45

Met Ala Glu Ala Ala Ser Arg Pro Gly Ala Pro Arg Asn Gly Lys Arg
50 55 60

<210> 101
<211> 59
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 101
Met Val Asn Val Glu Val Thr Met Thr Arg Tyr Gln Gly Met Leu Ile
1   5   10   15

Asn Thr His Thr Lys Glu Ile Val Phe Leu Ala Pro Ala Phe His Asp
            20   25   30

Thr Tyr Asn Glu Ala Glu Glu Asp Ala Arg Ile Ala Lys Ile His Pro
        35   40   45

Asp Glu Glu Ile Cys Val Arg Gln Gln Glu Gln
    50   55

<210> 102
<211> 76
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 102
gcuucaauag cucaguuggu agagcaaacg accgauaauc guuaggucac ugguucgagu 60

ccaguucgga guacca 76

<210> 103
<211> 77
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 103
ggucaguugg cagagauggu uuaugcacuc gcuucauacg ugagacuaca gugguucgag 60

uccacuauug accacca 77

<210> 104
<211> 76
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 104
acuugcuuag cucaaucggg agagcaucgu cuuuacacgg cgaggguagc ugguucgaaa 60

ccagcagcaa guacca 76

<210> 105
<211> 93
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 105
Met Glu Lys Ile Thr Ala Thr Gly Ile Glu Ser Ala Leu Val Val Asp
1 5 10 15

Trp Ala Gly Trp Asp Gly Asp His Glu Trp Met Val Phe Tyr Ser Cys
20 25 30

Thr Leu Gln Pro Glu Leu Trp Thr Arg Leu Thr Asp Glu His Ala Met
35 40 45

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

Thr Ile Met Val His Arg Ala Glu Gly Asp His Lys Glu Ile Phe Arg
65 70 75 80

Lys Ser Ile Lys Leu Val Val Ser Thr Gly Asp Phe Ile
85 90

<210> 106
<211> 125
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 106
Met Tyr Thr Arg Pro Thr Asn Gly Asn Ser Ala Val Val Arg Leu Met
1 5 10 15

Ile Val Gln Asp Asn Leu Ser Asn Asn Ile Glu Ser Leu Asp Arg Arg
20 25 30

Ile Glu Glu Tyr Arg Thr Glu Met Leu Ser Leu Met Arg Glu Arg Glu
35 40 45

Ala Lys Ile Glu Glu Gln Leu Glu Val Cys Glu Ala Ile Asp Arg Leu
50 55 60

Val Asp Gly Thr Ala Val Phe Met Ala Glu Ala Pro Ala Glu Pro Thr
65 70 75 80

Phe Thr Pro Val Ala Pro Ala Asp Met Gln Tyr Ala Ile Leu Pro Phe
85 90 95

His Leu Glu Glu Glu Asp Gly Glu Gly Pro Ser Leu Glu Asp Val Val
100 105 110

Arg Phe Leu Leu Ala Ser Gly Phe Pro Asn Gly Gly Arg
115 120 125

<210> 107
<211> 71

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 107
Met Asp Phe Ile Val Val Cys Gly Ala Asn Thr Asp Cys Phe Glu Leu
1   5   10   15

Leu Asn Asp Ala Leu Asp Lys Val Asp Glu His Met Gln Glu Gly Arg
            20   25   30

Thr Pro Thr Phe Ile Asp Leu Ser Gln Gly Lys Thr Tyr Phe Tyr Pro
        35   40   45

Ser Leu Asp Val Glu Pro Thr Val Leu Pro Ile Phe Met His Ser Leu
    50   55   60

Ser Trp Asp Glu Glu Asp Asp
65   70

<210> 108
<211> 77
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 108
gcggcuaugg uguucagcgg ucaacauacc ggccugucac gucggagcca cggguucgaa 60

ucccguuagc cgcgcca 77

<210> 109
<211> 78
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 109
gggagagaag caguaagugg uauaggcggu cgccuguuaa gcgaaugaca gugaguucga 60

aucucaccuc ucccgcca 78

<210> 110
<211> 74
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 110
gcaucauugg ccgagugacu aggcagaggc uugcaaaccc ucgaagcaug guuaaaaucc 60

augauggugc ucca 74

<210> 111
<211> 59
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 111
Met Ile Lys Tyr Lys Ala Phe Val Thr Arg Glu Ser Gln Thr Gly Asp
1 5 10 15

Ser Ser Ile Lys Phe Glu Gly Thr Thr Leu His Asp Thr Phe Glu Ala
20 25 30

Ala Leu Thr Glu Ala Glu Thr His Ile Val Ser Lys Ser Cys Tyr Ala
35 40 45

His Val Trp Glu Val Asn Thr Ile Leu Asp Arg
50 55

<210> 112
<211> 76
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 112
agaucgcuag cucaaugguu agagcacucg ccuuuuaagc gauagguucc ggguucgagu 60

cccgggcggu cuacca 76

<210> 113
<211> 78
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 113
gcaacuguag cucagcgagg ugagagcacu gguuugaaag uccagggguc guucguucaa 60

aucgaaccgg uugcacca 78

<210> 114
<211> 64
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 114
Met Asn Gln Lys Ile Leu Met Arg Tyr Asn Pro Arg Ala Leu Trp Phe
1 5 10 15

Arg Trp Glu Val Ile Val Ser Tyr Gln Ile Arg Val Arg Asn Gly Asp

20 25 30

Pro Glu Asn Asn Ile Ile Val Leu Glu Thr Phe Ser Asn Arg Asp Ala
35 40 45

Ala Val Lys Phe Leu Asn Thr Ile Asp Asn Thr Leu Ile Lys Val Tyr
50 55 60

<210> 115
<211> 112
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 115
Met Asp Ile Phe Thr Thr Pro Ala Ile Asn Leu Val Gly Val Gly Leu
1 5 10 15

Phe Gln Ala Thr Val Tyr Arg Ile Asp Asp Ser Thr Asp Val Val Thr
20 25 30

Phe Ile Val Pro Glu Phe Phe Leu Glu Lys Phe Phe Glu Glu Phe Glu
35 40 45

Gln Phe Arg Glu Glu His Asp Ala Tyr Ser Asn Met Glu Asp Leu Ala
50 55 60

Ala Met Phe Pro Thr Val Tyr Gly Tyr Ile Phe Glu Gly Asn Asp Leu
65 70 75 80

Leu Leu Asp Lys Ser Glu Leu Val Glu Leu Asn Trp Gly Ile Ser Phe
85 90 95

Glu Val Gly Ser Pro Phe Pro Arg Tyr Phe Gln Gly Leu Glu Ile Arg
100 105 110

<210> 116
<211> 49
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 116
Met Gly Gly Tyr Ser Asn Phe Ile Glu Asn Tyr Ile Asn Ser Val Asp
1 5 10 15

Ser Trp Asn Gln Glu Thr Leu Val Val Val Leu Lys Glu Arg Phe Asn
20 25 30

Ile Ser Thr Leu Glu Ala Leu Glu Ala Ile Glu Ala Tyr Leu Asp Asn
35 40 45

Asp

<210> 117
<211> 78
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 117
acccacuugg uccaaucugg uagaggcaug aggcuuaaga cuucaggguu cccgguucga 60

guccgggagu ggguacca 78

<210> 118
<211> 77
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 118
uuccccuuag cucagucugg cagagcgggc gcuuugggag cgucagguca aguguucaaa 60

ucacuuaggg gagacca 77

<210> 119
<211> 76
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 119
gccucaauag cucagccggg agagcaaccg ccuuguaagc gguaggucgu ggguucgauu 60

ccuacuuggg gcacca 76

<210> 120
<211> 76
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 120
gcgacuaacu guacggguua cagcguccgc cuuccaagcg guacugagug ggguucgauu 60

cccccuaguc gcucca 76

<210> 121
<211> 33
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 121
Met Lys Ala Phe Asp Ala Glu Leu Val Phe Ser Leu Leu Ala Glu Met
1 5 10 15

Glu Ala Cys Val Asp Arg Val Arg Ala Leu Arg Leu Ser Met Phe Ser
20 25 30

Ser

<210> 122
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 122
Met Leu Thr Val Lys Val Met Ser Pro Asn Gly Gly Glu Glu Ile His
1 5 10 15

Asp Gly Ser Ser Val Gly Phe Asn Pro Lys Gln Lys Ser Ile Ser Ile
20 25 30

Ala Gly Leu Asp Gln His Ile Phe Leu Lys Glu Asp Glu Val Ala Tyr
35 40 45

Val Met Asn Gln Asn Gly Lys Thr Val Ser Val Tyr His Gly Ser
50 55 60

<210> 123
<211> 77
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 123
auuccccgag uguuacugga cagcacgccg gucuccaaaa ccgugcagua ggaguucgag 60

ucuccugggg uuugcca 77

<210> 124
<211> 118
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 124
Met Ile Thr Tyr Ser Thr Asn Phe Met Gly Pro Val Ser Asn Asn Trp
1 5 10 15

Tyr Ile Arg Met Gly Ile Pro Tyr Thr Glu Val Thr Glu Pro Asn Arg
20 25 30

Phe Ala Asp Gly Gly Gln Leu Thr Arg Lys Val Phe Ala Lys Arg Tyr
35 40 45

Ala Gly Gly Arg Ile Asp Val Arg Gly Thr Asp Asp Tyr Phe Gly Gln
50 55 60

Glu Ile Gly Val Pro Ile Met Glu Ala Glu Ser Trp Asn Glu Leu Gln
65 70 75 80

Gln Phe Leu Trp Thr Phe Ser Ser Asp Lys Val Leu Thr Leu Glu Gln
85 90 95

Ile Val Gln Ala Leu Glu Asp Glu Thr Gly Phe Arg Ile Val Trp Phe
100 105 110

Lys Glu Pro Ala Cys Thr
115

<210> 125
<211> 126
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 125
Met Tyr Ile Asp Arg Asn Gln Leu Phe Lys Phe Leu Glu Leu Asp Leu
1 5 10 15

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

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

Ala Val Tyr Val Ala Ser Gly Val Arg Glu Met Ala Arg Leu Glu Lys
50 55 60

Lys Tyr Asn Glu Leu Gln Pro His Val Lys Ile Thr Thr Tyr Ser Met
65 70 75 80

Leu Glu Pro Tyr Arg Ile Gly Arg Arg Phe Ser Cys Ile Met Phe Asp
85 90 95

Glu Pro Ser Leu Ala Ile Lys Tyr Gly Val Asn Ala Tyr Val Val Arg
100 105 110

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

<210> 126

<211> 58
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 126
Val Glu Gln Glu Phe Gln Val Phe Val Asp Ala Ser Lys Arg Val Leu
1   5   10   15

Phe Ile Gln Ala Thr Asp Glu Gly His Gly Leu Gln Leu Ser Phe Asp
            20   25   30

Ser Leu Glu Gln Ile Asn Gln Ile Val Leu Arg Ala Gln Lys Ser Leu
        35   40   45

Glu Lys Asn Thr Glu Ala Pro Pro Asp Leu
    50   55

<210> 127
<211> 71
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 127
Met Arg Glu Ile Ser Lys Met Lys Val Thr Met Glu Asn Thr Glu Glu
1   5   10   15

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

Met Asp Asp His Thr Met Gln Leu Val Ala Asp Ile Tyr Arg Leu Ala
        35   40   45

Glu Leu Ala Lys Glu Gln His Asn Arg Leu Val Tyr Val Lys Glu Arg
    50   55   60

Leu Glu Met Met Asp Lys Glu
65   70

<210> 128
<211> 90
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 128
Met Asn Glu Leu Asn Glu Leu Asn Glu Leu His Tyr Ala Glu Arg Ala
1   5   10   15

Ile Asp Glu Leu Asp Phe Ala Gly Gly Tyr Tyr Thr Arg His Val Asn
            20   25   30

Ala Met Thr Ala Glu Gly Leu Asn Ser Lys Ser Ala Ile Ala Ala Glu
35 40 45

Leu Ala Val Arg Asp Phe Val Ile Asp Ser Leu Gln Lys Thr Ile Ser
50 55 60

Asn Leu Ser Glu Asn Asn Lys Ala Ala Leu Glu Ala Leu Asp Lys Leu
65 70 75 80

Ser Asn His Leu Leu Ala Leu Gly Ile Lys
85 90

<210> 129
<211> 180
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 129
Met Asn Lys Gln Ser Leu Arg Gly Ile Arg Val Phe Arg Ser Ser Leu
1 5 10 15

Val Asp Ser Phe Tyr Ile Trp Gly Lys Ala Thr Arg Arg Thr Val Glu
20 25 30

Gln Ala Leu Asp Gly Thr Phe Tyr Asp Trp Arg Glu Lys Glu Arg Asn
35 40 45

Pro Val Phe Ser Arg Pro Gly Leu Tyr His Asp Arg Val Ser Lys Thr
50 55 60

Ala Trp Tyr Glu Ile Glu Val Thr Pro Gly Val Ile Arg Ala Phe Tyr
65 70 75 80

Thr Asp Trp Glu His Glu Lys Trp Val Trp Asp Asn Gln Ile Ala Pro
85 90 95

Gly Asp Arg Ile Met Asn Tyr Ala Glu Tyr Lys Glu Met Lys Arg Met
100 105 110

Phe Glu Leu Tyr Asp Val Pro Arg Leu Ser Arg Pro Ala Ile Phe Ile
115 120 125

Ala Ser Gln Glu Tyr Trp His Thr Val Arg Met Lys Arg Asp Phe Asn
130 135 140

Lys His His Leu Arg Tyr Glu Lys Glu His Gly Thr Leu Arg Glu Arg
145 150 155 160

Val Ala Lys Arg Lys Ala Glu Leu Arg Glu Lys Arg Leu Glu Lys Lys

165 170 175

Tyr Gly Glu Ser
180

<210> 130
<211> 75
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 130
Met Val Lys Ala Ser Leu Leu Arg Phe Thr Pro Gly Val Gly Leu Gln
1 5 10 15

Tyr Lys Ile Val Gly Gly His Lys Phe Gln Tyr Phe Thr Pro Gly Lys
20 25 30

Leu Tyr Phe Val Glu Leu His Asp Ser Arg Ala Gly Tyr Lys Leu Arg
35 40 45

Ser Asp Ala Asn Glu Gly Ile Trp Val Ser Phe Thr Gln Val Lys Arg
50 55 60

Trp Phe Thr Val Glu Gly Tyr Asn Asp Tyr Glu
65 70 75

<210> 131
<211> 122
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 131
Met Ile Met Ser Lys Val Val Tyr Phe Val Lys Cys Cys Arg Asp Thr
1 5 10 15

Leu Glu Leu Val Asp His Lys Met Gln Thr Cys Lys Cys Gly Ala Ser
20 25 30

Ser Ile Asp Gly Val Ala Gly Ala Tyr Val Arg Phe Leu Gly Asp Lys
35 40 45

Ser Asn Phe Met Arg Leu Asn Glu Phe Gln Leu Glu Val Glu Lys Asn
50 55 60

Arg Pro Ala Leu Glu Ala Glu Ala Glu Arg Leu Lys Asp Phe Asp Gly
65 70 75 80

Asn Ile Val Ala Tyr Asn Met Val Ser Gly Lys Asp Phe Trp Ser Glu
85 90 95

Leu Ala Glu Lys Leu Asn Met Pro Arg Gln Ala Ala Lys Ala Leu Tyr
100 105 110

His Gly Phe Asn Tyr Ser Pro Arg Trp Asn
115 120

<210> 132
<211> 88
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 132
Met Ala Ser Thr Thr Arg His Val Gly Ile Lys Phe Ser Asn Ser Asn
1 5 10 15

Arg Thr Tyr Val Tyr Arg Val Pro Ser Tyr Trp Lys Tyr Ser Pro Glu
20 25 30

Ile Gly Asp Val Val Val Ile Pro Gly Asn Val Met Phe Asn Asn Pro
35 40 45

Arg Arg Ala Lys Val Val Glu Val His Gly Met Tyr Gly Lys Pro Glu
50 55 60

Tyr Lys Glu Arg Lys Asn Ile Ser Tyr Val Glu Leu His Asp Tyr Leu
65 70 75 80

Pro Lys Glu Glu Arg Asn Gly Arg
85

<210> 133
<211> 101
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 133
Met Asp Asp Lys Ile Ala Arg Glu Ala Ile Glu Leu Val Arg Lys Arg
1 5 10 15

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

Gly Gly Ile Gly Gly Phe Pro Ser Phe Thr Asp Leu Glu Arg Met Glu
35 40 45

Arg Glu Ser Gln Ala Ser Phe Leu Glu Leu Glu Ser Tyr Ala Arg Glu
50 55 60

Met Glu His Glu His Pro Ile Gly Asn Asn Phe Met Pro Arg Ser Ser

65 70 75 80

Arg Gln Glu Val Thr His Gly Lys Thr Asn Ser Trp Pro Thr Pro Lys
85 90 95

Arg Arg Gly Arg Lys
100

<210> 134
<211> 69
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 134
Met Ile Thr Thr Gly Phe Gly Tyr Ser His Glu Glu Leu Cys Lys Met
1 5 10 15

Val Glu Ser Ala Pro Phe Ile Lys Lys Leu Val Glu Glu Gln Arg Pro
20 25 30

Val Cys Leu His Ala Ala Cys Thr Lys Cys His Gly Thr Gly Val Asp
35 40 45

Lys Asn Gly Lys Met Cys Val His Ala Leu Ser Cys Pro Cys Pro Lys
50 55 60

Cys Ser Trp Ser Cys
65

<210> 135
<211> 145
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 135
Met Asp Leu Gly Tyr Cys Val Val His Glu Phe Met Glu Gln Gly Leu
1 5 10 15

Pro Asp Arg Ile Cys Val Val Thr Ser Arg Asn Leu Glu Ala Ala Gln
20 25 30

Ser Leu Val Glu Arg Leu Ser Gly Tyr Tyr Arg Asp His Glu Arg Tyr
35 40 45

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

Asp Met Pro Thr Pro Gln Leu Asp Asp Leu Lys Gln Phe Ser Pro Glu
65 70 75 80

```
Ala Trp Tyr Ser Val Lys Asp Ala Ser Pro Val Asp Tyr Thr Val Gln
                85                  90                  95


Val Phe Ser His Tyr Gly Thr Arg His Trp Ile Asn Arg Lys Trp Asp
            100                 105                 110


Ser Met Val Asp Tyr Leu Asn Ser Glu Leu Glu Lys Gly Ala Ala Glu
        115                 120                 125


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


Leu
145


<210> 136
<211> 107
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 136
Met Ser Lys Leu Ser Ile Glu Ser Ile Ile Arg Pro Leu Met His Gly
1               5                   10                  15


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


Glu Glu Glu Leu Val Ala Asn Gly Tyr Asn Leu His Glu Gly Val Ile
        35                  40                  45


Glu Asp Leu Phe Trp Gln Thr Ala Glu Asp Met Glu Ile Phe Arg Cys
    50                  55                  60


Val Asn Cys Gly Trp Trp Cys Pro Ala Phe Glu Arg Ala Glu Asn Gln
65                  70                  75                  80


Ile Glu Glu Ile Cys Arg Asp Cys Glu Pro Asp Leu Glu Gly Glu Val
                85                  90                  95


Asp Glu Gln Asp Asn Glu Gly Glu Asp Tyr Glu
            100                 105


<210> 137
<211> 99
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 137
Met Asn Lys Ile Thr Lys Val Lys Thr Met Ser Lys Arg Ser Ile Ala
```

1 5 10 15

Ala Ile Ile Ala Phe Ser Met Met Tyr Ser Gly Val Ser Leu Ala Ala
20 25 30

Glu Arg Asn Lys Val Glu Ile Ser Asp Asn Gly Arg Val Arg Val Thr
35 40 45

Thr Asn Gly Ile Thr Lys Gly Ala Gly Lys Phe Arg Lys Ser Glu Thr
50 55 60

Arg Phe Gly Glu Thr Lys Ile Tyr Thr Asn Lys Thr Tyr Gly Lys Pro
65 70 75 80

Ala Val Thr Leu Asp Arg Tyr Gly Arg Gln Val Glu Asp Glu Asp Asp
85 90 95

Ser Asp Glu

<210> 138
<211> 144
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 138
Met Ser Asn Leu His Pro Lys Leu Gln Glu Thr Leu Asp Trp Ile Asn
1 5 10 15

Glu Glu Cys Ala Phe Glu Glu Ala Pro Tyr Cys Val Trp Ala Arg Ala
20 25 30

Gly Ala Ala Pro Ser Glu Trp Cys Thr Val Phe Asp Asn Arg Tyr Arg
35 40 45

Ile Thr Val Glu Leu Ser Leu Lys Glu Asp Lys Val Tyr Ala Lys Ala
50 55 60

Ser Met Thr Ala Leu Gly Leu Ser Gly Phe Val Glu Met Gln Glu Leu
65 70 75 80

Cys Met Pro Asn Thr His Leu Arg Val Gln Ile Glu Gln Leu Ala Thr
85 90 95

Ile Arg Leu Met Leu Pro Glu Asp Asn Ile Asn Asp His Phe His Lys
100 105 110

Val Ile Glu Asn Glu Tyr Lys Leu Arg Arg Gln Arg Arg Lys Ala Arg
115 120 125

Arg Glu Val Glu Lys Thr Arg Met Met Cys Asn Met Asn Pro His Val
    130   135   140

<210> 139
<211> 130
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 139
Met Phe Thr Leu Phe Ile Leu Ala Val Ser Ala Trp Met Ala Val Gly
1   5   10   15

Ile Asn His Gly Leu Asp Ser Ala Lys Leu Leu Ser Ala Lys Ala Phe
            20   25   30

Glu Phe Leu Ala Lys Phe Ala Thr Arg Lys Asp Ile Glu Ala Ile Ile
        35   40   45

Ala Lys Gly Gly Ala Lys Asp Ala Ser Ser Val Leu Lys Ser Phe Asp
    50   55   60

Lys Ile Leu Glu Leu Arg Asn Gly Lys His Ala Ala Glu Leu Arg Cys
65   70   75   80

Met Ser Arg Lys Thr Ile Gly Arg Leu Cys Lys Ala Ile Phe Ile Val
                85   90   95

Gln Gly Ala Leu Lys Gly Pro Phe Ala Lys Tyr Lys Pro Asp Ser Ile
            100   105   110

Lys Arg Ala Lys Ile Phe Asn Asp Tyr Cys Val Glu His His Pro Leu
        115   120   125

Asn Arg
    130

<210> 140
<211> 232
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 140
Met Arg Ile Ile Ser Lys Leu Lys Asp Val Tyr Asp Leu Gln Gly Thr
1   5   10   15

Met Tyr Asp Ala Glu Arg Ala Trp Tyr Arg Glu Glu Val Lys Glu Val
            20   25   30

Val Asn Val Ser Ala Asp Phe Glu Gln Ile Ile Phe Tyr Ala Glu Ile
        35   40   45

```
Leu Arg Asn Arg Thr Ser Ser Gly Tyr Gly Gly Val Asn Met Gly Thr
    50                  55                  60

Leu Glu Val Arg Pro Val Leu Ile Cys Gly Thr Leu Arg Trp Leu Tyr
65                  70                  75                  80

Gly Tyr His Thr Gly Leu Gly Ala Asp Ala Val His Ile Gln Thr Phe
                85                  90                  95

Asp Pro Val Lys Val Lys Glu Val Leu Glu Glu Gln Gly Tyr Tyr Leu
            100                 105                 110

Arg Met Gly Trp Asp Met Asn Thr Ile Glu Lys Ile Asp Ala His Val
        115                 120                 125

Arg Asn Ala Thr Ala Thr Ala Ser Ala Phe Leu Glu Thr Phe Asn Lys
    130                 135                 140

Pro Ile Ala Met Ala Trp Asp Ala Ala Lys Ser Lys Thr Asp Pro Thr
145                 150                 155                 160

Val Asn Ile Thr Val Lys Thr Asp Phe Asn Phe His Ala Glu Asp Phe
                165                 170                 175

Pro Trp Gln Glu Ile Asp Pro Asn Leu Tyr Arg Trp His Gln Thr Leu
            180                 185                 190

Glu Ser Tyr Ile Phe Gly Val Leu Gly Gln Gly Glu Pro Lys Thr Glu
        195                 200                 205

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

Val Ser Phe Arg Asn Met Glu Arg
225                 230


<210> 141
<211> 153
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 141
Met Leu Lys Phe Leu Ser Gly Ile Trp Ser Gly Lys Thr Gly Ala Ile
1               5                   10                  15

Leu Phe Leu Ala Ile Ala Ala Gly Thr Phe Gly Gly Ala Tyr Tyr Ile
            20                  25                  30

Thr Asn Lys Leu Thr Asp Met Ser Ser Ser Leu Gln Ser Leu Ser Asn
```

35 40 45

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

Arg Asn Arg Asp Arg Asn Thr Thr Thr Tyr Ile Thr Asn Leu Ala Lys
65 70 75 80

Asn Gln Glu Asp Leu Asp Gly Arg Ile Asn Lys Leu Asp Ala Ala Arg
85 90 95

Ala Lys Glu Gly Val Val Ala Ala Lys Pro Lys Leu Ala Thr Lys Val
100 105 110

Ala Lys Asp Lys Val Asn Glu Phe Gln Glu Arg Leu Ser Cys Val Thr
115 120 125

Gly Asn Met Asp Ser Cys Ser Arg Leu Gln Leu Ser His Pro Gly Val
130 135 140

Gln Asn Gly Gln Thr Gln Val Ala Gln
145 150

<210> 142
<211> 109
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 142
Met Arg Asn Trp Lys Tyr Gly Leu Leu Leu Ser Ala Ala Ile Ile Ala
1 5 10 15

Ser Gly Cys Ala Glu Arg Pro Asp Pro Ser Ser Thr Val Thr Gly Val
20 25 30

Glu Pro Gln His Leu Pro Trp Pro Ala Ser Leu Gln Thr Cys Pro Phe
35 40 45

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

Tyr Gln Asp Trp Ile Thr Met Gly Lys Cys Asn Glu Gln Val Tyr Thr
65 70 75 80

Tyr Ile Ala Asn Leu Thr Ala Leu Thr Cys Thr Tyr Arg Val Ser Leu
85 90 95

Asn Glu Tyr Arg Cys Lys Pro Phe Asn Lys Glu Thr Lys
100 105

<210> 143
<211> 253
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 143
Met Lys Tyr Val Leu Gly Leu Ile Gly Asp Ala Gly Ala Gly Lys Asp
1 5 10 15

Thr Phe Ala Asp Met Ala Lys Val Trp Ala Trp Glu Val Leu Gly Pro
20 25 30

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

Ala Ala Val Ile Leu Gly Val Thr Pro Glu Lys Leu Ala Glu Arg Arg
50 55 60

Thr Lys Glu Ile Lys Gln Trp Phe Trp Val Thr Gln Glu Ala Leu Glu
65 70 75 80

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

Phe Ser Tyr Val Trp Pro Gln Phe Glu Ala Ser Ala Leu Tyr Pro Leu
100 105 110

Ile Ala Lys Thr Ala Pro Asp Phe Tyr Gln Gly Arg Glu Thr Pro Leu
115 120 125

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

Glu Leu Gly Arg Ala Leu Val Asp Glu Asn Leu Trp Leu Asn Ile Val
145 150 155 160

Val Asp Arg Ile Thr Ala Thr Lys Ala Asp Ile Ser Ile Ile Ser Asp
165 170 175

Val Arg Phe Asp Asn Glu Ala Ala Leu Val Arg Asn Phe Pro Gly Ala
180 185 190

Gln Asn Ser Ser Ile Leu Lys Val His Ala Pro Asn Asn Ile His Ala
195 200 205

Ile Gln Ser Thr His Ala Ser Ala Arg Gly Val Ala Pro Glu Phe Ile
210 215 220

Asp Asp Val Val Thr Asn Asn Phe Asp Gly Leu Glu Asn Phe Arg Lys
225 230 235 240

Asn Val Asn Ala Phe Cys Asp Glu Arg Ile Leu Phe Ile
245 250

<210> 144
<211> 203
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 144
Met Gly Gln Ile Asn Asn Val Glu Gln Lys Gly Gly Asn Lys Thr Pro
1 5 10 15

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

His Tyr His Leu Asp Gly Pro Ile Val Asp Val Asp Tyr Tyr Arg Asp
35 40 45

Leu Ser Val Thr Leu Ala Thr Met Gln Glu Gly Asp Thr Leu Asn Leu
50 55 60

Tyr Ile Asn Ser Pro Gly Gly Tyr Val Asp Thr Ala Val Gln Leu Cys
65 70 75 80

Asn Leu Ile Met Asn Cys Gln Gly Thr Val Ile Gly His Leu Val Gly
85 90 95

Pro Ser Ala Ser Ala Ala Cys Ser Ile Phe Leu Ala Cys His Gly Trp
100 105 110

Leu Val His Pro Tyr Val Met Leu Met Gly His Thr Tyr Arg Gly Ala
115 120 125

His Tyr Gly Lys Gly Lys Asn Glu Ile Gln His Tyr Ala Asp Gln Phe
130 135 140

Asn Ser Phe Phe Glu Asp Met Met Leu Asp Leu Tyr Tyr Pro Phe Phe
145 150 155 160

Ser Leu Glu Glu Ile Thr Glu Met Ile Glu Gly Gly Lys Asp Ile Trp
165 170 175

Leu Thr Ser Lys Glu Ile Asn Glu Arg Val Asp Arg Met Ala Ala His
180 185 190

Arg Glu Gln Glu Ala Arg Lys Ala Ala Gly Gln
195 200

<210> 145
<211> 220

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 145
Met Asp Lys Phe Ile Gln Leu Ile Ser Leu Leu Leu Gln Glu Ala Lys
1 5 10 15

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

Val Ile Tyr Leu Phe Ile Ala Asn Thr Ser Glu Val Met Ser Tyr Leu
35 40 45

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

Thr Leu Glu Phe Pro Asn Val Ala Arg Glu Lys Ala Met Ile Leu Phe
65 70 75 80

Ser Gln Thr Arg Ala Asp Ala Val Phe Val Val Lys Tyr Lys Pro Glu
85 90 95

Ala Ile Asn Asp Tyr Gln Thr Ile Ile Ala Trp Glu Ser Asn Val Gln
100 105 110

Leu Asp Lys Ser Asp Val Ser Asp Lys Ala Val Asp Lys Thr Ser Met
115 120 125

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

Glu Lys Arg Gly Leu Ser Lys Trp Ser Gly Thr Gly Leu Pro Pro Phe
145 150 155 160

Lys Ser Ala Asn Phe Glu Tyr Val Tyr Thr Cys Pro Tyr Phe Asn Leu
165 170 175

Asn Asn Ile Tyr Ser Gly Tyr Val Ala Val Ala Trp Glu Lys Tyr Pro
180 185 190

Leu Gln Asp Glu Asp Met Gly Met Phe Asn Asp Tyr Met Ala Lys Ile
195 200 205

Cys Ala Ser Pro Gln Arg Ser Leu Gly Arg Ser Ile
210 215 220

<210> 146
<211> 137
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 146
Met Ser Phe Arg Phe Gly Asn Arg Ser Leu Gln Gln Leu Asp Thr Val
1   5   10   15

Asp Pro Lys Leu Lys Ala Leu Ala Ile Arg Ala Leu Glu Leu Ser Pro
            20   25   30

His Asp Phe Thr Ile Ile Gln Gly Lys Arg Thr Val Gln Gln Ser Ala
        35   40   45

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

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

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

Phe Lys Lys Ala Ala Asn Glu Met Asn Ile Ala Val Arg Phe Gly Ala
            100   105   110

Asp Trp Asn Asn Ser Gly Asp Tyr Arg Asp Glu Ile Gln Arg Gly Thr
        115   120   125

Tyr Asp Gly Gly His Val Glu Leu Leu
    130   135

<210> 147
<211> 134
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 147
Met Ser Asp Arg Phe Tyr Thr Gln Met Cys Glu His Phe Lys Val Ser
1   5   10   15

Pro Tyr Glu Leu Asn Ile Ala Leu Trp Asp Arg Glu Ser Pro Glu Phe
            20   25   30

Lys Lys Ile Ala Lys Lys Ser Glu Gly Val Met Ser Asn Gly Lys Lys
        35   40   45

Met Thr Arg Ile Asp Leu Asn Asn Ala Leu Thr Lys Leu Leu Gly Val
    50   55   60

Asn Ile Glu Gly Gln Lys Leu Ser Met Pro Thr Leu Thr Thr Ile Leu
65   70   75   80

Glu Lys Val Lys Ala Gly Asp Val Lys Lys Val Ala Val Pro Glu Gly
85 90 95

Arg Leu Lys Lys Pro Tyr Gln Glu Ala Ile Ile Glu Ala Phe Gly Glu
100 105 110

Lys Leu Asp Leu Asp Thr Ala Thr Val Lys Thr Met Lys Ala Leu Leu
115 120 125

Glu Ser Ile Asn Asn Val
130

<210> 148
<211> 94
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 148
Met Ser Lys Lys Ile Val Phe Leu Lys Gly Ser Ser Cys Val Pro Cys
1 5 10 15

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

Pro Val Glu Lys Arg Thr Asp Asp Val Asp Ser Leu Arg Lys Phe Gly
35 40 45

Leu Arg Thr Val Pro Ala Val Val Leu Val Asp Val Glu Asn Gly Arg
50 55 60

Glu Glu Ala His His Ile Leu Ser Gly Ala Thr Leu Arg Ser Ala Val
65 70 75 80

Val Ser Lys Ala Ile Gln Asp Phe Ile Asp Tyr Val Glu Glu
85 90

<210> 149
<211> 134
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 149
Met Thr Lys Gln Ala Tyr Leu Ile Leu Asn Asn Gly Phe Ala Val Gly
1 5 10 15

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

Asp Ala Ala Gln Lys Asn Gln Leu Val Asn Glu Ala Ala Trp Glu Tyr

35 40 45

Ala Glu Ala Tyr Val Glu Ala Val Asp Asp Glu Leu Val Ile Val Val
50 55 60

Ser Leu Gly Ala Val Gly Cys Asp Ala His Val His Thr Asp Phe Gln
65 70 75 80

Ser Glu Glu Glu Trp Asp Glu Leu Asp Leu Thr His Gln Asn Ala Leu
85 90 95

Ile Asn Glu Ala Phe Trp Glu Val Val Asp Cys Tyr Val Ala Phe Cys
100 105 110

Lys Asp Asp Asp Glu Ala Asn Thr Cys Thr Asn Tyr Gly Tyr Glu His
115 120 125

Asp Asp Val Glu Cys Ala
130

<210> 150
<211> 120
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 150
Met Gln Lys Phe Ser Arg Asp Trp Ser Ser Asp Met Ala Arg Lys Asn
1 5 10 15

Arg Ala Ala Ala Tyr Tyr Asn Lys Lys Ile Gln Leu Asp Lys Leu Ile
20 25 30

Lys Gly Ile Thr Tyr Asn Val Glu Arg Gly Phe Ser Gly Ile Lys Val
35 40 45

Asp Ala Arg Ser Leu Asp Tyr Ser Cys Ile Leu Trp Ala Lys Gln Asn
50 55 60

Gly Tyr Ala Phe Lys Arg Ile Gly Asn Glu Ile Leu Ile Ala Trp Glu
65 70 75 80

Pro Glu Gly Leu Val Gln Tyr Val Ile Tyr Asp Pro Tyr Arg Gly Glu
85 90 95

Tyr Val Arg Asp His Arg Gln Gln Pro Thr Asp Phe Ser Leu Pro Lys
100 105 110

Arg Tyr Tyr Leu Glu Thr Arg Tyr
115 120

<210> 151
<211> 276
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 151
Met Asn Val His Glu Thr Val Thr Val Pro Asp Asn Ala Asn Ile Phe
1 5 10 15

Phe Ile Gly Asp Ile His Gly Glu Tyr Asp Met Met Met Gly Ala Leu
20 25 30

Lys Leu Ala Gly Tyr Glu Glu Gly Arg Asp Tyr Val Phe Cys Val Gly
35 40 45

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

Leu Tyr Asn Pro Lys Phe Arg Ser Val Arg Gly Asn His Asp Glu Phe
65 70 75 80

Met Ile Gln Asp Asp Tyr Ala Asn Trp Met Tyr Asn Gly Gly Ser Trp
85 90 95

Thr Ile Thr Glu Gly Phe Asp Thr Asp Thr Met Lys Gly Ile Ala Glu
100 105 110

Asp Met Asp Ser Lys Met Pro Tyr Ile Met Thr Val Glu His Arg Gly
115 120 125

Lys Arg Tyr Gly Val Val His Ala Gly Ile Pro Leu Arg Tyr Gln Ala
130 135 140

Gln Gly Met Gly Val Thr Val Pro Val Trp Asp Asp Ile Val His Glu
145 150 155 160

His Glu Ser Thr Pro Asp Leu Arg Arg Leu Gly Val Leu Leu Trp Asp
165 170 175

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

Lys His Pro Tyr Phe Asp Arg Tyr Ala Ser Phe Ser Glu Glu Cys Ala
195 200 205

Val Asp Val Pro Glu Ile Val Gly Val Asp Tyr Thr Phe His Gly His
210 215 220

Thr Gly Val Pro Phe Pro Ile Arg Trp Lys Asn Arg Val Tyr Leu Asp
225 230 235 240

Thr Gly Gly Thr Phe Asn Gly Arg Met Thr Val Ala Ser Pro Val Leu
245 250 255

Gly Gln Leu Tyr Thr Phe Thr Thr Asp Arg Asp Asp Pro Cys Gly Ser
260 265 270

Ala Asp Ile Ile
275

<210> 152
<211> 77
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 152
Met Lys Leu Phe Lys Asp Leu Glu Glu Gly Glu Val Phe Val Val Ala
1 5 10 15

Gly Gly Phe Glu Leu Gln Lys Cys Val Ala Met Leu Asp Asn Gly Asn
20 25 30

Ser Val Phe Thr Asp Asp Ala Asn Ile Ser Val Thr Ile Ala Pro Asp
35 40 45

Thr Glu Thr Trp Lys Pro Lys Glu Phe Trp Glu Ile His Lys Asp Arg
50 55 60

Pro Leu Asp Asp Leu Leu Asp Asp Ile Leu Phe Thr Ala
65 70 75

<210> 153
<211> 122
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 153
Met Lys Leu Glu Ser Arg Tyr Ile Val Phe Lys Gln Ser Asp Ala Ala
1 5 10 15

Lys Tyr Leu Thr Ser Thr Ala Ile Arg Glu Ile Asn Asp Ser Leu Ser
20 25 30

Leu Ile Tyr Lys Gly Arg Glu Ala Asp Gly Lys Val Gly Phe Pro Asn
35 40 45

Tyr Ile Val Leu Glu Glu Asp Trp Pro Glu Tyr Pro Ile Ala Lys Glu
50 55 60

Ala Leu Glu Gly Arg Ile Val Leu Glu Glu Phe Asn Lys Arg Ala Glu

65 70 75 80

Lys Lys Arg Gly Ala Lys Ala Ala Glu Asp His Tyr Lys Gln His Gln
85 90 95

Ser Thr Glu Leu Leu Arg Gly Ile Ser Pro Phe Cys Ala Gly Trp Asn
100 105 110

Asp Tyr Met Arg Arg Leu Val Ile Glu Glu
115 120

<210> 154
<211> 39
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 154
Met Tyr Thr Gly Met Gly Asn Asp Met Ala Lys Met Phe Ile Gly Leu
1 5 10 15

Leu Ile Leu Ala Ala Leu Val Gly Ala Ala Ile Val Gly Gly Ile Trp
20 25 30

Ala Leu Val Ala Phe Val Phe
35

<210> 155
<211> 142
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 155
Met Lys Asn Ala Met Ile Glu Leu Asn Ala Asn Met Glu Ser Leu Arg
1 5 10 15

His Ala Val Asn Thr Ala Arg Ala Ser Phe Asn Leu Leu Met Arg Asp
20 25 30

Glu Ser Ile Pro Leu Ser Ala Arg Val Lys Ala Phe Glu Glu Phe Ala
35 40 45

Asp Glu Leu Leu His Met Gly Asp Tyr Leu Ser Asp Ser Pro Phe Asn
50 55 60

Glu Asp Arg Arg Asp Tyr Gln His Ala Tyr Cys Asn Arg Gly Glu Ile
65 70 75 80

Val Tyr Leu Thr Asp Val Leu Glu Ser Val Leu Glu Tyr Ala Asn Ser
85 90 95

```
Phe Met Arg Thr Pro Asp Glu Trp Glu Asp Ala Ser Asn Asp Tyr Val
            100                 105                 110


Leu Asp Glu Ile Gln Lys Asn Trp Pro Glu Ile Lys Lys Leu Val Glu
        115                 120                 125


Glu His Ile His Ser Glu Val Tyr Ala Tyr Arg Ile Asp Trp
    130                 135                 140


<210> 156
<211> 101
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 156
Met Ala Lys Asn Thr Ile Ser Tyr Thr Thr Gly Lys Thr Ala Asp Glu
1               5                   10                  15


Gln Ala Asn Thr Leu Thr Lys Asp Glu Met Val Ala Val Leu Val Ile
            20                  25                  30


Leu Leu Asp Met Ser Gly Phe Glu Gly Gln Leu Ala Lys Leu Ser Leu
        35                  40                  45


Pro Ala Leu Arg Ala Leu Tyr Glu Gly Thr Asn Lys Asn Ala Ala Ala
    50                  55                  60


Tyr Asn Leu Ala Lys Asn Glu Ala Arg Trp Ala Lys Glu His Gln Gln
65                  70                  75                  80


Val Ala Glu Arg Arg Ala Glu Ser Phe Glu Arg Asp Leu Lys Arg Glu
                85                  90                  95


Lys Ala Lys Lys Lys
            100


<210> 157
<211> 93
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 157
Met Val Leu Glu Ile Leu Ser Gly Leu Leu Ile Ala Ala Leu Val Thr
1               5                   10                  15


Gly Thr Gly Leu Ala Val Trp Val Ser Ile Leu Arg Glu Asn Asn Arg
            20                  25                  30


Arg Met Arg Leu Thr Asn Asn Gly Leu His Glu Lys Leu Met Asp Gln
```

35 40 45

Val Gln Asp Ala Asp Glu Phe Ser Ala Ala Ala Glu Arg Leu Leu Val
50 55 60

Arg Leu Ala Lys Ile Glu Glu Ile Ile Gly Gln Asp Ser Thr Met Ser
65 70 75 80

Lys Thr Thr Lys Met Arg Leu Ile Thr Glu Ile Lys Lys
85 90

<210> 158
<211> 82
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 158
Met Ile Ser Pro Ile Val Ala Ala Leu Tyr Leu Val Val Val Gly Tyr
1 5 10 15

Leu Ser Gly Lys Tyr His Gly Phe Gly Leu Lys Gly Thr Ile Lys Ala
20 25 30

Ala Met Leu Val Pro Leu Tyr Pro Leu Ala Ile Leu Leu Thr Gly Tyr
35 40 45

Tyr Ala Cys Val Leu Arg Ile Phe Gly Arg Gly Lys Val Asn Tyr Asp
50 55 60

Asn Cys Thr Ala Leu Leu Asp Asp Ile Glu Asn Thr Ile Lys Lys Glu
65 70 75 80

Glu Lys

<210> 159
<211> 113
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 159
Met Asn Leu Asn Ser Lys Glu Arg Gln Val Leu Val Asp Ala Leu Arg
1 5 10 15

Gln Val Val Asp His Asp Leu Leu Cys Asp Glu Asp Ile Val Glu Ser
20 25 30

Ile Ala Leu Ile Ala Lys Ile Glu Leu Ala Glu Lys Asp Ser Trp Arg
35 40 45

Pro Leu Ser Glu Leu Pro Pro Leu Gly Leu Ala Ile Val Val Gln Arg
50 55 60

Ala Asp Gly Ala Pro Phe Asn Thr Val Met Val Arg Arg Asp Leu Ala
65 70 75 80

Lys Ser Tyr Ser Pro Asp Ile Ile Thr Leu His Thr Lys Ile Thr Asn
85 90 95

Glu Pro Phe Glu Phe Asn Thr Arg His Tyr Tyr Trp Arg Leu Thr Asn
100 105 110

Ala

<210> 160
<211> 75
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 160
Met Leu Asn Gln Leu Arg Ile Tyr Asn Phe Leu Asp Cys Asn Phe Gln
1 5 10 15

Val Trp Arg Glu Leu Pro Ser Arg Phe Leu Gly Trp Ala Leu Phe Leu
20 25 30

Ser Met Val Val Ser Val Phe His Asn Val Pro Ala Thr Phe Tyr Met
35 40 45

Glu Ala Ile Gln Pro Val Thr Val Phe Ile Tyr Glu Met Tyr Leu Val
50 55 60

Ala Ile Asn Gly Trp Lys Asp Gly Arg Ile Asn
65 70 75

<210> 161
<211> 155
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 161
Met Ala Ala Ser Thr Glu Val Leu Asn Gln Tyr Phe Asn Arg Glu His
1 5 10 15

Gln Glu Phe Ser Asp Leu Phe Ile Gln Met Phe Val Asn Ala Asn Asn
20 25 30

Ala Leu Asp Tyr Arg Phe Phe Asn Glu Phe His Glu Thr Thr Phe Ser

35 40 45

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

Ile Pro Phe Arg Gln Thr Ala Asn Ala Glu Thr Leu Glu Leu Ser Val
65 70 75 80

Val Trp Gly Leu Phe Lys Lys Ala Tyr Glu Phe Gly Lys Tyr Gln Asn
85 90 95

Ala Arg His Trp Ile Tyr Glu Val Tyr Leu Asn Thr Glu Val Ile Leu
100 105 110

Pro Arg Gln Met Met Leu Gly Trp Ile Ala Lys Gln Arg Pro Glu Arg
115 120 125

Asn Ala Lys Ser Phe Ala Pro Ile Asn Asp Gly Asn Leu Tyr His Ala
130 135 140

Ser Glu Lys Phe Asp Ala Pro Lys Ser Val Ala
145 150 155

<210> 162
<211> 108
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 162
Met Leu Leu Val Glu Gly Leu Thr Glu Glu Asp Ile Cys Leu Asn Ser
1 5 10 15

Phe Tyr Asn Cys Lys Thr His Val Met Gln Ala Leu Asp Glu Glu Arg
20 25 30

Val Glu Leu Ser Lys Phe Met Val Asn Ile Ala Thr Ala Gln Val His
35 40 45

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

Asn Ala Ile Ala Glu Tyr Gly Lys Ala Arg Gly Glu Ala Leu Leu Ala
65 70 75 80

Ser Lys Lys Glu Phe Asp Lys Ser Glu Ser Met Leu Lys Met Ala Ile
85 90 95

Asp Ile His Met Glu Gly Ile Asp Gly Thr Ile His
100 105

<210> 163
<211> 95
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 163
Met Ala Lys Lys Arg Val Val Val Asn Phe Leu Glu Glu Asp Ser Gly
1   5   10   15

Asp Cys Glu Tyr Gly Cys Trp Asn Thr Gly Tyr Gly Val Glu Val Met
            20   25   30

Val Asp Gly Lys Cys Val His Arg Gln Glu Ala Trp Ala Ser Cys Thr
        35   40   45

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

Ile Lys Thr Lys Glu Gly Tyr Pro Val Lys Ala Asp His Ile Asp Phe
65   70   75   80

Gly Asp Pro Ser Asp Tyr Pro Glu Glu Phe Leu Asp Leu Phe Thr
                85   90   95

<210> 164
<211> 62
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 164
Met Lys Ser Ile Asp Asn Tyr Leu Arg Gly Glu Asn Pro Val Asp Gln
1   5   10   15

Ala Ala Val Thr Val Glu Lys Val Arg Lys Glu Cys Phe Ile Leu Thr
            20   25   30

Gln Arg Gly Gly Gly Asn Arg Pro Asn Arg Val Tyr Leu Asn Trp Thr
        35   40   45

Gln Ser Lys Asp Leu Tyr Glu Arg Leu Lys Arg Glu Phe Glu
    50   55   60

<210> 165
<211> 158
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 165
Val Glu Glu Leu Arg Gln Lys Ile Asn Gln Glu Leu Val Trp Glu Ala

1 5 10 15

Lys Ser Phe Pro Ile Asn Gln Phe Leu Lys Arg Asp Gly Ser Ile Asn
20 25 30

His Asn Lys Ile Lys Gln Leu Arg Pro Asp Phe Arg Gln Asp Ala Lys
35 40 45

Asn Leu Ile Phe Ile Asn Arg Ala Leu Asp Ala His Gly Val Phe Phe
50 55 60

Gly Tyr Glu Lys Leu Val Phe His Ser Leu Asn Gln Leu Val Glu Ile
65 70 75 80

Trp Cys Pro Asp His Gln Asp Tyr Phe Met Gln Thr Ala Arg Ser His
85 90 95

Leu Glu Gly Asn Gly Cys Gln Lys Cys Arg His Arg Met Val Thr Arg
100 105 110

Val Thr Asp Tyr Gly Ser Tyr Thr Val Pro Ala Tyr Tyr His Lys Phe
115 120 125

Ser Ile Asp Gly Asp Ser Ile Ile Trp Tyr Asn Asn Ser Ser Lys Leu
130 135 140

Ile Lys Pro Leu Glu Val Lys Asp Glu Ile Arg Phe Pro Glu
145 150 155

<210> 166
<211> 133
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 166
Met Lys Tyr Asp Ser Leu Asn Asn Pro Ser Thr Asn Tyr Leu Thr Asp
1 5 10 15

Gln Ser Val Ser Glu Ile Lys Phe His Pro Asn Tyr Ser Pro Asp Ser
20 25 30

Ser Lys Pro Ser Val Ala Ala Ile Ser Phe Arg Phe Arg Asn Leu Arg
35 40 45

Phe Thr Phe Val Gly Glu Glu Asp Lys Met Ile Ser Ile Ile Asp Lys
50 55 60

Val Lys Ala Val Ser Glu Leu Ser Gly Ser Asp Thr Val Lys Phe Glu
65 70 75 80

Ala Leu Thr Ser Leu Leu Leu Thr Ser Gly Ala Thr Val Gly Lys Phe
85 90 95

Glu Leu Ile Gln Pro His Val Ser Ala Leu Thr Asn Thr Arg Asn Phe
100 105 110

Trp Asp Gln Ala Asn Val Glu Ser Leu Ile Lys Trp Asp Ser Ala Thr
115 120 125

Glu Phe Tyr Asn Lys
130

<210> 167
<211> 169
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 167
Met Leu Phe Cys Thr Val Asp Phe Glu Glu Ala Asn Glu Thr Tyr Ile
1 5 10 15

Val Tyr Gly Met Ser Glu Ser Lys Val Arg Ile Leu Trp Asn Gln Phe
20 25 30

Gln Leu Glu Val Pro Asp Asp Ile Ser Lys Thr Pro Lys Asp Phe Phe
35 40 45

His Leu Ile Asp Ile Lys Ala Val Lys Ala Arg Lys Lys Leu Thr Pro
50 55 60

Tyr Val Phe Pro Gly Ala Val Phe Val His Glu Leu Thr Ala Tyr Thr
65 70 75 80

Asn Val Val Leu Lys Lys Ser Arg Gln His Pro Gly Tyr Leu Thr Met
85 90 95

Leu Thr Tyr Lys Val Gly Ala Ile His Asp Gly Glu Leu Val Val Arg
100 105 110

Val Asp Ala Arg Leu Gln Gln Glu Val Glu Glu Met Ile Arg Gln Cys
115 120 125

Gln Asn Lys Ala Glu Leu Lys Gln Arg Ala Arg Leu Phe Asp Met Ala
130 135 140

Ala Pro Ser Glu Ala Val Ala Ala Tyr His Gly Phe Tyr Lys Glu Ile
145 150 155 160

Ala Glu Ser Asp Glu Asp Phe Phe Met
165

<210> 168
<211> 106
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 168
Met Asn Glu Lys Tyr Glu Val Trp Thr Pro Val Gly Glu Asn Cys Ser
1 5 10 15

Tyr Leu Leu Arg Thr Leu Cys Thr Arg Glu Asp Gly Thr Ser Phe Ser
20 25 30

Glu Tyr Leu Ser Glu Cys His Ala Lys Ala Gln Gln Asp Asn Pro Leu
35 40 45

Phe Lys Ile Arg Gly Glu Asp Ile Leu Lys Val Asn Gly Val Pro Tyr
50 55 60

Thr Pro Val Asp Ser Phe Ala Ala Leu Gln Val Phe Lys Glu His Arg
65 70 75 80

Glu Arg Glu His Arg Arg Met Ile Glu Arg Leu Thr Gly Arg Glu Pro
85 90 95

Phe Ser His Pro Arg Trp Asn Glu Glu Thr
100 105

<210> 169
<211> 254
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 169
Met Ser Arg Val Glu Lys Leu Gln His Ile Tyr Asn Leu Val Lys Lys
1 5 10 15

Ala Asp Gln Lys Lys Leu Ser Glu Leu Ser Glu Glu Glu Tyr Gln Ala
20 25 30

Val Leu Phe Cys Cys Ser Ala Met Pro Ala Lys Leu Asp Gly Val Leu
35 40 45

Ala Lys Ser Asp Ile His Asn Gly Lys Glu Thr Thr Phe Gln Pro Pro
50 55 60

Tyr Lys Trp Leu Ala Ser Asn Ile Gln Gln Met Val Gly Lys Val Thr
65 70 75 80

Gly Phe Ser Asn Arg Lys Thr Pro Asn Ile Phe Ile Asp Ile Thr Pro

85 90 95

Arg Thr Pro Glu Phe Thr Lys Asp Trp Arg Asp Ala Leu Asp Ser Phe
100 105 110

Pro Ser Trp Lys Val Phe Tyr Lys Pro Asp Asp Glu Thr Tyr Ala His
115 120 125

Leu Pro Phe Leu Lys His Pro Gly Tyr Thr Val Glu Asp Pro Ser Ser
130 135 140

Gly Val Asn Phe Lys Asp Phe Lys Cys Thr Asp Glu Asn Ile Ala Tyr
145 150 155 160

Gly Leu Met Arg Thr Ser Val Arg Ile Ala Met Asp His Glu Leu Asp
165 170 175

Lys Gln Asp Leu Ala Val Ile Ala Leu Cys Lys Asp Arg Tyr Ile Lys
180 185 190

Val Lys Arg Ile Ala Glu Lys Leu Ser Val Leu Ser Cys Phe Glu Thr
195 200 205

Ile Arg Asp Cys Glu Pro Glu Gly Glu Tyr Pro Lys Gly Ser Leu Tyr
210 215 220

Trp Lys Asp Val Lys His Leu Gly Leu Ser Glu Glu Ala Val Phe Leu
225 230 235 240

Gly Leu Val Val Thr Gly Arg Phe Leu Arg Leu Gln Glu Lys
245 250

<210> 170
<211> 109
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 170
Val Gly Tyr Ser Arg Asp Pro Phe Tyr Arg Leu Asn Ser Leu Gln Leu
1 5 10 15

His Arg Leu Pro His Arg Gly Leu Gln Asp Ile Val Ile His Ser Val
20 25 30

Tyr Ile Ile Asp Asp Ala Ser Glu Phe Ser Ala Lys Leu Leu Glu Lys
35 40 45

Ala Ala His Lys Lys Phe Lys Pro Met Arg Val Asn Phe Gly Asp Lys
50 55 60

Phe Asp Gly His Thr Glu Trp Phe Asp Val Glu Pro His Val Ile Glu
65 70 75 80

Lys Phe Phe Leu Ser Val Gly Ala Lys Gln Val Pro Ile Asp Lys Leu
85 90 95

Ile Ala Gln Glu Gln Lys Ile Arg Lys Ser Thr Lys Lys
100 105

<210> 171
<211> 56
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 171
Met Arg Thr Leu Arg Gly Gly Ser Pro Lys Ser Arg Ser His Asn Thr
1 5 10 15

Tyr Gln Leu Asn Val Ile Arg Asp Gly Gln Lys Lys Gly Gly Asp Gly
20 25 30

Gly Gly Gly Glu Trp Gly Phe Arg Val Ile Met Val Ile Ile Met Thr
35 40 45

Leu Val Phe Leu Gln Ser Cys Gln
50 55

<210> 172
<211> 321
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 172
Met Leu Gln Lys Phe Thr Pro Val Ala Asn Leu Pro Met Val Arg Gly
1 5 10 15

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

Ile Leu Gly Val Tyr Arg Ser Asn Met Glu Ser Arg Thr Ser Arg Ala
35 40 45

Phe Glu His Ser Arg Asp Tyr Val Leu Ala Asn Pro Gly Ala Ala Ile
50 55 60

Val Ile Phe His Asp Asp Gln Tyr Leu Val Asp Ser Gln Pro Ile Asp
65 70 75 80

Leu Ile Val Ser Thr Thr Thr Asp Ala Tyr Leu Tyr Lys Ala Ser Glu
85 90 95

```
Gly Lys Gln Ala Ser Arg Arg Phe Cys Tyr His Glu Ser Glu Leu Leu
            100                 105                 110

Ala Phe Thr Asp Ala Arg Ala Trp Ile Lys Asn Leu Cys Asp His Leu
        115                 120                 125

Glu Leu Pro Pro Ala Arg Ile Ser Ser Glu Met Met Ile Phe Val Leu
    130                 135                 140

Asp Lys Asp Gly Ser Ile Leu Leu Pro Cys Asp Pro Tyr Asp Ile Asp
145                 150                 155                 160

Ile Glu Glu Gly Ala Arg Thr Gly Asn Tyr Arg Tyr Asp Gly Glu Leu
                165                 170                 175

Glu Glu Val Ala Pro Ala Val Thr Glu Asn Val Val Asn Pro Asn Asn
            180                 185                 190

Phe Glu Thr Gly Ala Leu Gln Met Asn Thr Ile Lys Ser Thr Ala Thr
        195                 200                 205

Ala Ile Val Ala Ala Asn Lys Asn Ala Ala Val Asn Ala Ala Lys Leu
    210                 215                 220

Glu Ala Gly Ser Ile Val Leu Lys Lys Val Ser Gly Ile Ala Ala Ser
225                 230                 235                 240

Lys Ala Pro Phe Met Val Arg Gly Tyr Val Asp Thr Ala Val Gly Arg
                245                 250                 255

Val Val Ile Ala Asn Leu Leu Asn Phe Ala Val Ser Gln Tyr Ala Pro
            260                 265                 270

Asn Asn Arg Lys Ala Val Ile Ala Ala Asp Ala Ala Met Gln Ala Ala
        275                 280                 285

Met Leu Glu Leu Val Gln Ser Phe Asn Val Gly Glu Met Ile Asp Glu
    290                 295                 300

Val Leu Lys Gly Val Asn Leu Ser Ser Leu Ile Glu Ser Asp Val Ala
305                 310                 315                 320

Glu
```

<210> 173
<211> 164
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F391/08

<400> 173
Met Glu Arg Leu Thr Ala Thr Phe Glu Gly Glu Lys Met Thr Ile Ala
1   5   10   15

Asn Val Trp Gln Arg Leu Arg Gln Asn Gly Asp Arg Gly Asn Phe Ala
            20   25   30

Ile Phe Ile Glu Pro Lys Asn Leu Asp Asn Leu Ala Arg Gln Ile Asp
        35   40   45

Arg Arg Asp Cys Tyr Pro Asp Thr Asp Asp Met Leu Gly Ile Pro Leu
    50   55   60

Arg Ile Ile Gly Val Tyr Gly Tyr Gly Phe Asp Ile Cys Ile Gly Asp
65   70   75   80

Ser Ser Phe Glu Ile Asp Cys Glu Ser Gly Ala Thr Glu Ile Glu Val
                85   90   95

Phe Leu Ile Asn Leu Gly Ser Leu Thr Phe Leu Asp Thr Pro Pro Ala
            100   105   110

Glu Pro Glu Pro Glu Lys Leu Glu Val Lys Thr Ser Val Ile Val Ser
        115   120   125

Ser Leu Thr Met Asp Glu Leu Ala Asp Ile Val Ser Thr Tyr Asp Glu
    130   135   140

Ile His Ala Asp Ala Ile Lys Glu Leu Asn Asn Arg Leu Asp Thr Phe
145   150   155   160

Arg Asp Lys Leu

<210> 174
<211> 175
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 174
Met Phe His Val Lys Ser Cys Val Pro Gly Ile Asn Tyr Thr Val Glu
1   5   10   15

Ala Glu Glu Gly Leu Tyr Leu Glu Gly Gly Arg Ile Glu Ser Gln Glu
            20   25   30

Val Ala Ala Val Leu Lys Cys Asp Thr Asn Val Cys Gly Thr Ser Trp
        35   40   45

Thr Asp Leu His Phe Leu Gly Arg Gly Ile Asp Val Asp Ser Leu Ser
50 55 60

Trp Glu Lys Ala Cys Glu His Ala Glu Ser Met Leu Asn Glu Asp Asp
65 70 75 80

Trp Asp Asp Asp Asp Ser Asp Glu Lys Tyr Ala Asn Ala Gly Val Glu
85 90 95

Gly Ser Phe Tyr Met Tyr Trp Pro Gly His Ser Cys Asn Leu Val Asn
100 105 110

Gly Gly Ser Pro Leu His Ser Val Leu Glu Arg Ala Ile Tyr Leu Gly
115 120 125

Tyr Ile Gln Ile Val Asp Gly Lys Ala Val Ile Asn Leu Arg Glu Leu
130 135 140

Lys Thr Phe Ile Tyr Ile Pro Asp Ala Glu Thr Ile Leu His Ile Glu
145 150 155 160

Glu Gly Leu Lys Ser Gly Trp Lys Val Ser Gly Val Val Tyr Leu
165 170 175

<210> 175
<211> 115
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 175
Met Ile Tyr Ile Tyr Val Asn Lys Tyr Phe Leu Ala His Tyr Lys Thr
1 5 10 15

Met Glu Ser Val Ile Gln Tyr Val Ser Arg Gln Asn Ala Arg His Ile
20 25 30

Asp Glu Val Ala Thr Leu Lys Ile Gly Leu Arg Gly Asp Ala Ile Asn
35 40 45

Ile Ser Trp Pro Leu Leu Ile Leu Ile Cys Arg Asp Leu Val Ala Gly
50 55 60

Lys Pro Val Ser Val Ser Ala Leu Gly Glu Ser Tyr Pro Leu Ser Asp
65 70 75 80

Asp Leu Asp Leu Tyr Asp Leu Leu Thr Lys Tyr Lys Thr Glu Arg Leu
85 90 95

Phe Tyr Arg Gly Gly Ser Val Cys Ser Ser Gly Glu Thr Ile Glu Thr
100 105 110

Val Phe Arg
        115

<210> 176
<211> 44
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F391/08

<400> 176
Met Leu Lys Glu Asn Val Met Ser Ser Glu Ile Val Asn Glu Phe Thr
1   5   10   15

Val Ala Asp Ala Glu His Phe Ile Glu Thr Tyr Leu Asn Val Tyr Asp
            20   25   30

Val Asp Leu Ala Phe Ile His Lys Asp Gly Gln Ile
        35   40

<210> 177
<211> 88
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 177
Asn Pro Glu Gln Gly Gln Ala Ala Ala Ala Glu Ser Thr Pro Ala Asp
1   5   10   15

Pro Ala Ala Asn Val Ser Arg Glu Thr Lys Pro Glu Asp Leu Ile Lys
            20   25   30

Asn Asp Val Ala Pro Ala Glu Leu Thr Pro Ala Phe Tyr Val Val Ala
        35   40   45

Glu Gly Arg Ala Ile Thr Ser Lys Arg Gly Ile Leu Ala Ala Gly Glu
    50   55   60

Ala Val Glu Ala Arg Asp Phe Val Gly Gly Glu Glu Thr Leu Asn Ser
65   70   75   80

Leu Leu Glu Arg Gly Leu Val Glu
                85

<210> 178
<211> 151
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 178

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

Asp Lys Asn Ser Gly Phe Gly Val Pro Val Val Leu Ile Ala Pro Asp
20 25 30

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

Ile Asp Pro Glu Thr Gly Val Leu Val Ala Gly Arg Val Ala Ser Val
50 55 60

Thr Phe Ala Asn Lys Ala Ile Arg Ala Ala Gly Phe Ala Glu Met Pro
65 70 75 80

Val Ala Val Ala Asp Ser Asn Lys Arg Pro Trp Val Val Cys Phe Arg
85 90 95

Asp Pro Glu Gly Ile Pro Tyr Leu Phe Lys Val Val Lys Ala Met Pro
100 105 110

Asp Arg Ala Ile Ser Gly Ile Val Leu Glu Leu Glu Val Tyr Lys Arg
115 120 125

Ser Ile Tyr Phe Asn Gly Ala Tyr Lys Phe Asp Gly Thr Thr Leu Tyr
130 135 140

Asp Gly Val Leu Asp Leu Leu
145 150

<210> 179
<211> 225
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 179
Met Asn Ile Glu Gly Phe Lys Lys Leu Gln Ser Pro Ile Asn Lys Leu
1 5 10 15

Asp Ser Phe Glu Ile Val Arg Asp Gln Ile Ala Ala Ile Leu Phe Leu
20 25 30

Glu Leu Glu Asn Gln Lys Ala Ile Ala Gly Arg Ala Gln Ile Asp Pro
35 40 45

Ala Arg Phe Asp Met Lys Val Tyr Lys Glu Arg Ser Asn Pro Trp Asp
50 55 60

Leu Phe Asp Asp Gly Glu Asn Lys Pro Ile Ile Asn Val Trp Phe Ser
65 70 75 80

```
Asn Ser Asp Phe Asp Tyr Thr Asn Ser Ser Thr Val Asp Lys Gln Lys
                85                  90                  95

Thr Thr Ala Ile Phe Asn Ile Asp Cys Ile Ala Thr Ala Ile Ser Gln
            100                 105                 110

Glu Thr Ala Thr Gly Gln Thr Leu Gly Asp Glu Met Ala Ser Leu Glu
        115                 120                 125

Val Gln Arg Val Ala Lys Val Ile Arg Asn Ile Leu Met Ser Asp Thr
    130                 135                 140

Asn Thr Tyr Leu Gln Leu Arg Gly Leu Val Trp Ser Arg Arg Val Leu
145                 150                 155                 160

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

Leu Cys Ala Ala Arg Leu Val Leu Gln Ala Thr Phe Ser Glu Phe Ser
            180                 185                 190

Pro Gln Tyr Glu Pro Gln Glu Leu Glu Ile Leu Ser Val Thr Val His
        195                 200                 205

Asn Cys Asp Gly Gln Ile Leu Phe Asn Lys Glu Ile Ala Lys Asn Gly
    210                 215                 220

Asn
225


<210> 180
<211> 500
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 180
Met Ala Ile Ser Thr Ala Val Asp Ile Ser Ala Val Ala Arg Val Leu
1               5                   10                  15

Gly Ile Lys Thr Asn Phe Lys Asn Leu Arg Asp Gly Arg Val Val Ile
            20                  25                  30

Leu Pro Gln Arg Ile Ala Leu Ile Gly Gln Gly Ser Thr Gly Met Val
        35                  40                  45

Phe Ala Thr Ser Lys Arg Gln Val Thr Ser Ala Asn Glu Val Gly Ser
    50                  55                  60

Leu Tyr Gly Tyr Gly Ser Pro Leu His Leu Ala Ala Lys Gln Leu Phe
65                  70                  75                  80
```

```
Pro Asn Asn Gly Asp Gly Val Gly Thr Ile Pro Val Thr Val Tyr Pro
                85                  90                  95

Leu Ser Asp Ala Asp Gly Ser Gln Ala Ala Thr Gly Ser Ile Glu Leu
            100                 105                 110

Leu Gly Thr Gln Leu Glu Ser Gly Ala Tyr Arg Val Val Val Asn Gly
        115                 120                 125

Ile Arg Ser Glu Gln Phe Ser Ile Leu Ile Asn Glu Ala Gly Gln Thr
    130                 135                 140

Val Leu Asn Arg Val Ala Ala Ala Ile Asn Ser Val Leu Asp Met Pro
145                 150                 155                 160

Val Arg Ala Thr Ala Asp Ser Glu Leu Gln Lys Val Thr Leu Val Ser
                165                 170                 175

Lys Trp Lys Gly Leu Ser Ala Asn Ala Ile Ser Val Gln Val Asp Gly
            180                 185                 190

Asp Leu Gly Gln Gly Ile Glu Phe Ala Val Thr Gln Pro Ala Gly Gly
        195                 200                 205

Leu Ile Asn Pro Ser Val Ser Gly Ala Leu Ser Gln Phe Gly Asn Val
    210                 215                 220

Trp Glu Thr Met Val Leu Asn Cys Leu Asn Ile Gln Asp Thr Glu Ala
225                 230                 235                 240

Leu Ser Ala Tyr Ser Asp Phe Gly Glu Gly Arg Trp Gly Ala Leu Val
                245                 250                 255

Arg Lys Pro Leu Ile Val Phe Thr Gly Asn Thr Glu Ala Asp Val Asn
            260                 265                 270

Ser Ala Val Ser Val Pro Asp Ala Arg Lys Arg Asp Arg Thr Asn Val
        275                 280                 285

Gln Leu Val Ala Pro Asp Ser Ile Asp Leu Pro Phe Val Val Ala Ser
    290                 295                 300

Arg Gln Leu Ala Arg Ile Val Lys Ile Ala Asn Glu Asn Pro Ala Cys
305                 310                 315                 320

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

Lys Gln Trp Leu Tyr Asn Val Arg Asp Met Ala Val Lys Lys Gly Ser
            340                 345                 350
```

```
Ser Thr Ile Glu Ile Arg Asp Asn Gln Val Phe Ile Gly Asp Val Val
        355                 360                 365

Thr Phe Tyr His Pro Glu Gly Glu Glu Asn Pro Pro Tyr Arg Tyr Val
    370                 375                 380

Cys Asp Ile Val Lys Leu Gln Asn Ile Ile Phe Asn Leu Asn Leu Ile
385                 390                 395                 400

Phe Ala Val Pro Glu Trp Asp Gly Ala Pro Leu Ile Pro Asn Asp Gln
                405                 410                 415

Pro Thr Thr Asn Pro Arg Ala Lys Lys Pro Ser Met Ala Val Ala Ala
            420                 425                 430

Ile Ala Ser Leu Val Asp Ser Leu Gly Leu Asn Ala Ile Ile Ser Asp
        435                 440                 445

Ala Ala Phe Thr Lys Lys Asn Thr Phe Ala Gln Ile Asn Glu Gln Asn
    450                 455                 460

Pro Lys Arg Leu Asp Val Ser Thr Thr Val Lys Leu Ser Gly Asn Thr
465                 470                 475                 480

Asn Ile Leu Ser Val Asp Leu Asn Phe Gly Phe Tyr Phe Gly Asn Ser
                485                 490                 495

Val Ile Val Gly
            500


<210> 181
<211> 125
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 181
Met Ser Val Gly Gly Ser Ile Glu Ser Leu Thr Leu Asp Gly Arg Thr
1               5                   10                  15

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

Asp Asn Glu Val Glu Met Asn Gly Asp Gly Thr Tyr Arg Ile Val Lys
        35                  40                  45

Thr Arg Val Pro Ser Lys Leu Asp Gly Ile Thr Val Ala Ile Asp Asp
    50                  55                  60

Val Arg Gly Asp Ala Glu Tyr Leu Gln Glu Leu Lys Asp Arg Lys Glu
```

65 70 75 80

Gly Phe Pro Tyr Ser Ile Thr Tyr Ala Ser Gly Val Ile Tyr Gln Gly
85 90 95

Thr Gly Thr Ile Val Gly Glu Thr Gly Ile Ser Ser Gln Asn Ala Thr
100 105 110

Ala Ser Ile Thr Ile Ser Gly Ser Ala Leu Thr Lys Gln
115 120 125

<210> 182
<211> 148
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 182
Val Glu His Ile Glu Asn Thr Glu Asn Gln Thr Leu Trp Gly Leu Pro
1 5 10 15

Val Lys Val Ala Arg Glu Val Ala Glu Ala Glu Phe Ile Arg Phe Cys
20 25 30

Asp Ala Met Asp Val Asp Tyr Asn Thr Asp Arg Met Thr Asp Glu Asp
35 40 45

Ala Lys Asp Phe Asn Glu Ser Lys Gly Leu Leu Leu Asp Ala Leu Gln
50 55 60

Ile Gly Val Leu Glu Ile Asp Ser Asp Gly Met Ala Val Val Tyr Pro
65 70 75 80

Lys Lys Gly Asp Ile Lys Gln Ile Lys Phe Asn Glu Leu Cys Gly Ala
85 90 95

Asp Tyr Val Ala Met Asp Asn Lys Lys Asp Thr Gln Ser Phe Ala Lys
100 105 110

Met Phe Ala Met Met Gly Ser Ile Thr Lys Leu Pro Pro Ala Thr Phe
115 120 125

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

Leu Phe Leu Val
145

<210> 183
<211> 497
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 183

```
Met Gln Ser Gly Ile Ser Arg Phe Thr Arg Arg Ala Glu Ser Gly Leu
1               5                  10                  15

Arg Arg Val Ser Asp Met Thr Trp Asn Ile Ser Lys Val Ser Gly Ala
            20                  25                  30

Ala Ala Ala Ala Ile Gly Gly Ala Phe Met Ala Ala Ala Gly Gly Ile
        35                  40                  45

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

Met Ser Lys Ala Met Gly Val Ser Ala Leu Ser Ala Arg Ala Ala Asp
65                  70                  75                  80

Ser Leu Leu Thr Pro Leu Gly Met Asn Trp Glu Asn Tyr Thr Asp Leu
                85                  90                  95

Ile Glu Glu Leu Gly Asn Lys Met Gly Glu Leu Lys Asn Thr Gly Glu
            100                 105                 110

Met Lys Thr Phe Gln Glu Ala Ile Gly Leu Thr Asn Ile Lys Met Lys
        115                 120                 125

Glu Leu Lys Ala Leu Lys Pro Glu Gln Gln Phe Thr Arg Ile Met Asp
    130                 135                 140

Ser Leu Ala Lys Met Glu Asp Gln Gln Lys Ala Gln Phe Ile Ala Asp
145                 150                 155                 160

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

Arg Gly Leu Thr Met Thr Ser Leu Ile Glu Asn Tyr Lys Lys Tyr Asn
            180                 185                 190

Phe Tyr Asn Glu Gln Gly Glu Lys Ala Thr Ala Ala Phe Asn Ala Ala
        195                 200                 205

Leu Thr Pro Leu Thr Thr Thr Ala Asn Ser Ala Lys Ser Gln Ile Ala
    210                 215                 220

Ala Leu Thr Gly Gly Ala Met Val Pro Tyr Ile Gln Lys Ala Thr Glu
225                 230                 235                 240

Trp Ala Ala Ala Asn Lys Glu Leu Ile Asn Ser Lys Ile Glu Val Phe
                245                 250                 255
```

```
Ala Lys Gly Leu Ala Asp Ser Leu Val Trp Val Val Val Asn Phe Ser
            260                 265                 270

Glu Ile Val Thr Trp Val Lys Arg Val Ala Ile Gly Ile Gly Ile Phe
        275                 280                 285

Leu Ala Leu Thr Ala Val Leu Lys Thr Phe Val Leu Ile Met Thr Ala
    290                 295                 300

Val Asn Leu Val Met Met Met Asn Pro Ile Gly Leu Ile Ile Ile Ala
305                 310                 315                 320

Val Val Ala Leu Ile Ala Val Ile Ala Tyr Leu Ile Asn Lys Phe Phe
                325                 330                 335

Gly Leu Gln Gly Val Ile Ala Ala Ala Asn Gly Val Leu Met Gly Ile
            340                 345                 350

Gly Ala Ala Ile Leu Val Ala Met Gly Pro Ile Gly Trp Leu Ile Gly
        355                 360                 365

Ala Ala Val Leu Ile Trp Lys Asn Trp Gly Val Leu Ser Gly Phe Phe
    370                 375                 380

Ser Gly Leu Trp Ala Gly Ile Val Ser Val Phe Gln Gly Ala Gln Asn
385                 390                 395                 400

Ile Ile Met Gly Ile Ile Asn Gly Ile Met Gly Ala Ile Asp Asn Val
                405                 410                 415

Ile Asn Lys Ala Val Ser Met Gly Ser Ala Val Lys Gly Phe Phe Ser
            420                 425                 430

Phe Gly Gly Gly Gly Gly Asp Gln Lys Gln Ala Ala Ala Ala Gly Gly
        435                 440                 445

Arg Val Ala Ser Pro Gln Glu Arg Thr Ala Lys Ser Val Thr Glu Asn
    450                 455                 460

Asn Ser His Ser Thr Val Thr Ile Gln Asp Lys Thr Gly Arg Ala Lys
465                 470                 475                 480

Met Ser Gly Lys Pro Gly Asn Gly Val Arg Leu Val Lys Thr Gly Thr
                485                 490                 495

Met
```

<210> 184
<211> 410
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 184
Met Ser Trp Glu Asp Arg Leu Lys Glu Ala Ala Tyr Thr Ala Pro Gly
1   5   10   15

Gly Thr Arg Ala Thr Phe Leu Val Glu Asp Val Ser Arg Ser Phe Asp
            20   25   30

Lys Lys Thr Asn Gly Phe Thr Phe Pro Asp Ala Ser Gly Thr Tyr Val
        35   40   45

Gln Asp Ser Gly Val Ser Gly Phe Lys Tyr Pro Leu Thr Ile Tyr Phe
    50   55   60

Ser Gly Pro Asp Cys Asp Val Glu Ala Glu Ala Phe Glu Ala Leu Leu
65   70   75   80

Arg Glu Thr Gly Ile Gly Arg Leu Glu His Pro Leu Tyr Gly Val Ile
                85   90   95

Asn Val Val Pro Phe Gly Thr Ile Thr Arg Thr Asp Ala Ile Lys Thr
            100   105   110

Glu Ala Asn Gln Thr Lys Ile Glu Leu Glu Phe Trp Glu Thr Asn Leu
        115   120   125

Leu Ile Tyr Pro Leu Pro Gln Ala Asp Gln Leu Ser Ala Val Phe Glu
    130   135   140

Ala Ile Ser Asp Val Lys Ala Ala Leu Ser Gly Asp Val Leu Asp Ser
145   150   155   160

Ile Asp Val Thr Asp Ala Ser Ala Leu Ala Arg Phe Lys Asn Lys Ile
                165   170   175

Thr Gly Ala Leu Ser Lys Val Lys Thr Ala Leu Gly Lys Ile Lys Asn
            180   185   190

Leu Ala Asp Leu Pro Gly Gln Leu Met Asp Lys Val Asn Gly Leu Ile
        195   200   205

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

Val Val Asn Ser Phe Phe Glu Leu Ala Thr Leu Pro Glu Gln Ile Val
225   230   235   240

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

```
Leu Thr Ser Phe Glu Gly Ile Phe Pro Ser Asn Glu Glu Tyr Glu Ala
            260                 265                 270

Ala Cys Thr Gly Val Thr Val Thr Leu Ser Gly Leu Val Val Asp Leu
        275                 280                 285

Val Glu Ser Glu Phe Asn Thr Gln Ser Glu Ala Leu Glu Ala Ala Glu
    290                 295                 300

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

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

His Ser Ala Val Met Thr Ala Ala Ser Tyr Leu Val Gln Gln Ser Phe
            340                 345                 350

Thr Leu Lys Lys Glu Arg Lys Leu Val Leu Asn Arg Ser Arg Thr Ile
        355                 360                 365

Ile Asp Leu Cys Ala Glu Leu Tyr Gly Glu Val Asp Ser Ala Leu Asp
    370                 375                 380

Phe Phe Ile Thr Ser Asn Asp Leu Ser Gly Ala Glu Ile Leu Glu Ile
385                 390                 395                 400

Pro Lys Gly Arg Glu Val Phe Tyr Tyr Val
                405                 410


<210> 185
<211> 398
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 185
Met Ser Asp Val Ser Met Met Ile His Gly Thr Arg Phe His Phe Trp
1               5                   10                  15

Ser Gly Val Arg Ile Ser Leu Asn Ile Asp Ala Val Ala Thr Ile Ser
            20                  25                  30

Phe Asn Ala Pro Phe Asp His Glu Ala Pro Gly Phe Lys Arg Asn Phe
        35                  40                  45

Ala Pro Phe Gly Phe Ser Pro Val Ala Ile Asp Val Asp Asp Gln Arg
    50                  55                  60

Leu Phe Thr Gly Thr Met Leu Asp Val Ser Pro Val Ile Ser Glu Asp
```

65 70 75 80

Gly Lys Lys Glu Ile Ser Val Asn Ala Tyr Ala Lys Cys Gly Val Leu
85 90 95

Gln Asp Cys Thr Ala Pro Pro Glu Ser Met Pro Leu Glu Phe Asn Lys
100 105 110

Leu Asn Leu Leu Asp Ile Ala Arg Lys Met Ala Ser Tyr Phe Gly Val
115 120 125

Gly Val Val Phe Asn Ala Asp Pro Gly Pro Ala Phe Asp Arg Val Ala
130 135 140

Cys Asp Pro Asp Lys Lys Val Leu Glu Phe Leu Ala Asp Leu Ala Lys
145 150 155 160

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

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

Ser Pro Leu Leu Ser Val Ser Pro Thr Phe Asn Pro Gln Glu Tyr Tyr
195 200 205

Ser His Ile Thr Gly Leu Ser Pro Val Glu Val Ala Lys Pro Ala Ala
210 215 220

Lys Ser Thr Ala Lys Val Lys Lys Asp Ala Ala Thr Pro Glu Lys Ala
225 230 235 240

Gly Gln Gly Ser Glu Lys Ala Thr Asp Lys Ala Gly Gln Ala Glu Ile
245 250 255

Lys Lys Glu Pro Lys Lys Glu Glu Lys Thr Lys Lys Glu Lys Gln Lys
260 265 270

Pro Lys Pro Thr Thr Tyr Lys Lys Phe Thr Ala Ile Asp Glu Ala Pro
275 280 285

Val Tyr Arg Pro Leu Val Phe Lys Ile Asp Asp Ala Glu Gly Ala Thr
290 295 300

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

Met Cys Thr Tyr Ala Ile Thr Val Ser Thr Trp Phe Asp Ala Ser Gly
325 330 335

Asp Leu Trp Arg Pro Asn Thr Lys Ile Lys Leu Lys Ala Pro Asp Ser

340 345 350

Met Ile Tyr Asp Phe Phe Glu Phe Asp Ile Lys Ser Val Glu Leu Ser
355 360 365

Ala Asp Glu Asn Ser Gln Gln Ala Asn Leu Thr Leu Cys Leu Pro Gly
370 375 380

Ser Phe Thr Gly Glu Pro Pro Glu Ile Phe Pro Trp Glu Leu
385 390 395

<210> 186
<211> 161
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 186
Val Gly Ile Val Ala Thr Val Leu Ser Asn Asp Gly Lys Asp Leu Lys
1 5 10 15

Val Asp Arg Gly Asn Gly Asp Asn Val Thr Ala Gln Gln Phe Gly Pro
20 25 30

Ser Gly Asp Asp Ala Pro Pro Leu Lys Asn Asp Tyr Ser Val Leu Gly
35 40 45

Ser Ala Lys Gly Ser Gly Asn Ala Ser Ala Val Ala Tyr Arg Asp Gln
50 55 60

Lys Ala Glu Asn Tyr Ile Ala Lys Ala Gly Glu Lys Arg Ile Tyr Ser
65 70 75 80

Arg Asp Glu Ser Gly Ala Val Lys Ala Glu Val Tyr Leu Lys Ala Asp
85 90 95

Gly Thr Ala Glu Ile Lys Asn Ala Ser Gly Leu Phe Val Met Glu Pro
100 105 110

Gly Gly Asp Val Val Ile Asn Gly Val Arg Ile Thr Lys Ala Gly Val
115 120 125

Ile Gln Thr Pro Gly Gly Ala Ser Met Ser Ser Asp Phe Thr Asn Ala
130 135 140

Gly Gly Ile Thr Leu Gly Asp His Ala Ala Asp Thr Ser Leu His Lys
145 150 155 160

Pro

<210> 187
<211> 245
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 187
Met Ser Phe Phe Asp Val His Leu Phe Asp Ser Val Asp Gly Gly Asn
1 5 10 15

Val Thr Asp Asp Leu Glu Thr Arg Asp Gly Leu Glu Thr Ala Val Tyr
20 25 30

Leu Ser Leu Phe Gly Gly Asn Ala Leu Asp Asp Gly Arg Pro Gln Asn
35 40 45

Leu Ser Thr Trp Trp Gly Asn Ile Gly Glu Asn Glu Ala Ala Lys Gln
50 55 60

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

Ala Asn Leu Lys Arg Ile Glu Ala Ala Ala Ser Arg Asp Leu Ala Trp
85 90 95

Leu Ile Pro Glu Tyr Val Asn Lys Ile Gln Val Lys Ala Phe Met Pro
100 105 110

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

Leu Gln Phe Arg Thr Asn Trp Gly Glu Lys Val Lys Glu Pro Val Tyr
130 135 140

Arg Leu Leu Pro Pro Lys Val Ser Arg Asn Asn Gly Val Asn Leu Glu
145 150 155 160

Gly Thr Ala Glu Thr Lys Thr Lys Leu Ile Leu Ile Arg Ala Asp Gly
165 170 175

Ser Arg Leu Ser Thr Leu Val Asp Gly Ser Gly Asn Trp Lys Phe Asp
180 185 190

Phe Tyr Pro Leu Tyr Gly Gly Glu Arg Ala Arg Met Tyr Val Glu Gly
195 200 205

Val Gly Gly Lys Ile Ser Ala Ile Val Thr Val Ile Gly Val Leu Pro
210 215 220

Leu Arg Tyr Asp Gly Met Ala Ile Tyr Asp Gly Thr His Lys Tyr Asn
225 230 235 240

Gly Val Arg Leu Asn
245

<210> 188
<211> 387
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 188
Met Ser Thr Pro Thr Thr Lys Glu Ile Ser Asn Arg Ile Leu Ser Lys
1 5 10 15

Leu Glu Thr Thr Phe Gly Gln Ser Leu Pro Lys Ser Phe Thr Arg Val
20 25 30

Leu Ser Thr Val Leu Gly Gly Val Phe Val Ile Leu Tyr Lys Tyr Gly
35 40 45

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

Thr Asp Phe Asn Gly Lys Thr Ile Asn Pro Leu Arg Glu Trp Gly Arg
65 70 75 80

Leu Ile Gly Ala Gly Asp Pro Asn Pro Ala Val Asn Ala Ile Ile Leu
85 90 95

Thr Arg Ile Val Val Glu Lys Pro Gly Glu Ile Leu Pro Ala Gly Thr
100 105 110

Gln Leu Val Asn Ser Gly Asn Gly Val Thr Tyr Ile Thr Gln Glu Asp
115 120 125

Ile Glu Leu Val Glu Gly Ala Gln Asp Ile Glu Val Leu Ala Ala Ser
130 135 140

Asp Thr Ser Gly Asn Ser Gly Ala Gly Lys Ala Gly Asn Leu Asn Ala
145 150 155 160

Gly Asp Val Leu Thr Phe Ala Asn Pro Leu Gly Ser Val Gly Arg Tyr
165 170 175

Ser Thr Val Val Thr Thr Ile Arg Glu Gly Leu Asp Ala Glu Ala Ile
180 185 190

Glu Thr Tyr Arg Ala Arg Val Val Ser Arg Phe Gln Leu Arg Ala Gln
195 200 205

Gly Gly Ala Met Val Asp Tyr Lys Ile Trp Gly Glu Ser Val Ser Gly
210 215 220

Val Ser Arg Ile Tyr Pro Tyr Thr Ser Asp Leu Pro Gly Gln Val Asp
225 230 235 240

Ile Tyr Val Asp Val Leu Glu Gly Val Ala Ser Gln Ala Ile Leu Asn
245 250 255

Gln Val Lys Asn Ala Val Glu Phe Asp Ala Asn Asn Gly Leu Ala Gln
260 265 270

Asn Arg Pro Leu Asn Ala Leu Val Asn Tyr Leu Pro Met Glu Phe Val
275 280 285

Glu Phe Asn Val Thr Ile Ser Gly Leu Ser Val Glu Gly Ala Leu Ser
290 295 300

Val Arg Ala Glu Ile Arg Ala Ala Leu Glu His Tyr Phe Asn Ile Arg
305 310 315 320

Ala Pro Tyr Ile Val Gly Leu Ser Thr Asp Ser Arg Ala Asp Arg Ile
325 330 335

Thr Leu Ala Ala Ala Ser Gly Val Val Asp Asp Val Val Asn Lys Ala
340 345 350

Gly Gly Ile Phe Asn Asp Met Gln Leu Phe Lys Gly Gln Thr Pro Ile
355 360 365

Ser Phe Tyr Met Leu Gly Ile Gly Glu Lys Ala Thr Leu Val Asn Val
370 375 380

Glu Tyr Leu
385

<210> 189
<211> 239
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 189
Met Asn Met Phe Lys His Leu Leu Pro Ser Gly Arg Ala Trp Asn Leu
1 5 10 15

Thr Ala Glu Lys Pro Leu Lys Ala Phe Phe Arg Cys Leu Asp Val Leu
20 25 30

Arg Thr Asp Ala Val Asn Tyr Phe Asn Leu Leu Phe Leu Asp Ile Asn
35 40 45

Pro Lys Thr Thr Arg Leu Leu Asp Gln Trp Glu Gln Gln Phe Gly Ile

50 55 60

Asn Arg Gly Phe Leu Thr Glu Ala Gln Arg Arg Glu Arg Val Ala Ala
65 70 75 80

Ala Trp Arg Asp Val Gly Gly Gln Ser Pro Ala Tyr Ile Gln Glu Val
85 90 95

Leu Arg Asn Asn Gly Phe Asp Val Tyr Ile His Glu Trp Phe Asp Pro
100 105 110

Ala Asp Arg Gly Glu Val Gly Glu Lys Gln Pro Ile Thr Pro Arg Asn
115 120 125

Pro Leu Ser Ile Met Ser Ala Gln Tyr Ala Glu Val Leu Pro Val Val
130 135 140

Asp Cys Gly Glu Pro Leu Ala Leu Cys Gly Glu Glu Phe Ala His Ala
145 150 155 160

Gly Asn Tyr Leu Gly Leu Val Gly Tyr Pro Leu Val Asn Lys Phe Val
165 170 175

Tyr Asp Ala Asp Lys Tyr Gly Tyr Thr Val Pro Val Asp Pro Ala Tyr
180 185 190

Trp Tyr His Phe Phe Tyr Val Cys Gly Pro Asn Phe Gly Asp Val Ala
195 200 205

Gln Val Glu Ala Thr Arg Arg Ala Glu Phe Glu Ala Leu Ile Leu Arg
210 215 220

Ile Lys Pro Ala His Leu Trp Ala Gly Val Ile Val Arg Tyr Val
225 230 235

<210> 190
<211> 200
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 190
Met Ser Leu Val Phe Asn Glu Lys Phe Pro Gly Lys Thr Ala Gly Ala
1 5 10 15

Thr Gln Asn Tyr Pro Tyr Gly Glu Ala Arg Asn Val Ser Gly Pro Gly
20 25 30

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

```
Gly Leu Leu Gln Gly Leu Leu Val Arg Ala Asn Ile Gln Pro Asn Gly
    50                  55                  60

Gln Ser Asp Thr Ala Leu Asn Ser Gln Tyr Leu Gln Ala Leu Leu Ala
65                  70                  75                  80

Leu Phe Met Pro Lys Gln Thr Pro Ile Ser Gly Lys Leu Glu Gln Asn
                85                  90                  95

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

Glu Arg Glu Phe Thr Ile Gln Trp Gly Ser Lys Asp Trp Ser Ser Tyr
        115                 120                 125

Pro Gly Glu Ile Gln Asp Ser Ile Val Phe Glu Lys Pro Phe Lys Thr
    130                 135                 140

Ala Cys Phe Gly Val Phe Pro Ile Arg Lys Met Ser Gln His Ser Ala
145                 150                 155                 160

Tyr Gly Asp Gly Gly Val Lys Pro Ile Ser Val Ser Lys Thr Gly Phe
                165                 170                 175

Thr Val Ser Leu Gln Ala Tyr Gly Gly Ser Val Gly His Leu Leu Gly
            180                 185                 190

Tyr Tyr Trp Phe Ala Val Gly Val
        195                 200


<210> 191
<211> 128
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 191
Met Glu Pro Ile Ser Thr Gly Gly Thr Ala Ala Phe Leu Lys Val Tyr
1               5                   10                  15

Gly Val Trp Leu Ala Val Val Thr Ala Leu Val Phe Val Ala Thr Val
            20                  25                  30

Val Leu Met Met Arg Leu Pro Arg Ser Pro Gln Glu Phe Leu Val Gly
        35                  40                  45

Ile Ile Thr Thr Val Val Ser Ser Leu Met Gly Gly Ser Phe Leu Ile
    50                  55                  60

Leu Tyr Phe Asp Leu Gln Ile Trp Ala Asn Ser Ala Tyr Gly Leu Met
65                  70                  75                  80
```

Val Ile Gly Gly Leu Tyr Phe Val Ala Gly Ile Pro Gly Trp Ala Leu
85 90 95

Val Arg Trp Val Phe Asn Phe Ile Asp Ala Arg Glu Gly Ser Thr Leu
100 105 110

Leu Asp Ile Phe Arg Glu Phe Asn Glu Glu Phe Arg Gly Gly Lys Lys
115 120 125

<210> 192
<211> 182
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 192
Met Ser Lys Ile Ile Ala Ile Cys Ala Gly His Ser Asp Lys Asp Pro
1 5 10 15

Gly Ala Val Asn Gly Lys Arg Thr Glu Ala Ala Ile Val Leu Asp Met
20 25 30

Arg Lys Met Val Ala Ser Tyr Leu Glu Lys Ala Gly Val Lys Tyr Leu
35 40 45

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

Val Ala Lys Gln Ala Ser Ile Ala Val Glu Phe His Cys Asn Ala Ala
65 70 75 80

Thr Ser Lys Lys Ala Thr Gly Val Glu Val Leu Ser Ala Glu Lys Asn
85 90 95

Lys Ala Leu Ala Lys Gln Ile Ala Ala Lys Ile Asn Gly Val Leu Asn
100 105 110

Ile Pro Leu Arg Gly Glu Ser Gly Trp Lys Ser Glu Gly Ser Gly Gln
115 120 125

His Ser Arg Leu Gly Phe Ile Ser Ser Gly Gly Gly Leu Ile Val Glu
130 135 140

Leu Phe Phe Ile Ser Asn Asp Asp Asp Leu Ala Lys Trp Asp Ala Lys
145 150 155 160

Lys Trp Leu Val Ala Lys Glu Val Ala Ala Val Leu Ile Glu Gln Val
165 170 175

Lys Lys Ala Glu Ala Ala
180

<210> 193
<211> 85
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 193
Met Ala Ala Leu Thr Ile Phe Asn Ala Ile Ser Glu Val Thr Ser Phe
1 5 10 15

Ala Gly Val Ala Arg Glu Ile Phe Asp Thr Ala Ala Asn Ala Met Asp
20 25 30

Ala Ala Gln Asn Glu Lys Lys Gly Gly Gly Asn Lys Lys Val Trp Val
35 40 45

Met Ala Tyr Met Glu Ser Phe Ile Asn Asp Leu Gly Glu Asn Trp Glu
50 55 60

Arg Trp Ala Lys Ala Ile Phe Ser Phe Ile Asp Phe Ala Lys Ser Ile
65 70 75 80

Phe Asn Ser Lys Arg
85

<210> 194
<211> 79
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 194
Met Arg Asn Thr Ala Asp Lys Ser Thr Ile Asp Phe Ile Glu Glu Thr
1 5 10 15

Thr Gly Asp Ala Tyr Lys Pro Val Lys Gly Cys Gly Thr Val Arg Gly
20 25 30

Tyr Lys Ala Gly Cys Ala Cys Asn Asn Cys His Lys Ala Gln Ile Gly
35 40 45

Arg Met Ala Asp Lys Ile Val Lys Ala Ala Leu Arg Thr Arg Ile Lys
50 55 60

Ser Ser Glu Pro Thr His Gln Pro Lys Glu Gln Ala Trp Asn Phe
65 70 75

<210> 195
<211> 138
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 195
Met Thr Lys Thr Glu Leu Lys Thr Ala Ile Ile Glu Phe Ser Ala Leu
1   5   10   15

Thr Thr Leu Gln Val Ala Gly Gln Phe Ser Ile Glu Glu Leu Thr Gly
            20   25   30

Leu Lys Thr His Leu Asn Gly Gln Arg Glu Ala Leu Leu Met Asp Lys
        35   40   45

Ala Pro Ala His Ile Lys Gly Glu Lys Glu Ala Lys Ile Asn Ala Gln
    50   55   60

Leu Ser Asp Val Asn Asn Leu Ile Lys Lys Ala Asn Lys Ala Ile Gly
65   70   75   80

Leu Ile Gln Val Asn Gln Ala Glu Leu Lys Gln Ser Lys Val Lys Gln
                85   90   95

Asp Thr His Phe Leu Ser Thr Phe His Asp Val Ala Gln Ser Tyr Leu
            100   105   110

Thr Asn Glu Leu Tyr Ala Asp Leu Lys Gln Lys Ala Leu Asn Val Met
        115   120   125

Arg Ile Ala Lys Ala Asn Gly Lys Asn Asp
    130   135

<210> 196
<211> 75
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 196
Met Ser Glu Thr Thr Asn Leu Phe Asn Pro Asp Ala Leu Asp Ala Asn
1   5   10   15

Phe Phe Tyr Glu Asn Ser Gly Gln Ala Leu Ala Ala Ala Leu Asp Pro
            20   25   30

Ile Glu Lys Cys Val Leu Glu Lys Ala Leu Lys Tyr Ser Lys Tyr Asn
        35   40   45

Ile Ala Glu Val Ser Arg Ile Leu Gly Ile Asn Arg Leu Thr Val Ile
    50   55   60

Lys Lys Met Lys Lys His Gly Leu Thr Glu Ile
65   70   75

<210> 197
<211> 76
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 197
Met Lys Gln Pro Val Ile Gln Arg Gln Gln Leu Ser Asn Phe Ser Gln
1 5 10 15

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

Phe Phe Cys Phe Met Leu Ala Ala Leu Ser Tyr Met Phe Ile Ile Lys
35 40 45

Gln Ala Asp Glu Ile Asp Lys Gln Ala Glu Phe Val Ala Glu Tyr Asn
50 55 60

Ala Gln Phe Lys Glu Tyr Pro Asn Glu Arg Asn His
65 70 75

<210> 198
<211> 323
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 198
Val Lys Lys Phe Asn Thr Lys Phe Lys Gln Asn Leu Asp Asp Ala Asn
1 5 10 15

Asn Asn Ala Phe Ile Pro Asn Ser Phe Gln Ile Thr Asn Ala Phe Val
20 25 30

Asp Asn Ile Met Asp Lys Ile Ser Asp Ala Ala Val Lys Ile Tyr Leu
35 40 45

Ile Thr Val Arg Lys Thr Thr Gly Trp Gly Lys Gln Ile Asp Ser Ile
50 55 60

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

Val Lys Cys Leu Lys Glu Leu Val Lys Val Gly Leu Leu Val Glu His
85 90 95

Thr Gly Thr Arg Tyr Gly Asn Ser Tyr Ser Val Ala Leu Val Asn Ser
100 105 110

```
Ile Gly Phe Glu Leu Leu Ser Ala Ser Lys Lys Ile Leu Leu Val Lys
        115                 120                 125

Ser Phe Asn Tyr Thr Ser Lys Lys Ser Leu Leu Pro Leu Val Lys Ile
    130                 135                 140

Phe Asn Thr Gln Lys Gln Leu Ser Lys Asn Thr Asn Gln Lys Gln Ile
145                 150                 155                 160

Asn Lys Arg Asp Trp Phe Ser Leu Lys Thr Leu Lys Asp Glu Leu Phe
                165                 170                 175

Lys Thr Gly Leu Gln Ile Glu Ala Glu Asp Leu Thr Ala Ala Lys Trp
            180                 185                 190

Phe Asp Arg Glu Lys Thr Ala Phe Glu Asn Tyr Ala Pro Asn Gln Asn
        195                 200                 205

Leu Ser Asp Pro Gln Lys Met Tyr Tyr Phe Val Asp Trp Leu Leu Lys
    210                 215                 220

Ala Lys Arg Lys Tyr Asp Ala Ala Glu Arg Gln Gln Ala Ala Lys Ala
225                 230                 235                 240

Lys Ala Glu Gly Lys Asn Gln Asn Gln Asn Pro Glu Asp Thr Lys Thr
                245                 250                 255

Glu Asn Asp Pro Phe Lys Leu Ser Thr Lys Gln Ile Ser Phe Phe Ala
            260                 265                 270

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

Lys Gly Phe Lys Glu Phe Glu Met Trp Ile Ala Ser Met Leu Asn Asn
    290                 295                 300

Pro Glu Asn Val Lys Lys Trp Asn Lys Tyr Leu Asn Glu Leu Gly Tyr
305                 310                 315                 320

Leu Ile Gly
```

<210> 199
<211> 76
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 199

```
Met Lys Ile Ser Asn Phe His Phe Gln Met Gln Ile Leu Leu Leu Ile
1               5                   10                  15
```

Ser Lys Asn Thr Val Leu Asp Phe Glu Gly Leu Lys Glu Lys Leu Ala
            20   25   30

Pro Ser Ile Thr Asp Asn Ala Leu Thr Glu Cys Leu Glu Glu Leu Leu
        35   40   45

Met Trp Gly Trp Val Gln Val Gln Lys Gly Leu Tyr Met Val Ser Gly
    50   55   60

Val Ala Tyr Gln Ile Met Gly Asp Ile Cys Gln Cys
65   70   75

<210> 200
<211> 74
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 200
Met Glu Lys Tyr Lys Tyr Ser Glu Ser Asn Ala Val Leu Ser Pro His
1   5   10   15

Leu Asn Cys Gly Leu Thr Ser Val Ser Arg Val Gly Ser Ser Gly Gln
            20   25   30

Ala Lys His Lys Pro His Lys Arg Ser Glu Ile Ala Asp Gln Ala Glu
        35   40   45

Lys Glu Ile Cys Lys Asn Trp Ala Leu Arg Gln Gln Ala Phe Leu Asn
    50   55   60

Asn Ser Val Ser Asn Ala Val Leu Gly Gly
65   70

<210> 201
<211> 173
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 201
Met Asn Lys Phe Ile His Ile Glu Gly Lys Pro Thr Ala Gln Gln Val
1   5   10   15

Arg Glu Ala Leu Ala Met Tyr Ala Lys Asp Ile Lys Arg Pro Glu Phe
            20   25   30

Ser Leu Ile Val Gln Arg Glu Leu Ile Glu Ser Phe Arg Asn Asp Thr
        35   40   45

Ala His Ala Leu Lys Ser Ala Val Ala Phe Tyr Phe Lys Asn Arg Val

50 55 60

Ile Gln Arg Pro Gly Leu Val Leu Ala Ser Gly Lys Asp Gln Ala Leu
65 70 75 80

Ile Val Glu Ser Cys Glu Asn Lys Ala Leu Lys Arg His Leu Val Ala
85 90 95

Val Ser Gly Tyr Ser Ser Gln Phe Leu Gln Met Val Ile Asp His Lys
100 105 110

Thr Pro Leu Ser Ala Val Ala Ala Arg Asp Leu Lys Gln Ala Leu Pro
115 120 125

Lys Ala Glu Lys Leu Tyr Lys Ala Glu Cys Lys Glu Lys Asp Ala Lys
130 135 140

Leu Lys Lys Asn Ile Cys Gly Phe Val Ala Cys Tyr Arg Asn Gly Cys
145 150 155 160

His Cys Thr Lys Cys Thr Thr Ala Tyr Lys Lys Tyr Arg
165 170

<210> 202
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 202
Met Gly Val Ser Ile Ile Asn Leu Val Leu Leu Val Gly Val Cys Leu
1 5 10 15

Leu Leu Thr Asn Ile Ala Leu Asn Cys Leu Phe His Thr Glu Asn Lys
20 25 30

Thr Tyr Leu Val Tyr Ala Cys Gly Phe Ser Ala Ala Ser Val Ala Gly
35 40 45

Ala Ile Ala Gly Val Ile Gly Cys Leu Ala Tyr Gly Val Thr Val
50 55 60

<210> 203
<211> 91
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 203
Met Lys Asn Lys Ser Ile Leu Met Gly Leu Phe Val Ala Ala Ala Gly
1 5 10 15

Val Val Phe Tyr Met Gly Ala Asp Ser Ala Cys Asn Gln Lys Ala Val
20 25 30

Ile Asp Pro Gly Ala Leu Met Ser Leu Gly Gly Ile Thr Val Glu Asn
35 40 45

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

Leu Val Ser Phe Val Leu Ile Lys Asp Gly Leu Arg Val Gly Gly Val
65 70 75 80

Val Asp Lys Ser His Val Ala Leu Ile Gly Glu
85 90

<210> 204
<211> 55
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 204
Met Ser Leu Gly Lys Arg Pro Ala Gly Ala Thr His Ile Glu Ser Asp
1 5 10 15

Gly Thr Tyr Trp Lys Asn Glu Asp Ala Asp Trp Tyr Phe Trp Arg Asp
20 25 30

Leu Trp Gly Trp Cys Gln Tyr Val Gly Pro Lys Asn Arg Asn Phe Leu
35 40 45

Asn Lys Phe Ser Val Leu Gly
50 55

<210> 205
<211> 61
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 205
Met Asp Leu Tyr Ile Gly Gln Ile Val Gly His Ser Ser Pro Thr Trp
1 5 10 15

Val Val Gln Gly Lys Leu Lys Ile Thr Lys Ile Asn Glu Gly Lys Arg
20 25 30

Ser Gly Leu Lys Ile Ile Thr Ala Thr Asp Glu Ser Gly Lys Glu Phe
35 40 45

Thr Ala Val Tyr Gly Val Phe Phe Ser Val Asp Arg Tyr

50 55 60

<210> 206
<211> 135
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 206
Val Arg Asn Glu Asn Phe Glu Asp Tyr Leu Lys Gln Thr Asp Asp Tyr
1 5 10 15

Ala Val Leu Leu Asn Asn Tyr Gly Ser Ser Leu Phe Ile His Glu Asn
20 25 30

Gly Val Tyr Arg Ala Leu Pro Val Arg Val Ala Tyr Ala Ala Trp Val
35 40 45

Ser Gly Gly Asp Arg Trp Gly Glu Val Gln His Leu Lys Gly Lys Ile
50 55 60

Lys Lys Met Ala Glu Arg Ala Ala Glu Thr Ala Asp Phe Tyr His Thr
65 70 75 80

Lys Ile Glu Lys Leu Glu Ser Ser Thr Val Lys Lys Ala Gly Leu Leu
85 90 95

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

Glu Leu Asn Arg Val Gln Glu Ser Ile Tyr Lys Arg Cys Ala Tyr Leu
115 120 125

Leu Arg Val Ala Val Asn Gly
130 135

<210> 207
<211> 166
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 207
Met Gly Asn Arg Trp Thr Leu Ser Gly Lys Val Lys Gly Leu Lys Asp
1 5 10 15

Leu Pro Glu Ser Ile Thr Ala Ala Gln Phe Arg Glu Met Ile Glu Arg
20 25 30

Gly Gln Val Lys Asn Thr Pro Gln Ala Pro Lys Lys Arg Arg Ser Gly
35 40 45

Lys Val Ser Ser Pro Gly Glu Ala Thr Leu Ala Gln Ala Leu Lys Ala
50 55 60

Leu Lys Ile Glu Phe Val Gln Glu Tyr Arg Phe Cys Glu Tyr Arg Lys
65 70 75 80

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

Glu Gly Gly Val Arg Ser Gly Gly Arg His Val Arg Pro Gln Gly Tyr
100 105 110

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

Val Leu Arg Phe Asp Thr Glu Thr Val Ser Arg Gly Thr Ala Ile Asn
130 135 140

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

Leu Thr Cys Glu Glu Ser
165

<210> 208
<211> 90
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 208
Val Lys Lys Val Lys Lys Phe Lys Tyr Asp Trp Arg Ala Val Pro Asp
1 5 10 15

His Ile Asn Trp Leu Ala Thr Tyr Glu Gly Gly Glu Met Ala Trp Gly
20 25 30

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

Thr Gly Gly Glu Trp Arg His Arg Val Pro Val Ala Pro Tyr Arg Gly
50 55 60

His Trp Thr Gln Ser Leu Glu Lys Arg Pro Ser Lys Ala Gln Leu Val
65 70 75 80

Glu Trp Val Leu Asn Gly Ala Val Val Val
85 90

<210> 209
<211> 685

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 209
Met Ala Glu Asn Ser Phe Ile Gln Pro Ile Ala Arg Lys Asp Ala Ile
1 5 10 15

Ala Leu Ile Gly Arg Asp Glu Leu Val Glu Gly Gly Pro Glu Gly Ala
20 25 30

Ala Asn Lys Gln Ala Ile Ala Leu Ala Asn Asn Ile Lys Tyr Leu Met
35 40 45

Gly Leu Ile Pro Glu Asn Trp Gly Val Glu Lys Thr Glu Tyr Gly Leu
50 55 60

Asp Glu Val Val Arg Leu Ser Asn Gly Asp Val Val Lys Ser Val Ile
65 70 75 80

Asp Glu Asn Ile Asn Asn Pro Asn Glu Asn Leu Ser Gly Trp Ser Phe
85 90 95

Val Thr Ser Asn Ser Val Asn Thr Ile Ser Asp Leu Leu Ser Ile Lys
100 105 110

Asn Pro Lys Asn Gly Met Lys Val Tyr Val Leu Gly Tyr His Lys Pro
115 120 125

Asp Asn Phe Ala Leu Leu Ser Pro Tyr Glu Gly Gly Gly Leu Phe Ile
130 135 140

Tyr Ser Gly Asn Lys Ala Ala Glu Asn Asp Gly Gly Val Val Leu Asn
145 150 155 160

Gly Trp Ile Arg Gln Tyr Val Gly Asp Val Asp Ile Ser Trp Phe Gly
165 170 175

Ala Lys Gln Gly Gln Asp Ala Ser Pro Phe Ile Glu Ala Ala Leu Lys
180 185 190

Val Lys Met Ser Ile Val Ile Arg Gly Glu Tyr Lys Leu Glu Thr Ile
195 200 205

Cys Gly Ile Pro Arg Gln Asn Asn Tyr Ala Ala Lys Val Ile Arg Ile
210 215 220

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

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

245 250 255

Ile Phe Thr Ala Lys Ile Asp Val Phe Gly Ile Asn Phe Val Gly Thr
260 265 270

Thr Val Ala Asn Ser Val Leu Phe Asn Gly Asp Arg Leu Tyr Asn Ile
275 280 285

Asn Ile His His Asn Asn Phe Lys Thr Asn Ile Thr Ile Val Lys Ala
290 295 300

Tyr Leu Lys Arg Glu Ala Ser Arg Gln Tyr Thr Gln Ser Val Ser Ile
305 310 315 320

Asn His Asn His Leu Ala Glu Ile His Arg Val Ile Glu Ser Asp Lys
325 330 335

Ser Tyr Asn Phe Asp Phe Ala Tyr Asn Met Cys Glu Ala Cys Lys Gly
340 345 350

Gly Met Tyr Ile Gly Val Asp Ala Pro Tyr Asp Pro Ser Gly Ile Ser
355 360 365

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

Thr Asn Gly Gly Ile Ile Ala Gly Ser Val Ser Lys Asn Tyr Phe Glu
385 390 395 400

Ala Asn Val Tyr Gln Asp Ala Ala Ile Asp Lys Cys Leu Ile Tyr Ile
405 410 415

Asn Arg Ser Gly Thr Gly Ala Gly Tyr Ser Gly Gly Leu Thr Phe Glu
420 425 430

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

Arg Val Leu Gly Gln Ser Thr Glu Thr Ser Gly Asn Ser Lys Ser Ala
450 455 460

Thr Thr Arg Pro Pro Val Phe Ile Gly Asn Trp Ser Asn Ser Tyr Met
465 470 475 480

Leu Thr Asn Met Ala Gln Ala Ile Leu Ile Gly Asn Lys Cys Ser Asn
485 490 495

Arg Glu Lys Met Leu Asn Ala Tyr Ser Pro Gln Glu Ala Arg Val Thr
500 505 510

Tyr Tyr Ser Gly Tyr Phe Thr Lys Gln Leu Ala Asn Ile Leu Thr Asp

515 520 525

Lys Lys Leu Asn Leu Leu Lys Val Asn Thr Ser Ala Val His Ala Ile
530 535 540

Gly Ser Ser Gln Ala Asn Phe Lys Thr Thr Leu Asp Val Ile Val Phe
545 550 555 560

Phe Lys Thr Ser Gly Ala Val Gly Thr Ala Met Ala Thr Phe Lys Leu
565 570 575

Asp Leu Phe Val Tyr Glu Ser Val Gly Leu Gly Ala Gly Asn Val Pro
580 585 590

Lys Ala Asn Leu Lys Ala Val Met Tyr Asn Phe Met Gln Ser Thr Ala
595 600 605

Asp Asp Lys Ile Thr Pro Thr Val Asn Met Phe Ser Ala Ile Ser Asp
610 615 620

Pro Leu Ile Asn Val Val Asp Asn Ser Asp Gly Thr Tyr Ser Ile Glu
625 630 635 640

Leu Ser Ser Phe Thr Asn Lys Ser Ser Pro Asn Trp Gly Phe Val Ser
645 650 655

Glu Leu His Ile Glu Tyr Thr Ala Gln Ala Thr Leu Ile Ala Ser His
660 665 670

Thr Ser Ser Tyr Ser Ala Ala Asn Leu Leu Thr Ile Ser
675 680 685

<210> 210
<211> 226
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 210
Met Phe Asp Ile Asp Thr Lys Gln Leu His Gly Leu Glu Arg Arg Leu
1 5 10 15

Glu Arg Leu Asn Arg Arg Gly Leu Pro Tyr Ala Thr Arg Gln Thr Met
20 25 30

Asn Asp Leu Ala Phe Glu Ser Arg Ala Val Ala Arg Ala Glu Leu Pro
35 40 45

Thr Arg Met Val Leu Arg Asn Lys His Ala Ile Asn Ser Ile Gln Val
50 55 60

```
Thr Lys Ala Thr Ser Leu Asn Ile Ser Gln Gln Ala Ala His Val Gly
65                  70                  75                  80

Ser Thr Ala Asp Tyr Met Ala Thr Gln Glu Thr Gly Gly Ile Lys Thr
                85                  90                  95

Lys Gln Gly Gly Ala Ala Val Ser Ile Pro Thr Thr Thr Ala Ala Gly
            100                 105                 110

Gln Gly Arg Asn Ala Lys Pro Arg Thr Arg Leu Pro Arg Ala Ala Leu
        115                 120                 125

Lys Met Gly Ala Ile His Leu Lys Arg Ile Ala Ala Ser Arg Asn Ala
    130                 135                 140

Lys Asn Arg Lys Gln Arg Asn Ala Ile Ala Met Ala Thr Ser Asp Lys
145                 150                 155                 160

Tyr Val Phe Leu Asp Leu Gly Arg Arg Lys Gly Ile Phe Arg Lys Asp
                165                 170                 175

Lys Gly Gly Gly Val Thr Met Leu His Asp Leu Thr Arg Ala Ser Val
            180                 185                 190

Gln Ile Pro Lys Asn Glu Trp Leu Lys Pro Ala Thr Glu Ala Ala Glu
        195                 200                 205

Arg Lys Leu Pro Gly Phe Tyr Gly Arg Ala Leu Glu Phe Gln Leu Arg
    210                 215                 220

Arg Phe
225


<210> 211
<211> 283
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 211
Met Val Lys Lys Leu Ile Ser Arg Ser Asp Phe Ala Ala Lys Ala Gly
1               5                   10                  15

Val Ser Gly Ala Ala Ile Ser Lys Ala Cys Lys Gly Pro Leu Leu Asp
            20                  25                  30

Ala Val Glu Gly Lys Phe Ile Asp Leu Asn His Lys Ser Ala Ile Ala
        35                  40                  45

Tyr Leu Glu Ser Lys Lys Asn Gly Lys Thr Thr Pro Ala Leu Glu Gly
    50                  55                  60
```

Ile Asp Ser Leu Tyr Glu Glu Ala Leu Glu Val Cys Arg Glu Ala Gly
65 70 75 80

Arg Cys Ser Gln Thr Leu Leu Arg Asp Lys Leu Met Ile Gly Ser Asp
85 90 95

Arg Ala Arg Lys Leu Val Ala Leu Ile Gln Asn Ala Asn Ile Gln Asp
100 105 110

Phe Glu Lys Pro Ala Ala Glu Lys Val Lys Arg Glu Glu Lys Ala Arg
115 120 125

Pro His Thr Arg Gly Thr Ala Ala Lys Lys Gln Gln Ala Ile Gln Glu
130 135 140

Asp Asp Glu Glu Leu Phe Glu Leu Leu Asp Arg Asn Val Ala Gln Tyr
145 150 155 160

Ala Asp Met Thr Leu Arg Asp Ile Val Arg Lys Phe Gly Thr Ala Thr
165 170 175

Arg Phe Ala Glu Tyr Leu Arg Ala Met Lys Glu Ile Ser Met Ile Glu
180 185 190

Asp Arg Glu Ile Lys Ile Ala Gln Thr Lys Gly Glu Leu Val His Arg
195 200 205

Asp Leu Val Ser Gln Leu Ile Ile Glu Pro Ile Asp Ser Ala His Val
210 215 220

Lys Leu Met Arg Asp Gly Ser Lys Thr Ile Ala Val Arg Met Ala Ala
225 230 235 240

Met His Gly Ser Gly Ala Asp Ile Asn Glu Met Gln Leu Val Thr Ser
245 250 255

Glu Leu Ile Ala Ser Phe Ile Lys Pro Val Lys Ala Lys Val Asn Lys
260 265 270

Ile Ala Thr Glu Leu Lys Arg Gly Ala Glu Ala
275 280

<210> 212
<211> 659
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 212
Met Asn Phe Ile Gly Met Asp Trp Leu Cys Asp Lys Val Glu Asn Leu
1 5 10 15

```
Thr Glu Tyr Ile Lys His Val Thr Pro Ser Gln Phe Asn Glu Glu Asn
            20                  25                  30

Arg Tyr Leu Pro Glu Ser Val Thr Ser Ile Pro Gly Phe Ile Arg Tyr
        35                  40                  45

Asp Val Asn Pro Phe Met Arg Glu Ile Val Asp Cys Phe Asp Ile Asn
    50                  55                  60

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

Ser Thr Val Leu Glu Ser Gly Ala Leu Tyr Tyr Met Gly His Val Lys
                85                  90                  95

Thr Leu Pro Ile Met Tyr Met Thr Ala Asp Lys Glu Leu Ala Lys Ala
            100                 105                 110

Arg Ile Glu Asn Asn Phe Ile Pro Met Leu Ala Gln Ser Asp Met Ala
        115                 120                 125

His Ile Val Arg Ser Ser Asp Glu Gly Asn Ser Arg Lys Thr Gly Lys
    130                 135                 140

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

Gly Ala Ile Asn Ala Asn Lys Met Arg Ser Phe Ser Ile Ala Val Met
                165                 170                 175

Leu Lys Asp Glu Ile Asp Ala Trp Pro Asp Arg Val Gly Lys Asp Gly
            180                 185                 190

Asp Pro Asp Lys Leu Ser Asp Asp Arg Cys Ser Ala Tyr Trp Glu Arg
        195                 200                 205

Arg Lys Ile Phe Arg Gly Ser Thr Pro Leu Ile Lys Gly Ser Ser Lys
    210                 215                 220

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

Cys Lys Lys Cys Ser Phe Pro Gln Glu Leu Arg Trp Ser Thr Pro Asp
                245                 250                 255

Gly Val Gly Gly Phe Lys Trp Asp Thr Asp Glu Asp Gly Ile Leu Lys
            260                 265                 270

Leu Asp Ser Val Arg Tyr Cys Cys Gln Gln Cys Gly Glu Pro His Phe
        275                 280                 285
```

```
Glu His Asp Lys Glu Arg Leu Phe Ser Glu Lys Phe Gly Ala Lys Trp
    290                 295                 300

Ile Pro Thr Ala Arg Pro Val Glu Pro Gly Ile Arg Ser Tyr His Leu
305                 310                 315                 320

Pro Ala Leu Tyr Ser Pro Phe Gly Met Gln Pro Trp Tyr Lys Cys Val
                325                 330                 335

Ile Ala Tyr Leu Asp Ala Phe Asp Pro Val Glu Arg Lys Val Lys Asp
            340                 345                 350

Ile Glu Leu Tyr Gln Val Phe Tyr Asn Asn Val Leu Ala Glu Pro Phe
        355                 360                 365

Glu Ile Gln Gly Ala Lys Val Arg Phe Glu Thr Val Ser His His Arg
    370                 375                 380

Arg Thr Val Tyr Arg Leu Gly His Ile Pro Asn Arg Tyr Ala Val Gln
385                 390                 395                 400

Tyr Ala Gly Ser Pro Ile Leu Phe Leu Thr Cys Gln Val Asp Val His
                405                 410                 415

Lys Ser Phe Leu Ala Val Ser Val Met Gly Trp Ala Lys Asp Ala Lys
            420                 425                 430

Cys Phe Val Ile Asp Tyr Leu Arg Ile Glu Gly Glu Asp Phe Ser Asp
        435                 440                 445

Ser Ala Glu Pro Gly Trp Gly Lys Leu Arg Glu Leu Ile Glu Glu Lys
    450                 455                 460

Gln Tyr Ile Ala Asp Asp Gly Lys Lys Tyr Arg Val Ala Leu Thr Phe
465                 470                 475                 480

Ile Asp Ser Gly Tyr Ala Asn Asp Thr Val Val Lys Phe Cys Ser Glu
                485                 490                 495

Tyr Ser Ser Ser Val Tyr Pro Ile Leu Gly Arg Asp Arg Pro Ser Lys
            500                 505                 510

Asn Gln Ala Ile Lys Glu Phe Ala Asp Phe Lys Thr Gln Glu Gly Thr
        515                 520                 525

Thr Gly Phe Arg Ile Ile Val Asp His Tyr Lys Asp Arg Leu Ala Pro
    530                 535                 540

Val Leu Arg Arg Glu Trp Asp Glu Met Gly Gly Gly Leu Gln Pro Val
545                 550                 555                 560
```

```
Tyr His Phe Asn Ala Pro Val Asp Leu Ser Asp Lys Ser Leu Lys Glu
                565                 570                 575


Leu Thr Val Glu Thr Arg Lys Glu Lys Thr Asp Ala Ser Gly Asn Thr
            580                 585                 590


Ser Tyr Phe Trp His Arg Pro Gly Asn Ala Arg Asn Glu Leu Trp Asp
        595                 600                 605


Leu Leu Cys Tyr Gly His Ala Ala Val Glu Ile Phe Ala Trp Ser Leu
    610                 615                 620


Cys Val Lys Asn Met Glu Gln Lys Glu Val Asp Trp Ala Trp Phe Trp
625                 630                 635                 640


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


Ala Ser Glu



<210> 213
<211> 69
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 213
Met Gln Tyr Glu Asn Asn Leu Glu Lys Leu Lys Gly Asn Lys Pro Glu
1               5                   10                  15


Gly Ala Thr Ile Val Ala Val Lys Gly Asp Arg Ile Ala Tyr Phe Lys
            20                  25                  30


Glu Ala Glu Gln Lys Gly Arg Leu Leu Thr Phe Asn Arg Ile Met Trp
        35                  40                  45


Val Lys Thr Trp Phe Thr Pro Asp His Leu Asn Leu Lys His Phe Asp
    50                  55                  60


Phe Ile Ala Val Leu
65


<210> 214
<211> 74
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 214
```

Met Asn Asn Gln Ser Phe Asn Asn Trp Arg Gly His Lys Ile Glu Ile
1   5   10   15

Val Gln Ala Gly Ala Thr Ile Gln Gln His Gly Tyr Pro Val Gln Ile
            20   25   30

Thr Asp Gln Asn Thr Ile Ala Phe Asp Gly Lys Ile Tyr Met Thr Gln
        35   40   45

Asn Thr Tyr Asn Ser Ile Ala Lys Asn Met Pro Gln Cys Gln Thr Pro
    50   55   60

Asn Phe Asn Asn Gln Gly Leu Asn Ile Phe
65   70

<210> 215
<211> 82
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 215
Met Ile Asp Lys Lys Tyr Leu Val Phe Gly Gly Trp Val Arg Ser Lys
1   5   10   15

His Asp Lys Gln Ser His Tyr Val Ala Pro Arg Met Val Ala Tyr Leu
            20   25   30

Tyr Asn Val Asn Pro His Glu Cys Ile Phe Ile Thr Asp Lys Thr Glu
        35   40   45

Leu Asn Pro Arg Thr His Leu Pro Tyr Gly Leu Asn Glu Asn His Asn
    50   55   60

Leu Ile Lys Leu Gly Pro Gln Thr Asn Gly Lys Tyr Asn Leu Pro Ala
65   70   75   80

Thr Asn

<210> 216
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 216
Met Gly Gln Ser Glu Ala Arg Gln Lys Gln Lys Ser Asp Tyr Glu Lys
1   5   10   15

Lys Arg Val Ile Lys Asn Phe Ser Leu Leu Lys Glu Arg Asp Lys His
            20   25   30

Leu Ile Glu Tyr Ile Glu Thr Val Pro Asn Val Gly Asp Leu Val Arg
35 40 45

Asp Leu Leu Asn Gln His Leu Lys Asn Glu Ala Val Ser Lys Lys
50 55 60

<210> 217
<211> 71
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 217
Met Leu Met Ile Gly Asn Thr Gln Val Lys Thr Pro Arg Glu Leu Thr
1 5 10 15

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

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

Ile Glu Ser Ile Gly Leu Phe Ala Asn Asp Met Gly Gly Phe Leu Thr
50 55 60

Val Phe Met Ala Glu Glu Met
65 70

<210> 218
<211> 84
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 218
Leu Asp Gln Ala Phe Leu Lys Glu Arg Ile Glu Ala Thr Lys Arg Gln
1 5 10 15

Ile Val Ala Tyr Glu Asp Ala Val Asn Gln Leu Ser Ser Gly Ala Val
20 25 30

Gln Ser Tyr Ser Leu Asn Thr Gly Gln Thr Thr Gln Asn Val Thr Arg
35 40 45

Phe Asp Val Ala Arg Leu Asn Gly Asp Ile Asp Gly Leu Tyr Asn Arg
50 55 60

Leu Ala Thr Leu Glu Ala Arg Leu Asn Gly Ser Gly Ser Thr Leu Val
65 70 75 80

Arg Pro Gly Trp

<210> 219
<211> 557
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 219
Met Asn Tyr Asp Phe Ser Arg Gly Leu Val Lys Val Pro Thr Val Gly
1 5 10 15

Leu Lys Thr Glu Phe Lys Tyr Ser Gly Ala Thr Ile Ala Pro Pro Pro
20 25 30

Met Gln Gly Ala Lys Ser Asp Ala Ile Glu Ile Asn Ala Leu Gly Gly
35 40 45

Gly Phe Asn His Ser Ala Phe Thr Gly Glu Lys Phe Ile Gly Gly Phe
50 55 60

Gly Pro Thr Ser Leu Phe Thr Met Asp Tyr Trp Thr Leu Arg Lys Arg
65 70 75 80

Ser Glu Gln Leu Phe Ser Glu Asn Leu Tyr Ala Ala Gly Leu Ile Glu
85 90 95

Arg Leu Val Thr Asn Glu Ile Asn Thr Gly Leu Thr Pro Glu Ala Cys
100 105 110

Pro Asp Glu Arg Ile Leu Gly Leu Lys Pro Gly Asp Leu Glu Asp Trp
115 120 125

Thr Glu Leu Val Glu Asn Arg Phe Ser Ile Trp Ala Asn Ser Ser Glu
130 135 140

Tyr Cys Asp Phe Tyr Gly Gln Asn Ser Leu Gly Glu Ile Gln Arg Ile
145 150 155 160

Ala Arg Arg Glu Ala Leu Ile Cys Gly Asp Val Leu Val Val Leu Arg
165 170 175

Gln Asn Gln Ser Thr Lys Met Pro Gln Val Gln Leu Val Ser Gly Ser
180 185 190

Leu Ile Arg Thr Pro Pro Asp Ile Pro Arg Lys Gly His Lys Ile Lys
195 200 205

His Gly Val Glu Leu Asp Thr Gln Gly Arg Gln Cys Ala Tyr Trp Val
210 215 220

```
Leu Gln Asp Asp Gly Thr Tyr Lys Arg Leu Pro Ala Phe Gly Glu Lys
225                 230                 235                 240

Ser Lys Arg Arg Ile Ala Trp Met Val Tyr Gly Ala Gln Arg Arg Leu
                245                 250                 255

Gly Glu Leu Arg Gly Gln Pro Leu Leu Ser Ile Val Leu Gln Ser Leu
            260                 265                 270

Lys Glu Ile Asp Arg Tyr Arg Asp Ala Ala Gln Arg Lys Ala Val Val
        275                 280                 285

Asn Ser Ile Leu Ala Met Phe Ile Glu Lys Thr Gln Asp Lys Met Ser
    290                 295                 300

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

Asn Ser Asn Thr Ala Ala Pro Arg Ser Phe Glu Ile Ala Ser Gln Val
                325                 330                 335

Pro Gly Val Val Leu Gln Glu Leu Gln Ala Gly Glu Lys Pro Val Gly
            340                 345                 350

Phe His Ser Gln Gly Thr Asp Ile Asn Phe Pro Ala Phe Glu Glu Ala
        355                 360                 365

Val Ile Ser Ala Val Ala Trp Cys Lys Gln Ile Pro Pro Glu Ile Leu
    370                 375                 380

Lys Leu Ser Phe Ser Ser Asn Tyr Ser Ala Ser Gln Ala Ala Ile Asn
385                 390                 395                 400

Glu Phe Lys Ile Tyr Leu Asn Met Val Trp Asn Glu Trp Gly Ala Asn
                405                 410                 415

Phe Cys Gln Pro Ile Tyr Thr Glu Phe Leu Ile Ser Glu Ala Leu Leu
            420                 425                 430

Gly Lys Ile Asp Ala Pro Gly Phe Leu Asp Ala Trp Arg Asp Pro Val
        435                 440                 445

Lys Met Asp Ile Phe Gly Ala Trp Leu Trp Cys Asp Trp Phe Gly Ser
    450                 455                 460

Ile Lys Pro Ser Thr Asp Met Arg Lys Met Gly Gln Gly Leu Ala Leu
465                 470                 475                 480

Ala Val Glu Gln Gly Trp Thr Thr Asn Ala Gln Ala Ser Arg Gln Met
                485                 490                 495
```

Phe Gly Thr Lys Phe Thr Lys Asn Ile Ala Arg Gln Arg Arg Glu Arg
500 505 510

Glu Leu Gln Ala Ser Leu Leu Arg Pro Met Leu Glu Leu Gln Lys Glu
515 520 525

Tyr Gly Ile Ser Ala Glu His Leu Val Asn Val Ala His Ala Ile Gly
530 535 540

Gly Thr Ile Ser Ala Gln Thr Glu Glu Thr Glu Glu Ile
545 550 555

<210> 220
<211> 383
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 220
Met Asp Trp Phe Leu Thr Pro Glu Ala Leu Lys Glu Ile Gln Glu Leu
1 5 10 15

His Ala Arg Gly Leu Val Leu Thr Ala Glu Gln Met Thr Glu Phe Asn
20 25 30

Ala Leu Tyr Ser Asp Asp Phe Pro Gly Ser Arg Ile Phe Gln Lys Val
35 40 45

Gly Thr Val Ala Gln Val Asn Ile Ala Gly Val Leu Thr Lys Glu Pro
50 55 60

Asn Trp Met Tyr Arg Tyr Tyr Gly Gly Gly Asn Thr Ala Tyr Ser Glu
65 70 75 80

Ile Ile Ser Ala Ile Asn Glu Ala Glu Arg Asp Pro Ala Ile Lys Glu
85 90 95

Ile Ile Leu Ala Ile Asp Ser Pro Gly Gly Gln Thr Asn Gly Leu Cys
100 105 110

Ser Ala Met Asp Ala Ile Lys Asn Thr Lys Lys Thr Val Leu Ala Val
115 120 125

Val Glu Gly Gln Ala Ala Ser Ala Ala Tyr Gly Leu Ala Ser Gln Ala
130 135 140

Asn Lys Ile Ile Ala Ala Asp Arg Gly Cys Met Val Gly Ser Val Gly
145 150 155 160

Ala Ala Ala Ser Ile Val Val Ser Glu Asn Val Val Asp Ile Ala Ser
165 170 175

Thr Asn Ala Pro Lys Lys Arg Pro Asp Val Thr Thr Asp Ala Gly Lys
180 185 190

Ala Val Ile Arg Glu Thr Leu Asp Gln Ile Glu Ser Ile Phe Ile Ala
195 200 205

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

Phe Gly Gln Gly Gly Met Tyr Val Ala Ala His Ala Leu Glu Arg Gly
225 230 235 240

Met Ile Asp Glu Ile Lys Thr Ala Asp Ser Ser Ala Thr Thr Asn Ala
245 250 255

Lys Ser Ser Ala Thr Tyr Thr Ala Ser Glu Glu Asn Ser Thr Met Asp
260 265 270

Ala Ala Thr Leu Lys Ala Gln Phe Pro Ala Val Tyr Thr Ala Ile Tyr
275 280 285

Asn Glu Gly Lys Thr Ala Glu Asn Glu Arg Val Ser Ala His Leu Thr
290 295 300

Leu Gly Glu Ala Ser Gly Asp Met Gln Thr Ala Ile Ser Ala Ile Asn
305 310 315 320

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

Asn Met Lys Arg Gly Gln Val Ala Gly Arg Glu Thr Asp Asp Thr Ala
340 345 350

Ala Ala Asn Ala Leu Asp Gly Val Lys Pro Gly Ala Thr Ala Thr Asp
355 360 365

Ala Asn Ala Val Thr Asn Met Val Ala Lys Asn Leu Gly Val Ala
370 375 380

<210> 221
<211> 129
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 221
Met Met Gln Val Thr Gln His Thr Asn Ser Ser Ile Asn Trp Gly Glu
1 5 10 15

Val Ala Cys Gln Asp Asp Thr Leu Thr Leu Gly Ala Asn Ala Thr Leu

20 25 30

Lys Glu Gly Thr Ile Leu Ala Arg Ala Ala Thr Gly Lys Leu Ile Pro
35 40 45

Phe Val Lys Gly Gly Ala Asp Gly Ala Gly Val Pro Val Ala Ile Ala
50 55 60

Met His Glu Ile Lys Thr Val Ala Ala Gly Asp Val Ser Val Arg Ala
65 70 75 80

Gly Ile Ser Gly Gln Val Arg Lys Asn Asn Leu Val Ile His Ala Asp
85 90 95

Gly Asn Ala Thr Asn Ile Asp Gly Ala Val Thr Asp Ala Leu Arg Ser
100 105 110

Tyr Gly Ile Val Ala Phe Thr Val Asn Ser Thr Asn Lys Pro Asp Asn
115 120 125

Gln

<210> 222
<211> 361
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 222
Met Thr Thr Ser Thr Ile Ala Gly Val Tyr Thr Gln Val Ala Pro Lys
1 5 10 15

Pro Leu Phe Leu Ser Gly Phe Phe Lys Ala Pro Pro Gln Asn His Phe
20 25 30

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

Ala Ala Val Val Gln Ser Leu Gly Ser Asp Tyr Asn Lys Asn Glu Thr
50 55 60

Gly Glu Phe Thr Asn Lys Lys Phe Thr Pro Pro Val Tyr Lys Glu Gly
65 70 75 80

Phe Ser Leu Asn Ala Phe Asp Leu Leu Lys Arg Glu Ala Gly Gln Ser
85 90 95

Gly Phe Asn Thr Pro Ser Glu Gln Ile Arg Gly Asn Leu Ile Thr Arg
100 105 110

```
Phe Ile Lys Gly Ala Arg Lys Val Glu Ala Lys Ile Leu Arg Gly Ile
        115                 120                 125

Glu Leu Gln Ala Ser Gln Ile Leu Gln Thr Gly Asn Leu Leu Leu Lys
    130                 135                 140

Asp Gln Glu Gly Lys Asp Ala Phe Lys Ile Asp Tyr Lys Pro Lys Ala
145                 150                 155                 160

Thr His Phe Val Asn Val Ala Asn Val Trp Thr Gly Ala Asn Ala Asp
                165                 170                 175

Pro Met Lys Asp Leu Glu Ser Leu Ser Glu Val Ile Gln Thr Asp Gly
            180                 185                 190

Leu Val Ile Pro Asp Ile Ile Ile Met Gly Ala Ser Ala Leu Ala Ala
        195                 200                 205

Ala Lys Gly Asn Glu Lys Phe Ile Lys Asn Phe Asp Ser Arg Asn Ile
    210                 215                 220

Ser Gly Asn Val Leu Ala Asp Met Gln Ile Thr Ala Arg Gly Gly Ile
225                 230                 235                 240

Tyr Gln Gly Thr Leu Arg Val Gly Asn Ala Val Cys Glu Leu Tyr Thr
                245                 250                 255

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

Leu Asn Thr Asn Lys Val Leu Met Leu Ser Ser Glu Ser Gln Leu Asp
        275                 280                 285

Ala Leu Phe Gly Ala Val Pro Asn Ile Ala Asp Ile Leu Gly Val Ser
    290                 295                 300

Leu Arg Glu Gln Leu Leu Pro Glu Leu Pro Thr Arg Phe Asp Ser Asn
305                 310                 315                 320

Ser Thr Asp Leu Phe Thr Asn Val Tyr Leu Ser Ala Ser Gly Glu Gln
                325                 330                 335

Leu Met Gly Gly Val Ala Ser Arg Pro Ile Leu Val Pro Thr Ala Ile
            340                 345                 350

Asp Ser Phe Gly Cys Leu Thr Val Ala
        355                 360
```

<210> 223
<211> 55
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F394/08

<400> 223
Met Asn Pro Leu Gln Trp Gly Phe Phe Leu Leu Asn Leu Glu Ile Phe
1   5   10   15

Asp Val Thr Lys Thr Asp Leu Ile Asn Ala Ile Lys Ala Ile Asp Ser
            20   25   30

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

Thr Glu Leu Gln Ala Lys Ala
    50   55

<210> 224
<211> 410
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 224
Met Ala Lys Ile Asn Glu Leu Leu Arg Glu Ser Thr Thr Thr Asn Ser
1   5   10   15

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

Lys Leu Ile Tyr Ser Asp Ile Val Ala Thr Gln Arg Thr Asn Gln Pro
        35   40   45

Val Ala Ala Phe Tyr Gly Ile Lys Tyr Leu Asn Pro Asp Asn Glu Phe
    50   55   60

Thr Phe Lys Thr Gly Ala Thr Tyr Ala Gly Glu Ala Gly Tyr Val Asp
65   70   75   80

Arg Glu Gln Ile Thr Glu Leu Thr Glu Glu Ser Lys Leu Thr Leu Asn
                85   90   95

Lys Gly Asp Leu Phe Lys Tyr Asn Asn Ile Val Tyr Lys Val Leu Glu
            100   105   110

Asp Thr Pro Phe Ala Asp Ile Glu Glu Ser Asp Leu Glu Leu Ala Leu
        115   120   125

Gln Ile Ala Ile Val Leu Leu Lys Val Arg Leu Phe Ser Asp Ala Ala
    130   135   140

Ser Thr Ser Lys Phe Glu Ser Ser Asp Ser Glu Ile Ala Asp Ala Arg
145   150   155   160

```
Phe Gln Ile Asn Lys Trp Gln Thr Ala Val Lys Ser Arg Lys Leu Lys
                165                 170                 175

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

Asp Ala Pro Asn Phe Leu Glu Asp Leu Leu Ala Thr Glu Met Ala Asp
        195                 200                 205

Glu Ile Asn Lys Asp Ile Leu Gln Ser Leu Ile Thr Val Ser Lys Arg
    210                 215                 220

Tyr Lys Val Thr Gly Ile Thr Asp Thr Gly Phe Ile Asp Leu Ser Tyr
225                 230                 235                 240

Ala Ser Ala Pro Glu Ala Gly Arg Ser Leu Tyr Arg Met Val Cys Glu
                245                 250                 255

Met Val Ser His Ile Gln Lys Glu Ser Thr Tyr Thr Ala Thr Phe Cys
            260                 265                 270

Val Ala Ser Ala Arg Ala Ala Ala Ile Leu Ala Ala Ser Gly Trp Leu
        275                 280                 285

Lys His Lys Pro Glu Asp Asp Lys Tyr Leu Ser Gln Asn Ala Tyr Gly
    290                 295                 300

Phe Leu Ala Asn Gly Leu Pro Leu Tyr Cys Asp Thr Asn Ser Pro Leu
305                 310                 315                 320

Asp Tyr Val Ile Val Gly Val Val Glu Asn Ile Gly Glu Lys Glu Ile
                325                 330                 335

Val Gly Ser Ile Phe Tyr Ala Pro Tyr Thr Glu Gly Leu Asp Leu Asp
            340                 345                 350

Asp Pro Glu His Val Gly Ala Phe Lys Val Val Val Asp Pro Glu Ser
        355                 360                 365

Leu Gln Pro Ser Ile Gly Leu Leu Val Arg Tyr Ala Leu Ser Ala Asn
    370                 375                 380

Pro Tyr Thr Val Ala Lys Asp Glu Lys Glu Ala Arg Ile Ile Asp Gly
385                 390                 395                 400

Gly Asp Met Asp Lys Met Ala Gly Arg Ser
                405                 410
```

<210> 225
<211> 521

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 225
Met Thr Ile Lys Thr Lys Ala Glu Leu Leu Asn Lys Trp Lys Pro Leu
1   5   10   15

Leu Glu Gly Glu Gly Leu Pro Glu Ile Ala Asn Ser Lys Gln Ala Ile
            20   25   30

Ile Ala Lys Ile Phe Glu Asn Gln Glu Lys Asp Phe Gln Thr Ala Pro
        35   40   45

Glu Tyr Lys Asp Glu Lys Ile Ala Gln Ala Phe Gly Ser Phe Leu Thr
    50   55   60

Glu Ala Glu Ile Gly Gly Asp His Gly Tyr Asn Ala Thr Asn Ile Ala
65   70   75   80

Ala Gly Gln Thr Ser Gly Ala Val Thr Gln Ile Gly Pro Ala Val Met
                85   90   95

Gly Met Val Arg Arg Ala Ile Pro Asn Leu Ile Ala Phe Asp Ile Cys
            100   105   110

Gly Val Gln Pro Met Asn Ser Pro Thr Gly Gln Val Phe Ala Leu Arg
        115   120   125

Ala Val Tyr Gly Lys Asp Pro Ile Ala Ser Gly Ala Lys Glu Ala Phe
    130   135   140

His Pro Met Tyr Gly Pro Asp Ala Met Phe Ser Gly Gln Gly Ala Ala
145   150   155   160

Lys Lys Phe Ala Ala Leu Lys Ala Ser Asp Thr Leu Glu Val Gly Thr
                165   170   175

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

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

Asp Ala Glu Ile Lys Lys Gln Met Glu Ala Gly Val Leu Val Glu Ile
    210   215   220

Ala Glu Gly Met Ala Thr Ser Ile Ala Glu Leu Gln Glu Gly Phe Asn
225   230   235   240

Gly Ser Thr Asp Asn Pro Trp Asn Glu Met Gly Phe Arg Ile Asp Lys

245 250 255

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

Glu Leu Ala Gln Asp Leu Arg Ala Val His Gly Met Asp Ala Asp Ala
275 280 285

Glu Leu Ser Gly Ile Leu Ala Thr Glu Ile Met Leu Glu Ile Asn Arg
290 295 300

Glu Val Val Asp Trp Ile Asn Tyr Ser Ala Gln Val Gly Lys Ser Gly
305 310 315 320

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

Pro Ile Asp Ile Arg Gly Ala Arg Trp Ala Gly Glu Ser Phe Lys Ala
340 345 350

Leu Leu Phe Gln Ile Asp Lys Glu Ala Val Glu Ile Ala Arg Gln Thr
355 360 365

Gly Arg Gly Glu Gly Asn Phe Ile Ile Ala Ser Arg Asn Val Val Asn
370 375 380

Val Leu Ala Ser Val Asp Thr Gly Ile Ser Tyr Ala Ala Gln Gly Leu
385 390 395 400

Ala Thr Gly Phe Asn Thr Asp Thr Thr Lys Ser Val Phe Ala Gly Val
405 410 415

Leu Gly Gly Lys Tyr Arg Val Tyr Ile Asp Gln Tyr Ala Lys Gln Asp
420 425 430

Tyr Phe Thr Val Gly Tyr Lys Gly Pro Asn Glu Met Asp Ala Gly Ile
435 440 445

Tyr Tyr Ala Pro Tyr Val Ala Leu Thr Pro Leu Arg Gly Ser Asp Pro
450 455 460

Lys Asn Phe Gln Pro Val Met Gly Phe Lys Thr Arg Tyr Gly Ile Gly
465 470 475 480

Ile Asn Pro Phe Ala Glu Ser Ala Ala Gln Ala Pro Ala Ser Arg Ile
485 490 495

Gln Ser Gly Met Pro Ser Ile Leu Asn Ser Leu Gly Lys Asn Ala Tyr
500 505 510

Phe Arg Arg Val Tyr Val Lys Gly Ile

515 520

<210> 226
<211> 269
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 226
Met Leu Lys Glu Gln Leu Ile Ala Glu Ala Gln Lys Ile Asp Ala Ser
1 5 10 15

Val Ala Leu Asp Ser Ile Phe Glu Ser Val Asn Ile Ser Pro Glu Ala
20 25 30

Lys Glu Thr Phe Gly Thr Val Phe Glu Ala Thr Val Lys Gln His Ala
35 40 45

Val Lys Leu Ala Glu Ser His Ile Ala Lys Ile Ala Glu Lys Ala Glu
50 55 60

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

Lys Ile Ala Glu Gln Ala Ser Lys Phe Leu Asp His Leu Ala Lys Glu
85 90 95

Trp Leu Thr Glu Asn Lys Leu Ala Val Asp Lys Gly Ile Lys Ala Glu
100 105 110

Leu Phe Glu Ser Met Leu Gly Gly Leu Lys Glu Leu Phe Val Glu His
115 120 125

Asn Val Val Val Pro Glu Glu Ser Val Asp Val Val Ala Glu Met Glu
130 135 140

Glu Glu Leu Gln Glu His Lys Glu Glu Ser Ala Arg Leu Phe Glu Glu
145 150 155 160

Leu Asn Lys Arg Asp Ala Tyr Ile Asn Tyr Val Gln Arg Glu Val Ala
165 170 175

Leu Ser Glu Ser Thr Lys Asp Leu Thr Glu Ser Gln Lys Glu Lys Val
180 185 190

Ser Ala Leu Val Glu Gly Met Asp Tyr Ser Asp Ala Phe Ser Ser Lys
195 200 205

Leu Ser Ala Ile Val Glu Met Val Lys Lys Ser Asn Lys Asp Glu Ser
210 215 220

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

Asn Phe Val Thr Glu Ala Val Glu Asp Lys Ser Ala Gln Gly Ala Glu
245 250 255

Asp Ile Val Ser Val Tyr Ala Lys Val Ala Ser Arg Phe
260 265

<210> 227
<211> 212
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 227
Met Asn Glu Pro Gln Leu Leu Ile Glu Thr Trp Gly Gln Pro Gly Glu
1 5 10 15

Ile Ile Asp Gly Val Pro Met Leu Glu Ser His Asp Gly Lys Asp Leu
20 25 30

Gly Leu Lys Pro Gly Leu Tyr Ile Glu Gly Ile Phe Met Gln Ala Glu
35 40 45

Val Val Asn Arg Asn Lys Arg Leu Tyr Pro Lys Arg Ile Leu Glu Lys
50 55 60

Ala Val Lys Asp Tyr Ile Asn Glu Gln Val Leu Thr Lys Gln Ala Leu
65 70 75 80

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

Ala Ile Ile Ile Glu Asp Met Trp Trp Lys Gly Asn Asp Val Tyr Gly
100 105 110

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

Ala Asn Ile Arg Ala Gly Trp Ile Pro Gly Val Ser Ser Arg Gly Leu
130 135 140

Gly Ser Leu Thr Asp Thr Asn Lys Gly Tyr Arg Ile Val Asn Glu Gly
145 150 155 160

Phe Lys Leu Thr Val Gly Val Asp Ala Val Trp Gly Pro Ser Ala Pro
165 170 175

Asp Ala Trp Val Thr Pro Lys Glu Ile Thr Glu Ser Gln Thr Ala Glu
180 185 190

Ala Asp Thr Ser Ala Asp Asp Ala Tyr Met Ala Leu Ala Glu Ala Met
195 200 205

Lys Lys Ala Leu
210

<210> 228
<211> 141
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 228
Met Leu Leu Ile Pro Glu Thr His Glu Leu Val Leu Glu Asn Val Glu
1 5 10 15

Ala Leu Ile Pro Glu Ala Gln Gly Arg Phe Asp Glu Leu Ser Ser Ala
20 25 30

Leu Asn Lys Asp Asp Ile Asn Thr Ile Val Glu Asn Met Leu Asp Asp
35 40 45

Glu Thr Asp Leu Ala Val Ala Leu Ala Ser Ile Asn Glu Asn Met Pro
50 55 60

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

Arg Thr Lys Asp Arg Lys Thr Arg Glu Arg Asn Ala Phe Gln Thr Thr
85 90 95

Gly Leu Ser Lys Ala Lys Arg Arg Gln Ile Ala Arg Lys Ala Thr Lys
100 105 110

Thr Lys Ile Ala Asn Pro Ala Gly Gln Ser Arg Ala Gln Arg Lys Arg
115 120 125

Lys Lys Ala Leu Lys Arg Arg Lys Ala Leu Gly Leu Ser
130 135 140

<210> 229
<211> 79
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 229
Met Glu Gly Leu Ile Glu Ala Ile Lys Ser Asn Asp Leu Val Ala Ala
1 5 10 15

Arg Lys Leu Phe Ala Glu Ala Met Ala Ala Arg Thr Thr Asp Leu Ile

20 25 30

Lys Glu Glu Lys Ile Ala Ile Ala Arg Asn Phe Leu Ile Glu Gly Glu
35 40 45

Glu Pro Asp Asp Glu Asp Asp Asp Glu Asp Glu Asp Ser Asp Asp Lys
50 55 60

Asp Asp Lys Lys Asp Lys Asp Ser Asp Glu Asp Glu Asp Asp Glu
65 70 75

<210> 230
<211> 524
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 230
Met Lys Phe Asn Val Leu Ser Leu Phe Ala Pro Trp Ala Lys Met Asp
1 5 10 15

Glu Arg Asn Phe Lys Asp Gln Glu Lys Glu Asp Leu Val Ser Ile Thr
20 25 30

Ala Pro Lys Leu Asp Asp Gly Ala Arg Glu Phe Glu Val Ser Ser Asn
35 40 45

Glu Ala Ala Ser Pro Tyr Asn Ala Ala Phe Gln Thr Ile Phe Gly Ser
50 55 60

Tyr Glu Pro Gly Met Lys Thr Thr Arg Glu Leu Ile Asp Thr Tyr Arg
65 70 75 80

Asn Leu Met Asn Asn Tyr Glu Val Asp Asn Ala Val Ser Glu Ile Val
85 90 95

Ser Asp Ala Ile Val Tyr Glu Asp Asp Thr Glu Val Val Ala Leu Asn
100 105 110

Leu Asp Lys Ser Lys Phe Ser Pro Lys Ile Lys Asn Met Met Leu Asp
115 120 125

Glu Phe Ser Asp Val Leu Asn His Leu Ser Phe Gln Arg Lys Gly Ser
130 135 140

Asp His Phe Arg Arg Trp Tyr Val Asp Ser Arg Ile Phe Phe His Lys
145 150 155 160

Ile Ile Asp Pro Lys Arg Pro Lys Glu Gly Ile Lys Glu Leu Arg Arg
165 170 175

```
Leu Asp Pro Arg Gln Val Gln Tyr Val Arg Glu Ile Ile Thr Glu Thr
            180                 185                 190

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

Asp Thr Ala His Glu Ser Tyr Ala Cys Asp Gly Arg Met Tyr Glu Ala
    210                 215                 220

Gly Thr Lys Ile Lys Ile Pro Lys Ala Ala Val Val Tyr Ala His Ser
225                 230                 235                 240

Gly Leu Val Asp Cys Cys Gly Lys Asn Ile Ile Gly Tyr Leu His Arg
                245                 250                 255

Ala Val Lys Pro Ala Asn Gln Leu Lys Leu Leu Glu Asp Ala Val Val
            260                 265                 270

Ile Tyr Arg Ile Thr Arg Ala Pro Asp Arg Arg Val Trp Tyr Val Asp
        275                 280                 285

Thr Gly Asn Met Pro Ala Arg Lys Ala Ala Glu His Met Gln His Val
    290                 295                 300

Met Asn Thr Met Lys Asn Arg Val Val Tyr Asp Ala Ser Thr Gly Lys
305                 310                 315                 320

Ile Lys Asn Gln Gln His Asn Met Ser Met Thr Glu Asp Tyr Trp Leu
                325                 330                 335

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

Ala Asp Asn Thr Gly Asn Met Glu Asp Ile Arg Trp Phe Arg Gln Ala
        355                 360                 365

Leu Tyr Met Ala Leu Arg Val Pro Leu Ser Arg Ile Pro Gln Asp Gln
    370                 375                 380

Gln Gly Gly Val Met Phe Asp Ser Gly Thr Ser Ile Thr Arg Asp Glu
385                 390                 395                 400

Leu Thr Phe Ala Lys Phe Ile Arg Glu Leu Gln His Lys Phe Glu Glu
                405                 410                 415

Val Phe Leu Asp Pro Leu Lys Thr Asn Leu Leu Leu Lys Gly Ile Ile
            420                 425                 430

Thr Glu Asp Glu Trp Asn Asp Glu Ile Asn Asn Ile Lys Ile Glu Phe
        435                 440                 445
```

His Arg Asp Ser Tyr Phe Ala Glu Leu Lys Glu Ala Glu Ile Leu Glu
    450   455   460

Arg Arg Ile Asn Met Leu Thr Met Ala Glu Pro Phe Ile Gly Lys Tyr
465   470   475   480

Ile Ser His Arg Thr Ala Met Lys Asp Ile Leu Gln Met Thr Asp Glu
                485   490   495

Glu Ile Glu Gln Glu Ala Lys Gln Ile Glu Glu Glu Ser Lys Glu Ala
            500   505   510

Arg Phe Gln Asp Pro Asp Gln Glu Gln Glu Asp Phe
        515   520

<210> 231
<211> 163
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 231
Met Phe Val Asp Asp Val Thr Arg Ala Phe Glu Ser Gly Asp Phe Ala
1   5   10   15

Arg Pro Asn Leu Phe Gln Val Glu Ile Ser Tyr Leu Gly Gln Asn Phe
            20   25   30

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

Ile Pro Val Gly Phe Met Asn Arg Lys Ile Asn Val Ala Gly Asp Arg
    50   55   60

Thr Phe Asp Asp Trp Thr Val Thr Val Met Asn Asp Glu Ala His Asp
65   70   75   80

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

Asn Glu Ile Thr Gly Gly Lys Pro Ala Glu Tyr Lys Lys Ser Ala Ile
            100   105   110

Val Arg Gln Tyr Ala Arg Asp Ala Lys Thr Val Thr Lys Glu Ile Glu
        115   120   125

Ile Lys Gly Leu Trp Pro Thr Asn Val Gly Glu Leu Gln Leu Asp Trp
    130   135   140

Asp Ser Asn Asn Glu Ile Gln Thr Phe Glu Val Thr Leu Ala Leu Asp
145   150   155   160

Tyr Trp Glu

<210> 232
<211> 659
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 232
Met Thr Leu Leu Ser Pro Gly Ile Glu Leu Lys Glu Thr Thr Val Gln
1 5 10 15

Ser Thr Val Val Asn Asn Ser Thr Gly Thr Ala Ala Leu Ala Gly Lys
20 25 30

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

Asp Leu Val Asn Thr Phe Gly Gln Pro Thr Ala Glu Thr Ala Asp Tyr
50 55 60

Phe Met Ser Ala Met Asn Phe Leu Gln Tyr Gly Asn Asp Leu Arg Val
65 70 75 80

Val Arg Ala Val Asp Arg Asp Thr Ala Lys Asn Ser Ser Pro Ile Ala
85 90 95

Gly Asn Ile Glu Tyr Thr Ile Ser Thr Pro Gly Ser Asn Tyr Ala Val
100 105 110

Gly Asp Lys Ile Thr Val Lys Tyr Val Ser Glu Asp Val Glu Thr Glu
115 120 125

Gly Lys Ile Thr Glu Val Asp Ala Asp Gly Lys Ile Lys Lys Ile Asn
130 135 140

Ile Pro Thr Ala Lys Ile Ile Ala Lys Ala Lys Glu Val Gly Glu Tyr
145 150 155 160

Pro Thr Leu Gly Ser Asn Trp Thr Ala Glu Ile Ser Ser Ser Ser Ser
165 170 175

Gly Leu Ala Ala Val Ile Thr Leu Gly Lys Ile Ile Thr Asp Ser Gly
180 185 190

Ile Leu Leu Ala Glu Ile Glu Ser Ala Glu Thr Ala Met Thr Ala Val
195 200 205

Asp Phe Gln Ala Asn Leu Glu Lys Tyr Gly Ile Pro Gly Val Val Ala
210 215 220

```
Leu Tyr Pro Gly Glu Leu Gly Asp Lys Ile Glu Ile Glu Ile Val Ser
225                 230                 235                 240

Lys Ala Asp Tyr Ala Lys Gly Ala Ser Ala Leu Leu Pro Ile Tyr Pro
                245                 250                 255

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

Pro Gln Thr Asp Ser Gln Tyr Ala Ile Ile Val Arg Arg Asn Asp Ala
        275                 280                 285

Ile Val Gln Ser Val Val Leu Ser Thr Lys Arg Gly Glu Lys Asp Ile
    290                 295                 300

Tyr Asp Ser Asn Ile Tyr Ile Asp Asp Phe Phe Ala Lys Gly Gly Ser
305                 310                 315                 320

Glu Tyr Ile Phe Ala Thr Ala Gln Asn Trp Pro Glu Gly Phe Ser Gly
                325                 330                 335

Ile Leu Thr Leu Ser Gly Gly Leu Ser Ser Asn Ala Glu Val Thr Ala
            340                 345                 350

Gly Asp Leu Met Glu Ala Trp Asp Phe Phe Ala Asp Arg Glu Ser Val
        355                 360                 365

Asp Val Gln Leu Phe Ile Ala Gly Ser Cys Ala Gly Glu Ser Leu Glu
    370                 375                 380

Thr Ala Ser Thr Val Gln Lys His Val Val Ser Ile Gly Asp Ala Arg
385                 390                 395                 400

Gln Asp Cys Leu Val Leu Cys Ser Pro Pro Arg Glu Thr Val Val Gly
                405                 410                 415

Ile Pro Val Thr Arg Ala Val Asp Asn Leu Val Asn Trp Arg Thr Ala
            420                 425                 430

Ala Gly Ser Tyr Thr Asp Asn Asn Phe Asn Ile Ser Ser Thr Tyr Ala
        435                 440                 445

Ala Ile Asp Gly Asn Tyr Lys Tyr Gln Tyr Asp Lys Tyr Asn Asp Val
    450                 455                 460

Asn Arg Trp Val Pro Leu Ala Ala Asp Ile Ala Gly Leu Cys Ala Arg
465                 470                 475                 480

Thr Asp Asn Val Ser Gln Thr Trp Met Ser Pro Ala Gly Tyr Asn Arg
                485                 490                 495
```

```
Gly Gln Ile Leu Asn Val Ile Lys Leu Ala Ile Glu Thr Arg Gln Ala
            500                 505                 510

Gln Arg Asp Arg Leu Tyr Gln Glu Ala Ile Asn Pro Val Thr Gly Thr
        515                 520                 525

Gly Gly Asp Gly Tyr Val Leu Tyr Gly Asp Lys Thr Ala Thr Ser Val
    530                 535                 540

Pro Ser Pro Phe Asp Arg Ile Asn Val Arg Arg Leu Phe Asn Met Leu
545                 550                 555                 560

Lys Thr Asn Ile Gly Arg Ser Ser Lys Tyr Arg Leu Phe Glu Leu Asn
                565                 570                 575

Asn Ala Phe Thr Arg Ser Ser Phe Arg Thr Glu Thr Ala Gln Tyr Leu
            580                 585                 590

Gln Gly Ile Lys Ala Leu Gly Gly Ile Tyr Glu Tyr Arg Val Val Cys
        595                 600                 605

Asp Thr Thr Asn Asn Thr Pro Ser Val Ile Asp Arg Asn Glu Phe Val
    610                 615                 620

Ala Thr Phe Tyr Ile Gln Pro Ala Arg Ser Ile Asn Tyr Ile Thr Leu
625                 630                 635                 640

Asn Phe Val Ala Thr Ala Thr Gly Ala Asp Phe Asp Glu Leu Thr Gly
                645                 650                 655

Leu Ala Gly
```

<210> 233
<211> 610
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

```
<400> 233
Met Glu Gln Pro Ile Asn Ala Leu Asn Asp Phe His Pro Leu Asn Glu
1               5                   10                  15

Ala Gly Lys Ile Leu Ile Lys His Pro Ser Leu Ala Glu Arg Lys Asp
            20                  25                  30

Glu Asp Gly Ile His Trp Ile Lys Ser Gln Trp Asp Gly Lys Trp Tyr
        35                  40                  45

Pro Glu Lys Phe Ser Asp Tyr Leu Arg Leu His Lys Ile Val Lys Ile
```

50 55 60

Pro Asn Asn Ser Asp Lys Pro Glu Leu Phe Gln Thr Tyr Lys Asp Lys
65 70 75 80

Asn Asn Lys Arg Ser Arg Tyr Met Gly Leu Pro Asn Leu Lys Arg Ala
85 90 95

Asn Ile Lys Thr Gln Trp Thr Arg Glu Met Val Glu Glu Trp Lys Lys
100 105 110

Cys Arg Asp Asp Ile Val Tyr Phe Ala Glu Thr Tyr Cys Ala Ile Thr
115 120 125

His Ile Asp Tyr Gly Val Ile Lys Val Gln Leu Arg Asp Tyr Gln Arg
130 135 140

Asp Met Leu Lys Ile Met Ser Ser Lys Arg Met Thr Val Cys Asn Leu
145 150 155 160

Ser Arg Gln Leu Gly Lys Thr Thr Val Val Ala Ile Phe Leu Ala His
165 170 175

Phe Val Cys Phe Asn Lys Asp Lys Ala Val Gly Ile Leu Ala His Lys
180 185 190

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

Leu Leu Pro Asp Phe Leu Gln Pro Gly Ile Val Glu Trp Asn Lys Gly
210 215 220

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

Pro Asp Ala Val Arg Gly Asn Ser Phe Ala Met Ile Tyr Ile Asp Glu
245 250 255

Cys Ala Phe Ile Pro Asn Phe His Asp Ser Trp Leu Ala Ile Gln Pro
260 265 270

Val Ile Ser Ser Gly Arg Arg Ser Lys Ile Ile Ile Thr Thr Thr Pro
275 280 285

Asn Gly Leu Asn His Phe Tyr Asp Ile Trp Thr Ala Ala Val Glu Gly
290 295 300

Lys Ser Gly Phe Glu Pro Tyr Thr Ala Ile Trp Asn Ser Val Lys Glu
305 310 315 320

Arg Leu Tyr Asn Asp Glu Asp Ile Phe Asp Asp Gly Trp Gln Trp Ser

325 330 335

Ile Gln Thr Ile Asn Gly Ser Thr Leu Ala Gln Phe Arg Gln Glu His
340 345 350

Thr Ala Ala Phe Glu Gly Thr Ser Gly Thr Leu Ile Ser Gly Met Lys
355 360 365

Leu Ala Val Met Asp Phe Ile Glu Val Thr Pro Asp Asp His Gly Phe
370 375 380

His Arg Phe Lys Gly Pro Glu Pro Asp Arg Lys Tyr Ile Ala Thr Leu
385 390 395 400

Asp Cys Ser Glu Gly Arg Gly Gln Asp Tyr His Ala Leu His Ile Ile
405 410 415

Asp Val Thr Asp Asp Val Trp Glu Gln Val Gly Val Leu His Ser Asn
420 425 430

Thr Ile Ser His Leu Ile Leu Pro Asp Ile Val Met Arg Tyr Leu Val
435 440 445

Glu Tyr Asn Glu Cys Pro Val Tyr Ile Glu Leu Asn Ser Thr Gly Val
450 455 460

Ser Val Ala Lys Ser Leu Tyr Met Asp Leu Glu Tyr Glu Gly Val Ile
465 470 475 480

Cys Asp Ser Tyr Thr Asp Leu Gly Met Lys Gln Thr Lys Arg Thr Lys
485 490 495

Ala Val Gly Cys Ser Thr Leu Lys Asp Leu Ile Glu Lys Asp Lys Leu
500 505 510

Ile Ile His His Arg Ala Thr Ile Gln Glu Phe Arg Thr Phe Ser Glu
515 520 525

Lys Gly Val Ser Trp Ala Ala Glu Glu Gly Tyr His Asp Asp Leu Val
530 535 540

Met Ser Leu Val Ile Phe Gly Trp Leu Ser Thr Gln Ser Lys Phe Ile
545 550 555 560

Asp Tyr Ala Asp Lys Asp Asp Met Arg Leu Ala Ser Glu Val Phe Ser
565 570 575

Lys Glu Leu Gln Asp Met Gly Asp Glu Tyr Ala Pro Val Ile Phe Val
580 585 590

Asp Ser Val His Ser Ala Glu Tyr Val Pro Val Ser His Gly Met Ser

595 600 605

Met Val
610

<210> 234
<211> 164
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 234
Met Glu Gly Leu Asp Ile Asn Lys Leu Leu Asp Ile Ser Asp Leu Pro
1 5 10 15

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

Glu Val Lys Ser Asn Pro Gln Asn Arg Thr Pro Asp Leu Glu Asp Asp
35 40 45

Tyr Gly Val Val Arg Arg Asn Met His Phe Gln Gln Gln Met Leu Met
50 55 60

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

Arg His Met Glu Val Phe Ala Thr Leu Met Gly Gln Met Thr Thr Thr
85 90 95

Asn Arg Glu Ile Leu Lys Leu His Lys Asp Met Lys Asp Ile Thr Ser
100 105 110

Glu Gln Val Gly Thr Lys Gly Ala Val Pro Thr Gly Gln Met Asn Ile
115 120 125

Gln Asn Ala Thr Val Phe Met Gly Ser Pro Thr Glu Leu Met Asp Glu
130 135 140

Ile Gly Asp Ala Tyr Glu Ala Gln Glu Ala Arg Glu Lys Val Ile Asn
145 150 155 160

Gly Thr Thr Asp

<210> 235
<211> 272
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 235
Met Phe Gly Tyr Phe Tyr Asn Ser Ser Phe Arg Arg Tyr Ala Thr Leu
1   5   10   15

Met Gly Asp Leu Phe Ser Asn Ile Gln Ile Lys Arg Gln Leu Glu Ser
            20   25   30

Gly Asp Lys Phe Ile Arg Val Pro Ile Thr Tyr Ala Ser Lys Glu His
        35   40   45

Phe Met Met Lys Leu Asn Lys Trp Thr Ser Ile Asn Ser Gln Glu Asp
    50   55   60

Val Ala Lys Val Glu Thr Ile Leu Pro Arg Ile Asn Leu His Leu Val
65   70   75   80

Asp Phe Ser Tyr Asn Ala Pro Phe Lys Thr Asn Ile Leu Asn Gln Asn
                85   90   95

Leu Leu Gln Lys Gly Thr Thr Ser Val Val Ser Gln Tyr Asn Pro Ser
            100   105   110

Pro Ile Lys Met Ile Tyr Glu Leu Ser Ile Phe Thr Arg Tyr Glu Asp
        115   120   125

Asp Met Phe Gln Ile Val Glu Gln Ile Leu Pro Tyr Phe Gln Pro His
    130   135   140

Phe Asn Thr Thr Met Tyr Glu Gln Phe Gly Asn Asp Ile Pro Phe Lys
145   150   155   160

Arg Asp Ile Lys Ile Val Leu Met Ser Ala Ala Ile Asp Glu Ala Ile
                165   170   175

Asp Gly Asp Asn Leu Ser Arg Arg Arg Ile Glu Trp Ser Leu Thr Phe
            180   185   190

Glu Val Asn Gly Trp Met Tyr Pro Pro Val Asp Asp Ala Glu Gly Leu
        195   200   205

Ile Arg Thr Thr Tyr Thr Asp Phe His Ala Asn Thr Arg Asp Leu Pro
    210   215   220

Asp Gly Glu Gly Val Phe Glu Ser Val Asp Ser Glu Val Val Pro Arg
225   230   235   240

Asp Ile Asn Pro Glu Asp Trp Asp Gly Thr Val Lys Gln Thr Phe Thr
                245   250   255

Ser Asn Val Asn Arg Pro Thr Pro Pro Glu Pro Pro Gly Pro Arg Thr
            260   265   270

<210> 236
<211> 256
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 236
Met Ala Thr Tyr Asp Lys Asn Leu Phe Ala Lys Leu Glu Asn Arg Thr
1 5 10 15

Gly Tyr Ser Gln Thr Asn Glu Thr Glu Ile Leu Asn Pro Tyr Val Asn
20 25 30

Phe Asn His Tyr Lys Asn Ser Gln Ile Leu Ala Asp Val Leu Val Ala
35 40 45

Glu Ser Ile Gln Met Arg Gly Val Glu Cys Tyr Tyr Val Pro Arg Glu
50 55 60

Tyr Val Ser Pro Asp Leu Ile Phe Gly Glu Asp Leu Lys Asn Lys Phe
65 70 75 80

Thr Lys Ala Trp Lys Phe Ala Ala Tyr Leu Asn Ser Phe Glu Gly Tyr
85 90 95

Glu Gly Ala Lys Ser Phe Phe Ser Asn Phe Gly Met Gln Val Gln Asp
100 105 110

Glu Val Thr Leu Ser Ile Asn Pro Asn Leu Phe Lys His Gln Val Asn
115 120 125

Gly Lys Glu Pro Lys Glu Gly Asp Leu Ile Tyr Phe Pro Met Asp Asn
130 135 140

Ser Leu Phe Glu Ile Asn Trp Val Glu Pro Tyr Asp Pro Phe Tyr Gln
145 150 155 160

Leu Gly Gln Asn Ala Ile Arg Lys Ile Thr Ala Gly Lys Phe Ile Tyr
165 170 175

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

Ile Pro Glu Phe Ser Glu Leu Glu Leu Asn Pro Val Arg Asn Leu Asn
195 200 205

Gly Ile His Asp Ile Asn Ile Asp Gln Tyr Ala Glu Val Asp Gln Ile
210 215 220

Asn Ser Glu Ala Lys Glu Tyr Val Glu Pro Tyr Val Val Val Asn Asn
225 230 235 240

Arg Gly Lys Ser Phe Glu Ser Ser Pro Phe Asp Asn Asp Phe Met Asp
245 250 255

<210> 237
<211> 309
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 237
Met Ser Gly Tyr Asn Ser Gln Asn Pro Lys Glu Leu Lys Asp Val Ile
1 5 10 15

Leu Arg Arg Leu Gly Ala Pro Ile Ile Asn Val Glu Leu Thr Pro Asp
20 25 30

Gln Ile Tyr Asp Cys Ile Gln Arg Ala Leu Glu Leu Tyr Gly Glu Tyr
35 40 45

His Phe Asp Gly Leu Asn Lys Gly Phe His Val Phe Tyr Val Gly Asp
50 55 60

Asp Glu Glu Lys Tyr Lys Thr Gly Val Phe Asp Leu Arg Gly Ser Asn
65 70 75 80

Val Phe Ala Val Thr Arg Ile Leu Arg Thr Asn Ile Gly Ser Ile Thr
85 90 95

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

Gly Met Ala Gly Ile Asn Gly Gly Met Gly Thr Ser Cys Asn Arg Phe
115 120 125

Tyr Gly Pro Asn Ala Phe Gly Ala Asp Leu Gly Tyr Phe Thr Gln Leu
130 135 140

Thr Ser Tyr Met Gly Met Met Gln Asp Met Leu Ser Pro Ile Pro Asp
145 150 155 160

Phe Trp Phe Asn Ser Ala Asn Glu Gln Leu Lys Val Met Gly Asn Phe
165 170 175

Gln Lys Tyr Asp Leu Ile Ile Val Glu Ser Trp Thr Lys Ser Tyr Ile
180 185 190

Asp Thr Asn Lys Met Val Gly Asn Thr Val Gly Tyr Gly Thr Val Gly
195 200 205

Pro Gln Asp Ser Trp Ser Leu Ser Glu Arg Tyr Asn Asn Pro Asp His

210 215 220

Asn Leu Val Gly Arg Val Val Gly Gln Asp Pro Asn Val Lys Gln Gly
225 230 235 240

Ala Tyr Asn Asn Arg Trp Val Lys Asp Tyr Ala Thr Ala Leu Ala Lys
245 250 255

Glu Leu Asn Gly Gln Ile Leu Ala Arg His Gln Gly Met Met Leu Pro
260 265 270

Gly Gly Val Thr Ile Asp Gly Gln Arg Leu Ile Glu Glu Ala Arg Leu
275 280 285

Glu Lys Glu Ala Leu Arg Glu Glu Leu Tyr Leu Leu Asp Pro Pro Phe
290 295 300

Gly Ile Leu Val Gly
305

<210> 238
<211> 485
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 238
Met Ile Glu Leu Lys Asp Leu Pro Phe Val Asp Ser Val Pro Asp Glu
1 5 10 15

Gly Gln Glu Arg Ile Ser Trp Ile Lys Asn Gly Glu Glu Ile Leu Gly
20 25 30

Ala Ser Thr Lys Tyr Gly Asn Asp Gly Ser Met Asn Arg Pro Ile Val
35 40 45

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

Lys Thr Ala Ile Glu Thr Ser Gln Lys Asp Ile Lys Thr Ile Gln Gly
65 70 75 80

Val Leu Asp Val Ser Gly Asp Ile Glu Ala Leu Ser Gln Ile Ser Val
85 90 95

Asn Lys Asn Asp Ile Ser Asn Leu Lys Thr Leu Thr Asn Glu His Thr
100 105 110

Asp Ile Leu Thr Gly Thr Asn Asn Thr Val Asp Lys Ile Ile Ala Asp
115 120 125

```
Ile Gly Pro Phe Asn Asp Glu Glu Asn Ser Val Tyr Arg Thr Ile Arg
    130                 135                 140

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

Asp Ile Asn Gly Leu Pro Val Val Gly Asn Ala Ser Thr Gly Met Lys
                165                 170                 175

His Arg Ile Ile Thr Asn Ser Thr Leu Leu Ser Ser Gln Gly Ile Arg
            180                 185                 190

Leu Ser Glu Leu Glu Asn Lys Phe Thr Glu Ser Asp Val Gly Ser Leu
        195                 200                 205

Thr Val Glu Val Gly Lys Leu Arg Asp Glu Leu Gly Asn Lys Pro Val
    210                 215                 220

Asp Phe Gly Pro Asn Ile Tyr Asn Arg Leu Asn Thr Ile Asp Asp Lys
225                 230                 235                 240

Gln Thr Leu Ile Asn Ser Asp Ile Ala Glu Ile Lys Ser Ser Ile Gly
                245                 250                 255

Tyr Pro Glu Asn Val Ser Ile Ile Thr Glu Ile Asn Asn Asn Lys Ser
            260                 265                 270

Ser Ile Glu Ser Ile Asn Asn Glu Leu Asn Gln Ser Glu Gly Val Lys
        275                 280                 285

Gln Arg Leu Thr Ala Ile Glu Thr Ser Ile Gly Ser Asp Asp Ile Pro
    290                 295                 300

Ser Ser Ile Lys Gly Lys Ile Lys Asn His Thr Thr Ser Ile Glu Ser
305                 310                 315                 320

Leu Asn Gly Ile Val Gly Glu Asn Thr Ser Ser Gly Leu Arg Ala Asn
                325                 330                 335

Val Ser Trp Leu Asn Gln Ile Val Gly Thr Asp Ser Ser Gly Gly Gln
            340                 345                 350

Pro Ser Pro Ser Gly Ser Leu Leu Asn Lys Val Ser Val Leu Glu Gly
        355                 360                 365

Glu Val Ser Val Leu Asn Asn Asn Val Gln Asn Ile Gln Val Glu Ile
    370                 375                 380

Gly Asn Asn Arg Thr Gly Ile Lys Gly Gln Val Ile Glu Leu Thr Ser
385                 390                 395                 400
```

Leu Ile Asn Gly Asn Asn Pro Asp Gly Ser Thr Val Glu Glu Arg Gly
405 410 415

Leu Thr Asn Ser Ile Lys Thr Asn Glu Thr Asn Ile Ala Ala Val Thr
420 425 430

His Glu Val Asn Thr Ala Lys Asp Asn Ile Ser Ser Leu Gln Ser Ser
435 440 445

Val Gln Ala Leu Gln Glu Ala Gly Tyr Ile Pro Glu Ala Pro Lys Asp
450 455 460

Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr
465 470 475 480

Phe Leu Ser Pro Ala
485

<210> 239
<211> 516
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 239
Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Lys Tyr Val
1 5 10 15

Lys Phe Asp Pro Val Gly Ser Asn Phe Pro Gly Thr Val Thr Thr Val
20 25 30

Gln Ser Ala Leu Ser Lys Ile Ser Asn Ile Gly Val Asn Gly Ile Pro
35 40 45

Asp Ala Thr Met Glu Val Lys Gly Ile Ala Met Ile Ala Ser Glu Gln
50 55 60

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

Leu Ala Thr Arg Leu Leu Tyr Pro Asn Ala Thr Glu Thr Lys Tyr Gly
85 90 95

Leu Thr Arg Tyr Ser Thr Asn Glu Glu Thr Leu Glu Gly Ser Asp Asn
100 105 110

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

Phe Arg Asn Arg Tyr Ser Ser Glu Ser Ser Asn Gly Val Ile Lys Ile
130 135 140

```
Ser Ser Thr Pro Ala Ala Leu Ala Gly Val Asp Asp Thr Thr Ala Met
145                 150                 155                 160

Thr Pro Leu Lys Thr Gln Lys Leu Ala Ile Lys Leu Ile Ser Gln Ile
                165                 170                 175

Ala Pro Ser Glu Asp Thr Ala Ser Glu Ser Val Arg Gly Val Val Gln
            180                 185                 190

Leu Ser Thr Val Ala Gln Thr Arg Gln Gly Thr Leu Arg Glu Gly Tyr
        195                 200                 205

Ala Ile Ser Pro Tyr Thr Phe Met Asn Ser Val Ala Thr Gln Glu Tyr
    210                 215                 220

Lys Gly Val Ile Arg Leu Gly Thr Gln Ser Glu Ile Asn Ser Asn Leu
225                 230                 235                 240

Gly Asp Val Ala Val Thr Gly Glu Thr Leu Asn Gly Arg Gly Ala Thr
                245                 250                 255

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

Pro Glu Gly Asp Ser Ser Gly Ala Leu Ala Trp Asn Ala Asp Val Ile
        275                 280                 285

Asn Thr Arg Gly Gly Gln Thr Ile Asn Gly Ser Leu Asn Leu Asp His
    290                 295                 300

Leu Thr Ala Asn Gly Ile Trp Ser Arg Gly Gly Met Trp Lys Asn Gly
305                 310                 315                 320

Asp Gln Pro Val Ala Thr Glu Arg Tyr Ala Ser Glu Arg Val Pro Val
                325                 330                 335

Gly Thr Ile Met Met Phe Ala Gly Asp Ser Ala Pro Pro Gly Trp Ile
            340                 345                 350

Met Cys His Gly Gly Thr Val Ser Gly Asp Gln Phe Pro Asp Tyr Arg
        355                 360                 365

Asn Val Val Gly Thr Arg Phe Gly Gly Asp Trp Asn Asn Pro Gly Val
    370                 375                 380

Pro Asp Met Arg Gly Leu Phe Val Arg Gly Ala Gly Thr Gly Gly His
385                 390                 395                 400

Ile Leu Asn Gln Arg Gly Gln Asp Gly Tyr Gly Lys Asp Arg Leu Gly
                405                 410                 415
```

```
Val Gly Cys Asp Gly Met His Val Gly Gly Val Gln Ala Gln Gln Met
            420                 425                 430

Ser Tyr His Lys His Ala Gly Gly Trp Gly Glu Tyr Asn Arg Ser Glu
        435                 440                 445

Gly Pro Phe Gly Ala Ser Val Tyr Gln Gly Tyr Leu Gly Thr Arg Lys
    450                 455                 460

Tyr Ala Asp Trp Asp Asn Ala Ser Tyr Phe Thr Asn Asp Gly Phe Glu
465                 470                 475                 480

Leu Gly Gly Pro Arg Asp Ala Leu Gly Thr Leu Asn Arg Glu Gly Leu
                485                 490                 495

Ile Gly Tyr Glu Thr Arg Pro Trp Asn Ile Ser Leu Asn Tyr Ile Ile
            500                 505                 510

Lys Val His Tyr
        515


<210> 240
<211> 219
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 240
Met Ser Leu Leu Asn Asn Lys Ala Gly Val Ile Ser Arg Leu Ala Asp
1               5                   10                  15

Phe Leu Gly Phe Arg Thr Lys Lys Asn Asp Ile Ser Val Met Asn Asn
            20                  25                  30

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

Asp Ser Asn Val Glu Ser Ala Ile Asn Asp Val Arg Asn Met Ala Glu
    50                  55                  60

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

Gly Val Gln Gln Thr Asp Tyr Trp Ser Phe Glu Gly Thr Val Thr Asp
                85                  90                  95

Thr Ser Ala Lys Pro Gly Asp Pro Val Ile Val Asn Met Phe Gly Ile
            100                 105                 110

Pro Val Lys Ala Thr Asn Gly Met Thr Ser Ile Glu Phe Thr Ser Ala
        115                 120                 125
```

```
Val Arg Thr Ala Leu Gln Glu Met Val Val Lys Phe Ile Ala Ile Asp
    130                 135                 140

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

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

Thr Phe Lys Gln Glu Ile Ile Ser Pro Ser Lys Pro Gly Tyr Gly Thr
            180                 185                 190

Trp Gln Leu Leu Gly Ala Gln Thr Val Thr Leu Asp Ser His Thr Gln
        195                 200                 205

Pro Thr Val Phe Tyr Tyr Phe Glu Arg Ile Ala
    210                 215


<210> 241
<211> 601
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 241
Met Lys Gln Asn Ile Asn Ile Gly Asn Val Val Asp Asp Gly Thr Gly
1               5                   10                  15

Asp Tyr Leu Arg Lys Gly Gly Ile Lys Ile Asn Glu Asn Phe Asp Glu
            20                  25                  30

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

Trp Lys Thr Tyr Asn Ala Ser Ser Gly Gln Thr Leu Thr Ala Glu Trp
    50                  55                  60

Gly Lys Ser Tyr Ala Ile Asn Thr Ser Ser Gly Arg Val Thr Leu Gln
65                  70                  75                  80

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

Asp Val Phe Ala Thr Trp Asn Val Asn Pro Val Thr Leu Val Ala Ala
            100                 105                 110

Ser Gly Asp Thr Ile Lys Gly Ser Ser Ser Ser Val Glu Ile Asn Val
        115                 120                 125

Gln Phe Ser Asp Leu Glu Leu Val Tyr Cys Ala Pro Gly Arg Trp Glu
```

```
130                 135                 140

Tyr Val Lys Asn Lys Gln Ile Asp Lys Ile Ile Ser Ser Asp Ile Ser
145                 150                 155                 160

Asn Val Ala Arg Lys Glu Phe Leu Val Glu Val Gln Gly Gln Thr Asp
                165                 170                 175

Phe Leu Asp Val Phe His Gly Thr Ser Tyr Asn Val Asn Asn Ile Arg
            180                 185                 190

Val Lys His Arg Gly Asn Glu Leu Tyr Tyr Gly Asp Val Phe Ser Glu
        195                 200                 205

Asn Ser Asp Phe Gly Ser Pro Gly Glu Asn Glu Gly Glu Leu Ile Pro
    210                 215                 220

Leu Asp Gly Phe Asn Ile Arg Leu Arg Gln Pro Cys Asn Ile Gly Asp
225                 230                 235                 240

Thr Val Gln Ile Glu Thr Phe Met Asp Gly Val Ser Gln Trp Arg Ser
                245                 250                 255

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

Lys Thr Ser Leu Glu Gly Ser Ile Tyr Val Thr Asp Leu Ser Ala Met
        275                 280                 285

Lys Ser Ile Pro Phe Ser Ala Phe Gly Leu Ile Pro Gly Glu Pro Ile
    290                 295                 300

Asn Pro Asn Ser Leu Glu Val Arg Phe Asn Gly Ile Leu Gln Gln Gln
305                 310                 315                 320

Ala Gly Thr Ala Gly Tyr Pro Leu Phe Leu Cys Glu Gly Ala Asn Ser
                325                 330                 335

Asp Thr Gln Glu Gly Cys Ile Ser Leu Gly Gly Glu Trp Lys Glu Ser
            340                 345                 350

Asn Thr Asp Tyr Ser Ile Glu Tyr Glu Asp Gly Lys Pro Val Ser Leu
        355                 360                 365

Leu Phe Asp Arg Lys Phe Glu Ser Gly Asp Ile Ile Val Ile Thr Trp
    370                 375                 380

Phe Asn Asn Asp Leu Gly Thr Leu Leu Glu Lys Asp Asp Ile Ile Glu
385                 390                 395                 400

Leu Thr Asp Asp Arg Tyr Val Ser Lys Gly Ser Ser Thr Glu Val Thr
```

405 410 415

Gly Asp Val Ala Leu Thr Asp Phe Asp Lys Ile Gly Trp Pro Asn Val
420 425 430

Glu Lys Val Asp Ser Tyr Thr Arg Thr Tyr Asn Ser Ile Ser Ser Ile
435 440 445

Phe Asp Ser Ile Tyr Pro Val Gly Ser Ile Tyr Glu Asn Ala Ile Asn
450 455 460

Pro Asn Asn Pro Val Thr Tyr Met Gly Phe Gly Ser Trp Lys Leu Phe
465 470 475 480

Gly Lys Gly Gln Val Leu Val Gly Trp Asn Asp Asp Val Thr Asp Pro
485 490 495

Asn Phe Ala Leu Asn Asn Asn Asp Leu Asp Ser Ser Gly Asn Pro Ser
500 505 510

His Thr Ala Gly Gly Thr Val Gly Thr Thr Ser Val Thr Leu Glu Asn
515 520 525

Ala Asn Leu Pro Ala Thr Lys Thr Asp Glu Arg Val Leu Ile Glu Asp
530 535 540

Glu Asn Gly Ser Val Ile Ile Gly Gly Cys Gln Tyr Asp Pro Asp Glu
545 550 555 560

Thr Gly Pro Ile Tyr Thr Lys Tyr Arg Glu Asp Tyr Ala Thr Thr Asn
565 570 575

Ser Ser His Thr Pro Pro Thr Asn Ile Ser Asn Ile Gln Pro Ser Ile
580 585 590

Thr Val Tyr Arg Trp Ile Arg Ile Ala
595 600

<210> 242
<211> 288
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 242
Met Phe Ile Gln Glu Pro Lys Lys Leu Ile Asp Thr Gly Glu Ile Gly
1 5 10 15

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

```
Ser Asp Phe Asn Ala Ile Tyr Asn Ala Phe Gly Asp Gln Arg Lys Met
        35                  40                  45

Ala Val Ala Asn Gly Thr Gly Ala Asp Gly Gln Ile Ile His Ala Thr
    50                  55                  60

Gly Tyr Tyr Gln Lys His Ser Ile Thr Glu Tyr Ala Thr Pro Val Lys
65                  70                  75                  80

Val Gly Thr Arg His Asp Ile Asp Thr Ser Thr Val Gly Val Lys Val
                85                  90                  95

Ile Ile Glu Arg Gly Glu Leu Gly Asp Cys Val Glu Phe Ile Asn Ser
            100                 105                 110

Asn Gly Ser Ile Ser Val Thr Asn Pro Leu Thr Ile Gln Ala Ile Asp
        115                 120                 125

Ser Ile Lys Gly Val Ser Gly Asn Leu Val Val Thr Ser Pro Tyr Ser
    130                 135                 140

Lys Val Thr Leu Arg Cys Ile Ser Ser Asp Asn Ser Thr Ser Val Trp
145                 150                 155                 160

Asn Tyr Ser Ile Glu Ser Met Phe Gly Gln Lys Glu Ser Pro Ala Glu
                165                 170                 175

Gly Thr Trp Asn Ile Ser Thr Ser Gly Ser Val Asp Ile Pro Leu Phe
            180                 185                 190

His Arg Thr Glu Tyr Asn Met Ala Lys Leu Leu Val Thr Cys Gln Ser
        195                 200                 205

Val Asp Gly Arg Lys Ile Lys Thr Ala Glu Ile Asn Ile Leu Val Asp
    210                 215                 220

Ala Val Asn Ser Glu Val Ile Ser Ser Glu Tyr Ala Val Met Arg Val
225                 230                 235                 240

Gly Asn Glu Thr Glu Glu Asp Glu Ile Ala Asn Ile Ala Phe Ser Ile
                245                 250                 255

Lys Thr Asn Tyr Val Thr Ala Thr Ile Ser Ser Ser Thr Val Gly Met
            260                 265                 270

Arg Ala Ala Val Lys Val Ile Ala Thr Gln Lys Ile Gly Val Ala Gln
        275                 280                 285
```

<210> 243
<211> 334
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 243

```
Met Asn Asp Ser Ser Val Ile Tyr Arg Ala Ile Val Thr Ser Lys Phe
1               5                  10                  15

Arg Thr Glu Lys Met Leu Asn Phe Tyr Asn Ser Ile Gly Ser Gly Pro
            20                  25                  30

Asp Lys Asn Thr Ile Phe Ile Thr Phe Gly Arg Ser Glu Pro Trp Ser
        35                  40                  45

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

Val Leu Gly Val Thr Asp Met Trp Thr His Met Met Gly Thr Val Lys
65                  70                  75                  80

Val Leu Pro Ser Met Leu Asp Ala Val Ile Pro Arg Arg Asp Trp Gly
                85                  90                  95

Asp Thr Arg Tyr Pro Asp Pro Tyr Thr Phe Arg Ile Asn Asp Ile Val
            100                 105                 110

Val Cys Asn Ser Ala Pro Tyr Asn Ala Thr Glu Ser Gly Ala Gly Trp
        115                 120                 125

Leu Val Tyr Arg Cys Leu Asp Val Pro Asp Thr Gly Met Cys Ser Ile
    130                 135                 140

Ala Ser Leu Thr Asp Lys Asp Glu Cys Leu Lys Leu Gly Gly Lys Trp
145                 150                 155                 160

Thr Pro Ser Val Arg Ser Met Thr Pro Pro Glu Gly Arg Gly Asp Ala
                165                 170                 175

Glu Gly Thr Ile Glu Pro Gly Asp Gly Tyr Val Trp Glu Tyr Leu Phe
            180                 185                 190

Glu Ile Pro Pro Asp Val Ser Ile Asn Arg Cys Thr Asn Glu Tyr Ile
        195                 200                 205

Val Val Pro Trp Pro Glu Glu Leu Lys Glu Asp Pro Thr Arg Trp Gly
    210                 215                 220

Tyr Glu Asp Asn Leu Thr Trp Gln Gln Asp Asp Phe Gly Leu Ile Tyr
225                 230                 235                 240

Arg Val Lys Ala Asn Thr Ile Arg Phe Lys Ala Tyr Leu Asp Ser Val
                245                 250                 255
```

```
Tyr Phe Pro Asp Ala Ala Leu Pro Gly Asn Lys Gly Phe Arg Gln Ile
            260                 265                 270

Ser Ile Ile Thr Asn Pro Leu Glu Ala Lys Ala His Pro Asn Asp Pro
        275                 280                 285

Asn Val Lys Ala Glu Lys Asp Tyr Tyr Asp Pro Glu Asp Leu Met Arg
    290                 295                 300

His Ser Gly Glu Met Ile Tyr Met Glu Asn Arg Pro Pro Ile Ile Met
305                 310                 315                 320

Ala Met Asp Gln Thr Glu Glu Ile Asn Ile Leu Phe Thr Phe
                325                 330

<210> 244
<211> 1032
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 244
Met Thr Val Lys Ala Pro Ser Val Thr Ser Leu Arg Ile Ser Lys Leu
1               5                   10                  15

Ser Ala Asn Gln Val Gln Val Arg Trp Asp Asp Val Gly Ala Asn Phe
            20                  25                  30

Tyr Tyr Phe Val Glu Ile Ala Glu Thr Lys Thr Asp Ser Gly Glu Asn
        35                  40                  45

Leu Pro Ser Asp Gln Tyr Arg Trp Ile Asn Leu Gly Tyr Thr Ala Asn
    50                  55                  60

Asn Ser Phe Phe Phe Asp Asp Ala Asp Pro Leu Thr Ser Tyr Ile Ile
65                  70                  75                  80

Arg Val Ala Thr Ala Ala Gln Asp Phe Glu Gln Ser Asp Trp Val Tyr
                85                  90                  95

Thr Glu Glu Phe Glu Thr Phe Ala Thr Asn Ala Tyr Thr Phe Gln Asn
            100                 105                 110

Met Ile Glu Met Gln Leu Ala Asn Lys Phe Ile Gln Glu Lys Phe Thr
        115                 120                 125

Leu Asn Asn Ser Asn Tyr Val Asn Phe Asn Asn Asp Thr Ile Met Ala
    130                 135                 140

Ala Leu Met Asn Glu Ser Phe Gln Phe Ser Pro Ser Tyr Val Asp Val
145                 150                 155                 160
```

```
Ser Ser Ile Ser Asn Phe Ile Ile Gly Glu Asn Glu Tyr His Glu Ile
                165                 170                 175

Gln Gly Ser Ile Gln Gln Val Cys Lys Asp Ile Asn Arg Val Tyr Leu
            180                 185                 190

Met Glu Ser Glu Gly Ile Leu Tyr Leu Phe Glu Arg Tyr Gln Pro Val
        195                 200                 205

Val Lys Val Ser Asn Asp Lys Gly Gln Thr Trp Lys Ala Val Lys Leu
    210                 215                 220

Phe Asn Asp Arg Val Gly Tyr Pro Leu Ser Lys Thr Val Tyr Tyr Gln
225                 230                 235                 240

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

Arg Lys Ser Thr Asp Val Arg Trp Ser Ala Asp Asp Val Arg Phe Ser
            260                 265                 270

Ser Gln Asp Ile Thr Phe Ala Lys Leu Gly Asp Gln Leu His Leu Gly
        275                 280                 285

Phe Asp Val Glu Ile Phe Gly Thr Tyr Ala Thr Leu Pro Ala Asn Val
    290                 295                 300

Tyr Arg Ile Ala Glu Ala Ile Thr Cys Thr Asp Asp Tyr Ile Tyr Val
305                 310                 315                 320

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

Asp Ser Asp Pro Leu Ser Pro Thr Tyr Ser Glu Arg Leu Phe Glu Pro
            340                 345                 350

Asp Thr Met Thr Ile Thr Gly Asn Pro Lys Ala Val Cys Tyr Lys Met
        355                 360                 365

Asp Ser Ile Gly Asp Lys Val Phe Ala Leu Ile Ile Gly Glu Val Glu
    370                 375                 380

Thr Leu Asn Ala Asn Pro Arg Thr Ser Lys Ile Ile Asp Ser Ala Asp
385                 390                 395                 400

Lys Gly Ile Tyr Val Leu Asn His Asp Glu Lys Thr Trp Lys Arg Val
                405                 410                 415

Phe Gly Asn Thr Glu Glu Glu Arg Arg Arg Ile Gln Pro Gly Tyr Ala
            420                 425                 430
```

```
Asn Met Ser Thr Asp Gly Lys Leu Val Ser Leu Ser Ser Ser Asn Phe
        435                 440                 445

Lys Phe Leu Ser Asp Asn Val Val Asn Asp Pro Glu Thr Met Val Lys
    450                 455                 460

Tyr Gln Leu Ile Gly Ala Val Lys Tyr Glu Phe Pro Arg Glu Trp Leu
465                 470                 475                 480

Ala Asp Lys His Tyr His Met Met Ala Phe Ile Ala Asp Glu Lys Ser
                485                 490                 495

Asp Trp Glu Thr Phe Thr Pro Gln Pro Met Lys Tyr Tyr Ala Glu Pro
            500                 505                 510

Phe Phe Asn Trp Ser Lys Lys Ser Asn Thr Arg Cys Trp Ile Asn Asn
        515                 520                 525

Ser Asn Arg Ala Val Val Val Tyr Ala Asp Leu Lys Tyr Thr Lys Val
    530                 535                 540

Ile Glu Asn Ile Pro Glu Thr Ser Pro Asp Arg Leu Val His Glu Tyr
545                 550                 555                 560

Trp Asp Asp Gly Asp Cys Thr Ile Val Met Pro Asn Val Lys Phe Thr
                565                 570                 575

Gly Phe Lys Lys Tyr Ala Ser Gly Met Leu Phe Tyr Lys Ser Ser Gly
            580                 585                 590

Glu Ile Ile Ser Tyr Tyr Asp Phe Asn Tyr Arg Val Arg Asp Thr Val
        595                 600                 605

Glu Ile Ile Trp Lys Pro Thr Gly Val Phe Leu Lys Ala Phe Leu Gln
    610                 615                 620

Asn Gln Glu His Glu Thr Pro Trp Ser Pro Glu Glu Glu His Gly Leu
625                 630                 635                 640

Ala Asp Pro Asp Leu Arg Pro Leu Ile Gly Thr Met Met Pro Asp Ser
                645                 650                 655

Tyr Leu Leu Gln Asp Ser Asn Phe Glu Ala Phe Cys Glu Ala Tyr Ile
            660                 665                 670

Gln Tyr Leu Ser Asp Gly Tyr Gly Thr Gln Tyr Asn Asn Leu Arg Asn
        675                 680                 685

Leu Ile Arg Asn Gln Tyr Pro Arg Glu Glu His Ala Trp Glu Tyr Leu
    690                 695                 700
```

```
Trp Ser Glu Ile Tyr Lys Arg Asn Ile Tyr Leu Asn Ala Asp Lys Arg
705                 710                 715                 720

Asp Ala Val Ala Arg Phe Phe Glu Ser Arg Ser Tyr Asp Phe Tyr Ser
                725                 730                 735

Thr Lys Gly Ile Glu Ala Ser Tyr Lys Phe Leu Phe Lys Val Leu Tyr
            740                 745                 750

Asn Glu Glu Val Glu Ile Glu Ile Glu Ser Gly Ala Gly Thr Glu Tyr
        755                 760                 765

Asp Ile Ile Val Gln Ser Asp Ser Leu Thr Glu Asp Leu Val Gly Gln
    770                 775                 780

Thr Ile Tyr Thr Ala Thr Gly Arg Cys Asn Val Thr Tyr Ile Glu Arg
785                 790                 795                 800

Ser Tyr Ser Asn Gly Lys Leu Gln Trp Thr Val Thr Ile His Asn Leu
                805                 810                 815

Leu Gly Arg Leu Ile Ala Gly Gln Glu Val Lys Ala Glu Arg Leu Pro
            820                 825                 830

Ser Phe Glu Gly Glu Ile Ile Arg Gly Val Lys Gly Lys Asp Leu Leu
        835                 840                 845

Gln Asn Asn Ile Asp Tyr Ile Asn Arg Ser Arg Ser Tyr Tyr Val Met
    850                 855                 860

Lys Ile Lys Ser Asn Leu Pro Ser Ser Arg Trp Lys Ser Asp Val Ile
865                 870                 875                 880

Arg Phe Val His Pro Val Gly Phe Gly Phe Ile Ala Ile Thr Leu Leu
                885                 890                 895

Thr Met Phe Ile Asn Val Gly Leu Thr Leu Lys His Thr Glu Thr Ile
            900                 905                 910

Ile Asn Lys Tyr Lys Asn Tyr Lys Trp Asp Ser Gly Leu Pro Thr Glu
        915                 920                 925

Tyr Ala Asp Arg Val Ala Lys Leu Thr Pro Thr Gly Glu Ile Glu His
    930                 935                 940

Asp Ser Val Thr Gly Glu Ala Ile Tyr Glu Pro Gly Pro Met Ala Gly
945                 950                 955                 960

Val Glu Tyr Pro Leu Pro Asp Asp Tyr Asn Ala Glu Asn Asn Asn Ser
                965                 970                 975
```

Ile Phe Gln Gly Gln Leu Pro Ser Glu Arg Arg Lys Leu Met Ser Pro
980 985 990

Leu Phe Asp Ala Ser Gly Thr Thr Phe Ala Gln Phe Arg Asp Leu Val
995 1000 1005

Asn Lys Arg Leu Lys Asp Asn Ile Gly Asn Pro Arg Asp Pro Glu
1010 1015 1020

Asn Pro Thr Gln Val Lys Ile Asp Glu
1025 1030

<210> 245
<211> 660
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 245
Met Ala Asn Thr Pro Val Asn Tyr Gln Leu Thr Arg Thr Ala Asn Ala
1 5 10 15

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

Leu Ile Glu Trp Leu Asn Gly Gln Asn Glu Phe Leu Asp Tyr Asp Phe
35 40 45

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

Leu Tyr Ile Gln Gln Phe Gly Asn Ala Ala Val Tyr Glu Ser Phe Met
65 70 75 80

Arg Thr Ala Asn Leu Arg Ser Ser Val Val Gln Ala Ala Gln Asp Asn
85 90 95

Gly Tyr Leu Pro Thr Ser Lys Ser Ala Ala Gln Thr Glu Ile Met Leu
100 105 110

Thr Cys Thr Asp Ala Leu Asn Arg Asn Tyr Ile Thr Ile Pro Arg Gly
115 120 125

Thr Arg Phe Leu Ala Tyr Ala Lys Asp Thr Ser Val Asn Pro Tyr Asn
130 135 140

Phe Val Ser Thr Glu Asp Val Ile Ala Ile Arg Asp Lys Asn Asn Gln
145 150 155 160

Tyr Phe Pro Arg Leu Lys Leu Ala Gln Gly Arg Ile Val Arg Thr Glu

```
                165                 170                 175

Ile Ile Tyr Asp Lys Leu Thr Pro Ile Ile Ile Tyr Asp Lys Asn Ile
            180                 185                 190

Asp Arg Asn Gln Val Lys Leu Tyr Val Asp Gly Ala Glu Trp Ile Asn
        195                 200                 205

Trp Thr Arg Lys Ser Met Val His Ala Gly Ser Thr Ser Thr Ile Tyr
    210                 215                 220

Tyr Met Arg Glu Thr Ile Asp Gly Asn Thr Glu Phe Tyr Phe Gly Glu
225                 230                 235                 240

Gly Glu Ile Ser Val Asn Ala Ser Glu Gly Ala Leu Thr Ala Asn Tyr
                245                 250                 255

Ile Gly Gly Leu Lys Pro Thr Gln Asn Ser Thr Ile Val Ile Glu Tyr
            260                 265                 270

Ile Ser Thr Asn Gly Ala Asp Ala Asn Gly Ala Val Gly Phe Ser Tyr
        275                 280                 285

Ala Asp Thr Leu Thr Asn Ile Thr Ile Ile Asn Ile Asn Glu Asn Pro
    290                 295                 300

Asn Gly Asp Pro Asp Phe Val Gly Ala Asp Gly Gly Gly Asp Pro Glu
305                 310                 315                 320

Asp Ile Glu Arg Ile Arg Glu Leu Gly Thr Ile Lys Arg Glu Thr Gln
                325                 330                 335

Gln Arg Cys Val Thr Ala Thr Asp Tyr Asp Thr Phe Val Ser Glu Arg
            340                 345                 350

Phe Gly Ser Ile Ile Gln Ala Val Gln Thr Phe Thr Asp Ser Thr Lys
        355                 360                 365

Pro Gly Tyr Ala Phe Ile Ala Ala Lys Pro Lys Ser Gly Leu Tyr Leu
    370                 375                 380

Thr Thr Val Gln Arg Glu Asp Ile Lys Asn Tyr Leu Lys Asp Tyr Asn
385                 390                 395                 400

Leu Ala Pro Ile Thr Pro Ser Ile Ile Ser Pro Asn Tyr Leu Phe Ile
                405                 410                 415

Lys Thr Asn Leu Lys Val Thr Tyr Ala Leu Asn Lys Leu Gln Glu Ser
            420                 425                 430

Glu Gln Trp Leu Glu Gly Gln Ile Ile Asp Lys Ile Asp Arg Tyr Tyr
```

435 440 445

Thr Glu Asp Val Glu Ile Phe Asn Ser Ser Phe Ala Lys Ser Lys Met
450 455 460

Leu Thr Tyr Val Asp Asp Ala Asp His Ser Val Ile Gly Ser Ser Ala
465 470 475 480

Thr Ile Gln Met Val Arg Glu Val Gln Asn Phe Tyr Lys Thr Pro Glu
485 490 495

Ala Gly Ile Lys Tyr Asn Asn Gln Ile Lys Asp Arg Ser Met Glu Ser
500 505 510

Asn Thr Phe Ser Phe Asn Ser Gly Arg Lys Val Val Asn Pro Asp Thr
515 520 525

Gly Leu Glu Glu Asp Val Leu Tyr Asp Val Arg Ile Val Ser Thr Asp
530 535 540

Arg Asp Ser Lys Gly Ile Gly Lys Val Ile Ile Gly Pro Phe Ala Ser
545 550 555 560

Gly Asp Val Thr Glu Asn Glu Asn Ile Gln Pro Tyr Thr Gly Asn Asp
565 570 575

Phe Asn Lys Leu Ala Asn Ser Asp Gly Arg Asp Lys Tyr Tyr Val Ile
580 585 590

Gly Glu Ile Asn Tyr Pro Ala Asp Met Ile Tyr Trp Asn Ile Ala Lys
595 600 605

Ile Asn Leu Thr Ser Glu Lys Phe Glu Val Gln Thr Ile Glu Leu Tyr
610 615 620

Ser Asp Pro Thr Asp Asp Val Ile Phe Thr Arg Asp Gly Ser Leu Ile
625 630 635 640

Val Phe Glu Asn Asp Leu Arg Pro Gln Tyr Leu Thr Ile Asp Leu Glu
645 650 655

Pro Ile Ser Gln
660

<210> 246
<211> 97
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 246

```
Met Ser Gly Leu Ser Tyr Asp Lys Cys Val Thr Ala Gly His Glu Ala
1               5                   10                  15

Trp Pro Pro Thr Val Val Asn Ala Thr Gln Ser Lys Val Phe Thr Gly
            20                  25                  30

Gly Ile Ala Val Leu Val Ala Gly Asp Pro Ile Thr Glu His Thr Glu
        35                  40                  45

Ile Lys Lys Pro Tyr Glu Thr His Gly Gly Val Thr Gln Pro Arg Thr
    50                  55                  60

Ser Lys Val Tyr Val Thr Gly Lys Lys Ala Val Gln Met Ala Asp Pro
65                  70                  75                  80

Ile Ser Cys Gly Asp Thr Val Ala Gln Ala Ser Ser Lys Val Phe Ile
                85                  90                  95

Lys
```

<210> 247
<211> 164
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 247

```
Met Glu Gly Ser Ser Ile Asp Val Thr Phe Thr Ala Gln Leu Glu Thr
1               5                   10                  15

Gly Glu Thr Leu Val Ser Ile Asn Ile Thr Ser Tyr Glu Glu Thr Pro
            20                  25                  30

Gly Val Leu Val Glu Glu Asn Arg Leu Tyr Gly Thr Tyr Glu Ser Val
        35                  40                  45

Phe Gly Phe Gly Asn Asp Ala Leu Lys Tyr Arg Leu Gly Asp Glu Phe
    50                  55                  60

Lys Thr Ala Ala Ser Trp Glu Glu Leu Pro Thr Asp Ser Asp Thr Gln
65                  70                  75                  80

Leu Tyr Leu Trp Lys Ala Pro Gln Asn Leu Gln Lys Thr Phe Thr Tyr
                85                  90                  95

Glu Val Thr Leu Ile Tyr Asp Tyr Gln Glu Gln Ser Glu Ser Gly Gly
            100                 105                 110

Ser Gly Ser Asn Ser Arg Ser Ser Ser Asp Thr Thr Glu Pro Thr Asp
        115                 120                 125
```

```
Pro Pro Ala Pro Val Arg Lys Thr Leu Val Lys Asn Tyr Thr Lys Thr
    130                 135                 140

Ile Val Gly Asn Trp Ser Arg Trp Ala Asn Lys Leu Arg Ser Tyr Val
145                 150                 155                 160

Tyr Glu Arg Ser
```

<210> 248
<211> 575
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 248

```
Met Glu Met Ile Ser Asn Asn Leu Asn Trp Phe Val Gly Val Val Glu
1               5                   10                  15

Asp Arg Met Asp Pro Leu Lys Leu Gly Arg Val Arg Val Arg Val Val
            20                  25                  30

Gly Leu His Pro Pro Gln Arg Ala Gln Gly Asp Val Met Gly Ile Pro
        35                  40                  45

Thr Glu Lys Leu Pro Trp Met Ser Val Ile Gln Pro Ile Thr Ser Ala
    50                  55                  60

Ala Met Ser Gly Ile Gly Gly Ser Val Thr Gly Pro Val Glu Gly Thr
65                  70                  75                  80

Arg Val Tyr Gly His Phe Leu Asp Lys Trp Lys Thr Asn Gly Ile Val
                85                  90                  95

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

Gly Phe Ser Asp Pro Thr Gly Gln Tyr Pro Arg Arg Leu Gly Asn Asp
        115                 120                 125

Thr Asn Val Leu Asn Gln Gly Gly Glu Val Gly Tyr Asp Ser Ser Ser
    130                 135                 140

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

Arg Pro Leu Ser Glu Ile Pro Thr Asp Asp Asn Pro Asn Met Ser Met
                165                 170                 175

Ala Asp Met Leu Arg Arg Asp Glu Gly Leu Arg Leu Lys Val Tyr Trp
            180                 185                 190
```

```
Asp Thr Glu Gly Tyr Pro Thr Ile Gly Ile Gly His Leu Ile Met Lys
        195                 200                 205

Gln Pro Val Arg Asp Met Ala Gln Ile Asn Lys Val Leu Ser Lys Gln
    210                 215                 220

Val Gly Arg Glu Ile Thr Gly Asn Pro Gly Ser Ile Thr Met Glu Glu
225                 230                 235                 240

Ala Thr Thr Leu Phe Glu Arg Asp Leu Ala Asp Met Gln Arg Asp Ile
                245                 250                 255

Lys Ser His Ser Lys Val Gly Pro Val Trp Gln Ala Val Asn Arg Ser
            260                 265                 270

Arg Gln Met Ala Leu Glu Asn Met Ala Phe Gln Met Gly Val Gly Gly
        275                 280                 285

Val Ala Lys Phe Asn Thr Met Leu Thr Ala Met Leu Ala Gly Asp Trp
    290                 295                 300

Glu Lys Ala Tyr Lys Ala Gly Arg Asp Ser Leu Trp Tyr Gln Gln Thr
305                 310                 315                 320

Lys Gly Arg Ala Ser Arg Val Thr Met Ile Ile Leu Thr Gly Asn Leu
                325                 330                 335

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

Met Ala Ala Thr Val Ala Lys Ser Ser Asp Pro Ala Asp Pro Pro Ile
        355                 360                 365

Pro Asn Asp Ser Arg Ile Leu Phe Lys Glu Pro Val Ser Ser Tyr Lys
    370                 375                 380

Gly Glu Tyr Pro Tyr Val His Thr Met Glu Thr Glu Ser Gly His Ile
385                 390                 395                 400

Gln Glu Phe Asp Asp Thr Pro Gly Gln Glu Arg Tyr Arg Leu Val His
                405                 410                 415

Pro Thr Gly Thr Tyr Glu Glu Val Ser Pro Ser Gly Arg Arg Thr Arg
            420                 425                 430

Lys Thr Val Asp Asn Leu Tyr Asp Ile Thr Asn Ala Asp Gly Asn Phe
        435                 440                 445

Leu Val Ala Gly Asp Lys Lys Thr Asn Val Gly Gly Ser Glu Ile Tyr
    450                 455                 460
```

```
Tyr Asn Met Asp Asn Arg Leu His Gln Ile Asp Gly Ser Asn Thr Ile
465                 470                 475                 480

Phe Val Arg Gly Asp Glu Thr Lys Thr Val Glu Gly Asn Gly Thr Ile
                485                 490                 495

Leu Val Lys Gly Asn Val Thr Ile Val Val Glu Gly Asn Ala Asp Ile
            500                 505                 510

Thr Val Lys Gly Asp Ala Thr Thr Leu Val Glu Gly Asn Gln Thr Asn
        515                 520                 525

Thr Val Asn Gly Asn Leu Ser Trp Lys Val Ala Gly Thr Val Asp Trp
    530                 535                 540

Asp Val Gly Gly Asp Trp Thr Glu Lys Met Ala Ser Met Ser Ser Ile
545                 550                 555                 560

Ser Ser Gly Gln Tyr Thr Ile Asp Gly Ser Arg Ile Asp Ile Gly
                565                 570                 575


<210> 249
<211> 196
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 249
Met Leu Phe Thr Phe Phe Asp Pro Ile Glu Tyr Ala Ala Lys Thr Val
1               5                   10                  15

Asn Lys Asn Ala Pro Thr Ile Pro Met Thr Asp Ile Phe Arg Asn Tyr
            20                  25                  30

Lys Asp Tyr Phe Lys Arg Ala Leu Ala Gly Tyr Arg Leu Arg Thr Tyr
        35                  40                  45

Tyr Ile Lys Gly Ser Pro Arg Pro Glu Glu Leu Ala Asn Thr Ile Tyr
    50                  55                  60

Gly Asn Pro Gln Leu Tyr Trp Val Leu Leu Met Cys Asn Asp Asn Tyr
65                  70                  75                  80

Asp Pro Tyr Tyr Gly Trp Ile Thr Ser Gln Glu Ala Ala Tyr Gln Ala
                85                  90                  95

Ser Ile Gln Lys Tyr Lys Asn Val Gly Gly Asp Gln Ile Val Tyr His
            100                 105                 110

Val Asn Glu Asn Gly Glu Lys Phe Tyr Asn Leu Ile Ser Tyr Asp Asp
```

115 120 125

Asn Pro Tyr Val Trp Tyr Asp Lys Gly Asp Lys Ala Arg Lys Tyr Pro
130 135 140

Gln Tyr Glu Gly Ala Leu Ala Ala Val Asn Thr Tyr Glu Asp Ala Val
145 150 155 160

Leu Glu Asn Glu Lys Leu Arg Gln Ile Lys Ile Ile Ala Lys Ser Asp
165 170 175

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

Gly Asn Asp Lys
195

<210> 250
<211> 150
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 250
Met Ala Tyr Ser Gly Lys Trp Val Pro Lys Asn Ile Ser Lys Tyr Arg
1 5 10 15

Gly Asp Pro Lys Lys Ile Thr Tyr Arg Ser Asn Trp Glu Lys Phe Phe
20 25 30

Phe Glu Trp Leu Asp Lys Asn Pro Glu Ile Ile Ala Trp Gly Ser Glu
35 40 45

Thr Ala Val Ile Pro Tyr Phe Cys Asn Ala Glu Gly Lys Lys Arg Arg
50 55 60

Tyr Phe Met Asp Ile Trp Met Lys Asp Ser Ser Gly Gln Glu Phe Phe
65 70 75 80

Ile Glu Ile Lys Pro Lys Lys Glu Thr Gln Pro Pro Val Lys Pro Ala
85 90 95

His Leu Thr Thr Ala Ala Lys Lys Arg Phe Met Asn Glu Ile Tyr Thr
100 105 110

Tyr Ser Val Asn Thr Asp Lys Trp Lys Ala Ala Gln Ala Leu Ala Glu
115 120 125

Lys Arg Gly Ile Lys Phe Arg Ile Leu Thr Glu Asp Gly Leu Arg Ala
130 135 140

Leu Gly Phe Lys Gly Ala
145 150

<210> 251
<211> 274
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 251
Met Ala Ile Phe Gln Ile Ile Asn Glu Ser Thr Pro Gln Val Pro Lys
1 5 10 15

Val Lys Gln Ser Leu Asn Glu Lys Lys Trp Ile Gln Ile Gly Leu Glu
20 25 30

Tyr Lys Lys Ala Lys Ala Lys Gly Met Thr Gly Lys Gln Phe Ala Glu
35 40 45

Glu Arg Gly Ile Lys Tyr Ser Thr Phe Thr Ser Ala Met Ser Lys Tyr
50 55 60

Ala Ser Gly Ile Lys Thr Ala Glu Lys Ile Gln Lys Leu Glu Ser Lys
65 70 75 80

Pro Met Asn Lys Leu Asn Lys Gln Glu Arg Gln Leu Leu Met Ile Asn
85 90 95

Ser Phe Arg Gln Thr Leu Arg Asp Lys Ile Arg Asn Glu Gly Ala Ala
100 105 110

Ile Asn Asn Lys Thr Arg Lys Trp Phe Ala Glu Thr Ile Lys Gln Val
115 120 125

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

Ala Tyr Asp Ala Lys His Lys Glu Thr Leu Pro Tyr Trp Asp Lys Phe
145 150 155 160

Pro Leu Ile Ile Tyr Leu Gly Leu Gly Lys His Asn Leu Met Tyr Gly
165 170 175

Leu Asn Leu His Tyr Ile Pro Pro Lys Ala Arg Gln Gln Phe Leu Glu
180 185 190

Glu Leu Leu Lys Gln Tyr Ala Asn Thr Pro Thr Ile Thr Asn Lys Thr
195 200 205

Lys Leu Lys Ile Asp Trp Ser Gln Val Lys Gly Phe Arg Gly Ala Asp
210 215 220

Gln Met Ile Lys Ala Tyr Ile Pro Gly Asn Ile Met Gly Ser Leu Val
225 230 235 240

Glu Ile Ala Pro Lys Asp Trp Ala Asn Val Val Leu Met Pro Leu Gln
245 250 255

Gln Phe Val Ser Lys Gly Lys Arg Phe Ser Ala Asn Lys Val Trp Ser
260 265 270

Asn Ile

<210> 252
<211> 176
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 252
Met Ser Gln Ala Leu Gln Gln Ile Phe Asn Gln Ala Asn Thr Thr Asn
1 5 10 15

Phe Val Val Ser Ile Pro His Ser Asn Thr Thr Ser Ala Phe Thr Leu
20 25 30

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

Thr Val Thr Gly Pro Phe Gly Leu Gly Arg Ala Gln Arg Pro Gly Ala
50 55 60

Thr Phe Glu Tyr Asp Pro Leu Ile Val Arg Phe Ile Val Asp Glu Glu
65 70 75 80

Leu Lys Ser Trp Ile Gly Met Tyr Glu Trp Met Leu Gly Thr Ser Asn
85 90 95

Tyr Leu Thr Gly Glu Asn Thr Ala Gln Lys Thr Gly Pro Glu Tyr Ile
100 105 110

Thr Leu Tyr Ile Leu Asp Asn Ser Lys Thr Glu Ile Val Met Ser Ile
115 120 125

Asn Phe Tyr Lys Pro Trp Val Ser Asp Leu Ser Glu Val Glu Phe Ser
130 135 140

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

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

<210> 253
<211> 241
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 253
Met Lys Leu Ile Phe Leu Ser Gly Val Lys Arg Ser Gly Lys Asp Thr
1 5 10 15

Thr Ala Asp Phe Ile Met Ser Asn Tyr Ser Ala Val Lys Tyr Gln Leu
20 25 30

Ala Gly Pro Ile Lys Asp Ala Leu Ala Tyr Ala Trp Gly Val Phe Ala
35 40 45

Ala Asn Thr Asp Tyr Pro Cys Leu Thr Arg Lys Glu Phe Glu Gly Ile
50 55 60

Asp Tyr Asp Arg Glu Thr Asn Leu Asn Leu Thr Lys Leu Glu Val Ile
65 70 75 80

Thr Ile Met Glu Gln Ala Phe Cys Tyr Leu Asn Gly Lys Ser Pro Ile
85 90 95

Lys Gly Val Phe Val Phe Asp Asp Glu Gly Gln Glu Ser Val Asn Ser
100 105 110

Val Ala Phe Asn Lys Ile Ile Asp Val Ile Asn Asn Ile Glu Asp Gln
115 120 125

Trp Ser Val Arg Arg Leu Met Gln Ala Leu Gly Thr Asp Leu Ile Val
130 135 140

Asn Asn Phe Asp Arg Met Tyr Trp Val Lys Leu Phe Ala Leu Asp Tyr
145 150 155 160

Leu Asp Lys Phe Asn Ser Gly Tyr Asp Tyr Tyr Ile Val Pro Asp Thr
165 170 175

Arg Gln Asp His Glu Met Asp Ala Ala Arg Ala Met Gly Ala Thr Val
180 185 190

Ile His Val Val Arg Pro Gly Gln Lys Ser Asn Asp Thr His Ile Thr
195 200 205

Glu Ala Gly Leu Pro Ile Arg Asp Gly Asp Leu Val Ile Thr Asn Asp
210 215 220

Gly Ser Leu Glu Glu Leu Phe Ser Lys Ile Lys Asn Thr Leu Lys Val

225 230 235 240

Leu

<210> 254
<211> 76
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 254
Met Ser Glu Gln Thr Ile Glu Gln Lys Leu Ser Ala Glu Ile Val Thr
1 5 10 15

Leu Lys Ser Arg Ile Leu Asp Thr Gln Asp Gln Ala Ala Arg Leu Met
20 25 30

Glu Glu Ser Lys Ile Leu Gln Gly Thr Leu Ala Glu Ile Ala His Ala
35 40 45

Val Gly Ile Thr Gly Asp Thr Ile Lys Val Glu Glu Ile Val Glu Ala
50 55 60

Val Lys Asn Leu Thr Ala Glu Ser Ala Asp Glu Glu
65 70 75

<210> 255
<211> 151
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 255
Met Glu Phe Lys Asp Phe Ser Thr Gly Leu Tyr Val Ala Ala Lys Phe
1 5 10 15

Ser Glu Leu Thr Leu Asp Ala Leu Glu Glu Leu Gln Arg Ser Leu Arg
20 25 30

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

Ser Arg Val Asn Val Pro Tyr Val Pro Ser Ser Gly Ser Phe Glu Val
50 55 60

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

Leu Val Leu Val Leu Asp Ser Glu Tyr Leu Arg Cys Arg His Met Tyr
85 90 95

Ala Arg Ala Leu Gly Ala Thr His Asp Phe Asp Asp Tyr Thr Pro His
100 105 110

Ile Thr Leu Ser Tyr Asn Val Gly Pro Leu Ser Phe Ser Gly Asp Val
115 120 125

Gln Ile Pro Val Val Leu Asp Arg Glu Tyr Lys Glu Pro Leu Lys Leu
130 135 140

Asp Trp Ala Asp Asp Leu Lys
145 150

<210> 256
<211> 85
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 256
Met Lys Thr Phe Lys Glu Phe Ala Thr Lys Thr Thr Ile Thr Glu Ser
1 5 10 15

Ser His Gly Met Glu Val Lys Leu Gly Met Ala Leu Ala Glu Ala Glu
20 25 30

Arg Leu Phe Ser Arg Ile Lys Glu Leu Ala Ala Ala Val Asp Pro Ser
35 40 45

Ser Phe Lys Gly Asp Gln Thr Lys Val Lys Ala Leu Leu Ala Leu Cys
50 55 60

Ser Asp Ala Gly Glu Ile Ala Lys Asn Gly Ser Lys Met Lys Lys Arg
65 70 75 80

Leu Glu Asp Leu Lys
85

<210> 257
<211> 81
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 257
Met Glu Ile Lys Met Lys Thr Tyr Gln Glu Phe Ile Ala Glu Thr Ala
1 5 10 15

Asp Val Lys Val Glu Phe Ile Tyr Thr Gly Lys Lys Asp Lys Met Gly
20 25 30

Glu Met Pro His Gly Val Leu Arg Asp Ala Leu Asp Asn Phe Gly Gln

35 40 45

Leu Ala Ala Glu Asp Tyr Gly Asp Lys Ile Val Val Thr Gly Pro Ala
50 55 60

Ala Val Ile Glu Lys Trp Ala Ala Glu Asn Lys Ser Ile Phe Arg Lys
65 70 75 80

Lys

<210> 258
<211> 61
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 258
Met Lys Arg Cys Glu Leu Ile Arg Asn Val Ala Ile Ala Ile Ser Ala
1 5 10 15

Ser Ala Phe Ser Phe Ser Met Phe Val Gly Phe Ile Cys Gly Leu Leu
20 25 30

Thr Thr Ala Glu Asn Val Phe Ser Leu Val Val Ala Phe Leu Ile Gly
35 40 45

Leu Ile Ala Ile Val Met Asp Lys Ile Ser Lys Gly Glu
50 55 60

<210> 259
<211> 132
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 259
Met Asn Val Glu Tyr Tyr Val Tyr Ala Asp Tyr Glu Asn Asn Pro Ser
1 5 10 15

Lys Asp Glu Asp Asn Arg Leu Gly Val Asp Ala Phe Asp Ser Pro Ala
20 25 30

Ala Ala Trp Gln Trp Val Glu Arg Thr Asp Ile Pro Tyr Arg Tyr Ile
35 40 45

Glu Val Val Asp His Ala Gly Asn Lys Tyr Pro Lys Glu Ala Tyr Val
50 55 60

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

Pro Arg Gly Gly Tyr Thr Asp Leu Ile Ala Lys Ala Phe Ser Glu Asp
85 90 95

Glu Leu Arg Asp Ile Ile Lys Glu Asn Glu Asn Lys Pro Met Asp Ser
100 105 110

Asn Arg Phe Asp Trp Trp Gln Ile Val Asn Ala Asn Thr His Thr Ile
115 120 125

Val Asp Glu Gly
130

<210> 260
<211> 95
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 260
Met Ile Leu Tyr Ala Lys Val Ser Ser Ile Glu Asn Gly Tyr Lys Tyr
1 5 10 15

Asp Gln Asp Ala Ala Lys Ala Leu Ile Asp Asp Tyr Gly Ile Leu Thr
20 25 30

Cys Phe Glu Val Glu Lys Val Tyr Ile Asp Arg Ser Ser Ser Gln Val
35 40 45

Lys Leu Val Lys Glu Glu Arg Lys Phe Asn Thr Val Asn Phe Asp Phe
50 55 60

Phe Ile Glu Thr Glu Lys Gly Pro Leu Glu Tyr Asp Ile Phe Lys Asn
65 70 75 80

Pro Leu Gly Leu Glu Cys Ile Val Asn Met Tyr Tyr Tyr Lys Trp
85 90 95

<210> 261
<211> 73
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 261
ugggaauuag ccaaguuggu aaggcacugg auuuugauuc caggaugcaa agguucgagu 60

ccuuuauucc cag 73

<210> 262
<211> 84
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 262
gcgagaaugg ccaaauuggu aaaggcacag cacuuaaaau gcugcggaau gauuuccuug 60

uggguucgag ucccacuucu cgca 84

<210> 263
<211> 71
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 263
gcggauaucg uauaauggua uuaccucaga cuuccaaucu gaugauguga guucgauucu 60

cauuauccgc u 71

<210> 264
<211> 74
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 264
cuccguguag cucaguuugg uagagcgucu gcuuugggag cagaaugucg uagguucaaa 60

uccugccacg gaga 74

<210> 265
<211> 87
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 265
ggaggcgugg cagagugguu uaaugcaccg gucuugaaaa ccggcagucg cuccggcgac 60

ucauagguuc aaauccuauc gccuccg 87

<210> 266
<211> 73
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 266
gcugauuuag cucaguaggu agagcaacuc acuuguaaug agaaggucgg cgguucgauu 60

ccgucaauca gca 73

<210> 267
<211> 72

<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 267
ggcccuguag cuggaagguu caagcaagcg acucauaauc gccagauggu gguucaauuc 60

cacccagggc ca 72

<210> 268
<211> 84
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 268
ggggaguuau cccguagagg uagcggugug gacuguaaau ccauugucau ugcgacucgg 60

gugguucgac uccaccacuc ccca 84

<210> 269
<211> 72
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 269
ggauguguag cucaauggca gagcgaucgc cuguuaagcg auugguuaua gguucgaauc 60

cuaucacguc cg 72

<210> 270
<211> 73
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 270
guggccguag uucaguuggu agaacucgag auugugauuc ucguagucau ggguucgacu 60

cccaucgguc acc 73

<210> 271
<211> 73
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 271
cggggcauag cucagaagga agagcaagga ccuucuaagu ccuaggucgu agguucgauc 60

ccuacugccu cga 73

<210> 272
<211> 116
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 272
Met Lys Gly Asn Val Tyr Leu Val Val His Asp Leu Thr Phe Tyr Phe
1 5 10 15

Asn His Asn Asp Thr Val Ile Ser Glu Arg Val Ile Asn Leu Leu Tyr
20 25 30

Gln His Ala Asp Tyr Val Tyr Val Glu Asn Glu Tyr Gly His Trp Gln
35 40 45

Phe Leu Lys Asn Arg Ser Phe Gly Leu Asp Gly Tyr Glu Tyr Phe Asp
50 55 60

Arg Lys Asp Leu Leu Asp Thr Ile Pro Leu Ser Thr Gln Tyr Gln Asn
65 70 75 80

His Lys Ser Leu His Lys Cys Arg Leu Ile Arg Asn Ala Glu Ser Ala
85 90 95

Tyr Glu Ala Ile Asp Leu Trp Arg Lys Arg Arg Glu Tyr Ile Asp Ser
100 105 110

Leu Lys Glu Tyr
115

<210> 273
<211> 157
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 273
Met Lys Ser Tyr Thr Gln Phe Leu Asn Glu Ala Val Leu Asn Glu Ala
1 5 10 15

Ser Ser Thr Glu Ile Gln Ala Val Ala Lys Ala Ala Ile Ala Ala Gly
20 25 30

Lys Tyr Ser Tyr Lys Asp Ala Ser Asp Glu Ser Arg Phe Gln Phe Ala
35 40 45

Arg Asp Met Lys Ala Glu Gly Phe Thr Gly Asn Ala Val Ser Met Ala
50 55 60

Trp Lys Ser Leu Val Ala Thr Gly Ala Ala Phe Ala Lys Ala Ser Gly
65 70 75 80

```
Lys Pro Ala Pro Lys Ala Asp Pro Lys Ala Ala Gln Glu Lys Asn Ile
                85                  90                  95

Val Lys Gly Ile Ile Ala Lys Tyr Glu Ala Ile Leu Lys Glu Leu Leu
            100                 105                 110

Val Ile Lys Thr Glu Gly Gln Lys Leu Ala Arg Ala Tyr Ser Phe Lys
        115                 120                 125

Asp Asn Pro His Val His Ser Leu Glu Tyr Val Glu Asp Ile Gln Lys
    130                 135                 140

Ile Ile Lys Asp Arg Ile Trp Ser Ala Lys Gln Ile Lys
145                 150                 155


<210> 274
<211> 187
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 274
Met Lys Thr Tyr Ala Glu Phe Leu Thr Glu Ala Ala Lys Leu Pro Ser
1               5                   10                  15

Glu Ala Asp Leu Thr Lys Val Phe Phe Gln Leu Asp Pro Lys Asp Arg
            20                  25                  30

Gly Asp Phe Leu Lys Trp Lys Ala Lys Ala Ile Glu Met Tyr Asn Ile
        35                  40                  45

Asp Asn Ser Ser Phe Thr Met Ser Gln Glu Asn Lys Phe Asn Lys Ala
    50                  55                  60

Phe Phe Lys Ile Ser Lys Lys Leu Ala Ser Gly Ala Gln Val Pro Lys
65                  70                  75                  80

Ser Val Leu Ala Thr Pro Glu Arg Ala Pro Val Lys Ile Ser Lys Asn
                85                  90                  95

Met Phe Asp Thr Lys Lys Tyr Val Asn Ala Leu Asn Lys Ala Leu Asp
            100                 105                 110

Ala Leu Asp Asp Ala Lys Lys Ala Ala Arg Asp Leu Gln Asp Val Tyr
        115                 120                 125

Thr Asp Phe Asp Arg Lys Thr Lys Gly Ser Ile Ser Asn Ser Glu Arg
    130                 135                 140

Asn Ser Val Ser Val Tyr Ser Asp Ser Leu Asp Val Leu Gly Asp Ala
```

145 150 155 160

Tyr Thr Glu Ile Lys Asn Arg Ile Asn Thr Ala Ser Lys Leu Lys Ala
165 170 175

Ala Ala Glu Ala Ile Ile Ser Lys Leu Gly Lys
180 185

<210> 275
<211> 87
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 275
Met Asp Asn Tyr Gly Glu Leu Phe Asn Phe Phe Met Lys Cys Val Ser
1 5 10 15

Glu Asp Phe Gly Arg Thr Val Asn Asp Ile Lys Val Ile Gly Pro Asp
20 25 30

His Pro Met Phe Glu Thr Tyr Ala Val Met Gly Asn Glu Asp Gly Gln
35 40 45

Trp Tyr Thr Val Lys Val Val Ile Asn Met Phe Thr Ala Glu Gly Tyr
50 55 60

Val Lys Leu Ser Ser Lys Val Tyr His Asp Asn Asp Glu Ile Ala Glu
65 70 75 80

Glu Tyr Phe Asn Asn Met Lys
85

<210> 276
<211> 197
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 276
Met Asn Thr Leu Lys Lys Ile Val Glu Phe Ile Arg Thr Lys Leu Gly
1 5 10 15

Ser Ala Met Ala Lys Asn Leu Ser Val Glu Glu Gln Tyr Thr Ala Ala
20 25 30

Ala Ala Lys Leu Leu Asp Lys Ile Lys Asp Leu Lys Thr Ala Ser Val
35 40 45

Lys Ser Ile Asn Glu Glu Lys Arg Ile Arg Glu Leu Val Ile Glu Lys
50 55 60

Asn Arg Gln Ala Glu Ser Lys Glu Arg Glu Ile Arg Lys Leu Leu Ser
65 70 75 80

Glu Gly Gln Asp Val Thr Met His Ala Lys Leu Gly Leu Leu Tyr Arg
85 90 95

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

Arg Ile Glu Ile Ala Lys Lys Val Val Glu Leu Asp Asp Ala Arg Gln
115 120 125

Glu Leu Ala Val Lys Leu Glu Tyr Ile Arg Glu Thr Arg Ala Ala Asn
130 135 140

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

Thr Lys Val Asp Ile Glu Asp Thr Leu Ala Arg Val Glu Thr Phe Asn
165 170 175

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

Ile Asn Ser Leu Lys
195

<210> 277
<211> 202
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 277
Met Lys Met Gln Ser Asp Phe Asn Ser Met Phe Glu Glu Phe Gln Arg
1 5 10 15

Gln Val Asp Val Pro Asp Gln Leu Leu Asn Ala Leu Lys Arg Met Ala
20 25 30

Glu Gly Arg Asn Tyr Tyr Trp Gly Ser Ser Tyr Glu Thr Asp Glu Ser
35 40 45

Leu Ser Gly Arg Phe Ser Arg Gly Lys Lys Ser Leu Ile Arg Pro Gly
50 55 60

Ile Leu Ile Asn Ser Ile Glu Ser Ile His Ser Leu Thr Cys Asp Phe
65 70 75 80

Asp Val Glu Phe Thr Asp Phe Ile Ser Pro Glu Trp Thr Val Cys Tyr
85 90 95

```
Leu Asn Asp Asp Phe Asp Tyr Leu Gly Val Tyr Ser Leu Ser Asp Ala
            100                 105                 110

Trp Phe Lys Arg Asn Leu Gln Lys Ser Asn Leu Phe Tyr Ile Asp Thr
        115                 120                 125

Thr Val Lys Phe Gln Gly Lys Lys Tyr Phe Phe Thr Leu Ile Val Asp
    130                 135                 140

Ser Glu Thr Lys His Glu Asn Lys Arg Ile Leu Ser Lys Lys Asn Ile
145                 150                 155                 160

Leu Thr Ile Val Asp Asp Leu Phe Asp Lys Phe Val Glu Asn Pro Asn
                165                 170                 175

Phe Glu Ser Asp Leu Leu Leu Glu Lys Phe Val Lys Glu Cys Arg Glu
            180                 185                 190

Tyr Val Lys Thr Ile Thr Ile Pro Ser Lys
        195                 200


<210> 278
<211> 130
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 278
Met Ser Lys Pro Ser Leu Tyr Leu Pro Ser Lys Pro Val Lys Tyr Glu
1               5                   10                  15

Pro Lys Arg Gln Ile Ile Ser Thr Asp Val Leu Ile Gly Pro Val Ile
            20                  25                  30

Leu Ile Ser Phe Val Ile Leu Leu Ile Ile Gly Gly Val Leu Asp Val
        35                  40                  45

Met Thr Asp Ile Asp Ser Gly Glu Ile Leu Val Leu Met Leu Ile Leu
    50                  55                  60

Pro Leu Ile Val Pro Leu Leu Leu Val Pro Val Asn Trp Val Gly Tyr
65                  70                  75                  80

Trp Tyr Gln Gly Arg His Tyr Arg Lys Arg Val Arg Asp Trp Lys Ala
                85                  90                  95

Gln Cys Lys Lys Ile Lys Lys Glu His Gln Leu Lys Leu Asp Met Tyr
            100                 105                 110

Glu Phe Asp Glu Ile Met Lys Phe Val Lys Glu Ser Arg Cys Lys Ser
```

115 120 125

Gln Asn
130

<210> 279
<211> 120
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 279
Met Gln Lys Pro Lys Leu Asn Lys Val Lys Tyr Ser Phe Pro Glu Ala
1 5 10 15

Leu Leu Ile Leu Ala Val Ser Val Phe Thr Ala Leu Ala Gly Ser Leu
20 25 30

Ile Gly Leu Leu Ile Asp Cys Phe Ile Leu Asn Ile Asp Gly Thr Val
35 40 45

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

Leu Phe Ser Phe Phe Gly Thr Met Leu Tyr Phe His Tyr Asp Asn Phe
65 70 75 80

Lys Ile Asn Trp Gln Arg Lys Lys Asp Tyr Lys Ile Gln Leu Lys Glu
85 90 95

Tyr Asn Ser Tyr Met Ser Tyr Ile Glu Lys Glu Ser Met Glu Glu Phe
100 105 110

Val Ser Asp Cys Arg Lys Ile Lys
115 120

<210> 280
<211> 162
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 280
Met Ile Leu Lys Thr Arg Trp Tyr Asp Leu Asp Asp Gly Asp Asp Gly
1 5 10 15

Ile Ser Val Asp Arg Val Asp Trp Ser Gly Cys Ser Glu Asp Thr Lys
20 25 30

Lys Arg Leu Ile Arg Glu Phe Arg Met Gly Tyr Gln Ala Val Lys Pro
35 40 45

```
Ser Thr Val Thr Asp Asp Lys Phe Val Cys Ile His Asn Gly Arg Ala
    50                  55                  60

Lys Leu Thr Asn Ala Glu Trp Phe Thr Asp Lys Ile Met Ile Leu Trp
65                  70                  75                  80

Tyr Ile Ile Ser Leu Pro Val Ser Ser Phe Val Phe Tyr Phe Phe Ile
                85                  90                  95

Lys Asn Pro Met Asp Arg Ile Gly Asp Trp Ile Leu Leu Thr Ile Leu
            100                 105                 110

Val Asn Ile Phe Thr Ala Ser Ile Leu Ser Gly Ile Trp Tyr Thr Phe
        115                 120                 125

Ile Glu Met Pro Trp Arg Leu Arg Arg Gln Gln Lys Ile Phe Asp Glu
    130                 135                 140

Lys Lys Tyr Thr Gln Asn Leu Asn Asn Phe Ile Thr Glu Cys Arg Lys
145                 150                 155                 160

Leu Lys
```

<210> 281
<211> 146
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 281

```
Met Lys Thr Leu Ser Ala Gly Ile Ile Phe Met Thr Glu Asp Lys Asp
1               5                   10                  15

Leu Phe Met Gly Arg Val Thr Gly Ser Arg Lys Pro Gly Met Met Ala
            20                  25                  30

His Arg Trp Asp Ile Pro Lys Gly Arg Val Glu Ser Ser Asp Leu Asn
        35                  40                  45

Ala Leu Glu Ala Ala Lys Arg Glu Cys Leu Glu Glu Thr Gly Phe Ser
    50                  55                  60

Asn Tyr Asn Pro Asp Leu Leu Glu Asp Leu Gly Val Phe Lys Tyr Ser
65                  70                  75                  80

Ser Asn Lys Asp Leu Gln Leu Phe Tyr Tyr Thr Ile Pro Val Glu His
                85                  90                  95

Glu Met Phe Arg Asn Cys His Cys Glu Ser Tyr Phe Glu Asn Lys Asp
            100                 105                 110
```

Gly Val Met Ile Pro Glu Met Asp Ala Phe Ala Leu Ile Pro Arg Thr
115 120 125

Gln Trp Gln Tyr Val Met Gly Pro Ser Leu Tyr Arg Ile Met Asn Ser
130 135 140

Leu Phe
145

<210> 282
<211> 164
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 282
Met Asn Ile Phe Glu Met Leu Arg Ile Asp Glu Gly Leu Arg Leu Lys
1 5 10 15

Ile Tyr Lys Asp Thr Glu Gly Tyr Tyr Thr Ile Gly Ile Gly His Leu
20 25 30

Leu Thr Lys Ser Pro Ser Leu Ser Val Ala Lys Ser Glu Leu Asp Lys
35 40 45

Ala Ile Gly Arg Asn Cys Asn Gly Val Ile Thr Lys Asp Glu Ala Glu
50 55 60

Lys Leu Phe Asn Gln Asp Val Asp Ala Ala Val Arg Gly Ile Leu Arg
65 70 75 80

Asn Ala Lys Leu Lys Pro Val Tyr Asp Ser Leu Asp Ala Val Arg Arg
85 90 95

Cys Ala Leu Ile Asn Met Val Phe Gln Met Gly Glu Thr Gly Val Ala
100 105 110

Gly Phe Thr Asn Ser Leu Arg Met Leu Gln Gln Lys Arg Trp Asp Glu
115 120 125

Ala Ala Val Asn Leu Ala Lys Ser Arg Trp Tyr Asn Gln Thr Pro Asn
130 135 140

Arg Ala Lys Arg Val Ile Ala Thr Phe Arg Thr Gly Thr Trp Asp Ala
145 150 155 160

Tyr Lys Asn Leu

<210> 283

<211> 138
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 283
Met Thr Arg Ile Asn Leu Thr Leu Val Ser Glu Leu Ala Asp Gln His
1   5   10   15

Leu Ile Ala Glu Tyr Arg Glu Leu Pro Arg Val Phe Gly Ile Val Arg
            20   25   30

Lys His Val Ala Asn Gly Lys Arg Val Lys Asp Phe Lys Ile Ser Ser
        35   40   45

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

Glu Phe Leu Arg Lys Arg Gln Ser Asp Ile Ile Thr Glu Cys Leu Lys
65   70   75   80

Arg Gly Phe Ser Ile Lys Asp Thr Glu Val Pro Asp Ile Ser Asp Ile
                85   90   95

Pro Val Glu Trp Lys Asn Asp Tyr Asn Pro Cys Lys Ser Ala Ile Lys
            100   105   110

Leu Ser Gln Gln Arg Leu Asp Glu Lys Ile Leu Met Lys Pro His Trp
        115   120   125

Tyr Lys Tyr Tyr Gly Lys Asn Ile Tyr Ile
    130   135

<210> 284
<211> 179
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 284
Met Arg Thr Phe Leu Thr Gly Pro Tyr Leu Ser Leu Met Asn Ala Phe
1   5   10   15

Thr His His Ser Asp Ala Arg Val Glu Glu Ile Cys Lys Asn Glu Tyr
            20   25   30

Ile Pro Pro Phe Glu Asp Leu Leu Lys Gln Tyr Cys Thr Leu Arg Leu
        35   40   45

Asp Gly Gly Arg Gln Ser Gly Lys Ser Thr Ala Val Thr Asn Phe Ala
    50   55   60

Ala Asn Trp Leu Tyr Asp Gly Gly Thr Val Ile Val Leu Ser Asn Thr
65 70 75 80

Ser Ala Tyr Ala Lys Ile Ser Ala Asp Asn Ile Lys Lys Glu Phe Ser
85 90 95

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

Arg Ser Phe Ile Gly Asn Lys Gly Ser Lys Phe Arg Gly Leu Ser Leu
115 120 125

Ser Arg Ile Leu Tyr Ile Ile Asp Glu Pro Val Lys Ser Pro Asp Met
130 135 140

Asp Lys Ile Tyr Ser Val His Ile Asp Thr Val His Cys Cys Cys Asn
145 150 155 160

Ile Lys Cys Cys Ile Gly Gly Ile Thr Arg Pro Gln Phe Phe Val Ile
165 170 175

Gly Met Gln

<210> 285
<211> 109
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 285
Met Met Thr Asp Thr Gln Leu Phe Glu Tyr Leu Tyr Phe Ser Pro Lys
1 5 10 15

Thr Ile Lys Asn Lys Leu Val Asn His Phe Glu Ile Leu Ala Lys Asn
20 25 30

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

Val Phe Lys Gly Cys Arg Val Leu Cys Thr Ala Pro Asn Ala Arg Leu
50 55 60

Met Asn Lys Ile Pro Tyr Phe Thr Met Glu Phe Ile Asp Gly Pro Phe
65 70 75 80

Lys Gly Leu Ile Thr Gln Ser Leu Met Ala Tyr Asp Ser Glu Pro Phe
85 90 95

Leu Ile Lys Glu Gln Ser Trp Ile Asn Leu Phe Phe Asn
100 105

<210> 286
<211> 120
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 286
Met Lys Ala Tyr Gln Ile Leu Glu Gly Thr His Lys Gly Thr Ile Tyr
1 5 10 15

Phe Glu Asp Gly Ile Gln Ala Arg Ile Ile Val Ser Lys Thr Phe Lys
20 25 30

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

Glu Ile Glu Ile Glu Gln Gln Pro Thr Val Lys Ile Glu Gly Gly Gln
50 55 60

His Leu Asn Val Asn Val Leu Arg Arg Glu Thr Leu Glu Asp Ala Val
65 70 75 80

Lys His Pro Glu Lys Tyr Pro Gln Leu Thr Ile Arg Val Ser Gly Tyr
85 90 95

Ala Val Arg Phe Asn Ser Leu Thr Pro Glu Gln Gln Arg Asp Val Ile
100 105 110

Ala Arg Thr Phe Thr Glu Ser Leu
115 120

<210> 287
<211> 73
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 287
Met Ala Lys Ile Ile Ile Glu Gly Ser Glu Asp Val Leu Asn Ala Phe
1 5 10 15

Ala Glu Trp Phe Ser Asn Ser Gly Glu Gln Gln Phe Asn Glu Ala Trp
20 25 30

Asn Met Gly Asp Ile Asn Gly Ile Tyr Pro Thr Thr Glu Ile Ser Val
35 40 45

Gln Gly Tyr Gly Ile His Glu Pro Ile Arg Leu Val Glu Tyr Asp Leu
50 55 60

Gly Thr Gly Glu Glu Val Lys Tyr Asp
65 70

<210> 288
<211> 88
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 288
Met Ile Glu Asp Ile Lys Gly Tyr Lys Pro His Thr Asp Asp Lys Ile
1 5 10 15

Ser Lys Val Asn Ala Ile Lys Asp Ala Glu Val Arg Leu Gly Leu Ile
20 25 30

Phe Asp Ala Leu Tyr Asp Glu Phe Trp Glu Ala Phe Asp Ser Cys Glu
35 40 45

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

Ile Ala Lys Met Lys Leu Lys Glu Ala Ser Met Trp Ala Cys Arg Ala
65 70 75 80

Val Phe Gln Pro Glu Glu Lys Tyr
85

<210> 289
<211> 92
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 289
Met Ala Gln Leu Ser Ala Gly Phe Gly Tyr Glu Tyr Tyr Thr Ala Pro
1 5 10 15

Arg Arg Val Ser Val Ala Pro Lys Lys Ile Gln Ser Leu Asp Asp Phe
20 25 30

Gln Glu Val Val Arg Asn Ala Phe Gln Asp Tyr Ala Arg Tyr Leu Lys
35 40 45

Glu Asp Ser Gln Asp Cys Leu Glu Glu Asp Glu Ile Ala Tyr Tyr Glu
50 55 60

Gln Arg Leu Glu Gln Leu Lys Asn Leu His Glu Val Arg Ala Glu Val
65 70 75 80

Ser Lys Ser Met Asn Lys Leu Ile Arg Phe Lys Glu
85 90

<210> 290
<211> 153
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 290
Met Thr Ile Asn Thr Glu Val Phe Ile Arg Arg Asn Lys Leu Arg Arg
1 5 10 15

His Phe Glu Ser Glu Phe Arg Gln Ile Asn Asn Glu Ile Arg Glu Ala
20 25 30

Ser Lys Ala Ala Gly Val Ser Ser Phe His Leu Lys Tyr Ser Gln His
35 40 45

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

Glu Leu Phe His Lys Ile Lys Asp His Val Leu Glu Val Asn Glu Phe
65 70 75 80

Leu Ser Met Pro Pro Arg Pro Asp Ile Asp Glu Asp Phe Ile Asp Gly
85 90 95

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

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

Leu Gln Cys Arg Met Ala Ile Ile Asn Ser Arg Arg Leu Pro Gly Lys
130 135 140

Ala Ser Lys Ala Val Ile Lys Thr Gln
145 150

<210> 291
<211> 181
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 291
Met Arg Lys Ala Leu Leu Ala Gly Leu Leu Ala Ile Ser Met Met Ala
1 5 10 15

His Ser Ser Glu His Thr Phe Ser Asn Val Gln Leu Asp Asn Met Arg
20 25 30

Tyr Ala Tyr Gln Phe Gly Glu Gln Phe Ser Lys Asp Gly Lys Tyr Lys
35 40 45

Thr His Lys Asn Ile His Lys Ser Gly Leu Gly His Ile Met Ala Ala
50 55 60

Ile Leu Trp Gln Glu Ser Ser Ala Gly Val Asn Leu Lys Ser Lys Pro
65 70 75 80

Lys His His Ala Tyr Gly Met Phe Gln Asn Tyr Leu Pro Thr Met Arg
85 90 95

Ala Arg Val Lys Glu Leu Gly Tyr Asn Met Thr Asp Ala Glu Ile Lys
100 105 110

Arg Met Leu Asn Lys Arg Ser Asn Ser Ala Ser Trp Ala Tyr Ile Glu
115 120 125

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

Ser Ser Tyr Asn Ser Gly Trp Asn Val Lys Ala Gly Ser Lys Tyr Ala
145 150 155 160

Ser Glu Val Leu Glu Lys Ala Asn Tyr Leu Lys Asn Asn Lys Leu Leu
165 170 175

Glu Ile Val Asn Asp
180

<210> 292
<211> 113
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 292
Met Thr Lys Ile Leu Val Leu Cys Ile Gly Leu Ile Ser Phe Ser Val
1 5 10 15

Leu Ala Asp Thr Ser Tyr Thr Glu Ile Arg Glu Tyr Val Asn Arg Thr
20 25 30

Ala Ala Asp Tyr Cys Gly Lys Asn Lys Ala Cys Gln Ala Glu Phe Ala
35 40 45

Gln Lys Leu Ile Tyr Ala Tyr Lys Asp Gly Glu Arg Asp Lys Ser Ser
50 55 60

Arg Tyr Lys Asn Asp Thr Leu Leu Lys Arg Tyr Ala Lys Lys Trp Asn
65 70 75 80

Thr Leu Glu Cys Ser Val Ala Glu Glu Lys Asp Lys Ala Ala Cys His
85 90 95

Ser Met Val Asp Arg Leu Val Asp Ser Tyr Asn Arg Gly Leu Ser Thr
100 105 110

Arg

<210> 293
<211> 159
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 293
Met Ile Val Lys Tyr Ile Lys Gly Asp Ile Val Ala Leu Phe Leu Gln
1 5 10 15

Gly Asn Ile Ile Ala His Gly Cys Asn Cys Phe His Thr Met Gly Ser
20 25 30

Gly Val Ala Gly Gln Leu Ala Arg Ala Tyr Pro Lys Ile Leu Glu Ile
35 40 45

Asp Lys Thr Thr Thr Glu Tyr Gly Ser Arg Asp Lys Leu Gly Asp Met
50 55 60

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

Leu Tyr Thr Gln Tyr Glu Pro Gly Pro Asn Leu Asp Tyr Gly Ala Leu
85 90 95

Val Asn Cys Met Ile Glu Leu Asn Leu Gln Ala Glu Thr Leu Leu Phe
100 105 110

Lys Pro Val Ile Tyr Ile Pro Arg Ile Gly Cys Gly Ile Ala Gly Gly
115 120 125

Asp Trp Asp Lys Val Ser Lys Leu Ile Asp Met Phe Thr Pro Asp Ile
130 135 140

Asp Leu Ile Val Val Asp Tyr Glu Ser Thr Leu Pro Ala Ser Val
145 150 155

<210> 294
<211> 70
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F488/08

<400> 294
Met Lys Val His Tyr Pro His Pro Phe Asp Pro Lys Asn Lys Val Glu
1   5   10   15

Ile Ile Arg Gln Trp Glu Arg Ile Cys Arg Thr Lys Cys Pro Ile Asn
            20   25   30

Ser Pro His Asp Val Asp Lys Asp Tyr Ile Gly Thr Phe Val Glu Tyr
        35   40   45

Thr Phe Ile Asp Arg Lys Gly Arg Lys Gln His Val Glu Glu Tyr Cys
    50   55   60

Leu Lys Val Thr Trp Leu
65   70

<210> 295
<211> 68
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 295
Met Ser Gln Thr Ser Ile Leu Lys Asn Ala His Cys Glu Lys Cys Glu
1   5   10   15

Trp Pro Val Val Phe Ala Leu Cys Asn Asp Glu Met Ala Cys Asp Phe
            20   25   30

Asp Tyr Trp Cys Tyr Cys Ser Asn Lys Gly Cys Ile Asn His Lys Gly
        35   40   45

Glu Gly Phe Tyr Ser Gly Phe Tyr Pro Tyr Pro Asp Phe Val Lys Glu
    50   55   60

Gly Lys Pro Lys
65

<210> 296
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 296
Met Asn Ser Phe Glu Leu Gln Tyr Glu Val Leu Arg Glu Leu Asp Asn
1   5   10   15

Leu Ile Glu Leu Ala Val Asn Lys Gly Phe Ala Ile Gly Ile Gly Gln
            20   25   30

Lys Asp Thr Gly His Leu Thr Met Glu Ile Phe Lys Gln Lys Arg Ile
35 40 45

Ile Leu Lys Leu Leu Glu Ile Asn Ile
50 55

<210> 297
<211> 61
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 297
Met Ser Leu Ser Lys Glu Gln Lys Asp Lys Leu Phe Glu Leu Ile His
1 5 10 15

Glu Leu Leu Asp Glu His Thr Glu Ala Asn Thr Phe Tyr Asp Glu Tyr
20 25 30

Gly Pro Leu Ser Pro Glu Gln Gln Glu Glu Phe Ala Asp Arg Phe Asp
35 40 45

Lys Lys Glu Asn Glu Leu Ile Ala Tyr Val Asn Met Leu
50 55 60

<210> 298
<211> 193
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 298
Met Ala Ser Leu Ile Phe Thr Tyr Ala Ala Met Asn Ala Gly Lys Ser
1 5 10 15

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

Val Leu Val Leu Lys Pro Ala Ile Asp Thr Arg Asp Ser Val Cys Glu
35 40 45

Val Val Ser Arg Ile Gly Ile Lys Gln Glu Ala Asn Ile Ile Thr Asp
50 55 60

Asp Met Asp Ile Phe Glu Phe Tyr Lys Trp Ala Glu Ala Gln Lys Asp
65 70 75 80

Ile His Cys Val Phe Val Asp Glu Ala Gln Phe Leu Lys Thr Glu Gln
85 90 95

Val His Gln Leu Ser Arg Ile Val Asp Thr Tyr Asn Val Pro Val Met

100 105 110

Ala Tyr Gly Leu Arg Thr Asp Phe Ala Gly Lys Leu Phe Glu Gly Ser
115 120 125

Lys Glu Leu Leu Ala Ile Ala Asp Lys Leu Ile Glu Leu Lys Ala Val
130 135 140

Cys His Cys Gly Lys Lys Ala Ile Met Thr Ala Arg Leu Met Glu Asp
145 150 155 160

Gly Thr Pro Val Lys Glu Gly Asn Gln Ile Cys Ile Gly Asp Glu Ile
165 170 175

Tyr Val Ser Leu Cys Arg Lys His Trp Asn Glu Leu Thr Lys Lys Leu
180 185 190

Gly

<210> 299
<211> 70
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 299
Met Leu Gln Leu Thr Glu Lys Gln Leu Arg Asn Leu Thr Val Leu Gln
1 5 10 15

Leu Asp Glu Ile Arg Arg Glu Val Gly Asn Ile Ile Ser Ala Leu Arg
20 25 30

Arg Glu Val Ser Leu Asn Gln Ser Pro Ala Asp Tyr Thr Arg Leu Arg
35 40 45

Asn Phe Glu Lys Tyr Leu Asp Lys Val Lys Ala Val His Arg His Lys
50 55 60

Val Asn Thr Gly Gln Lys
65 70

<210> 300
<211> 97
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 300
Met Ala Leu Lys Ala Thr Ala Leu Phe Ala Met Leu Gly Leu Ala Phe
1 5 10 15

Ala Leu Ser Pro Pro Ile Glu Ala Asn Val Asp Pro His Phe Asp Lys
            20   25   30

Phe Met Glu Ser Gly Ile Arg His Val Tyr Met Leu Phe Glu Asn Lys
        35   40   45

Ser Val Glu Ser Ser Glu Gln Phe Tyr Ser Phe Met Arg Thr Thr Tyr
    50   55   60

Lys Asn Asp Pro Cys Ser Ser Asp Phe Glu Cys Ile Glu Arg Gly Ala
65   70   75   80

Glu Met Ala Gln Ser Tyr Ala Arg Ile Met Asn Ile Lys Leu Glu Thr
                85   90   95

Glu

<210> 301
<211> 128
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 301
Met Lys Phe Ser Asp Phe Ser Gln Ser Gly Lys Pro Ser Lys Ala Asp
1   5   10   15

Glu Tyr Leu Gly Leu Leu Met Ala Ala Gln Ala Tyr Phe His Ser Ala
            20   25   30

His Phe Glu Thr Lys Ser Tyr Ala Arg His Lys Ala Tyr Asp Phe Ile
        35   40   45

Phe Ser Glu Leu Pro Asp Leu Ile Asp Lys Phe Gly Glu Gln Tyr Leu
    50   55   60

Gly Tyr Ser Gly Arg Lys Tyr Thr Pro Ser Ile Pro Asp Ala Ser Lys
65   70   75   80

Leu Pro Thr Asp Thr Ile Lys Met Ile Asp Arg Ile Leu Asp Gln Ser
                85   90   95

Asn Ser Ile Tyr Lys Glu Met Pro Pro Ala Ile Gln Ser Thr Ile Asp
            100   105   110

Asp Ile Thr Gly Met Phe Tyr Gln Ser Lys Tyr Leu Leu Ser Leu Glu
        115   120   125

<210> 302
<211> 62

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 302
Met Lys Ile Glu Ala Leu Asn Gln Glu Gly Asn Ile Tyr Val Ile Ile
1   5   10   15

Asn Gly Asp Phe Phe Val Asp Met Asp Glu Val Thr Ser Glu Glu Leu
            20   25   30

Val Glu Leu Leu Lys Lys Arg Tyr Asp Met Cys Asp Glu Ala Ala Thr
        35   40   45

His Met Ala Cys Ala Ile Phe Ser Leu Ser Tyr Val Val Glu
    50   55   60

<210> 303
<211> 67
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 303
Met Thr Arg Ile Glu Gln Ala Asp Lys Ile Lys Glu Leu Val Ala Leu
1   5   10   15

Ile Arg Lys Ala Asp Glu Glu Leu Ser Asp Phe Ala Trp Phe Ser Ala
            20   25   30

Gly Ile Ala Asn Lys Gly Ile Glu Lys Phe Glu Ala Lys Val Asp Asn
        35   40   45

Ala Leu Glu Ala Leu Asp Met Phe Leu Asp Glu Ile Ile Asp His Asn
    50   55   60

Thr Arg Val
65

<210> 304
<211> 64
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 304
Met Leu Thr Arg Glu Gln Phe Glu Lys Ile Ile Lys Leu Ala Arg Asp
1   5   10   15

Ile Glu Ile Asp Ser Tyr Gln Leu Ala Val Glu His Cys Glu Gly Tyr
            20   25   30

Ser Tyr Asp Gly Ile Glu Ala Ala Lys Lys Asp Leu Asp Lys Ser Lys
        35   40   45

Ala Lys Leu Val Gln Tyr Leu Glu Met Ile Arg Trp Asn Asn Glu Asn
    50   55   60

<210> 305
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 305
Met Lys Thr Glu Lys Gln Met Phe Leu Met Lys Leu Ile Glu Glu Tyr
1   5   10   15

Ala Asn Ala Val Ser Asp Tyr Glu Cys Ser Ser Arg Glu Arg Gly Thr
            20   25   30

Ala Phe Ala Lys Glu Glu Leu Lys Ile Met Val Asp Ala His Thr Lys
        35   40   45

Leu Gln Asn Phe Ile Glu Asn Val Ile
    50   55

<210> 306
<211> 61
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 306
Met Thr Ser Glu Gln Ala Phe Lys Leu Lys Glu Leu Ile Glu Thr Tyr
1   5   10   15

Ser Lys Ala Val His Thr Ala Thr Val Ile Asp Glu Ser Ala Phe Ser
            20   25   30

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

Val Asn Leu Asp Ser Tyr Ile Glu Thr Leu Ile Gly Glu
    50   55   60

<210> 307
<211> 88
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 307

```
Met Gly Phe Pro Lys Leu Glu Val Gly Asp Leu Val Leu Thr Lys Leu
1               5                   10                  15

Trp Asn Gly Val Gln Ser Val Glu Ile Cys Gln Tyr Arg Gly Ala Thr
            20                  25                  30

Gly Asn Leu Met Tyr Thr Ile Tyr Asn Pro Glu Ile Leu Leu Glu Cys
        35                  40                  45

His Leu Glu Arg Phe Ile Lys Asp Thr Asp Ser Met Pro Tyr Ser Val
    50                  55                  60

Ser Ile Val Arg Lys Ser Asp Thr Lys Glu Tyr Ser Lys Ile Leu Glu
65                  70                  75                  80

Gln Ile Arg Ala Asn Lys Lys Asp
                85
```

<210> 308
<211> 177
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 308

```
Met Lys Arg Leu Val Leu Glu Val Ser Pro Leu Phe Gly Glu Leu Ala
1               5                   10                  15

Ile Glu Lys Val Asn Asn Met Tyr Arg Leu Thr Gln Glu Asp Asp Met
            20                  25                  30

Leu Tyr Phe Thr Pro Ser Glu Ile Ile His Leu Thr Gln Ile Glu Tyr
        35                  40                  45

Pro Tyr Thr Asp Lys Ile Val Ser Ile Asn Asp Glu His Lys Ile His
    50                  55                  60

Phe Tyr Ser Ser Cys Pro Gly Phe Asn Ile Lys Ser Glu Ser Met Cys
65                  70                  75                  80

Leu Ser Val Ile His Trp Asp Ser Phe Ile Asp Lys Ile Lys Tyr Phe
                85                  90                  95

Tyr Tyr Ser Asn Glu Arg Lys His Ser Leu Lys Trp Leu Lys Asn Cys
            100                 105                 110

Asn Ala Ile Ile Thr Asn Ala Cys Asn Gln Asn Asp Glu Thr Leu Leu
        115                 120                 125

Asn Val Ser Lys Cys Tyr Glu Glu Gly Asp Val Leu Thr Ile Arg Gln
    130                 135                 140
```

Ile Asp Asp Phe Arg Ser His Ile Val Thr Phe Thr Lys Asp Glu Ala
145 150 155 160

Ile Ala Leu Lys Thr Tyr Leu Asp Ser Val Ile Pro Thr Met Ile Ser
165 170 175

Lys

<210> 309
<211> 173
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 309
Met Phe Ile Ser Ser Gly Ser Gly Leu Ile Arg Val Glu Phe Lys Asn
1 5 10 15

Asp Ile Phe Leu Ser Gln Gly Asp Asp Ile Ile Lys Met Ser Tyr Asp
20 25 30

Glu Ile Lys Lys Ile Cys His Ala Leu Glu Ser His Gly Lys Glu Asn
35 40 45

Ala Thr Ile Asp Ile Gly Asp Leu Trp Val Thr Leu Tyr Glu Val Ser
50 55 60

Glu Gly Phe Asn Ile Glu Asp Glu Asn Asn Ile Leu Ala Ile Asp Lys
65 70 75 80

Arg Ser Asp Leu Phe Asp Val Leu Lys Val Tyr Glu Gln Ser Asn Gly
85 90 95

Gly Arg Lys Ala Val Leu Val Tyr Gln Lys Pro His Ser Cys Gly Thr
100 105 110

Ala Ser Ile Ile Ser Asn Ile Glu Asp Glu Thr Asp Thr Tyr Met Cys
115 120 125

Val Leu Lys Ala Gly Gly Asp Arg His Pro Asp Phe Ile Ser Ile Arg
130 135 140

Gln Asn Asn Gly Glu Ile Ser Leu Ser Lys Ser Glu Ala Glu Ala Met
145 150 155 160

Ile Lys Tyr Leu Thr Thr Val Thr Pro Ser Met Lys Gly
165 170

<210> 310
<211> 153

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 310
Met Ile Ile Asn Glu Asn Ser Trp His Tyr Lys Leu Phe Lys Met Phe
1   5   10   15

Asn Asp Glu Trp Lys Arg Pro Lys Thr Leu Cys Ala Tyr Phe Trp Ser
            20   25   30

Ile Val Ile Pro Thr Phe Phe Val Ser Phe Phe Gly Cys Thr Ile Leu
        35   40   45

Ala Gly Leu Thr Ile Ile Cys Ala Glu Ile Ile Gln Lys Trp Leu Ile
    50   55   60

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

Leu Leu Val Leu Leu Ile Ile Gly Ser Phe Val Ile Pro Ala Gln Leu
                85   90   95

His Glu Lys Tyr Lys Asp Tyr Lys Trp Lys Lys Asp Tyr Ala Leu His
            100   105   110

Val Glu Asn Ile Asp Arg Ala Tyr Lys Gly Leu Pro Pro Ile Gln Pro
        115   120   125

Lys Lys Ser Ile Ile Val Glu Phe Leu Lys Ala Arg Lys Ala Lys Val
    130   135   140

Cys Pro Val Ile Glu Tyr Lys Ala Glu
145   150

<210> 311
<211> 336
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 311
Met Lys Thr Val Met Lys Ser Tyr Phe Gly Ser His Leu Tyr Gly Thr
1   5   10   15

Ser Thr Pro Glu Ser Asp Val Asp Phe Lys Glu Ile Phe Val Pro Pro
            20   25   30

Ala Arg Asp Ile Leu Ile Gly Asn Val Lys Glu His Met Ser Lys Asn
        35   40   45

```
Thr Asn Asn Thr Ser Ser Lys Asn Thr Lys Asp Asp Ile Asp His Glu
    50                  55                  60

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

Val Ala Leu Asp Met Leu His Thr Pro Pro Glu Leu Val Val Lys Ser
                85                  90                  95

Asp Leu Pro Asp Val Trp Lys Phe Ile Gln Asp Asn Arg Ser Arg Phe
            100                 105                 110

Tyr Thr Thr Asn Met Lys Ser Tyr Leu Gly Tyr Val Arg Lys Gln Ala
        115                 120                 125

Ser Lys Tyr Gly Val Lys Gly Ser Arg Leu Ala Ala Leu Arg Asp Val
    130                 135                 140

Leu Lys Val Val Asn Gln Ile Pro Glu Gln Trp Val Asp Tyr Gln Glu
145                 150                 155                 160

Asp Gly Ser Ile Lys Gln Arg Arg Thr Lys Val Glu Asp Ile Lys His
                165                 170                 175

Arg Leu Pro Glu Asn Glu Phe Cys Glu Trp Val Phe His Asn His Glu
            180                 185                 190

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

Thr Thr Leu Ser Leu Ile Glu Leu Lys Gln Ser Leu Asn Lys Leu Asp
    210                 215                 220

Ala Glu Tyr Gly Glu Arg Ala Arg Lys Ala Glu Ala Asn Glu Gly Ile
225                 230                 235                 240

Asp Trp Lys Ala Leu Ser His Ala Cys Arg Gly Gly Leu Gln Leu Leu
                245                 250                 255

Glu Ile Tyr Lys Thr Gly Asp Leu Val Tyr Pro Leu Gln Asp Ala Pro
            260                 265                 270

Phe Ile Leu Asp Val Lys Leu Gly Lys His Pro Phe Lys Thr Val Gln
        275                 280                 285

Glu Phe Leu Glu Asp Val Val Asp Gln Val Glu Ala Ala Ser Thr Glu
    290                 295                 300

Ala Ser Lys Asn Gly Met Gln Gln Lys Val Asp Met Ser Phe Trp Asp
305                 310                 315                 320
```

Asp Phe Leu Glu Lys Val Tyr Leu Glu Asn His Arg Ser Tyr Tyr Lys
325 330 335

<210> 312
<211> 49
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 312
Met Lys Ile Thr Pro Ile Glu Val Lys Lys Leu Ile Asp Thr Glu Glu
1 5 10 15

Ile Ser Glu Cys Phe Glu Ser Phe Leu Glu Asp Ala Thr Glu Asp Asn
20 25 30

Ala Val Tyr Leu Ala Gln Lys Ile Ile Glu Thr Tyr Leu Glu Lys Asn
35 40 45

Gln

<210> 313
<211> 87
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 313
Met Thr Val Tyr Val Asp Val Leu Met Asn His Gly Trp Lys Leu Arg
1 5 10 15

Gly His Pro Thr Lys Asn Cys His Met Phe Thr Asp Gly Asp Ile Glu
20 25 30

Glu Leu His Glu Met Ala Glu Ala Ile Gly Met Lys Arg Ser Trp Phe
35 40 45

Gln Asp Lys Arg Ile Lys His Tyr Asp Leu His Ala Arg Arg Arg Gln
50 55 60

Lys Ala Val Glu Leu Gly Ala Val Glu Val Ser Arg Arg Glu Ala Val
65 70 75 80

Lys Ile Trp Arg Thr Leu Lys
85

<210> 314
<211> 322
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F488/08

<400> 314

```
Met Lys Thr Val Thr Ile Asn Lys Gly Ile Tyr Phe Gly Lys Glu Ile
1               5                  10                  15

Ser Gly Thr Phe Glu Leu Leu Gly Glu Trp Phe Pro Asp Asn Ala Pro
            20                  25                  30

Val Asp Ala Gln Gly Asp Gly Lys Val Phe Val Glu Ile Asp Gly Lys
        35                  40                  45

Arg Arg Gly Val Trp Val Tyr Lys Ser Asp Ile Ser Tyr Asp Gly Val
    50                  55                  60

Lys Val Glu Glu Val Lys Glu Ser Tyr Glu Asp Met Lys Thr Arg Ile
65                  70                  75                  80

Asn Lys Arg Phe Asn Val Met Gly Met Met Thr Asn Gly Ile Ile Asn
                85                  90                  95

Gly Asn Ile Arg Ser Leu Ile Ile Ser Gly Ala Ala Gly Ile Gly Lys
            100                 105                 110

Thr Tyr Ser Leu Asp Lys Ala Leu Asn Lys Ala Asn Asp Asn Gly Tyr
        115                 120                 125

Ile Glu Tyr Lys Ser Ile Asn Gly Lys Ile Ser Gly Ile Gly Leu Tyr
    130                 135                 140

Glu Gln Leu Trp Asn Asn Arg Glu Glu Asn Ser Val Leu Leu Ile Asp
145                 150                 155                 160

Asp Val Asp Val Phe Ser Asp Met Asp Ile Leu Asn Leu Leu Lys Ala
                165                 170                 175

Ala Leu Asp Thr Gly Glu Thr Arg Lys Val Cys Trp Ser Thr Ala Ser
            180                 185                 190

Ser Tyr Leu Glu Glu Lys Gly Ile Glu Arg Glu Phe Glu Phe Lys Gly
        195                 200                 205

Thr Ile Val Phe Ile Thr Asn Val Asp Ile Asp Arg Glu Leu Asp Arg
    210                 215                 220

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

Tyr Leu Asp Leu Gly Val His Thr Asn Glu Glu Ile Met Val Arg Val
                245                 250                 255

Glu Asp Val Ile Leu Ser Thr Asp Met Met Gln Lys Arg Gly Leu Ser
```

260 265 270

Asp Glu Glu Thr Tyr Lys Ala Leu Ser Trp Met Lys Val Asn Val Asn
275 280 285

Arg Leu Arg Asn Val Ser Leu Arg Thr Ala Leu Tyr Leu Ala Asp Phe
290 295 300

Ile Met Thr Asp Lys Asn Gly Trp Glu Glu Ile Ala Glu Val Thr Leu
305 310 315 320

Leu Lys

<210> 315
<211> 100
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 315
Met Leu Tyr Ser Lys Ala Arg Glu Ile Tyr Glu Thr Lys Ile Lys Glu
1 5 10 15

Ala Val Phe Lys Phe Ala Thr Thr Met Arg Trp Thr Asn Asp Trp Glu
20 25 30

Tyr Ser Lys Asn His Lys Lys Pro Met Val Thr Arg Lys Ala His Met
35 40 45

Leu Val Leu Ile Asp Arg Glu Gln Ile Lys Ala Arg Glu Ala Leu Gln
50 55 60

Asn His Lys Lys Ala Ala Phe Glu Trp Phe Met Asp Asn Thr Ala Pro
65 70 75 80

Glu Thr Lys Lys Ala Val Ser Ala Trp Phe Ser Gly Lys Asn Cys Glu
85 90 95

Arg Ser Phe Phe
100

<210> 316
<211> 175
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 316
Met Asn Ala Lys Asp Ile Phe Asn Leu Val Asn Tyr Asn Asp Gly Lys
1 5 10 15

```
Phe Lys Ser Glu Ala Gln Ser Lys Phe Phe Asn Asp Ile Ser Ile Gly
            20                  25                  30

Gly Glu Ile Thr Val Asp Gly Gly Gln Ile Tyr Lys Ser Arg Trp Asn
        35                  40                  45

Trp Ile Val Ile Ile Asp Glu Ile Gly Ile Val Glu Ile Tyr Lys Asn
    50                  55                  60

Thr Asn Lys Asn Arg Thr Leu His Trp Ser Arg Asp Thr Asn Glu Gln
65                  70                  75                  80

Tyr Lys Lys Asp Lys Ala Ser Lys Leu Ser Arg Val Thr Gln Glu Asp
                85                  90                  95

Ile Glu Phe Ile Lys Lys Asp Ile Leu Met Tyr Asp Asn Leu Ile Ala
            100                 105                 110

Glu Glu Gln Ala Val Ile Asp Lys Phe Asp Glu Ile Lys Ala Ser Arg
        115                 120                 125

Glu Ile Pro Asp Phe Met Lys Glu Ser Val Asn Glu Arg Tyr Thr Leu
    130                 135                 140

Ile Ser Glu Arg Ile Glu Thr Tyr Lys Lys Gln Arg Ala Glu Arg Gln
145                 150                 155                 160

Asn Thr Leu Arg Lys Phe Glu Glu Arg Leu Lys Thr Val Leu Ala
                165                 170                 175


<210> 317
<211> 135
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 317
Met Lys Gln Leu Ile Ile Lys Arg Leu Asn Leu Leu Ile Cys Cys Leu
1               5                   10                  15

Cys Ile Ala Ile Ala Tyr Gly Tyr Tyr Ala Ile Asn Asp Tyr Met His
            20                  25                  30

Tyr Lys Asp Tyr Asp Val Thr Val Val Asn Thr Ile Thr Gly Thr Gln
        35                  40                  45

Gly Lys Gly Ser Ser Leu Ser Phe Ile Ala Val Tyr Glu Leu Lys Asp
    50                  55                  60

Gly Tyr Arg Phe Ser Glu Tyr Ile Ser Pro Glu Met Tyr Ser Ser Ile
65                  70                  75                  80
```

Glu Lys Gly Asp Asn Ile Thr Val Ser Leu Arg Pro Phe Asp Val Lys
85 90 95

Gln Thr Leu Phe Asp Asn Ile Val Trp Phe Phe Gly Met Val Leu Val
100 105 110

Gln Ser Val Cys Gly Ala Tyr Ile Val Cys Ser Ile Leu Phe Cys Ile
115 120 125

Phe Ser Lys Ile Glu Ile Glu
130 135

<210> 318
<211> 295
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 318
Met Ser Val Val Ile Asn Asn Val Asn Ala Val Ile Lys Ser Leu Val
1 5 10 15

Asn Lys Lys Leu Asn Glu Trp Thr Val Leu Arg Arg Gly Glu Pro Asp
20 25 30

Lys Phe Phe His Arg Phe Asn Pro Thr Leu Asp Leu Asn Val Ile Asp
35 40 45

Arg Asp Val His Ala Glu Ile Leu Asp Lys Phe Lys Val Asp Ile Gly
50 55 60

Phe Gly Leu Asp Lys His Leu Gln Arg Thr Asn Gly Ser Gly Met Gly
65 70 75 80

Leu Ser Asn Arg Ile Met Lys Ala Leu Asn Lys Ile Gly Ala Leu Ser
85 90 95

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

Leu Tyr Gly Arg Leu Met Pro Lys Leu Ser Phe Asp Gln Met Ile Ala
115 120 125

Asp Leu Trp Glu Asn Gln Arg Arg Leu Leu Ala Leu Gly Ala Arg Leu
130 135 140

Ala Lys Gly Leu Asp Lys Gln Met Ile Phe Lys Thr Asn Asn Thr Glu
145 150 155 160

Asp Leu Lys Cys Phe Lys Phe Ser Thr Arg Gly Asp Asp Tyr Tyr Ile

165 170 175

Arg Ala Arg Ser Thr Asp Tyr Val Asn Met Gly His His Leu Cys Leu
180 185 190

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

Ala Lys Cys Pro Ile Gly Ser Asn Cys Ile Leu Ile Tyr Arg Pro Asp
210 215 220

Glu Ser Ser Ser Thr Lys Leu Pro Thr Lys Pro Val Pro Val Arg Ser
225 230 235 240

Asn Glu Lys His Ser Glu Gln Ile Ala Tyr Phe Asn Lys Gln Ile Glu
245 250 255

Glu Leu Asn Ile Ser Ile Gln Gln Tyr Asp Asp Glu Ile Phe Arg Leu
260 265 270

Ser Gly Leu Ser Ser Lys Ala Lys Ser Glu Arg Glu Lys Leu Ile Lys
275 280 285

Ile Val Asp Leu Leu Lys Ser
290 295

<210> 319
<211> 342
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 319
Met Lys Thr Arg Ser Gln Ile Glu Asp Met Val Arg Asn Ala Ser Tyr
1 5 10 15

Thr Arg Asp Val Met Thr Phe Leu Cys Glu Asn Asn Leu Asp Pro Asp
20 25 30

Lys Val Asn Arg Val Ile His His Phe Lys Tyr Thr Asn Ser Ser Glu
35 40 45

Trp Val Arg Asn Phe Ser Lys Ala Gly Tyr Ile Thr Gln Met Thr Ala
50 55 60

Arg Glu Gln Leu Thr Asp Phe Cys Lys Thr Ile Asp Tyr Lys Asn Pro
65 70 75 80

Leu Ile Val Gln Gly Val Gly Gln Ser Lys Val Asp Leu Ser Ser Gly
85 90 95

```
Phe Phe Asn Pro Asn His Tyr Arg Ile Glu Trp Arg Phe Ile Ala Leu
            100                 105                 110

Phe Arg Lys Gln Leu Lys Gln Ile Leu Ser Thr Ala Ser Arg Leu Lys
        115                 120                 125

Gly Ser Asp Ile Asn Leu Lys Asn Leu Lys Phe Asp Gly Tyr Thr Leu
    130                 135                 140

Gln Met Glu Val Arg Pro Leu Lys Glu Asn Asn Arg Thr Ala Arg Ile
145                 150                 155                 160

Ser Phe Lys Pro Asn Thr Lys Asn Ser Leu Ser Ile Cys Glu Cys Leu
                165                 170                 175

Lys Ser Gln Leu Thr Glu Ala Phe Lys Tyr Met Asp Val Val Ala Ala
            180                 185                 190

Val Gln Ser Lys Ile Leu Pro Arg Phe Glu Arg Asn Trp Glu His Thr
        195                 200                 205

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

Arg Lys Asp Glu Ile Val Gln Glu Lys Lys Gln Glu Val Gln Asp Thr
225                 230                 235                 240

Leu Asn Leu Asn Leu Ser Asn Tyr Leu Ser Asn Asp Pro Lys Phe Trp
                245                 250                 255

Met Tyr Ser Ser Ser Asn Ile Asp Ala Cys Lys Leu Asn Lys Val Ser
            260                 265                 270

Phe Leu Pro Thr Glu Asn Ser Asn Phe Lys Pro Val Glu Lys Trp His
        275                 280                 285

Ala Asp Ala Ile Glu Lys Ser Leu Lys Ala Val Asp Asp Glu Leu Val
    290                 295                 300

Lys Ala Thr Asn Glu Val Leu Glu Ala Glu Lys Ala Leu Glu Gln Ala
305                 310                 315                 320

Gln Ser Arg Val Gln Asn Leu Thr Lys Gln Arg Ser Lys Leu Asn Asn
                325                 330                 335

Ala Leu Asn Ala Leu Asn
            340


<210> 320
<211> 333
<212> PRT
<213> Unknown
```

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 320
Met Thr Arg Asn Glu Tyr Ile Lys Ser Phe Asn Ser Val Ile Asp Asp
1 5 10 15

Lys Ala Ile Pro Met Phe Gly Gln Asn Ser Val Leu Ser Ile Ile Asn
20 25 30

Gln Trp Leu Asn Ser Val Asp Ala Ser Ile Val Ser Ser Thr Lys Phe
35 40 45

Ile His Glu Ile Arg Lys Ile Ser Ser Arg Val Asp Lys Asp Val Ile
50 55 60

Lys Lys Thr Phe Lys Glu Ser Arg Leu Leu Ser Tyr Leu Val Asn Arg
65 70 75 80

Asp Ile Leu Gly Asn Phe Gly Lys Glu Ile Lys Arg Thr Lys Asp Val
85 90 95

Val Gly Tyr Asn Trp Phe Gly Asp Val Asn Ser Tyr His Leu Asn Ile
100 105 110

Lys Glu Asp Pro Glu Asn Ile Phe Thr Arg Arg Trp Ile Ser Asn Phe
115 120 125

Arg Leu Phe Lys Lys Gln Ile Leu Lys Ser Ala Ser Lys Leu Cys Tyr
130 135 140

Gly Asp Tyr Arg Gln Ile His Pro Leu Ala Ser Asp Met Ile Ile Ile
145 150 155 160

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

Gly Phe Phe Thr Pro Glu Thr Asn Gln Lys Asn Ile Asn Lys Phe Phe
180 185 190

Ser Ile Ala Ser Thr Ile Thr Arg Gln Leu Glu Thr Ala Leu Leu Cys
195 200 205

Met Glu Thr Val Glu Asn Ile His Thr Tyr Pro Phe Lys Asn Ile Cys
210 215 220

Gly Trp Glu Gly Tyr Lys Leu Val Ile Ser Leu Arg Glu Val Lys Cys
225 230 235 240

Ala Tyr Ser Pro Thr Asp Lys Glu Ile Tyr Gln Gln Lys Cys Asp Glu
245 250 255

```
Ile Val Asn Thr Pro Lys Glu Glu Thr Thr Leu Glu Glu Leu Met Glu
            260                 265                 270


Cys Leu Asp Asp Ser Pro Glu Pro Ile Glu Ile Arg Pro Glu Val Ile
        275                 280                 285


Ala Leu Glu Lys Ala Tyr Lys Glu Val Leu Glu Ile Ser Asn Lys Ala
    290                 295                 300


Gln Lys Glu Tyr Glu Gln Ala Lys Arg Ile Trp Glu Glu Ser Val Asn
305                 310                 315                 320


Arg Leu Asp Arg Leu Glu Gln Ala Leu Gln Leu Ile Lys
                325                 330


<210> 321
<211> 308
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 321
Met Lys Thr Arg Lys His Tyr Ile Asp Tyr Phe Asp Ser Leu Ile Thr
1               5                   10                  15


Lys His Arg Asn Tyr Gln Ile Gly His Arg Ala Val Ile Asn Asn Ile
            20                  25                  30


Leu Arg Asp Phe Leu Asp Tyr Ile Gly Trp Glu Asn His Ile Cys Lys
        35                  40                  45


Asp Thr Gln Asn Ala Tyr Ser His Ser Leu Gly Ser Leu Leu Glu Trp
    50                  55                  60


Phe Lys Arg Ser Arg Leu Leu Ser Ser Val Ile Ala Val Asn Asn Val
65                  70                  75                  80


Lys Lys Phe Met Tyr Pro Ser Tyr Ile Glu Thr Asn Val Ser Asn Ala
                85                  90                  95


Ser Val Val Thr Phe Asn Ile Ile Asn Asp Val Lys Arg Thr Tyr Leu
            100                 105                 110


Glu Glu Trp Phe Ser Lys Asp Ser Lys Glu Lys Phe Ala Ser Glu Phe
        115                 120                 125


Ser His Glu Phe Asn Asn Asn Val Asn Met Leu Phe Lys His Ser Arg
    130                 135                 140


Arg Leu Phe Cys His Gly Asp Asn Arg Thr Ile Asn Val Asn Val Lys
145                 150                 155                 160
```

```
Asp Trp Val Thr Ala Lys Phe Thr Pro Ser Ser Gln Asn Gly Gln Phe
                165                 170                 175

Glu Leu Ser Ile Ile Ile Cys Ala Pro His Glu Ile Tyr Lys Asn Leu
            180                 185                 190

Pro Tyr Met Lys Pro Arg Glu Ala Asn Lys His Asn Glu Thr Ile Ser
        195                 200                 205

Ser Leu Ala Tyr Asn Leu Arg Val Leu Leu Ser Asp Met Asp Val Val
    210                 215                 220

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

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

Lys Ser Asn His Gly Asn Asp Thr Met Lys Glu Glu Arg Glu Tyr Leu
            260                 265                 270

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

Val Leu Lys Ala Leu Thr Ala Lys Ala Asn Gly Leu Arg Asn Ala Ile
    290                 295                 300

Glu Val Leu Lys
305


<210> 322
<211> 129
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 322
Met Lys Lys Arg Leu Leu Glu Asp Ile Ala Ala Ser Ser Asn Ser Ser
1               5                   10                  15

Leu Ile Lys Ile Ile Met Ala Gly Glu Glu Asp Asp Met Glu Met Arg
            20                  25                  30

Gly Lys Ile His Gly Cys Asp Asp Leu Asp Phe Lys Pro Pro Ala Trp
        35                  40                  45

Asp Ala Ile Met Ala Met Val Glu Arg Arg Glu Arg Ala Ser Lys Asn
    50                  55                  60

Val Pro Asn Cys Pro Glu Cys Gly Thr Glu Gln Val Gln Leu Ile Asn
```

65 70 75 80

Trp Arg Lys Pro Glu Leu Glu Tyr Lys Cys Arg Gln Cys Lys His Lys
85 90 95

Phe Ser Lys His Ala Pro Glu Met Val Lys Leu Pro Asp Ser Thr Glu
100 105 110

Phe Phe Lys Glu Leu Val Ser Val Gln Pro Met Pro Asn Asn Ile Leu
115 120 125

Asp

<210> 323
<211> 80
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 323
Met Thr Lys Arg Lys Glu Tyr Met Glu Ala Ala Glu Lys Ala Val Arg
1 5 10 15

Glu Leu Ala Ile Ala Tyr Tyr Asn Glu His Gly Lys Phe Pro Asp Arg
20 25 30

Tyr Ser Val Leu Lys Ser Ala Leu Thr Arg Ser Tyr Lys Asn Met Leu
35 40 45

Ser Glu Val Ser Asp Ile Ile Tyr Lys His Lys Glu Gln Thr Gly Gln
50 55 60

Ser Leu Asp Tyr Asp Glu Thr Phe Lys Gln Val Leu Gly Ile Lys Glu
65 70 75 80

<210> 324
<211> 87
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 324
Met Phe Lys Val Tyr Gly Tyr Asp Ser Asn Ile His Lys Cys Val Tyr
1 5 10 15

Cys Asp Asn Ala Lys Arg Leu Leu Thr Val Lys Lys Gln Pro Phe Glu
20 25 30

Phe Ile Asn Ile Met Pro Glu Lys Gly Val Phe Asp Asp Glu Lys Ile
35 40 45

Ala Glu Leu Leu Thr Lys Leu Gly Arg Asp Thr Gln Ile Gly Leu Thr
50 55 60

Met Pro Gln Val Phe Ala Pro Asp Gly Ser His Ile Gly Gly Phe Asp
65 70 75 80

Gln Leu Arg Glu Tyr Phe Lys
85

<210> 325
<211> 71
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 325
Met Met Leu Glu Gly Thr Asp Tyr Ile His Asp Tyr Arg Gly Ser Ala
1 5 10 15

Val Tyr Val Gly Asp Glu Val Ala Val Tyr Tyr Gly Tyr Gly Thr Leu
20 25 30

Met Thr Ala Lys Val Ile Gln Ile Lys Asn Asn Arg Ala Lys Leu Glu
35 40 45

Val Tyr Tyr Ser Asn Gly Glu Lys Ser Ile Ser Lys Trp Lys Tyr Gly
50 55 60

Asp Cys Met Val Lys Leu Gly
65 70

<210> 326
<211> 56
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 326
Met Ile Tyr Asp Ile Asn Val Ser Arg Thr Pro Ser Met Val Thr Ile
1 5 10 15

Pro Ala Glu Glu Leu Asp Arg Leu Gln Lys Ile Glu Glu Leu Leu Trp
20 25 30

Glu Ile Glu Ser Asp Leu Pro Ser Gly Leu Glu Ser Trp Ile Asp Tyr
35 40 45

Glu Glu Leu Asn Lys Leu Arg Gly
50 55

<210> 327

<211> 57
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 327
Leu Ile Met Lys Asn Leu Ile Ser Phe Gly Val Lys Pro Trp Trp Ala
1   5   10   15

Ala Arg Trp Glu Thr Val Glu Pro Glu Pro Glu Glu Pro Val Tyr Ile
            20   25   30

Asp Glu Glu Thr Val Tyr Asn Glu Pro Thr Ile Asn Asp Leu Ile Asp
        35   40   45

Met Glu Met Gly His Asp Tyr Ser Arg
    50   55

<210> 328
<211> 161
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 328
Met Ile Thr Val Asp Lys Trp Phe Arg Ile Asn Arg Val Asp Thr Gly
1   5   10   15

Leu Cys Asn Tyr Trp Pro Glu Leu Ser Ala Gly Thr Val Phe Lys Val
            20   25   30

Arg Glu Leu Ala Lys Glu Cys Glu Asp Asp Ile Glu Pro Asp Thr Gly
        35   40   45

Ile Ile Glu Ile Glu Leu Ser Asp Gly Lys Ile Ile Asn Ile Tyr Asp
    50   55   60

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

Gly Glu Ile Glu Glu Val Val Glu Arg Thr Ser Gln Asp Val Gln Lys
                85   90   95

Pro Lys Ala Ala Phe Gln Gly Glu Arg Ile Ser Tyr Ala Leu Ala Lys
            100   105   110

Leu Ala Ala Gln Glu Asn Asn Asp Gly Tyr Glu Gly Asn Leu Met Gln
        115   120   125

Ala Ala Ala Glu Tyr Ile Glu Trp Leu Glu Thr Gln Ile Ser Phe Ser
    130   135   140

Asp Gln Lys Ile Arg Gln Tyr Lys Arg Leu His Gln Met Phe Tyr Asn
145 150 155 160

Thr

<210> 329
<211> 58
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 329
Met Lys Thr Glu Leu Val Tyr Thr Glu Lys Leu Asn Gly Gly Lys Val
1 5 10 15

Trp Lys Leu Phe Ile Lys Gly His Ser Thr Asp Pro His Met Thr Thr
20 25 30

Cys Val Gly Thr Tyr Ser Arg Pro Thr Lys Lys Met Ile Arg Gln Tyr
35 40 45

Lys Arg Leu His Arg Met Phe Tyr Asn Thr
50 55

<210> 330
<211> 157
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 330
Met Leu Leu Thr Gly Lys Leu Tyr Lys Glu Glu Lys Gln Lys Phe Tyr
1 5 10 15

Asp Ala Gln Asn Gly Lys Cys Leu Ile Cys Gln Arg Glu Leu Asn Pro
20 25 30

Asp Val Gln Ala Asn His Leu Asp His Asp His Glu Leu Asn Gly Pro
35 40 45

Lys Ala Gly Lys Val Arg Gly Leu Leu Cys Asn Leu Cys Asn Ala Ala
50 55 60

Glu Gly Gln Met Lys His Lys Phe Asn Arg Ser Gly Leu Lys Gly Gln
65 70 75 80

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

Ser Asp Tyr Thr Gln Asn Asn Ile His Pro Asn Phe Val Gly Asp Lys

100 105 110

Ser Lys Glu Phe Ser Arg Leu Gly Lys Glu Glu Met Met Ala Glu Met
115 120 125

Leu Gln Arg Gly Phe Glu Tyr Asn Glu Ser Asp Thr Lys Thr Gln Leu
130 135 140

Ile Ala Ser Phe Lys Lys Gln Leu Arg Lys Ser Leu Lys
145 150 155

<210> 331
<211> 605
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 331
Met Thr Ile Glu Lys Glu Ile Glu Gly Leu Ile His Lys Thr Asn Lys
1 5 10 15

Asp Leu Leu Asn Glu Asn Ala Asn Lys Asp Ser Arg Val Phe Pro Thr
20 25 30

Gln Arg Asp Leu Met Ala Gly Ile Val Ser Lys His Ile Ala Lys Asn
35 40 45

Met Val Pro Ser Phe Ile Met Lys Ala His Glu Ser Gly Ile Ile His
50 55 60

Phe His Asp Ile Asp Tyr Ser Pro Ala Leu Pro Phe Thr Asn Cys Cys
65 70 75 80

Leu Val Asp Leu Lys Gly Met Leu Glu Asn Gly Phe Lys Leu Gly Asn
85 90 95

Ala Gln Ile Glu Thr Pro Lys Ser Ile Gly Val Ala Thr Ala Ile Met
100 105 110

Ala Gln Ile Thr Ala Gln Val Ala Ser His Gln Tyr Gly Gly Thr Thr
115 120 125

Phe Ala Asn Val Asp Lys Val Leu Ser Pro Tyr Val Lys Arg Thr Tyr
130 135 140

Ala Lys His Ile Glu Asp Ala Glu Lys Trp Gln Ile Ala Asp Ala Leu
145 150 155 160

Asn Tyr Ala Gln Ser Lys Thr Glu Lys Asp Val Tyr Asp Ala Phe Gln
165 170 175

```
Ala Tyr Glu Tyr Glu Val Asn Thr Leu Phe Ser Ser Asn Gly Gln Thr
            180                 185                 190

Pro Phe Val Thr Ile Thr Phe Gly Thr Gly Thr Asp Trp Thr Glu Arg
        195                 200                 205

Met Ile Gln Lys Ala Ile Leu Lys Asn Arg Ile Lys Gly Leu Gly Arg
    210                 215                 220

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

Gly Val Asn Leu Tyr Lys Asp Asp Pro Asn Tyr Asp Ile Lys Gln Leu
                245                 250                 255

Ala Leu Glu Cys Ala Ser Lys Arg Met Tyr Pro Asp Ile Ile Ser Ala
            260                 265                 270

Lys Asn Asn Lys Ala Ile Thr Gly Ser Ser Ile Pro Val Ser Pro Met
        275                 280                 285

Gly Cys Arg Ser Phe Leu Ser Ala Trp Lys Asp Ser Thr Gly Asn Glu
    290                 295                 300

Ile Leu Asp Gly Arg Asn Asn Leu Gly Val Val Thr Leu Asn Leu Pro
305                 310                 315                 320

Arg Ile Ala Leu Asp Ser Tyr Ile Gly Thr Gln Phe Asn Glu Gln Lys
                325                 330                 335

Phe Thr Glu Leu Phe Asn Glu Arg Met Asp Leu Cys Phe Glu Ala Leu
            340                 345                 350

Met Cys Arg Ile Ser Ser Leu Lys Gly Val Lys Ala Thr Val Ala Pro
        355                 360                 365

Ile Leu Tyr Gln Glu Gly Ala Phe Gly Val Arg Leu Lys Pro Asp Asp
    370                 375                 380

Asp Ile Ile Glu Leu Phe Lys Asn Gly Arg Ser Ser Val Ser Leu Gly
385                 390                 395                 400

Tyr Ile Gly Ile His Glu Leu Asn Ile Leu Val Gly Arg Asp Ile Gly
                405                 410                 415

Gln Glu Ile Leu Thr Lys Met Asn Ala Arg Leu Lys Gln Trp Ala Glu
            420                 425                 430

Arg Thr Gly Phe Ala Phe Ser Leu Tyr Ser Thr Pro Ala Glu Asn Leu
        435                 440                 445
```

```
Cys Tyr Arg Phe Cys Lys Leu Asp Thr Glu Lys Tyr Gly Ser Val Lys
    450                 455                 460

Asp Val Thr Asp Lys Gly Trp Tyr Thr Asn Ser Phe His Val Ser Val
465                 470                 475                 480

Glu Glu Asn Ile Thr Pro Phe Glu Lys Ile Ser Arg Glu Ala Pro Tyr
                485                 490                 495

His Phe Ile Ala Thr Gly Gly His Ile Ser Tyr Val Glu Leu Pro Asp
            500                 505                 510

Met Lys Asn Asn Leu Lys Gly Leu Glu Ala Val Trp Asp Tyr Ala Ala
        515                 520                 525

Gln His Leu Asp Tyr Phe Gly Val Asn Met Pro Val Asp Lys Cys Phe
    530                 535                 540

Thr Cys Gly Ser Thr His Glu Met Thr Pro Thr Glu Asn Gly Phe Val
545                 550                 555                 560

Cys Ser Ile Cys Gly Glu Thr Asp Pro Lys Lys Met Asn Thr Ile Arg
                565                 570                 575

Arg Thr Cys Gly Tyr Leu Gly Asn Pro Asn Glu Arg Gly Phe Asn Leu
            580                 585                 590

Gly Lys Asn Lys Glu Ile Met His Arg Val Lys His Gln
        595                 600                 605


<210> 332
<211> 156
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 332
Met Asn Tyr Asp Arg Phe Tyr Pro Cys Asp Phe Val Asn Gly Pro Gly
1               5                   10                  15

Cys Arg Thr Val Leu Phe Val Thr Gly Cys Leu His Lys Cys Glu Gly
            20                  25                  30

Cys Tyr Asn Lys Ser Thr Trp Asn Ala Arg Asn Gly Ile Pro Phe Thr
        35                  40                  45

Gly Glu Thr Leu Glu Gln Leu Ile Glu Cys Leu Asn Asn Asp Tyr Ile
    50                  55                  60

Glu Gly Leu Thr Ile Thr Gly Gly Asp Pro Leu Tyr Pro Asp Asn Arg
65                  70                  75                  80
```

Asp Val Ile His Cys Ile Val Gln Thr Val Lys Asn Leu Tyr Pro Asn
85 90 95

Lys Ser Ile Trp Leu Trp Thr Gly Tyr Lys Phe Glu Asp Ile Lys Gln
100 105 110

Leu Glu Met Leu Lys Tyr Val Asp Val Ile Ile Asp Gly Lys Tyr Glu
115 120 125

Lys Asn Leu Pro Thr Lys Lys Leu Trp Arg Gly Ser Asp Asn Gln Arg
130 135 140

Leu Trp Ser Asn Thr Asp Gly Val Trp Lys His Asp
145 150 155

<210> 333
<211> 37
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 333
Met Ile Lys Leu Asn Tyr Ile Met Asp Thr Ile Asn Asp Met Ile Phe
1 5 10 15

His Phe Gly Pro Glu Phe Tyr Ser Gln Tyr Ser Leu Val Leu Ile Asn
20 25 30

Ala Trp Leu Ile Asn
35

<210> 334
<211> 71
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 334
Met Tyr Lys Phe Arg Lys Gly Leu Ala Asp Phe Leu Thr Thr Val Thr
1 5 10 15

Phe Phe Leu Phe Met Ala Val Gly Ala Ile Phe Leu Ile Pro Phe Ile
20 25 30

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

Ser Ser Glu Phe Asn Glu Arg Leu Asp Lys Ile Thr Asn Lys Leu Asn
50 55 60

Ala Val Leu Asp Lys Lys Ala

65 70

<210> 335
<211> 103
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 335
Met Ile Ser Phe Glu Arg Tyr Val Val Glu Ser Trp Asn Gly Phe Asp
1 5 10 15

Met Phe Gly Asn Asp Tyr Tyr Phe Tyr Glu Cys Ser Leu Asn Pro Ser
20 25 30

Phe Trp Ala Gly Arg Glu Gln Asp Leu Glu Glu Ile Asn Ala Arg Ala
35 40 45

Asp Leu Leu Gly Glu Leu Pro Thr Thr Tyr Phe Thr Phe Asp Glu Ser
50 55 60

Gly Phe Val Ile Gln Val Tyr Phe Pro Glu Glu Asn Ser Gly Glu Asp
65 70 75 80

Ser Val Asn Pro Pro Tyr Trp Ala Tyr Gln Gly Ile Ile Ser Arg Gly
85 90 95

Thr Lys Leu Glu Leu Lys Glu
100

<210> 336
<211> 107
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 336
Val Glu Gln Asn Ser Asn Leu Lys Asn Lys Ile Glu Val Tyr Gly Ile
1 5 10 15

Pro Asp Glu Val Gly Arg Cys Pro Gly Cys Gln Ser Val Thr Lys Leu
20 25 30

Leu Lys Glu Leu Asn Ala Pro Phe Thr Phe Tyr Lys Val Leu Thr Asn
35 40 45

Asn Gly Lys Ile Glu Tyr Asp Arg Pro Leu Ile Val Ser Leu Ala Lys
50 55 60

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

Asn Asp Ser Arg Gln Lys Asn Ile Lys His Phe Lys Glu Thr Leu Ile
85 90 95

Ser Leu Gly Tyr Asp Arg Asp Ile Ile Glu Asp
100 105

<210> 337
<211> 60
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 337
Met Val Val Val Asp Lys Glu Ile Lys Lys Gly Gln Tyr Tyr Phe Ile
1 5 10 15

Asn Gly Asn Val Val Arg Val Thr Tyr Val Asn Gly Phe Glu Val Tyr
20 25 30

Tyr Leu Ile Leu Lys Leu His Lys Gln Met Ile Cys Asp Arg Ala Val
35 40 45

Phe Ser Ser Val Ala Lys Glu Ile Lys Leu His Gly
50 55 60

<210> 338
<211> 97
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 338
Met Gly Lys Thr Tyr Arg Arg Lys Asp Leu Lys Val Arg Asp Tyr Asp
1 5 10 15

Tyr Phe Gly Lys Arg Lys Ala Pro Asp Gly Val Ser His Lys Asp Met
20 25 30

Val Glu Asn Ile Phe Arg Ser Asp Lys Trp Arg Arg Met Lys Gly Ile
35 40 45

Asp Ser Glu Val Lys Asp Glu Leu Asn Arg Gln Leu Arg Ser Glu Val
50 55 60

Arg Lys Leu Lys Lys Ser Val Tyr Ile Asp Asp Asp Phe Asp Tyr Asn
65 70 75 80

Thr Ser Gln Arg Val Ala Lys Arg Lys Ser Asn Glu Cys Tyr Arg Tyr
85 90 95

Ser

<210> 339
<211> 43
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 339
Met Asn Ile Lys Arg Met Leu Phe Lys Gln Gly Leu Tyr Thr Leu Asn
1 5 10 15

Ala Thr Pro Lys Gly Asp Thr Thr Lys Trp Ser Val Asn Asp Trp Ile
            20 25 30

Lys Phe Ile Asp Glu Asn Gly Asn Trp Glu Ile
        35 40

<210> 340
<211> 66
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 340
Met Asn Pro Glu Ser Lys Leu Ser Gln Arg Ile Ala Glu Glu Arg Ala
1 5 10 15

Lys Phe Phe Gln Asn Met Lys His Asn Gly Ile Glu Asp Glu Val Phe
            20 25 30

Leu Asn Trp Phe Trp Asn Asn Lys Tyr Ala Ala Cys Glu Gly Ala Leu
        35 40 45

Ser Leu Ser Val Ala Met Met Tyr Glu Gly Trp Lys Gly Ala Lys Lys
    50 55 60

Phe Ser
65

<210> 341
<211> 108
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 341
Met Thr Ile Gln Ile Lys Asn Ala Ile Asn Ser Tyr Ala Tyr Asp Lys
1 5 10 15

Val Val Ser Leu Leu Glu Lys Gly Asp Ile Val Thr Pro Gln Ile Leu
            20 25 30

```
Asp Lys Trp Glu Lys Glu Leu His Gln Thr Met Lys Gln Asn Asp Gln
        35                  40                  45

Lys Ile Gly Arg Asn Thr Val Arg Glu Leu Leu Val Gln Tyr Ile Leu
    50                  55                  60

Ser Glu Phe Asp Val Lys Ala Phe Gly Val Glu Ser Lys Ala Tyr Gln
65                  70                  75                  80

Lys His Glu Ile Ser Asp Lys Thr Ile Arg Arg Met Lys Asn Gln Arg
                85                  90                  95

Lys Lys Lys Phe Ala Asp Leu Lys Ile Thr Lys Val
            100                 105
```

<210> 342
<211> 71
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 342

```
Met Asn Glu Ala Leu Ile Asn Asp Leu Arg Leu Ala Gly Tyr Glu Val
1               5                   10                  15

Asn Thr Asn Gly Ile Gly Leu Thr Gln Ile Glu Gly Asn Gly Phe Ile
            20                  25                  30

Leu Glu Tyr Glu Phe Ser Gln Trp Trp Leu Tyr Ala Asn Tyr Gly Glu
        35                  40                  45

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

Ala Ala Lys Leu Met Asn Val
65                  70
```

<210> 343
<211> 89
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 343

```
Met Lys Leu Ile Asn Ile Ser Ile Ala Ile Glu Asn Phe Gly Ile Phe
1               5                   10                  15

Tyr Val Asp Gln Tyr Met Lys Ile Ser Phe Phe Pro Asn Lys Thr Gly
            20                  25                  30
```

Val Gly Tyr Trp Glu Ser His Val Ser Glu Leu Asn Glu Ser Glu Tyr
        35   40   45

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

Asn Asp His Tyr Ile Asp Ile His Glu Phe Lys Lys Met Met Glu Lys
65   70   75   80

Val Phe Gln Ala Tyr Cys Leu Leu Arg
                85

<210> 344
<211> 185
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 344
Met Ser Glu Thr Lys Pro Lys Tyr Asn Tyr Val Asn Asn Lys Glu Leu
1   5   10   15

Leu Gln Ala Ile Ile Asp Trp Lys Thr Glu Leu Ala Asn Asn Lys Asp
            20   25   30

Pro Asn Lys Val Val Arg Gln Asn Asp Thr Ile Gly Leu Ala Ile Met
        35   40   45

Leu Ile Ala Glu Gly Leu Ser Lys Arg Phe Asn Phe Ser Gly Tyr Thr
    50   55   60

Gln Ser Trp Lys Gln Glu Met Ile Ala Asp Gly Ile Glu Ala Ser Ile
65   70   75   80

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

Tyr Ile Thr Gln Ala Cys Phe Asn Ala Phe Val Gln Arg Ile Lys Lys
            100   105   110

Glu Arg Lys Glu Val Ala Lys Lys Tyr Ser Tyr Phe Val His Asn Val
        115   120   125

Tyr Asp Ser Arg Asp Asp Asp Met Val Ala Leu Val Asp Glu Thr Phe
    130   135   140

Ile Gln Asp Ile Tyr Asp Lys Met Thr His Tyr Glu Glu Ser Thr Tyr
145   150   155   160

Arg Thr Pro Gly Ala Glu Lys Lys Ser Val Val Asp Asp Ser Pro Ser
                165   170   175

Leu Asp Phe Leu Tyr Glu Ala Asn Asp
180 185

<210> 345
<211> 72
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 345
Met Arg Leu Thr Ile Asn Leu Ser Gly Phe Leu Glu Glu Ile Pro Glu
1 5 10 15

Val Glu Ala Ile Pro Tyr Leu Leu Lys Met Tyr Leu Arg Glu Val Leu
20 25 30

Ala Leu Asp Ile Asp Ile Asp Pro Glu Asn Pro Tyr Asp Thr Ala Phe
35 40 45

Lys Ser Asn Gly Val Glu Leu Asn Tyr Arg Tyr His Leu Thr Asp Asp
50 55 60

Asp Phe Tyr Phe Ile Leu Glu Lys
65 70

<210> 346
<211> 105
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 346
Met Thr Asp Lys Pro Glu Ile Asn Asp Glu Val Glu Lys Leu Ile Ser
1 5 10 15

Ser Ile Glu Glu Lys Asn Arg Leu Glu Ala Glu Arg Lys Ala Asn Lys
20 25 30

Leu Leu Ser Lys Asn Lys Arg Glu Leu Asn Arg Leu Tyr Lys His Ala
35 40 45

Gln Ile Ala Ala Glu Asn Asn Asn Phe Ala Gln Tyr Glu Tyr Ala Ile
50 55 60

Lys Lys Ser Arg Asp Ile Leu Lys Gln Pro Tyr Asn Asp Glu Leu Ile
65 70 75 80

Ser Ile Leu Trp Lys Thr Thr Arg Ser Gln Ile Glu Asp Met Ile Asp
85 90 95

Ala Tyr Thr Arg Lys Ile Gln Ala Ser

100 105

<210> 347
<211> 67
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 347
Met Leu Thr His Val Lys Phe Lys Arg Leu Lys Ile Asn Ala Gly Phe
1 5 10 15

Thr Glu Ser Leu Asn Gly His Leu Cys Val Lys Ile Ser Glu Lys Glu
20 25 30

Tyr His Asp Ser Ser Ile Lys Glu Val Asn Pro Pro Ile Val Arg Ala
35 40 45

Asp Pro Asn Met Lys Val Trp Val Asp Ser Tyr Gln Val Lys Lys Trp
50 55 60

Trp Gln Leu
65

<210> 348
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 348
Met Asn Thr Gln Thr Ser Glu Ile Asp Tyr Asn Lys Ile Arg Ser Ser
1 5 10 15

Lys Glu Glu Met Met Arg Arg Phe Lys Glu Ser His Asp Lys Ala Lys
20 25 30

Ala Glu Gly Thr Ile Lys Tyr Lys Arg Ile Lys Phe Lys Ser Ser Asn
35 40 45

Glu Pro Leu Tyr Gly Val Leu Cys Gly
50 55

<210> 349
<211> 400
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 349
Met Lys Val Cys Ile Phe Met Ala Arg Gly Leu Glu Gly Cys Gly Val
1 5 10 15

```
Thr Lys Phe Ser Leu Glu Gln Arg Asp Trp Phe Ile Lys Asn Gly His
            20                  25                  30

Glu Val Thr Leu Val Tyr Ala Lys Asp Lys Ser Phe Thr Arg Asn Cys
        35                  40                  45

Ala His Asp Tyr Lys Ser Phe Ser Ile Pro Val Leu Leu Ala Lys Glu
    50                  55                  60

Tyr Asp Lys Thr Leu Lys Leu Val Asn Asp Cys Asp Ile Leu Ile Ile
65                  70                  75                  80

Asn Ser Val Pro Ala Thr Ser Val Glu Glu Asp Thr Ile Asn Asn Tyr
                85                  90                  95

Lys Lys Ile Ile Asp Asn Ile Lys Pro Ser Val Arg Val Val Val Tyr
            100                 105                 110

Gln His Asp His Ser Ser Leu Ser Leu Arg Arg Asn Leu Gly Leu Glu
        115                 120                 125

Glu Thr Ile Arg Arg Ala Asp Val Ile Phe Ser His Ser Asp Asn Gly
    130                 135                 140

Asp Phe Asn Lys Val Leu Met Lys Glu Trp Tyr Pro Glu Thr Val Ser
145                 150                 155                 160

Leu Phe Asp Asp Ile Glu Glu Ala Pro Thr Val Tyr Asn Phe Gln Pro
                165                 170                 175

Pro Met Asp Ile Ala Lys Val Arg Ser Thr Tyr Trp Lys Asp Val Ser
            180                 185                 190

Glu Ile Asn Met Asn Ile Asn Arg Trp Ile Gly Arg Thr Thr Thr Trp
        195                 200                 205

Lys Gly Phe Tyr Gln Met Phe Asp Phe His Glu Lys His Leu Lys Pro
    210                 215                 220

Ala Gly Leu Ser Thr Ile Met Glu Gly Leu Glu Arg Ser Pro Ala Phe
225                 230                 235                 240

Ile Pro Ile Lys Glu Lys Gly Ile Pro Tyr Glu Tyr Tyr Arg Leu His
                245                 250                 255

Gln Val Asp Gln Ile Lys Ile Ala Pro Asn Leu Pro Thr Gln Ile Leu
            260                 265                 270

Asp Arg Tyr Val Asn Ser Glu Met Leu Glu Arg Met Ser Lys Ser Gly
        275                 280                 285
```

Phe Gly Tyr Gln Leu Ser Lys Leu Asp Lys Lys Tyr Leu Gln Arg Ser
290 295 300

Leu Glu Tyr Thr His Leu Glu Leu Gly Ala Cys Gly Thr Ile Pro Val
305 310 315 320

Phe Trp Lys Ser Thr Gly Glu Asn Leu Lys Phe Arg Val Asp Asn Thr
325 330 335

Pro Leu Thr Ser His Asp Ser Gly Ile Ile Trp Phe Asp Glu Asn Asp
340 345 350

Met Glu Ser Thr Phe Glu Arg Ile Lys Glu Leu Ser Ser Asp Arg Thr
355 360 365

Leu Tyr Asp Arg Glu Arg Glu Lys Ala Tyr Glu Phe Leu Tyr Gln His
370 375 380

Gln Asp Ser Ser Phe Cys Phe Lys Glu Gln Phe Asp Ile Ile Thr Lys
385 390 395 400

<210> 350
<211> 339
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 350
Met Lys Ile Leu Asn Leu Gly Asp Trp His Leu Gly Val Lys Ala Asp
1 5 10 15

Asp Glu Trp Val Gln Ser Ile Gln Leu Asp Gly Ile Lys Gln Ala Ile
20 25 30

Glu Tyr Ser Lys Lys Asn Gly Ile Thr Thr Trp Ile Gln Tyr Gly Asp
35 40 45

Ile Phe Asp Val Arg Lys Ala Ile Thr His Lys Thr Met Glu Phe Ala
50 55 60

Arg Glu Ile Val Gln Met Leu Asp Asp Ala Gly Ile Thr Leu His Thr
65 70 75 80

Ile Val Gly Asn His Asp Met His Phe Lys Asn Thr Leu Thr Pro Asn
85 90 95

Ala Ser Thr Glu Leu Leu Ala Lys Tyr Pro Asn Val Lys Val Tyr Asp
100 105 110

Lys Pro Thr Thr Val Asp Phe Asp Gly Cys Leu Ile Asp Leu Ile Pro

115 120 125

Trp Met Cys Glu Glu Asn Thr Gly Glu Ile Leu Glu His Ile Lys Thr
130 135 140

Ser Ser Ala Ser Phe Cys Val Gly His Trp Glu Leu Asn Gly Phe Tyr
145 150 155 160

Phe Tyr Lys Gly Met Lys Ser His Gly Leu Glu Pro Asp Phe Leu Lys
165 170 175

Thr Tyr Lys Glu Val Trp Ser Gly His Phe His Thr Ile Ser Glu Ala
180 185 190

Ala Asn Val Arg Tyr Ile Gly Thr Pro Trp Thr Leu Thr Ala Gly Asp
195 200 205

Glu Asn Asp Pro Arg Gly Phe Trp Met Phe Asp Thr Glu Thr Glu Arg
210 215 220

Met Glu Phe Ile Pro Asn Asn Thr Thr Trp His Arg Arg Ile His Tyr
225 230 235 240

Pro Phe Lys Gly Lys Ile Asp Tyr Lys Asp Phe Thr Asn Leu Ser Val
245 250 255

Arg Val Ile Val Thr Glu Val Asp Lys Asn Leu Thr Lys Phe Glu Ser
260 265 270

Glu Leu Glu Lys Val Val His Ser Leu Arg Val Val Ser Lys Ile Asp
275 280 285

Asn Ser Val Glu Ser Asp Asp Ser Glu Glu Val Glu Val Gln Ser Leu
290 295 300

Gln Thr Leu Met Glu Glu Tyr Ile Asn Ala Ile Pro Asp Ile Thr Asp
305 310 315 320

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

Ala Thr Gln

<210> 351
<211> 87
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 351

Met Thr Phe Asp Glu Phe Lys Asn Val Met Met Ser Gln His Phe Glu
1   5   10   15

Cys Glu Val Lys Asp Asp Ile Gly His Lys Glu Ile Ile Glu Tyr Trp
            20   25   30

Phe Glu Pro Leu Glu Val Glu Asp Asn Cys Ile Lys Lys Val Thr Val
        35   40   45

Cys Thr Asp Trp Ala Val Ser Phe Asn Phe Asn Ile Leu Asp Asn Asp
    50   55   60

Thr Pro Lys Ser Leu Arg Asp Met Ala Val Ser Cys Ile Lys Asp Ala
65   70   75   80

Tyr Cys Glu Val Phe Asp Ile
                85

<210> 352
<211> 68
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 352
Val Lys Phe Ser Thr Phe Asp Ile Asn Asp Glu Phe Ile Ala Asn Ile
1   5   10   15

Asp Tyr Thr Glu Glu Asp Ser Arg Tyr Val Gly Ile Ile Tyr Ile Thr
            20   25   30

Ser Lys Thr Ala Gln Gly Val Val Cys Met Ala Glu Phe Asp Glu Tyr
        35   40   45

Phe Leu Asp Tyr Asp Asp Met Ile Glu Trp Ser Lys Arg Tyr Ile Lys
    50   55   60

Arg Asn Leu Leu
65

<210> 353
<211> 546
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 353
Met Ser Val Gly Gly Asn Pro Ile Asp Ile Gln Leu Asp Lys Val Gln
1   5   10   15

Lys Thr Leu Ile Thr Gly Arg Asn Gly Gly Gly Lys Ser Thr Met Leu
            20   25   30

```
Glu Ala Ile Thr Phe Gly Leu Phe Gly Lys Pro Phe Arg Asp Val Lys
        35                  40                  45

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

Leu Trp Met Glu Tyr Asp Glu Lys Lys Tyr Tyr Ile Lys Arg Gly Gln
65                  70                  75                  80

Lys Pro Asn Val Phe Glu Ile Thr Val Asn Gly Thr Arg Leu Asn Glu
                85                  90                  95

Ser Ala Ser Ser Lys Asp Phe Gln Ala Glu Phe Glu Gln Leu Ile Gly
            100                 105                 110

Met Ser Tyr Ala Ser Phe Lys Gln Ile Val Val Leu Gly Thr Ala Gly
        115                 120                 125

Tyr Thr Pro Phe Met Gly Leu Ser Thr Pro Ala Arg Arg Lys Leu Val
    130                 135                 140

Glu Asp Leu Leu Glu Val Gly Thr Leu Ala Glu Met Asp Lys Leu Asn
145                 150                 155                 160

Lys Ala Leu Ile Arg Glu Leu Asn Ser Gln Asn Gln Val Leu Asp Val
                165                 170                 175

Lys Lys Asp Ser Ile Ile Gln Gln Ile Lys Ile Tyr Asn Asp Asn Val
            180                 185                 190

Glu Arg Gln Lys Lys Leu Thr Gly Asp Asn Leu Thr Arg Leu Gln Asn
        195                 200                 205

Met Tyr Asp Asp Leu Ala Lys Glu Ala Arg Thr Leu Lys Ser Glu Ile
    210                 215                 220

Glu Glu Ala Asn Glu Arg Leu Val Asn Ile Val Leu Asp Glu Asp Pro
225                 230                 235                 240

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

Lys Ile Asp Ser Tyr Asn Lys Val Ile Asn Met Tyr His Glu Gly Gly
            260                 265                 270

Leu Cys Pro Thr Cys Leu Ser Gln Leu Ser Ser Gly Asp Lys Val Val
        275                 280                 285

Ser Lys Ile Lys Asp Lys Val Ser Glu Cys Thr His Ser Phe Glu Gln
    290                 295                 300
```

Leu Ser Thr His Arg Asp Asn Leu Lys Val Leu Val Asp Glu Tyr Arg
305 310 315 320

Asp Asn Ile Lys Thr Gln Gln Ser Leu Ala Asn Asp Ile Arg Asn Lys
325 330 335

Lys Gln Ser Leu Ile Thr Thr Val Asp Lys Ala Lys Lys Val Lys Ala
340 345 350

Ala Ile Glu Lys Ala Ser Ser Glu Phe Ile Asp His Ala Asp Glu Ile
355 360 365

Ala Leu Leu Gln Glu Glu Leu Asp Lys Ile Val Lys Thr Lys Thr Asn
370 375 380

Leu Val Met Glu Lys Tyr His Arg Gly Ile Leu Thr Asp Met Leu Lys
385 390 395 400

Asp Ser Gly Ile Lys Gly Ala Ile Ile Lys Lys Tyr Ile Pro Leu Phe
405 410 415

Asn Lys Gln Ile Asn His Tyr Leu Lys Ile Met Glu Ala Asp Tyr Val
420 425 430

Phe Thr Leu Asp Glu Glu Phe Asn Glu Thr Ile Lys Ser Arg Gly Arg
435 440 445

Glu Asp Phe Ser Tyr Ala Ser Phe Ser Gln Gly Glu Lys Ala Arg Ile
450 455 460

Asp Ile Ala Leu Leu Phe Thr Trp Arg Asp Ile Ala Glu Lys Val Ser
465 470 475 480

Gly Val Lys Ile Asn Thr Leu Ile Leu Asp Glu Val Phe Asp Ser Ala
485 490 495

Thr Asp Val Glu Gly Val Lys Ala Ile Ser Thr Ile Leu Asp Ser Leu
500 505 510

Lys Asn Thr Asn Val Phe Val Ile Ser His Arg Asp His Asp Pro Gln
515 520 525

Ala Tyr Gly Gln His Leu Gln Met Lys Lys Val Gly Arg Phe Thr Val
530 535 540

Met Val
545

<210> 354
<211> 62

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 354
Met Glu Tyr Ser Thr Gly Gln His Leu Leu Thr Ile Pro Glu Ile Lys
1   5   10   15

Arg Tyr Ile Leu Arg Asn Asn Phe Ser Asn Glu Glu His Ile Val Thr
            20   25   30

Glu Ser Met Leu Arg Asn Ala Phe Lys Ala Glu Tyr Thr Lys Ile Met
        35   40   45

Ser Asn Arg Asn Glu Ala Trp Thr Val Thr Asp Tyr Tyr Asp
    50   55   60

<210> 355
<211> 129
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 355
Met Thr Lys Ile Thr Val Asn Tyr Thr Val Asp Val Lys Asp Ile Gln
1   5   10   15

Pro Lys His Val Arg Ser Glu Ser Asn Pro Gln Asn Gln Asn Lys Ile
            20   25   30

Arg Arg Ala Trp Val Leu Ser Leu Ser Asp Asn Ala Met Glu Val Ile
        35   40   45

Gln Asn Lys Ile Lys Ser Ala Pro Ala Arg His Ala Tyr Tyr Glu Ala
    50   55   60

Ile Asp Arg Glu Val Ser Asn Lys Trp Ile Glu Leu Met Arg Lys His
65   70   75   80

Thr Thr Glu Ser Leu Asn Ala Gly Ala Lys Phe Ile Met Thr Ser Cys
                85   90   95

Gly Glu Arg Leu Glu Asp Glu Tyr Cys Gly Asn Ala Asp Glu Arg Leu
            100   105   110

Ile Val Ala Ala Gln Ile Val Ala Glu Thr Ile Ala Ala Asp Phe Asn
        115   120   125

Arg

<210> 356
<211> 228
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 356
Met Lys Leu Ser Lys Asp Thr Thr Ala Leu Leu Lys Asn Phe Ala Thr
1   5   10   15

Ile Asn Ser Gly Ile Met Leu Lys Ser Gly Gln Phe Ile Met Thr Arg
            20   25   30

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

Asp Phe Asp Val Ala Ile Tyr Asp Leu Asn Gly Phe Leu Gly Ile Leu
    50   55   60

Ser Leu Val Asn Asp Asp Ala Glu Ile Ser Gln Ser Glu Asp Gly Asn
65   70   75   80

Ile Lys Ile Ala Asp Ala Arg Ser Thr Ile Phe Trp Pro Ala Ala Asp
                85   90   95

Pro Ser Thr Val Val Ala Pro Asn Lys Pro Ile Pro Phe Pro Val Ala
            100   105   110

Ser Val Val Thr Glu Ile Lys Ala Glu Asp Leu Gln Gln Leu Leu Arg
        115   120   125

Val Ser Arg Gly Leu Gln Ile Asp Thr Ile Ala Ile Thr Val Lys Glu
    130   135   140

Gly Lys Ile Val Ile Asn Gly Phe Asn Lys Val Glu Asp Ser Ala Leu
145   150   155   160

Thr Arg Val Lys Tyr Ser Leu Thr Leu Gly Asp Tyr Asp Gly Glu Asn
                165   170   175

Thr Phe Asn Phe Ile Ile Asn Met Ala Asn Met Lys Met Gln Pro Gly
            180   185   190

Asn Tyr Lys Leu Leu Leu Trp Ala Lys Gly Lys Gln Gly Ala Ala Lys
        195   200   205

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

Thr His Asp Phe
225

<210> 357
<211> 319
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 357
Met Ile Thr Val Asn Glu Lys Glu His Ile Leu Glu Gln Lys Tyr Arg
1   5   10   15

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

Phe Lys Ser Ile Thr Ser Lys Gly Lys Ile Pro His Ile Ile Leu His
        35   40   45

Ser Pro Ser Pro Gly Thr Gly Lys Thr Thr Val Ala Lys Ala Leu Cys
    50   55   60

His Asp Val Asn Ala Asp Met Met Phe Val Asn Gly Ser Asp Cys Lys
65   70   75   80

Ile Asp Phe Val Arg Gly Pro Leu Thr Asn Phe Ala Ser Ala Ala Ser
                85   90   95

Phe Asp Gly Arg Gln Lys Val Ile Val Ile Asp Glu Phe Asp Arg Ser
            100   105   110

Gly Leu Ala Glu Ser Gln Arg His Leu Arg Ser Phe Met Glu Ala Tyr
        115   120   125

Ser Ser Asn Cys Ser Ile Ile Ile Thr Ala Asn Asn Ile Asp Gly Ile
    130   135   140

Ile Lys Pro Leu Gln Ser Arg Cys Arg Val Ile Thr Phe Gly Gln Pro
145   150   155   160

Thr Asp Glu Asp Lys Ile Glu Met Met Lys Gln Met Ile Arg Arg Leu
                165   170   175

Thr Glu Ile Cys Lys His Glu Gly Ile Ala Ile Ala Asp Met Lys Val
            180   185   190

Val Ala Ala Leu Val Lys Lys Asn Phe Pro Asp Phe Arg Lys Thr Ile
        195   200   205

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

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

```
Ser Leu Lys Asn Lys Asp Val Lys Gln Leu Arg Ala Leu Ala Pro Lys
                245                 250                 255

Tyr Ala Ala Asp Tyr Ser Trp Phe Val Gly Lys Leu Ala Glu Glu Ile
            260                 265                 270

Tyr Ser Arg Val Thr Pro Gln Ser Ile Ile Arg Met Tyr Glu Ile Val
        275                 280                 285

Gly Glu Asn Asn Gln Tyr His Gly Ile Ala Ala Asn Thr Glu Leu His
    290                 295                 300

Leu Ala Tyr Leu Phe Ile Gln Leu Ala Cys Glu Met Gln Trp Lys
305                 310                 315


<210> 358
<211> 187
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 358
Met Ser Leu Phe Glu Asp Asp Ile Gln Leu Asn Glu His Gln Val Ala
1               5                   10                  15

Trp Tyr Ser Lys Asp Trp Thr Ala Val Gln Ser Ala Ala Asp Ser Phe
            20                  25                  30

Lys Glu Lys Ala Glu Asn Glu Phe Phe Glu Ile Ile Gly Ala Ile Asn
        35                  40                  45

Asn Lys Thr Lys Cys Ser Ile Ala Gln Lys Asp Tyr Ser Lys Phe Met
    50                  55                  60

Val Glu Asn Ala Leu Ser Gln Phe Pro Glu Cys Met Pro Ala Val Tyr
65                  70                  75                  80

Ala Met Asn Leu Ile Gly Ser Gly Leu Ser Asp Glu Ala His Phe Asn
                85                  90                  95

Tyr Leu Met Ala Ala Val Pro Arg Gly Lys Arg Tyr Gly Lys Trp Ala
            100                 105                 110

Lys Leu Val Glu Asp Ser Thr Glu Val Leu Ile Ile Lys Leu Leu Ala
        115                 120                 125

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

Leu Thr Lys Asn Gly Lys Leu Pro Leu Val Leu Lys Glu Leu Lys Gly
```

145 150 155 160

Leu Val Thr Asp Asp Phe Leu Lys Glu Val Thr Lys Asn Val Lys Glu
165 170 175

Gln Lys Gln Leu Lys Lys Leu Ala Leu Glu Trp
180 185

<210> 359
<211> 122
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 359
Met Ile Glu Ile Thr Leu Lys Lys Pro Glu Asp Phe Leu Lys Val Lys
1 5 10 15

Glu Thr Leu Thr Arg Met Gly Ile Ala Asn Asn Lys Asp Lys Val Leu
20 25 30

Tyr Gln Ser Cys His Ile Leu Gln Lys Lys Gly Leu Tyr Tyr Ile Val
35 40 45

His Phe Lys Glu Met Leu Arg Met Asp Gly Arg Gln Val Glu Met Thr
50 55 60

Glu Glu Asp Glu Val Arg Arg Asp Ser Ile Ala Trp Leu Leu Glu Asp
65 70 75 80

Trp Gly Leu Ile Glu Ile Val Pro Gly Gln Arg Thr Phe Met Lys Asp
85 90 95

Leu Thr Asn Asn Phe Arg Val Ile Ser Phe Lys Gln Lys His Glu Trp
100 105 110

Lys Leu Val Pro Lys Tyr Thr Ile Gly Asn
115 120

<210> 360
<211> 73
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 360
Met Thr Ala Ile Thr Pro Gln Glu Tyr Met Ala Ser Leu Lys Glu Lys
1 5 10 15

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

```
Gln Leu Lys Phe Gln Val Glu Phe Gln Lys Leu Val His Pro Glu Gln
        35                  40                  45


Lys His Phe Thr Ala Val Val Lys Ser Ile Asn Ala Asp Gly Met Ile
    50                  55                  60


Ile Phe Thr Arg Gln Ile Val Leu Ile
65                  70


<210> 361
<211> 898
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 361
Met Lys Glu Phe Tyr Ile Ser Ile Glu Thr Val Gly Asn Asn Ile Val
1               5                   10                  15


Glu Arg Tyr Ile Asp Glu Asn Gly Lys Glu Arg Thr Arg Glu Val Glu
            20                  25                  30


Tyr Leu Pro Thr Met Phe Arg His Cys Lys Glu Glu Ser Lys Tyr Lys
        35                  40                  45


Asp Ile Tyr Gly Lys Asn Cys Ala Pro Gln Lys Phe Pro Ser Met Lys
    50                  55                  60


Asp Ala Arg Asp Trp Met Lys Arg Met Glu Asp Ile Gly Leu Glu Ala
65                  70                  75                  80


Leu Gly Met Asn Asp Phe Lys Leu Ala Tyr Ile Ser Asp Thr Tyr Gly
                85                  90                  95


Ser Glu Ile Val Tyr Asp Arg Lys Phe Val Arg Val Ala Asn Cys Asp
            100                 105                 110


Ile Glu Val Thr Gly Asp Lys Phe Pro Asp Pro Met Lys Ala Glu Tyr
        115                 120                 125


Glu Ile Asp Ala Ile Thr His Tyr Asp Ser Ile Asp Asp Arg Phe Tyr
    130                 135                 140


Val Phe Asp Leu Leu Asn Ser Met Tyr Gly Ser Val Ser Lys Trp Asp
145                 150                 155                 160


Ala Lys Leu Ala Ala Lys Leu Asp Cys Glu Gly Gly Asp Glu Val Pro
                165                 170                 175


Gln Glu Ile Leu Asp Arg Val Ile Tyr Met Pro Phe Asp Asn Glu Arg
            180                 185                 190
```

```
Asp Met Leu Met Glu Tyr Ile Asn Leu Trp Glu Gln Lys Arg Pro Ala
        195                 200                 205

Ile Phe Thr Gly Trp Asn Ile Glu Gly Phe Asp Val Pro Tyr Ile Met
    210                 215                 220

Asn Arg Val Lys Met Val Leu Gly Glu Arg Ser Met Lys Arg Phe Ser
225                 230                 235                 240

Pro Ile Gly Arg Val Lys Ser Lys Leu Ile Gln Asn Met Tyr Gly Ser
                245                 250                 255

Lys Glu Ile Tyr Ser Ile Asp Gly Val Ser Ile Leu Asp Tyr Leu Asp
            260                 265                 270

Leu Tyr Lys Lys Phe Ala Phe Thr Asn Leu Pro Ser Phe Ser Leu Glu
        275                 280                 285

Ser Val Ala Gln His Glu Thr Lys Lys Gly Lys Leu Pro Tyr Asp Gly
    290                 295                 300

Pro Ile Asn Lys Leu Arg Glu Thr Asn His Gln Arg Tyr Ile Ser Tyr
305                 310                 315                 320

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

Phe Ile Asp Leu Val Leu Ser Met Ser Tyr Tyr Ala Lys Met Pro Phe
            340                 345                 350

Ser Gly Val Met Ser Pro Ile Lys Thr Trp Asp Ala Ile Ile Phe Asn
        355                 360                 365

Ser Leu Lys Gly Glu His Lys Val Ile Pro Gln Gln Gly Ser His Val
    370                 375                 380

Lys Gln Ser Phe Pro Gly Ala Phe Val Phe Glu Pro Lys Pro Ile Ala
385                 390                 395                 400

Arg Arg Tyr Ile Met Ser Phe Asp Leu Thr Ser Leu Tyr Pro Ser Ile
                405                 410                 415

Ile Arg Gln Val Asn Ile Ser Pro Glu Thr Ile Arg Gly Gln Phe Lys
            420                 425                 430

Val His Pro Ile His Glu Tyr Ile Ala Gly Thr Ala Pro Lys Pro Ser
        435                 440                 445

Glu Glu Tyr Ser Cys Ser Pro Asn Gly Trp Met Tyr Asp Lys His Gln
    450                 455                 460
```

```
Glu Gly Ile Ile Pro Lys Glu Ile Ala Lys Val Phe Phe Gln Arg Lys
465                 470                 475                 480

Asp Trp Lys Lys Lys Met Phe Ala Glu Glu Met Asn Ala Glu Ala Ile
                485                 490                 495

Lys Lys Ile Ile Met Lys Gly Ala Gly Ser Cys Ser Thr Lys Pro Glu
            500                 505                 510

Val Glu Arg Tyr Val Lys Phe Ser Asp Asp Phe Leu Asn Glu Leu Ser
        515                 520                 525

Asn Tyr Thr Glu Ser Val Leu Asn Ser Leu Ile Glu Glu Cys Glu Lys
    530                 535                 540

Ala Ala Thr Leu Ala Asn Thr Asn Gln Leu Asn Arg Lys Ile Leu Ile
545                 550                 555                 560

Asn Ser Leu Tyr Gly Ala Leu Gly Asn Ile His Phe Arg Tyr Tyr Asp
                565                 570                 575

Leu Arg Asn Ala Thr Ala Ile Thr Ile Phe Gly Gln Val Gly Ile Gln
            580                 585                 590

Trp Ile Ala Arg Lys Ile Asn Glu Tyr Leu Asn Lys Val Cys Gly Thr
        595                 600                 605

Asn Gly Glu Asp Phe Ile Ala Ala Gly Asp Thr Asp Ser Val Tyr Val
    610                 615                 620

Cys Val Asp Lys Val Ile Glu Lys Val Gly Leu Asp Arg Phe Lys Glu
625                 630                 635                 640

Gln Asn Asp Leu Val Glu Phe Met Asn Gln Phe Gly Lys Lys Lys Met
                645                 650                 655

Glu Pro Met Ile Asp Val Ala Tyr Arg Glu Leu Cys Asp Tyr Met Asn
            660                 665                 670

Asn Arg Glu His Leu Met His Met Asp Arg Glu Ala Ile Ser Cys Pro
        675                 680                 685

Pro Leu Gly Ser Lys Gly Val Gly Gly Phe Trp Lys Ala Lys Lys Arg
    690                 695                 700

Tyr Ala Leu Asn Val Tyr Asp Met Glu Asp Lys Arg Phe Ala Glu Pro
705                 710                 715                 720

His Leu Lys Ile Met Gly Met Glu Thr Gln Gln Ser Ser Thr Pro Lys
                725                 730                 735
```

```
Ala Val Gln Glu Ala Leu Glu Glu Ser Ile Arg Arg Ile Leu Gln Glu
            740                 745                 750

Gly Glu Glu Ser Val Gln Glu Tyr Tyr Lys Asn Phe Glu Lys Glu Tyr
        755                 760                 765

Arg Gln Leu Asp Tyr Lys Val Ile Ala Glu Val Lys Thr Ala Asn Asp
    770                 775                 780

Ile Ala Lys Tyr Asp Asp Lys Gly Trp Pro Gly Phe Lys Cys Pro Phe
785                 790                 795                 800

His Ile Arg Gly Val Leu Thr Tyr Arg Arg Ala Val Ser Gly Leu Gly
                805                 810                 815

Val Ala Pro Ile Leu Asp Gly Asn Lys Val Met Val Leu Pro Leu Arg
            820                 825                 830

Glu Gly Asn Pro Phe Gly Asp Lys Cys Ile Ala Trp Pro Ser Gly Thr
        835                 840                 845

Glu Leu Pro Lys Glu Ile Arg Ser Asp Val Leu Ser Trp Ile Asp Tyr
    850                 855                 860

Ser Thr Leu Phe Gln Lys Ser Phe Val Lys Pro Leu Ala Gly Met Cys
865                 870                 875                 880

Glu Ser Ala Gly Met Asp Tyr Glu Glu Lys Ala Ser Leu Asp Phe Leu
                885                 890                 895

Phe Gly



<210> 362
<211> 126
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 362
Met Lys Ile Ala Ile Leu Val Ile Ala Leu Gly Leu Thr Gly Cys Val
1               5                   10                  15

Ala Gln Gly Pro Val Val Asn Gln Ser Asp Val Gly Lys Ile Val Asn
            20                  25                  30

Cys Ser Ser Lys Phe Tyr Asn Pro Asn Val Lys Cys Tyr Lys Glu Ala
        35                  40                  45

Pro Lys Gln Thr Val Glu Gln Met Gln Ala Asn Phe Asp Glu Ala Ile
```

50 55 60

Arg Pro Asp Glu Ser Ala Gln Ala Tyr Arg Asn Ser Asp Val Ile Thr
65 70 75 80

Arg Glu Glu Lys Ile Glu Asn Tyr Cys Ala Glu Leu Trp Ala Asn Trp
85 90 95

Ala Asn Asn Tyr Gln Trp Arg Thr Gly Lys Asn Ala Pro Met Glu Tyr
100 105 110

Val Val Asn Ser Tyr Asn Ser Cys Val Lys Asn Leu Thr Lys
115 120 125

<210> 363
<211> 83
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 363
Met Glu Thr Leu Val Ala Gly Ser Ile Phe Met Val Leu Val Ser Gly
1 5 10 15

Val Leu Ala Ile Ile Ile Tyr Met Leu Pro Trp Phe Ile Ala Leu Met
20 25 30

Arg Gly Ser Lys Ser Thr Val Gly Ile Phe Phe Thr Ser Leu Leu Phe
35 40 45

Asn Trp Ser Ile Ile Gly Trp Phe Ile Thr Phe Ile Trp Ser Ile Ala
50 55 60

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

Glu Lys Glu

<210> 364
<211> 246
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 364
Met Ile Ser Asp Ser Met Thr Val Glu Glu Ile Arg Leu His Leu Gly
1 5 10 15

Leu Ala Leu Lys Glu Lys Asp Phe Val Val Asp Lys Thr Gly Val Lys
20 25 30

```
Thr Ile Glu Ile Ile Gly Ala Ser Phe Val Ala Asp Glu Pro Phe Ile
        35                  40                  45

Phe Gly Ala Leu Asn Asp Glu Tyr Ile Gln Arg Glu Leu Glu Trp Tyr
    50                  55                  60

Lys Ser Lys Ser Leu Phe Val Lys Asp Ile Pro Gly Glu Thr Pro Lys
65                  70                  75                  80

Ile Trp Gln Gln Val Ala Ser Ser Lys Gly Glu Ile Asn Ser Asn Tyr
                85                  90                  95

Gly Trp Ala Ile Trp Ser Glu Asp Asn Tyr Ala Gln Tyr Asp Met Cys
            100                 105                 110

Leu Ala Glu Leu Gly Gln Asn Pro Asp Ser Arg Arg Gly Ile Met Ile
        115                 120                 125

Tyr Thr Arg Pro Ser Met Gln Phe Asp Tyr Asn Lys Asp Gly Met Ser
    130                 135                 140

Asp Phe Met Cys Thr Asn Thr Val Gln Tyr Leu Ile Arg Asp Lys Lys
145                 150                 155                 160

Val Asn Ala Val Val Ser Met Arg Ser Asn Asp Cys Trp Ala Gly Tyr
                165                 170                 175

Arg Asn Asp Tyr Ala Trp Gln Lys Tyr Val Leu Asp Lys Leu Val Ser
            180                 185                 190

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

Ile Trp Asn Val Gly Ser Leu His Val Tyr Glu Asn Gln Phe Tyr Leu
    210                 215                 220

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

Tyr Thr Gly Lys Trp Lys
                245


<210> 365
<211> 213
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 365
Met Glu Val Asn Val Pro His Val Tyr Lys Tyr Lys His Pro Lys Thr
1               5                   10                  15
```

```
Lys Lys Trp Tyr Ile Gly Ser His Asp Gly His Asn Pro Asn Tyr Asp
            20                  25                  30

Gly Ser Gly Val Val Trp Gln His Val Lys Lys Lys Tyr Gly Ile Lys
        35                  40                  45

Ser Phe Asn Lys Glu Ile Leu Tyr Glu Gly Pro Met Phe Arg Gln Val
    50                  55                  60

Glu Glu Ile Ile Leu Thr Cys Leu Asp Ala Ala Asn Cys Pro Asp Ser
65                  70                  75                  80

Tyr Asn Leu Lys Asn Glu Ala Trp Gly Gly Ser Phe Pro Gly Lys Leu
                85                  90                  95

Asn Gly Met Tyr Gly Lys Lys Leu Ser Pro Glu Glu Arg Tyr Lys Cys
            100                 105                 110

Gly Asn Ala Phe Arg Gly Ile Lys Arg Pro Asp His Ser Lys Arg Met
        115                 120                 125

Lys Gly Glu Gly Asn Pro Met Tyr Gly Lys Asn Glu Gln Ala Tyr Gly
    130                 135                 140

Ile Ile Asn Arg Ala Lys Glu Asn Ser Gly Lys Thr Tyr Glu Glu Ile
145                 150                 155                 160

Phe Gly Val Glu Lys Ala Lys Ile Ile Lys Glu Thr Met Ser Lys Asn
                165                 170                 175

Arg Lys Gly Lys Pro His Asn Leu Ile Glu Lys Ile Cys Pro His Cys
            180                 185                 190

Gly Leu Lys Gly Arg Gly Pro Asn Met Thr Arg Tyr His Phe Asp Lys
        195                 200                 205

Cys Lys Ala Leu Lys
    210


<210> 366
<211> 280
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 366
Met Ile Gln Phe Val Ile Pro Ser Tyr Gln Arg Val Gly Ala Val Ser
1               5                   10                  15

Ala Leu Asp Met Phe Pro Thr Asp Tyr Glu Pro His Ile Val Val Arg
```

```
            20                  25                  30

Glu His Glu Glu Lys Ala Tyr Tyr Asp Ala Tyr Gly Ser Lys Ala Lys
        35                  40                  45

Ile Val Thr Ile Pro Asp Asp Val Asn Gly Ile Ala Gly Thr Arg Lys
    50                  55                  60

Ala Ile Thr Asp Met Tyr Ala Gly Gln Arg Ile Trp Met Ile Asp Asp
65                  70                  75                  80

Asp Thr Thr Ile Arg Met Ser Ser Met Arg Lys Arg Asp Asp Arg Arg
                85                  90                  95

Cys Val Asp Lys Val Asn Gln Leu Thr Arg Glu Gln Phe Tyr Glu Leu
            100                 105                 110

Ile Gln Tyr Val Glu Asp Ala Met Asp Cys Gly Tyr Tyr His Gly His
        115                 120                 125

Ala Arg Leu Pro Ile Phe Lys Ile Thr Ser Ser Trp Gly Asn Tyr Arg
    130                 135                 140

Glu Asn Ser Tyr Gly Phe Thr Asn Thr Trp Tyr Asp Leu Gly Lys Leu
145                 150                 155                 160

Thr Thr Glu Gln Ile Gly Tyr Gly Lys Ile Asp Leu Cys Glu Asp Met
                165                 170                 175

Tyr Ala Phe Leu Asn Leu Ile Asn Gln Gly Tyr Pro His Leu Ala Leu
            180                 185                 190

Phe Lys Tyr Leu Val Val Ser Gly Lys Ala Gln Ala Pro Gly Gly Cys
        195                 200                 205

Ser Ser Ile Arg Ser Asn Ser Lys His Asn Arg Ala Leu Glu Gln Ile
    210                 215                 220

Asn Arg Glu Phe Pro Glu Gln Ala Arg Trp Lys Thr Ser Asn Ile Glu
225                 230                 235                 240

Lys Arg Lys Ser Leu Gly Glu Glu Asp Glu Pro Leu Lys Val Leu Arg
                245                 250                 255

Met Cys Val Ser Arg Lys Glu Lys Ser Glu Ala Phe His Lys Phe Asn
            260                 265                 270

Ala Ile His Pro Ile Ala Val Asp
        275                 280

<210> 367
```

<211> 393
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 367
Met Ser Ile Ala Asp Leu Lys Ser Arg Leu Ile Lys Ala Ser Thr Ser
1   5   10   15

Lys Met Thr Ala Glu Leu Thr Thr Ser Lys Phe Phe Asn Glu Lys Asp
            20   25   30

Val Ile Arg Thr Lys Ile Pro Met Leu Asn Ile Ala Ile Ser Gly Ala
        35   40   45

Ile Asp Gly Gly Met Gln Ser Gly Leu Thr Ile Phe Ala Gly Pro Ser
    50   55   60

Lys His Phe Lys Ser Asn Met Ser Leu Thr Met Val Ala Ala Tyr Leu
65   70   75   80

Asn Lys Tyr Pro Asp Ala Val Cys Leu Phe Tyr Asp Ser Glu Phe Gly
                85   90   95

Ile Thr Pro Ala Tyr Leu Arg Ser Met Gly Val Asp Pro Glu Arg Val
            100   105   110

Ile His Thr Pro Ile Gln Ser Val Glu Gln Leu Lys Ile Asp Met Val
        115   120   125

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

Asp Ser Ile Gly Asn Met Ala Ser Lys Lys Glu Thr Glu Asp Ala Leu
145   150   155   160

Asn Glu Lys Ser Val Ala Asp Met Thr Arg Ala Lys Ser Leu Lys Ser
                165   170   175

Leu Phe Arg Ile Val Thr Pro Tyr Phe Ser Ile Lys Asn Ile Pro Cys
            180   185   190

Val Ala Val Asn His Thr Ile Glu Thr Ile Glu Met Phe Ser Lys Thr
        195   200   205

Val Met Thr Gly Gly Thr Gly Val Met Tyr Ser Ala Asp Thr Val Phe
    210   215   220

Ile Ile Gly Lys Arg Gln Ile Lys Asp Gly Ser Asp Leu Gln Gly Tyr
225   230   235   240

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

Lys Phe Phe Ile Asp Val Lys Phe Asp Gly Gly Ile Asp Pro Tyr Ser
260 265 270

Gly Leu Leu Asp Met Ala Leu Glu Leu Gly Phe Val Val Lys Pro Lys
275 280 285

Asn Gly Trp Tyr Ala Arg Glu Phe Leu Asp Glu Glu Thr Gly Glu Met
290 295 300

Ile Arg Glu Glu Lys Ser Trp Arg Ala Lys Asp Thr Asn Cys Thr Thr
305 310 315 320

Phe Trp Gly Pro Leu Phe Lys His Gln Pro Phe Arg Asp Ala Ile Lys
325 330 335

Arg Ala Tyr Gln Leu Gly Ala Ile Asp Ser Asn Glu Ile Val Glu Ala
340 345 350

Glu Val Asp Glu Leu Ile Asn Ser Lys Val Glu Lys Phe Lys Ser Pro
355 360 365

Glu Ser Lys Ser Lys Ser Ala Ala Asp Leu Glu Thr Asp Leu Glu Gln
370 375 380

Leu Ser Asp Met Glu Glu Phe Asn Glu
385 390

<210> 368
<211> 112
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 368
Met Ser Lys Asp Asp Leu Asp Leu Glu Ile Ile Asp Glu Ser Pro Ser
1 5 10 15

Ser Glu Gly Glu Glu Glu Arg Lys Glu Arg Leu Phe Asn Glu Ser Leu
20 25 30

Lys Ile Ile Lys Ser Ala Met Glu Asn Val Ile Gln Glu Ile Val Ile
35 40 45

Lys Leu Glu Asp Gly Ser Thr His Ile Val Tyr Val Thr Lys Leu Asp
50 55 60

Trp Val Asp Gly Lys Val Val Met Asp Phe Ala Val Leu Asp Gln Glu
65 70 75 80

Arg Lys Ala Glu Leu Ala Pro His Val Glu Lys Cys Ile Thr Met Gln
85 90 95

Leu Gln Asp Ala Phe Asn Lys Arg Ser Lys Lys Lys Phe Lys Phe Phe
100 105 110

<210> 369
<211> 475
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 369
Val Val Glu Ile Ile Leu Ser His Leu Ile Phe Asp Gln Ala Tyr Phe
1 5 10 15

Ser Lys Val Trp Pro Tyr Met Asp Ser Glu Tyr Phe Glu Ser Gly Pro
20 25 30

Ala Lys Asn Thr Phe Lys Leu Ile Lys Ser His Val Asn Glu Tyr His
35 40 45

Ser Val Pro Ser Ile Asn Ala Leu Asn Val Ala Leu Glu Asn Ser Ser
50 55 60

Phe Thr Glu Thr Glu Tyr Ser Gly Val Lys Thr Leu Ile Ser Lys Leu
65 70 75 80

Ala Asp Ser Pro Glu Asp His Ser Trp Leu Val Lys Glu Thr Glu Lys
85 90 95

Tyr Val Gln Gln Arg Ala Met Phe Asn Ala Thr Ser Lys Ile Ile Glu
100 105 110

Ile Gln Thr Asn Ala Glu Leu Pro Pro Glu Lys Arg Asn Lys Lys Met
115 120 125

Pro Asp Val Gly Ala Ile Pro Asp Ile Met Arg Gln Ala Leu Ser Ile
130 135 140

Ser Phe Asp Ser Tyr Val Gly His Asp Trp Met Asp Asp Tyr Glu Ala
145 150 155 160

Arg Trp Leu Ser Tyr Met Asn Lys Ala Arg Lys Val Pro Phe Lys Leu
165 170 175

Lys Ile Leu Asn Lys Ile Thr Lys Gly Gly Ala Glu Thr Gly Thr Leu
180 185 190

Asn Val Leu Met Ala Gly Val Asn Val Gly Lys Ser Leu Gly Leu Cys
195 200 205

```
Ser Leu Ala Ala Asp Tyr Leu Gln Leu Gly His Asn Val Leu Tyr Ile
    210                 215                 220

Ser Met Glu Met Ala Glu Glu Val Cys Ala Lys Arg Ile Asp Ala Asn
225                 230                 235                 240

Met Leu Asp Val Ser Leu Asp Asp Ile Asp Asp Gly His Ile Ser Tyr
                245                 250                 255

Ala Glu Tyr Lys Gly Lys Met Glu Lys Trp Arg Glu Lys Ser Thr Leu
            260                 265                 270

Gly Arg Leu Ile Val Lys Gln Tyr Pro Thr Gly Gly Ala Asp Ala Asn
        275                 280                 285

Thr Phe Arg Ser Leu Leu Asn Glu Leu Lys Leu Lys Lys Asn Phe Val
    290                 295                 300

Pro Thr Ile Ile Ile Val Asp Tyr Leu Gly Ile Cys Lys Ser Cys Arg
305                 310                 315                 320

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

Glu Glu Leu Arg Ala Leu Ala Val Glu Thr Glu Thr Val Leu Trp Thr
            340                 345                 350

Ala Ala Gln Val Gly Lys Gln Ala Trp Asp Ser Ser Asp Val Asn Met
        355                 360                 365

Ser Asp Ile Ala Glu Ser Ala Gly Leu Pro Ala Thr Ala Asp Phe Met
    370                 375                 380

Leu Ala Val Ile Glu Thr Glu Glu Leu Ala Ala Ala Glu Gln Gln Leu
385                 390                 395                 400

Ile Lys Gln Ile Lys Ser Arg Tyr Gly Asp Lys Asn Lys Trp Asn Lys
                405                 410                 415

Phe Leu Met Gly Val Gln Lys Gly Asn Gln Lys Trp Val Glu Ile Glu
            420                 425                 430

Gln Asp Ser Thr Pro Thr Glu Val Asn Glu Val Ala Gly Ser Gln Gln
        435                 440                 445

Ile Gln Ala Glu Gln Asn Arg Tyr Gln Arg Asn Glu Ser Thr Arg Ala
    450                 455                 460

Gln Leu Asp Ala Leu Ala Asn Glu Leu Lys Phe
465                 470                 475
```

<210> 370
<211> 60
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 370
Met Glu Leu Val Lys Val Val Phe Met Gly Trp Phe Lys Asn Glu Ser
1   5   10   15

Met Phe Thr Lys Glu Ile Thr Met Met Lys Asp Asp Val Gln Trp Ala
            20   25   30

Thr Thr Gln Tyr Ala Glu Val Asn Lys Ala Leu Val Lys Ala Phe Ile
        35   40   45

Asp Asp Lys Lys Val Cys Glu Val Asp Cys Arg Gly
    50   55   60

<210> 371
<211> 80
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 371
Met His Ile Val Leu Phe Lys Pro Thr Pro Tyr Asn Val Arg Lys Asn
1   5   10   15

Thr Gln Phe Lys Ala Leu Ile Ala Asp Thr Trp Glu Leu Val Leu Asp
            20   25   30

Ile Pro Ala Glu Glu Ser Pro Pro Phe Gly Arg Val Glu Phe Ile Lys
        35   40   45

Phe Ala Val Arg Pro Thr Lys Arg Gln Ile Arg Gln Cys Lys Arg Tyr
    50   55   60

Phe Arg Lys Ile Val Lys Leu Glu Lys Gln Leu Leu Met Leu Val Lys
65   70   75   80

<210> 372
<211> 84
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 372
Met Met Leu Val Asn Arg Glu Tyr Gln Phe Lys Ser Glu Glu Asp Leu
1   5   10   15

Glu Lys Phe Ala Ser Gly Cys Glu Leu Asn Arg Arg Thr Ala Lys Val
20 25 30

Ile Gly Leu Lys Pro Phe Thr Val Leu Asp Cys Glu Val Ser Lys Phe
35 40 45

Arg Arg Gly Cys Ser Ile Ser Gly His Ala Leu Val Asp Gly Asn Thr
50 55 60

Phe Phe Phe Val Phe Ser Val Arg Glu Leu Leu Leu Ile Asn Glu Leu
65 70 75 80

Glu Glu Ile Lys

<210> 373
<211> 60
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 373
Met Ser Lys Val Ser Gly Tyr Gln Leu Leu Thr Gln Glu Gln Arg Ser
1 5 10 15

Glu Met Asp Ser Leu Gln Glu Arg Cys Gln His Arg Asn Asn Ala Leu
20 25 30

Asp Ser Phe Leu Leu Val Glu Tyr Glu Asn Leu Cys Ser Arg Leu Glu
35 40 45

Lys Glu Tyr Val His Gln His Glu Gly Gly Glu Glu
50 55 60

<210> 374
<211> 97
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 374
Met Lys Lys Phe Ile Phe Ala Ala Ile Phe Ala Leu Ser Ser Cys Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Gly Tyr Asp Lys Asp Leu Cys Glu Trp Ser
20 25 30

Met Thr Ala Asp Gln Thr Glu Val Glu Thr Gln Ile Glu Ala Asp Ile
35 40 45

Met Asn Ile Val Glu Arg Asp Arg Pro Glu Met Lys Ala Glu Val Gln

50 55 60

Lys Gln Leu Lys Ser Gly Gly Val Met Gln Tyr Asn Tyr Val Leu Tyr
65 70 75 80

Cys Asp Lys Asn Phe Asn Asn Lys Asn Ile Ile Ala Glu Val Val Gly
85 90 95

Glu

<210> 375
<211> 33
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 375
Met Leu Ser Asp Glu Ile Asn Asp Leu Leu Asn Asp Ala Glu Lys Val
1 5 10 15

Ala Ile Pro Ser Ile Asp Asp Gln Ile Phe Asn Ala Phe Met Asn Arg
20 25 30

Gly

<210> 376
<211> 54
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 376
Met Lys Thr Phe Lys Glu Phe Ile Lys Glu Asp Met Val Ala Gly Asp
1 5 10 15

Ser Gly Gly Asn Pro Glu Asn Ile Ser Thr Gly Thr Thr Ser Gly Ala
20 25 30

Val Val Asn Lys Gly Pro Glu Gln Ile Pro Lys Lys Lys Lys Glu Glu
35 40 45

Ser Lys Glu Lys Glu Glu
50

<210> 377
<211> 342
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 377
Met Ser Ser Ile Pro Trp Ile Asp Asn Glu Phe Ala Tyr Arg Ala Leu
1   5   10   15

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

Leu Arg Phe Arg Cys Pro Val Cys Gly Asp Ser Lys Thr Asp Gln Asn
        35   40   45

Lys Ala Arg Gly Trp Tyr Tyr Gly Asp Asn Asn Glu Gly Asn Ile His
    50   55   60

Cys Tyr Asn Cys Asn Tyr His Ala Pro Ile Gly Ile Tyr Leu Lys Glu
65   70   75   80

Phe Glu Pro Asp Leu Tyr Arg Glu Tyr Ile Phe Glu Ile Arg Lys Glu
                85   90   95

Lys Gly Lys Ser Arg Pro Val Glu Lys Pro Lys Glu Leu Pro Lys Gln
            100   105   110

Pro Glu Lys Lys Ile Ile Lys Ser Leu Pro Ser Cys Ile Arg Leu Asp
        115   120   125

Lys Leu Ala Glu Asp His Pro Ile Ile Lys Tyr Val Lys Ala Arg Cys
    130   135   140

Ile Pro Lys Asp Lys Trp Lys Tyr Leu Trp Phe Thr Thr Glu Trp Pro
145   150   155   160

Lys Leu Val Asn Ser Ile Ala Pro Gly Thr Tyr Lys Lys Glu Ile Pro
                165   170   175

Glu Pro Arg Leu Val Ile Pro Ile Tyr Asn Ala Asn Gly Lys Ala Glu
            180   185   190

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

Thr Ile Lys Ala Tyr Pro Glu Ala Thr Lys Ile Tyr Gly Val Glu Arg
    210   215   220

Val Lys Asp Gly Asp Val Tyr Val Leu Glu Gly Pro Ile Asp Ser Leu
225   230   235   240

Phe Ile Glu Asn Gly Ile Ala Ile Thr Gly Gly Gln Leu Asp Leu Glu
                245   250   255

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

```
Arg His Pro Asp Thr Ile Lys Arg Met Thr Lys Leu Val Asp Ala Gly
        275                 280                 285


Glu Arg Val Met Phe Trp Asp Lys Ser Pro Trp Lys Ser Lys Asp Val
    290                 295                 300


Asn Asp Met Ile Arg Lys Glu Gly Ala Thr Pro Glu Gln Ile Met Glu
305                 310                 315                 320


Tyr Met Lys Asn Asn Ile Ala Gln Gly Leu Met Ala Lys Met Arg Leu
                325                 330                 335


Ser Lys Tyr Ala Lys Ile
            340


<210> 378
<211> 66
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 378
Met Val Gln Lys Leu Met Ala Leu Val Asn Ala Ile Lys Gly Asn Lys
1               5                   10                  15


Lys Arg Ile Ala Phe Thr Ile Ser Ala Met Ile Gly Ile Leu Leu Trp
            20                  25                  30


Asn Phe Val Leu Ser Pro Val Ala Ile Ala His Gly Val Ser Ile Pro
        35                  40                  45


Val Ile Thr Leu Asp Thr Phe Val Asp Leu Ala Phe Ala Leu Val Gly
    50                  55                  60


Leu Ile
65


<210> 379
<211> 172
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 379
Met Ala Tyr Phe Asn Glu Cys Ala His Leu Ile Glu Gly Val Asp Lys
1               5                   10                  15


Ala Asn Arg Ala Tyr Ala Glu Asn Ile Met His Asn Ile Asp Pro Leu
            20                  25                  30
```

Gln Val Met Leu Asp Met Gln Arg His Leu Gln Ile Arg Leu Ala Asn
35 40 45

Asp Lys Pro Glu Thr Asn Arg His Pro Asp Ser Leu Glu Thr Ala Gly
50 55 60

Glu Val Leu Ala Trp Leu Arg Asn Gln Asp Asp Tyr Ile Ala Asp Glu
65 70 75 80

Thr Arg Glu Leu Tyr Thr Ser Leu Gly Gly Met Ser Asn Gly Glu Lys
85 90 95

Glu Ala Ser Ala Val Trp Lys Pro Trp Lys Lys Arg Tyr Ser Glu Met
100 105 110

Gln Ser Lys Lys Ile Gln Asp Leu Ser Pro Glu Asp Gln Leu Glu Ile
115 120 125

Lys Phe Glu Leu Ile Asp Gln Phe His Phe Phe Met Asn Lys Phe Ile
130 135 140

Ala Leu Gly Met Ser Ala Glu Glu Ile Phe Lys Leu Tyr Tyr Leu Lys
145 150 155 160

Asn Ala Glu Asn Phe Ala Arg Gln Asp Arg Gly Tyr
165 170

<210> 380
<211> 66
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 380
Met Ala Arg Leu Asn Lys Arg Gln Leu Lys Lys Ala His Lys Lys Arg
1 5 10 15

Ile Asp Gln Leu Phe Lys Asn Tyr Asp Lys Glu Leu Val Cys Glu Leu
20 25 30

Leu Ser Asn Gln Leu Arg Ala Val Asp Trp Val Val Glu Glu Gly Pro
35 40 45

Asp Glu Ile Phe Val Ser Glu Glu Ala Leu Lys Leu Ile Ile Glu His
50 55 60

Ser Lys
65

<210> 381
<211> 57
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 381
Met Lys Ile Ser Lys Glu Glu Phe Ile Arg Arg Gln Lys Ala Leu Ile
1   5   10   15

Asn Leu His Glu Trp Tyr Ala Tyr Gln Leu Lys Val Asp Ser Ser Asn
            20   25   30

Ile Asn Ala Val Met Ala Leu Tyr Lys Gln Ile Gln Asp Glu His Glu
        35   40   45

Phe Leu Ala Gln Val Phe Ile Glu Asp
    50   55

<210> 382
<211> 78
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 382
Met Gly Gly Phe Val Asn Ile Lys Thr Phe Thr His Pro Ala Gly Glu
1   5   10   15

Gly Lys Glu Val Lys Gly Met Glu Val Ser Val Pro Phe Glu Ile Tyr
            20   25   30

Ser Asn Glu His Arg Ile Ala Asp Ser His Tyr Gln Ile Phe Pro Ser
        35   40   45

Glu Lys Ala Ala Tyr Ser Thr Val Val Ser Asp Ala Ala Asp Trp Lys
    50   55   60

Thr Lys Asn Ala Ala Met Phe Thr Pro Thr Gln Ile Gly Gly
65   70   75

<210> 383
<211> 68
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 383
Met Leu Asn Arg Trp Ile Lys Pro Asn Glu Asp Leu Asp Ile Ile Ile
1   5   10   15

Ser Arg His Val Met Lys Lys Tyr Glu Leu Gln Pro Trp Ser Thr Glu
            20   25   30

Val Val Val His Ser Phe Met Met Tyr Ala Asp Gly Ser Val Glu Phe
        35   40   45

Asn Ala Glu Ile Arg Tyr Asp Tyr Gly Glu Lys Gln Val Glu Phe Lys
    50   55   60

Arg Gly Phe Leu
65

<210> 384
<211> 113
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 384
Met Phe Ile Phe Asn Trp Phe Lys Ser Phe Phe Thr Asp Phe Phe Ser
1   5   10   15

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

Leu Thr Val Val Glu Tyr Val Tyr Met Gly Asp Gly Thr Val Glu Ala
        35   40   45

Val Thr Met Thr Tyr Glu Glu Ala Gln Glu Tyr Tyr Lys Asn Pro Trp
    50   55   60

Arg Trp Ser Thr Pro Ile Thr Ser Ser Asn Thr Gln Asn Thr Gln Ser
65   70   75   80

Ser Ser Asp Ser Tyr Asp Thr Asn Val Pro Val His Val Trp Thr Gly
                85   90   95

Asp Ser Cys Gly Ser Ser Cys Asp Ser Ser Cys Ser Ser Thr Ser Cys
            100   105   110

Asp

<210> 385
<211> 161
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 385
Met Glu Ala Ile Leu Phe Glu Met Tyr Ile Ser Ser Asn Ser Met Ser
1   5   10   15

Phe Ala Lys Asp Val Pro Ile Thr Val Ala Val Met Ile Asp Lys Gly
            20   25   30

Tyr Cys Asp Pro Met Tyr Leu Val Glu Asn Phe Val Ser Met Pro Val
35 40 45

Pro Glu Asp Ala Glu Ile Lys Leu Lys Lys Ile Gly Ile Ile Glu Thr
50 55 60

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

Tyr Ile Asn Val Ser Ala Glu Gln Tyr Asn Asp Lys Pro Ile Ser Phe
85 90 95

Tyr Ser Tyr Asp Ser Val Tyr Ser Trp Lys Ile Asp Lys Gly Asn Lys
100 105 110

Phe Ile Ile Val Ser Glu Asp Ala Leu Ser Tyr Phe Ile Ser Ser Ile
115 120 125

Trp Asn Ser Leu His Pro Asn Leu Leu Lys Ile His Glu Phe Asp Asp
130 135 140

Ala Pro Thr Val Val Leu Gly Lys Thr Asn Glu Ser Ser Glu Glu Asn
145 150 155 160

Val

<210> 386
<211> 67
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 386
Met Lys Val Leu Lys Lys Met Phe Glu Trp Phe Ser Arg Pro Asn Ser
1 5 10 15

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

Asn Glu Ser Glu Glu Trp Met Lys Ser Met Ile Ser Val Glu Lys Glu
35 40 45

Lys Lys Leu Glu Arg Ser Ala Leu Lys Leu Met Arg Asp Ile Tyr Gly
50 55 60

Asp Lys Ser
65

<210> 387

<211> 54
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 387
Val Asn Arg Asp Met Thr Leu Glu Glu Ala Lys Ala Lys Ala Asn Glu
1   5   10   15

Ala Leu Asp Leu Leu Leu Lys Ile Gly Ser Lys Met Met Glu Glu Asn
            20   25   30

Glu Lys Tyr Ile Gln Glu Asn Lys Ile Pro Asp Gly Pro Leu Val Gly
        35   40   45

Lys Arg Lys Ser His Asp
    50

<210> 388
<211> 160
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 388
Met Ile Glu Val Ala Lys His Tyr Ser Ile Glu Phe Met Ser Lys Glu
1   5   10   15

Gly Lys Ser Val Asn Thr Leu Asp Lys Lys Cys Ser Leu Ile Ile Pro
            20   25   30

Leu Ala Glu Asn Pro Asp Ile Leu Ile Lys Asp Ile Lys Glu Arg Lys
        35   40   45

Tyr Pro Glu Asn Val Ile Leu Ile Ile Lys His Thr Glu Asp Ile Leu
    50   55   60

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

Gly Tyr Lys Arg Ala His Glu Tyr Gly Leu Phe Asp Leu Phe Glu Asp
                85   90   95

Asp Lys Val Lys Leu Ala Leu Asn Leu Ala Gly Gln Ser Ser Lys Ser
            100   105   110

Lys Thr Phe Ile Ile Glu Asp Ile Lys Asp Ile Asn Ala Phe Val Lys
        115   120   125

Met Val Trp Ala His Phe Asp Val Gly Leu Arg Trp Arg Met Ser Glu
    130   135   140

Glu Glu Arg Lys Ile Ile Glu Ala Asn Arg Tyr Phe Gly Phe Tyr Arg
145 150 155 160

<210> 389
<211> 60
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 389
Met Asp Leu Phe Glu Met Leu Glu Asp Asn His Ser Thr Asn Ile Gln
1 5 10 15

Asn Asp Ser Ser Asp Tyr Lys Lys Glu Tyr Arg Ile Val Leu Gln Asn
20 25 30

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

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

<210> 390
<211> 207
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 390
Met Ile Ile Asn Leu Ala Asp Val Glu Gln Leu Ser Ile Lys Ala Glu
1 5 10 15

Ser Val Asp Phe Gln Tyr Asp Met Tyr Lys Lys Val Cys Glu Lys Phe
20 25 30

Thr Asp Phe Glu Gln Ser Val Leu Trp Gln Cys Met Glu Ala Lys Lys
35 40 45

Asn Lys Ala Leu His Arg Gln Leu Asn Lys Ile Ile Lys Lys His Leu
50 55 60

Thr Lys Ser Pro Tyr Gln Leu Tyr Arg Gly Ile Ser Lys Ser Thr Lys
65 70 75 80

Glu Leu Ile Lys Asp Leu Gln Val Gly Glu Val Phe Ser Thr Asn Arg
85 90 95

Val Asp Ser Phe Thr Thr Ser Leu His Thr Ala Cys Gly Phe Ser Tyr
100 105 110

Val Glu Tyr Phe Thr Glu Ile Ile Phe Arg Leu Lys Thr Asp Lys Ala

115 120 125

Phe Asn Tyr Ser Asp His Ile Ser Asp Ile Ile Leu Ser Ser Pro Asn
130 135 140

Thr Glu Phe Lys Tyr Thr Tyr Glu Asp Thr Asp Gly Leu Asp Ser Glu
145 150 155 160

Arg Thr Asp Asn Leu Met Met Ile Val Arg Glu Gln Glu Trp Met Ile
165 170 175

Pro Ile Gly Lys Tyr Lys Ile Thr Ser Ile Ser Lys Glu Lys Leu His
180 185 190

Asp Ser Phe Gly Thr Phe Lys Val Tyr Asp Ile Glu Val Val Glu
195 200 205

<210> 391
<211> 200
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 391
Met Lys Tyr Ser Ala Met Gln Leu Lys Asp Phe Lys Ile Lys Ser Met
1 5 10 15

Asp Ala Ser Val Arg Ala Ser Ile Arg Glu Glu Leu Leu Ser Glu Gly
20 25 30

Phe Asn Leu Ser Glu Ile Glu Leu Leu Ile His Cys Ile Thr Asn Lys
35 40 45

Pro Asp Asp His Ser Trp Leu Asn Glu Ile Ile Lys Ser Arg Leu Val
50 55 60

Pro Asn Asp Lys Pro Leu Trp Arg Gly Val Pro Val Glu Thr Lys Gln
65 70 75 80

Val Leu Asn Gln Gly Ile Asp Ile Ile Thr Phe Asp Lys Val Val Ser
85 90 95

Ala Ser Tyr Asp Lys Asn Val Glu Leu His Phe Ala Ser Gly Leu Glu
100 105 110

Tyr Asn Thr Gln Val Ile Phe Glu Phe Lys Ala Pro Met Val Phe Asn
115 120 125

Phe Gln Glu Tyr Ala Ile Lys Ala Leu Arg Cys Lys Glu Tyr Ser Pro
130 135 140

Ser Phe Lys Phe Pro Asp Ser His Arg Tyr Arg Asn Met Glu Leu Val
145 150 155 160

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

Ala Asp Arg Tyr Glu Tyr Lys Lys His Ser Thr Tyr Thr Ile Tyr Thr
180 185 190

Leu Asp Phe Glu Gly Phe Asn Leu
195 200

<210> 392
<211> 248
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 392
Met Lys Leu Ser Lys Asn Gln Ile Arg Lys Ile Thr Arg Arg Leu Glu
1 5 10 15

His Thr Gln Ala Ser Ala Lys Arg Arg Ser Lys Asp Phe Asn Leu Asp
20 25 30

Phe Asn Tyr Ile Lys Asn Ile Leu Asp Gln Lys Val Cys Ala Tyr Ser
35 40 45

Gly Glu Pro Phe Asp Asn Arg Ile Glu Gly Glu Lys Leu Ser Leu Glu
50 55 60

Arg Phe Asp Asn Asn Val Gly Tyr Ile Lys Gly Asn Val Ile Ala Val
65 70 75 80

Lys Lys Lys Tyr Asn Thr Phe Arg Ser Asp Tyr Thr Leu Glu Glu Leu
85 90 95

Ile Glu Lys Arg Asp Leu Phe Ala Leu Arg Ile Gly Arg Ser Ser Ala
100 105 110

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

Lys Lys Thr Tyr Asn Gln Ile Lys Ala Ile Gln Lys Lys Arg Glu Asn
130 135 140

Arg Ile Glu His Ile Ser Gln Leu Ser Lys Ser Lys Gln Thr Ser Asp
145 150 155 160

Val Lys Leu Thr Ile Ile Ala Leu Lys Ala Arg Ile Asp Gly Ser Arg
165 170 175

Ile Ala Glu Gly Ala Glu Val Val Lys Leu Asn Val Leu Leu Lys Gly
180 185 190

Ser Asp Trp Lys Thr Val Lys Lys Leu Ser Glu Ala Glu Met Gln Tyr
195 200 205

Asp Met Cys Asp Lys Ile Ile Gln Gly Val Glu Arg Tyr Gln Asn Leu
210 215 220

Ser Phe Ile Asp Lys Leu Lys Leu Lys Arg Gly Tyr Pro Leu Asn Cys
225 230 235 240

Ser Ile Phe Lys Leu Ile Arg Gly
245

<210> 393
<211> 103
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 393
Met Phe Tyr Val Tyr Ala Ile Val Tyr Arg Asp Lys Asp Gly Phe Ala
1 5 10 15

Val Pro Val Pro Leu Asp Glu His Arg Pro Ala Val Phe Phe Glu Arg
20 25 30

Glu Ile Ala Asp Lys Val Phe Thr Thr Leu Lys Glu Gln Tyr Gln Leu
35 40 45

Ala Leu Gly Met Gly Ile Pro Arg Leu Val Glu Thr Pro Arg Lys Phe
50 55 60

Trp Phe Asn Lys Ile Glu Val Lys His Val Lys Pro Asp Val Asp Thr
65 70 75 80

Gln Arg Leu Tyr Arg Arg Ile Leu Asp Thr Gly Arg Ile Val Ser Ile
85 90 95

Pro Ile Ala Gly Asn Leu Arg
100

<210> 394
<211> 439
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 394
Met Thr Phe Asp Asp Leu Thr Glu Gly Gln Lys Asn Ala Phe Asn Ile

1 5 10 15

Val Met Arg Ala Ile Lys Glu Lys Lys His His Val Thr Ile Asn Gly
20 25 30

Pro Ala Gly Thr Gly Lys Thr Thr Leu Thr Lys Phe Ile Ile Glu Ala
35 40 45

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

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

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

Leu Phe Glu Gln Lys Glu Val Pro Asp Leu Ala Lys Cys Arg Val Leu
100 105 110

Ile Cys Asp Glu Val Ser Met Tyr Asp Arg Lys Leu Phe Lys Ile Leu
115 120 125

Leu Ser Thr Ile Pro Pro Trp Cys Thr Ile Ile Gly Ile Gly Asp Asn
130 135 140

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

Pro Phe Phe Thr His Lys Asp Phe Tyr Gln Cys Glu Leu Thr Glu Val
165 170 175

Lys Arg Ser Asn Ala Pro Ile Ile Asp Val Ala Thr Asp Val Arg Asn
180 185 190

Gly Lys Trp Ile Tyr Asp Lys Val Val Asp Gly His Gly Val Arg Gly
195 200 205

Phe Thr Gly Asp Thr Ala Leu Arg Asp Phe Met Val Asn Tyr Phe Ser
210 215 220

Ile Val Lys Ser Leu Asp Asp Leu Phe Glu Asn Arg Val Met Ala Phe
225 230 235 240

Thr Asn Lys Ser Val Asp Lys Leu Asn Ser Ile Ile Arg Lys Lys Ile
245 250 255

Phe Glu Thr Asp Lys Asp Phe Ile Val Gly Glu Ile Ile Val Met Gln
260 265 270

Glu Pro Leu Ile Lys Thr Tyr Lys Ile Asp Gly Lys Pro Val Ser Glu

275 280 285

Ile Ile Phe Asn Asn Gly Gln Leu Val Arg Ile Ile Glu Ala Glu Tyr
290 295 300

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

Arg His Trp Asp Leu Thr Val Glu Thr Tyr Gly Asp Asp Glu Tyr Tyr
325 330 335

Arg Glu Lys Ile Lys Ile Ile Ser Ser Asp Glu Glu Leu Tyr Lys Phe
340 345 350

Asn Leu Phe Leu Gly Lys Thr Ala Glu Thr Tyr Lys Asn Trp Asn Lys
355 360 365

Gly Gly Lys Ala Pro Trp Ser Asp Phe Trp Asp Ala Lys Ser Gln Phe
370 375 380

Ser Lys Val Lys Ala Leu Pro Ala Ser Thr Phe His Lys Ala Gln Gly
385 390 395 400

Met Ser Val Asp Arg Ala Phe Ile Tyr Thr Pro Cys Ile His Tyr Ala
405 410 415

Asp Ala Glu Leu Ala Gln Gln Leu Leu Tyr Val Gly Val Thr Arg Gly
420 425 430

Arg Tyr Asp Val Phe Tyr Val
435

<210> 395
<211> 86
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 395
Met Ile Asn Ile Asn Ser Lys Tyr Leu Asn Arg Leu Ile Asp Gly Ile
1 5 10 15

Arg Lys His Thr Asn Lys Gln Asp Asn Leu Asp Val Met Val Thr Gly
20 25 30

Ala Glu Leu Leu His Lys Leu Tyr Leu Ile Ser Asp Thr Ile Leu Ala
35 40 45

Ile Lys Arg Ile Glu Lys Gln Ser Tyr His Ser Asn Thr Asp Thr Val
50 55 60

Ile Thr Leu Asp Glu Ser Val Cys Lys Leu Leu Ile Lys Phe Glu Glu
65 70 75 80

Ala Ile Arg Gly Asn Asn
85

<210> 396
<211> 81
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 396
Val Glu Ile Thr Lys Asp Gln Phe Tyr Leu Leu Gln Asp Lys Val Ser
1 5 10 15

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

Glu Ser Ser Lys Leu Met Leu Gln Leu Glu Glu Ile Glu Arg Asp Leu
35 40 45

Ile Ala Leu Glu Phe Phe Cys Gly Glu Val Lys Thr Val Thr Ile Ser
50 55 60

Asp Tyr Val Leu Gly Glu Ile Ser Tyr Leu Tyr Lys Ala Ile Ile Asn
65 70 75 80

Asp

<210> 397
<211> 80
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 397
Met Ile Glu Leu Ser Trp Cys Gln Phe Lys Ser Leu Met Thr Asn Val
1 5 10 15

Lys Ala Val Ile Glu Lys Asn Ser Gly Pro Glu Asn Ile Thr Ile Arg
20 25 30

Glu Lys Ala Leu Lys Ile Ile Tyr Ser Leu Glu Glu Met Gln Lys Asp
35 40 45

Ile Glu Ser Met Ala Lys Phe Ile Asp Glu Pro Ile Asn Lys Val Tyr
50 55 60

Ile Gln Asp Tyr Thr Val Gly Gln Ile Arg Asp Leu Ala Arg Lys Ile
65 70 75 80

<210> 398
<211> 227
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 398
Met Phe Asp Phe Ile Ile Asp Phe Glu Thr Met Gly Ser Gly Glu Lys
1   5   10   15

Ala Ala Val Ile Asp Leu Ala Val Ile Ala Phe Asp Pro Asn Pro Glu
            20   25   30

Val Val Glu Thr Phe Asp Glu Leu Val Ser Arg Gly Ile Lys Ile Lys
        35   40   45

Phe Asp Leu Lys Ser Gln Lys Gly His Arg Leu Phe Thr Lys Ser Thr
    50   55   60

Ile Glu Trp Trp Lys Asn Gln Ser Pro Glu Ala Arg Lys Asn Ile Ala
65   70   75   80

Pro Ser Asp Glu Asp Val Ser Thr Ile Asp Gly Ile Ala Lys Phe Asn
                85   90   95

Asp Tyr Ile Asn Ala His Asn Ile Asp Pro Trp Lys Ser Gln Gly Trp
            100   105   110

Cys Arg Gly Met Ser Phe Asp Phe Pro Ile Leu Val Asp Leu Ile Arg
        115   120   125

Asp Ile Gln Arg Leu Asn Gly Val Ser Glu Asn Glu Leu Asp Thr Phe
    130   135   140

Lys Leu Glu Pro Cys Lys Phe Trp Asn Gln Arg Asp Ile Arg Thr Arg
145   150   155   160

Ile Glu Ala Leu Leu Leu Val Arg Asp Met Thr Thr Cys Pro Leu Pro
                165   170   175

Lys Gly Thr Leu Asp Gly Phe Val Ala His Asp Ser Ile His Asp Cys
            180   185   190

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

Leu Glu Asp Ala Pro Ser Glu Glu Asp Cys Asp Pro Leu Ser Leu Pro
    210   215   220

Thr Lys Arg

225

<210> 399
<211> 166
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 399
Met Lys Ile Tyr Arg Val Glu Ser Ser Phe Ser Ile Leu Asp Tyr Glu
1 5 10 15

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

Arg Ser Ile Ile Asp Ser Trp Ser Glu Glu Trp Leu Leu His Val Gly
35 40 45

Tyr Asp Arg Pro Asn Phe Met His His Ser Asp Asn Asn Lys Arg Ile
50 55 60

Pro Leu Pro His Glu Asp Lys Leu Leu Val Lys Asn Ala Asn Ile Val
65 70 75 80

Ile Asn Thr Lys Phe Lys Lys Asp Tyr Val Gly Val Glu Tyr His Ile
85 90 95

Pro Gly Trp Phe Ile Ala Leu Tyr His Phe Ala Phe Ala Ser Glu Tyr
100 105 110

Asp Met Met Arg Trp Phe Thr Arg Glu Glu Arg Glu Glu Leu Ala Ser
115 120 125

Lys Gly Phe Tyr Leu Ala Val Tyr Glu Val Pro Asp Asp Gln Val Ile
130 135 140

Val Gly Gly His Gln Val Met Phe Arg Lys Ser His Ala Glu Leu Val
145 150 155 160

Asp Phe Ile Glu Met Arg
165

<210> 400
<211> 181
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 400
Met Lys Phe Asn Tyr Asn Pro Glu Tyr Thr Pro Asn Pro Ala Ala Lys
1 5 10 15

```
Leu Ile Asp Phe Asp Val Val Ser Thr Tyr Val Cys Pro Val Lys Pro
            20                  25                  30

Leu Glu Ile Lys Glu Pro Thr Met Thr Thr Ala Ile Glu Ile Gly Lys
        35                  40                  45

Thr Tyr Lys Leu Val Glu Pro Lys Ile Lys Thr Asn Ala Leu Ile Ser
    50                  55                  60

Gly His Lys Thr Leu Thr Asp Val Phe Gly Glu Gly Glu Phe Ile Val
65                  70                  75                  80

Glu Glu Phe Ala Lys Ser Glu Trp Phe Asp Lys Ser Tyr Val Ile His
                85                  90                  95

Gly Arg Arg Leu Asp Asn Asn Lys Ile Lys Lys Asn Leu Val Tyr Glu
            100                 105                 110

Asp Glu Phe Ile Leu Phe Gln Glu Val Glu Glu Gln Asp Pro Thr Asp
        115                 120                 125

Leu Leu Cys Ala Ala Val Ser Ile Arg Arg Pro Phe Asp Asn Pro Ile
    130                 135                 140

Cys Gly Trp Val Thr Asp Gln Trp Ile Glu Asp Gly Val Glu Leu Leu
145                 150                 155                 160

Asn Val Val His Ala Gly Asp Phe Ser Val Val Pro Arg Ser Ala Val
                165                 170                 175

Val Ala Ile Leu Asn
            180


<210> 401
<211> 162
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 401
Met Ile Ile Asn Ile Gly Glu Ile Ala Arg Val Ser Asp Lys Ser Arg
1               5                   10                  15

Ser Lys Ala Ala Gly Lys Leu Val Glu Val Val Ser Ile Gln Leu Lys
            20                  25                  30

His Gly Val Lys Asp Glu Asp Ser Glu Val Lys Val Arg Ile Ile Ala
        35                  40                  45

Lys Asp Gly Met Ser Lys Pro Gln Phe Gly Tyr Val Arg Trp Lys Phe
    50                  55                  60
```

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

Ile Asp Thr Ser His Val Gly Val Asp Phe Lys Trp Lys Leu Gly Gln
85 90 95

Ala Ile Lys Phe Ile Ala Pro Cys Glu Phe Lys Phe Ile Lys Asp Asp
100 105 110

Gly Lys Ala Val Tyr Thr Arg Ala Met Cys Gly Tyr Ile Thr Asp Gln
115 120 125

Trp Val Glu Asp Gly Val Lys Leu Tyr Asn Val Val Phe Leu Gly Thr
130 135 140

Tyr Lys Val Ile Pro Glu Ser Trp Ile Lys His Tyr Ser Asn Ala Leu
145 150 155 160

Tyr Ala

<210> 402
<211> 71
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 402
Met Lys Arg Lys Ile Val Gln Asn Cys Thr Asn Asp Glu Phe Glu Asp
1 5 10 15

Val Leu Phe Asp Pro Asp Leu Val Val Val Gln Lys Glu His Thr Ile
20 25 30

Lys Phe Thr His Leu Thr Ser Val Tyr Val Tyr Glu Lys Val Gly Asp
35 40 45

Lys Gln Pro Ile Tyr Gly Val Phe Arg Glu Ile Thr Glu Asp Gly Thr
50 55 60

Thr Tyr Trp Lys Glu Ile Tyr
65 70

<210> 403
<211> 137
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 403

Met Ala Ile Lys Phe Glu Val Asn Lys Trp Tyr Gln Phe Lys Asn Lys
1 5 10 15

Gln Ala Gln Glu Asn Phe Ile Lys Asp His Thr Asp Asn Gly Ile Tyr
20 25 30

Ala Arg Arg Leu Gly Met His Pro Phe Lys Ile Leu Asp Val Asp Ala
35 40 45

Leu Gly Arg Pro Ile Lys Ile Met Ser Phe Ala Gly Asn Leu Val Leu
50 55 60

Ser Ser Gly Lys Asp Ile Leu Asp Glu Asp Phe Ile Trp Leu Ser Ser
65 70 75 80

Asn Glu Ala Glu Phe Phe Asn Glu Val Glu Asn Pro Tyr Gln Ala Ala
85 90 95

Glu Glu Gln Glu Glu Ser Ala Pro Ile Thr Asp Gln Ser Lys Phe Pro
100 105 110

Val Met Lys Val Thr Ile Glu Asn Asp Glu Gln Ala Trp Ser Leu Tyr
115 120 125

Gln Met Leu Lys Ala His Phe Lys Glu
130 135

<210> 404
<211> 58
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 404
Met Pro Leu Tyr Asp Tyr Lys Cys Gln Ser Lys Asp Cys Ala Lys Glu
1 5 10 15

Tyr Glu Lys Ile Lys Lys Ile Ser Glu Arg Asp Thr Asp Val Cys Pro
20 25 30

Asp Cys His Arg Ile Ala Ile Arg Leu Val Ser Ala Pro Lys His Val
35 40 45

Asn Gly Gly Phe Tyr Asp Leu Leu Lys Gly
50 55

<210> 405
<211> 123
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 405
Met Phe Lys Ile Gly Lys Lys Tyr Arg Ile Arg Glu Gly Glu Glu Lys
1   5   10   15

Lys Tyr Leu Phe Ser Ala Ile Tyr Arg Asn Gly Ser Ile Asn Ala Val
            20   25   30

Ile Ser Thr Ser Glu Phe Ile Val Glu Asp Met Lys Gly Asn Asn Val
        35   40   45

Thr Met Ile Ser Thr Ala Ser Gly Asn Asp Gly Lys Ile Leu His Ser
    50   55   60

Phe Gln Ser Asn Val Leu Ile Tyr Asp Glu Glu Phe Asp Phe Phe Glu
65   70   75   80

Glu Val Pro Glu Gly Phe Ala Phe Glu Cys Thr Ile Thr Met Lys Ser
                85   90   95

Gly Asp Pro Leu Ser Phe Thr Val Lys Asp Glu Gly Ser Arg Leu Arg
            100   105   110

Ile Ile Ser Leu Leu Gln Ala Ile Lys Phe Lys
        115   120

<210> 406
<211> 86
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 406
Met Lys Tyr Ile Asn Arg Ser Ile Ala Ala Leu Val Leu Ala Val Ser
1   5   10   15

Leu Val Gly Cys Thr Asp Ala Asp Asn Ala Thr Lys Val Leu Ser Ser
            20   25   30

Ser Gly Phe Thr Asn Ile Glu Ile Thr Gly Tyr Asn Trp Phe Gly Cys
        35   40   45

Ser Glu Asn Asp Phe Gln His Thr Gly Phe Arg Ala Ile Gly Pro Thr
    50   55   60

Gly Gln Lys Val Glu Gly Thr Val Cys Ser Gly Leu Phe Phe Lys Asp
65   70   75   80

Ser Thr Ile Arg Phe Lys
                85

<210> 407

<211> 605
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 407
Met Ile Lys Asn Glu Ile Lys Ile Leu Ser Asp Ile Glu His Ile Lys
1   5   10   15

Lys Arg Ser Gly Met Tyr Ile Gly Ser Ser Ala Asn Glu Met His Glu
            20   25   30

Arg Phe Leu Phe Gly Lys Trp Glu Ser Val Gln Tyr Val Pro Gly Leu
        35   40   45

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

Arg Thr Lys Phe Lys Phe Ala Asn Lys Ile Asn Val Thr Ile Lys Asn
65   70   75   80

Asn Gln Val Thr Val Glu Asp Asn Gly Arg Gly Ile Pro Gln Ala Met
                85   90   95

Val Lys Thr Pro Thr Gly Glu Glu Ile Pro Gly Pro Val Ala Ala Trp
            100   105   110

Thr Ile Pro Lys Ala Gly Gly Asn Phe Gly Asp Asp Lys Glu Arg Val
        115   120   125

Thr Gly Gly Met Asn Gly Val Gly Ser Ser Leu Thr Asn Ile Phe Ser
    130   135   140

Val Met Phe Val Gly Glu Thr Gly Asp Gly Gln Asn Asn Ile Val Val
145   150   155   160

Arg Cys Ser Asn Gly Met Glu Asn Lys Ser Trp Glu Thr Ile Pro Gly
                165   170   175

Lys Trp Lys Gly Thr Arg Val Thr Phe Ile Pro Asp Phe Met Ser Phe
            180   185   190

Glu Thr Asn Glu Leu Ser Gln Val Tyr Leu Asp Ile Thr Leu Asp Arg
        195   200   205

Leu Gln Thr Leu Ala Val Val Tyr Pro Asp Ile Gln Phe Thr Phe Asn
    210   215   220

Gly Lys Lys Val Gln Gly Asn Phe Lys Lys Tyr Ala Arg Gln Tyr Asp
225   230   235   240

```
Glu His Ala Ile Val Gln Glu Gln Glu Asn Cys Ser Ile Ala Val Gly
               245                 250                 255

Arg Ser Pro Asp Gly Phe Arg Gln Leu Thr Tyr Val Asn Asn Ile His
           260                 265                 270

Thr Lys Asn Gly Gly His His Ile Asp Cys Val Met Asp Asp Ile Cys
       275                 280                 285

Glu Asp Leu Ile Pro Gln Ile Lys Arg Lys Phe Lys Ile Asp Val Thr
   290                 295                 300

Lys Ala Arg Val Lys Glu Cys Leu Thr Ile Val Met Phe Val Arg Asp
305                 310                 315                 320

Met Lys Asn Met Arg Phe Asp Ser Gln Thr Lys Glu Arg Leu Thr Ser
               325                 330                 335

Pro Phe Gly Glu Ile Arg Ser His Ile Gln Leu Asp Ala Lys Lys Ile
           340                 345                 350

Ser Arg Ala Ile Leu Asn Asn Glu Ala Ile Leu Met Pro Ile Ile Glu
       355                 360                 365

Ala Ala Leu Ala Arg Lys Leu Ala Ala Glu Lys Ala Ala Glu Thr Lys
   370                 375                 380

Ala Ala Lys Lys Ala Ser Lys Ala Lys Val His Lys His Ile Lys Ala
385                 390                 395                 400

Asn Leu Cys Gly Lys Asp Ala Asp Thr Thr Leu Phe Leu Thr Glu Gly
               405                 410                 415

Asp Ser Ala Ile Gly Tyr Leu Ile Asp Val Arg Asn Lys Glu Leu His
           420                 425                 430

Gly Gly Tyr Pro Leu Arg Gly Lys Val Leu Asn Ser Trp Gly Met Ser
       435                 440                 445

Tyr Ala Asp Met Leu Lys Asn Lys Glu Leu Phe Asp Ile Cys Ala Ile
   450                 455                 460

Thr Gly Leu Val Leu Gly Glu Lys Ala Glu Asn Leu Asn Tyr His Asn
465                 470                 475                 480

Ile Ala Ile Met Thr Asp Ala Asp His Asp Gly Leu Gly Ser Ile Tyr
               485                 490                 495

Pro Ser Leu Leu Gly Phe Phe Ser Asn Trp Pro Glu Leu Phe Glu Gln
           500                 505                 510
```

Gly Arg Ile Arg Phe Val Lys Thr Pro Val Ile Ile Ala Gln Val Gly
515 520 525

Lys Lys Gln Glu Trp Phe Tyr Thr Val Ala Glu Tyr Glu Ser Ala Lys
530 535 540

Asp Ala Leu Pro Lys His Ser Ile Arg Tyr Ile Lys Gly Leu Gly Ser
545 550 555 560

Leu Glu Lys Ser Glu Tyr Arg Glu Met Ile Gln Asn Pro Val Tyr Asp
565 570 575

Val Val Lys Leu Pro Glu Asn Trp Lys Glu Leu Phe Glu Met Leu Met
580 585 590

Gly Asp Asn Ala Asp Leu Arg Lys Glu Trp Met Ser Gln
595 600 605

<210> 408
<211> 67
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 408
Met Lys Ser Tyr Lys Val Asn Leu Glu Leu Phe Asp Lys Ala Val His
1 5 10 15

Arg Glu Tyr Arg Ile Ile Gln Arg Phe Phe Asp Met Gly Glu Ala Glu
20 25 30

Glu Phe Lys Asn Arg Phe Lys Asp Ile Arg Asp Lys Ile Gln Ser Asp
35 40 45

Thr Ala Thr Lys Asp Glu Leu Leu Glu Val Ala Glu Val Ile Lys Arg
50 55 60

Asn Met Asn
65

<210> 409
<211> 725
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 409
Met Ile Ile Thr Thr Glu Lys Glu Thr Ile Leu Gly Asn Gly Ser Lys
1 5 10 15

Ser Lys Ala Phe Ser Ile Thr Ala Ser Pro Lys Val Phe Lys Ile Leu
20 25 30

```
Ser Ser Asp Leu Tyr Thr Asn Lys Ile Arg Ala Val Val Arg Glu Leu
        35                  40                  45

Ile Thr Asn Met Ile Asp Ala His Ala Leu Asn Gly Asn Pro Glu Lys
    50                  55                  60

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

Asp Phe Gly Pro Gly Met Ser Asp Phe Asp Ile Gln Gly Asp Asp Asn
                85                  90                  95

Ser Pro Gly Leu Tyr Asn Ser Tyr Phe Ser Ser Ser Lys Ala Glu Ser
            100                 105                 110

Asn Asp Phe Ile Gly Gly Phe Gly Leu Gly Ser Lys Ser Pro Phe Ser
        115                 120                 125

Tyr Thr Asp Thr Phe Ser Ile Thr Ser Tyr His Lys Gly Glu Ile Arg
    130                 135                 140

Gly Tyr Val Ala Tyr Met Asp Gly Asp Gly Pro Gln Ile Lys Pro Thr
145                 150                 155                 160

Phe Val Lys Glu Met Gly Pro Asp Asp Lys Thr Gly Ile Glu Ile Val
                165                 170                 175

Val Pro Val Glu Glu Lys Asp Phe Arg Asn Phe Ala Tyr Glu Val Ser
            180                 185                 190

Tyr Ile Met Arg Pro Phe Lys Asp Leu Ala Ile Ile Asn Gly Leu Asp
        195                 200                 205

Arg Glu Ile Asp Tyr Phe Pro Asp Phe Asp Asp Tyr Tyr Gly Ile Asn
    210                 215                 220

Pro Glu Arg Tyr Trp Pro Asp Arg Gly Gly Leu Tyr Ala Ile Tyr Gly
225                 230                 235                 240

Gly Ile Val Tyr Pro Ile Asp Gly Val Ile Lys Asp Arg Asn Trp Leu
                245                 250                 255

Ser Ile Arg Asn Glu Val Asn Tyr Ile Lys Phe Pro Met Gly Ser Leu
            260                 265                 270

Asp Ile Ala Pro Ser Arg Glu Ala Leu Ser Leu Asp Asp Arg Thr Arg
        275                 280                 285

Lys Asn Ile Ile Glu Arg Val Lys Glu Leu Ser Glu Lys Ala Phe Asn
    290                 295                 300
```

```
Glu Asp Val Lys Arg Phe Lys Glu Ser Thr Ser Pro Arg His Thr Tyr
305                 310                 315                 320

Arg Glu Leu Met Lys Met Gly Tyr Ser Ala Arg Asp Tyr Met Ile Ser
                325                 330                 335

Asn Ser Val Lys Phe Thr Thr Lys Asn Leu Ser Tyr Lys Lys Met Gln
            340                 345                 350

Ser Met Phe Glu Pro Asp Asn Lys Leu Cys Asn Ala Gly Val Val Tyr
        355                 360                 365

Glu Val Asn Leu Asp Pro Arg Leu Lys Arg Ile Lys Gln Ser His Glu
    370                 375                 380

Thr Ser Ala Val Ala Ser Ser Tyr Arg Leu Phe Gly Ile Asn Thr Thr
385                 390                 395                 400

Lys Ile Asn Ile Val Ile Asp Asn Ile Lys Asn Arg Val Asn Ile Val
                405                 410                 415

Arg Gly Leu Ala Arg Ala Leu Asp Asp Ser Glu Phe Asn Asn Thr Leu
            420                 425                 430

Asn Ile His His Asn Glu Arg Leu Leu Phe Ile Asn Pro Glu Val Glu
        435                 440                 445

Ser Gln Ile Asp Leu Leu Pro Asp Ile Met Ala Met Phe Glu Ser Asp
    450                 455                 460

Glu Val Asn Ile His Tyr Leu Ser Glu Ile Glu Ala Leu Val Lys Ser
465                 470                 475                 480

Tyr Ile Pro Lys Val Val Lys Ser Lys Ala Pro Arg Pro Lys Ala Ala
                485                 490                 495

Thr Ala Phe Lys Phe Glu Ile Lys Asp Gly Arg Trp Glu Lys Glu Glu
            500                 505                 510

Leu Phe Thr Leu Thr Ser Glu Ala Asp Glu Ile Thr Gly Tyr Val Ala
        515                 520                 525

Tyr Met His Arg Ser Asp Ile Phe Ser Met Asp Gly Thr Thr Ser Leu
    530                 535                 540

Cys His Pro Ser Met Asn Ile Leu Ile Arg Met Ala Asn Leu Ile Gly
545                 550                 555                 560

Ile Asn Glu Phe Tyr Val Ile Arg Pro Leu Leu Gln Lys Lys Val Lys
                565                 570                 575
```

```
Glu Leu Gly Gln Cys Gln Cys Ile Phe Glu Thr Leu Arg Asp Leu Tyr
            580                 585                 590

Val Asp Ala Phe Asp Asp Val Asp Tyr Asp Lys Tyr Val Gly Tyr Ser
        595                 600                 605

Ser Ser Ala Lys Arg Tyr Ile Asp Lys Ile Ile Lys Tyr Pro Glu Leu
    610                 615                 620

Asp Phe Met Met Lys Tyr Phe Ser Val Asp Glu Val Ser Glu Glu Tyr
625                 630                 635                 640

Thr Arg Leu Ala Asn Met Val Ser Ser Leu Gln Gly Val Tyr Phe Asn
                645                 650                 655

Gly Gly Lys Asp Thr Ile Gly His Asp Ile Trp Thr Val Thr Asn Leu
            660                 665                 670

Phe Asp Glu Leu Ser Arg Asn Ala Ser Lys Asn Ser Asp Lys Met Val
        675                 680                 685

Ala Glu Phe Thr Lys Lys Phe Arg Ile Val Ser Asp Phe Ile Gly Tyr
    690                 695                 700

Arg Asn Ser Leu Ser Asp Asp Glu Val Ser Gln Ile Ala Lys Thr Met
705                 710                 715                 720

Lys Ala Leu Ala Ala
                725


<210> 410
<211> 312
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 410
Met Tyr Asn Ile Lys Cys Leu Thr Lys Asn Glu Gln Ala Glu Ile Val
1               5                   10                  15

Lys Leu Tyr Ser Ser Gly Asn Tyr Thr Gln Gln Glu Leu Ala Asp Trp
            20                  25                  30

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

Glu Ala Glu Arg Ser Lys Val Thr Ile Ser Gly Asp Ile Thr Val Lys
    50                  55                  60

Val Asn Ser Asp Ala Val Ile Ala Pro Val Ala Lys Ser Asp Ile Ile
```

65 70 75 80

Trp Asn Ala Ser Lys Lys Phe Ile Ser Ile Thr Val Asp Gly Val Thr
85 90 95

Tyr Asn Ala Thr Pro Asn Thr His Ser Asn Phe Gln Glu Ile Leu Asn
100 105 110

Leu Leu Val Ala Asp Lys Leu Glu Glu Ala Ala Gln Lys Ile Asn Val
115 120 125

Arg Arg Ala Val Glu Lys Tyr Ile Ser Gly Asp Val Arg Ile Glu Gly
130 135 140

Gly Ser Leu Phe Tyr Gln Asn Ile Glu Leu Arg Ser Gly Leu Val Asp
145 150 155 160

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

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

Arg Leu Phe Asp Phe Leu Val Ala Asn Asp Ile Glu Ile Thr Glu Asp
195 200 205

Gly Tyr Phe Tyr Ala Trp Lys Val Val Arg Ser Asn Tyr Phe Asp Cys
210 215 220

His Ser Asn Thr Phe Asp Asn Ser Pro Gly Lys Val Val Lys Met Pro
225 230 235 240

Arg Thr Arg Val Asn Asp Asp Asp Thr Gln Thr Cys Ser Arg Gly Leu
245 250 255

His Val Cys Ser Lys Ser Tyr Ile Arg His Phe Gly Ser Ser Thr Ser
260 265 270

Arg Val Val Lys Val Lys Val His Pro Arg Asp Val Val Ser Ile Pro
275 280 285

Ile Asp Tyr Asn Asp Ala Lys Met Arg Thr Cys Gln Tyr Glu Val Val
290 295 300

Glu Asp Val Thr Glu Gln Phe Lys
305 310

<210> 411
<211> 64
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 411
Met Leu Gly Tyr Gln Ala Arg Val Lys Glu Glu Tyr Asp Gln Leu Met
1   5   10   15

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

Thr Val Ser Ala Val Glu Gln Glu Leu Leu Leu Ser Gln Phe Ile Ser
        35   40   45

Met Lys Ser Tyr Ala Asp Cys Leu Glu Lys Arg Ile Ala Gln Phe Lys
    50   55   60

<210> 412
<211> 185
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 412
Met Gln Lys Thr Asn Pro Gly Leu Gln Arg Leu Phe Gln Ile Pro Ser
1   5   10   15

Phe Thr Leu Ser Asn Ser Asp Leu Thr Ser Glu Met Lys Val Lys Ile
            20   25   30

Ala Asp Thr Ala Arg Tyr Ser Leu Lys Gln Asn Pro Asn Gln Asp Lys
        35   40   45

Ala Glu Val Ile Glu Arg Cys Arg Ile Ala Val Tyr Ala Glu Phe Phe
    50   55   60

Val Ala Asp Trp Leu Arg Gly Tyr Val Asn Lys Gly Gln Glu Asp Val
65   70   75   80

Asn Asp Pro Tyr Thr Tyr Ala Trp Asp Val Leu Ala His Pro Lys Tyr
                85   90   95

Cys Gly Leu Arg Val Glu Val Lys Thr His Gln Thr Asp Ser Arg Trp
            100   105   110

Ile Ser Val Thr Thr Gly Cys Ser Gly Glu Tyr Pro Tyr Gly Ser Gly
        115   120   125

Ile Asn Leu Gly Pro Ile Leu Asn His Gln Val Ala Asp Cys Ile Ile
    130   135   140

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

Lys Phe Ile Gly Asp Arg Glu Asp Leu Arg Lys Val Val Arg Lys Ser
165 170 175

Asn Tyr Asn Gly Trp Tyr Leu Ser Ile
180 185

<210> 413
<211> 87
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 413
Met Lys Phe Lys Phe Tyr Tyr Ala Lys His Lys Ile Thr Gly Glu Phe
1 5 10 15

Ile Ala Phe Thr Thr Ser Thr Thr Asp Glu Gly Asp Ile Phe Thr Ala
20 25 30

Val Phe Leu Ser Lys Trp Glu Ser Asp Gln Pro Tyr Leu Ser Ser Arg
35 40 45

Glu Asp Leu Gln Arg Leu Val Asn Gly Glu Tyr Asn Asp Ser Trp Ser
50 55 60

Tyr Leu Val His Asp Cys Val Lys Lys Ala Ile Lys Gln Lys His Leu
65 70 75 80

Glu Ile Val Glu Ile Glu Leu
85

<210> 414
<211> 32
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 414
Met Lys Ile Leu Asn Ser Val Leu Ile Ala Cys Ala Trp Trp Val Ala
1 5 10 15

Gln Val Ser Ala Val Val Val Gly Ile His Ile Tyr Tyr Glu Tyr Phe
20 25 30

<210> 415
<211> 37
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 415

Met Lys Lys Ile Val Lys Ala Ile Trp Asn Val Val Ile Ile Leu Ile
1   5   10   15

Val Leu Ser Ile Phe Pro Ile Val Leu Met Ile Asp Val Leu Asn Ala
            20   25   30

Tyr Phe Gly Phe Met
        35

<210> 416
<211> 65
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 416
Met Lys Arg Lys Arg Ser Ala Phe Thr Phe Ile Glu Trp Phe Phe Asp
1   5   10   15

Asn Ile Phe Pro Ala Leu Phe Ile Phe Met Leu Ile Phe Ala Leu Gly
            20   25   30

Ser Val Val Val Gly Ile Tyr Leu Met Thr Val Val Gly Ile Asp Ile
        35   40   45

His Gln Asn Gly Leu Lys Ser Val Val Glu Thr Ile Trp Asn Gly Val
    50   55   60

Lys
65

<210> 417
<211> 36
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 417
Met Met Asn Leu Leu Ser Gly Trp Phe Tyr Ile Leu Met Phe Tyr Ile
1   5   10   15

Gly Ala Asn Phe Pro Tyr Trp Met Gly Trp Ser Thr Thr Ala Phe Gly
            20   25   30

Phe Tyr Thr Pro
        35

<210> 418
<211> 71
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F488/08

<400> 418
Met Lys Ile Phe Lys Asp Val Lys Val Gly Glu Ile Phe Cys Leu Asp
1   5   10   15

Asn Gly Asp Gln Leu Ile Arg Ile Ser Pro Leu Lys Ser Thr Ser Glu
            20   25   30

Lys Pro Thr Val Asn Ala Thr Leu Ala Asn Asn Ser Asn Glu Arg Phe
        35   40   45

Cys Ile Glu Asn Asp Thr Glu Thr Tyr Thr Val Glu Glu Phe Trp Glu
    50   55   60

Leu Ser Val Asp Cys Asp Asp
65   70

<210> 419
<211> 152
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 419
Met Lys Tyr Met Thr Val Thr Asp Leu Asn Asn Ala Gly Ala Thr Val
1   5   10   15

Ile Gly Thr Ile Lys Asn Gly Glu Trp Phe Leu Gly Val Pro His Lys
            20   25   30

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

Gly Arg Pro Phe Ser Asn Pro Cys Val Ser Ala Arg Phe Tyr Val Gly
    50   55   60

Asn Gln Arg Ser Lys Gln Gly Phe Ser Ala Val Leu Ser His Ile Arg
65   70   75   80

Gln Arg Arg Ser Gln Leu Ala Arg Thr Ile Ala Asn Asn Asn Val Pro
                85   90   95

Tyr Thr Val Phe Tyr Leu Pro Ala Ser Lys Met Lys Pro Leu Thr Thr
            100   105   110

Gly Phe Gly Lys Gly Gln Leu Ala Leu Ala Phe Ile Arg Asn His His
        115   120   125

Ser Glu Tyr Gln Thr Leu Glu Glu Met Asn Arg Met Leu Ala Asp Asn
    130   135   140

Phe Lys Phe Val Leu Gln Ala Tyr
145 150

<210> 420
<211> 52
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 420
Met Asn Ile Ala Lys Leu Leu Gly Val Ile Ser Phe Ile Cys Trp Ile
1 5 10 15

Val Ala Cys Val Leu Thr Ile Cys Ile Asp Val Ser Ser Val Phe Ser
20 25 30

Gln Ala Leu Ala Gln Gly Met Cys Ala Tyr Leu Thr Phe Val Leu Leu
35 40 45

Ser Thr Asn Asp
50

<210> 421
<211> 442
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 421
Met Gln Leu Asn Asn Arg Asp Leu Lys Ser Ile Ile Asp Asn Glu Ala
1 5 10 15

Leu Ala Tyr Ala Met Tyr Thr Val Glu Asn Arg Ala Ile Pro Asn Met
20 25 30

Ile Asp Gly Phe Lys Pro Val Gln Arg Phe Val Ile Ala Arg Ala Leu
35 40 45

Asp Leu Ala Arg Gly Asn Lys Asp Lys Phe His Lys Leu Ala Ser Ile
50 55 60

Ala Gly Gly Val Ala Asp Leu Gly Tyr His His Gly Glu Asn Ser Ala
65 70 75 80

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

Leu Leu Asp Gly Gln Gly Asn Phe Gly Ser Arg Thr Val Gln Lys Ala
100 105 110

Ala Ala Ser Arg Tyr Ile Phe Ala Arg Val Ser Lys Asn Phe Tyr Asn
115 120 125

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

Ile Pro Pro Ala Phe Tyr Leu Pro Ile Ile Pro Thr Val Leu Leu Asn
145                 150                 155                 160

Gly Val Ser Gly Ile Ala Thr Gly Tyr Ala Thr Tyr Ile Leu Pro His
                165                 170                 175

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

Lys Val Thr Lys Pro Lys Val Glu Phe Pro Glu Phe Arg Gly Glu Val
        195                 200                 205

Val Glu Ile Asp Gly Gln Tyr Glu Ile Arg Gly Thr Tyr Lys Phe Thr
    210                 215                 220

Ser Arg Thr Gln Met His Ile Thr Glu Ile Pro Tyr Lys Tyr Asp Arg
225                 230                 235                 240

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

Ile Thr Trp Asp Asp Ala Cys Gly Glu His Gly Phe Gly Phe Lys Val
            260                 265                 270

Lys Phe Arg Lys Glu Tyr Ser Leu Ser Asp Asn Glu Glu Glu Arg His
        275                 280                 285

Ala Lys Ile Met Lys Asp Phe Gly Leu Ile Glu Arg Arg Ser Gln Asn
    290                 295                 300

Ile Thr Val Ile Asn Glu Lys Gly Lys Leu Gln Val Tyr Asp Asn Val
305                 310                 315                 320

Val Asp Leu Ile Lys Asp Phe Val Glu Val Arg Lys Thr Tyr Val Gln
                325                 330                 335

Lys Arg Ile Asp Asn Lys Ile Lys Glu Thr Glu Ser Ala Phe Arg Leu
            340                 345                 350

Ala Phe Ala Lys Ala His Phe Ile Lys Lys Val Ile Ser Gly Glu Ile
        355                 360                 365

Val Val Gln Gly Lys Thr Arg Lys Glu Leu Thr Glu Glu Leu Ser Lys
    370                 375                 380

Ile Asp Met Tyr Ser Ser Tyr Val Asp Lys Leu Val Gly Met Asn Ile
385                 390                 395                 400
```

Phe His Met Thr Ser Asp Glu Ala Lys Lys Leu Ala Glu Glu Ala Lys
405 410 415

Ala Lys Lys Glu Glu Asn Glu Tyr Trp Lys Thr Thr Asp Val Val Thr
420 425 430

Glu Tyr Thr Lys Asp Leu Glu Glu Ile Lys
435 440

<210> 422
<211> 49
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 422
Met Ser Pro Phe Ile Gly Ile Thr Ser Ala Ala Leu Val Ser Gly Gly
1 5 10 15

Ile Leu Leu Ala Gly Leu Gly Val Val Pro Ala Val Ala Gly Gly Leu
20 25 30

Leu Ala Phe Gly Ile Gln Arg Val Ile Met Thr Val Ile Thr Val Met
35 40 45

Gln

<210> 423
<211> 75
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 423
Met Lys Phe Lys Ile Glu Asn Glu Ile Val Lys Ala Lys Asn Ala Leu
1 5 10 15

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

Val Arg Glu Glu Lys Pro Gly Val Leu Thr Phe Phe Thr Met Ile Phe
35 40 45

Lys Phe Lys Gly Asp Thr Glu Phe Lys Gln Phe Asp Phe Ala His Glu
50 55 60

Asp Glu Ile Glu Val Arg Asn Leu Asn Ile Lys
65 70 75

<210> 424
<211> 211
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 424
Met Ser Lys Val Thr Tyr Ile Ile Lys Ala Ser Asn Asp Val Leu Asn
1   5   10   15

Glu Lys Thr Ala Ala Ile Leu Ile Thr Ile Ala Lys Lys Asp Phe Ile
            20   25   30

Thr Ala Ala Glu Val Arg Glu Val His Pro Asp Leu Gly Asn Ala Val
        35   40   45

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

Ser Gly Asp Gly Leu Ile Ile Thr Gly Glu Ala Gln Asp Ile Ile Ser
65   70   75   80

Asn Ala Ala Thr Leu Tyr Ala Gln Glu Asn Ala Pro Glu Leu Leu Lys
                85   90   95

Lys Arg Ala Thr Arg Lys Ala Arg Glu Ile Thr Ser Asp Met Glu Glu
            100   105   110

Asp Lys Asp Leu Met Leu Lys Leu Leu Asp Glu Asn Gly Phe Val Leu
        115   120   125

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

Arg Thr His Gly Ile Arg Asn Phe Glu Ile Asn Asn Asn Gly Asn Met
145   150   155   160

Arg Ile Phe Gly Tyr Lys Met Met Glu His His Ile Gln Lys Phe Thr
                165   170   175

Asp Ile Gly Met Ser Cys Lys Ile Ala Lys Asn Gly Asn Val Tyr Leu
            180   185   190

Asp Ile Lys Arg Ser Ala Glu Asn Ile Glu Ala Val Ile Thr Val Ala
        195   200   205

Ser Glu Leu
    210

<210> 425
<211> 109
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 425
Met Asn Lys Leu Glu Ile Val Asn Glu Leu Arg Arg Cys Val Glu Pro
1   5   10   15

Thr Gln Glu Gly Trp Asp Ile Trp Tyr His Gly Ala Tyr Leu Gly Thr
            20   25   30

Ile Val Lys Ile Lys Thr Gly Lys Tyr Met Ile Ile Arg Glu Ser Lys
        35   40   45

Asp Ala Pro Val Gly Ile Arg Asn Asn Phe Met Ala Ala Ile Ser Ser
    50   55   60

Phe Thr Asp Ala Ala Tyr Glu Ile Tyr Leu Ala Asp Tyr Lys Glu Phe
65   70   75   80

Gln Glu Ser Gln Pro Val Ile Arg Ser Ile Gly Val Asn Lys Ala Gln
                85   90   95

Gln Lys Thr Leu Trp Gln Arg Ile Lys Gly Trp Phe Lys
            100   105

<210> 426
<211> 153
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 426
Met Asn Pro Phe Ile Asn Arg Leu Lys Met Leu Asn Val Pro Leu Ser
1   5   10   15

Arg Glu Thr Pro Glu Ser Leu Val Glu Lys Phe Lys Ala His Gly Tyr
            20   25   30

Lys Cys Thr Glu Glu Asp Ile Leu Lys Glu Val Pro Glu Ile Cys Trp
        35   40   45

Gln Thr Ala Tyr Trp Asp Glu Asn Gln Lys Tyr Gln Arg Arg Ile Val
    50   55   60

Cys Ala Ala Asn Arg Phe Lys Leu Lys Asp Gly Arg Thr Leu Ile Ile
65   70   75   80

Pro Gly Ala Arg His Tyr Ser Lys Asp Met Ala Glu Val Leu Asp Val
                85   90   95

Val Lys Pro Gln Leu Val Thr Gln Gln Val Cys Asp Asp Asp Gln Gly

100 105 110

Phe Ile Asp Gln Tyr Ser Asn Tyr Trp Thr Arg Glu Glu Ala Met Ile
115 120 125

Ile Ala Thr Tyr Ala Gly Gln Val Arg Ile Glu Arg Gly Gly Ser Glu
130 135 140

Lys Glu Leu Tyr Ser Glu Asp Leu Tyr
145 150

<210> 427
<211> 98
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 427
Met Asn Ile Lys Lys Phe Gln Ile Asp Gly Ile Thr Asn Gln Ile Lys
1 5 10 15

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

Ala Asn Glu Pro Ala Phe Lys Phe Cys Asp Met Glu Phe Thr Lys Lys
35 40 45

Leu Val Gly Lys Asp His Val Cys Pro Phe Ser Ser Pro Val Asn Gly
50 55 60

Met Leu Lys Pro Ala Leu Arg Asp Leu Tyr Ile Ala Met Asn Glu Glu
65 70 75 80

Met Ile Lys Glu Leu Lys Arg Gln Leu Lys Val Ile Gln Phe Gly Gln
85 90 95

Gly Asn

<210> 428
<211> 72
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 428
Leu Ala Arg Glu Ile Asn Ser Lys Ser Asp Tyr Phe Asn Ser Leu Asn
1 5 10 15

Asp Lys Asp Lys Asn Leu Ile Arg His Phe Ile Val Glu Met Gly Tyr
20 25 30

Thr Asp Thr His Asp Leu Arg Glu His Ile Phe Glu Cys Gly Val Ala
35 40 45

Lys Lys Phe Ser Phe Thr Cys Lys Cys Leu Arg Glu Val Ile Gln His
50 55 60

Tyr Glu Gln Phe Ser Arg Lys Thr
65 70

<210> 429
<211> 92
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 429
Met Ile Ile Asp Ser Gln Ser Val Val Gln Tyr Thr Ile Lys Ile Asp
1 5 10 15

Ile Leu Glu Lys Leu Tyr Lys Phe Leu Pro Asn Leu Tyr His Ser Ile
20 25 30

Val Asn Glu Leu Val Glu Glu Leu His Leu Gly Asn Asn Asp Phe Leu
35 40 45

Ile Gly Thr Tyr Lys Asp Leu Ser Lys Ala Gly Tyr Phe Tyr Ile Ile
50 55 60

Pro Ala Pro Gly Lys Ser Ile Asp Asp Val Leu Lys Thr Ile Met Ile
65 70 75 80

Tyr Val His Asp Tyr Glu Ile Glu Asp Tyr Phe Glu
85 90

<210> 430
<211> 50
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 430
Met Ser His Asn Leu Glu Lys Val Ile Glu His Asn Val Ala Gln Glu
1 5 10 15

Arg Lys Ser Phe Lys Glu Phe Val Glu Lys Ile Phe Glu Glu Asn Thr
20 25 30

Thr Asp Gln Phe Thr Asn Gln Ala Ser Asp Asp Ile Ile Thr Lys Ser
35 40 45

Thr Asn

50

<210> 431
<211> 90
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 431
Met Asn Lys Asn Ile Asp Thr Val Arg Glu Ile Ile Thr Val Ala Ser
1 5 10 15

Ile Leu Ile Lys Phe Ser Arg Glu Asp Ile Val Glu Asn Arg Ala Asn
20 25 30

Phe Ile Ala Phe Leu Asn Glu Ile Gly Val Thr His Glu Gly Arg Lys
35 40 45

Leu Asn Gln Asn Ser Phe Arg Lys Ile Val Ser Glu Leu Thr Gln Glu
50 55 60

Asp Lys Lys Thr Leu Ile Asp Glu Phe Asn Glu Gly Phe Glu Gly Val
65 70 75 80

Tyr Arg Tyr Leu Glu Met Tyr Thr Asn Lys
85 90

<210> 432
<211> 218
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 432
Met Ala Ala Pro Arg Ile Ser Phe Ser Pro Ser Asp Ile Leu Phe Gly
1 5 10 15

Val Leu Asp Arg Leu Phe Lys Asp Asn Ala Thr Gly Lys Val Leu Ala
20 25 30

Ser Arg Val Ala Val Val Ile Leu Leu Phe Met Met Ala Ile Val Trp
35 40 45

Tyr Arg Gly Asp Ser Phe Phe Glu Tyr Tyr Lys Gln Ser Lys Tyr Glu
50 55 60

Thr Tyr Ser Glu Ile Ile Glu Lys Glu Arg Asn Ala Arg Phe Glu Ser
65 70 75 80

Val Ala Leu Glu Gln Leu Gln Ile Val His Ile Ser Ser Glu Ala Asp
85 90 95

```
Phe Ser Ala Val Tyr Ser Phe Arg Pro Lys Asn Leu Asn Tyr Phe Val
            100                 105                 110

Asp Ile Ile Ala Tyr Glu Gly Lys Leu Pro Ser Thr Ile Ser Glu Lys
        115                 120                 125

Ser Leu Gly Gly Tyr Pro Val Asp Lys Thr Met Asp Glu Tyr Thr Val
    130                 135                 140

His Leu Asn Gly Arg His Tyr Tyr Ser Asp Ser Lys Phe Ala Phe Leu
145                 150                 155                 160

Pro Thr Lys Lys Pro Thr Pro Glu Ile Asn Tyr Met Tyr Ser Cys Pro
                165                 170                 175

Tyr Phe Asn Leu Asp Asn Ile Tyr Ala Gly Thr Ile Thr Met Tyr Trp
            180                 185                 190

Tyr Arg Asn Asp His Ile Ser Asn Asp Arg Leu Glu Ser Ile Cys Ala
        195                 200                 205

Gln Ala Ala Arg Ile Leu Gly Arg Ala Lys
    210                 215


<210> 433
<211> 260
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 433
Met Ala Val Val Gly Val Pro Gly Trp Ile Gly Ser Ser Ala Ala Asn
1               5                   10                  15

Glu Thr Gly Gln Arg Trp Met Ser Gln Ala Ala Gly Gln Leu Arg Leu
            20                  25                  30

Gly Val Pro Cys Trp Met Ser Gln Phe Ala Gly Arg Ser Arg Glu Ile
        35                  40                  45

Ile His Thr Val Gly Ala Asn His Asn Phe Asn Gly Gln Trp Phe Arg
    50                  55                  60

Asp Arg Cys Phe Glu Ala Gly Gly Ala Pro Ile Val Phe Asn Ile Val
65                  70                  75                  80

Gly Asp Ile Val Ser Tyr Ser Lys Asp Val Pro Leu Phe Phe Met Tyr
                85                  90                  95

Gly Asp Thr Pro Asn Glu Tyr Val Gln Leu Asn Ile His Gly Val Thr
            100                 105                 110
```

```
Met Tyr Gly Arg Gly Gly Asn Gly Gly Ser Asn Ser Pro Gly Ser Ala
        115                 120                 125

Gly Gly His Cys Ile Gln Asn Asp Ile Gly Gly Arg Leu Arg Ile Asn
    130                 135                 140

Asn Gly Gly Ala Ile Ala Gly Gly Gly Gly Gly Gly Gly Gly Gly Tyr
145                 150                 155                 160

Tyr Ser Pro Phe Ser Gln Met Arg Leu Thr Phe Gly Gly Gly Gly Gly
                165                 170                 175

Arg Pro Phe Gly Ala Pro Gly Gly Ser Ile Asp Met Gln Ser Gly Ala
            180                 185                 190

Thr Gly Gly Thr Ile Ser Ala Pro Gly Ser Gly Ser Val Asn Gly Ile
        195                 200                 205

Tyr Asn Gly Gly Asn Gly Gly Glu Val Gly Ser Ala Gly Gly Arg Cys
    210                 215                 220

Asn Ile Arg Gly Gln Gly Ser Glu Tyr Asn Gly Gly Ala Ala Gly Tyr
225                 230                 235                 240

Ala Val Ile Gly Ser Ala Pro Thr Trp Gln Asn Val Gly Ala Ile Tyr
                245                 250                 255

Gly Pro Arg Val
            260


<210> 434
<211> 982
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 434
Met Ala Thr Leu Lys Gln Ile Gln Phe Lys Arg Ser Lys Thr Ala Gly
1               5                   10                  15

Gln Arg Pro Ala Ala Ser Val Leu Ala Glu Gly Glu Leu Ala Ile Asn
            20                  25                  30

Leu Lys Asp Lys Thr Ile Phe Thr Lys Asp Asp Ser Gly Ser Val Ile
        35                  40                  45

Glu Leu Gly Leu Lys Tyr Gly Gly Thr Ile Asn Gly Ser Leu Glu Val
    50                  55                  60

Thr Glu Asn Ile Thr Gly Thr Leu Ile Gly Asn Ser Ser Thr Ala Thr
```

65 70 75 80

Lys Leu Gln Thr Pro Arg Lys Ile Asn Gly Ile Ser Phe Asp Gly Ser
85 90 95

Lys Asp Ile Thr Leu Thr Pro Ser Asp Ile Asn Val Asn Ser Thr Thr
100 105 110

Phe Ile Lys Asn Asn Gly Glu Leu Pro Thr Asp Ala Asn Leu Asp Thr
115 120 125

Tyr Gly Pro Ile Glu Glu Tyr Leu Gly Val Trp Ser Lys Ser Thr Ser
130 135 140

Thr Asn Ala Gln Pro Ala Asn Lys Phe Pro Glu Glu Asn Ala Val Gly
145 150 155 160

Val Leu Glu Val Phe Val Ala Gly Gln Phe Ala Gly Thr Gln Arg Tyr
165 170 175

Thr Val Arg Ser Gly Asn Val Tyr Ile Arg Ser Leu Ser Ala Lys Trp
180 185 190

Asn Gly Val Asp Gly Pro Trp Gly Val Trp Arg Asn Val Gln Ala Ser
195 200 205

Thr Arg Pro Leu Ser Gln Thr Ile Asp Leu Asp Ser Leu Gly Glu Leu
210 215 220

Glu His Cys Gly Leu Trp Arg Asn Ser Ser Ser Ala Ile Ala Ser Phe
225 230 235 240

Asp Arg His Tyr Pro Glu Glu Gly Ser Ala Ala Gln Gly Phe Leu Glu
245 250 255

Ile Phe Glu Gly Gly Leu Tyr Thr Arg Thr Gln Arg Tyr Thr Thr Arg
260 265 270

Met Gly Met Val Tyr Thr Arg Cys Leu Ala Ala Ala Trp Asp Ala Ser
275 280 285

Ala Pro Lys Trp Glu Glu Trp Lys Gln Val Gly His Gly Thr Pro Ala
290 295 300

Thr Phe Tyr Asp Gly Asp Leu Asn Asp Phe Lys Thr Pro Gly Leu Tyr
305 310 315 320

Asn Ile Leu Gly Thr Asp Ala Val Ile Asn Cys Pro Thr Gly Glu Gly
325 330 335

Leu Pro Thr Val Ile Val Gly Leu Leu Glu Val Lys Gln Arg Ala Ser

340 345 350

Gly Gly Ala Ile Phe Gln Arg Phe Thr Thr Ala Gly Thr Gly Ala Thr
355 360 365

Thr Arg Asp Arg Ile Phe Glu Arg Ala Tyr Thr Gly Gly Ala Trp Gly
370 375 380

Ala Trp Asn Glu Val Tyr Thr Ser Tyr Ser Leu Pro Ile Thr Leu Gly
385 390 395 400

Met Gly Gly Ile Lys Ala Gln Leu Ala Glu Leu Asp Trp Gln Thr Phe
405 410 415

Asp Phe Val Pro Gly Ser Met Phe Ser Val Pro Leu Asn Lys Ile Lys
420 425 430

Asn Met Pro Ala Asn Met Asp Trp Gly Thr Ile Asp Gly Asn Leu Val
435 440 445

Met Phe Ser Val Gly Pro Ser Glu His Thr Gly Thr Gly Arg Thr Val
450 455 460

Gln Val Trp Arg Gly Thr Val Ser Gln Ala Asn Tyr Arg Tyr Phe Val
465 470 475 480

Val Arg Ile Ala Gly Asn Pro Gly Ser Arg Thr Asn Thr Cys Arg Arg
485 490 495

Val Val Leu Glu Asp Gly Ser His Thr Trp Thr Ala Gln Gln Asn Phe
500 505 510

Arg Gly Leu Leu Asn Ile Thr Ala Ala Val Asn Leu Gly Ala Asn Gln
515 520 525

Lys Ile Ser Leu Ala Pro Gly Ala Tyr Ile Gln Ala Pro Ala Ser Gly
530 535 540

Ser Gly Ser Asn Thr Tyr Ala Asn Gln Asn Thr Thr Ile Ala Pro Leu
545 550 555 560

Tyr Gln Ala Ile Asp Asp Ser Asn Lys Asn Gln Phe Ala Pro Ile Val
565 570 575

Lys Gln Lys Asn Thr Val Thr Asn Ile Thr Met Ala Ser Gly Met Asp
580 585 590

Ile Ala Ser Ser Glu Tyr Arg Ile Val Ala Gln Gly Asp Leu Ser Ala
595 600 605

Thr Gly Thr Thr Ala Thr Glu Leu Ala Thr Trp Arg Phe Leu Pro Ser

610 615 620

Gly Arg Phe Met Ser Gln Ser Arg Val Tyr Ala Gly Ala Ala Phe Leu
625 630 635 640

Asn Thr Asp Gly Asn Ile Ala Gly Ser Ile Trp Lys Lys Tyr Asn Asp
645 650 655

Ala Thr Asn Leu Asp Ala Ala Leu Asn Thr Arg Leu Gly Lys Gly Gly
660 665 670

Asp Thr Met Thr Gly Arg Leu Thr Ile Asn Ala Pro Asn Asp Ser Ile
675 680 685

Val Leu Ser Thr Thr Ala Ser Asn Ser Leu His Ile Arg Gly Asp Ile
690 695 700

Asp Gly Thr Gly Asn Trp Tyr Ile Gly Lys Gly Gly Ala Asp Asn Ser
705 710 715 720

Leu Ala Phe Tyr Ser Tyr Ala Ser Gln Ala Ala Val His Ile Thr Asn
725 730 735

Asn Gly Glu Ile Ala Leu Asn Pro Gln Asn Thr Ala Met Val Asn Val
740 745 750

Asn Arg Asp Arg Val His Ile Asn Gly Ser Gly Trp Ile Ala Arg Gln
755 760 765

Pro Gly Asp Trp Gly Asn Gln Trp Arg Val Glu Ala Pro Leu Phe Val
770 775 780

Asp His Gly Tyr Val Gly Gln Asp Ser Tyr Tyr Pro Ile Leu Lys Ala
785 790 795 800

Arg Ser Val Ile Thr Asn Gln Gly Tyr Ser Thr Ala Val Asp Phe Gly
805 810 815

Met Arg Arg Ile Pro Ser Gln Trp Gly Gln Ala Ile Ile Arg Val Gly
820 825 830

Ser Thr Glu Ala Ser Pro Asp Ala Gly His Pro Gln Ala Val Phe Glu
835 840 845

Phe His His Asp Gly Phe Phe Tyr Thr Pro Gly Asn Gly Ser Phe Ser
850 855 860

Asp Val Tyr Ile Arg Ser Asp Ser Arg Leu Lys Ile Asn Lys Glu Glu
865 870 875 880

Leu Glu Tyr Gly Ala Val Glu Lys Val Cys Arg Leu Lys Val Tyr Ile

885 890 895

Tyr Asp Lys Val Lys Ser Ile Lys Asp Arg Ser Val Ile Lys Arg Glu
900 905 910

Val Gly Ile Ile Ala Gln Asp Leu Glu Lys Glu Leu Pro Glu Ala Val
915 920 925

Ser Lys Val Glu Val Asp Gly Ser Asp Val Leu Thr Ile Ser Asn Ser
930 935 940

Ala Val Asn Ala Leu Leu Ile Lys Ala Ile Gln Glu Met Ser Glu Glu
945 950 955 960

Ile Lys Glu Leu Lys Thr Pro Leu Phe Thr Lys Ile Ala Arg Lys Ile
965 970 975

Ser Lys Tyr Phe Lys Phe
980

<210> 435
<211> 216
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 435
Met Ala Asp Leu Lys Val Gly Ser Thr Val Gly Gly Ser Val Ile Trp
1 5 10 15

His Gln Gly Asn Phe Pro Leu Asn Ser Ala Gly Asp Asp Val Leu Tyr
20 25 30

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

Asn Asp Phe Val Ser Lys Ala Asn Gly Gly Thr Tyr Ala Gly Pro Ile
50 55 60

Thr Ile Asn Tyr Gly Val Asn Ser Tyr Leu Gln Leu Ser Asn Asn Glu
65 70 75 80

Thr Pro Ile Arg Ile Arg Ser Gly Gly Gly Thr Gly Asn Thr Leu Val
85 90 95

Val Gly Gly Ser Ser Gly Gly Ile Ser Phe Arg Pro Ala Gly Ser Glu
100 105 110

Ile Thr Thr Gly Gln Ile Thr Ile Thr Pro Glu Gly Leu Thr Thr Phe
115 120 125

```
Thr Arg Ala Val Thr Ala Pro Ser Val Thr Val Thr Ser Thr Pro Ser
    130                 135                 140

Ala Ala Ser Asp Val Thr Arg Lys Asp Tyr Val Asp Gly Ala Ile Asn
145                 150                 155                 160

Thr Val Thr Ala Asn Ala Asn Ser Arg Val Leu Arg Ser Gly Asp Thr
                165                 170                 175

Met Thr Gly Asn Leu Thr Ala Pro Asn Leu Phe Ser Gln Asn Pro Ala
            180                 185                 190

Ser Gln Pro Ser His Val Pro Arg Phe Asp Gln Ile Val Ile Lys Asp
        195                 200                 205

Ser Val Gln Asp Phe Gly Tyr Tyr
    210                 215


<210> 436
<211> 371
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 436
Met Glu Lys Phe Met Ala Glu Phe Gly Gln Gly Tyr Val Gln Thr Pro
1               5                   10                  15

Phe Leu Ser Glu Ser Asn Ser Val Arg Tyr Lys Ile Ser Ile Ala Gly
            20                  25                  30

Ser Cys Pro Leu Ser Thr Ala Gly Pro Tyr Val Lys Phe Gln Asp Asn
        35                  40                  45

Pro Val Gly Asn Gln Thr Phe Ser Ala Gly Leu His Leu Arg Val Phe
    50                  55                  60

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

Ala Ser Asn Asn Thr Thr Ser Ala Ala Phe Val Ser Phe Met Asn Ser
                85                  90                  95

Leu Ser Asn Asn Arg Leu Val Ala Ile Leu Thr Ser Gly Lys Val Asn
            100                 105                 110

Phe Pro Pro Glu Val Val Ser Trp Leu Arg Gly Ala Gly Thr Ser Val
        115                 120                 125

Phe Pro Ser Asp Ser Val Leu Ser Arg Phe Asp Val Ser Tyr Ala Ala
    130                 135                 140
```

```
Phe Tyr Thr Ser Ser Lys Arg Ala Ile Ala Leu Glu His Val Lys Leu
145                 150                 155                 160

Ser Asn Arg Lys Ser Thr Asp Asp Tyr Gln Thr Ile Leu Asp Val Val
                165                 170                 175

Phe Asp Ser Leu Glu Asp Val Gly Ala Thr Gly Phe Pro Lys Arg Thr
            180                 185                 190

Tyr Glu Ser Val Glu Gln Phe Met Ser Ala Val Gly Gly Thr Asn Asn
        195                 200                 205

Glu Ile Ala Arg Leu Pro Thr Ser Ala Ala Ile Ser Lys Leu Ser Asp
    210                 215                 220

Tyr Asn Leu Ile Pro Gly Asp Val Leu Tyr Leu Lys Ala Gln Leu Tyr
225                 230                 235                 240

Ala Asp Ala Asp Leu Leu Asp Leu Gly Thr Thr Asn Ile Ser Ile Arg
                245                 250                 255

Phe Tyr Asp Ala Ser Asn Gly Tyr Ile Ser Ser Thr Gln Ala Glu Phe
            260                 265                 270

Thr Gly Gln Ala Gly Ser Trp Glu Leu Lys Glu Asp Tyr Val Val Val
        275                 280                 285

Pro Glu Asn Ala Val Gly Phe Thr Ile Tyr Ala Gln Arg Thr Ala Gln
    290                 295                 300

Ala Gly Gln Gly Gly Met Arg Asn Leu Ser Phe Ser Glu Val Ser Arg
305                 310                 315                 320

Asn Gly Gly Ile Ser Lys Pro Ala Glu Phe Gly Val Asn Gly Ile Arg
                325                 330                 335

Val Asn Tyr Val Cys Glu Ser Ala Ser Pro Pro Asp Ile Met Val Leu
            340                 345                 350

Pro Thr Gln Ala Ser Ser Lys Thr Gly Lys Val Phe Gly Gln Glu Phe
        355                 360                 365

Arg Glu Val
    370


<210> 437
<211> 1289
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08
```

<400> 437
Met Ala Glu Ile Lys Arg Lys Phe Arg Ala Glu Asp Gly Leu Asp Ala
1   5   10   15

Gly Gly Asp Lys Ile Ile Asn Val Ala Leu Ala Asp Arg Thr Val Gly
            20   25   30

Thr Asp Gly Val Asn Val Asp Tyr Leu Ile Gln Glu Asn Thr Val Gln
        35   40   45

Gln Tyr Asp Pro Thr Arg Gly Tyr Leu Lys Asp Phe Val Ile Ile Tyr
    50   55   60

Asn Asn Arg Phe Trp Ala Ala Thr Asp Asn Ile Pro Lys Pro Ala Gly
65   70   75   80

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

Thr Thr Val Ser Ser Gly Pro Tyr Gln Leu Lys Ser Gly Glu Ala Ile
            100   105   110

Ser Val Asp Thr Ser Val Gly Asn Asp Ile Glu Phe Thr Leu Pro Pro
        115   120   125

Ser Pro Leu Asp Gly Glu Thr Val Ile Ile Gln Asp Ile Gly Gly Lys
    130   135   140

Pro Gly Ile Asn Gln Val Lys Ile Asn Ser Ser Asn Gln Ser Ile Val
145   150   155   160

Asn Phe Arg Gly Glu Gln Val Arg Ser Val Leu Met Thr His Pro Lys
                165   170   175

Ser Gln Met Ile Phe Ile Phe Asn Asn Arg Leu Trp Gln Met Tyr Val
            180   185   190

Ala Asp Tyr Ser Arg Glu Ala Ala Ile Val Thr Pro Ser Thr Ala Tyr
        195   200   205

Gln Ala Gln Ser Asn Asp Phe Ile Val Arg Arg Phe Thr Ser Ala Ala
    210   215   220

Pro Ile Asn Val Lys Leu Pro Arg Phe Ala Asn His Gly Asp Ile Ile
225   230   235   240

Asn Phe Val Asp Leu Asp Lys Leu Asn Pro Leu Tyr His Thr Ile Val
                245   250   255

Thr Thr Tyr Asp Glu Thr Thr Ser Val Gln Glu Val Gly Thr His Ser
            260   265   270

```
Ile Glu Gly Arg Thr Ser Ile Asp Gly Phe Leu Met Phe Asp Asp Asn
        275                 280                 285

Glu Lys Leu Trp Arg Leu Phe Asp Gly Asp Ser Lys Ala Arg Leu Arg
    290                 295                 300

Ile Ile Thr Thr Asn Ser Asn Ile Arg Pro Asn Glu Glu Val Met Val
305                 310                 315                 320

Phe Gly Ala Asn Asn Gly Thr Thr Gln Thr Ile Glu Leu Gln Leu Pro
                325                 330                 335

Thr Asp Ile Ser Val Gly Asp Thr Val Lys Ile Ser Met Asn Tyr Met
            340                 345                 350

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

Ala Ser Ser Val Gln Leu Leu Gln Phe Pro Lys Arg Ser Glu Tyr Pro
    370                 375                 380

Pro Glu Ala Glu Trp Val Thr Val Gln Glu Leu Val Phe Asn Gly Glu
385                 390                 395                 400

Thr Asn Tyr Val Pro Val Leu Gln Leu Ala Tyr Ile Glu Asp Ser Asp
                405                 410                 415

Gly Lys Tyr Trp Val Val Gln Gln Asn Val Pro Thr Val Glu Arg Val
            420                 425                 430

Asp Ser Leu Asn Ala Ser Thr Arg Ala Arg Leu Gly Val Ile Ala Leu
        435                 440                 445

Ala Thr Gln Ala Gln Ala Asn Ala Asp Leu Glu Asn Ser Pro Gln Lys
    450                 455                 460

Glu Leu Ala Ile Thr Pro Glu Thr Leu Ala Asn Arg Thr Ala Thr Glu
465                 470                 475                 480

Thr Arg Arg Gly Ile Ala Arg Ile Ala Thr Thr Ala Gln Val Asn Gln
                485                 490                 495

Asn Thr Thr Phe Ser Phe Ala Asp Asp Leu Ile Ile Thr Pro Lys Lys
            500                 505                 510

Leu Asn Glu Arg Thr Ala Thr Glu Thr Arg Arg Gly Val Ala Glu Ile
        515                 520                 525

Ala Thr Gln Gln Glu Thr Asn Thr Gly Thr Asp Asp Thr Thr Ile Ile
    530                 535                 540
```

```
Thr Pro Lys Lys Leu Gln Ala Arg Gln Gly Ser Glu Ser Leu Ser Gly
545                 550                 555                 560

Ile Val Thr Phe Val Ser Thr Ala Gly Ala Thr Pro Ala Ser Ser Arg
                565                 570                 575

Glu Leu Asn Gly Thr Asn Val Tyr Asn Lys Asn Thr Asn Asn Leu Val
            580                 585                 590

Val Ser Pro Lys Ala Leu Asp Gln Tyr Lys Ala Thr Pro Thr Gln Gln
        595                 600                 605

Gly Ala Val Ile Leu Ala Val Glu Ser Glu Val Ile Ala Gly Gln Ser
    610                 615                 620

Gln Glu Gly Trp Ala Asn Ala Val Val Thr Pro Glu Thr Leu His Lys
625                 630                 635                 640

Lys Thr Ser Thr Asp Gly Arg Ile Gly Leu Ile Glu Ile Ala Thr Gln
                645                 650                 655

Ser Glu Val Asn Thr Gly Thr Asp Tyr Thr Arg Ala Val Thr Pro Lys
            660                 665                 670

Thr Leu Asn Asp Arg Arg Ala Thr Glu Ser Leu Ser Gly Ile Ala Glu
        675                 680                 685

Ile Ala Thr Gln Val Glu Phe Asp Ala Gly Val Asp Asp Thr Arg Ile
    690                 695                 700

Ser Thr Pro Leu Lys Ile Lys Thr Arg Phe Asn Ser Thr Asp Arg Thr
705                 710                 715                 720

Ser Val Val Ala Leu Ser Gly Leu Val Glu Ser Gly Thr Leu Trp Asp
                725                 730                 735

His Tyr Thr Leu Asn Ile Leu Glu Ala Asn Glu Thr Gln Arg Gly Thr
            740                 745                 750

Leu Arg Val Ala Thr Gln Val Glu Ala Ala Ala Gly Thr Leu Asp Asn
        755                 760                 765

Val Leu Ile Thr Pro Lys Lys Leu Leu Gly Thr Lys Ser Thr Glu Ser
    770                 775                 780

Gln Glu Gly Val Ile Lys Val Ala Thr Gln Ser Glu Thr Val Thr Gly
785                 790                 795                 800

Thr Ser Ala Asn Thr Ala Val Ser Pro Lys Asn Leu Lys Trp Ile Val
                805                 810                 815
```

```
Gln Ser Glu Pro Thr Trp Ala Ala Thr Thr Leu Ile Arg Gly Phe Val
            820                 825                 830

Lys Thr Ser Ser Gly Ser Leu Thr Phe Val Gly Asn Asp Thr Val Gly
        835                 840                 845

Ser Thr Gln Pro Leu Glu Ser Tyr Glu Lys Asn Gly Tyr Ala Val Ser
    850                 855                 860

Pro Tyr Glu Leu Asn Arg Val Leu Ala Asn Tyr Leu Pro Leu Lys Ala
865                 870                 875                 880

Lys Ala Val Asp Ser Asn Leu Leu Asp Gly Leu Asp Ser Leu Gln Phe
                885                 890                 895

Ile Arg Arg Asp Ile Ala Gln Thr Val Asn Gly Ser Leu Thr Leu Thr
            900                 905                 910

Gln Gln Thr Asn Leu Gly Ala Pro Leu Val Ser Ser Ser Thr Ala Thr
        915                 920                 925

Phe Gly Gly Ser Val Ser Ala Asn Ser Thr Leu Thr Ile Ser Asn Thr
    930                 935                 940

Gly Thr Ala Thr Arg Leu Ile Phe Glu Lys Gly Pro Gln Thr Gly Thr
945                 950                 955                 960

Asn Pro Ala Gln Thr Met Thr Val Arg Val Trp Gly Asn Gln Phe Ser
                965                 970                 975

Gly Glu Ser Asp Thr Thr Arg Ser Thr Val Phe Glu Val Ser Asp Glu
            980                 985                 990

Thr Ser Ser His Phe Tyr Ser Gln  Arg Asn Lys Ala Gly  Asn Ile Thr
        995                 1000                1005

Phe Asn  Ile Asn Gly Thr Val  Thr Pro Ile Asn Val  Asn Ala Ser
    1010                1015                1020

Gly Thr  Leu Asn Ala Asn Gly  Val Ala Thr Phe Gly  Asn Ser Val
    1025                1030                1035

Thr Ala  Thr Gly Glu Ile Ile  Ser Arg Ser Ala Asn  Ala Phe Arg
    1040                1045                1050

Ala Ile  Asn Gly Asn Tyr Gly  Phe Ile Val Arg Asn  Asp Gly Ser
    1055                1060                1065

Val Thr  Asn Phe Met Leu Thr  Ala Ser Gly Asp Gln  Thr Gly Gly
    1070                1075                1080
```

```
Phe Asn  Gly Leu Arg Pro Leu  Ala Ile Asn Asn Ala  Ser Gly Gln
    1085                 1090                 1095

Val Thr  Ile Gly Glu Ser Leu  Ile Ile Ala Lys Gly  Ala Thr Ile
    1100                 1105                 1110

Asn Ser  Gly Gly Leu Thr Val  Asn Ser Arg Ile Arg  Ser Gln Gly
    1115                 1120                 1125

Thr Lys  Thr Ser Asp Leu Tyr  Thr Arg Ala Pro Thr  Ser Asp Thr
    1130                 1135                 1140

Val Gly  Phe Trp Ser Ile Asp  Ile Asn Asp Ser Ala  Thr Tyr Asn
    1145                 1150                 1155

Gln Phe  Pro Gly Tyr Phe Lys  Met Val Glu Lys Thr  Asn Glu Val
    1160                 1165                 1170

Thr Gly  Leu Pro Tyr Leu Glu  Arg Gly Glu Glu Val  Lys Ser Pro
    1175                 1180                 1185

Gly Thr  Leu Thr Gln Phe Gly  Asn Thr Leu Asp Ser  Leu Tyr Gln
    1190                 1195                 1200

Asp Trp  Ile Thr Tyr Pro Thr  Thr Pro Glu Ala Arg  Thr Thr Arg
    1205                 1210                 1215

Trp Thr  Arg Thr Trp Gln Lys  Thr Lys Asn Ser Trp  Ser Ser Phe
    1220                 1225                 1230

Val Gln  Val Phe Asp Gly Gly  Asn Pro Pro Gln Pro  Ser Asp Ile
    1235                 1240                 1245

Gly Ala  Ile Pro Ser Asp Asn  Gly Ile Ile Gly Asn  Leu Thr Ile
    1250                 1255                 1260

Arg Asp  Phe Leu Arg Ile Gly  Asn Val Arg Ile Ile  Pro Asp Pro
    1265                 1270                 1275

Val Asn  Lys Thr Val Lys Phe  Glu Trp Val Glu
    1280                 1285
```

<210> 438
<211> 305
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 438
Met Asp Leu Glu Met Met Leu Asp Glu Asp Tyr Lys Glu Gly Ile Cys

1 5 10 15

Phe Ile Asp Phe Ser Gln Ile Ala Leu Ser Thr Ala Leu Val Asn Phe
20 25 30

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

Asn Ser Ile Lys Phe Asn Val Lys Lys Ala Lys Thr Leu Gly Tyr Thr
50 55 60

Lys Ile Val Leu Cys Ile Asp Asn Ala Lys Ser Gly Tyr Trp Arg Arg
65 70 75 80

Asp Phe Ala Tyr Tyr Tyr Lys Lys Asn Arg Gly Lys Ala Arg Glu Glu
85 90 95

Ser Thr Trp Asp Trp Glu Gly Tyr Phe Glu Ser Ser His Lys Val Ile
100 105 110

Asp Glu Leu Lys Ala Tyr Met Pro Tyr Ile Val Met Asp Ile Asp Lys
115 120 125

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

Glu Gly His Lys Ile Leu Ile Ile Ser Ser Asp Gly Asp Phe Thr Gln
145 150 155 160

Leu His Lys Tyr Pro Asn Val Lys Gln Trp Ser Pro Met His Lys Lys
165 170 175

Trp Val Lys Ile Lys Ser Gly Ser Ala Glu Ile Asp Cys Met Thr Lys
180 185 190

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

Ser Asp Phe Trp Phe Thr Arg Val Glu Gly Glu Arg Thr Pro Ser Met
210 215 220

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

Val Leu Leu Thr Glu Ser Glu Tyr Asn Arg Tyr Lys Glu Asn Leu Val
245 250 255

Leu Ile Asp Phe Asp Tyr Ile Pro Asp Asn Ile Ala Ser Asn Ile Val
260 265 270

Asn Tyr Tyr Asn Ser Tyr Lys Leu Pro Pro Arg Gly Lys Ile Tyr Ser

275 280 285

Tyr Phe Val Lys Ala Gly Leu Ser Lys Leu Thr Asn Ser Ile Asn Glu
290 295 300

Phe
305

<210> 439
<211> 89
<212> PRT
<213> Unknown

<220>
<223>
Bacteriophage F488/08

<400> 439
Met Ala Lys Lys Glu Met Val Glu Phe Asp Glu Ala Ile His Gly Glu
1 5 10 15

Asp Leu Ala Lys Phe Ile Lys Glu Ala Ser Asp His Lys Leu Lys Ile
20 25 30

Ser Gly Tyr Asn Glu Leu Ile Lys Asp Ile Arg Ile Arg Ala Lys Asp
35 40 45

Glu Leu Gly Val Asp Gly Lys Met Phe Asn Arg Leu Leu Ala Leu Tyr
50 55 60

His Lys Asp Asn Arg Asp Val Phe Glu Ala Glu Thr Glu Glu Val Val
65 70 75 80

Glu Leu Tyr Asp Thr Val Phe Ser Lys
85

<210> 440
<211> 112
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 440
Met Thr Gln Phe Ser Leu Asn Asp Ile Arg Pro Val Asp Glu Thr Gly
1 5 10 15

Leu Ser Glu Lys Glu Leu Ser Ile Lys Lys Glu Lys Asp Glu Ile Ala
20 25 30

Lys Leu Leu Asp Arg Gln Glu Asn Gly Phe Ile Ile Glu Lys Met Val
35 40 45

Glu Glu Phe Gly Met Ser Tyr Leu Glu Ala Thr Thr Ala Phe Leu Glu
50 55 60

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


Ile Ile Glu Lys Ile Gln Ser Glu Ala Ile Asp Glu Asn Leu Leu Arg
                85                  90                  95


Pro Ser Val Val Arg Cys Glu Lys Thr Asn Thr Leu Asp Phe Leu Leu
            100                 105                 110


<210> 441
<211> 217
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 441
Met Ile Lys Leu Arg Met Pro Ala Gly Gly Glu Arg Tyr Ile Asp Gly
1               5                   10                  15


Lys Ser Val Tyr Lys Leu Tyr Leu Met Ile Lys Gln His Met Asn Gly
            20                  25                  30


Lys Tyr Asp Val Ile Lys Tyr Asn Trp Cys Met Arg Val Ser Asp Ala
        35                  40                  45


Ala Tyr Gln Lys Arg Arg Asp Lys Tyr Phe Phe Gln Lys Leu Ser Glu
    50                  55                  60


Lys Tyr Lys Leu Lys Glu Leu Ala Leu Ile Phe Ile Ser Asn Leu Val
65                  70                  75                  80


Ala Asn Gln Asp Ala Trp Ile Gly Asp Ile Ser Asp Ala Asp Ala Leu
                85                  90                  95


Val Phe Tyr Arg Glu Tyr Ile Gly Arg Leu Lys Gln Ile Lys Phe Lys
            100                 105                 110


Phe Glu Glu Asp Ile Arg Asn Ile Tyr Tyr Phe Ser Lys Lys Val Glu
        115                 120                 125


Val Ser Ala Phe Lys Glu Ile Phe Glu Tyr Asn Pro Lys Val Gln Ser
    130                 135                 140


Ser Tyr Ile Phe Lys Leu Leu Gln Ser Asn Ile Ile Ser Phe Glu Thr
145                 150                 155                 160


Phe Ile Leu Leu Asp Ser Phe Leu Asn Ile Ile Asp Lys His Asp Glu
                165                 170                 175


Gln Thr Asp Asn Leu Val Trp Asn Asn Tyr Ser Ile Lys Leu Lys Ala
```

180 185 190

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

Ile Glu Thr Val Lys Ser Cys Lys Tyr
210 215

<210> 442
<211> 302
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 442
Met Phe Lys Arg Lys Ser Thr Ala Glu Leu Ala Ala Gln Met Ala Lys
1 5 10 15

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

Lys Leu Lys Leu Asp Asn Ala Gly Asn Gly Gln Ala Val Ile Arg Phe
35 40 45

Leu Pro Ser Lys Asn Asp Glu Gln Ala Pro Phe Ala Leu Leu Val Asn
50 55 60

His Gly Phe Lys Lys Asn Gly Lys Trp Tyr Ile Glu Thr Cys Ser Ser
65 70 75 80

Thr Tyr Gly Asp Tyr Asp Ser Cys Pro Val Cys Gln Tyr Ile Ser Lys
85 90 95

Asn Asp Leu Tyr Asn Thr Asp Asn Lys Glu Tyr Ser Leu Val Lys Arg
100 105 110

Lys Thr Ser Tyr Trp Ala Asn Ile Leu Val Val Lys Asp Pro Ala Ala
115 120 125

Pro Glu Asn Glu Gly Lys Val Phe Lys Tyr Arg Phe Gly Lys Lys Ile
130 135 140

Trp Asp Lys Ile Asn Ala Met Ile Ala Val Asp Val Glu Met Gly Glu
145 150 155 160

Thr Pro Val Asp Val Thr Cys Pro Trp Glu Gly Ala Asn Phe Val Leu
165 170 175

Lys Val Lys Gln Val Ser Gly Phe Ser Asn Tyr Asp Glu Ser Lys Phe
180 185 190

Leu Asn Gln Ser Ala Ile Pro Asn Ile Asp Asp Glu Ser Phe Gln Lys
        195   200   205

Glu Leu Phe Glu Gln Met Val Asp Leu Ser Glu Met Thr Ser Lys Asp
    210   215   220

Lys Phe Lys Ser Phe Glu Glu Leu Ser Thr Lys Phe Ser Gln Val Met
225   230   235   240

Gly Thr Ala Ala Met Gly Gly Ala Ala Ala Thr Ala Ala Lys Lys Ala
                245   250   255

Asp Lys Val Ala Asp Asp Leu Asp Ala Phe Asn Val Asp Asp Phe Lys
            260   265   270

Thr Lys Thr Glu Asp Asp Phe Met Ser Ser Ser Ser Gly Ser Ser Ser
        275   280   285

Ser Ala Asp Asp Thr Asp Leu Asp Asp Leu Leu Asn Asp Leu
    290   295   300

<210> 443
<211> 76
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 443
Met Ala Lys Val Asp Ile Asp Ile Val Asp Phe Glu Tyr Ile Glu Glu
1   5   10   15

Ile Ile Arg Asn Arg Tyr Pro Glu Leu Ser Ile Thr Ser Ile His Asp
            20   25   30

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

Asp Leu Thr Arg Phe Met Ala Asn Glu Tyr Cys Asp Gly Met Asp Ser
    50   55   60

Glu Asp Ala Glu Phe Tyr Met Gly Leu Ile Glu Gln
65   70   75

<210> 444
<211> 121
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 444
Met Tyr Ile Gly Lys Lys Tyr Glu Leu Val Pro Arg Leu Ile Asp Thr
1   5   10   15

Phe Ile Asn Tyr Arg Pro Arg Ser Asn Ser Ser Ile Val Lys Ile Ile
            20   25   30

Gln Glu Asn Gly Gly Trp Phe Glu Val Lys Glu Ala Phe Phe Val Asp
        35   40   45

Gly Phe Arg Val Ile Lys His Ile Glu Cys Ala Asn Gly Lys His Phe
    50   55   60

Tyr Phe Asn Val Cys Glu Asp Glu Phe His Cys Phe Arg Glu Tyr Lys
65   70   75   80

Glu Pro Thr Ser Glu Glu Asp Gly Ala Glu Asp Ile Val Ser Gly Val
                85   90   95

Thr Lys Ile His Cys Ile Val Asp Glu Asn Asn Val Asp Glu Ile Ile
            100   105   110

Glu Leu Leu Arg Lys Thr Phe Lys Lys
        115   120

<210> 445
<211> 80
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 445
Met Arg Leu Gln Arg Gln Ser Ile Lys Asp Ser Glu Val Arg Gly Lys
1   5   10   15

Trp Tyr Phe Asn Ile Ile Gly Lys Asp Ser Glu Leu Val Glu Lys Ala
            20   25   30

Glu His Leu Leu Arg Asp Met Gly Trp Glu Asp Glu Cys Asp Gly Cys
        35   40   45

Pro Leu Tyr Glu Asp Gly Glu Ser Ala Gly Phe Trp Ile Tyr His Ser
    50   55   60

Asp Val Asp Gln Phe Lys Ala Asp Trp Lys Ile Val Lys Lys Ser Val
65   70   75   80

<210> 446
<211> 110
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 446

Met Ser Gly Ile His Val Thr Gly Ile Ala Gln Val Asn Ile Arg Cys
1 5 10 15

Gln Phe Lys Thr Val Pro Gly Val Thr His Ile Thr Leu Ser His Asp
20 25 30

Pro Tyr Ser Arg Gly Arg Gln Leu Thr Gly Val Ile Lys Phe Phe Gly
35 40 45

Gly Ile Gly Gly Ser Glu Phe Thr Ile Gly Asp Asp Glu Ile Val Gly
50 55 60

Cys Lys Leu Lys Val Gln Lys Gly Val Leu Glu Leu Phe Ser Asp Glu
65 70 75 80

Val Phe Asp Glu Ile Ser Arg Ala Val Asn Lys Gly Met Leu Thr Leu
85 90 95

Ile Lys Met Ile Lys Ala Ser Gly Tyr Val Thr Asp Pro Phe
100 105 110

<210> 447
<211> 81
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 447
Met Ile Phe Val Phe Glu Phe Met Asn Asp Glu Phe Asp Tyr Ala Ile
1 5 10 15

Phe Asn Ala Leu His Asn Pro Asp Leu Ser Glu Phe Asn Glu Met Phe
20 25 30

Ser Asp Ala Leu Ser Met Ser Glu Glu Tyr Cys Gly Glu Cys Gln Arg
35 40 45

Val Cys Val Thr Val Phe Glu Asn Lys Glu Lys Thr Tyr Glu Glu Leu
50 55 60

Phe Phe Asp Ala Asn Lys Ala Thr Glu Trp Phe Val Glu Arg Gly Phe
65 70 75 80

Ala

<210> 448
<211> 193
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 448
Met Ile Lys Leu Val Phe Ala Tyr Ser Pro Thr Lys Thr Val Glu Gly
1 5 10 15

Phe Asn Glu Leu Ala Phe Gly Leu Gly Asp Gly Leu Pro Trp Gly Arg
20 25 30

Ile Lys Lys Asp Leu Gln Asn Phe Lys Ala Arg Thr Glu Gly Thr Ile
35 40 45

Leu Ile Met Gly Ala Lys Thr Phe Gln Ser Leu Ser Thr Leu Leu Pro
50 55 60

Gly Arg Ser His Ile Val Val Cys Asp Leu Ala Arg Asp Tyr Pro Val
65 70 75 80

Thr Lys Asp Gly Asp Leu Ala His Phe Tyr Ile Thr Trp Glu Gln Tyr
85 90 95

Ile Thr Tyr Ile Ser Gly Gly Glu Ile Gln Val Ser Ser Pro Asn Ala
100 105 110

Pro Phe Glu Thr Met Leu Gly Gln Asn Ser Lys Val Ser Val Ile Gly
115 120 125

Gly Pro Ala Leu Leu Tyr Ala Ala Leu Pro Tyr Ala Asp Glu Val Val
130 135 140

Val Ser Arg Ile Val Lys Arg His Arg Val Asn Ser Thr Val Gln Leu
145 150 155 160

Asp Ala Ser Phe Leu Asp Asp Ile Ser Lys Arg Glu Met Val Glu Thr
165 170 175

His Trp Tyr Lys Ile Asp Glu Val Thr Thr Leu Thr Glu Ser Val Tyr
180 185 190

Lys

<210> 449
<211> 68
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 449
Met Ser Asn Lys Leu Lys Val Lys Asp Val Pro Asn Ala Met Ala Leu
1 5 10 15

Phe Ile Cys Arg Gln Met His Gln Gly Pro Met Thr Pro Lys Gln Tyr

20 25 30

Leu Lys Gly Glu Arg Ser Leu Gly Phe Thr Arg Lys Ala Lys Gln Met
35 40 45

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

Ser Trp Met Asn
65

<210> 450
<211> 183
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 450
Met Lys Gln Tyr Gln Phe Leu Ile Lys Asp Ile Leu Glu Asn Gly Tyr
1 5 10 15

Glu Thr Asp Asp Arg Thr Gly Thr Gly Thr Ile Ala Leu Phe Gly Thr
20 25 30

Lys Leu Arg Trp Asp Leu Thr Lys Gly Phe Pro Ala Val Thr Thr Lys
35 40 45

Lys Leu Ala Trp Asn Ala Cys Ile Ser Glu Leu Leu Trp Phe Leu Ser
50 55 60

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

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

Asp Leu Gly Tyr His Ser Gly Glu Leu Gly Pro Ile Tyr Gly Lys Gln
100 105 110

Trp Arg Asp Phe Gly Gly Val Asp Gln Ile Ile Glu Val Ile Asp Arg
115 120 125

Ile Lys Lys Leu Pro Asn Asp Arg Arg Gln Ile Val Ser Ala Trp Asn
130 135 140

Pro Ala Glu Leu Lys Gln Met Ala Leu Pro Pro Cys His Met Phe Tyr
145 150 155 160

Gln Phe Asn Val Arg Asn Gly Tyr Leu Asp Leu Gln Trp Tyr Gln Arg
165 170 175

Ser Val Asp Val Phe Leu Gly
            180

<210> 451
<211> 245
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 451
Met Lys Ser Gly Ile Tyr Gln Ile Lys Asn Thr Leu Asn Asn Lys Val
1   5   10   15

Tyr Val Gly Ser Ala Lys Asp Phe Glu Lys Arg Trp Lys Arg His Phe
            20   25   30

Lys Asp Leu Glu Lys Gly Cys His Ser Ser Ile Lys Leu Gln Arg Ser
        35   40   45

Phe Asn Lys His Gly Asn Val Phe Glu Cys Ser Ile Leu Glu Glu Ile
    50   55   60

Pro Tyr Glu Lys Asp Leu Ile Ile Glu Arg Glu Asn Phe Trp Ile Lys
65   70   75   80

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

Gly Asp Thr Cys Ser Thr His Pro Leu Lys Glu Glu Ile Ile Lys Lys
            100   105   110

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

Arg Lys Ala Leu Tyr Ser Lys Pro Gly Ser Lys Asn Gly Arg Trp Asn
    130   135   140

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

Ala Tyr Thr Cys Ser Lys Cys Arg Asn Arg Ser Gly Glu Asn Asn Ser
                165   170   175

Phe Phe Asn His Lys His Ser Asp Ile Thr Lys Ser Lys Ile Ser Glu
            180   185   190

Lys Met Lys Gly Lys Lys Pro Ser Asn Ile Lys Lys Ile Ser Cys Asp
        195   200   205

Gly Val Ile Phe Asp Cys Ala Ala Asp Ala Ala Arg His Phe Lys Ile
    210   215   220

Ser Ser Gly Leu Val Thr Tyr Arg Val Lys Ser Asp Lys Trp Asn Trp
225 230 235 240

Phe Tyr Ile Asn Ala
245

<210> 452
<211> 104
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 452
Met Leu Pro Phe Asn Ile Ala Ser Tyr Ala Thr Leu Val His Ile Val
1 5 10 15

Ala Lys Met Cys Asn Leu Ile Pro Gly Asp Leu Ile Phe Ser Gly Gly
20 25 30

Asn Thr His Ile Tyr Met Asn His Val Glu Gln Cys Lys Glu Ile Leu
35 40 45

Arg Arg Glu Pro Lys Glu Leu Cys Glu Leu Val Ile Gly Gly Leu Pro
50 55 60

Tyr Lys Phe Arg Tyr Leu Ser Thr Lys Glu Gln Leu Glu Tyr Ile Leu
65 70 75 80

Lys Leu Arg Pro Lys Asp Phe Val Leu Lys Asp Tyr Gln Ser His Gly
85 90 95

Val Leu Lys Gly Lys Met Ala Val
100

<210> 453
<211> 87
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 453
Met Ile Leu Arg Phe Lys Asp Thr Ser Gly Ala Val Leu Phe Thr Leu
1 5 10 15

Pro Asn Pro Ser Glu Leu Glu Val Pro Gly Pro Asn Gln Pro Ile Ile
20 25 30

Ile Tyr Gly Lys Lys Tyr Tyr Thr His Lys Met Thr Arg Glu Tyr Phe
35 40 45

Asp Asn Lys Ile Ser Thr Val Lys Thr Ser Ser Asp Cys Tyr Tyr Asp

50 55 60

Ile Thr Val Leu Thr Glu Lys Gln Tyr Asp Glu Leu Ser Pro Arg Gly
65 70 75 80

Pro Ser Met Pro Gly Ser Glu
85

<210> 454
<211> 108
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 454
Met Thr Asn Tyr His Arg Ala Gly Arg Leu Cys Gln Val Val Asn Lys
1 5 10 15

Tyr Lys Ser Asp Phe Asp Val Asn Ile His Arg Gly Thr Phe Trp Gly
20 25 30

Asn Tyr Val Gly Lys Asp Ala Gly Ser Arg Glu Ala Ala Ile Glu Leu
35 40 45

Phe Lys Lys Asp Phe Ile Arg Arg Ile Lys Ser Gly Glu Ile Thr Lys
50 55 60

Ala His Leu Glu Pro Leu Arg Gly Met Arg Leu Gly Cys Thr Cys Lys
65 70 75 80

Pro Lys Pro Cys His Gly Asp Ile Ile Ala His Ile Val Asn Arg Leu
85 90 95

Phe Lys Asp Asp Phe Gln Val Glu Asp Leu Cys Asn
100 105

<210> 455
<211> 754
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 455
Met Gln Leu Ile Asn Val Ile Lys Ser Ser Gly Val Ser Gln Ser Phe
1 5 10 15

Asp Pro Gln Lys Ile Ile Lys Val Leu Ser Trp Ala Ala Glu Gly Thr
20 25 30

Ser Val Asp Pro Tyr Glu Leu Tyr Glu Asn Ile Lys Ser Tyr Leu Arg
35 40 45

```
Asp Gly Met Thr Thr Asp Asp Ile Gln Thr Ile Val Ile Lys Ala Ala
    50                  55                  60

Ala Asn Ser Ile Ser Val Glu Glu Pro Asp Tyr Gln Tyr Val Ala Ala
65                  70                  75                  80

Arg Cys Leu Met Phe Ala Leu Arg Lys His Val Tyr Gly Gln Tyr Glu
                85                  90                  95

Pro Arg Ser Phe Ile Asp His Ile Ser Tyr Cys Val Asn Glu Gly Lys
            100                 105                 110

Tyr Asp Pro Glu Leu Leu Ser Lys Tyr Ser Ala Glu Glu Ile Thr Phe
        115                 120                 125

Leu Glu Ser Lys Ile Lys His Glu Arg Asp Met Glu Phe Thr Tyr Ser
    130                 135                 140

Gly Ala Met Gln Leu Lys Glu Lys Tyr Leu Val Lys Asp Lys Thr Thr
145                 150                 155                 160

Gly Gln Ile Tyr Glu Thr Pro Gln Phe Ala Phe Met Thr Ile Gly Met
                165                 170                 175

Ala Leu His Gln Asp Glu Pro Val Asp Arg Leu Lys His Val Ile Arg
            180                 185                 190

Phe Tyr Glu Ala Val Ser Thr Arg Gln Ile Ser Leu Pro Thr Pro Ile
        195                 200                 205

Met Ala Gly Cys Arg Thr Pro Thr Arg Gln Phe Ser Ser Cys Val Val
    210                 215                 220

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

Ile Val Glu Tyr Ile Ser Lys Arg Ala Gly Ile Gly Ile Asn Val Gly
                245                 250                 255

Met Ile Arg Ala Glu Gly Ser Lys Ile Gly Met Gly Glu Val Arg His
            260                 265                 270

Thr Gly Val Ile Pro Phe Trp Lys His Phe Gln Thr Ala Val Lys Ser
        275                 280                 285

Cys Ser Gln Gly Gly Ile Arg Gly Gly Ala Ala Thr Ala Tyr Tyr Pro
    290                 295                 300

Ile Trp His Leu Glu Val Glu Asn Leu Leu Val Leu Lys Asn Asn Lys
305                 310                 315                 320
```

```
Gly Val Glu Glu Asn Arg Ile Arg His Met Asp Tyr Gly Val Gln Leu
                325                 330                 335

Asn Asp Leu Met Met Glu Arg Phe Gly Lys Asn Asp Tyr Ile Thr Leu
            340                 345                 350

Phe Ser Pro His Glu Met Gly Gly Glu Leu Tyr Tyr Ser Tyr Phe Lys
        355                 360                 365

Asp Gln Asp Arg Phe Arg Glu Leu Tyr Glu Ala Ala Glu Lys Asp Pro
    370                 375                 380

Asn Ile Arg Lys Lys Arg Ile Lys Ala Arg Glu Leu Phe Glu Leu Leu
385                 390                 395                 400

Met Thr Glu Arg Ser Gly Thr Ala Arg Ile Tyr Val Gln Phe Ile Asp
                405                 410                 415

Asn Thr Asn Asn Tyr Thr Pro Phe Ile Arg Glu Lys Ala Pro Ile Arg
            420                 425                 430

Gln Ser Asn Leu Cys Cys Glu Ile Ala Ile Pro Thr Asn Asp Val Asn
        435                 440                 445

Ser Pro Asp Ala Glu Ile Gly Leu Cys Thr Leu Ser Ala Phe Val Leu
    450                 455                 460

Asp Asn Phe Asp Trp Gln Asp Gln Asp Lys Ile Asn Glu Leu Ala Glu
465                 470                 475                 480

Val Gln Val Arg Ala Leu Asp Asn Leu Leu Asp Tyr Gln Gly Tyr Pro
                485                 490                 495

Val Pro Glu Ala Glu Lys Ala Lys Lys Arg Arg Asn Leu Gly Val Gly
            500                 505                 510

Val Thr Asn Tyr Ala Ala Trp Leu Ala Ser Asn Phe Ala Ser Tyr Glu
        515                 520                 525

Asp Ala Asn Asp Leu Thr His Glu Leu Phe Glu Arg Leu Gln Tyr Gly
    530                 535                 540

Leu Ile Lys Ala Ser Ile Lys Leu Ala Lys Glu Lys Gly Pro Cys Glu
545                 550                 555                 560

Tyr Tyr Ser Asp Thr Arg Trp Ser Arg Gly Glu Leu Pro Ile Asp Trp
                565                 570                 575

Tyr Asn Lys Lys Ile Asp Gln Ile Ala Ala Pro Lys Tyr Val Cys Asp
            580                 585                 590
```

Trp Ser Ser Leu Arg Glu Asp Leu Lys Leu Phe Gly Ile Arg Asn Ser
595 600 605

Thr Leu Ser Ala Leu Met Pro Cys Glu Ser Ser Ser Gln Val Ser Asn
610 615 620

Ser Thr Asn Gly Ile Glu Pro Pro Arg Gly Pro Val Ser Val Lys Glu
625 630 635 640

Ser Lys Glu Gly Ser Phe Asn Gln Val Val Pro Asn Ile Glu His Asn
645 650 655

Ile Asp Leu Tyr Asp Tyr Thr Trp Lys Leu Ala Lys Lys Gly Asn Lys
660 665 670

Pro Tyr Leu Thr Gln Val Ala Ile Met Leu Lys Trp Val Cys Gln Ser
675 680 685

Ala Ser Ala Asn Thr Tyr Tyr Asp Pro Gln Ile Phe Pro Lys Gly Lys
690 695 700

Val Pro Met Ser Ile Met Ile Asp Asp Leu Leu Tyr Phe Trp Tyr Phe
705 710 715 720

Gly Gly Lys Asn Phe Tyr Tyr His Asn Thr Arg Asp Gly Ser Gly Thr
725 730 735

Asp Asp Tyr Glu Ile Glu Thr Pro Lys Ala Glu Asp Cys Ser Ser Cys
740 745 750

Lys Leu

<210> 456
<211> 392
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 456
Met Ser Thr Val Phe Asn Thr Asn Pro Val Asp Val Leu Lys Glu Pro
1 5 10 15

Met Phe Phe Gly Ser Gly Leu Gly Ile Ala Arg Tyr Asp Ile Gln Arg
20 25 30

His Lys Val Phe Glu Asp Leu Thr Glu Lys Gln Leu Ser Phe Phe Trp
35 40 45

Arg Pro Glu Glu Val Asn Leu Met Met Asp Ala Ala Gln Phe Asn Lys
50 55 60

```
Leu Pro Gln Tyr Gln Gln Asn Ile Phe Thr Asn Asn Leu Lys Tyr Gln
65                  70                  75                  80

Ser Leu Leu Asp Ser Ile Gln Gly Arg Ala Pro Ser Ala Val Leu Met
                85                  90                  95

Ser Leu Ile Ser Asp Pro Ser Leu Asp Thr Trp Val Ala Thr Trp Thr
            100                 105                 110

Phe Ser Glu Thr Ile His Ser Arg Ser Tyr Thr His Ile Met Arg Asn
        115                 120                 125

Leu Tyr Thr Asp Pro Ser Lys Val Phe Asp Glu Ile Val Leu Asp Glu
    130                 135                 140

Ala Ile Met Lys Arg Ala Glu Ser Ile Gly Arg Tyr Tyr Asp Asp Val
145                 150                 155                 160

Leu Ile Lys Thr Arg Tyr Trp Glu Asn Ala Lys Ala Asp Ile Glu Tyr
                165                 170                 175

Gln Lys Glu Ile Asn Ala Asp Glu Asp Val Ile Glu Asp Ala Ile Glu
            180                 185                 190

His Glu Thr Tyr Trp Lys Arg Glu Leu Met Lys Ser Leu Tyr Leu Cys
        195                 200                 205

Leu His Val Ile Asn Ala Leu Glu Ala Ile Arg Phe Tyr Val Ser Phe
    210                 215                 220

Ala Cys Thr Phe Asn Phe His Lys Asn Met Glu Ile Met Glu Gly Asn
225                 230                 235                 240

Ala Lys Ile Met Lys Phe Ile Ala Arg Asp Glu Gln Leu His Leu Lys
                245                 250                 255

Gly Thr Gln Tyr Ile Ile Arg Gln Leu Gln Leu Gly Thr Asp Gly Asp
            260                 265                 270

Glu Trp Val Lys Ile Ala Gln Glu Cys Glu Gln Glu Ala Val Asp Ile
        275                 280                 285

Phe Met Glu Val Asn Arg Gln Glu Lys Asp Trp Ala Val His Leu Phe
    290                 295                 300

Lys Asp Gly Asp Val Pro Gly Leu Asn Thr Asn Ser Met Trp Ser Phe
305                 310                 315                 320

Ile Asp Tyr Leu Thr Val Ser Arg Met Lys Gln Cys Gly Leu Pro Cys
                325                 330                 335
```

```
Pro Ile Thr Asp Ala Pro Val Lys His Pro Tyr Pro Trp Ile Arg Glu
            340                 345                 350

Tyr Leu Asn Ser Asp Asn Val Gln Ser Ala Pro Gln Glu Val Glu Leu
        355                 360                 365

Ser Ser Tyr Leu Val Ala Gln Ile Asp Asn Asp Val Asp Asp Lys Val
    370                 375                 380

Met Met Ser Phe Lys Lys Tyr Phe
385                 390


<210> 457
<211> 136
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 457
Met Lys Glu Ile Ala Thr Glu Tyr Ser Phe Ile Lys Tyr Thr Glu Leu
1               5                   10                  15

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

Tyr Asn Val Ile Tyr Ala Ile Ala Ile Asn Asp Glu Leu Val Tyr Ile
        35                  40                  45

Gly Lys Thr Lys Asn Leu Arg Lys Arg Ile Asn Tyr Tyr Arg Thr Ala
    50                  55                  60

Ile Asn Arg Lys Asp Lys Thr Ser Asp Ser Thr Lys Ser Ala Leu Ile
65                  70                  75                  80

His Ala Ala Leu Lys Glu Gly Ser Lys Val Glu Phe Tyr Ala Arg Gln
                85                  90                  95

Cys Phe Asn Leu Ser Met Thr Asn Glu Leu Gly Thr Met Thr Ile Ala
            100                 105                 110

Thr Ile Asp Leu Glu Glu Pro Leu Phe Ile Lys Leu Phe Asn Pro Pro
        115                 120                 125

Trp Asn Ile Gln His Lys Lys Lys
    130                 135


<210> 458
<211> 374
<212> PRT
<213> Unknown
```

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 458
Met Gln Glu Leu Phe Asn Asn Leu Met Glu Leu Cys Lys Asp Ser Gln
1   5   10   15

Arg Lys Phe Phe Tyr Ser Asp Asp Val Ser Ala Ser Gly Arg Thr Tyr
            20   25   30

Arg Ile Phe Ser Tyr Asn Tyr Ala Ser Tyr Ser Asp Trp Leu Leu Pro
        35   40   45

Asp Ala Leu Glu Cys Arg Gly Ile Met Phe Glu Met Asp Gly Glu Lys
    50   55   60

Pro Val Arg Ile Ala Ser Arg Pro Met Glu Lys Phe Phe Asn Leu Asn
65   70   75   80

Glu Asn Pro Phe Thr Met Asn Ile Asp Leu Asn Asp Val Asp Tyr Ile
                85   90   95

Leu Thr Lys Glu Asp Gly Ser Leu Val Ser Thr Tyr Leu Asp Gly Asp
            100   105   110

Glu Ile Leu Phe Lys Ser Lys Gly Ser Ile Lys Ser Glu Gln Ala Leu
        115   120   125

Met Ala Asn Gly Ile Leu Met Asn Ile Asn His His Arg Leu Arg Asp
    130   135   140

Arg Leu Lys Glu Leu Ala Glu Asp Gly Phe Thr Ala Asn Phe Glu Phe
145   150   155   160

Val Ala Pro Thr Asn Arg Ile Val Leu Ala Tyr Gln Glu Met Lys Ile
                165   170   175

Ile Leu Leu Asn Val Arg Glu Asn Glu Thr Gly Glu Tyr Ile Ser Tyr
            180   185   190

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

Tyr Glu Ile Asp Ser Pro Lys Trp Val Glu Glu Ala Lys Asn Ala Glu
    210   215   220

Asn Ile Glu Gly Tyr Val Ala Val Met Lys Asp Gly Ser His Phe Lys
225   230   235   240

Ile Lys Ser Asp Trp Tyr Val Ser Leu His Ser Thr Lys Ser Ser Leu
                245   250   255

```
Asp Asn Pro Glu Lys Leu Phe Lys Thr Ile Ile Asp Gly Ala Ser Asp
            260                 265                 270

Asp Leu Lys Ala Met Tyr Ala Asp Asp Glu Tyr Ser Tyr Arg Lys Ile
        275                 280                 285

Glu Ala Phe Glu Thr Thr Tyr Leu Lys Tyr Leu Asp Arg Ala Leu Phe
    290                 295                 300

Leu Val Leu Asp Cys His Asn Lys His Cys Gly Lys Asp Arg Lys Thr
305                 310                 315                 320

Tyr Ala Met Glu Ala Gln Gly Val Ala Lys Gly Ala Gly Met Asp His
                325                 330                 335

Leu Phe Gly Ile Ile Met Ser Leu Tyr Gln Gly Tyr Asp Ser Gln Glu
            340                 345                 350

Lys Val Met Cys Glu Ile Glu Gln Asn Phe Leu Lys Asn Tyr Lys Lys
        355                 360                 365

Phe Ile Pro Glu Gly Tyr
    370


<210> 459
<211> 167
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 459
Met Asp Leu Gln Leu Ile Thr Thr Glu Met Val Val Glu Ala Tyr Gly
1               5                   10                  15

Asp Thr Thr Asp Gly Ile Ser Val Phe Lys Gly Asn Arg Arg Val Gly
            20                  25                  30

Tyr Ile Thr Asp Leu Lys Lys Asp Leu Ala Lys Gln Val Lys Arg Lys
        35                  40                  45

Thr Thr Ile Lys Glu Tyr Arg Asn Arg Arg Leu Glu Gln Ala Arg Asp
    50                  55                  60

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

Leu Ala Lys Tyr Asp Cys Asp Val Phe Ile Asn Gln Thr Gln Pro Asn
                85                  90                  95

Val His Ile Asn Ser Cys Lys Cys Tyr Ile Ile Val Asn Pro Leu Thr
            100                 105                 110
```

Gly Lys His Arg Leu Gly Ile Ser Asn Pro Asn Arg Ser Ala Ser Asp
        115   120   125

Met Ala Glu Asp Val Glu Ala Cys Phe Lys Ile Ser Lys Ser Pro Ala
    130   135   140

Glu His His Ile Leu Ile Asn Gly Leu Ser Gln Asp Asp Ile Ile Glu
145   150   155   160

Val Ile Lys Thr Leu Cys Met
                165

<210> 460
<211> 117
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 460
Met His Val Ser Asn Phe Thr Ala Gly Leu Leu Leu Leu Val Ile Ala
1   5   10   15

Phe Gly Gly Thr Ser Ile Ile Leu Lys Asn Lys Val Glu Arg Leu Glu
            20   25   30

Thr Ser Val Thr Glu Ile Thr Lys Thr Ala Asn Glu Asn Ala Leu Ala
        35   40   45

Leu Asn Asn Leu Arg Ile Gln Tyr Asn Tyr Ile Asp Ala Met Asn Asn
    50   55   60

Lys Asn Arg Glu Ala Ile Ala Ala Ile Glu Arg Glu Asn Glu Lys Leu
65   70   75   80

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

Val Glu Lys Gln Ile Asn Asn Ser Phe Asn Lys Phe Ala Glu Asp Ile
            100   105   110

Gln Asp Leu Ser Lys
        115

<210> 461
<211> 99
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 461
Met Ile Lys Leu Ser Ala Val Ile Leu Ser Ile Gly Leu Leu Val Gly

1 5 10 15

Cys Ser Thr Lys Pro Leu Glu Val Lys Lys Glu Thr Val His Pro Asn
20 25 30

Trp Pro Val Gln Ile Lys Ser Tyr Asp Glu Ala Lys Leu Ser Trp Gln
35 40 45

Val Lys Val Ile Asp Gly Lys Ala Trp Val Gly Met Pro Phe Glu Asp
50 55 60

Ser Gln Glu Phe Arg Ile Trp Leu Asn Asp Val Lys Arg Tyr Val His
65 70 75 80

Asp Gln Lys Thr Met Ile Cys Tyr Tyr Arg Gln Glu Leu Lys Glu Asp
85 90 95

Lys Cys Lys

<210> 462
<211> 76
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 462
Met Ile Ser Trp Tyr Gln Phe Glu His Leu Lys Gly Leu Ile Tyr Glu
1 5 10 15

Ser Glu Met Ala Ala Met Ile Tyr Gly Arg Gln Ile Gln Arg Leu Glu
20 25 30

Ser Leu Pro Pro Thr Asn Asp Val Leu Leu Ala Gln Ser Arg Ala Asn
35 40 45

Leu Lys Asn Glu Tyr Gln Asn Lys Trp Gly Lys Ala Ser Lys Asp Leu
50 55 60

His Asp Tyr Ile Gln Ser Leu Val Glu Lys Asn Lys
65 70 75

<210> 463
<211> 100
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 463
Met Lys Thr Leu Leu Glu Arg Tyr Ile Glu Cys Ser Asp Arg Tyr Ile
1 5 10 15

Asp Val Cys His Asp Asn Ala Ser Ser Ile Ser Glu Asp Ile Glu His
20 25 30

Ala Lys Ala Leu Asp Asp Ala Gly Lys Ala Leu Arg Lys Glu Ala Lys
35 40 45

Ala Arg Gly Phe Asp Met Tyr Gln Leu Lys Asn His Met Ile Lys Phe
50 55 60

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

Leu Tyr Lys Gly Arg Arg Glu His Asn Ile Arg Ile Leu Glu Val Phe
85 90 95

Leu Gly Ile Lys
100

<210> 464
<211> 301
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 464
Met Met Lys Lys Ile Ile Leu Thr Ile Gly Cys Pro Gly Ser Gly Lys
1 5 10 15

Ser Thr Trp Ala Arg Glu Phe Ile Ala Lys Asn Pro Gly Phe Tyr Asn
20 25 30

Ile Asn Arg Asp Asp Tyr Arg Gln Ser Ile Met Ala His Glu Glu Arg
35 40 45

Asp Glu Tyr Lys Tyr Thr Lys Asn Lys Glu Gly Ile Val Thr Tyr Met
50 55 60

Gln His Asp Val Ala Asn Met Ile Leu Cys Gln Asp Ala Thr Lys Gly
65 70 75 80

Val Ile Val Ser Asp Thr Asn Leu Asn Pro Glu Arg Arg Lys Val Trp
85 90 95

Glu Glu Phe Ala Lys Glu Leu Gly His Gln Ile Glu Tyr Lys Val Phe
100 105 110

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

Lys Ala Val Pro Ile Asp Val Leu Arg Ser Met Tyr Lys Ser Met Arg
130 135 140

```
Glu Tyr Leu Gly Leu Pro Val Tyr Lys Gly Thr Pro Gly Lys Pro Lys
145                 150                 155                 160

Ala Val Ile Phe Asp Val Asp Gly Thr Leu Ala Lys Met Asn Gly Arg
                165                 170                 175

Gly Pro Tyr Asp Leu Glu Lys Cys Asp Ile Asp Ile Ile Asn Pro Met
            180                 185                 190

Val Val Glu Leu Ser Lys Met Tyr Ala Leu Met Gly Tyr Gln Ile Val
        195                 200                 205

Val Val Ser Gly Arg Glu Ser Gly Thr Glu Glu Asp Pro Thr Lys Tyr
    210                 215                 220

Tyr Arg Met Thr Arg Lys Trp Val Glu Asp Ile Ala Gly Val Pro Leu
225                 230                 235                 240

Val Met Gln Cys Gln Arg Glu Gln Gly Asp Thr Arg Lys Asp Asp Val
                245                 250                 255

Val Lys Glu Glu Ile Phe Trp Lys His Ile Ala Pro His Phe Asp Val
            260                 265                 270

Lys Leu Ala Ile Asp Asp Arg Thr Gln Val Val Glu Met Trp Arg Arg
        275                 280                 285

Ile Gly Val Glu Cys Trp Gln Val Ala Ser Gly Asp Phe
    290                 295                 300


<210> 465
<211> 58
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 465
Leu Gly Phe Val Ile Val Asn Ser Gly Leu Val Gly Thr Ser Asn Gly
1               5                   10                  15

Gln Phe Cys Val Phe Thr Ser Glu Asn Arg Ala Trp Glu Glu Cys Leu
            20                  25                  30

Lys Leu Arg Glu Lys Asn Pro Asp Val Glu Leu Val Val Lys Lys Thr
        35                  40                  45

Lys Leu Pro Leu Pro Trp Lys Thr Tyr Glu
    50                  55


<210> 466
```

<211> 66
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 466
Met Asn Asn Leu Glu Lys Ile Tyr Arg Leu Cys Asp Lys Ile Glu Lys
1   5   10   15

Glu Lys Lys Tyr Leu Phe Cys Leu Trp Pro Ile Val Asp Gly Arg Val
            20   25   30

Gly Leu Asp Val Leu Asp Tyr Glu Thr Glu Asp Lys Val Asp Gly Ala
        35   40   45

Thr Phe Asp Asn Ala Leu Asp Val Ile Asp Trp Leu Glu Glu Asn Tyr
    50   55   60

Val Arg
65

<210> 467
<211> 91
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 467
Met Phe Pro Thr Tyr Ser Lys Ile Val Glu Val Val Phe Ser Gln Ile
1   5   10   15

Ile Ala Asn Asn Met Phe Glu Lys Leu Asp Asn Ala Ala Glu Leu Arg
            20   25   30

Ile His Ala Gln Val Thr His Val Leu Asn Ala Leu Leu Pro Asp Gln
        35   40   45

Val Asp Ser Ile Ala Ile Thr Leu Tyr Pro Gly Ser Ala His Ile Ile
    50   55   60

Val Val Phe Gly Leu Asp Ala Glu Leu Val Ile Lys Gly Asp Ile Arg
65   70   75   80

Phe Glu Ser Gln Thr Ser Glu Phe Lys Ala Ile
                85   90

<210> 468
<211> 175
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 468
Met Ser Glu Trp Phe Glu Glu Asp Lys Val Tyr Arg Phe Lys Ala Gly
1 5 10 15

Tyr Lys Asp Ile Phe Asn Glu Thr Cys Gly Ala Asn Lys Arg Ile Ala
20 25 30

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

Asn Val Ile Ser Ile Lys Arg Glu Ile Asp Asp Cys Trp Tyr Lys Ala
50 55 60

Val Asp Val Met Gly Glu Ser Tyr Lys Val Ser Pro Leu Phe Ser Ile
65 70 75 80

Ala Tyr Met Leu Glu Tyr Ser Phe Phe Glu Glu Val Gln Lys Asp Asp
85 90 95

Ser Val Ser Lys Phe Glu Ile Lys Thr Asp Lys Glu Ile Lys Trp Lys
100 105 110

Val Val Gly Ile Thr Gly Cys Met Phe Tyr Ile Tyr Ala Gln Thr Asp
115 120 125

Thr Lys Glu Glu Ala Lys Lys Lys Ala Leu Glu Tyr Leu Glu Glu His
130 135 140

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

Lys Leu Val Lys Asn Val Glu Ser Lys Glu Leu Gly Ser Thr Cys
165 170 175

<210> 469
<211> 78
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 469
Met Leu Ser Glu Lys Pro Ile Thr Val Lys Glu Phe Gln Glu Lys Val
1 5 10 15

Lys Leu Phe Ala Gln Glu Leu Val Asn Lys Val Ser Glu Arg Phe Pro
20 25 30

Glu Thr Ser Val Arg Val Ile Thr Glu Thr Pro Arg Ser Val Leu Val
35 40 45

Ile Val Asn Pro Gly Asp Gly Asp Gln Ile Ser His Leu Lys Leu Asp

50 55 60

Phe Asp Gly Leu Val Glu Ala Gln Arg Val Tyr Gly Val Leu
65 70 75

<210> 470
<211> 112
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 470
Met Met Asn Leu Thr Asp Ile Ile Asp Asn Cys Leu Glu Asn Asp Thr
1 5 10 15

Gly Asp His Arg Ala Leu Asp Ser Glu Thr Ala Gln Phe Ile Arg Ile
20 25 30

Thr Leu Met Asn Asp Thr Leu Val Asn Ser Ile His Pro Ser Val Tyr
35 40 45

Asp Ala Ile Ile Val Thr Lys Tyr Pro Val Glu Leu His Lys Lys Met
50 55 60

Thr Gly Ala Val Phe Ile Asp Lys Lys Asn Arg Phe Lys Asp Gly Gln
65 70 75 80

Asn Ile Thr Ser Ser Val Ile Lys Ser Ile Thr Lys Leu Arg His Glu
85 90 95

Ile Tyr Arg Val Glu Thr Ala Lys Ser Ala Tyr Leu Val Ile Met Lys
100 105 110

<210> 471
<211> 193
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 471
Met Lys Ala Ser Thr Val Leu Gln Ile Ala Tyr Leu Val Ser Gln Glu
1 5 10 15

Ser Lys Cys Cys Ser Trp Lys Val Gly Ala Val Ile Glu Lys Asn Gly
20 25 30

Arg Ile Ile Ser Thr Gly Tyr Asn Gly Ser Pro Ala Gly Gly Val Asn
35 40 45

Cys Cys Asp Tyr Ala Ala Glu Gln Gly Trp Leu Leu Asn Lys Pro Lys
50 55 60

```
His Thr Ile Ile Gln Gly His Lys Pro Glu Cys Val Ser Phe Gly Ser
65                  70                  75                  80


Thr Asp Arg Phe Val Leu Ala Lys Glu His Arg Ser Ala His Ser Glu
                85                  90                  95


Trp Ser Ser Lys Asn Glu Ile His Ala Glu Leu Asn Ala Ile Leu Phe
            100                 105                 110


Ala Ala Arg Asn Gly Ser Ser Ile Glu Gly Ala Thr Met Tyr Val Thr
        115                 120                 125


Leu Ser Pro Cys Pro Asp Cys Ala Lys Ala Ile Ala Gln Ser Gly Ile
    130                 135                 140


Lys Lys Leu Val Tyr Cys Glu Thr Tyr Asp Lys Asn Lys Pro Gly Trp
145                 150                 155                 160


Asp Asp Ile Leu Arg Asn Ala Gly Ile Glu Val Phe Asn Val Pro Lys
                165                 170                 175


Lys Asn Leu Asn Lys Leu Asn Trp Glu Asn Ile Asn Glu Phe Cys Gly
            180                 185                 190


Glu



<210> 472
<211> 78
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 472
Met Lys Phe Arg Leu Val Lys Leu Thr Ala Ile Ser Ser Tyr Ser Asn
1               5                   10                  15


Glu Asn Ile Ser Phe Ala Val Glu Tyr Lys Lys Tyr Phe Phe Ser Lys
            20                  25                  30


Trp Lys Gln Tyr Tyr Lys Thr Asp Trp Thr Ser Ile Asp Arg Pro Tyr
        35                  40                  45


Ser Trp Lys Ser Asp Leu Glu Lys Cys Gln Lys Leu Leu Ser Thr Leu
    50                  55                  60


Lys Glu Arg Gly Thr Thr His Ile Lys Thr Val Ile Gly Lys
65                  70                  75


<210> 473
<211> 102
```

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 473
Met Lys Leu Thr Thr Glu Gln Lys Val Ala Ile Arg Glu Ile Leu Lys
1   5   10   15

Thr Lys Leu Ser Met Gly Ile Ser Asn Val Val Phe Glu Lys Ser Asp
            20   25   30

Gly Thr Ile Arg Ile Met Lys Cys Thr Arg Asp Ala Asp Phe Met Pro
        35   40   45

Thr Met Gln Thr Gly Lys Leu Thr Glu Ser Thr Arg Lys Glu Ser Thr
    50   55   60

Asp Met Ile Pro Val Phe Asp Val Glu Leu Gly Ala Trp Arg Gly Phe
65   70   75   80

Ser Ile Asp Lys Leu Ile Ser Val Asn Gly Met Lys Val Glu His Leu
                85   90   95

Leu Gln Phe Ile Gly Lys
            100

<210> 474
<211> 111
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 474
Met Ser Glu Val Gln Gln Leu Pro Ile Arg Ala Val Gly Glu Tyr Val
1   5   10   15

Ile Leu Val Ser Glu Pro Ala Gln Ala Gly Asp Glu Glu Val Thr Glu
            20   25   30

Ser Gly Leu Ile Ile Gly Lys Arg Ile Gln Gly Glu Val Pro Glu Leu
        35   40   45

Cys Val Val His Ser Val Gly Pro Asp Val Pro Glu Gly Phe Cys Glu
    50   55   60

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

His Pro Phe Val Ala Leu Gly Leu Lys Gln Pro Lys Glu Ile Lys Gln
                85   90   95

Lys Phe Val Thr Cys His Tyr Lys Ala Ile Pro Cys Leu Tyr Lys
100 105 110

<210> 475
<211> 82
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 475
Met Ile Lys Gln Leu Gln His Ala Leu Glu Leu Gln Arg Asn Ala Trp
1 5 10 15

Asn Asn Gly His Glu Asn Tyr Gly Ala Ser Ile Asp Val Glu Ala Glu
20 25 30

Ala Leu Glu Ile Leu Arg Tyr Phe Lys His Leu Asn Pro Ala Gln Thr
35 40 45

Ala Leu Ala Ala Glu Leu Gln Glu Lys Asp Glu Leu Lys Tyr Ala Lys
50 55 60

Pro Leu Ala Ser Ala Ala Arg Lys Ala Val Arg His Phe Val Val Thr
65 70 75 80

Leu Lys

<210> 476
<211> 72
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 476
Met Pro Ile Ser Pro Ala Phe Ser Phe Lys Arg Glu Phe Ile Met Ala
1 5 10 15

Lys Gln Val Lys Ala Lys Lys Ala Val Glu Lys Lys Val Gly Asp Ser
20 25 30

Lys Arg Ala Gly Tyr Lys Arg Gly Ser Asn Ser Arg Ile Asn Gln Thr
35 40 45

Val Glu Lys Ile Met Arg Arg Ala Arg Ala Val Leu Arg Asp Asp Ala
50 55 60

Ser Arg Phe Gly Lys Gln Lys Ala
65 70

<210> 477
<211> 121

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 477
Met Asn Tyr Ile Asn Phe Glu Arg Lys Tyr Val Ser Asn Gly Ile Ala
1   5   10   15

Gly Ser Ile Asp Thr Ile Cys Leu Trp Lys His Gln Asn Gly Ser Val
            20   25   30

Cys Glu Ile Asp Gln Tyr Met Thr Pro Asn Tyr Val Tyr Met Arg Phe
        35   40   45

Glu Asn Gly Ile Thr Val Ser Ile Thr Lys Glu Gly Ser Asn Phe Lys
    50   55   60

Ile Ala Leu Asp Asp Asp Phe Arg Glu Arg Asp Leu Gly Thr His Pro
65   70   75   80

Cys Trp Asn Gly Val His Arg Lys Leu Leu Ile Lys Thr Trp Ile Arg
                85   90   95

His Ile Leu Ser Asn Lys Ala Lys Pro Glu His Leu Glu Ala Ile Phe
            100   105   110

Asp Val Val Leu Asn Glu Phe Asp Ile
        115   120

<210> 478
<211> 95
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 478
Met Phe Met Thr Thr Tyr Phe Asp Thr Arg Lys Asn Phe Cys Glu Val
1   5   10   15

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

Ser Glu Ser Ile Lys Asn Tyr Val Asn Val Val Cys Pro Leu Glu Phe
        35   40   45

Arg Thr Val Asn Gly Arg Asp Thr Leu Ala Ile Thr Lys Leu Asn Arg
    50   55   60

Glu Ile Asp Ile Asp Pro Ser Ile Ala Arg Glu Ile Asn Ser Ser Asp
65   70   75   80

Ile Asn Gly Gly Asn Val Lys Ser His Gly Phe Gln Met Arg Phe
85 90 95

<210> 479
<211> 65
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 479
Met Lys Phe Phe Leu Gly Gln Thr Val Glu Leu Lys Gly Val Gly Ile
1 5 10 15

Pro Gly Leu Ile Ser Lys Val Leu Pro Pro Phe Lys Trp Ser Gly Ile
20 25 30

Gln Ile Lys Glu Ala Tyr Ile Val Ser Trp Val Asp Gly Asn Glu Asp
35 40 45

Leu Arg Met Gly Asp Glu Leu Ser Pro Ile Tyr Gly Leu Lys Glu Leu
50 55 60

Val
65

<210> 480
<211> 68
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 480
Met Asn Ile Ile Asn Lys Ile Phe Gly Ile Gln Tyr Ile Lys Val Thr
1 5 10 15

Tyr Lys Val Thr Asp Lys Asn Pro Tyr Thr Asp Glu His Glu Glu Pro
20 25 30

Gln Val Lys Ser Ile Ile Leu Glu Lys Gly Ser Asp Trp Pro Val Glu
35 40 45

Phe Arg Leu Pro Asn Tyr Gly His Trp Ala Asp Val Glu Ile Ile Ser
50 55 60

Ile Glu Asn Val
65

<210> 481
<211> 152
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F488/08

<400> 481
Met Ser Glu Leu Glu Ile Arg Ser Asn Phe Lys Trp Pro Ser Cys Ala
1   5   10   15

Leu Ser Asn Phe Ala Gln Trp Pro Phe Val Met Asp Gly Ile Gln Phe
            20   25   30

Gly Gly Leu Glu Gly Phe Leu Gln Gly Cys Lys Val Lys Asn Val Glu
        35   40   45

Gln Gln Arg Arg Ile Phe Gly Leu Ser Gly Leu Ala Ala Gln Gln Ala
    50   55   60

Gly Arg Ser Tyr Ala Arg Ala Gln Asp Arg Gly Thr Leu Phe Trp Leu
65   70   75   80

Gly Val Pro Phe Ser Arg Tyr Ser Pro Ala Trp Lys Glu Leu Tyr Thr
                85   90   95

Asn Ala Tyr Phe Glu Ala Ala Ile Gln Asn Lys Gly Phe Arg Asp Ala
            100   105   110

Leu His Ala Ser Lys Gly Lys Val Leu Lys His Ser Met Ala Ser Gly
        115   120   125

Leu Thr Lys Asp Asp Thr Ile Leu Thr Glu Ala Glu Phe Ile Asp Val
    130   135   140

Leu Asn Leu Leu Arg Asp Ser Leu
145   150

<210> 482
<211> 279
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 482
Met Lys Pro Thr Ile Leu Thr Asp Ile Asp Gly Val Cys Leu Ser Trp
1   5   10   15

Gln Ser Gly Leu Pro Tyr Phe Ala Gln Lys Tyr Asn Leu Pro Leu Glu
            20   25   30

His Ile Leu Lys Met Ile Gln Asp Glu Lys Phe Ile Ser Pro Gly Lys
        35   40   45

Leu Phe Asn Cys Asp Glu Glu Leu Gly Val Lys Leu Ile Glu Lys Tyr
    50   55   60

```
Asn Arg Ser Asp Phe Ile Arg Tyr Leu Ser Pro Tyr Lys Asp Ala Leu
65                  70                  75                  80

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

Ala Leu Gly Asp Ser Ile Asp Ala Leu Leu Asn Arg Gln Phe Asn Leu
            100                 105                 110

Asn Ala Leu Phe Pro Gly Ala Phe Ser Glu Val Leu Met Cys Gly His
        115                 120                 125

Asp Ser Ser Lys Glu Glu Leu Phe Lys Lys Ala Lys Glu Lys Tyr Asn
    130                 135                 140

Val Ile Cys Tyr Ile Asp Asp Leu Ala His His Cys Asp His Ala Ser
145                 150                 155                 160

Glu Ile Leu Asn Val Pro Val Tyr Trp Met Ala Arg Gly Glu Arg Asp
                165                 170                 175

Ser Ile Pro Lys Thr Ala Gln Arg Val Tyr Thr Trp Asn Asp Val Glu
            180                 185                 190

Asn Lys Leu Phe Ser Pro Lys Glu Asn Lys Glu Ser Phe Asp Ser Glu
        195                 200                 205

Lys Ala Ile Lys Asp Val Ile Glu Lys Met Ile Lys Asn Asp Ser Phe
    210                 215                 220

Pro Trp Asn Thr Thr Trp Arg Thr Pro Gly Phe Asn Pro Tyr Asn His
225                 230                 235                 240

Leu Tyr His Pro Tyr Gln Thr His Pro Phe Gln Thr Trp Asn Tyr Ile
                245                 250                 255

Lys Pro Gly Gly Ile Glu Tyr Leu Tyr Asn Arg Pro Thr Ser Gly Asp
            260                 265                 270

Asn Ile Phe Gln Gly Ala Phe
        275
```

<210> 483
<211> 89
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 483

```
Met Phe Val Val His Thr Ile Tyr Glu Asn Glu Gly Asn Thr Thr Arg
1               5                   10                  15
```

```
Asp Tyr Gly His Val Asn Gln Phe Phe Arg Cys Asn Pro Glu Phe Arg
            20                  25                  30

Ala Gln Lys Asp Glu Arg Ile Phe Lys Lys Cys Val Glu Gln Gly Phe
        35                  40                  45

Ile Tyr Val Lys His Trp Met Gln Gly Asn Lys Val Arg Thr Thr Tyr
    50                  55                  60

His Arg Ser Leu Thr Glu Leu Asn Asp Glu Leu Ile Tyr Asn Arg Ala
65                  70                  75                  80

Val Asn Gln Thr Leu Lys Asp Glu Gln
                85
```

<210> 484
<211> 487
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 484

```
Met Ile Leu Lys Ile Leu Asn Glu Ile Ala Ser Ile Gly Ser Thr Lys
1               5                   10                  15

Gln Lys Gln Ala Ile Leu Glu Lys Asn Lys Asp Asn Glu Leu Leu Lys
            20                  25                  30

Arg Val Tyr Arg Leu Thr Tyr Ser Arg Gly Leu Gln Tyr Tyr Ile Lys
        35                  40                  45

Lys Trp Pro Lys Pro Gly Ile Ala Thr Gln Ser Phe Gly Met Leu Thr
    50                  55                  60

Leu Thr Asp Met Leu Asp Phe Ile Glu Phe Thr Leu Ala Thr Arg Lys
65                  70                  75                  80

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

Gly Lys Lys Asp Asp Val Glu Val Leu Arg Arg Val Met Met Arg Asp
            100                 105                 110

Leu Glu Cys Gly Ala Ser Val Ser Ile Ala Asn Lys Val Trp Pro Gly
        115                 120                 125

Leu Ile Pro Glu Gln Pro Gln Met Leu Ala Ser Ser Tyr Asp Glu Lys
    130                 135                 140

Gly Ile Asn Lys Asn Ile Lys Phe Pro Ala Phe Ala Gln Leu Lys Ala
145                 150                 155                 160
```

```
Asp Gly Ala Arg Cys Phe Ala Glu Val Arg Gly Asp Glu Leu Asp Asp
                165                 170                 175

Val Arg Leu Leu Ser Arg Ala Gly Asn Glu Tyr Leu Gly Leu Asp Leu
            180                 185                 190

Leu Lys Glu Glu Leu Ile Lys Met Thr Thr Glu Ala Arg Gln Ile His
        195                 200                 205

Pro Glu Gly Val Leu Ile Asp Gly Glu Leu Val Tyr His Glu Gln Val
    210                 215                 220

Glu Lys Glu Pro Glu Gly Leu Asp Phe Leu Phe Asp Ala Tyr Pro Glu
225                 230                 235                 240

Ile Ser Lys Ala Lys Glu Phe Ala Glu Val Ala Glu Ser Arg Thr Ala
                245                 250                 255

Ser Asn Gly Ile Ala Asn Lys Ser Leu Lys Gly Thr Ile Ser Glu Lys
            260                 265                 270

Glu Ala Gln Cys Met Lys Phe Gln Val Trp Asp Tyr Val Pro Leu Val
        275                 280                 285

Glu Ile Tyr Gly Leu Pro Ala Phe Arg Leu Lys Tyr Asp Val Arg Phe
    290                 295                 300

Ser Lys Leu Glu Gln Met Thr Ser Gly Tyr Asp Lys Val Ile Leu Ile
305                 310                 315                 320

Glu Asn Gln Val Val Asn Asn Leu Asp Glu Ala Lys Val Ile Tyr Lys
                325                 330                 335

Lys Tyr Ile Asp Gln Gly Leu Glu Gly Ile Ile Leu Lys Asn Thr Asp
            340                 345                 350

Gly Leu Trp Glu Asn Ala Arg Ser Lys Asn Leu Tyr Lys Phe Lys Glu
        355                 360                 365

Val Ile Asp Val Asp Leu Lys Ile Val Gly Ile Tyr Pro His Arg Lys
    370                 375                 380

Asp Pro Thr Lys Ala Gly Gly Phe Ile Leu Glu Ser Glu Cys Gly Lys
385                 390                 395                 400

Ile Lys Val Asn Ala Gly Ser Gly Leu Lys Asp Lys Ala Ser Val Lys
                405                 410                 415

Ser His Glu Leu Asp Arg Thr Arg Ile Met Glu Asn Gln Asn Tyr Tyr
            420                 425                 430
```

Ile Gly Lys Ile Leu Glu Cys Glu Cys Asn Gly Trp Leu Lys Ser Asp
435 440 445

Gly Arg Thr Asp Tyr Val Lys Leu Phe Leu Pro Ile Ala Ile Arg Leu
450 455 460

Arg Glu Asp Lys Thr Lys Ala Asn Thr Phe Glu Asp Val Phe Gly Asp
465 470 475 480

Phe His Glu Val Thr Gly Leu
485

<210> 485
<211> 62
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 485
Met Lys Ala Tyr Leu Glu Thr Ile Val Val Ala Gln Lys Glu Gly Gly
1 5 10 15

Asp Val Ser Thr Ser Val Ser Gln Val Ile Leu Glu Phe Val Asp Ala
20 25 30

Tyr Ala Tyr Asn Lys Phe Thr Glu Thr Phe Asp Ala Tyr Glu Lys Gly
35 40 45

Pro Lys Phe Glu Ile Tyr Arg Thr Leu Leu Pro Leu Asp Tyr
50 55 60

<210> 486
<211> 697
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 486
Met Glu Leu Ile Thr Glu Leu Phe Asp Glu Asp Thr Thr Leu Pro Ile
1 5 10 15

Thr Asn Leu Asn Pro Lys Lys Lys Ile Pro Gln Ile Phe Ser Val His
20 25 30

Val Asp Asp Ala Ile Glu Gln Pro Gly Phe Arg Leu Cys Thr Tyr Thr
35 40 45

Ser Gly Gly Asp Thr Asn Arg Asp Leu Lys Met Gly Asp Lys Met Met
50 55 60

```
His Ile Val Pro Phe Thr Leu Thr Ala Lys Gly Ser Ile Ala Lys Leu
65                  70                  75                  80

Lys Gly Leu Gly Pro Ser Pro Ile Asn Tyr Ile Asn Ser Val Phe Thr
                85                  90                  95

Val Ala Met Gln Thr Met Arg Gln Tyr Lys Ile Asp Ala Cys Met Leu
            100                 105                 110

Arg Ile Leu Lys Ser Lys Thr Ala Gly Gln Ala Arg Gln Ile Gln Val
        115                 120                 125

Ile Ala Asp Arg Leu Ile Arg Ser Arg Ser Gly Gly Arg Tyr Val Leu
    130                 135                 140

Leu Lys Glu Leu Trp Asp Tyr Asp Lys Lys Tyr Ala Tyr Ile Leu Ile
145                 150                 155                 160

His Arg Lys Asn Val Ser Leu Glu Asp Ile Pro Gly Val Pro Glu Ile
                165                 170                 175

Ser Thr Glu Leu Phe Thr Lys Val Glu Ser Lys Val Gly Asp Val Tyr
            180                 185                 190

Ile Asn Lys Asp Thr Gly Ala Gln Val Thr Lys Asn Glu Ala Ile Ala
        195                 200                 205

Ala Ser Ile Ala Gln Glu Asn Asp Lys Arg Ser Asp Gln Ala Val Ile
    210                 215                 220

Val Lys Val Lys Ile Ser Arg Arg Ala Ile Ala Gln Ser Gln Ser Leu
225                 230                 235                 240

Glu Ser Ser Arg Phe Glu Ser Glu Leu Phe Gln Lys Tyr Glu Ser Thr
                245                 250                 255

Ala Ala Asn Phe Asn Lys Pro Ala Thr Ala Pro Leu Ile Pro Glu Ala
            260                 265                 270

Glu Glu Met Lys Ile Gly Ile Asn Ser Leu Ala Ser Lys Thr Lys Ala
        275                 280                 285

Ala Lys Ile Ile Ala Glu Gly Thr Ala Asp Glu Leu His Tyr Asp Tyr
    290                 295                 300

Lys Phe Phe Pro Met Ser Gln Val Gly Glu Val Ser Glu Lys Ile Lys
305                 310                 315                 320

Glu Val Ile Phe Asn Ala Ile Lys Asn Glu Pro Thr Thr Ser Ile Lys
                325                 330                 335
```

```
Cys Leu Glu Lys Tyr Ala Ala Ala Ala Asn Gln Leu Phe Glu Glu Tyr
            340                 345                 350

Lys Asp Asn Trp Leu Asp Lys His Asn Lys Thr Arg Lys Gly Gln Pro
        355                 360                 365

Asp Glu Val Trp Glu Glu Met Thr Lys Asn Ser Trp Asn Ala Ala Lys
    370                 375                 380

Thr Lys Phe Leu Lys Arg Met Ile Tyr Ser Phe Ser Gly Ile Gly Ala
385                 390                 395                 400

Gly Pro Met Ile Asp Ile Thr Ile Ala Arg Asp Gly Ser Lys Tyr Thr
                405                 410                 415

Pro Ser Gln Lys Arg Gly Ile Arg Glu Tyr Cys Gly Ser Gly Tyr Thr
            420                 425                 430

Asp Ile Asn Asn Leu Leu Leu Gly Arg Tyr Asp Pro Glu Arg Tyr Glu
        435                 440                 445

Val Met Ser Glu Lys Glu Ile Glu Ala Ala Ile Thr Asn Leu Asp Ser
    450                 455                 460

Ala Phe Glu Asn Gly Asp Arg Ile Pro Glu Gly Ile Thr Val Tyr Arg
465                 470                 475                 480

Ala Gln Ser Met Thr Ala Pro Ile Tyr Glu Ala Leu Val Lys Asn Lys
                485                 490                 495

Val Phe Tyr Phe Arg Asn Phe Val Ser Thr Ser Leu Thr Pro Ile Ile
            500                 505                 510

Phe Gly Arg Phe Gly Ile Thr His Ala Gly Ile Gly Leu Leu Glu Pro
        515                 520                 525

Glu Ala Arg Asn Glu Leu Thr Val Asp Lys Asn Glu Glu Gly Ile Thr
    530                 535                 540

Ile Asn Pro Asn Glu Ile Arg Ala Tyr Lys Glu Asn Pro Glu Tyr Val
545                 550                 555                 560

Lys Val Gln Ile Gly Trp Ala Ile Asp Gly Ala His Lys Val Asn Val
                565                 570                 575

Val Tyr Pro Gly Ser Leu Gly Ile Ala Thr Glu Ala Glu Val Ile Leu
            580                 585                 590

Pro Arg Gly Leu Met Val Lys Val Asn Lys Ile Thr Asp Ala Ser Asn
        595                 600                 605
```

```
Asn Asp Gly Thr Thr Ser Asn Asn Thr Lys Leu Ile Gln Ala Glu Val
    610                 615                 620

Met Thr Thr Glu Glu Leu Thr Glu Ser Val Ile Tyr Asp Gly Asp His
625                 630                 635                 640

Leu Met Glu Thr Gly Glu Leu Val Ala Met Thr Gly Asp Ile Glu Ile
                645                 650                 655

Glu Asp Arg Val Asp Phe Ala Ser Phe Val Ser Ser Asn Val Lys Gln
            660                 665                 670

Lys Val Glu Ser Ser Leu Gly Ile Ile Ala Ser Cys Ile Asp Ile Thr
        675                 680                 685

Asn Met Pro Tyr Lys Phe Val Gln Gly
    690                 695

<210> 487
<211> 685
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 487
Met Glu Leu Ile Thr Glu Leu Phe Asp Gly Ala Ser Ala Pro Val Val
1               5                   10                  15

Asn Leu Asn Pro Lys His Lys Ile Pro Gln Ile Phe Ala Ile Gln Ala
            20                  25                  30

Gly Glu Glu Ser Val Leu Pro Gly Phe Arg Phe Cys Thr Tyr Thr Ser
        35                  40                  45

Gly Gly Asp Thr Asn Lys Asn Val Lys Pro Gly Asp Lys Met Met His
    50                  55                  60

Ile Val Met Ile Gly Val Asn Glu Lys Leu Ser Leu Val Lys Leu Arg
65                  70                  75                  80

Asn Leu Gly Gly Asn Pro Ile Gly Val Ile Asn Ala Val Phe Asp Thr
                85                  90                  95

Ala Leu Gln Thr Met Lys Gln Tyr Lys Ile Asp Ala Cys Leu Phe Arg
            100                 105                 110

Val Leu Lys Ser Lys Thr Asn Gly Ala Ala Arg Gln Met Gln Val Ile
        115                 120                 125

Ala Asp Arg Leu Val Arg Thr Lys Gly Ala Gly Arg Tyr Val Leu Leu
    130                 135                 140
```

```
Lys Glu Ile Trp Gly Tyr Asp Lys Lys Tyr Ala Tyr Ile Met Val Tyr
145                 150                 155                 160

Arg Lys Asn Ala Asn Leu Glu Asp Ile Pro Gly Val Pro Pro Ile Ser
                165                 170                 175

Thr Glu Leu Phe Thr Lys Val Glu Ser Lys Val Gly Asp Val Tyr Val
            180                 185                 190

Asp Val Lys Thr Gly Asn Ala Val Pro Lys Ala Val Ala Val Ala Ala
        195                 200                 205

Ser Ile Ala Leu Glu Asn Asp Lys Arg Thr Asp Gln Ala Val Ile Gln
    210                 215                 220

Lys Thr Lys Ile Ser Arg Arg Leu Ala Ala Gln Ala Gln Tyr Ser Thr
225                 230                 235                 240

Val Asp Ala Ser Leu Gln Gly Asp Ser Phe Ala Ala Lys Lys Tyr Gln
                245                 250                 255

Glu Phe Glu Ser Lys Val Pro Val Tyr Lys Ala Glu Gly Pro Met Asn
            260                 265                 270

Ser Gly Val Ile Gln Ile Gly Ser Asn Phe Ser Lys Gly Ala Ile Gly
        275                 280                 285

Gly Met Arg Ser Ala Ser Arg Phe Lys Ser Asn Asp Tyr Glu Leu Glu
    290                 295                 300

Ser Phe Arg Asn His Ile Ala Leu Ala His Ala Arg Leu Arg Asp Pro
305                 310                 315                 320

Ser Ile Lys Leu Gln Ser Asp Ile Thr Tyr Gln Gly Ser Gln Glu Tyr
                325                 330                 335

Leu Lys Asn Lys Glu Phe Phe Asp Tyr Lys Thr Asp Lys Ile Leu Ser
            340                 345                 350

Asp Leu Ala Asp Ile Asn Ile Ser Asn Ser Phe Asp Val Ile Lys Lys
        355                 360                 365

Ile Ile Asn Asp Leu Val Lys Gly Ser Lys Ala Thr Pro Asp Glu Lys
    370                 375                 380

Thr Ala Ile Ile Gln Phe Val Met Asn Gly Ile Tyr Lys Leu Ile Asn
385                 390                 395                 400

Glu Ser Ala Ala Gln Ala Tyr Glu Tyr Ala Ser Thr Glu Val Thr Pro
                405                 410                 415
```

```
Lys Gly Leu Thr Gln Ala Glu Ser Asp Val Ile Glu Asp Tyr Cys Ala
            420                 425                 430

Asp Ser Tyr Val Glu Met Asn Ser Phe Leu Leu Gly Lys Pro Asp Ser
        435                 440                 445

Thr Arg Glu Glu Tyr Met Glu Arg Ala Ile Lys His Ile Glu Thr Leu
    450                 455                 460

Asp Ser Ala Phe Ala Lys Gly Ser Val Leu Pro Pro Gly Thr Thr Leu
465                 470                 475                 480

Tyr Arg Gly Gln Glu Val Thr Phe Lys Thr Leu Arg His Asn Ile Glu
                485                 490                 495

Asn Lys Met Phe Tyr Phe Lys Asn Phe Val Ser Thr Ser Leu Lys Pro
            500                 505                 510

Asn Ile Phe Gly Glu His Gly Lys Asn Tyr Met Ala Leu Asp Asp Ser
        515                 520                 525

Gly Ala Val Phe Ser Gly Glu Gly Glu Gly Ser Ile Asp Ala Glu Asp
    530                 535                 540

Leu Met His Met Gly Ser His Ser Thr Tyr Val Asn Glu Asp Ala Glu
545                 550                 555                 560

Thr Ser Val Gly Met Val Ile Lys Gly Ala Glu Arg Ile Lys Val Ile
                565                 570                 575

Val Pro Gly His Leu Ser Gly Phe Pro Ser Glu Ala Glu Val Ile Leu
            580                 585                 590

Pro Arg Gly Ile Leu Leu Lys Ile Asn Lys Val Ser Thr Tyr Phe Met
        595                 600                 605

Lys Glu Thr Ala Tyr Asn Lys Tyr Leu Ile Glu Gly Thr Ile Val Pro
    610                 615                 620

Pro Ser Glu Gln Leu Glu Glu Ser Val Tyr Asp Gly Asp His Leu Met
625                 630                 635                 640

Glu Thr Gly Glu Val Arg Pro Met Thr Gly Phe Asn Gln Phe Leu Val
                645                 650                 655

Glu Glu Ser Lys Glu Glu Glu Asn Glu Val Ser Gln Ile Leu Ala Ser
            660                 665                 670

Leu Val Asn Ile Asn Gly Met Ser Lys Lys Phe Lys Met
        675                 680                 685
```

<210> 488
<211> 96
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 488
Met Lys Ser Ser Leu Arg Phe Leu Gly Gln Glu Leu Val Val Glu Gly
1   5   10   15

Val Ile Pro Ala Asp Asn Ala Phe Asn Glu Ala Val Tyr Asn Glu Phe
            20   25   30

Ile Lys Ile Phe Gly Thr Asp Lys Lys Phe Gly Ile Phe Pro Ser Glu
        35   40   45

Asn Phe Ser Lys Pro Glu Gln Thr Glu Ser Ile Phe Gln Gly Val Val
    50   55   60

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

Glu Asp Ser Leu Val Ala Ser Val Ala Ala Phe Ile Ser Phe Arg Lys
                85   90   95

<210> 489
<211> 321
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 489
Met Tyr Ser Leu Glu Glu Phe Asn Asn Gln Ala Ile Asn Ala Asp Phe
1   5   10   15

Gln Arg Asn Asn Met Phe Ser Cys Val Phe Ala Thr Thr Pro Ser Thr
            20   25   30

Lys Ser Ser Ser Leu Ile Ser Ser Ile Ser Asn Phe Ser Tyr Asn Asn
        35   40   45

Leu Gly Leu Asn Ser Asp Trp Leu Gly Leu Thr Gln Gly Asp Ile Asn
    50   55   60

Gln Gly Ile Thr Thr Leu Ile Thr Ala Gly Thr Gln Lys Leu Ile Arg
65   70   75   80

Lys Ser Gly Val Ser Lys Tyr Leu Ile Gly Ala Met Ser Gln Arg Thr
                85   90   95

Val Gln Ser Leu Leu Gly Ser Phe Thr Val Gly Thr Tyr Leu Ile Asp

100 105 110

Phe Phe Asn Met Ala Tyr Asn Ser Ser Gly Leu Met Ile Tyr Ser Val
115 120 125

Lys Met Pro Glu Asn Arg Leu Ser Tyr Glu Thr Asp Trp Asn Tyr Asn
130 135 140

Ser Pro Asn Ile Arg Ile Thr Gly Arg Glu Leu Asp Pro Leu Val Ile
145 150 155 160

Ser Phe Arg Met Asp Ser Glu Ala Cys Asn Tyr Arg Ala Met Gln Asp
165 170 175

Trp Val Asn Ser Val Gln Asp Pro Val Thr Gly Leu Arg Ala Leu Pro
180 185 190

Gln Asp Val Glu Ala Asp Ile Gln Val Asn Leu His Ser Arg Asn Gly
195 200 205

Leu Pro His Thr Ala Val Met Phe Thr Gly Cys Ile Pro Ile Ser Val
210 215 220

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

Asp Val Thr Phe Ala Tyr Arg Val Met Gln Ala Gly Ala Val Asp Arg
245 250 255

Gln Ala Ala Leu Glu Trp Leu Glu Ser Ala Ala Ile Asn Gly Ile Gln
260 265 270

Ser Val Leu Gly Asn Ser Gly Gly Val Thr Gly Leu Ser Asn Ser Leu
275 280 285

Ser Arg Leu Ser Arg Leu Gly Gly Thr Ala Gly Ser Ile Ser Asn Ile
290 295 300

Asn Thr Met Thr Gly Ile Val Asn Ser Gln Ser Lys Ile Leu Gly Ala
305 310 315 320

Ile

<210> 490
<211> 364
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 490

```
Met Ala Ile Val Lys Glu Ile Thr Ala Asp Leu Ile Lys Lys Ser Gly
1               5                  10                  15

Glu Lys Ile Ser Ala Gly Gln Ser Thr Lys Ser Glu Val Ala Thr Lys
            20                  25                  30

Thr Tyr Thr Ala Gln Phe Pro Thr Gly Arg Ala Ser Gly Asn Asp Thr
        35                  40                  45

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

Thr Ala Tyr Asn Met Ser Ser Arg Asp Ser Gly Ser Leu Arg Thr Met
65                  70                  75                  80

Arg Ser Asn Tyr Ser Ser Ser Ser Ser Ser Ile Leu Arg Thr Ala Arg
                85                  90                  95

Asn Thr Ile Ser Asn Thr Val Ser Lys Leu Ser Asn Gly Leu Ile Ser
            100                 105                 110

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

Leu Pro Arg Ser Lys Ser Asp Val Asp Thr Ser Ser His Arg Phe Asn
    130                 135                 140

Asp Val Gln Asp Ser Leu Ile Thr Lys Gly Gly Gly Thr Ala Thr Gly
145                 150                 155                 160

Val Leu Ser Asn Met Ala Ser Thr Ala Val Phe Gly Ala Leu Glu Ser
                165                 170                 175

Ile Thr Gln Gly Ile Met Ala Asp Asn Asn Glu Gln Ile Tyr Thr Thr
            180                 185                 190

Ala Arg Ser Met Tyr Gly Gly Ala Glu Asn Arg Thr Lys Val Phe Thr
        195                 200                 205

Trp Asp Leu Thr Pro Arg Ser Thr Glu Asp Leu Met Ala Ile Ile Asn
    210                 215                 220

Ile Tyr Gln Tyr Phe Asn Tyr Phe Ser Tyr Gly Glu Thr Gly Lys Ser
225                 230                 235                 240

Gln Tyr Ala Ala Glu Ile Lys Gly Tyr Leu Asp Glu Trp Tyr Arg Ser
                245                 250                 255

Thr Phe Ile Glu Pro Leu Thr Pro Glu Asp Ala Val Lys Asn Lys Thr
            260                 265                 270
```

```
Leu Phe Glu Lys Met Thr Ser Ser Leu Thr Asn Val Leu Val Val Ser
        275                 280                 285


Asn Pro Thr Ile Trp Met Val Lys Asn Phe Gly Ala Thr Ser Lys Phe
    290                 295                 300


Asp Gly Lys Thr Glu Ile Phe Gly Pro Cys Gln Ile Gln Ser Ile Arg
305                 310                 315                 320


Phe Asp Lys Thr Pro Asn Gly Asn Phe Asn Gly Leu Ala Ile Ala Pro
                325                 330                 335


Asn Leu Pro Ser Thr Phe Thr Leu Glu Ile Thr Met Arg Glu Ile Ile
            340                 345                 350


Thr Leu Asn Arg Ala Ser Leu Tyr Ala Gly Thr Phe
        355                 360


<210> 491
<211> 590
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 491
Met Lys Lys Pro Gln Glu Met Gln Thr Met Arg Arg Lys Val Ile Ser
1               5                   10                  15


Asp Asn Lys Pro Thr Gln Glu Ala Ala Lys Ser Ala Ser Asn Thr Leu
            20                  25                  30


Ser Gly Leu Asn Asp Ile Ser Thr Lys Leu Asp Asp Ala Gln Ala Ala
        35                  40                  45


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


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


Ser Glu Leu Ile Ala Glu Thr Val Glu Ile Gly Asn Asn Ile Asn Lys
                85                  90                  95


Glu Ile Gly Glu Ser Leu Gly Ser Lys Leu Asp Lys Leu Thr Ser Leu
            100                 105                 110


Leu Glu Gln Lys Ile Gln Thr Ala Gly Ile Gln Gln Thr Gly Thr Ser
        115                 120                 125


Leu Ala Thr Val Glu Ser Ala Ile Pro Val Lys Val Val Glu Asp Asp
    130                 135                 140
```

```
Thr Ala Glu Ser Val Gly Pro Leu Leu Pro Ala Pro Glu Ala Val Asn
145                 150                 155                 160

Asn Asp Pro Asp Ala Asp Phe Phe Pro Thr Pro Gln Pro Val Glu Pro
                165                 170                 175

Lys Gln Glu Ser Pro Glu Glu Lys Gln Lys Lys Glu Ala Phe Asn Leu
            180                 185                 190

Lys Leu Ser Gln Ala Leu Asp Lys Leu Thr Lys Thr Val Asp Phe Gly
        195                 200                 205

Phe Lys Lys Ser Ile Ser Ile Ser Asp Lys Ile Ser Ser Met Leu Phe
    210                 215                 220

Lys Tyr Thr Val Ser Ala Ala Ile Glu Ala Ala Lys Met Thr Ala Met
225                 230                 235                 240

Ile Leu Ala Val Val Val Gly Ile Asp Leu Leu Met Val His Phe Lys
                245                 250                 255

Tyr Trp Ser Asp Lys Phe Ser Gln Ala Trp Asp Leu Phe Ser Thr Asn
            260                 265                 270

Phe Thr Lys Phe Ser Ser Glu Thr Gly Thr Trp Gly Pro Leu Leu Gln
        275                 280                 285

Ser Ile Phe Gly Ser Ile Asp Lys Ile Lys Lys Leu Trp Glu Ala Gly
    290                 295                 300

Asp Trp Gly Gly Leu Thr Val Ala Ile Val Glu Gly Leu Gly Lys Val
305                 310                 315                 320

Leu Phe Asn Leu Gly Glu Leu Ile Gln Leu Gly Met Ala Lys Leu Ser
                325                 330                 335

Ala Ala Ile Leu Arg Val Ile Pro Gly Met Lys Asp Thr Ala Asp Glu
            340                 345                 350

Val Glu Gly Arg Ala Leu Glu Asn Phe Gln Asn Thr Thr Asn Ala Ser
        355                 360                 365

Leu Ser Lys Glu Asp Gln Glu Lys Val Ala Asn Tyr Gln Tyr Lys Arg
    370                 375                 380

Met Asn Asp Asp Leu Gly Pro Ile Ala Lys Gly Leu Asp Lys Ile Ala
385                 390                 395                 400

Asn Trp Lys Thr Arg Ala Ser Asn Trp Ile Arg Gly Val Asp Asn Lys
                405                 410                 415
```

```
Glu Ala Leu Thr Thr Asp Glu Glu Arg Ala Glu Glu Glu Glu Lys Leu
            420                 425                 430

Lys Gln Leu Ser Pro Glu Glu Ala Lys Ile Ala Leu Met Lys Ala Asn
        435                 440                 445

Glu Ala Arg Ala Ala Met Asn Arg Phe Asp Glu Tyr Ala Asn Ser Ala
    450                 455                 460

Asp Met Ser Lys Asp Ser Thr Val Lys Ser Val Glu Ala Ala Tyr Glu
465                 470                 475                 480

Asp Leu Lys Lys Arg Met Asp Asp Pro Asp Leu Asn Asn Ser Pro Ala
                485                 490                 495

Val Lys Lys Glu Leu Ala Ala Arg Phe Ser Lys Ile Asp Ala Thr Tyr
            500                 505                 510

Gln Glu Leu Lys Lys Asn Gln Pro Asn Ala Lys Pro Gln Thr Ser Ala
        515                 520                 525

Lys Ser Pro Glu Ala Lys Gln Val Gln Val Ile Glu Lys Asn Lys Ala
    530                 535                 540

Gln Gln Ala Pro Ile Gln Gln Ala Ser Pro Ser Ile Asn Asn Thr Asn
545                 550                 555                 560

Asn Val Ile Lys Lys Asn Thr Val Val His Asn Met Thr Pro Val Thr
                565                 570                 575

Ser Thr Thr Ala Pro Gly Val Phe Asp Ala Thr Gly Val Asn
            580                 585                 590


<210> 492
<211> 177
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 492
Met Asn Leu Lys Leu Ile Leu Pro Leu Lys Lys Val Val Leu Pro Ile
1               5                   10                  15

Ser Asn Lys Glu Val Ser Ile Pro Lys Met Gly Leu Lys His Tyr Asn
            20                  25                  30

Ile Leu Lys Asp Val Lys Gly Pro Asp Glu Asn Leu Lys Leu Leu Ile
        35                  40                  45

Asp Ser Ile Cys Pro Asn Leu Ser Pro Ala Glu Val Asp Phe Val Ser
    50                  55                  60
```

Ile His Leu Leu Glu Phe Asn Gly Lys Ile Lys Ser Arg Lys Glu Ile
65 70 75 80

Asp Gly Tyr Thr Tyr Asp Ile Asn Asp Val Tyr Val Cys Gln Arg Leu
85 90 95

Glu Phe Gln Tyr Gln Gly Asn Thr Phe Tyr Phe Arg Pro Pro Gly Lys
100 105 110

Phe Glu Gln Phe Leu Thr Val Ser Asp Met Leu Ser Lys Cys Leu Leu
115 120 125

Lys Val Asn Asp Glu Val Lys Glu Ile Asn Phe Leu Glu Met Pro Ala
130 135 140

Phe Val Leu Lys Trp Ala Asn Asp Ile Phe Thr Thr Leu Ala Ile Pro
145 150 155 160

Gly Pro Asn Gly Pro Ile Thr Gly Ile Gly Asn Ile Ile Gly Leu Phe
165 170 175

Glu

<210> 493
<211> 390
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 493
Met Ser Met Leu Gln Arg Pro Gly Tyr Pro Asn Leu Ser Val Lys Leu
1 5 10 15

Phe Glu Ser Tyr Asp Ala Trp Ser Asn Asn Arg Phe Val Glu Leu Ala
20 25 30

Ala Thr Ile Thr Thr Leu Thr Met Arg Asp Ser Leu Tyr Gly Arg Asn
35 40 45

Glu Gly Met Leu Gln Phe Tyr Asp Ser Lys Asn Ile His Thr Lys Met
50 55 60

Asp Gly Asn Glu Ile Ile Gln Ile Ser Val Ala Asn Ala Asn Asp Ile
65 70 75 80

Asn Asn Val Lys Thr Arg Ile Tyr Gly Cys Lys His Phe Ser Val Ser
85 90 95

Val Asp Ser Lys Gly Asp Asn Ile Ile Ala Ile Glu Leu Gly Thr Ile

100 105 110

His Ser Ile Glu Asn Leu Lys Phe Gly Arg Pro Phe Phe Pro Asp Ala
115 120 125

Gly Glu Ser Ile Lys Glu Met Leu Gly Val Ile Tyr Gln Asp Arg Thr
130 135 140

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

Pro Trp Thr Ser Thr Phe Glu Asn Tyr Leu Ser Tyr Val Arg Glu Val
165 170 175

Ala Leu Ala Val Gly Ser Asp Lys Phe Val Phe Val Trp Gln Asp Ile
180 185 190

Met Gly Val Asn Met Met Asp Tyr Asp Met Met Ile Asn Gln Glu Pro
195 200 205

Tyr Pro Met Ile Val Gly Glu Pro Thr Leu Ile Gly Gln Phe Val Gln
210 215 220

Glu Leu Lys Tyr Pro Leu Ala Tyr Asp Phe Val Trp Leu Thr Lys Ser
225 230 235 240

Asn Pro His Lys Arg Asp Pro Met Lys Asn Ala Thr Ile Tyr Ala His
245 250 255

Ser Phe Leu Asp Ser Ser Leu Pro Met Ile Thr Thr Gly Lys Gly Glu
260 265 270

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

Arg Asn Gly Tyr Glu Glu Ala Ile Arg Leu Gln Thr Met Ala Gln Tyr
290 295 300

Asp Gly Tyr Ala Lys Cys Ser Thr Val Gly Asn Phe Asn Leu Thr Pro
305 310 315 320

Gly Val Lys Ile Ile Phe Asn Asp Ser Lys Asn Gln Phe Lys Thr Glu
325 330 335

Phe Tyr Val Asp Glu Val Ile His Glu Leu Ser Asn Asn Asn Ser Val
340 345 350

Thr His Leu Tyr Met Phe Thr Asn Ala Thr Lys Leu Glu Thr Ile Asp
355 360 365

Pro Val Lys Val Lys Asn Glu Phe Lys Thr Asp Thr Thr Thr Glu Glu

370 375 380

Ser Ser Ser Ser Asp Lys
385 390

<210> 494
<211> 250
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 494
Met Ala Asn Ile Ile Arg Cys Lys Leu Pro Asp Gly Val His Arg Phe
1 5 10 15

Lys Pro Phe Thr Val Glu Asp Tyr Arg Asp Phe Leu Leu Val Arg Asn
20 25 30

Asp Ile Glu His Arg Ser Pro Gln Glu Gln Lys Glu Ile Ile Thr Asp
35 40 45

Leu Ile Asp Asp Tyr Phe Gly Asp Tyr Pro Lys Thr Trp Gln Pro Phe
50 55 60

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

Val Thr Phe Val Cys Pro Lys Cys Lys Lys Glu Lys Thr Val Pro Phe
85 90 95

Glu Ile Tyr Gln Lys Glu Leu Lys Glu Pro Val Phe Asp Val Ala Asn
100 105 110

Val Lys Ile Lys Leu Lys Phe Pro Ser Glu Phe Tyr Glu Asn Lys Ala
115 120 125

Lys Met Ile Thr Glu Asn Ile His Ser Val Gln Val Asp Glu Ile Trp
130 135 140

Tyr Asp Trp Lys Glu Ile Ser Glu Ser Ser Gln Ile Glu Leu Val Asp
145 150 155 160

Ala Ile Glu Ile Glu Thr Leu Glu Lys Ile Leu Asp Ala Met Asn Pro
165 170 175

Ile Asn Leu Thr Leu His Met Ser Cys Cys Asp Lys Tyr Ile Lys Lys
180 185 190

Tyr Thr Asp Ile Val Asp Val Phe Lys Leu Leu Val Asn Pro Asp Glu
195 200 205

Ile Phe Thr Phe Tyr Gln Ile Asn His Thr Leu Val Lys Ser Asn Tyr
210 215 220

Ser Leu Asn Ser Ile Met Lys Met Ile Pro Ala Glu Arg Gly Phe Val
225 230 235 240

Leu Lys Leu Ile Glu Lys Asp Lys His Gln
245 250

<210> 495
<211> 208
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 495
Met Tyr Glu Tyr Lys Phe Asp Val Arg Val Gly Ser Lys Ile Ile Asn
1 5 10 15

Cys Arg Ala Phe Thr Leu Lys Glu Tyr Leu Glu Leu Ile Thr Ala Lys
20 25 30

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

Thr Asn Ala Lys Asp Leu Asn Arg Gln Glu Ser Glu Leu Leu Leu Ile
50 55 60

His Leu Trp Ala His Ser Leu Gly Glu Val Asn His Glu Asn Ser Trp
65 70 75 80

Lys Cys Thr Cys Gly Thr Glu Ile Pro Thr His Ile Asn Leu Leu His
85 90 95

Thr Gln Ile Asp Ala Pro Glu Asp Leu Trp Tyr Thr Leu Gly Asp Ile
100 105 110

Lys Ile Lys Phe Arg Tyr Pro Lys Ile Phe Asp Asp Lys Asn Ile Ala
115 120 125

His Met Ile Val Ser Cys Ile Glu Thr Ile His Ala Asn Gly Glu Ser
130 135 140

Ile Pro Val Glu Asp Leu Asn Glu Lys Glu Leu Glu Asp Leu Tyr Ser
145 150 155 160

Ile Ile Thr Glu Ser Asp Ile Val Ala Ile Lys Asp Met Leu Leu Lys
165 170 175

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

Thr His Ala His Val Ile Arg Gly Leu Lys Glu Phe Phe Glu Leu Leu
195 200 205

<210> 496
<211> 132
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 496
Met Ala Asn Ile Asn Lys Leu Tyr Ser Asp Ile Asp Pro Glu Met Lys
1 5 10 15

Met Asp Trp Asn Lys Asp Val Ser Arg Ser Leu Gly Leu Arg Ser Ile
20 25 30

Lys Asn Ser Leu Leu Gly Ile Ile Thr Thr Arg Lys Gly Ser Arg Pro
35 40 45

Phe Asp Pro Glu Phe Gly Cys Asp Leu Ser Asp Gln Leu Phe Glu Asn
50 55 60

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

Val Arg Asn Tyr Glu Pro Arg Ile Asp Lys Leu Ala Val Asn Val Ile
85 90 95

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

Ile Asp Asn Pro Asp Asp Ile Glu Gln Ile Lys Leu Gln Leu Ala Ser
115 120 125

Ser Asn Arg Val
130

<210> 497
<211> 137
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 497
Met Arg Leu Glu Asp Leu Gln Glu Glu Leu Lys Lys Asp Val Phe Ile
1 5 10 15

Asp Ser Thr Lys Leu Gln Tyr Glu Ala Ala Asn Asn Val Met Leu Tyr
20 25 30

Ser Lys Trp Leu Asn Lys His Ser Ser Ile Lys Lys Glu Met Leu Arg

35 40 45

Ile Glu Ala Gln Lys Lys Val Ala Leu Lys Ala Lys Leu Asp Tyr Tyr
50 55 60

Ser Gly Arg Gly Asp Gly Asp Glu Phe Ser Met Asp Arg Tyr Glu Lys
65 70 75 80

Ser Glu Met Lys Thr Val Leu Ser Ala Asp Lys Asp Val Leu Lys Val
85 90 95

Asp Thr Ser Leu Gln Tyr Trp Gly Ile Leu Leu Asp Phe Cys Ser Gly
100 105 110

Ala Leu Asp Ala Ile Lys Ser Arg Gly Phe Ala Ile Lys His Ile Gln
115 120 125

Asp Met Arg Ala Phe Glu Ala Gly Lys
130 135

<210> 498
<211> 74
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 498
Met Arg Tyr Asn Ile Asp Asp Ala Phe Asn Tyr Glu Glu Glu Phe Glu
1 5 10 15

Thr Glu Ile Gln Phe Leu Met Lys Lys His Asn Leu Lys Arg Gln Asp
20 25 30

Ile Arg Ile Leu Ala Asp His Pro Cys Gly Glu Asp Val Leu Tyr Ile
35 40 45

Lys Gly Lys Phe Ala Gly Tyr Leu Asp Glu Tyr Phe Tyr Ser Lys Asp
50 55 60

Met Gly Ile Asp Met His Met Arg Val Val
65 70

<210> 499
<211> 55
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 499
Met Ser Asp Lys Ile Cys Val Val Cys Lys Thr Pro Ile Asp Ser Ala
1 5 10 15

Leu Val Val Glu Thr Asp Lys Gly Pro Val His Pro Gly Pro Cys Tyr
            20   25   30

Asn Tyr Ile Lys Glu Leu Pro Val Ser Glu Ser Ser Glu Glu Gln Leu
        35   40   45

Asn Glu Thr Gln Leu Leu Leu
    50   55

<210> 500
<211> 76
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 500
Met Leu Leu Glu Phe Lys Gln Phe Leu Tyr Glu Ala Ser Ile Asp Glu
1   5   10   15

Phe Met Gly Lys Ile Ala Ser Cys Gln Thr Leu Glu Gly Leu Glu Glu
            20   25   30

Leu Glu Ala Tyr Tyr Lys Lys Arg Val Lys Glu Thr Glu Leu Lys Asp
        35   40   45

Thr Asp Asp Ile Ser Val Arg Asp Ala Leu Ala Gly Lys Arg Ala Glu
    50   55   60

Leu Glu Asp Ser Asp Asp Glu Val Glu Glu Ser Phe
65   70   75

<210> 501
<211> 503
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 501
Met Thr Asp Ile Lys Val His Phe Tyr Asp Phe Ser His Val Arg Ile
1   5   10   15

Asp Cys Glu Glu Ser Thr Phe His Glu Leu Arg Asp Phe Phe Ser Phe
            20   25   30

Glu Ala Asp Gly Tyr Arg Phe Asn Pro Lys Tyr Lys Tyr Gly His Trp
        35   40   45

Asp Gly Arg Ile Arg Leu Leu Asp Tyr Asn Arg Leu Leu Pro Phe Gly
    50   55   60

Leu Val Gly Gln Ile Lys Lys Phe Cys Asp Asn Phe Gly Tyr Lys Ala

65 70 75 80

Trp Ile Asp Pro Gln Ile Asn Glu Lys Glu Glu Leu Ser Arg Lys Asp
85 90 95

Phe Asp Glu Trp Leu Ser Lys Leu Glu Ile Tyr Ser Gly Asn Lys Arg
100 105 110

Ile Glu Pro His Trp Tyr Gln Lys Asp Ala Val Phe Glu Gly Leu Val
115 120 125

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

Ile Gln Ala Leu Leu Ala Arg Tyr Tyr Leu Glu Asn Tyr Glu Gly Lys
145 150 155 160

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

Asp Phe Val Asp Tyr Arg Leu Phe Ser His Ala Met Ile Lys Lys Ile
180 185 190

Gly Gly Gly Ala Ser Lys Asp Asp Lys Tyr Lys Asn Asp Ala Pro Val
195 200 205

Val Val Gly Thr Trp Gln Thr Val Val Lys Gln Pro Lys Glu Trp Phe
210 215 220

Ser Gln Phe Gly Met Met Met Asn Asp Glu Cys His Leu Ala Thr Gly
225 230 235 240

Lys Ser Ile Ser Ser Ile Ile Ser Gly Leu Asn Asn Cys Met Phe Lys
245 250 255

Phe Gly Leu Ser Gly Ser Leu Arg Asp Gly Lys Ala Asn Ile Met Gln
260 265 270

Tyr Val Gly Met Phe Gly Glu Ile Phe Lys Pro Val Thr Thr Ser Lys
275 280 285

Leu Met Glu Asp Gly Gln Val Thr Glu Leu Lys Ile Asn Ser Ile Phe
290 295 300

Leu Arg Tyr Pro Asp Glu Phe Thr Thr Lys Leu Lys Gly Lys Thr Tyr
305 310 315 320

Gln Glu Glu Ile Lys Ile Ile Thr Gly Leu Ser Lys Arg Asn Lys Trp
325 330 335

Ile Ala Lys Leu Ala Ile Lys Leu Ala Gln Lys Asp Glu Asn Ala Phe

340 345 350

Val Met Phe Lys His Val Ser His Gly Lys Ala Ile Phe Asp Leu Ile
355 360 365

Lys Asn Glu Tyr Asp Lys Val Tyr Tyr Val Ser Gly Glu Val Asp Thr
370 375 380

Glu Thr Arg Asn Ile Met Lys Thr Leu Ala Glu Asn Gly Lys Gly Ile
385 390 395 400

Ile Ile Val Ala Ser Tyr Gly Val Phe Ser Thr Gly Ile Ser Val Lys
405 410 415

Asn Leu His His Val Val Leu Ala His Gly Val Lys Ser Lys Ile Ile
420 425 430

Val Leu Gln Thr Ile Gly Arg Val Leu Arg Lys His Gly Ser Lys Thr
435 440 445

Ile Ala Thr Val Trp Asp Leu Ile Asp Asp Cys Gly Val Lys Pro Lys
450 455 460

Ser Ala Asn Thr Lys Lys Lys Tyr Val His Leu Asn Tyr Leu Leu Lys
465 470 475 480

His Gly Ile Asp Arg Ile Gln Arg Tyr Ala Asp Glu Lys Phe Asn Tyr
485 490 495

Val Met Lys Thr Val Asn Leu
500

<210> 502
<211> 226
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 502
Met Ile Asp Lys Asp Tyr Ile Ala Glu Leu Lys Ala Leu Asp Asp Asn
1 5 10 15

Lys Glu Ala Lys Ala Lys Leu Ala Glu Tyr Ala Glu Gln Phe Gly Ile
20 25 30

Lys Val Lys Lys Asn Lys Ser Phe Asp Asn Ile Val Asn Asp Ile Glu
35 40 45

Glu Ala Leu Gln Lys Leu Ala Ser Glu Pro Met Pro Glu Thr Asp Gly
50 55 60

```
Leu Ser Ile Lys Asp Leu Ile Asp Ala Ala Asp Ala Ala Glu Gly Leu
65                  70                  75                  80

Lys Tyr Asp Asp Glu Glu Val Asn Pro Glu Ala Ala Leu Leu Ile Asp
                85                  90                  95

Ser Pro Val Lys Ser Asp Ile Lys Ile Glu Val Val Glu Thr Asp Lys
            100                 105                 110

Ile Pro Glu Asn Thr Asp Val Leu Ile Glu Asp Thr Pro Phe Val Glu
        115                 120                 125

Glu Lys Phe Glu Gln Ala Val Ala Glu Ile Ile Glu Ser Glu Lys Pro
    130                 135                 140

Ser Val Phe Thr Leu Pro Glu Asn Phe Ser Pro Asn Leu Gln Leu Ile
145                 150                 155                 160

Gly Lys Asn Pro Gly Phe Cys Thr Val Pro Trp Trp Ile Tyr Gln Trp
                165                 170                 175

Ile Ala Glu Thr Pro Asp Trp Lys Ser His Pro Thr Ser Phe Glu His
            180                 185                 190

Ala Ser Ala His Gln Thr Leu Phe Ser Leu Ile Tyr Tyr Ile Asn Arg
        195                 200                 205

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

Leu Lys
225


<210> 503
<211> 472
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 503
Met Thr Phe Thr Val Asp Ile Thr Pro Lys Thr Pro Thr Gly Val Ile
1               5                   10                  15

Asp Glu Thr Lys Gln Phe Thr Ala Thr Pro Ser Gly Glu Thr Gly Gly
            20                  25                  30

Gly Thr Ile Thr Tyr Ala Trp Thr Val Asp Asp Ala Pro Gln Glu Glu
        35                  40                  45

Thr Ser Ala Thr Phe Ser Tyr Val Leu Lys Gly Pro Ala Gly Gln Lys
    50                  55                  60
```

```
Thr Ile Lys Val Val Ala Thr Asn Gln Val Ala Glu Ser Glu Pro Glu
65                  70                  75                  80

Thr Ala Glu Ile Ser Thr Thr Ile Thr Val Gln Asn Lys Thr Gln Thr
                85                  90                  95

Thr Thr Leu Ala Val Thr Pro Gly Ser Pro Asp Ala Gly Val Ile Gly
            100                 105                 110

Thr Pro Ile Glu Phe Thr Ala Ala Leu Ala Ser Gln Pro Ser Gly Ala
        115                 120                 125

Asn Ala Thr Tyr Gln Trp Tyr Val Asp Gly Ser Pro Val Gly Glu Ala
    130                 135                 140

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

Ile Lys Cys Val Ala Gln Val Thr Ala Thr Asp Tyr Asp Thr Lys Glu
                165                 170                 175

Val Thr Ser Asn Glu Val Ser Leu Thr Val Asn Lys Lys Thr Gln Thr
            180                 185                 190

Thr Thr Leu Ala Val Thr Pro Asp Ser Pro Pro Ala Gly Val Ile Gly
        195                 200                 205

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

Ser Ala Thr Tyr Gln Trp Tyr Val Asp Asp Ser Gln Val Gly Gly Glu
225                 230                 235                 240

Thr Asn Ser Thr Phe Ser Tyr Thr Pro Thr Thr Ser Gly Val Lys Arg
                245                 250                 255

Ile Lys Cys Val Ala Gln Val Thr Ala Glu Asn Tyr Asn Glu Lys Glu
            260                 265                 270

Val Thr Ser Asn Glu Val Ser Leu Thr Val Asn Lys Lys Thr Met Asn
        275                 280                 285

Pro Gln Val Thr Leu Thr Pro Pro Ser Ile Asn Val Gln Gln Asp Ala
    290                 295                 300

Ser Ala Thr Phe Thr Ala Asn Val Thr Gly Ala Pro Glu Glu Ala Gln
305                 310                 315                 320

Ile Thr Tyr Ser Trp Lys Lys Asp Ser Ser Pro Val Glu Gly Ser Thr
                325                 330                 335
```

```
Asn Val Tyr Thr Val Asp Thr Ser Ser Val Gly Ser Gln Thr Ile Glu
            340                 345                 350

Val Thr Ala Val Val Thr Ala Thr Asp Tyr Asp Ser Lys Thr Ile Thr
        355                 360                 365

Ala Glu Gly Gln Val Gln Val Thr Asp Lys Val Ala Pro Glu Pro Glu
    370                 375                 380

Gly Glu Leu Pro Tyr Val His Pro Leu Pro His Arg Thr Ser Ala Tyr
385                 390                 395                 400

Ile Trp Cys Gly Trp Trp Val Met Asp Glu Ile Gln Lys Met Thr Glu
                405                 410                 415

Glu Gly Lys Asp Trp Lys Thr Asp Asp Pro Asp Ser Lys Tyr Tyr Leu
            420                 425                 430

His Arg Tyr Thr Leu Gln Lys Met Met Lys Asp Tyr Pro Glu Val Asp
        435                 440                 445

Val Gln Glu Ser Arg Asn Gly Tyr Ile Ile His Lys Thr Ala Leu Glu
    450                 455                 460

Thr Gly Ile Ile Tyr Thr Tyr Pro
465                 470


<210> 504
<211> 67
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 504
Met Arg Thr Glu Val Val Val Phe Thr Leu His Glu Ser Gly Lys Ser
1               5                   10                  15

Phe Ile Glu Ile Ala Arg Glu Leu Asn Leu Gln Ala Lys Glu Val Ala
            20                  25                  30

Val Leu Trp Ala Arg Ala Met Thr Ala Lys Asn Lys Phe Glu Thr Arg
        35                  40                  45

Glu Lys Val Val Tyr Arg Lys Arg His Ile Asn Lys Lys Val Lys Asn
    50                  55                  60

Gly Thr Val
65


<210> 505
<211> 92
```

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 505
Met Glu Gln Tyr Asp Leu Tyr Glu Asn Glu Ser Phe Ala Asn Gln Leu
1   5   10   15

Arg Glu Lys Ala Leu Lys Ser Lys Gln Phe Lys Leu Glu Cys Phe Ile
            20   25   30

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

His Phe Ser Tyr Tyr Cys Ile Ala Arg Asp Lys Leu Ile Thr Glu Glu
    50   55   60

Ile Gly Asp Trp Leu Arg Lys Glu Gly Phe Ser Phe Lys Val Asn Ser
65   70   75   80

Asp Gln Arg Asp Gly Asp Trp Leu Glu Ile Thr Phe
                85   90

<210> 506
<211> 334
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F488/08

<400> 506
Met Phe Lys Lys Tyr Ser Ser Leu Glu Asn His Tyr Asn Ser Lys Phe
1   5   10   15

Ile Glu Lys Leu Tyr Ser Leu Gly Leu Thr Gly Gly Glu Trp Val Ala
            20   25   30

Arg Glu Lys Ile His Gly Thr Asn Phe Ser Leu Ile Ile Glu Arg Asp
        35   40   45

Lys Val Thr Cys Ala Lys Arg Thr Gly Pro Ile Leu Pro Ala Glu Asp
    50   55   60

Phe Phe Gly Tyr Glu Ile Ile Leu Lys Asn Tyr Glu Asp Ser Ile Lys
65   70   75   80

Ala Val Gln Asp Ile Met Glu Thr Ser Ala Val Val Ser Tyr Gln Val
                85   90   95

Phe Gly Glu Phe Ala Gly Pro Gly Ile Gln Lys Asn Val Asp Tyr Gly
            100   105   110

```
Asp Lys Asp Phe Tyr Val Phe Asp Ile Ile Val Thr Thr Glu Ser Gly
        115                 120                 125


Asp Val Thr Tyr Val Asp Asp Tyr Met Met Glu Ser Phe Cys Asn Thr
    130                 135                 140


Phe Lys Phe Lys Met Ala Pro Leu Leu Gly Arg Gly Lys Phe Glu Glu
145                 150                 155                 160


Leu Ile Lys Leu Pro Asn Asp Leu Asp Ser Val Val Gln Asp Tyr Asn
                165                 170                 175


Phe Thr Val Asp His Ala Gly Leu Val Asp Ala Asn Lys Cys Val Trp
            180                 185                 190


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


Lys Pro Cys Tyr Pro Ser Trp Leu His Asn Gly Asn Arg Val Ala Ile
    210                 215                 220


Lys Cys Lys Asn Ser Lys Phe Ser Glu Lys Lys Lys Ser Asp Lys Pro
225                 230                 235                 240


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


Ile Leu Ala Cys Tyr Val Thr Leu Asn Arg Val Asn Asn Val Ile Ser
            260                 265                 270


Lys Ile Gly Glu Ile Gly Pro Lys Asp Phe Gly Lys Val Met Gly Leu
        275                 280                 285


Thr Val Gln Asp Ile Leu Glu Glu Thr Ser Arg Glu Gly Ile Thr Leu
    290                 295                 300


Thr Gln Ala Asp Asn Pro Ser Leu Val Lys Lys Glu Leu Val Lys Met
305                 310                 315                 320


Val Gln Asp Val Leu Arg Pro Ala Trp Ile Glu Leu Val Ser
                325                 330


<210> 507
<211> 40
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 507
Leu Leu Asn Glu Ala Val Ala Ser Lys Val Leu Asn Ser Arg Leu Gly
1               5                   10                  15
```

Trp Ser Ala Val Gly Glu Tyr Val Glu Leu Phe Asn Arg Thr Gln Ser
20 25 30

Arg Val Ala Gly Leu Ile Pro Glu
35 40

<210> 508
<211> 69
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 508
Met Leu Ser Arg Gln Asp Arg Gly Glu Arg Ala Trp His Gln Gln Asp
1 5 10 15

Ala Ala Trp Gln Arg Gln Ile Ala Thr Trp Ala Ala Gln Asp His Arg
20 25 30

His Tyr Ala Ala Pro Trp Arg Lys Arg Gln Ala Ser Gln Glu Tyr Ala
35 40 45

Val Ala Leu Thr Lys His Arg Glu Ala Leu Glu Arg Ser Arg His Tyr
50 55 60

Gly Gln Pro Lys Gly
65

<210> 509
<211> 117
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 509
Val Gly Ser Arg Ser Val Glu Phe Ala Leu Ser Ser Arg Asn Asn Ala
1 5 10 15

Ser Thr Gly Ser Leu Glu Thr Gly Leu Thr His Cys Gln Gly Ile Gly
20 25 30

Arg Val Arg Ser Gln Asn Asp Gly Arg Leu Gln Pro Ser Lys Arg Gly
35 40 45

Thr Ser His Arg Arg Lys Gly His Gly Lys Leu Leu Gly Gln Glu Pro
50 55 60

Gln Cys Val Arg Pro Ala Gly Ile Thr Glu Gly Ile Asp Thr Val Gln
65 70 75 80

Asp Thr Arg Tyr Ser Ser His His Leu Met Ala Thr Gln Gln Lys Gly

85 90 95

Leu Cys Gln Arg Thr Gly Arg Thr Asn Pro Arg Gln Arg Ile Asp Lys
100 105 110

Thr Ser Ala Ser Leu
115

<210> 510
<211> 94
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 510
Met Ala His Phe Lys Ala Lys Ala Pro Lys Ser Pro Phe Ala Ala Gln
1 5 10 15

Val Ala Tyr Trp Arg Asp Trp Glu Ala Lys Arg Thr Lys Leu Ile Ala
20 25 30

Gln Asp Asn Val Glu Gly Arg Lys Glu Leu Arg Lys Met Arg Asp Val
35 40 45

Arg Tyr Ala Thr Asp Pro Glu Pro Ala Pro Gly Arg Tyr His Asn Pro
50 55 60

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

Leu Lys Gly Trp Asn Ala Lys Lys Ser Gln Gly Lys Gly Leu
85 90

<210> 511
<211> 75
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 511
Met Pro Arg Val Asn Glu Leu Thr Pro Arg Gln Arg Lys Ala Ala Lys
1 5 10 15

Ala Arg Arg Asp Lys Ala Arg Arg Ile Asp Leu Ala His Arg Met Pro
20 25 30

Lys Gly Ala Asp Cys Pro Ile Phe Arg Lys Ala Glu Gln Ala Gln Ala
35 40 45

Lys Gln Pro Arg Val Asp Thr Leu Thr Thr Pro Arg Ser Ala Gly Tyr
50 55 60

Leu Ala Ala Ala Ala Tyr Leu Asn Lys Ser Ile
65 70 75

<210> 512
<211> 179
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 512
Met Thr Asn Ala Ile Ser Lys Thr Val Ile Ala Phe Arg Gly Thr Glu
1 5 10 15

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

Asp Glu Ala Ile Gln Leu Thr Gly Leu Ser Ile Ile His His Ile Asp
35 40 45

Gln Cys Gly Asp Val Thr Val Val Lys Ala Leu Tyr Glu Ala Met Pro
50 55 60

Lys Gly Ser Arg Arg Asn Ala Leu Val Glu Trp Leu Val Leu His Gly
65 70 75 80

Lys Val Gln Val Asn Thr Asp Lys Lys Ser Asn Lys Asp Leu Pro Phe
85 90 95

Leu Tyr Asn Lys Phe Gly Lys Thr Asp Leu Val Gly Ala Thr Asn Ser
100 105 110

Pro Trp Tyr Ser Phe Lys Pro Glu Lys Ala Leu Asp Gln Glu Phe Asn
115 120 125

Leu Ala Ala Ala Leu Ala Thr Ile Lys Lys Gln Val Leu Gln Ala Gln
130 135 140

Thr Lys Gly Lys Val Ile Val Gly Met Glu Leu Leu Gly Asp Leu Glu
145 150 155 160

Ala Leu Ala Ala Lys Ala Ala Pro Ile Ala Glu Gln Ser Lys Arg Ala
165 170 175

Ala Ala His

<210> 513
<211> 122
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F510/08

<400> 513
Met Gln Ala Leu Asn Thr Leu Leu Ile Ala Ile Pro Lys Asp Pro Thr
1 5 10 15

Ala Gly Met His Ala Ala Asp Lys Val Leu Cys Ala His Gly Phe Arg
            20 25 30

Met Gly Asp Leu Asn Thr Ala His Val Leu Thr Pro Gly Gly Phe Val
        35 40 45

Val Val Gly Ala Gly Val Thr Val Asn Arg Tyr Asp Glu Ala Tyr Arg
    50 55 60

Met Ser Arg Asn Leu Asp Ser Glu Gly Phe Asp Val Leu Leu Val Gln
65 70 75 80

Gly Ser Pro Leu Ser Gly Arg Val Thr Cys Gln Ala Tyr Gly Trp Ile
                85 90 95

Asn Ala Glu Tyr His Lys Gly Cys Ala Asn Gly Arg Pro Ile Phe Asp
            100 105 110

Ile Ala Gly Thr Ser Tyr His Val Ile Ala
        115 120

<210> 514
<211> 74
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 514
Met Ser Ser Arg Asp Pro Tyr Arg Ile Gly His Arg Val Gly Leu Val
1 5 10 15

Asn Tyr Ser Asp Arg Tyr Leu Gly Ala Asp Ala Ala Gly Thr Lys Gly
            20 25 30

Ile Ile Glu Ala Ile Thr Arg Pro Ser Arg Cys Met Thr Val Tyr His
        35 40 45

Val Arg Cys Glu Arg Thr Leu Arg Leu Ile Glu Ala Glu Ala Arg Asn
    50 55 60

Val Arg Phe Ile Arg Gln Arg Ala Glu Arg
65 70

<210> 515
<211> 86
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 515
Met Thr Leu Val Ala Thr Val Val Asp Ser Ala His Asn Leu Glu Val
1   5   10   15

Asp Asp Leu Thr Ala Gly Asn Leu Tyr Ala Ala Ser Ser Pro Ser Gly
            20   25   30

Asn Met Phe Ile Val Val Val Gly Asn His Asn Gly Arg Arg Leu Pro
        35   40   45

Val Val Leu Ser Ser Thr Asp Thr Arg Thr Ile Gly Asp Val Ile Ser
    50   55   60

Asn Thr Gly Phe Arg Tyr Ser Glu Ile Ala Gly Phe Ser Val Asn Leu
65   70   75   80

Ala Gln Gly Asp Tyr Asp
                85

<210> 516
<211> 96
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 516
Met Val Thr Arg Thr Val Tyr Val Thr Pro Glu Asp Pro Thr Pro Pro
1   5   10   15

Ile Leu Ser Val Gly Arg Leu Ala Pro Gly Glu Leu Tyr Lys Val Val
            20   25   30

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

Pro Ala Leu Ala Gln Ala Ala Val Val Leu His Ser Met Asn Pro Ala
    50   55   60

Gln Tyr Pro Ala Gly Ser Ala Ile Leu Asn Thr Ala Trp Lys Cys Arg
65   70   75   80

Arg Leu Gly Val Gly Glu Tyr Val Lys Leu Val Gln Gly Glu Glu Asp
                85   90   95

<210> 517
<211> 79
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F510/08

<400> 517
Met Ala Val Ala Ile Leu Ile Leu Ala Val Trp Leu Ile Gly Gly Ala
1   5   10   15

Leu Leu Phe Leu Pro Phe Asp Leu Val Val Ser Pro Arg Leu Pro Leu
            20   25   30

Ser Asp Glu Ala Leu Asn Arg Thr Ala Leu Tyr Thr Val Leu Trp Pro
        35   40   45

Val Thr Leu Pro Thr Leu Ile Ala Ile Thr Val Val Val Met Leu His
    50   55   60

Ser Ala Tyr Arg Gly Ala Ile Glu Leu Tyr Gln Glu Met Lys Ser
65   70   75

<210> 518
<211> 97
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 518
Met Ile Arg Thr His Thr His Asn Val Glu Arg Thr Pro His Arg Leu
1   5   10   15

Tyr Arg His Thr Glu Leu Ala Ser Gly Glu Leu Tyr Arg Val Val Gln
            20   25   30

Pro Asp Ser Lys Arg Gly Thr Leu Val Val Gly Val Ala Ala Trp Asp
        35   40   45

Ser Gln Gly Arg Pro Ala Val Leu Pro Val Val Ile His Asp Asp Gly
    50   55   60

Asp Ala Lys Val Thr Cys Ala Arg Pro Thr Val Leu Arg Asn Asp Gly
65   70   75   80

Trp Arg Met Val Leu Ala Asp Lys Gly Thr Gln Val Thr Leu Thr Ala
                85   90   95

Glu

<210> 519
<211> 138
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 519
Met Thr Asn Val Asn Thr Thr Thr Glu Thr Thr Thr Ala Ala Val Leu
1 5 10 15

Gly Ala Lys Leu Ile Lys Lys Pro Ala Thr Val Glu Asp Phe Arg Asn
20 25 30

Asn Val Val Phe His His Ser Ala Leu Thr Lys Leu Thr Glu Val Tyr
35 40 45

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

Val Ala Gly Asp Val Ile Thr Phe Asp His Gly Lys Gly Glu Lys Ala
65 70 75 80

Glu Val Leu Ser Gly Glu Val Ile Ser Val Val Ala Gly Val Tyr Gln
85 90 95

Val Leu Val Arg Phe Ser Asp Ser Ala Pro Ala Lys Leu Leu Asp Val
100 105 110

Lys Ala Ser Ala Ile Arg Ala Val Gln Ser Ser Ala Ala Gln Ala Ala
115 120 125

Thr Leu Asp Glu Ala Ile Ala Gln Gly Glu
130 135

<210> 520
<211> 119
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 520
Met Ser Lys Arg Asn Pro Glu His Ile Asn Gly Thr Val Arg Ser Val
1 5 10 15

Ser Val Gln Lys Leu Ala Ala Thr Gln Glu Leu Glu Asp Arg Leu Glu
20 25 30

Ala Ala Leu Ala Val Cys Gln Gln Arg Ala Glu Asp Ile Asp Leu Leu
35 40 45

Ser Arg Arg Leu Gln Ala Ala Glu Arg Ala Arg Arg Trp Glu Ile Asp
50 55 60

Glu Ile Arg Asn His Gln Ala Thr Ile Arg Leu Leu Gln Asn Asp Leu
65 70 75 80

Asn Ala Ala His Asp Ala His Glu Ala Gln Glu Arg Arg Ala Arg Lys
85 90 95

Ala Thr Ile Met Ala Trp Val Cys Leu Leu Thr Ala Gly Leu Ala Val
100 105 110

Thr Leu Lys Leu Ala Gly Val
115

<210> 521
<211> 269
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 521
Met Gln Cys Lys Asp Leu Tyr Thr Asn Leu Ala Ser Gly Met Phe Asn
1 5 10 15

Val Pro Cys Ser Gln Val Thr Pro Glu Met Arg Arg Val Ala Lys Ser
20 25 30

Arg Ala Phe Ala His Ala Tyr Thr Pro Lys Lys Gln Ala Ser Gly Gly
35 40 45

Thr Tyr Thr Ala Arg Val Ser Gly Val Thr Cys Asp Gly Gly Lys Val
50 55 60

Glu Val Arg Leu Asp Asn Val Glu Arg Val Ser Thr Phe Asp Tyr Ala
65 70 75 80

Glu Leu Glu Thr Arg Val Ala Ala Ser Leu Cys Gln Ala Asp Ala Lys
85 90 95

Arg Ala Ala Glu Tyr Glu Lys Leu Leu Leu Lys Ala Phe Pro Ser Val
100 105 110

Ser Pro Lys Asp Gly Pro Leu Ser Ala Lys Asp Phe Glu Leu Arg Leu
115 120 125

His Asp Leu Cys Ser Thr Lys Leu Val Val Leu Arg Ala Leu Arg Asp
130 135 140

Ala Gly Ile Glu Met Asp Gly Pro Leu Arg Ser Arg Val Arg Lys Leu
145 150 155 160

Ala Asp Arg Asn Asn Val Met Gly Ala Glu Leu Phe Ser Leu Lys Gln
165 170 175

Glu Leu Ala Gln Leu Val Ala Val Gly Gln Lys Ala Gly Leu Asn Trp
180 185 190

Asp Gly Ala Glu Thr Gln Arg Leu Leu Thr Val Ala Pro Thr Lys Ala

195 200 205

Leu Cys Arg Leu Ile Ser Ala Leu Thr Gly Val Arg Tyr Thr His His
210 215 220

Thr Val Val Ala Lys Ala Glu Ala Glu Ala Arg Glu Arg Ala Lys Ala
225 230 235 240

Glu Ala Lys Asp Ser Leu Gln Ala Ala Thr Phe Ala Ala Ala Ile Ala
245 250 255

Gly Gly Val Val Gly Ser Ala Leu Met Phe Leu Leu Gly
260 265

<210> 522
<211> 180
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 522
Met Ser Lys Thr Ser Leu Tyr Pro Leu Asn Leu His Pro Gly Leu Ile
1 5 10 15

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

Glu Asn Trp Trp Gln Trp Phe Leu Trp Gln Arg Lys Tyr His Pro Leu
35 40 45

Arg Glu Ser Leu Ser Pro Ala Gly Glu Leu Ser Ala Ser Ile Ala Glu
50 55 60

Cys Val Leu His Leu Arg Arg Asn Gly Trp Gln Asp Ser Asp Ile Trp
65 70 75 80

Arg Lys Lys Gly Gly Val Leu Ala Leu Gly Ala Phe Asp Leu Ser Gly
85 90 95

Leu Met Val Gly Ser Cys Leu Val Val Gly Gly Glu Leu Lys Ala Leu
100 105 110

Cys Val Asp Asp Arg His Ser Arg Gln Gly Ile Gly Ala Glu Leu Val
115 120 125

Arg Ala Ala Glu Leu Ala Gly Ala Glu Tyr Leu Thr Cys Phe Glu Phe
130 135 140

Leu Glu Pro Phe Tyr Ala Asp Leu Gly Trp Ser Thr Thr His Arg Glu
145 150 155 160

```
Ala Asn Trp Thr Ala Gly Glu Pro Asp Val Leu His Met Arg Ala Pro
                165                 170                 175


Gly His Asp Val
            180


<210> 523
<211> 274
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 523
Met Ala Leu Arg Arg Asp Ser Trp Leu Lys Gln Ala Gln Ser Leu Ala
1               5                   10                  15


Val Gly Gln Ala Gly Arg Phe Arg His Val Leu Gly Cys Gln Ser Met
            20                  25                  30


Ser Arg Gly Gly Thr Asn Met Thr Cys Lys Asn Leu Pro Asp Arg Trp
        35                  40                  45


Val Ala Tyr Cys Tyr Ser Cys Gln Glu Gly Gly Val Val Glu Lys Thr
    50                  55                  60


His Val Arg Arg Val Gln Cys Ala Asp Gln Glu Arg Phe Met Pro Trp
65                  70                  75                  80


Pro Glu Asp Ala Ser Asp Trp Thr Gln Ala Asp Cys Tyr Gln Ser Leu
                85                  90                  95


Tyr Gly Leu Leu Leu Ser Lys Gly Ile Asp Tyr Asn Val Met Thr Pro
            100                 105                 110


Gly Leu Pro Leu Leu Tyr Ser Glu Arg Gln His Arg Leu Ile Phe Pro
        115                 120                 125


Thr Asp Ala Gly Trp Ile Gly Arg Ala Thr Ala Asp Gln Asn Pro Lys
    130                 135                 140


Trp Val Gly Tyr Gly Tyr Pro Ala Pro Asp Tyr His Gly Trp Pro Gln
145                 150                 155                 160


Glu Leu Ser Met Gly Arg Pro Trp Val Leu Thr Glu Asp Tyr Leu Ser
                165                 170                 175


Ala Leu Lys Val Arg Trp Ala Cys Pro Glu Val Phe Ala Val Gly Leu
            180                 185                 190


Asn Gly Thr Arg Leu Arg Asp Arg Leu Ala Ala Ile Met Leu Gln Gln
        195                 200                 205
```

```
Thr Cys Lys Arg Ala Phe Ile Phe Leu Asp Gly Asp Arg Ala Gly Val
    210                 215                 220

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

Gly Gln Val Ile Pro Thr Pro Asp Gly Phe Asp Pro Lys Asp Leu Thr
                245                 250                 255

Arg Glu Gln Ile Arg Ser Leu Val Ile Gly Arg Ile Asp Ala Ser Arg
            260                 265                 270

Thr Glu
```

<210> 524
<211> 422
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 524

```
Leu Asp Val Leu Thr Leu His Ala Leu Ser Asp Arg Asp Arg Phe Arg
1               5                   10                  15

Thr Leu Arg Ser Val Val Pro Glu Gly Met Met Gly Pro Glu Thr Cys
            20                  25                  30

Phe Val Ile Asp Trp Ile Glu Gln Tyr Trp Lys Val Tyr Pro Ala His
        35                  40                  45

Gln Lys Val Asp Pro Gln Ala Leu Arg Glu Leu Ile Lys Leu Arg Gly
    50                  55                  60

Gly Tyr Gln Pro Glu Gln Leu Ala Val Val Leu Asn Leu Val Asn Gln
65                  70                  75                  80

Leu Asp Lys Pro Val Asp Pro Asp Ser Leu Gln Gly Val Val Ser Gln
                85                  90                  95

Leu Asn Glu Leu Asp Phe Ser Gly Arg Val Asp Ala Leu Leu Ala Gln
            100                 105                 110

Tyr Asn Gln Gly Glu Asp Ile Asp Leu Ala Tyr Glu Leu Arg Arg Leu
        115                 120                 125

Ser Asp Glu Ala Leu Arg Arg Gly Gly Val Ser Thr Pro Thr Asp Tyr
    130                 135                 140

Val Thr Asp Asp Val Phe Asp Ile Leu Ala Glu Glu Gln Gly Asp His
145                 150                 155                 160
```

```
Gly Ile Lys Leu Pro Gly Leu Val Leu Pro Ala Tyr Met Lys Gly Leu
                165                 170                 175

His Ala Gly Ala Ser Val Leu Val Ala Ala Pro Pro Asp Ala Gly Lys
            180                 185                 190

Thr Ser Phe Met Ala Trp Ile Ala Val His Ile Ala Pro Gln Leu Lys
        195                 200                 205

Arg Tyr Phe Asp Pro Gly Arg Pro Ile Leu Trp Leu Asn Asn Glu Gly
    210                 215                 220

Lys Gly Arg Arg Ile Lys Pro Arg Leu Tyr Ser Ala Ala Leu Gly Met
225                 230                 235                 240

Thr Val Gly Glu Ile Leu Ala Leu Asp Pro Glu Glu Val Arg Arg Met
                245                 250                 255

Tyr Ala Glu Lys Ile Gly Gly Asp Ser Glu Leu Ile Arg Ile Lys Asp
            260                 265                 270

Phe His Gly Gly Ser Leu Ala Gln Ala Glu Gln Val Ile Asp Ala Met
        275                 280                 285

Lys Pro Ser Val Val Phe Trp Asp Met Met Ala His Val Lys Gly Gly
    290                 295                 300

Gln Arg Lys Asp Gln Asn Arg Thr Asp Glu Met Glu Tyr Lys Val Ala
305                 310                 315                 320

Glu Val Arg Glu Met Ala Val Arg His Asp Phe Ile Ser Phe Met Thr
                325                 330                 335

Trp Gln Ile Ser Asn Asp Gly His Asp Gln Leu Phe Pro Pro Gln Ser
            340                 345                 350

Cys Leu Lys Asp Ser Lys Thr Ala Val Gln Gly Ala Val Asp Val Gln
        355                 360                 365

Ile His Leu Gly Arg Leu Asn Gly Ala Asp Gln Gln Val Met Arg Gly
    370                 375                 380

Leu Ser Leu Pro Lys Asn Lys Phe Gln Met Asp Gly Lys Pro Ser Asn
385                 390                 395                 400

Val Glu Ala Met Ile Asn Phe Asp Ala Ala Arg Cys Arg Phe Phe Glu
                405                 410                 415

Ser Val Asp His Ala Ser
            420
```

<210> 525
<211> 206
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 525
Met Gln Ala Lys His Ser Arg Val Leu Glu Gly Thr Lys Glu Ile Pro
1   5   10   15

Leu Gly Ser Ile Glu Pro Leu Leu Gly Ser Val Ala Gly Leu Leu Leu
            20   25   30

Cys Leu Tyr Ser Asp Ala Thr His Glu Glu Gly Val Ala Leu Ala Gly
        35   40   45

Gly Phe Pro Arg Asp Leu Met His Gly Ala Thr Pro Lys Asp Val Asp
    50   55   60

Val Ala Leu Tyr Ser Met Thr Trp Gly Arg Ala Glu His Leu Ile Gln
65   70   75   80

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

Arg Ser Asp Tyr Ala Asp Gly Gly Asp Gly Gly Ile Phe Lys Gly Val
            100   105   110

Met Ser Leu Val Gly Cys Arg Gly Leu Asn Gly Met Asp Leu Asp Phe
        115   120   125

Asn Tyr Tyr Asp Ala Asp Ser Leu Gly Arg Val Met Glu Ser Phe Asp
    130   135   140

Phe Thr Ile Asn Gln Val Gly Ile Ala Tyr Asn Trp Pro Asp Pro Glu
145   150   155   160

Gly Gly Pro Arg Leu Gly Ala Tyr Leu His Lys Asp Val Thr Trp Gly
                165   170   175

Val Asn Lys Glu Val Gly Ala Gly Ser Arg Leu Pro Glu Arg Cys Glu
            180   185   190

Lys Met Arg Ala Lys Ala Ala Tyr Tyr Gly Trp Glu Asn Val
        195   200   205

<210> 526
<211> 315
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 526
Met Ser Lys Arg Asp Val Val Leu Asp Ile Glu Lys Gly Ile Trp Arg
1   5   10   15

Gly Val Asp Gln Asn Asp Lys Ala Val Glu Ala Ile Ile Lys Lys Asn
            20   25   30

Gly Tyr Val Ile Val Glu Pro Lys Ile Asp Gly Cys Arg Ala Ile Val
        35   40   45

Gly Ala His Gly Val Val Ser Arg Ser Gly Arg Arg Phe Pro Ala Leu
    50   55   60

Asp Gly Leu Glu Asp Arg Ile Ile Glu Arg Leu Ala Arg Pro Gly Leu
65   70   75   80

Asp Ser Gly Leu Val Leu Asp Cys Glu Met Tyr Leu Ala Gly Met Pro
                85   90   95

Phe Ser Glu Ala Thr Gly Arg Met Ser Ser Lys Thr Pro Leu Thr Glu
            100   105   110

Glu Glu Leu Glu Cys Leu His Phe Ala Val Phe Asp Ala Thr His Ile
        115   120   125

Asp Val Leu Arg Lys Ala Arg Thr Ser His Leu Val Tyr Glu Glu Arg
    130   135   140

Arg Ala Met Ala Ser Ser Leu Leu Ala Ala Cys Arg Leu Ser Asp Thr
145   150   155   160

Pro Thr Phe Phe Gln Val Gly Phe Thr Val Cys Arg Arg Met Ser Asp
                165   170   175

Val Tyr Arg Gln Tyr Lys Phe Asn Arg Glu Val Gly Tyr Glu Gly Ser
            180   185   190

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

Cys Tyr Lys Arg Lys Pro Gly Ile Thr Val Asp Gly Arg Ile Val Gly
    210   215   220

Tyr Val Met Gly Lys Thr Gly Lys Asn Val Gly Arg Val Val Gly Tyr
225   230   235   240

Arg Val Glu Leu Glu Asp Gly Ser Gly Thr Val Ala Ala Thr Gly Leu
                245   250   255

Ser Glu Glu His Ile Gln Leu Leu Thr Tyr Ala His Leu Asn Ala His
260 265 270

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

Met Glu Arg Ser Ala Asn Thr Leu Arg His Pro Ser Phe Ser Arg Phe
290 295 300

Arg Asp Leu Ala Ser Asn Pro Gly Val Lys Val
305 310 315

<210> 527
<211> 94
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 527
Met Lys Ile Arg Lys Ser Arg Asn Arg Asn Tyr Pro Glu Asp Met Val
1 5 10 15

Tyr His Ala Thr Asn Arg Asp Ser Leu Leu Tyr Pro Lys Tyr Val Met
20 25 30

Gly Ser Val Phe Ile Ser Gln Asp Gly Thr Phe Arg Ile Cys Val Met
35 40 45

Ala Gly Thr Trp Asp His Val Gly Ser Glu Val Leu His His Ala Arg
50 55 60

Asp Ile Gln Ser Leu Gly Ala Gly Arg Arg Lys Leu His Arg Val Met
65 70 75 80

Arg Arg Leu Arg Arg Asn Leu Gln Gln Val Gly Val Lys Val
85 90

<210> 528
<211> 111
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 528
Met Arg Met Pro Thr Glu Glu Glu Arg Thr Ile Arg Cys Leu Leu Ala
1 5 10 15

Asp Ile His Glu Pro Leu Asn Leu Leu Phe Pro Gly Ile Arg Val Lys
20 25 30

Ala Glu Thr Met Pro Leu Gly Trp Gly Asp Ser Ile Cys Ala Leu Val
35 40 45

Leu Arg Val Ser Tyr Glu His Leu Thr Leu Gly Arg Leu Glu Tyr Met
50 55 60

His Glu Val Pro Ile Leu His Leu Ser Gln Trp Gly Arg Asp Gly Leu
65 70 75 80

Leu Gln His Leu Met Asn Glu Ile Pro Arg Arg Val Leu Asp Gly Met
85 90 95

Leu Arg Gln Ala Gln Lys Tyr Ser Gln Ser Asn Trp Tyr Ser Lys
100 105 110

<210> 529
<211> 807
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 529
Met Thr Thr Ile Arg Ile Leu Asp Leu Glu Thr Glu Ser Tyr Glu His
1 5 10 15

Lys Gly Arg Lys Ala Ser Pro Phe Asp Pro Arg Asn Tyr Ile Val Met
20 25 30

Ala Gly Trp Arg Asp Asp Val Asp Gly Lys Val Gly Gln Lys Val Glu
35 40 45

His Arg Phe Arg Ser Arg Ala Glu Ala Glu Asp Pro Asn Asn Arg Trp
50 55 60

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

Glu Ser Asn Trp Phe Phe Thr Arg Tyr Arg Asp Glu Tyr Leu Ala Phe
85 90 95

Leu Arg Arg Gly Gly Arg Val Trp Cys Thr Gln Gln Ala Glu Tyr Leu
100 105 110

Leu Ser His Gln Thr Trp Leu Tyr Pro Ala Leu Asp Glu Leu Ala Pro
115 120 125

Lys Tyr Gly Gly Thr His Lys Val Asp Gly Ile Lys Met Leu Trp Asp
130 135 140

Gln Gly Val Leu Thr Ser Glu Met Asp Gln Asp Leu Leu Ser Glu Tyr
145 150 155 160

Leu Ser Gly Pro Cys Gly Asp Ile Glu Asn Thr Ala Leu Val Phe Tyr

```
                165                 170                 175

Gly Gln Leu Met Lys Leu Gln Ala Arg Gly Met Trp Ala Gly Tyr Leu
            180                 185                 190

Glu Arg Cys Glu Ala Leu Ile Gly Phe Ser Ala Met Glu Cys Ala Gly
        195                 200                 205

Leu Lys Val Asp Leu Glu Val Ala Lys Val Asn His Ala Lys Gln Leu
    210                 215                 220

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

Phe Pro Glu Tyr Phe Glu Phe Lys Tyr Thr Ser Leu Tyr His Met Ser
                245                 250                 255

Ala Trp Leu Tyr Gly Gly Glu Val Arg Tyr Lys Gly Arg Val Pro Tyr
            260                 265                 270

Glu Asp Gly Arg Met Glu Lys Ala Asp Phe Val Arg Phe Gly Thr Ala
        275                 280                 285

Lys Arg Gly Thr Pro Ile Glu Ser Thr Ser Val Arg Val Pro Ile His
    290                 295                 300

Glu Val Thr Asp Gln Gly Glu Trp His Trp Pro Thr Ile Thr Glu Leu
305                 310                 315                 320

Ala Thr Lys His Gly Pro Val Ile Thr Phe Ser Ala Gly Lys Asn Lys
                325                 330                 335

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

Trp Asp Asp Asp Gln Arg Phe Arg Phe Pro Gly Leu Ile Asn Leu Thr
        355                 360                 365

Asn Leu Pro Glu Val Val Arg Glu Lys Phe Leu Gly Lys Arg Pro Glu
    370                 375                 380

Phe Gln Cys Ala Leu Thr Leu Ala Asp Gly Ser Pro Val Phe Ser Thr
385                 390                 395                 400

Ser Gly Asp Ala Leu Lys Ala Leu Glu Lys Gln Gly Phe Glu Ala Ala
                405                 410                 415

Lys Leu Leu Met Arg Leu Ala Glu Leu His Lys Asp Asn Ser Ser Phe
            420                 425                 430

Tyr Ile Thr His Thr Tyr Asn Lys Asp Gly Thr Ile Lys Asp Thr Lys
```

435 440 445

Gly Met Leu Gln Tyr Val Asp Asp Gly Ile Ile His His Ser Leu
450 455 460

Asn Thr Thr Ala Thr Ala Thr Thr Arg Leu Ser Ser Ser Arg Pro Asn
465 470 475 480

Leu Gln Gln Leu Pro Ser Lys Asp Glu Asp Asp Pro Glu Ala Gly Ser
485 490 495

Arg Val Lys Glu Met Phe Val Ser Arg Phe Gly Ala Asp Gly Met Ile
500 505 510

Gly Glu Thr Asp Tyr Thr Ala Leu Glu Val Val Met Leu Ala Ala Leu
515 520 525

Ser Lys Asp Arg Asn Leu Leu Ala Lys Leu Met Ala Gly Thr Asp Met
530 535 540

His Leu Tyr Arg Leu Ala Gly Lys His Asn Asn Trp Asn Gly Phe Asp
545 550 555 560

Tyr Asp Gln Leu Val Ala Ile Lys Lys Asp Pro Asn His Pro Trp His
565 570 575

Gly Arg Met Met Gln Ala Arg Lys Asn Ile Lys Pro Lys Ala Phe Ser
580 585 590

Ala Gln Tyr Gly Ala Ser Ala Ala Gly Ile Ala Phe Asn Thr Gly Cys
595 600 605

Thr Val Glu Glu Ala Gln Glu Phe Leu Asp Asn Glu Ala Ala Leu Phe
610 615 620

Pro Glu Ser Ile Ala Phe Arg Gln Ile Val Arg Asp Ser Ala Glu Ala
625 630 635 640

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

Phe Ser Glu Met Gly Pro Asp Gly Asn Trp Arg Gln Tyr Arg Arg Gly
660 665 670

Phe Trp Gln Ala Pro Gly Gly Thr Cys Tyr Ser Phe Arg Gln Gln Glu
675 680 685

Arg Trp Asp Lys Glu Gln Arg Lys Thr Val Met Asp Phe Lys Asp Thr
690 695 700

Gln Ile Ala Asn Tyr Trp Asn Gln Gly Glu Ala Gly Phe Met Met Thr

705 710 715 720

Val Ser Val Gly Arg Ile Phe Arg Trp Met Leu His Arg Pro Gly Phe
725 730 735

Met Val Thr Glu Phe Leu Ile Asn Asn Val His Asp Ala Val Tyr Thr
740 745 750

Asp Cys His Lys Asp Thr Ala Ala Glu Val Asn Lys Gly Val Arg Asp
755 760 765

Ile Met Ala Asp Ala Ala Arg Tyr Met Ser Glu Arg Leu Gly Tyr Asp
770 775 780

Ile Ala Asp Val Pro Phe Pro Ala Val Ala Glu Met Gly Pro Asn Met
785 790 795 800

Phe Asn Met Glu Val Ile Gln
805

<210> 530
<211> 103
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 530
Val Lys Glu Leu His Pro Leu His Thr Pro Glu Phe Val Lys Thr Phe
1 5 10 15

Leu Asp Gln Thr Gly Cys Leu Pro Gly Val Arg Arg Thr Gly Arg Thr
20 25 30

Thr Gly Ile Ala Leu Gln Ala Ile Gly Met Ala Leu Ser His Pro Arg
35 40 45

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

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

Leu Val Arg Pro Thr Thr Arg Ala Asp Gly Arg Ser Val Ser Ile Val
85 90 95

Phe Lys Thr Leu Pro Asn Ala
100

<210> 531
<211> 349
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 531
Met Thr Gln Gln Leu Asn Ala Leu Gln Ala Ala Leu Ala Leu Ala Asn
1 5 10 15

Lys Ala Ala Glu Thr Ala Thr Ile Asp Met Ser Glu Thr Ser Thr Gly
20 25 30

Gly Gly Gly Gly Arg Ile Phe Pro Ala Gly Thr Ala Met Gly Arg Phe
35 40 45

Cys Ile Tyr Ile Glu Leu Gly Asp His Ala Lys Glu Phe Gln Gly Lys
50 55 60

Leu Lys Asn Pro Ala Pro Gln Ile Arg Leu Gly Phe Ala Leu Trp Gly
65 70 75 80

Asp Val Asn Pro Gln Ala Gly Asn Pro Gln Ser Arg Pro Asp Asp Leu
85 90 95

Phe His Thr Tyr Glu Ala Asp Gly Ser Ile Lys Pro Gly Leu Phe Arg
100 105 110

Thr Phe Glu Met Thr Leu Gly Asn Asn Glu Lys Ser Lys Thr Lys Leu
115 120 125

Ala Phe Asp Lys Met Asn Trp Ser Gly Gln His Thr His Phe Ala Gln
130 135 140

Met Leu Gly Gln Ala Phe Ile Ile Pro Ile Lys Arg Thr Lys Ile Thr
145 150 155 160

Lys Gly Asn Asn Ala Gly Lys Glu Arg Asn Asp Ile Asp Trp Gly Gly
165 170 175

Ile Met Lys Pro Tyr Asn Pro Val Asp Gly Ser Pro Tyr Asn Val Pro
180 185 190

Glu Leu Pro Met Asp Leu Leu Gln Tyr Phe Phe Phe Asp Ala Pro Thr
195 200 205

Lys Glu Thr Trp Asp Ala Leu Tyr Ile Glu Gly Thr Ser Asp Asn Gly
210 215 220

Lys Ser Lys Asn Phe Leu Gln Glu Thr Ile Arg Ser Ala Thr Asn Phe
225 230 235 240

Pro Gly Ser Ala Leu His Ile Met Leu Gly Gly Gly Asp Asp Leu Ile
245 250 255

```
Ile Lys Pro Thr Ser Gln Ala Ala Gly Ser Asn Leu Pro Ala Val Pro
            260                 265                 270

Asn Val Ala Ala Asp Ala Gly Val Ala Ala Ala Pro Ala Val Pro Ala
        275                 280                 285

Val Pro Gln Ala Val Ala Gln Thr Ala Pro Ser Val Pro Gln Val Ala
    290                 295                 300

Asn Val Ala Ala Pro Val Val Gly Thr Ala Glu Ala Gln Asn Val Leu
305                 310                 315                 320

Pro Asp Val Pro Gln Val Ala Gln Thr Ala Ala Pro Ala Ala Val Glu
                325                 330                 335

Val Pro Ala Val Pro Val Val Pro Ala Val Pro Gln Val
            340                 345


<210> 532
<211> 313
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 532
Met Arg Leu Pro Ser Glu Glu Phe Leu Ala Gly Leu Ser Ala Gln Phe
1               5                   10                  15

Asp Arg Ser Met Ala Gly Gly Thr Leu Val Cys Asp Ala Asp Gly Pro
            20                  25                  30

Ala Tyr Val Ala Ala Ala Thr Ala Lys Thr Leu Asp Thr Ala Leu Arg
        35                  40                  45

Arg Phe Trp Lys Leu Ile Leu Glu Gln Gln Phe Leu Ala His Cys Thr
    50                  55                  60

Gly Thr Arg Val His Leu Thr Ala Ala Gly Gly Ala Lys Ala Tyr Arg
65                  70                  75                  80

Asp Thr Tyr Pro Thr Met Lys Pro Tyr Gln Gly Gln Arg Lys Gly Lys
                85                  90                  95

Ala Lys Pro Ala Leu Leu Glu Pro Leu Arg Arg Ala Val Ala Asp Val
            100                 105                 110

His Glu Arg Gly Gly Ala Pro Glu Gly Ile Asp Val Ile Leu His Thr
        115                 120                 125

Phe Phe Glu Ala Asp Asp Gly Met Met Met Asp Ala Tyr Ala Met Gln
    130                 135                 140
```

```
Asp Lys Ala Ile Ile Arg Ser Asp Asp Lys Asp Leu Arg Met Thr Ile
145                 150                 155                 160

Tyr Pro Tyr Trp Glu Ile Asp Thr Ala Cys Val Ser Arg Ile Glu Gly
                165                 170                 175

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

Leu Lys Gly His Gly Arg Lys Phe Phe Leu Ala Gln Trp Leu Gly Gly
        195                 200                 205

Asp Thr Ala Asp Asn Ile Arg Gly Ile Asp Arg Phe Asn Gly Lys Leu
    210                 215                 220

Cys Gly Met Lys Thr Ala Phe Asp Ile Leu His Pro Ile Thr Asp Glu
225                 230                 235                 240

Asp Glu Ala Ile Asp Met Ile Leu Glu Ala Tyr Ala Lys Ile Lys Gln
                245                 250                 255

Asn Pro Leu Ala Glu Ala Glu Val Leu Trp Met Arg Arg Thr Pro Thr
            260                 265                 270

Asp Asn Ala Ala Gln Tyr Leu Leu Ser Arg Asp Leu Arg Pro Ala Phe
        275                 280                 285

Arg Gln Trp Ile Ile Glu Leu Asp Ala Tyr His Glu Ala Leu Leu Gln
    290                 295                 300

Lys Arg Arg Glu Ser Asp Tyr Asp Glu
305                 310


<210> 533
<211> 146
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 533
Met Thr Ser Glu Pro Lys Val Tyr Gln Ile Pro Arg Ser Gln Gln Arg
1               5                   10                  15

Thr Phe Thr Leu Lys Leu Trp Ala Glu Gln Asn Lys Leu Cys Pro Leu
            20                  25                  30

Cys Gly Lys Pro Ile Asp Ile Ser Val Lys Gly Glu Ala Val Met Asp
        35                  40                  45

His Asp His Glu Thr Gly Leu Val Arg Gly Val Leu His Arg Ser Cys
```

50 55 60

Asn Thr Ala Glu Gly Lys Ile Thr Asn Ala Ala Gly Ser Trp Gly Cys
65 70 75 80

Lys Ser Met Lys Tyr Ser Asp Ile Ile Pro Tyr Leu Arg Ala Leu Leu
85 90 95

Thr Tyr Leu Glu Gly Pro Lys His Pro Leu Ile Tyr Pro Leu His Lys
100 105 110

Thr Asp Glu Glu Lys His Glu Ala Lys Leu Ala Lys Arg Arg Gln Ala
115 120 125

Ala Ala Lys Arg Lys Ala Ala Met Ala Val Ala Lys His Asn Ala Arg
130 135 140

Asn Val
145

<210> 534
<211> 348
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 534
Met Ser Lys Leu Arg Lys Gln Phe Thr Asn Glu Tyr Leu Arg Asn Val
1 5 10 15

Tyr Val Glu Leu Gly Leu Lys Lys Gly Ala Glu His Leu Thr Glu His
20 25 30

Ser Arg Phe Gly Glu Val Ser Arg Gln Cys Phe Arg Asn Trp Cys Ile
35 40 45

Lys Leu Gly Phe His Asp Ser Arg Thr Arg Gly Met Tyr Ala Lys Lys
50 55 60

Gly Ala Met His Trp Leu Gly Arg Lys Ala Ala Glu Val Val Arg Lys
65 70 75 80

Phe Pro Gly Ala Val Gly Asn Val Val Gly Gln Gly Pro Lys Val Leu
85 90 95

Ser Leu Asp Ile Glu Thr Ser Pro Ile Glu Gly Trp Val Trp Ser Leu
100 105 110

Trp Lys Gln Asn Val Gly Leu Asn Gln Ile Lys Arg Asp Trp Thr Ile
115 120 125

```
Leu Ser Phe Cys Ala Lys Trp Met His Ser Asp Glu Val Ile Tyr Met
    130                 135                 140

Asp Cys Gln Gly Asp Pro Leu Asp Asp Met His Leu Leu Val Ala Leu
145                 150                 155                 160

His Lys Leu Leu Asp Glu Ala Asp Ile Ile Ile Val Gln Asn Gly Lys
                165                 170                 175

Arg Phe Asp Val Pro Lys Ile Asn Ala Arg Phe Phe Leu Asn Lys Met
            180                 185                 190

Pro Pro Pro Arg Pro Phe Lys Val Ile Asp Thr Leu Ile Ile Ala Lys
        195                 200                 205

Gln Gln Phe Ala Phe Thr Ser Arg Lys Leu Glu Tyr Met Thr His Lys
    210                 215                 220

Ala Cys Thr Ile Lys Lys Arg Leu His Gly Lys Phe Pro Gly Phe Asp
225                 230                 235                 240

Leu Trp Ala Ala Cys Leu Gln Asp Asn Pro Glu Ala Trp Glu Glu Met
                245                 250                 255

Arg Leu Tyr Asn Ile Asp Asp Val Arg Ser Met Glu Glu Leu Tyr Ile
            260                 265                 270

Leu Met Arg Pro Trp Phe Val Gly His Pro Asn Val Ala Val Tyr Phe
        275                 280                 285

Asn Asp Ala Glu Pro Thr Ile Arg Cys Pro Lys Cys Gly Asp Thr Asp
    290                 295                 300

Val Lys Gln Glu Gly Trp Val His Thr Gln Thr Gly Lys Tyr Glu His
305                 310                 315                 320

Tyr His Cys Gly Gly Cys Gly Gly Trp Ser Arg Gly Arg Tyr Thr Arg
                325                 330                 335

Asn Thr Ser Glu Gln Arg Lys Ala Leu Leu Ser Asn
            340                 345


<210> 535
<211> 123
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 535
Met Ser Leu Ala Phe Pro Asp Ser Tyr Glu Ser Thr Ile Thr Thr Glu
1               5                   10                  15
```

```
Pro Tyr Arg Lys Gly Ala Ser Leu Glu Glu Arg Lys Val Gly Lys Leu
            20                  25                  30

Pro Met His Leu Val Val Glu Gly Phe Pro Leu Leu Lys Arg Glu Leu
        35                  40                  45

Ala Arg Met Met Gln Trp Ala Ala Glu Val Lys Gly Tyr Leu Pro His
    50                  55                  60

Asp Trp Lys Lys Met Thr Val Gly Glu Phe Lys Ser Ala Gln His Arg
65                  70                  75                  80

His Glu Ser Lys Arg Leu Ile Asp Gly Pro Leu Asp Asp Glu Ser Asn
                85                  90                  95

Leu Met His Leu Val His Glu Ala Phe Asn Ala Met Ala Ala Ala Glu
            100                 105                 110

Val Ala Leu Met Asp Arg Glu Lys Gly Asn Glu
        115                 120


<210> 536
<211> 116
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 536
Met Ser Lys Ile Cys Trp Cys Thr Arg Pro His Glu Thr Asp Glu Gly
1               5                   10                  15

Val Arg Val Ile Trp Ala Phe Asn Glu Arg Gly Ile Gly Val Asn Tyr
            20                  25                  30

Val Thr Ala Tyr Ile Thr Pro Ala Met Val Ser His Arg Asp Trp Ser
        35                  40                  45

Asp Val Ile Leu Pro Asp Ile Leu Arg Glu Met Ala Glu Arg Leu Glu
    50                  55                  60

Arg Glu Val Lys Leu Val Glu Leu Arg Trp Phe Arg Ala Glu Ile Leu
65                  70                  75                  80

Ser Cys Gly Glu Trp Arg Asp Tyr Arg Ala Met Thr Leu Glu Gly Ala
                85                  90                  95

Val Ser Leu Ala Glu Ala Glu Trp Gly Pro Glu Asp Ile Gly Arg Val
            100                 105                 110

Ile Glu Arg Arg
        115
```

<210> 537
<211> 816
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 537
Met Asp Leu Ile Gln Gln Gln Ile Ala His Glu Glu Ala Leu Val Gly
1 5 10 15

Ala Ala Gln Asn Asp Ala Arg Ile Ala Leu Glu Lys Ala Ile Ala Gln
20 25 30

Gly Ser Ile Asp Arg Ile Pro Arg Ala Arg Ile Met Leu Met Arg Met
35 40 45

Leu Pro Ile Val Thr Glu Ala Ile Phe Ala His Gln Glu Ala Lys Ala
50 55 60

Ala Gly Pro Ala Ala Lys Leu Arg His Leu Leu Arg Ile Ile Asp Ala
65 70 75 80

Gln Asp Leu Ala Val Met Ala Leu Arg Ala Gly Leu Ser Met Leu Ile
85 90 95

Asn Tyr Pro Thr Ile Thr Ala Thr Lys Tyr Tyr Thr His Met Gly Lys
100 105 110

Ile Leu Cys Arg Glu Ile Glu Val Arg Leu Ala Phe Lys Val Asn Gln
115 120 125

Pro Tyr Tyr Asp Arg Thr Leu Asp Tyr Leu Lys Thr Ser Arg Thr Arg
130 135 140

Ser Val Arg His Ile Gln Lys Thr Met Asp Ala Leu Leu Asp Ala Val
145 150 155 160

Leu Pro Glu Glu Ala Arg Ile Asp Leu Pro Asp Gly Asp Tyr Leu Arg
165 170 175

Leu Gly Lys Phe Ile Gly Asp Pro Leu Ile Gln Cys Gly Leu Phe Glu
180 185 190

Pro Asn Arg Phe Thr Gly Arg Gly Gly Thr Ser Val His Leu Glu Pro
195 200 205

Ser Pro Glu Ala Lys Glu Phe Leu Gln Asp Pro Ser Ala Ala Met Thr
210 215 220

Trp Gly Gly Pro Gly Arg Ser Val Met Leu Ala Pro Pro Arg Pro Trp

225 230 235 240

Asn Asp Trp Cys Asp Gly Gly Tyr Tyr Ser Ala Lys Ala Gln Lys His
245 250 255

His Val Leu Val Arg Arg Thr Lys His Gln Thr Lys Arg Ala Arg Gln
260 265 270

Met Gln Leu Arg His Leu Gly Arg Asp Lys Met Pro Arg Val Tyr Glu
275 280 285

Ala Val Asn Ala Leu Gln Ser Val Ala Tyr Glu Ile Asn His Asp Val
290 295 300

Tyr Glu Ile Ile Glu Arg Val Phe Thr Ser Gly Gly Gly Val Leu Gly
305 310 315 320

Ile Pro Gln Arg Thr Tyr Pro Asp Lys Pro Glu Phe Pro Leu Gly Asp
325 330 335

Glu Trp Ala Lys Glu Asn Ala Ser Glu Gln Glu Leu Glu Ala Phe Asn
340 345 350

Arg Trp Lys Arg Ser Val His Arg Trp Tyr Thr Gly Glu Arg Glu His
355 360 365

Thr Ala Lys Leu Arg Glu Phe Ala Ala Leu Tyr Arg Val Val Arg Glu
370 375 380

His His Gly Lys Ala Val Tyr Phe Pro Met His Val Asp Ser Arg Gly
385 390 395 400

Arg Met Tyr Tyr Trp Gly Thr Pro Asn Pro Gln Gly Ser Asp Ile Ala
405 410 415

Lys Ala Cys Leu Arg Phe His Glu Lys Arg Ala Leu Gly Lys Arg Gly
420 425 430

Leu Tyr Trp Leu Lys Val His Val Ala Asn Ser Leu Gly Cys Asp Lys
435 440 445

Val Tyr Phe Asp Asp Arg Ala Ala Trp Val Asp Glu Arg Trp Asp Asp
450 455 460

Phe Gln Arg Ala Leu Asp Glu Gly Pro Glu Asn Tyr Pro Asn Leu Phe
465 470 475 480

Pro Glu Asp Glu Ser Pro Leu Cys Ala Ile Ala Gly Leu Leu Glu Leu
485 490 495

Arg Ala Ala Tyr Ala Ser Gly Asn Pro Glu Gly Tyr Ala Ser Gly Phe

500 505 510

Ile Val His Met Asp Ala Thr Cys Ser Gly Leu Gln His Tyr Ser Ala
515 520 525

Ile Leu Arg Asp Glu Ile Gly Gly Ala Tyr Val Asn Leu Leu Pro Pro
530 535 540

Gly Leu Ala Lys Ala Asp Ile Tyr Ser Arg Val Leu Gly Leu Val Asn
545 550 555 560

Glu Ser Leu Glu Arg Asp Arg Ala Glu Gly Ala Asp Gly Glu Ala Arg
565 570 575

Gly Tyr Ala Ile Leu Trp Asp Lys Ala Gly Leu Thr Arg Ser Leu Thr
580 585 590

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

Val Asp His Cys Leu Asp Tyr Leu Asp Glu Ser Gly Val Glu Ile Pro
610 615 620

Glu Gly Val Pro Ser Tyr Arg Leu Gly Ser Tyr Met Ala Thr Leu Ile
625 630 635 640

Leu Asp Ala Ile Arg Glu Thr Val Pro Ser Ala Val Phe Ala Met Glu
645 650 655

Trp Leu Gln Arg Leu Ala Arg Ala Leu Pro Asp Ala Ser Lys Asp Leu
660 665 670

His Trp Thr Thr Pro Leu Gly Met Gln Val Phe Gln Ser Tyr Pro Lys
675 680 685

Thr Glu Glu Val Arg Val Arg Leu Arg Ala Glu Ala Val Glu Tyr Val
690 695 700

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

Gly Ile Ala Pro Asn Phe Val His Gly Leu Asp Ser Ser His Leu Gly
725 730 735

Leu Thr Ala Leu Ala Cys Ala Ala Glu Gly Ile Pro Ile Gln Ala Ile
740 745 750

His Asp Ser Met Gly Thr Tyr Ala Ala Asp Val Asp Arg Met His Val
755 760 765

His Ile Arg Glu Gln Phe Ile Ala Met Tyr Ser Gly Pro Cys Val Leu

770 775 780

Val Glu Leu Ala Lys Gln Leu Gly Ile Glu Ala Thr Pro Pro Arg Arg
785 790 795 800

Gly Ser Leu Asn Leu Glu Ala Val Arg Asp Ser Trp Ala Phe Phe Cys
805 810 815

<210> 538
<211> 83
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 538
Met Ala Thr Met Lys Thr His Arg Pro Thr Val Met Ser Pro Thr Val
1 5 10 15

Glu Gly Ser Arg Thr Gly Lys Gly Thr Ala Arg Pro Val Thr Phe Thr
20 25 30

Ser Gln Gln Ile Glu Trp Leu Glu Gln Thr Phe Pro Glu His Gln Ile
35 40 45

Gly Pro Gly Thr Thr Met Glu Asp Ile Gln Phe Gln Ala Gly Arg Arg
50 55 60

Asp Val Val Arg Ala Val Arg Leu Arg Arg Arg Asp Ala Ile Ala Val
65 70 75 80

Glu Leu Lys

<210> 539
<211> 157
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 539
Met Asn Lys Ser Ile Trp Arg Val His Ala Lys Ala Gly Thr Pro Ser
1 5 10 15

Glu Leu Gln Gly Leu Cys Trp Leu Ala Ile Gln Glu Leu Glu Glu Phe
20 25 30

Thr Leu Phe Arg Ser Lys Asp Asp Ala Leu Asn Ala Met Leu Asp Ser
35 40 45

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

Leu Ala Gly Gly Ala Cys Ile Val Phe Glu Asp Asp Pro His Val Gly
65 70 75 80

Pro Cys Val Thr Ala Gln Trp Gln Tyr Val Leu Pro Arg Tyr Arg Asn
85 90 95

Thr Gly Val Val Arg Glu Phe Ile Arg Glu Leu His Arg Gln Ala Gly
100 105 110

Trp Gly Gln Ile Pro Leu Val Cys Trp Ser His Arg Glu Ser Asp Ser
115 120 125

Arg Tyr Thr Ile His Tyr Arg Arg Ala Lys Pro Tyr Gly Gln Glu Ser
130 135 140

Lys Glu Gly Ala Gly Gln Asp His His Arg Gln Thr Arg
145 150 155

<210> 540
<211> 98
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 540
Met Gly Lys Lys Val Lys Lys Val Leu Gly Lys Thr Ile Ile Gly Lys
1 5 10 15

Leu Ala Asp Gly Leu Leu Gly Thr Asp Leu Ser Gly Ala Gln Ser Asp
20 25 30

Ala Arg Lys Met Glu Glu Gln Asn Arg Leu Met Gln Gln Gln Ala Asp
35 40 45

Gln Leu Ala Arg Asn Gln Gln Val Asp Leu Thr Ala Glu Asn Val Ala
50 55 60

Gln Val Asp Leu Gly Ala Met Ala Asp Ala Thr Gly Thr Gly Thr Arg
65 70 75 80

Arg Arg Arg Asn Gln Ala Gly Thr Gly Val Ser Gln Thr Leu Gly Ile
85 90 95

Asn Tyr

<210> 541
<211> 510
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F510/08

<400> 541

```
Met Lys Thr Thr Ala Ala Met Leu Trp Glu Lys Leu Arg Asp Gly Ser
1               5                  10                  15

Val Glu Ser Arg Ala Ile Glu Phe Ala Lys Thr Thr Leu Pro Tyr Leu
            20                  25                  30

Met Val Asp Pro Met Ser Gly Ser Arg Gly Val Val Glu His Asp Phe
        35                  40                  45

Gln Ser Ala Gly Ala Leu Leu Val Asn Asn Leu Ala Ala Lys Leu Ala
    50                  55                  60

Arg Ser Leu Phe Pro Thr Gly Ile Pro Phe Phe Arg Ser Glu Leu Thr
65                  70                  75                  80

Asp Ala Ile Arg Arg Glu Ala Asp Ser Arg Asp Thr Asp Ile Thr Glu
                85                  90                  95

Val Thr Ala Ala Leu Ala Arg Val Asp Arg Lys Ala Thr Gln Arg Leu
            100                 105                 110

Phe Gln Asn Ala Ser Leu Ala Val Leu Thr Gln Val Ile Lys Leu Leu
        115                 120                 125

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

Val Val Ala Trp Ser Leu Arg Ser Tyr Ala Val Arg Arg Asp Ala Thr
145                 150                 155                 160

Gly Arg Trp Met Asp Ile Val Leu Lys Gln Arg Tyr Lys Ser Lys Asp
                165                 170                 175

Leu Asp Glu Glu Tyr Lys Gln Asp Leu Met Arg Ala Gly Arg Asn Leu
            180                 185                 190

Ser Gly Ser Gly Ser Val Asp Leu Tyr Thr His Val Gln Arg Lys Lys
        195                 200                 205

Gly Thr Ala Met Glu Tyr Ala Glu Leu Tyr His Glu Ile Asp Gly Val
    210                 215                 220

Arg Val Gly Lys Glu Gly Arg Trp Pro Ile His Leu Cys Pro Tyr Ile
225                 230                 235                 240

Val Pro Thr Trp Asn Leu Ala Pro Gly Glu His Tyr Gly Arg Gly His
                245                 250                 255

Val Glu Asp Tyr Ile Gly Asp Phe Ala Lys Leu Ser Leu Leu Ser Glu
```

260 265 270

Lys Leu Gly Leu Tyr Glu Leu Glu Ser Leu Glu Val Leu Asn Leu Val
275 280 285

Asp Glu Ala Lys Gly Ala Val Val Asp Asp Tyr Gln Asp Ala Glu Met
290 295 300

Gly Asp Tyr Val Pro Gly Gly Ala Glu Ala Val Arg Ala Tyr Glu Arg
305 310 315 320

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

Val Val Arg Leu Asn Gln Ala Phe Met Tyr Gly Ala Asn Gln Arg Asp
340 345 350

Ala Glu Arg Val Thr Ala Glu Glu Val Arg Ile Thr Ala Glu Glu Ala
355 360 365

Glu Asn Thr Leu Gly Gly Thr Tyr Ser Leu Leu Ala Glu Asn Leu Gln
370 375 380

Ser Pro Leu Ala Tyr Val Cys Leu Ser Glu Val Asp Asp Ala Leu Leu
385 390 395 400

Gln Gly Leu Ile Thr Lys Gln His Lys Pro Ala Ile Glu Thr Gly Leu
405 410 415

Pro Ala Leu Ser Arg Ser Ala Ala Val Gln Ser Met Leu Asn Ala Ser
420 425 430

Gln Val Ile Ala Gly Leu Ala Pro Ile Ala Gln Leu Asp Pro Arg Ile
435 440 445

Ser Leu Pro Lys Met Met Asp Thr Ile Trp Ala Ala Phe Ser Val Asp
450 455 460

Thr Ser Gln Phe Tyr Lys Ser Ala Asp Glu Leu Glu Ala Glu Ala Glu
465 470 475 480

Gln Gln Arg Gln Gln Ala Ala Gln Ala Gln Ala Ala Gln Glu Thr Leu
485 490 495

Leu Glu Gly Ala Ser Asp Met Thr Asn Ala Leu Ala Gly Val
500 505 510

<210> 542
<211> 322
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 542
Met Thr Gln Pro Asn Asp Gln Gln Leu Pro Pro Gly Leu Ala Asn Leu
1   5   10   15

Val Ala Asn Val Pro Pro Ala Ala Ala Pro Thr Pro Ser His Val Gln
            20   25   30

Val Leu Pro Asn Pro Val Ile Gln Pro Gln Ala Pro Val Gln Pro Gly
        35   40   45

Gln Val Gly Ala Pro Gln Gln Leu Ala Ile Pro Thr Gln Gln Pro Gln
    50   55   60

Pro Val Pro Thr Ser Ala Met Thr Pro His Tyr Gln Pro Val Ala Val
65   70   75   80

Pro Val Ala Gly Gln Pro Val Val Pro Gln Ala Pro Ala Gln Pro Ala
                85   90   95

Pro Val Ala Pro Pro Ala Ala Gly Ala Val Leu Pro Glu Asn Leu Glu
            100   105   110

Val Pro Pro Pro Pro Ala Phe Thr Pro Asn Gly Glu Ile Val Gly Thr
        115   120   125

Leu Ala Gly Asn Leu Glu Gly Asp Pro Gln Leu Ala Pro Ser Ile Ser
    130   135   140

Tyr Leu Glu Ala Phe Ser Asp Lys Leu Asp Thr Val Arg Ala Phe Gly
145   150   155   160

Lys Ala Ala Glu Asn Arg Asp Pro Arg Phe Ile Asp Glu His Tyr Leu
                165   170   175

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

Lys Gly Val Leu Thr Tyr Val Asp Ala Gln Thr Lys Ala Val Leu Asn
        195   200   205

Gln Thr Tyr Ala Ala Val Gly Gly Glu Ala Val Leu Lys Gln Ala Ala
    210   215   220

Gly Val Phe Asn Gln His Ala Asp Pro Ala Thr Lys Ala Ala Ile Gly
225   230   235   240

Arg Leu Met Asp Ser Gly Asp Ala Gln Ala Met Gln Tyr Ala Ala Lys
                245   250   255

Gln Ile Val Ala Phe Ala Gln Gly Ser Gly Ala Val Val Gln Ala Thr
            260   265   270

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

Glu Gln Tyr Arg Leu Glu Val Ser Lys Leu Pro Leu Asn Ala Ser Glu
    290   295   300

Ala Glu Met Ala Ala Leu Arg Glu Arg Arg Lys Ala Gly Met Ala Gln
305   310   315   320

Gly Ile

<210> 543
<211> 335
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 543
Met Ser Phe Leu Asn Asp Leu Thr Arg Pro Asn Tyr Ala Gly Lys Asn
1   5   10   15

Ala Asp Val Asp Ile His Leu Glu Glu His Leu Gly Ile Val Asp Lys
            20   25   30

His Phe Ala Tyr Thr Ser Lys Phe Ala Pro Leu Met Asn Ile Arg Asp
        35   40   45

Leu Arg Gly Ser Asn Val Val Arg Leu Asp Arg Leu Gly Asn Val Glu
    50   55   60

Ala Lys Gly Arg Arg Ala Gly Glu Glu Leu Glu Arg Ser Arg Val Val
65   70   75   80

Asn Asp Lys Trp Asn Leu Thr Val Asp Thr Leu Leu Tyr Leu Arg His
                85   90   95

Gln Phe Asp His Gln Asp Glu Trp Thr Gln Ser Phe Asp Met Arg Lys
            100   105   110

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

Ala Cys Leu Ile Gln Val Ile Lys Ala Ala Ala Met Asp Ala Pro Val
    130   135   140

Asp Leu Glu Asp Ala Phe Ser Pro Gly Val Leu Glu Lys Leu Asp Leu
145   150   155   160

```
Thr Gly Leu Thr Ala Lys Gln Ala Ala Asp Lys Ile Val Arg Met His
                165                 170                 175

Arg Arg Val Val Glu Thr Phe Ile Asp Arg Asp Leu Gly Asp Ala Val
            180                 185                 190

Tyr Ser Glu Gly Leu Thr Pro Met Ser Pro Arg Val Phe Ser Leu Leu
        195                 200                 205

Leu Glu His Asp Lys Leu Met Asn Val Glu Tyr Gln Ala Thr Gly Ala
    210                 215                 220

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

Val Leu Glu Thr Pro Arg Phe Ala Thr Lys Ala Ile Ala Ala His Pro
                245                 250                 255

Leu Gly Arg His Phe Asn Val Ser Ala Glu Glu Ser Glu Arg Gln Ile
            260                 265                 270

Ala Leu Phe Leu Pro Ser Lys Thr Leu Ile Thr Ala Gln Val Ala Pro
        275                 280                 285

Val Gln Ala Lys Leu Trp Glu Asp Asn Glu Lys Phe Ser Trp Val Leu
    290                 295                 300

Asp Thr Phe Gln Met Tyr Asn Ile Gly Ala Arg Arg Pro Asp Thr Ala
305                 310                 315                 320

Gly Ala Ile Glu Leu Lys Gly Ile Gly Ala Phe Asp Ile Thr Ala
                325                 330                 335


<210> 544
<211> 184
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 544
Met Leu Leu Leu Asp Ala Val Asn Val Ile Leu Arg Lys Ile Gly Glu
1               5                   10                  15

Leu Pro Ile Pro Ser Met Asp Glu Thr Tyr Pro Thr Met Ala Ile Ala
            20                  25                  30

Leu Pro Glu Leu Glu Asp Gln Arg Ile Gln Leu Leu Thr Gln Gly Trp
        35                  40                  45

Trp Phe Asn Thr Trp Trp Lys His Lys Leu Thr Pro Asp Pro Gln Gly
    50                  55                  60
```

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

Asp Leu Gln Trp Asp Gly Leu Gly Val Arg Asp Ala Asn Thr Gly Asp
85 90 95

Asp Arg Ile Gly Lys Ser Val Glu Gly Arg Leu Val Leu Ser Arg Glu
100 105 110

Trp Asp Arg Ile Pro Glu Ile Ala Gln Arg Val Ile Ala His Gln Ala
115 120 125

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

Val Ile Ala Gln Glu Leu Gln Ala Tyr Gln Asn Glu Leu Ser Arg Met
145 150 155 160

His Thr Arg Ser Arg Pro Leu Asn Thr Gln Ala Lys Arg Ser Phe Ser
165 170 175

Arg Trp Arg Arg Ser Leu Arg Thr
180

<210> 545
<211> 826
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 545
Met Ser Tyr Lys Gln Ser Ala Tyr Pro Asn Leu Leu Met Gly Val Ser
1 5 10 15

Gln Gln Val Pro Phe Glu Arg Leu Pro Gly Gln Leu Ser Glu Gln Ile
20 25 30

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

Glu Leu Met Ala His Leu Leu His Thr Asp Gln Pro Trp Pro Arg Pro
50 55 60

Phe Leu Tyr His Thr Asn Leu Gly Gly Arg Ser Ile Ala Met Leu Val
65 70 75 80

Ala Gln His Arg Gly Glu Leu Tyr Leu Phe Asp Glu Arg Asp Gly Arg
85 90 95

Leu Leu Met Gly Gln Pro Leu Ala His Asp Tyr Leu Lys Ala Asp Asp

```
            100                 105                 110

Tyr Arg Gln Leu Arg Ala Ala Thr Val Ala Asp Asp Leu Phe Ile Ala
        115                 120                 125

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

Asp Pro Asn Lys Ala Gly Trp Leu Tyr Ile Lys Ala Gly Gln Tyr Ser
145                 150                 155                 160

Lys Ala Phe Ser Met Thr Ile Lys Val Lys Asp Asn Ala Thr Gly Thr
                165                 170                 175

Thr Tyr Ser His Thr Ala Thr Tyr Val Thr Pro Asp Asn Ala Ser Thr
            180                 185                 190

Asn Pro Asn Leu Ala Glu Ala Pro Phe Gln Thr Ser Val Gly Tyr Ile
        195                 200                 205

Ala Trp Gln Leu Tyr Gly Lys Phe Phe Gly Ala Pro Glu Tyr Thr Leu
    210                 215                 220

Pro Asn Ser Thr Lys Lys Tyr Pro Lys Val Asp Pro Asp Ala Asn Ala
225                 230                 235                 240

Ala Thr Ile Ala Gly Tyr Leu Asn Gln Arg Gly Val Gln Asp Gly Tyr
                245                 250                 255

Ile Ala Phe Arg Gly Asp Ala Asp Ile Val Val Glu Val Ser Thr Asp
            260                 265                 270

Met Gly Asn Asn Tyr Gly Ile Ala Ser Gly Gly Met Ser Leu Asn Ala
        275                 280                 285

Thr Ala Asp Leu Pro Ala Leu Leu Pro Gly Ala Gly Ala Pro Gly Val
    290                 295                 300

Gly Val Gln Phe Met Gly Gly Ala Val Met Ala Thr Gly Ser Thr Lys
305                 310                 315                 320

Ala Pro Val Tyr Phe Glu Trp Asp Ser Ala Asn Arg Arg Trp Ala Glu
                325                 330                 335

Arg Ala Ala Tyr Gly Thr Asp Trp Val Leu Lys Lys Met Pro Leu Ala
            340                 345                 350

Leu Arg Trp Asp Glu Ala Thr Asp Thr Tyr Ser Leu Asn Glu Leu Glu
        355                 360                 365

Tyr Asp Arg Arg Gly Ser Gly Asp Glu Asp Thr Asn Pro Thr Phe Asn
```

370 375 380

Phe Val Thr Arg Gly Ile Thr Gly Met Thr Thr Phe Gln Gly Arg Leu
385 390 395 400

Val Leu Leu Ser Gln Glu Tyr Val Cys Met Ser Ala Ser Asn Asn Pro
405 410 415

His Arg Trp Phe Lys Lys Ser Ala Ala Ala Leu Asn Asp Asp Asp Pro
420 425 430

Ile Glu Ile Ala Ala Gln Gly Ser Leu Thr Glu Pro Tyr Glu His Ala
435 440 445

Val Thr Phe Asn Lys Asp Leu Ile Val Phe Ala Lys Lys Tyr Gln Ala
450 455 460

Val Val Pro Gly Gly Gly Ile Val Thr Pro Arg Thr Ala Val Ile Ser
465 470 475 480

Ile Thr Thr Gln Tyr Asp Leu Asp Thr Arg Ala Ala Pro Ala Val Thr
485 490 495

Gly Arg Ser Val Tyr Phe Ala Ala Glu Arg Ala Leu Gly Phe Met Gly
500 505 510

Leu His Glu Met Ala Pro Ser Pro Ser Thr Asp Ser His Tyr Val Ala
515 520 525

Glu Asp Val Thr Ser His Ile Pro Ser Tyr Met Pro Gly Pro Ala Glu
530 535 540

Tyr Ile Gln Ala Ala Ala Ser Ser Gly Tyr Leu Val Phe Gly Thr Ser
545 550 555 560

Thr Ala Asp Glu Met Ile Cys His Gln Tyr Leu Trp Gln Gly Asn Glu
565 570 575

Lys Val Gln Asn Ala Phe His Arg Trp Thr Leu Arg His Gln Ile Ile
580 585 590

Gly Ala Tyr Phe Thr Gly Asp Asn Leu Met Val Leu Ile Gln Lys Gly
595 600 605

Gln Glu Ile Ala Leu Gly Arg Met His Leu Asn Ser Leu Pro Ala Arg
610 615 620

Glu Gly Leu Gln Tyr Pro Lys Tyr Asp Tyr Trp Arg Arg Ile Glu Ala
625 630 635 640

Thr Val Asp Gly Glu Leu Glu Leu Thr Lys Gln His Trp Asp Leu Ile

645 650 655

Lys Asp Ala Ser Ala Val Tyr Gln Leu Gln Pro Val Ala Gly Ala Tyr
660 665 670

Met Glu Arg Thr His Leu Gly Val Lys Arg Glu Thr Asn Thr Lys Val
675 680 685

Phe Leu Asp Val Pro Glu Ala Val Val Gly Ala Val Tyr Val Val Gly
690 695 700

Cys Glu Phe Trp Ser Lys Val Glu Phe Thr Pro Pro Val Leu Arg Asp
705 710 715 720

His Asn Gly Leu Pro Met Thr Ser Thr Arg Ala Val Leu His Arg Tyr
725 730 735

Asn Val Asn Phe Gly Trp Thr Gly Glu Phe Leu Trp Arg Ile Ser Asp
740 745 750

Thr Ala Arg Pro Asn Gln Pro Trp Tyr Asp Thr Thr Pro Leu Arg Leu
755 760 765

Phe Ser Arg Gln Leu Asn Ala Gly Glu Pro Leu Val Asp Ser Ala Val
770 775 780

Val Pro Leu Pro Ala Arg Val Asp Met Ala Thr Ser Lys Phe Glu Leu
785 790 795 800

Ser Cys His Ser Pro Tyr Asp Met Asn Val Arg Ala Val Glu Tyr Asn
805 810 815

Phe Lys Ser Asn Gln Thr Tyr Arg Arg Val
820 825

<210> 546
<211> 181
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 546
Met Ala Phe Trp Leu Pro Leu Leu Ala Ala Gly Gly Met Ser Ala Leu
1 5 10 15

Gln Gln Gly Leu Ala Asn Lys Glu Glu Arg Asn Lys Ile Lys Ala Glu
20 25 30

Asn Lys Ala Arg Leu Lys Thr Asp Leu Asp Asn Leu Gly Ala Ala Ala
35 40 45

Arg Asp Ile Ala Asn Leu Gly Val Met Ala Ala Ser Tyr Arg Lys Gln
50 55 60

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

Gly Ser Ala Glu Ala Gln Ala Gly Ala Phe Gly Val Lys Gly Ala Ser
85 90 95

Val Asp Ala Val Ala Leu Asp Ile Glu Arg Glu Val Gly Glu Ala Leu
100 105 110

Ile Gln Ile Asp Asp Asn Leu Asp Asn Gln Met Trp Asn Leu Ala Glu
115 120 125

Gln Ala His Ser Ile Gln Ala Gln Ala Lys Ala Gly Leu Leu Gly Gln
130 135 140

Lys Ser Thr Thr Ala Gly Gln Arg Ser Pro Leu Val Ala Gly Leu Met
145 150 155 160

Ser Ala Gly Ser Leu Tyr Ala Ser Gln Tyr Phe Lys Phe Gly Ala Thr
165 170 175

Pro Lys Gly Gly Asn
180

<210> 547
<211> 898
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 547
Met Ala Glu Ser Gln Arg Ala Ser Gln Glu Leu Gly Ile Asn Val Gly
1 5 10 15

Gln Thr Gln Leu Gln Pro Gly Gln Ser Ala Arg Arg Gly Val Arg Asp
20 25 30

Ser Glu Val Asn Tyr Ser Gly Pro Ser Val Gly Ser Gln Ile Leu Asp
35 40 45

Gly Ile Leu Gly Ala Gly Gln Gln Ile Ala Gly Lys Trp Phe Glu His
50 55 60

Asn Val Gln Gln Glu Val Leu Arg Gly Glu Arg Ala Arg Met Ala Gly
65 70 75 80

Glu Ala Glu Glu Ala Val Asp Ser Asn Val Leu Ala Lys Pro Phe Val
85 90 95

```
Lys Gly Gly Trp Arg Lys Gln Asp Tyr Arg Ile Ala Gln Ala Asp Phe
            100                 105                 110

Ser Leu Lys Met Gln Arg Phe Ile Ala Asn Lys Gly Arg Glu Met Thr
        115                 120                 125

Pro Glu Glu Phe Arg Lys Tyr Leu Ser Gln Glu Ala Thr His Val Leu
    130                 135                 140

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

Gln Gln Gln Lys Ala Glu Glu Gln Leu Phe Gly Met Gln Ala Lys Ala
                165                 170                 175

Tyr Met Asp Trp Ser Ile Asp Gln Ala Ala Arg Gly Phe Arg Thr Gln
            180                 185                 190

Gly Asn Ser Ile Leu Ala Lys Ala Val Gln Ala Gln Ala Thr Gly Asp
        195                 200                 205

Glu Leu Ser Arg Gln Leu Ser Leu Glu Glu Ala Gly Leu Phe Tyr Thr
    210                 215                 220

Asn Ile Met Thr Ser Glu Asp Ile Pro Leu Glu Val Arg Asp Lys Val
225                 230                 235                 240

Gly Met Gln Phe Leu Ala Ala Ser Leu Asp Met Asn Gln Arg Gly Ile
                245                 250                 255

Tyr Glu Gly Leu Arg Asp Ala Gly Phe Leu Asp Ser Met Ser Phe Asp
            260                 265                 270

Asp Arg Arg Ala Leu Asn Gly Leu Tyr Glu Lys Ser Lys Ala Gln Thr
        275                 280                 285

Arg Ala Lys Glu Ser Met Ala Thr Leu Arg Ala Asp Ala Asp Phe Gln
    290                 295                 300

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

Tyr Ser Arg Gly Met Val Glu Glu Gly Arg Trp Ser Asp Ala Gln Ala
                325                 330                 335

Ile Ser Phe Met Thr Lys Ala Met Thr Gly Leu Gly Asn Ala Gln Arg
            340                 345                 350

Met Gln Gly Ile Met Ala Ala Leu Glu Ala Gly Asp Ile Asn Ala Leu
        355                 360                 365
```

```
His Thr Leu Gly Thr Asn Val Thr Glu Ala Leu Glu Gln Trp Asp Lys
    370                 375                 380

Met Gln Ala Ala Asn Gly Ser Ser Leu Thr Asp Arg Leu Val Gln Gly
385                 390                 395                 400

Thr Gln Leu Gly Leu Arg Leu Gly Thr Phe Pro Lys Thr Tyr Gly Glu
                405                 410                 415

Ser Val Gly Ser Ala Val Arg Met Ile Gln Ala Ala Lys Glu Gly Glu
            420                 425                 430

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

Ala Ser Ala Gln Glu Ile Asn Pro Ser Ala Gly Asn Val Met Leu Ser
    450                 455                 460

Gly Ile Pro Glu Ala Glu Gln Gly Ala Val Ala Trp Ala Leu Lys Gln
465                 470                 475                 480

Met Lys Met Gly Ile Ala Pro Ala Gln Ala Leu Arg Glu Phe Ser Ala
                485                 490                 495

Asn Ala Glu Val Val Lys Gln Met Asp Glu Phe Glu Lys Gly Gln Asn
            500                 505                 510

Thr Lys Ala Phe Lys Asp Asn Leu Gly Lys Gln Val Asn Asp Lys Phe
        515                 520                 525

Val Asn Asn Ile Phe Gly Arg Ala Trp Asn Met Leu Thr Gly Glu Ser
    530                 535                 540

Asp Leu Ser Asn Asn Glu Ala Val Leu Ser Met Tyr Arg Arg Ala Thr
545                 550                 555                 560

Ile Asp Glu Ala Asn Trp Leu Ala Ser Asp Arg Lys His Ala Gly Leu
                565                 570                 575

Leu Thr Ser Asp Thr Gly Arg Glu Ala Leu Leu Glu Ile Ala Ala Ala
            580                 585                 590

Asn Val Arg Asn Arg Thr Ile Gln Val Gly Glu Gly Arg Asn Leu Lys
        595                 600                 605

Glu Gly Asp Leu Phe Ser Arg Arg Asp Ser Ala Pro Leu Ile Leu Pro
    610                 615                 620

Arg Gly Thr Thr Ala Glu Gln Leu Phe Gly Thr Asn Asp Thr Glu Thr
625                 630                 635                 640
```

```
Ile Gly Thr Val Leu Ala Glu Gln His Lys Pro His Val Glu Gly Leu
                645                 650                 655

Leu Gly Tyr Lys Ser Val Val Ala Phe Glu Tyr Asp Arg Thr Arg Gly
            660                 665                 670

Ser Leu Leu Ala Val Glu Tyr Asp Glu Asn Gly Val Ala Leu Asp Arg
        675                 680                 685

Thr Arg Val Asp Pro Gln Ala Val Gly Asn Glu Val Leu Lys Arg Asn
    690                 695                 700

Ala Asp Lys Leu Asn Ala Met Arg Gly Ala Glu Tyr Gly Ala Asn Val
705                 710                 715                 720

Lys Val Ser Gly Thr Asp Ile Arg Met Asn Gly Gly Asn Ser Ala Gly
                725                 730                 735

Met Leu Lys Gln Asp Val Phe Asn Trp Arg Lys Glu Leu Ala Gln Phe
            740                 745                 750

Glu Ala Tyr Arg Gly Glu Ala Tyr Lys Asp Ala Asp Gly Tyr Ser Val
        755                 760                 765

Gly Leu Gly His Tyr Leu Gly Ser Gly Asn Ala Gly Ala Gly Thr Thr
    770                 775                 780

Val Thr Pro Glu Gln Ala Ala Gln Trp Phe Ala Glu Asp Thr Asp Arg
785                 790                 795                 800

Ala Leu Asp Gln Gly Val Arg Leu Ala Asp Glu Leu Gly Val Thr Asn
                805                 810                 815

Asn Ala Ser Ile Leu Gly Leu Ala Gly Met Ala Phe Gln Met Gly Glu
            820                 825                 830

Gly Arg Ala Arg Gln Phe Arg Asn Thr Phe Gln Ala Ile Lys Asp Arg
        835                 840                 845

Asn Lys Glu Ala Phe Glu Ala Gly Val Arg Asn Ser Lys Trp Tyr Thr
    850                 855                 860

Gln Thr Pro Asn Arg Ala Glu Ala Phe Ile Lys Arg Met Ala Pro His
865                 870                 875                 880

Phe Asp Thr Pro Ser Gln Ile Gly Val Asp Trp Tyr Ser Ala Ala Thr
                885                 890                 895

Ala Glu
```

<210> 548
<211> 1337
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 548
Met Ala Lys Gln Phe Lys Gly Arg Met Thr Pro Lys Tyr Pro Leu Asp
1 5 10 15

Gln Val Gln Leu Asp Glu Ala Gln Val Gln Gly Gln Leu Asp Ala Val
20 25 30

Pro Thr Val Gly Phe Asp Ala Leu Thr Gly Gly Glu Ile Gly Glu Arg
35 40 45

Asn Val Ala Ala Gly Gln Arg Ala Asn Ala Arg Glu Leu Glu Arg Ile
50 55 60

Val Ala Asp Gln Glu Leu Pro Ala Leu Asp Arg Ala Ser Ala Leu Trp
65 70 75 80

Asn Gln Ser Thr Leu Val Gly Arg Trp Val Asp Ala Leu Gln Leu Asp
85 90 95

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

Ala Gly Thr Tyr Gly Val Gln Ala Leu Gln Ala Ala Gly Ile Gln Pro
115 120 125

Thr Asp Asn Tyr Leu Gln Ile Met Ala Arg Ala Gly Asn Ala Glu Asp
130 135 140

Ala Ala Tyr Leu Leu Ser Arg Ile Gln Arg Tyr Glu Gln Asp Glu Gln
145 150 155 160

Ile Val Arg Asp Asn Pro Tyr Trp Asn Phe Ala Val Gly Met Leu Asp
165 170 175

Pro Ala Ala Leu Ala Val Asp Ala Val Thr Phe Gly Ala Gly Arg Ala
180 185 190

Leu Arg Leu Gly Arg Ala Gly Met Ala Ala Ala Gly Gly Ala Gly Gln
195 200 205

Val Gly Tyr Val Ala Gly Leu Asp Ala Ala Gly Ala Asp Val Asp Ala
210 215 220

Gly Thr Tyr Ile Val Ala Gly Ala Leu Gly Ala Gly Val Gly Ala Leu
225 230 235 240

```
Leu Gly Ser Gly Ala Gly Arg Ile Ala Ala Glu Ala Pro Thr Gln Pro
               245                 250                 255

His Val Pro Glu Val Ser Ala Pro Thr Val Gly Leu Pro Glu Val Ala
           260                 265                 270

Met Thr Ala Glu Glu Ala Ala Ala Arg Gly Phe Lys Ala Gly Asp Val
       275                 280                 285

Val Asp Leu Leu Asp Glu Gly Thr Val Leu Ser Arg Val Ser Ala Arg
   290                 295                 300

Val Glu Gln Ala Glu Ile Pro Ala Ile Pro Arg Arg Asp Thr Ala Phe
305                 310                 315                 320

Gly Asp Glu Leu His Ser Leu Ser Gly Arg Lys Leu Ser Glu Val Leu
               325                 330                 335

Asp His Ile Lys Thr His Ala Glu Val Pro Lys Pro Leu Gln Gly Ile
           340                 345                 350

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

Arg Thr Ala Phe Arg Val Val Gln Gly Gly Asp Thr Ala Ser Ser Ala
   370                 375                 380

Phe Leu Lys Pro Gly Thr Ala Gly Ile His Ser Thr Gln Gly Leu Asp
385                 390                 395                 400

Thr Leu Val Gln Val Arg Gly Ser Thr Ala Pro Gly Arg Val Gly Thr
               405                 410                 415

Asn Pro Val Thr Val Leu His Glu Ala Val His Ala Ala Thr Val Gly
           420                 425                 430

Val Met Asn Ala Ala Leu Arg Asn Pro Gly Ala Met Ser Pro Lys Val
       435                 440                 445

Ala Gln Ala Met Gln Thr Leu Glu Asn Val Arg Gly Asn Val Leu Asn
   450                 455                 460

Ala Leu Lys Gln Asp Arg Ala Ala Gly Arg Gln Leu Ser Glu Phe Glu
465                 470                 475                 480

Glu Thr Leu Leu Ala Gly Asn Ser Asn Thr Leu Ala Asn Val Lys Glu
               485                 490                 495

Leu Val Ala Trp Gly Leu Thr Asp Thr Arg Phe Gln Arg Thr Leu Asn
           500                 505                 510
```

```
Arg Leu Arg Tyr Ser Asp Gly Gly Pro Gly Leu Trp Ser Arg Phe Val
        515                 520                 525

Glu Gly Ile Arg Thr Leu Leu Gly Leu Arg Ser Asp Ala Asp Thr Ala
    530                 535                 540

Leu Ser Arg Val Leu Ala Ala Ser Glu Thr Ile Met Glu Ala Met Pro
545                 550                 555                 560

Gly Tyr Thr Lys Ala Gln Ala Lys Trp Ala Asn Lys Gly Ala Pro Val
                565                 570                 575

Thr Glu Glu Ala Ser Leu Glu Thr Ile Val Arg Ser Thr Arg Glu Arg
            580                 585                 590

Ala Arg Glu Gly Ala Gly Phe Val Asn Arg Phe Phe Ser Glu Ala Asp
        595                 600                 605

Leu Leu Ala Gln Pro Gly Glu Gly Ala Arg Arg Leu Leu Ser Arg Leu
    610                 615                 620

Ile Asp Asp Pro Val Arg Arg Asp Gly Phe Ser Thr Asn Asp Asn Ala
625                 630                 635                 640

Ala Ser Tyr Leu Arg Arg Tyr Arg Asn Glu Phe Glu Gly Tyr Val Lys
                645                 650                 655

Ser Tyr Asp Glu Met Met Ala Lys Ala Met Ala Glu Gln Gly Val Gly
            660                 665                 670

Leu Thr Ala Arg Ala Leu Asn Ser Arg Arg Ala Met Ala Val Arg Asp
        675                 680                 685

Gln Leu Asn Glu Gln Val Thr Arg Glu Leu Leu Arg Arg Asp Arg Glu
    690                 695                 700

Trp Thr Ala Tyr Gly Ser Val Arg Val Asp Pro Asn Leu Pro Pro Thr
705                 710                 715                 720

Ile Lys Ala Leu Ala Asp Arg Ser Asp Glu Ile His Gly Leu Met Gly
                725                 730                 735

Gln Arg Ala Arg Glu Ala Gly Val Arg Gly Phe Glu Asn Phe Ala Pro
            740                 745                 750

Arg Pro Gly Tyr Phe His Arg Ser Trp Asn Trp Ser Lys Met Ala Gln
        755                 760                 765

Met Asp Glu Ala Ala Pro Gly Leu Ala Arg Arg Ala Ile Ser Glu Ala
    770                 775                 780
```

```
Val Phe Arg Gly Ile Pro Gly Leu Glu Arg Ala Asp Ala Asp Thr Ile
785                 790                 795                 800

Ala Gln Ala Ile Val Gln Arg Ala Arg Asp Arg Ala Thr Gly Ile Arg
                805                 810                 815

Ser Glu Phe Met Gly Ala Met Gly Val Ala Asp Thr Ala Phe Ile Arg
            820                 825                 830

Gln Ala Leu Glu Glu Ala Asn Val Ser Gln Ala Lys Phe Asp Ser Ile
        835                 840                 845

Met Ala Lys Ile Glu Gln Lys Gln Ser Asp Gln Gly Thr Val Lys Tyr
    850                 855                 860

Gly Lys Gly Arg Leu Ser Leu Asp Met Thr Ala Glu Ile Asn His Asn
865                 870                 875                 880

Gly Thr Val Tyr Arg Val Gln Asp Leu Ile Asp Arg Asp Leu Asp Arg
                885                 890                 895

Leu Met Glu Asn Tyr Ala Gly Ser Met Ser Gly Arg Ser Ala Leu Ala
            900                 905                 910

Arg Ala Gly Met Pro Gly Asp Ser Glu Ile Glu Ala Phe Ile Arg Glu
        915                 920                 925

Tyr Gln Arg Glu Ala Ala His Leu Gly Thr Asp Lys Val Gln Glu Leu
    930                 935                 940

Thr Gly Gln Leu Arg Gly Val Phe Gly Asp Phe Thr Gly Asn Val Pro
945                 950                 955                 960

Arg Glu His Gln Leu Gly Pro Val Ala Gln Arg Ala Ser Gly Leu Thr
                965                 970                 975

Ser Ala Thr Met Leu Gly Phe Ser Gly Val Tyr Gln Leu Ala Glu Leu
            980                 985                 990

Ala Thr Met Ala His Arg Gln Gly  Val Phe Asn Val Met  Lys Ala Met
        995                 1000                1005

Leu Asn  Ser Arg Leu Gly Asp  Phe Val Gly Ala Met  Arg Arg Asp
    1010                1015                1020

Pro Asp  Leu Ala Asp Glu Met  Gln Thr Val Leu Gly  Leu Asn Leu
    1025                1030                1035

Ala Asn  Asp Ile Arg Met Lys  Pro Trp Lys Arg Gln  Phe Asp Thr
    1040                1045                1050
```

```
Phe Leu  Val Ser Gln Asp Thr  Phe Met Asp Arg Phe  Leu His Ala
    1055                 1060                 1065

Gly Lys  Gln Ala Val Pro Val  Leu Asn Gly Met Lys  Phe Ile His
    1070                 1075                 1080

Asn Trp  Gln Ser Arg Met Asn  Ala Asn Leu Thr Leu  Asn Lys Val
    1085                 1090                 1095

Ala Arg  Ala Ala Gln Gly Asp  Glu Ala Ala Leu Arg  Val Leu Gln
    1100                 1105                 1110

Gln Tyr  Gly Lys Asp Val Asp  Trp Thr Pro Val Leu  Ala Arg Val
    1115                 1120                 1125

Arg Gly  Tyr Val Thr Tyr Arg  Gly Arg Asn Ala Arg  Ser Met Asn
    1130                 1135                 1140

Trp Gly  Ala Trp Ser Gln Ala  Asp Val Asn Thr Val  Met Asn Thr
    1145                 1150                 1155

Ala Leu  Arg Ile Met Asp Asp  Ser Leu Leu Tyr Gly  Arg Val Gly
    1160                 1165                 1170

Gln Asn  Ser Gly Phe Ala Arg  Ser Pro Val Gly Gln  Ile Leu Gly
    1175                 1180                 1185

Gln Phe  Arg Ser Phe Val Ala  Phe Ala His Asn Lys  Leu Leu Arg
    1190                 1195                 1200

Gly Thr  Tyr Glu Asn Ser Gly  Val Leu Gly Val Ala  Ser Leu Leu
    1205                 1210                 1215

Ala Phe  Gln Tyr Pro Leu Thr  Ala Leu Met Met Gly  Ala Lys Ala
    1220                 1225                 1230

Ala Ile  Asn Gly Lys Phe Asp  Thr Ser Asp Glu Gly  Ile Arg Lys
    1235                 1240                 1245

Met Ala  Ile Asp Gly Ile Gly  Tyr Thr Ala Gly Leu  Gly Phe Thr
    1250                 1255                 1260

Ala Asp  Met Trp Gly Val Ile  Thr Gly His Ser Arg  Met Ser Ala
    1265                 1270                 1275

Pro Val  Phe Gly Leu Ala Glu  His Ser Asn Glu Val  Phe Arg Gly
    1280                 1285                 1290

Val Lys  Asp Leu Val Thr Gly  Asp Asp Pro Ala Ala  Ala Thr Gly
    1295                 1300                 1305
```

Asp Ile Val Asn Gly Ala Ala Gly Ala Leu Pro Phe Val Asn Val
    1310   1315   1320

Phe Pro Ala Thr Lys Leu Leu Leu Glu Ser Ile Lys Gly Glu
    1325   1330   1335

<210> 549
<211> 251
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 549
Val Ala Arg Phe Lys Asn Pro Glu Thr Ile His Val Ala Asp Gly Val
1   5   10   15

Glu Ala Val Phe Ser Leu Asp Phe Pro Phe Leu Arg Arg Glu Asp Val
            20   25   30

Phe Val Gln Val Asp Lys Ile Leu Val Thr Asp Tyr Thr Trp Val Asp
        35   40   45

Asp Thr Asn Ile Gln Leu Ala Val Val Pro Lys Lys Asp Gln Glu Val
    50   55   60

Arg Ile Phe Arg Asp Thr Pro Ala Gln Val Pro Asp Thr Gln Phe Ser
65   70   75   80

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

Leu Leu Tyr Ala Val Gln Glu Gly Ile Asn Thr Ala Asn Leu Ala Leu
            100   105   110

Asp Gly Val Leu Asp Ala Ile Arg Ile Ala Glu Glu Ala Arg Arg Leu
        115   120   125

Ala Gln Glu Ala Leu Asp Ala Ala Asn Glu Ala Leu Arg Arg Ala Leu
    130   135   140

Gly Phe Ala Glu Ile Arg Thr Val Thr Glu Asp Ser Asp Ile Asp Pro
145   150   155   160

Ser Trp Arg Gly Tyr Trp Asn Arg Cys Ile Thr Ser Glu Gln Ser Leu
                165   170   175

Thr Leu Thr Met Gln Met Glu Asp Pro Asp Glu Pro Trp Ile Glu Phe
            180   185   190

Ser Glu Val His Phe Glu Gln Ala Gly Ile Arg Asp Leu Asn Ile Val

195 200 205

Ala Gly Pro Gly Val Thr Ile Asn Arg Leu Gln Asn Thr Thr Met Gln
210 215 220

Leu Tyr Gly Glu Asn Gly Val Cys Thr Leu Lys Arg Leu Gly Pro Asn
225 230 235 240

His Trp Ile Ile Phe Gly Ala Met Glu Asp Asp
245 250

<210> 550
<211> 146
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 550
Met Arg Gly Ile Ile Ala Gly Val Val Ala Ser Gln Ile Arg Arg Pro
1 5 10 15

Lys Pro Val Leu Thr Thr Ile Thr Tyr Pro Gln Ser Ser Ser Asp Arg
20 25 30

Gly Gly Met Thr Phe His Ala Ile Ala Gly Ile Ile Gln Asp Thr Val
35 40 45

Lys Phe Ala Asp Ser Lys Asp Leu Gly Ser Tyr Glu Met Leu Val Arg
50 55 60

Asp Ala Thr Leu Lys Ser Met Val Ile Thr Leu Thr Glu Val Lys Asp
65 70 75 80

Ser Ser Val Trp Ser Met Gly Val Leu Ser Ala Ala Ile Lys Ser Val
85 90 95

Val Gln Phe Leu Thr Pro Val Glu Glu Lys Ser Ser Leu Asp Met Ser
100 105 110

Ile Ile His Gly Glu His Lys Gln Ser Val Ile Pro Tyr Ser Arg Trp
115 120 125

Ala Glu Ala Gly Ser Leu Ser Met Gly Ile Thr Glu Gly Lys Val Tyr
130 135 140

Val Pro
145

<210> 551
<211> 292
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 551
Met Tyr His Ser Ser Thr Ile Arg Gly Glu Phe Asp Leu Glu Ile Val
1 5 10 15

Arg Pro Asp Gly Thr Val Arg Gln His Leu His Phe Lys Asn Leu Ile
20 25 30

Thr Asp Leu Ala Leu Glu Ala Met Ser Ser Lys Gly Val Pro Ser Gly
35 40 45

Gly Trp Thr Asn Met Phe Ala Gly Thr Gly Asn Arg Thr Pro Val Pro
50 55 60

Ala Asp Val Ser Leu Val Ala Pro Val Ala Asn Ala Ser Ala Ser Leu
65 70 75 80

Asn Tyr Gly Asn Arg Ala Val Trp Asp Ser Thr Thr Gly Glu Lys Val
85 90 95

His Thr Gly Thr Gly Thr Phe Arg Ala Gly Ser Phe Gln Gly Gln Ser
100 105 110

Leu Ala Glu Val Gly Ile Gly Arg Val Val Ser Glu Leu Tyr Ser Arg
115 120 125

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

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

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

Ser Met Arg Asp Arg Arg Thr Phe Arg Asp Leu Ser Pro Glu Pro Ala
180 185 190

Ala Glu Phe Gly Thr Arg Gly Ser Leu Ser Trp Ser Ala Ile Ser Ala
195 200 205

Pro Asp Ser Asn Gly Gln Thr Lys Thr Ala Asn Leu Ser Gly Asp Ala
210 215 220

Gly Thr Gly Ile Ile Gln Val Pro Ala Gln Ser Ala Gln Ile Met Arg
225 230 235 240

Ile Gln Pro Ala Asp Ala Asn Trp Thr Glu Gly Ile Gln Tyr Leu Arg
245 250 255

```
Trp Glu Thr Pro Ala Gly Arg Glu Leu Glu Ile Lys Leu Asp Pro Pro
            260                 265                 270

Leu Val Lys Asn Ser Leu Glu Arg Val Asp Ile Thr Val Thr His Ile
        275                 280                 285

Phe Asn Arg Val
    290
```

<210> 552
<211> 196
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 552

```
Met Ile Gln Phe Lys Phe Gly Asp Tyr Arg Thr Arg Val Pro Phe Gln
1               5                   10                  15

Gly Ala Arg Asp Arg Arg Asp Ile Asn Asp Arg Ser Asp Tyr Val Asp
            20                  25                  30

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

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

Glu Arg Val Thr Thr Arg Ile Gly Pro Gly Ile Asn Glu Gly Val Ala
65                  70                  75                  80

Ser Met Ala Val Thr Phe Asp Gln Asn Met Asn Tyr Val Leu Val Tyr
                85                  90                  95

Thr Lys Gln Gly Glu Gly Phe Ile Asp Phe Phe Asp Ser Ala Thr Glu
            100                 105                 110

Glu Arg Asn Val Met Asn Leu Gly Pro Val Asp Tyr Ile Lys Thr Asp
        115                 120                 125

Leu Asp Asp Arg Arg Pro Glu Gly Ser Ala Trp Ala Gln Val Leu Val
    130                 135                 140

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

Phe Thr Glu Glu Glu Leu Ile Val Gly Thr Gly Lys Val Thr Arg Pro
                165                 170                 175

Ile Val Lys Cys Gly Met Ala Ala Asn Trp Arg Phe Gln Val Leu Phe
            180                 185                 190
```

Arg Gly Arg Met
195

<210> 553
<211> 101
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 553
Met Ser Lys Lys Gln Thr Ala Ser Ala Glu Arg Leu Gly Leu Leu His
1 5 10 15

Glu Leu Val Cys Thr Ala Ile Glu Arg Asn Phe Lys Trp Tyr Met Asp
20 25 30

Asn Asp Ile Pro Ile Pro Ala Ser Asp Ile Ala Ala Ala Thr Lys Phe
35 40 45

Leu Lys Asp Asn Glu Ile Thr Cys Asp Pro Ser Asp Thr Ile Asn Ile
50 55 60

Asp Arg Leu Arg Glu Glu Met Arg Gln Ala Gln Ala Glu Asn Arg Arg
65 70 75 80

Ile Ala Leu Glu Gly Phe Ile Ala Gly Glu Thr Asp Asp Glu Met Glu
85 90 95

Arg Leu Tyr Thr His
100

<210> 554
<211> 601
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 554
Met Thr Pro Gln Glu Arg Phe Gln Ile Ala His Glu Val Arg Asp Met
1 5 10 15

Tyr Pro Arg Phe Arg Asp Phe Cys Leu Asp Ala Met Leu Phe Leu Gly
20 25 30

Phe Lys Met Thr Trp Met Gln Leu Asp Ile Ala Asp Phe Met Gln Asp
35 40 45

Ser Pro Asn Lys Ala Met Val Ala Ala Gln Arg Gly Glu Ala Lys Ser
50 55 60

```
Thr Ile Ala Cys Ile Tyr Val Val Trp Cys Ile Thr Gln Asn Pro Ala
65                  70                  75                  80

Thr Arg Ala Met Leu Val Ser Gly Ser Gly Asp Lys Ala Glu Glu Asn
                85                  90                  95

Gly Gln Leu Ile Thr Lys Leu Ile Met His Trp Asp Leu Leu Ala Tyr
            100                 105                 110

Leu Arg Pro Glu Ala Arg Met Gly Asp Arg Thr Ser Ala Thr Ser Phe
        115                 120                 125

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

Cys Ile Gly Ile Thr Ala Ala Leu Gln Gly Tyr Arg Ala Asp Ile Leu
145                 150                 155                 160

Ile Pro Asp Asp Ile Glu Thr Thr Lys Asn Gly Leu Thr Ala Thr Glu
                165                 170                 175

Arg Ala Lys Leu Thr Arg Gln Ser Gln Glu Phe Thr Ser Ile Cys Thr
            180                 185                 190

His Gly Lys Ile Leu Tyr Leu Gly Thr Pro Gln Ser Arg Glu Ser Ile
        195                 200                 205

Tyr Asn Gly Leu Pro Ala Arg Gly Phe Leu Met Arg Ile Trp Pro Gly
    210                 215                 220

Arg Phe Pro Thr Leu Asp Glu Gln Glu Arg Tyr Gly Asp Trp Leu Ala
225                 230                 235                 240

Pro Ser Ile Leu Ala Arg Ile Ala Arg Leu Glu Glu Lys Gly His Asn
                245                 250                 255

Pro Arg Thr Gly Lys Gly Leu Asp Gly Thr Arg Gly Trp Ala Ala Asp
            260                 265                 270

Pro Gln Arg Tyr Asn Glu Glu Asp Leu Leu Asp Lys Glu Leu Asp Gln
        275                 280                 285

Gly Pro Glu Gly Phe Gln Leu Gln Tyr Met Leu Asp Thr Ser Leu Ala
    290                 295                 300

Asp Glu Gln Arg Met Gln Leu Lys Leu Arg Asp Leu Leu Phe Ile Asp
305                 310                 315                 320

Ala Thr His Glu Ser Val Pro Glu Gln Val Ala Trp Ala Ala Asp Glu
                325                 330                 335
```

```
Arg Phe Lys Leu Lys Phe Asp Ala His Arg Phe Pro Val Ile Lys Pro
            340                 345                 350

Glu Leu Tyr Leu Pro Ala Leu Met Ala Gly Gly Trp Ala Pro Leu Gln
        355                 360                 365

Gln Met Thr Met Phe Val Asp Pro Ala Gly Asp Gly Gly Asp Glu Leu
    370                 375                 380

Ser Tyr Ala Val Gly Gly Thr Leu Gly Pro Tyr Ile His Val Val Ser
385                 390                 395                 400

Ile Gly Gly Trp Lys Gly Gly Phe Ala Glu Glu Asn Leu Glu Lys Cys
                405                 410                 415

Ile Ala Leu Ala Ala Arg Tyr Gly Val Lys Val Ile Tyr Val Glu Lys
            420                 425                 430

Asn Leu Gly Ala Gly Ala Val Gly Gln Leu Phe Arg Asn His Met Arg
        435                 440                 445

Ser Ile Asp Pro Asp Thr Asn Lys Pro Arg Tyr Glu Gly Ile Gly Val
    450                 455                 460

Glu Asp Arg Gln Lys Ser Gly Gln Lys Glu Arg Arg Ile Ile Asp Thr
465                 470                 475                 480

Leu Arg Pro Ile Met Gln Arg His Arg Leu Ile Phe His Val Ser Ala
                485                 490                 495

Met Asp Ser Asp His Val Ala Cys Gln Gln Tyr Pro Ala Asp Lys Arg
            500                 505                 510

Asn Glu Arg Ser Val Phe His Gln Ile His Asn Ile Thr Thr Asp Arg
        515                 520                 525

Gly Ser Leu Pro Lys Asp Asp Arg Ile Asp Ala Leu Glu Gly Leu Val
    530                 535                 540

Arg Glu Leu Ala Pro Thr Leu Val Lys Asp Asp Glu Ala Ala Thr Arg
545                 550                 555                 560

Ala Arg Glu Glu Ala Ala Lys Lys Glu Trp Leu Asn Asn Pro Met Gly
                565                 570                 575

Tyr Thr Lys Ser Val Leu Arg Ser Leu Gly Met Gly Arg Glu Arg Arg
            580                 585                 590

Lys Gly Arg Pro Lys Gly Arg Arg Leu
        595                 600
```

<210> 555
<211> 66
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 555
Met Met Leu Asp Thr Ala Thr Glu Ala Gly Lys Gly Thr Leu Ala Val
1   5   10   15

Thr Gly Val Gly Ile Ala Val Tyr Ser Pro Tyr Glu Ile Ala Ser Leu
            20   25   30

Cys Ala Ala Val Leu Thr Ala Leu Tyr Val Gly Ala Gln Leu Ile Thr
        35   40   45

Leu Leu Pro Lys Met Leu Asp Ser Ile Ala Glu Leu Arg Arg Arg Phe
    50   55   60

Lys Lys
65

<210> 556
<211> 160
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 556
Val Asn Lys Pro Leu Arg Gly Ala Ala Leu Ala Ala Ala Leu Ala Gly
1   5   10   15

Leu Val Ala Leu Glu Gly Ser Glu Thr Thr Ala Tyr Arg Asp Ile Ala
            20   25   30

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

Asp Lys Ala Thr Pro Glu Gln Cys Tyr Gln Met Thr Leu Lys Asp Tyr
    50   55   60

Gln Arg Phe Glu Arg Ile Val Leu Asp Ala Ile Lys Val Pro Leu Asn
65   70   75   80

Val Asn Glu Gln Thr Ala Leu Thr Phe Phe Cys Tyr Asn Val Gly Pro
                85   90   95

Val Cys Thr Thr Ser Thr Ala Phe Lys Arg Phe Asn Gln Gly Arg Ala
            100   105   110

Thr Glu Gly Cys Gln Ala Leu Ala Met Trp Asn Lys Val Thr Ile Asn
        115   120   125

Gly Gln Lys Val Val Ser Lys Gly Leu Val Asn Arg Arg Asn Ala Glu
130 135 140

Ile Lys Gln Cys Leu Glu Pro Ser Ser Gln Tyr Ser Ser Leu Leu Trp
145 150 155 160

<210> 557
<211> 109
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 557
Met Pro Arg Thr Ile Val Ala Ile Leu Val Leu Ala Val Val Ala Leu
1 5 10 15

Gly Ala Ser Tyr Gly Phe Val Gln Ser Tyr Arg Ala Leu Gly Ile Ala
20 25 30

Gln Glu Glu Ile Lys Arg Gln Thr Ala Arg Ala Glu Ala Leu Glu Val
35 40 45

Arg Tyr Ala Thr Leu Gln Arg His Val Lys Glu Val Ala Ala Arg Thr
50 55 60

Asn Thr Gln Arg Gln Glu Val Asp Arg Ala Leu Asp Gln Asn Arg Pro
65 70 75 80

Trp Ala Asp Arg Pro Val Pro Ala Ala Val Val Asp Ser Leu Cys Asn
85 90 95

Arg Pro Gly Ala Arg Cys Ala Val Arg Thr Pro Thr Asp
100 105

<210> 558
<211> 104
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 558
Met Ala Asn Thr Arg Glu Gln Tyr Leu Ala Gly Arg Asn Thr Gly Leu
1 5 10 15

Thr Phe Tyr Gln Val Cys Gln Pro Gly Thr Asp Asn Arg Ile Ala Leu
20 25 30

His Asp Met Asp Glu Ala Asp Val Lys Ala Lys Ala Thr Ala Val Ile
35 40 45

Ala Ala Ala Thr Ala Leu Gly Gly Glu Gly Gly Ala Thr Pro Pro Asp
    50   55   60

Pro Leu Thr Ala Tyr Lys Val Lys Asn Gly Asp Thr Leu Pro Val Asp
65   70   75   80

Gly Gly Gly Ser Val Lys Val Thr Val Ala Asn Gly Ala Ile Thr Lys
                85   90   95

Val Val Tyr Thr Ala Pro Ala Gly
            100

<210> 559
<211> 81
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F510/08

<400> 559
Met Ala Thr Phe Ala Ala Ala Thr Gln Lys Asp Leu Arg Ala Phe Ala
1   5   10   15

Gly Ala Ile Glu Asn Leu Ile Arg Pro Leu Glu Glu Ala Ala Leu Gly
            20   25   30

Ser Gly Phe Thr Glu Val Ile Thr Ile Thr Lys Gly Thr Asp Gly Asn
        35   40   45

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

Leu Asp Ala Leu Met Ala Ala Val Glu Thr Ala Lys Ala Ala Val Tyr
65   70   75   80

Lys

<210> 560
<211> 137360
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 560
aatttcatta gaaaagaatt tttttctttt tctatagtat ctttcttgtt atcgtattct   60

gaatacatca taaattctat aaatatacta tttctgtcag atgaaaacat atctatagaa   120

aacggacaat caaaacttat gtcatcttta ttaatactaa aacattcagt aacatttaag   180

tcatttattt catatacctc aaagtatcca tcaactcttt taagttctat agcactatta   240

tatctataat aacgttgttc ctctattaac ttatcttttg ttagataggg atattcattt   300

ataaatatag gattacttgt tccatagtta tttttaatat attcagcatc ttctaaggaa 360

tcagtataac ctaaaacttc gtaacttgtt gtatacacag tatcctcttc ccacaagtca 420

tagtccattt cctctatttc ttcctctagt atataaattt ttttcatata ttactcccaa 480

acaccaataa gatttttaag tttagctata acttcttctt ctgtttgata agaaaatact 540

cctgtaatgt gtccatagtt acctataatt tcataatcct gtgtaccatg tttgtctact 600

agatatgagt tacccataac atttaaacta tcctccgagt aactgaaatt tatattatag 660

tctactaaaa aattaataat ttttttcatt tacataacct ctcctatcgg atattgtcct 720

aacattcttg ttccattttc gttatagaag gtatattcta ctacaataat attcattata 780

tcgacatata tagcttctat ataaggtgta atattctctt cttcttgtat gtgtttacct 840

ataatattat ataataattc agagtgtatt cttttatctc tcattataga cctccgtaag 900

aaatgataca gtcttatctt ttaaagattt ttctactagt tccatagcat ctttataatg 960

ttttatatta gattcattag acttcagttt atcttttact tcttgaatta gaggttcaac 1020

tttagtaact aaatcttttt tattttctat actcacattg cttcttttat tatctaatac 1080

ttcctttggc atatacttaa cttttgcaaa gtctttatag ctaacattta agttatctaa 1140

atcatctaat aaatcattat aatattctaa atgattatag aatgtgtaaa acttaacaag 1200

gtctttacct gctagctctt ctttttttag tatattattg atattaccaa taacagaata 1260

tgctataggc ttaaaattag ccctaacata agttaaaaat ataaaatcat cataaaacaa 1320

gtctaaaaca gttttattga atctagtatt tttagcttgc tctaattgag cacataaatt 1380

aagaacatta tcaaacccac tctttaatac caaagagata aatctttcca ctgcatagta 1440

cctagatact tcagtatgtt tgcttgcttt ttcactattt ctaaaaatag tatctgataa 1500

aggttgaact actaaactca tataatcttt atctgaatat tcatccgatg ttccttgata 1560

agtacttcca aattctattg tagataataa aaaacttttt tctaaattca ttataacatc 1620

ctccttttac ttgttattat aatactaaca catatgttta ttaatgtcaa acattaaata 1680

tcttctgttg tgtcaacttc atcttgtata tacttaaagt attcataaat tttaaatagt 1740

ataactccta gtgttattaa tcctaaaata tatttcataa caatcctcct taaaagtatt 1800

tatccttccc atcctgataa agcatccata gccatatcat actcttcttc atttttagtt 1860

cttataattt tctctatttc ttttttttgct tgtttagagt tcataaaatc aatatctact 1920

gtatctaaat ttgtataatc aatattttct ctaataaagt tcttttgact tggtgttata 1980

gaattaactc gtacgttttc gtgatttaaa aattgataga agtccatact attcaccttc 2040

ttttaaacag tctgccatat cttttaaagt attaagtaca tatttcaaat ctctataata 2100

actatcagaa aaactaataa cagcatatgg tgtcatatca ctatagtgtg cacaatcaaa 2160

acctaatacc ctatagtcac cctcatgttc atcgtatgtt atacctccat gggaacaatc 2220

ttctatacta ttaaactgtt ctttggttat attcgtaggc acattaatat aaccatttag 2280

atgtcctgaa tgagggtgac gtttaacagt taggtttatt cccttataat ctatatttaa 2340

agttaagtcc tctcctaata tattatcctc tttatctata atttccataa tatgttctgg 2400

agcttttcca aacatcataa ttcctccctt ttctttatac tcttactata cactactttt 2460

tctattttgt caacaaaaaa aggctactaa ttaaagtagc ctaagaatta attatttagc 2520

attatatttc cattgccaat aaccattttt ctgtgagaac tcaaagtgaa aaccgtcata 2580

gtcaaattca atattatagt ctccatcttg aagtggtttt gaatttagta caggactatt 2640

actctttgcc aattctgcta gaaactcatg atttactttt tccatagggt ttattcctcc 2700

taattattct tacagtacta atatatcaca ggtctttttc taggtcgttt ttaaatttct 2760

cctcataaga actagcataa gttacttcat aacctattac cttagtataa tctatgcaaa 2820

gtaatttata attggacttt attttaatat cctctgattg ttctatttta ttgataactt 2880

catttagctc attcgaagag taatgtttat tatcaacttt tattgttttt ccttgggtat 2940

agatatcaat ttcttgtatc atcatttcat ccttttgatt attcattatt tgattataag 3000

tctctaaatc atcaatgtta tctgtatctg aacctttttac taaccattct cctctcttct 3060

taaggaggtc atcaaatttc tcatgttctt taattatctt ctctacttca ctcggtatta 3120

gaacagctct agcgtaattt atatgccaca tagacatatt atcaataaga taattaacca 3180

ttcttataag ttccttctca tttgccatat accaacctcc ttatatctaa tactaatata 3240

agagaaaagc agacttatta aaagtctgct tctgtaccta attctaatct tttatttttc 3300

atatgaggaa tcatttttct atctcctgtt aatagagata attctctagc tttttcttta 3360

gataatgtta atagtccatt ataattatct actttcttat tatattccat aattaagcgc 3420

tctagctcat atgatatatc ttcgagttct cctgatttaa ctccaagtaa ctttctatac 3480

atatcataat cttcagaaag actttctact ttatttttag atacagaatc ataaactgct 3540

tgtaaattac cttcttcaat aagtttaaag ttatgttcac ctatgattaa ttcctcctca 3600

gaagaatcaa gcgttactaa tccgcttgta ttacctgtaa agtcaccttt ataatctaca 3660

acaatacctt cagttacttt gtcacctaat tcaatagtcc catcttcatt ttctttaaat 3720

ttatgagcat catatacttc tactttgtca cctaatctca aatcttgagt taagttatgt 3780

ttaccaataa ttctatccat tactcaatct ctcctttatt aatagggtct tgtgttaaga 3840

acatttctag attctctttt gtaataggta accaaaaata tttactttcc ggaattgtaa 3900

ttgtatagaa atcctcatct ttgttaactt taatattaac atctgtaaac tcatcctgca 3960

ttaaccaatg agttacagtt aagttatatg aaccatcact aacataccct aaatcaatat 4020

catgtctaaa agccaaatct tctaaatgtt ctaataaatc gttcttttca ttatgttttt 4080

cttcttctgt attattttta attgggttaa ttaactctgt gcaaacaata tcgtacaatt 4140

caccatctgt aacctcatag ttcttttcaa ttaatacatc ttgtatttta ttgattgagt 4200

ttgtaactac tttcccatat tcttcttctg taaacttaca tttatctaaa tcaacatctg 4260

taattaattc tgcaatccat ttatttaaaa ttgatactgc cattgttcta gaaataatac 4320

tgtcgtatac catatttatt taatctcctt atttaggtga atgtggtctt ctaatgaaaa 4380

atcaaaaggc gctacaccat ttcttttatt atttgtttct tttttaagta taacataagt 4440

tagtgaaaaa gtcaagatag ttactacaac cattgataaa aatttaatca ggtttttcat 4500

aattactcta actccttaag tttatttttt actttctctt tatcgtactt ataatcttta 4560

ctagagtttt catttttttc tttctcttct tcattaagtt ctctatactg agcctcttct 4620

acctcttgtt ctttattatc attaccttct tctgcttttt gaatttctac atttttacta 4680

ctaccaccat ttacctttttt tctaaaaaga aaccaaagta ttaataaaat gatgagtaaa 4740

ataataatgc ttaatacaac agcccaaata ttattaacca ttacaaccta cctccgaata 4800

gtttttttac ggctcttaag ttttcagatg aatcattatt tatatcaata cctatgctag 4860

aatcaaaaat tacagcatta tcaagtatat gctctgtcaa tttattaccg taactacttt 4920

tacttaccac actaccataa ccatgattag ttaggtcaac catatcaggt tcaacttcta 4980

gtactctaaa agatattcta cgtaagaatg aaggatttac caagtaaaag gaagatttaa 5040

aaacatttaa tctttgataa gaatgtttta tattaacaac aaaccctgtt aacttatttt 5100

catattctga atttgataac ttacctaggt aaaggtttat actatatcct tttgtttcta 5160

atgtttgaat agcacttaac attatagccc ctctataagc aaggttttca gggtcttcca 5220

tccaactaat actagaatta taaaatacat caataacttt cttctctgct ttaactcttt 5280

gctgagacat catagaatta ggtaaccctt ttatagcatt aggtacgtga ggttgatacc 5340

cttccggagc tacgacaggt tttcttttta ctgacttatc cattctaaat aatgcatctg 5400

tcatttttt aagtttaact accatatcat atgattctct atcaccctta accattaagt 5460

tataggcttc ttgaaaacta tgagttcctg taaaatcata gctacctgta tctgatgaat 5520

tttctctacc tgaaactcta ttctttttta aagcagaaaa gaaatcaggt agaccatcat 5580

atttaattac atttaattct gagttatcta ttaatcgtct acccattgat tttcctccta 5640

ttctaatcct aacttatcca taattgtatc aaagtccatt gaatcttttg atgtactatt 5700

agattttcta ggttcctgtt taggttcttg ttgcatacct aaaagctttc ttgttgcttc 5760

tgtatatctg ttaccttcag gtaaagagct aataaattga ttaatctcat ctttcggtac 5820

agatttaaag ataatacttt ctacaacaaa ctcatcttcc attactccat ctaatttact 5880

accattaata attgcacgca ttgagaatac ataaggtaat ccttttttcat cattctcatg 5940

tcttaattgt tgtacaaagt ttactaagtc ttcattgctt gatagttgat gttccacctt 6000

agtatcatag tcaaattcaa cttgagcaaa gcggtctaat gtagctccat ctaattgttg 6060

tctacctaca taaatatggt ctgctcctgt tcccatagta ttacctgctg acacaactct 6120

gaaatcttca tgagctgtta cacgtccaat agggaagtca aagtatttat ttgcaatagc 6180

tgaattaaga attaatagta cttcaggaat agatgcatcc atttcatcta agaagaataa 6240

cccacctttt gtaaatgctt tatagaattg agtttcatga aacttaccat ttgcatcaat 6300

aaatcctgtt aatttaaatt cttgagtaat tgcattacta aaatagaaat ctaaatctag 6360

ggcttctgct acttgttcca atacatggtt cttacctgaa cctgctccgc cttttaaaaa 6420

tactggaata ttttggttaa ctaactttag tatatcttga tatctgtaat ggaagattcc 6480

tgagatatct ttaattgttt ttccttcttg ttgtaattca attttaactg gtaaattact 6540

aagttgttct tctacatact cttcaatttg ttttttaaca tcagtaataa taatttctct 6600

actctcagtt cctgctttct caacaattgc atctacaatt gcttgttcat acggattaga 6660

gtttttctct cctagttttt ttgctaaatc tgctgttgtt tccatttgtt gctctaccaa 6720

tctctctaat ctttcaatag tatcttgctt tgccatattt atcattctcc tttgatttgt 6780

tatacattta ttatattaca agtatttgaa tttgtcaaca actttctaaa actttttag 6840

ttgctaataa aaaaatacct tacacctata acttaacata gggtaaggta attgtcaaca 6900

cttttgttaa aaatacatta atttaaaaaa atcatcaata tctttagttc catgtgtatc 6960

catatcatac ataaacatac aattatatgt atgactattc attatttcta acatgttatg 7020

catagaagtt gcattattga attcctctaa atcaatagtt accgtaagtt cttgaccttc 7080

ataaagtatg tttgctatat aatatttcct aacaccttcc attgttccat gggaagtttc 7140

attatgatta agtacttcta cacctagtga aggtaaatat tctgaaaagt aatatttaca 7200

gaaatatata aaattgtctg ttcttttaga cacgagtact atctccgtac tttatatttc 7260

tttctaatcg tacataatat gttttaattt tttgtacttc tttatctact gcatcctttc 7320

ttcctaacct tgtagtatat tttacaatat taaatatcat agaatcaaca aagccatcat 7380

aagaaaaatg ttcttctaga aaagaaataa catccttact acctttataa tgttcaggta 7440

aatgtgcatc tacttgtata ttataataat cttctaaaag acctatactc tcaccaagac 7500

tagataaagc gtaacctaaa tcatttgaat cattagacca ttctttagat actgatagtg 7560

catcttctat aattgttact tttaatttat ctaaataatc ttctacttga gcttgtgttt 7620

tcataaattc ttttgcgttc atgtaatacc ctcctaaatt atataaaaaa aacaccctgc 7680

ttggatacaa gcaaggtgaa aaaggaaaga tattatggaa gtgtactatc taagtacacc 7740

tcataatata acagttttcc ttgctagtta ttacttattt tttaaggtct tcttctttga 7800

caaacactcc gttaataagc ttacctttcc tttcttttat ctcatcataa gccatatcaa 7860

tacactcttc aatatctata tctaactgta aacatagtac tgttaatact acaaaaatat 7920

ccccaacact atctcttgtt acatggtcat tacttttagc aatacctgaa gctaattctc 7980

ctgcttcttc taataatttt aacatttgac cctcgggttt acctgtttgt aagtttctat 8040

cttttgccca ttgtttaata agttctactt tttccattat tctatatctc ctttaatttc 8100

tgtatctttg ataattaggt tatcagagtc acttgttaca tttaagttat cttcaactaa 8160

ttcatgtaga ttattagtaa tatcttcttc atacctataa cctacacgaa cataagcttt 8220

aactctgata tctatattaa cataatcttc ttggaatttt tccatttcta acttccttta 8280

ttatatcata ttattatact attgtcaatt aatctgagta gtttccttta gcaagttgat 8340

acttttgtg taattcttca tataattctc tcataccttc gtagtttctc atatcatctt 8400

ccaagaaact aagataatct aataatactt ttacatcctc aggttctaaa gttataactg 8460

gttttaccat taggcaacct ccttaaattc ttctttattt attttcttaa tatctttttc 8520

taatgcttct tttaattcat taggtaattt ataggcatca attgattgtt gttgacctaa 8580

tacatatcca ttatctgtga tacgtatttc cactgtaaac catgaattat ctaaatcttc 8640

ttctaatctt gctaataata ttaaacaact atttttaaa attctattag catacccgcc 8700

aacacaatga gataacattt taccttcatc tttaagttta cttacagtat ctgcaggaag 8760

gaattttact tttctaccat cttttaattt ataagtttta tcaattattt tttctaattt 8820

attatcatat ttagctttaa gttccgcatc atctaattgt tgttgtatag attgtttctc 8880

atctgtaact atatcatgtt ctagttttaa tgagaatggt gttaggttaa cactttctaa 8940

tgttctataa ccttctctta ttaatattga taaatcatgt aagtaatcta agtaatagtt 9000

atctagtgca tatcctgtta tacgttgtct gtcttgagca tctacatcta aatagtgagt 9060

catcttttg tagttagcaa aagatataga taatatttca tttacaatag gttttacttt 9120

taaagcattt gtaacatctc ttgaatctct aaccattaaa aaggtatcgt caaataattg 9180

gtgtaaatta acttcattgt gtaaatgatt atagttctta tagagagtat tagcaaatct 9240

taagtaatta ccttgctcaa atttatttaa agttagtagc tttttataag tctgttttgt 9300

aagattgaag gcttcatgaa ctttccattt agggttttta ggtatatgga atagtaatgc 9360

atttctttca aataatccaa attcttctaa gttatttatt ttatcaatat ttttaacaat 9420

atctgttaaa gttattaagt aattagaagt tgaattttct cctataaaaa tcctatactt 9480

atcccctcta taatttatat gaccataaac atctatatta tcaggacacc aactagaaaa 9540

atcaaaatta tgatgctcta atgtttgttc tattatcttt attataattc ctctatttaa 9600

gttaggttgt gaatagtttt ttaaaataac atttaataaa acagataatg tcaattcatt 9660

tttgtattca cttttactaa tatcatcttt atataggttt aaagctattt ctttattaac 9720

aagactatct gttaagaaaa ccttgactgc tcctgtctta acgtcaaatg aacttttatt 9780

ttctaaaacc catttgttac ccatattatg cttatccctg atatgtctaa ctttaagacc 9840

aaaagatgaa ttattctcag tacttgggtg catgtaccaa acacgactat acaatgaatc 9900

tgacatttcc ttataatact cactagaacc tttttctata tcttcattca taacaataat 9960

agatgaattt ataagaacat atttaccttg gtctagtaca tccatgatat cattatttaa 10020

actatctact gcttccttat actcatctaa ttgtctagct tcatatcccc ataaacggtt 10080

ttcattttct aattctttaa ttttttcttc aacataccct ttagattgta tttgttttct 10140

acgtctacta ccatataaag gaaaatcttt tctttctcct ctatcagctt caatatactc 10200

tttgtaattt cttcctttat tattaccaat cacaccttca actaattttt caactgtttc 10260

ataggggtca ccttcaaagt ttgttacttc tttattacca catagggcta aaaataaatg 10320

tatttctgta gctgtatcaa aactaaatat attatgaata tctctaaata attctttaga 10380

acctaagtta attatattat ttttcttttt cttaagaaat acatcttctt ctcctatata 10440

gatacatcct ttattaacct taggtaaatt aataatttct tgttctgtta atccttttg 10500

tttataagtt attgccattt aaaatcactc cttatttgtt atgtactaat cataccatag 10560

taaataatat ttgtcaacaa aaaaagaaga acttttttaaa gttcttctaa atgagtttcg 10620

tatataactt tttgaatttt atttaatggt tctaaatcta aattcctaat aagtttttca 10680

tactttcttg aatttttaaa attgatagta tttggcatag caagagcttc atcaacatct 10740

ttagtatagc ttacaacatc tgaatagata tctacttctt ttacatatag accttgagtt 10800

aaactcctaa atactacctc attatgtgct ataatttctt ctttcttttc tatgctcatt 10860

tataaacctc ctggtctact ctacacaaac aagtacgtat tctaaattag ttaaagaaac 10920

tgatttaata ttgtttaatt cttgtaattt cttaatttcc acatcatagt tcttacttat 10980

agtccataat gtctctcctg ctcttacttt gtgataatat ttatttccct ctttgataag 11040

gtcattcaat attacctacc tccttgagta ataattagct tgtagataac atataagtat 11100

aagaacaaag tttacaaatt cagtagctat aatatgaaca taggtatgtg ttaaaaccat 11160

acttacaatt aatgaagcta atcctaatcc aataataaga aatagaaatc tatttgttcc 11220

ttctgcactt ttagttttat aaaaggttgt tatctgagtt acatacgcaa ggataatagt 11280

aatagttgct acagtttgtg ttaaggctgt aaagtcactt aataaaaata gtaacagtga 11340

gaacacaata ataaaaggta tagagaaata gtccttttttt ctatatgaag ctactaataa 11400

gcaaacaata cctagagtta aattaagacc aactgatact acttgaaaca tcgtagcatc 11460

agttagaagt aaattgtaaa aactaatacc tactgtagct acaattaaat accaaaaata 11520

actactaaca cctttaacac tatctgactt aactagggct attaaacctg gtatataacc 11580

tactgtaact aatatagcat ataatatact taagtaatgt gataaattat ccatcttgtt 11640

cccctaattt ctctaatcta ttagtaactt cttcccatga aataaatcct tctccgtttg 11700

ttaattctaa aaccatacca tacacaaatt ggtttgtact aaattcagct ctgtcagggt 11760

cattgtatgg tttaccatga ccctgtctaa tatcagagca gtagattaat acgggttttt 11820

ttaaaatata ttcctgctct ccaatttgtc cttgtaaaat atcatatgtt tctgatagtt 11880

catctatctc attgaactta aataactcag actgttcttt taattgtttt attgtttctt 11940

gtgcttgatg tttcatacct aataaaatac ctagttctgc aattgttcct aatccttcat 12000

taagaacatc aaatacaaaa atatctgatt cttgcatagc cttaaagtca ttagttaaaa 12060

tacgttctgc tagcttagtt tgttctgcat tagctttatc atttattgac ttatctttgt 12120

gagggctata cggagttact cctacaatgc catctacttc tttatgttgt ttatctctgt 12180

aatctaccat agcttcattt aggatatgtc cacccatata aattactttg tctttaattt 12240

tattaaccat ctatagtatc tccttttttct tctaaaattt ctcttaaaat atgtggcatt 12300

tttttcttaa tttgtttatc tactattttc agtatatttt ctttttcttc ttccataata 12360

tcatcaacaa agttttgacc tacttgtttc ataattagac cgaagttttc taattctaaa 12420

tcatcttcag ataatctatc ttcttctata gccctaaaaa tcatttttttc cattcttgct 12480

cttgtaatgg cataatctgc cactgactcg ttctttttta cttctgtttt catttttga 12540

cgactaaatt ctttaaactc attagatact aatttaaagt agtcatcata ttctgattta 12600

ccatctaagt atttaattac tataccttca cccttatcag gtttaactgt catgtcagat 12660

tttcctacta attcttgaat ttcttcaggt tttaaatcat ttaagtagtg agatggttta 12720

gctactagca aagttttaac tgtttttaac cctaaatgat gtgcaattac attcatgtct 12780

tctattgata aataaacttc attttcttta tcataaacat caaatacata aaaattgttg 12840

taaaattctt ctttgtactg aatcttatgt ttgactaacc attcaccaaa aataatgtat 12900

ttttctaagg ctgatacgta cgtatttctt acatttatat tttcatgtac ccaatcataa 12960

aaaccattta aagtttcatt ctcatttaat ttttttctac gtgaaaaaca tactaattca 13020

ccattttcta ctgtgaagct tgcattactt ccatctaatt tttcttgtac aactagacct 13080

ctttctttaa atttatctag tacaatacct ttatttttta ctttagtata cgatttcatt 13140

aattatcctc ctttgaatta tgtactatag aaaacaaaat aagacttaca ctagctaaaa 13200

atgctaatac tactaaacca ggtaaattaa gaactgttga taagaataat gatattgcac 13260

ttataacata aactagaccg cttagaaata aagttaataa tacaattgtt ataagtttca 13320

ccaaccaatt attattaata aataccttag ctaaataatt cataaaaaaa tcctccttag 13380

ttattataga ataactatac cataactaag gggatttgtc aacatattat tttaccattt 13440

aaaattgtct gcatattgtg caagcttaga gcggaaatta actgtaaaat tatgaaatac 13500

tgctccttca taatttttaa agtattccat ataatctcca aaacctgatt tactttcgtt 13560

ctttaaatct atttgtttaa aattaccttc tactattaca gtagaatttt ttgtatgaac 13620

ccttgtaaga actttttaa gttcactgcg tttaaagttc tgtgcttcat ttataattat 13680

agtagcatct cttagatttc cacctcttag gaataaatgg gatatttgag atacccaaca 13740

atctcctagt ttatcttctt taacattatc ttccatcatt aacatttcag ttatttgttg 13800

ttcaggattc atattaagtt caataagggc atcgtgtaat cccatgaaat aagccatttc 13860

tttttctgtc tgattacctg gtctgcttcc taaatcttct gatactggtg aaattataaa 13920

tactagcttt ctatttttat taagatagtc tgcgtaagca caggctactg agcacattgt 13980

tttacctgta ccggcttgac tctcattcca aagtatttca acattatcat taaagaaatc 14040

ctcacagaaa tctaactgct cggttgtagc tttttcaagg aattcattaa agattagatg 14100

ttctcccatg ttgtatctta cattaggata atcttttaac ttaaagtcta actcttttag 14160

ttgtattgcc atattttaaa gttcccctat ctataaatag ttttactctc ttttaatata 14220

gtactaattt ccgatatatt ctcctgttga agagcaataa ttactacatt cacattcagg 14280

gtagttatca caaacatctt catcttctac atcatcataa ccaatatcat aattattata 14340

attaaaatct acaatacaat tttcactatt acctttagat aatcctgtat aaataatatc 14400

atccacagaa tcccaatcgt tatctgccaa gtaatttaca ctatctagta ctgattcatt 14460

atcaggtaaa taaatactac cgtctgaaaa tttaattaaa atatcacctt gaggtaaggt 14520

atcattaatt aaatcaatct ctgtttcttc ttcaatagtg aatacagttc cttctaatct 14580

ttccggtgta gtatgtgtta aatgttttac agtatcccct gattcttcat agaatcctac 14640

tgcattcata tctttattat attttgcaat aaatttacca ttgtcactta ccaaatattg 14700

actagttgca ttatagtcgt ttgcgtcatc tactgtcatg caagggttat aatctttaac 14760

ataataacta attttcctaa catctgctgt ttgtactttc ttaccttcac ctttaattac 14820

tgaattaatt ttcttcataa tattttctcc tttttatata tcaattgatt tttttgcaag 14880

attatcggca tagtcattcc atttgtcatt tgaatggctc tttacttta caaagtttat 14940

atctattact ttttggtatt ctcgtatcat attaatatat gttttactta gaatatttct 15000

tgcagaccaa gtaccttcat accaatgtat taaaccaata taatctatat aaactattgc 15060

ctgattgtat cctagtttta tagcctcttc aataccataa caacaagcca atatttcacc 15120

cgcaacatta ttatacttta ttaatcctgg tttgtcaaca cttttactaa tttccgatat 15180

tatatttcct tctttactta ccaagacagc acctgagcct actttacctt tattatatga 15240

ggagctaccg tctgtgtata tatttacact atcctgcata cttataatcc tccataaatt 15300

gagggaattc acaatctgaa tagacttctc tgcaaaaaga tactgagata tagttaaaat 15360

caaaacattt gaaacagtgt tcttgaactt ctttttttatc tttagcaatc acattaaatt 15420

taaaaccatc agctatgact gtaaatactc ctttttttcat aaaacaaata cctccactaa 15480

ttttatttta aattaataac taactcaata aatgatttaa tagttttatt tttaccttca 15540

tcaatatctg aaaagaaatt aattaaactg tcatcctcat caaataaatc ttcaacatca 15600

tcaaatttat ttaatatgtc tgtaacactg taaccctctt ctgatatata ctcatgtaag 15660

tcttctccat cttctgacag tgttgcttct attttaccat ttttactttc aattaaatat 15720

aaagtattta atactttaac agaatctaca actacactgt agttactaat agtaggatac 15780

tctgtataaa gtatttctat attagtattc atataactat caattacaga gttaactgta 15840

tctcttttta gctcagatac attatgtttt cgtatagtag ggaattcttc atcatattct 15900

actaattctt ttctatctgt attcaataac ttgtctaaag aagacaacaa tactatttta 15960

tattggttat caggaagact gtctgtaatt tccattattg ttaaaaacgt atcttcacct 16020

agaactttgt ttatatcttg taattcaaat gaatctacca tttcaatagt atcatctata 16080

tcatctgtag tcattaaaaa attaactaaa ttattattct ccatcgtctt cctccaattc 16140

tttaaataac tcttttcctg gagtatttaa cgctttctct aaccgcatta aattagcact 16200

tcttggtttc ttttttccat actcccaata agatataaga gagtaatgaa cacctatctc 16260

agaagctaga cttcttaacg tatgtccttt ttctactcta atttttgaa ggtttagagg 16320

tttactttcc tttttttcat ccataattat ttctcctcta cttttaaaaa tttaaaatcc 16380

tcagattctt ttgcattttt tagtatatac tcttgtgatt tatttcttgc ctctgcctta 16440

cttttagcat ataactctat atgaaataca tgaggttttt ttaaagacgg tgactcgtat 16500

ctccaataaa ctttaaaaag tagtgtttct ttttttaaaa cattaattcg aaaccatctt 16560

ttaaatttat tcattcatta tcctcctcta tttatttgtt aaactaatta tagcatagtt 16620

aacttatgaa gtcaactata atatacaaaa aagactaaga aattaatctt agccttaata 16680

tattaataac tattatgtgc gttgtggtat gcaagagctc ctgatgttga accgtaacgg 16740

tcaatcatat attgttttgc acctttagtt tgttctgcta tagaaccacc actccatgat 16800

ttacctaatc cttggaatag tccttgagct cctgatgatg cattaacagc attagggttc 16860

attgtagatt cacgcatagc aatttcaatc attgcctcgt ctccacctgc ttgtctaatc 16920

tgttctgcta cagagcctcc tgtagaacta gttgattgtg taggttgttt agtttccttt 16980

tgaactggtg ctgatgttgt ttgtacttct tttttagtat cttgtttatt ttgagtatca 17040

aattgtgctt gttgttggtc tacttttgt tcaggtgttt gttcttctcc tgctaatcta 17100

gatactgtat tatctacttg agttgagcct gaatggtatt cataaccaaa gttaccatta 17160

taattataga aatgataagt aaattcaccg tcactaaatg agaaatcata attaccttct 17220

tgaattggtt ttgtattgac ttctgctgaa tttgatttag cctgttctgc taacttatta 17280

taatcaattt cgtctgcact agcttcgttt gtagcaatac ctccaaaagt aatagctgta 17340

cctaatgcta atgttgcaaa aattgttttc ttcataaatt taaaactcct taaataattt 17400

tttagaattg tttatttgta aaccgacata agtaatcata acatatatct ttaaataacg 17460

caagtataat atagcactaa ttagtgtaat attattaagg ttttattaca aacattacag 17520

ttatcagata attaaataca aaaaaaagag aggtattaac ctctctaatt tattattttc 17580

ctgttacatc tacaatagtt ccgtctccgc caatttgaat aggttgttta ccatcccatt 17640

tttcaattaa ctgttgacgt aatatcttat cagataagga agattctcta atctcattgg 17700

ctttttatc accattagcc tctacttctt ttttcttagc attttgttca gcaatttgtt 17760

tatcaacttt agtacgttct aattcttggt tagctttaac tcgactgtca attgcttttt 17820

gagtattctt atctgcttta gggctagata atgcaatgtc ctcaattaca aatccttgtt 17880

tttctaagtt gtcattcaag ctatctaaag tatctttttt aatttcccct gttttaactc 17940

caaatgcatc aattacagaa tacttagata ctgcttgacg gacattatct tgtacccgtg 18000

aacgtaaata tccttttttct agttcttcga tatctgcact accaaaacga ttaaataaat 18060

ctacagcttt agttgcatct actttataag atacatcaat atccatttgt aaattcttgc 18120

catctgaagt tgctacattt aaatctttat atttatgtgt ttgtgtttta gttgggtatt 18180

tatttacctt atcaaaaggt gctgttaaat gccaacctgg tgatttagta tcttccttaa 18240

caccatttac tgagtataca actccaacat gaccttgtgg aatcttagta atacacatta 18300

ataaaataat aaaccctata attgctaaaa accctaatac tcctgaaata actactgact 18360

ttctcattac atttctcctt tttctatttc ttttattaag ctatttaaag ctttttcctc 18420

ttggtctatt tcttgtttat cggctctagt tacaattgat tgtctacggt catttaagaa 18480

ttgtttttta tactttacat attgttctaa accgtattca tctaatgtac cttgcctaac 18540

taattccctg tattgttttc ttatgttact cttcttctct ttcattgaaa gaaaatcaaa 18600

taaataactt ataccaaaac ctacaaggac tagaaaaaca ataaaaatag caaaatatgt 18660

taaaagtagt gccatgtaat tcctccttta tttgattaca tatataacta tacactatgt 18720

atttaatttt gtcaacactt ttttgcaaaa aaaaatagac ggattttaaa tccgtctaaa 18780

tttatattct atttgaatac tccccaggca acgccaggta tttgattagg tggaacacct 18840

tgacaagttc taacagggca atatactctg ttaccgttgt aagcattata acctatccaa 18900

atatgacctg cttggataca aacttcgtca tatacaattg tagcccctgc cggtaagtta 18960

ccgcctactg gagcatttaa gaatggagaa cctattctgg ttactatagg ttggttacca 19020

ttaacaaatg ttgcgctttc cggtttatac caagttccga actggttctt tttccaagaa 19080

cctgtaactg gtctagttgc cggtgtactt gcactacttg ttttaccatc tttaactaca 19140

gtagagcttg aagttccgtt actcatgtag tttttaattt gtttaatgaa gtaatctttt 19200

aacttattca ttattgcttg tgatggtctt ccttgtgtta ctgggttaaa tcctgtatga 19260

agaaccatcg aacggtgagg gcaggcagtt ggtacaaatt ccatatgcaa tcttacagtt 19320

ttacggttag gagtaagacc ccattcttta aatttctctg ctgtaaattg gaatactgct 19380

tgttcatttt taaggaattg agcatcacta gcactcattg attgacagac ttcaatacct 19440

gcaaatctaa agttacctga gtttgctcct gttccatccc ctgtgtgcca agcaatttga 19500

ttcttagcat ctattgcttc ccatacataa ccttcagagc catagtaatg agcaatacca 19560

ttagcatatc tagcataacc tgcattagct aatgaattct cgtattgttg tcctgaagaa 19620

cgacctgcat cgttgtgtat taccattcct tcaggttttt taccacgttt atccattgta 19680

tagttaatgt gattcttaga aacttttagt gttgctttct ttttaggtgc aggtgtttta 19740

cttgcgcttt tcttagctgt ttctttttta acagtagttc ctgcttttac aggtatttca 19800

atgaagtgag ttaatccgta ataattatct acacgttttg taggtttttt attagcataa 19860

ccattccagt tttgctctaa aatagtaaat gtagaagtat tacctccatc atatacaata 19920

cctatgtgac cccactgttc ataactaccg gatgtaaata ccgcaatcca acctttttta 19980

ggtacagtag aaggtttatt ttcatgtatt ttaaatccag taccataact ctgtttaatt 20040

tggtctttag cattacccca agttctaact ttattatctg ttaaccataa aacatagtct 20100

gtaataaggt cttgacattg agcgtgatag tagccatctg cgtcaatggc tcctgcttcc 20160

attacaccaa atgacgggtc ataacttgta gctttttttaa ctctgtaagg gctatctact 20220

gttccttttg cataagcgtc taaacgttta tttatttctg cttgagtctt agccattact 20280

taacttcctc ctctgcaaat actttaccat gttcctcggt atcttcttca tcttgagaag 20340

gtgctgaacc accatcaatt tcatcttcaa tagcaggtac ttcatcacta tcatctgtgt 20400

caggttctgc attgttttcg tagctgtcta tctcaaaagt actagcgtta tttgcgtttg 20460

tttgccattg aacgaactca ttagggtctt tactatcacg aggtttaacg taatctgttt 20520

gaacaatatc actgtctcta agacctttag tattattatc aacaataata cctaaacctg 20580

ctaataatgt tagtatagaa cctacaatat ttacaccttg ctcaatttga gctgagtagt 20640

ctaaaccgaa agcacctgta atttggttag caaataatgc tactgctgat ataattgcta 20700

cccaaaatgt tttgctctta gttcttgtgc taaggtttat tcctccaaca actttaggtt 20760

gtttagtttc attagccatt aaaaaaccga cctttctatt atatttattt ctaacaataa 20820

tataacagta ggtcggtcat gtttatctat attaatttaa cacttactca ttaatttggt 20880

ttagtttttt gataacttca gacatttgtt tgttatctaa atcttctaat ttagtttccg 20940

gaagtagctc taacttatcc caaacttctt ctttattaga tactttatta ttaataattg 21000

ccttaccaac taaactttcc gtataatata attgttttgc tgatgccatt tgtatctctc 21060

cttttaaata tgtaaagtat atagctagta tcgtatccta ggaacaaaca cttgcgctat 21120

atactcaatg aaatcctacc ctcattcgag gacacagcaa accggttcgt caaccgcaca 21180

tatgaattct aagatttcat ttatgtaaaa cacaccctct ttgatttgca caaagactaa 21240

gggttttgga gacccttgta ctactaatta tactaagggt gtttattatg gtttctattg 21300

gatttgaacc aatgacacct agagcttcaa tctagtgctc taccatctga gctaagaaac 21360

cttaaaacga cccatacgag actcgaactc gtactctctg ccgtgacagg gcagtgtgtt 21420

aaccagttac accaatgagc caaaattata atgctatacc ctaaccttac cttaatgtat 21480

agcaggtttt ctcttaggct cgaagcaacg attattacca ctcataacaa ctatatatta 21540

agtgaaagga ggtgaaatga acaaaacgtg gtaattggta cctaagaagg taatatgtat 21600

aatctacaag gagtaagtta ttggttcata aaggagtgtg aacaataaat acatgaaaga 21660

gtgaaagttt actccctgta gattcttttt taattatcaa tcaaaggagg aaactgataa 21720

ttgttaataa taaactataa agaggaaaat atttatagtc acattctgat ataatgcaac 21780

taaatatcca agcataaccc gtctcacgag gaacctacct ataagacctg ttattaagtg 21840

aatcactacg attgactcta ttaaggagct accttaagtc catctcacgc aatttaaaag 21900

ggacttacaa accgtaaaac ggtaataagt ttattaaata atgtgatatt aacatattag 21960

ttaataactt tcacatggtc gaagaaaagt aaatttattt gattaccaaa ttatttttat 22020

caaatatagc tcttttgaac ctgtagattt atgctactca tactgataac ctctattatc 22080

taacacattt ctgtgctcca actacagtta gtcgttacag cgtatctttc taggattccg 22140

ctaagaccct agaaagaaat taaaccctag ccgttatcat actctacaga ccttataagt 22200

aagtaccaag tataccaatc gtatttaaca atactaatga cgacccatcc taccgatata 22260

tctccgataa gttttgattc gtttgattat cttgtacctt atgactacca aatcattatt 22320

cagtcactat gctcagatat ttagttgtat tatttatata ttaattataa catagttttt 22380

attacttgtc aagttaattt caaaaaaatt atagaagtag ggacgcttac ctacttccat 22440

ttaatttaca caaggatgat aacattgtta ttgttttata ctggaaaaca atgtaagaaa 22500

aacagtgatg tgtaaggtat ttgttttatt gttaattaca ttatagcata tactgatacc 22560

tttgtcaagt taatttaata ctttttttaaa atattagtta tcttttgtta attcttcctg 22620

aatagcatcc catcttcttt ctgcttcact acgattatct tctatatgtt ttgtagtttt 22680

acaacatttg atacaatata tatctttgat atgaccttct tctcttttat ttgctctttt 22740

tcttggtact ttgaatacat ttccacattc tttacatatt aaacttgagt aaaacatttt 22800

ttgtcttttc ataattaatc aattcctttt ctcttttatt tgataattta actatatact 22860

atattgataa ataagtcaac agttttctaa aaataattta aattattttg aagaatcctt 22920

taatatcaag ggttacaaga gaaaaagtac gtatttagaa aataaggagt actcctatta 22980

tatataatta tattctgata tagagtaata aataatatta aatatataat tataattaat 23040

aaggttggga aaattgatat aaacataact gatattgctt atagatactc agtataaaag 23100

taaaatccct tagtatcagt acttacaggc aaaaaagtac gtatttagaa aataaggaac 23160

tctcctatta tagttatata tattaattac tattattaat tactatttaa atatataatt 23220

ataattaaca atgttagaaa gtcaacaata gtataaataa aaaagtgact acttaaagtc 23280

actcaataat tagaatacta ttttaaaaga ttctattctg tttggattaa tatatacttg 23340

aggtgaagtt atagcacttt cagtatatac ttttatagag gtttcatcca ttcctcttaa 23400

catataatct atatcttgcc tattgtaact cttttcatca gtagatacta aaaagtattt 23460

agctccactt gacattgtta tttcaatatg ttttgacatc tacaatctct cctatgcaaa 23520

tttgttaaag acaaaggata atatagctcc tagaacaagt aaaagaactt tctcagttgt 23580

atccttcttc ttagtatcct tagtttttgt acttccagca agttctgaaa tcttttcatc 23640

aagtctttct aattggacgt aaattgctga ttgtttttca ctattgacag ctacatcttt 23700

atctatacta actatcattt ttcttagttc agctacctca acttctaaat ctttgaaagt 23760

ccctctatct atataattac cttcttgtat cttagactta atagtttcta cttgagaaac 23820

aaggttgttt atctccttat ccaactagaa tcacctctaa ggtctaaccg tttcagattc 23880

agaatggata tcataatttt ctaagaaatc attgataatc tccatataat tatccgtaac 23940

gacttttccg taagatgttt ttgtatcaat ttcaaaccta agcttaccaa aactttggag 24000

gtctaattct tttattacaa tattagggtc atcagaagga aggtaataat agtcgaagta 24060

tataattgag ccatttatta atactctgtc tattctatag acgtggaaat agcgtctgtc 24120

tcttttaaaa tgggctagtg catctttaaa ctctaactta aggatatcct tatatttagt 24180

caaagtggta acctccttac tattaatttt taaatttact tattttgtgg tataatagtt 24240

atgataaagg cagttattat aattatatta agaataatga taataattat tttttctgag 24300

aaaataagcc aaatactaaa aacagataaa gcatagatag ctgatagata tactatatta 24360

agagttacct tacttttatc ttttctatag atagaataac ctaaagacgt tgtaacacca 24420

ctaagtataa aataatagaa acaaaaaaga ggtatagaca gaaaaaaaga tacgataatc 24480

attgttaaac acctatttct ttttgaccta ttatttctag aacttttaga ttacaccact 24540

aatataacat taaaagccag tcataaaagt caattgttag attaataata taataaaaaa 24600

agacaatagg aggttaaagt ggttgaataa taacatagct atattcatat tcaaaacact 24660

ggttatcatt atattcttac tactaatttt gtctgttatt aattccttgt cccttattta 24720

ctcaataaga ccgagtgtag ttatgacata ctttatcttt ggtggtattg tttctaatgt 24780

cgcacttact gtaacagata agttcttact gaagaaagaa gacccctac ctgaatatgt 24840

tcttaaaaaa gtagagataa atgataaaga aataagaata atcaagaaaa tcatagaaag 24900

taattacgga ataacagcag aagagataaa agttagggct aaagcacaaa gaagaataga 24960

ggaagatagt aaaaaggaag attacgatga aaacaaagaa agaaattaaa gaacaaagga 25020

aagagcttaa ggatggtgct acatctgttt ctttagtaaa aaaaggagat aagagaatag 25080

ctagccctag tagaatttgt agtctatgtg gtcagcagtt atcaggtatg aattacacta 25140

aaggaaaagc attatcaaaa gttaatcatt ttcatttaca gtattctaag tatatttatt 25200

ttgatatttg cgcagatatc aacaattgtt ataaaaattt aagaaaacga ggtgaaatgg 25260

attgagtgca gaaaatatta gagatataat taacaagaaa aagttagaag aagaggatac 25320

aagaaaatat atagctgatg gatttatgaa tggtatcggt aaattaatgt acgaattcaa 25380

taaaaaagta gataataaag aaatagaagt taaagaccct aatgatttat ataaattatt 25440

tgtgatattc tctcaaatgc aaaatatggt caatgaaact tctgaaggtg gagcaatacc 25500

tcaactatct agacctcaac aggaattatt tgatgagatt acaacagaag atagtaatgg 25560

agaatctaca gttgatttac agaagatatc agaaatgtca gcagaagata ttacagcaat 25620

gatttctgaa aaggaaaaag taatgaatga ggaaaattca gaaacattct aaggagaaag 25680

atataaatgg atggaaaaga actaattaag atagcacaag aaacatttca aactgaaaaa 25740

ataacaagag aacagataga ccatataatc aatatgctaa acccttctac ctatatgctt 25800

aagtatcata cactgagagg tcatcctata acttttagta ttcctaacag ggatagaagt 25860

aaagcacagg ctcatagacc ttggcaaact aggattgtaa atgatactca tcctaataag 25920

gctgtaataa aatcacgtca gttaggtctt agtgaaatgg gtgtaatgga aatggttcat 25980

tttgcagata tgcatagtta tgctaacgca aagtgtctgt atacattccc tacaaatgaa 26040

caaatgaaaa aatttgttca gtcacgtttg aaccctgttt tagagaaaga atattttaga 26100

gacattgttg attgggataa agactcgtta ggttttaaaa agataagaaa ctctagttta 26160

ttctttagaa caagttctaa agcaagtacc gtagagggtg tggatattga ttatttatct 26220

ttagatgagt atgatagggt aaacttatta gcagaatcgt ctgcactaga atcaatgtct 26280

tcatcacctt ttaagattgt gagaagatgg agcacacctt ctgtacctgg gatgggtata 26340

cacaaattat accaacaatc agaccagtgg tattacggtc atagatgtca acattgtgat 26400

tacttaaatg aaatgagtta taatgattac aaccctgata atcttgaaga aagtggaaat 26460

atgttatgtg ttaatcctga aggtgtagat gagcaagcta aaacagtaca gaatggcagt 26520

taccaatttg tttgtcaaaa atgtggtaaa ccattggata gatggtataa cggtgagtgg 26580

cattgtaagt accctgagcg tacaaaaggt aataaagggg tacgaggata cctaataaca 26640

caaatgaacg ctgtatggat ttctgctgat gaattaaaag agaaagaaat gaatacagaa 26700

tctaagcaag cattctacaa ctatatttta ggttatcctt ttgaagatgt taaacttaga 26760

gttaatgaag aagatgttta tggtaacaaa tcacctattg cagaaacaca attaatgaaa 26820

cgagatagat attctcatat agctattggt atagattggg gaaatactca ctggataact 26880

gttcatggta tgttacctaa tggtaaggta gacttaatac gattattctc tgttaaaaaa 26940

atgacaagac ctgatttagt tgaagcagat ttagaaaaaa taatttggga aatatctaag 27000

tacgaccctg atattataat tgcagataac ggggactcag gtaataacgt tttaaaactc 27060

attaatcatt ttggaaaaga taaagtattt gggtgtactt ataaatcttc tcctaaatct 27120

acagggcaat taagacctga atttaatgag aacaataata gggttacagt agataaatta 27180

atgcagaata aaagatatgt acaagcactt aagacaaagg atataagtgt ttatagtaca 27240

gtagatgatg atttaaaaac tttcttaaaa cattggcaga atgttgttat tatggatgaa 27300

gaagatgaaa aaactggaga aatgtaccaa gttatcaaac gtaaaggtga cgaccactat 27360

gcacaagcaa gtgtctacgc ctatatagga ttaacaagaa taaaagaact tcttaaagaa 27420

ggaaacggta caagctttgg ttctacattt gtttctactg attacaatca agaaggaaat 27480

aaacaattct actttgatga atagaggtga aatagacttg acagataaat tattttatgg 27540

tacaattagt aatgaagaaa ttaataaaag tgtattgaat ttgttattgg gtgaggaatt 27600

atccttagat tatgtttcta aaaatagtga tactttagat gttaaatatg aacatgttta 27660

taaatctcta ggattcgata atttctttga ttgtttttta tatgctaata gagagcctga 27720

aatagtccat aaaggtggag ataaaaatct tggtggacta aataaggtta aacgtactgt 27780

tattcgtaat ggtaaagaaa tggaaatgac agtttacgaa gatggtaata aagagaacga 27840

tagtaaagaa aaacaagaag gaaaagaaga agttagtaga agtgcagtag gagcaagggc 27900

tatttctaat ggtgaagaag gaaaggtaaa ccctaaaaag gtagcaaatt cattatctaa 27960

tttaagtaaa aaaggtgtag atgtatcaca tattaataca aactcatcat tgtataaaga 28020

gtttgttgat gataacggtg atacattagg aattacatct tttaaacgaa ctgaaaatga 28080

tataatatta gaatcttatg caagttcaca tgattcagat ggtgtaggag caagagctat 28140

tatggaatta ttacgtttaa gtattaagga aaataaaaat gcagttgtgt atgatataga 28200

attacctgaa gcagtagagt atttaaaaac tttaggattt aaacctaata aagatggata 28260

catcttaaga aaaaaagatg taaaacaatt cttaggtgat tatagtgatt ttatttagca 28320

ctatagtcat ctattctatt gtatttattc tatatattgt attaaaaaca atttatataa 28380

agtctaatat gagtagaata gataacacaa ctgaattatt aaaaatatta caggaagata 28440

ttgaaggtaa gataaaaaag gaaggaagaa ataaatgact ttagaagaaa ataaattaac 28500

attagaagaa tcaataactc cacttagcaa agaggagaaa gaagatagta ttaaagaatt 28560

tagcagttta ttatgtgaaa tggtaaatag actatataag tcttataatg tatttagaca 28620

agaccctatg gatgaaactc aacgtctaga tggctcttta atggtctttc aaagtagatt 28680

aaatgaccct ttaacaggag atttacatga taagatgtat aaacttgctt tttcaaaacg 28740

tattgatatt ttcgaagcta ataagcaatt tagaaaagat gtagaagcag gtaaagcaat 28800

tgagttaggt gatgtagcta ttatagatac agcattaagt aacatccttt caggcaatga 28860

gttccaagga agtatttcat ttatgcttag aaaagacttt gaagaaaaag aacgaattag 28920

aaaagaagaa gaagagaaac ttaataactt ataaaaggga agaattatga gactatataa 28980

aatgaggtat cataattgaa aaagaaacca caaggcaatg aggtaatcat aaccataata 29040

acggttatga tagcagtatt tgtagtcatt atgaccatat tttttaataa atatcaagat 29100

gctaaagaag ataaagatag atatcaaaga ttagtagaga tttataaaaa agcagatgat 29160

aatgatggtg agactaaaaa gaaatatgtt aaaagattaa ataaggctga agaagaactt 29220

aaaaaagtaa aaaagaaaca aattataaag attataataa gaagtcaagt aaagaaagac 29280

aaaaagaaga taaagaaact agagagaaaa tatatgatgt aactggtgat gatgacttaa 29340

tattagtaaa aaataatatt gagtttagtg ataaagtaga caagcccgaa atacttatta 29400

gtgaagatgg aattggtacg ataactgttc ctgtagatag tgggtatgaa aaacaaacag 29460

taggttctat tattactagt gtattaggtt ctcctttcct atcacctggt tcaaatagta 29520

tagatggttt aagtgttatt aacgataatg tttatccaaa tacagtagat agcatagtag 29580

aagatacaaa accttctatt aacttaccaa cggataatcc tattataaca aatccagttg 29640

aaccaactat accttcagat attatacctc ctattgataa tccttcagtt ccgatatctc 29700

ctgagaaccc aggagataat aatcaaggaa atacagataa tccaaatcct ccccctccag 29760

ggtacacaga tgaagatggt ggaagaggct ccggtggtgg aggaaattct gaaccaccat 29820

caacggaaga accttcggat aatggtaaca ccggaggagg agattgggaa gaaaaacctg 29880

acccaggaga agaaccttca gataatggta atacaggagg aaatggtgga gaagttacgc 29940

ctgaacctga acctgaacct gaacctgaac ctgaacctga acctgaacaa ccgaatgaaa 30000

atcctgatga aggtaatgaa gaaaaaccat ctgaaccgtc tgacaatcct gatgaaaatg 30060

gaggatggga aactgaacca actgaacctg agtcaccttc agagccggac gataaagtgg 30120

acgaagaaga taaaaatgaa gatactacag atgataaaca gcccactgaa caaccggacg 30180

ataacaacat agataatgaa gataaaactg aagaggagta attactcctc ttttttgttt 30240

gctatattaa ataagagcta aatataaaaa aattgaacat tacggtggtg aaaactttgt 30300

taggaatgaa tattataacg tcactatcag tagtatttac ttgtttaagt cttttaactt 30360

taatgatttt tgttcatagt aagttctcta gtaaaaacgt ttttgttttg tatgtaattt 30420

atgctataat aggaataggt acatacatag ttttaactat gtttcaaaca acatctgtac 30480

ttattaagaa tgatgtaata gattccatag aaaatactga acattatatt ggattcaatg 30540

accctataat tatatttact ataagtttta taggtgcaat acttggagga atttggtaca 30600

agatgatgaa aattattaaa aagagtaact ttaaagataa aaaataaaaa agacggtgaa 30660

taggttgata ttctctaaag ataaaaaatg ggatgaagca aaagatttca tcaaaggtca 30720

aggtatgcaa gataattgga tagagattgt agattattat agacagatag gtggaaaaca 30780

cgtagctgtt tttattgctt taaacaaagt aaaatacatg attctagaag caacaaaaga 30840

caataaggta atattagtag ataaagataa taatatacta ttagaagatt atgatattgt 30900

tatggaaagt aagaagatgt tttattacat tgaagaaccg ttcgaggtta aaataaatat 30960

ccctcaacat attagagatg taacttataa taatactgtt gtattaacta cagtaagagg 31020

gagtagaggt gactagtaat tggcagattt atttaagcaa ttcagattag gtaaagacta 31080

tggtaataat agtaccattg ctcaagttcc tattgatgaa ggattacaag ctaacattaa 31140

aaaaatagaa caagacaata aagagtatca agatttaact aagtctttat acggacagca 31200

acaggcttat gcagagccat ttatagaaat gatggatacg aatcctgaat ttagagataa 31260

gagaagttac atgaagaacg aacataactt acatgatgtt ttgaaaaagt ttggtaataa 31320

ccctatcctt aatgctatca tacttacacg ttcaaatcaa gtagctatgt attgtcaacc 31380

tgcaagatat tcagagaaag gtttaggttt tgaggtaaga ttaagagacc tagatgcgga 31440

acccggtaga aaagaaaaag aagaaatgaa acgtatagaa gattttattg ttaatacagg 31500

taaagataaa gatgtagata gagattcatt tcaaactttc tgtaagaaaa ttgttagaga 31560

tacttacatc tatgaccaag ttaactttga aaaagtattt aataagaata ataaaactaa 31620

attagaaaaa ttcatagcag tagacccttc tactattttt tatgcaacag ataaaaaagg 31680

taaaattatt aagggtggta agagatttgt tcaagtagta gataaaagag tagtagctag 31740

ttttacttct agagagttag ctatgggtat aagaaaccct agaactgaat tatcttcttc 31800

aggatatgga ttatcagaag tagagatagc tatgaaagag tttattgcct acaataacac 31860

tgaatcattt aatgatagat tcttctccca cggtggtact actagaggta ttttacagat 31920

acgttcagac caacaacaat cacaacatgc attagagaac tttaagcgtg aatggaaatc 31980

tagtttatca ggtatcaacg gttcatggca aataccagtg gtaatggcag atgatattaa 32040

atttgtcaat atgacaccaa ctgctaatga tatgcaattt gagaaatggt taaattacct 32100

tatcaatatt atatctgctt tatatggtat tgaccctgca gaaattggtt tccctaatag 32160

aggaggagct acaggttcta aaggtggttc tactttaaat gaggctgacc cgggtaaaaa 32220

acaacaacaa tctcaaaata aaggtttaca acctttactt agatttattg aagacttagt 32280

taatagacat attatatcag aatatggaga taagtataca ttccaattcg taggtggaga 32340

tactaagagt gctactgata aacttaatat tcttaaacta gagactcaaa tatttaaaac 32400

agttaatgag gctagagaag agcaaggtaa gaaacctatt gaaggtggag acattattct 32460

agatgcttca ttcttacaag gaacagccca attacaacaa gataaacaat ataatgatgg 32520

taaacaaaaa gaacgtttac aaatgatgat gagtttacta gaaggagaca atgatgattc 32580

tgaagaaggg caatcaacag attctagtaa tgatgataaa gagataggaa cagatgcaca 32640

aataaaaggt gacgataatg tttatcgtac tcaaacatct aataaaggtc aaggaagaaa 32700

aggagaaaaa tcttctgact ttaaacatta attaataagc ctagaataaa tctaggcttt 32760

gtttattttt ttcgtaattt aattttgata aatgtaataa ctatgatata ctatatgtaa 32820

ttgatattaa tacataaaaa atattaatat ttcacttaca agttattatt gttatattat 32880

taacgtaaaa gtaaataaaa taacaagtgg aggtgtagac acctttggaa gaaataaaat 32940

ttaatgcttt tgtacctatg gatttgaaga aatctgtatc aacagcttct gatactaatg 33000

agtattctat cgtttcagga tgggctagta ctccaagtat ggatttacag aatgatatag 33060

ttaatcctaa aggaatagat atagagtatt ttaagtcaca agggtacatt aattatgagc 33120

atcaaagtga taaagttgta ggtataccta cagagaattg ctatgtggat atagaaaaag 33180

gtttatttat tgaagcaaag ctatggaaga atgacgaaaa tgttgttaag atgcttgatt 33240

tagctgagaa attagaaaaa tcaggtagtg gaagacgttt aggtttttct attgaaggtg 33300

cagttaaaaa acgtaatata aatgacaatc gagttattga tgaagttatg ataaccggag 33360

ttgcattagt taaaaaccct gctaatcctg aagcaacatg ggaaagcttt atgaaatcat 33420

ttttaactgg tcatggtaca tcacctgaca ctcaagttga tgcaggagct ttaagaaaag 33480

aagaaatagc atctagcatt acaaatttag cttacgtcac taagattaaa gatttaaaag 33540

agtttaatga tgtatggaat ggcgttgttg aagatttgag taaatctaat agtatgggat 33600

atgaggaatc agtccttacg ttacaactag ctaaaggttt atctcgtaaa gatgcagaac 33660

tagcagtaat ggatataaac aaacaaaaac tagaataggt aaggagaata cattctatga 33720

gtaaagaaat gcaaaatatt ttagaagagt atgataagtt aaatgctcaa gaggcagttt 33780

cgaaatctgt agaagatgat gaaaagaata cagtagaatc taccgaagag caagtagcag 33840

aaacaactga agaacctgct aaagaacctg aaaaagtatc tgaggaagat gctaaagaag 33900

cacaagagca aggtgaaaaa gttgaatctg aagaggtagc agagggcaat gaagatgagg 33960

aagttgaaaa atcagctaaa gaatcaaaag accctgtaga ccaaaaagat actaagacag 34020

aaaataaaga caacgagaaa cgtaaaaata aaaaagataa aaaagaagat tctgacgatg 34080

aagataaaga tactgacgat gataaagata agaaagaaga taagaaggaa aaaacttcta 34140

aatcaatttc tgatgaagat atcacaacag tatttaaatc tatcttaaca tcttttgaaa 34200

acttaaataa agagaaagaa aactttgcta ctaaagaaga tttaagtgaa gttagtaaat 34260

ctattaatga gttatcagca aaaatttctg aaatccaagc tgaagatgtt tctaaatcag 34320

tagacactga tgaagaagct gtagaaaaat cagtaacatc tacaaacgga gagcaagaaa 34380

aagtagaagg ttacgtttct aaatcagtag acactgaaga acaagctgaa actggtgaag 34440

caaaatcaga agaagctgaa gaagtacaag aagataacac atttaaagga ttaagtcaag 34500

aagaacgaac taagttcatg gattcttaca aagcacaagc taaagaccct agagcttcta 34560

aacatgactt acaatcagct taccaatctt acttgaacat taacactgac cctactaatg 34620

catcagagaa agatattaaa actgtaaaag actttgcaca aatttaatta atgcacaaag 34680

ttgtgttata ttatacggtg taactaaaga atataaatag ggtacatttt actgtaccct 34740

acataaaata aaaagaacac aaatgaaagg tgataaattt atatgactat cgaaaagaac 34800

ctgtcagacg ttcaacaaaa gtacgctgac caattccaag aagacgtagt aaagtcattc 34860

caaactggtt atggaatcac tcctgataca caaattgacg caggagcttt acgtagagaa 34920

attttagatg accaaatcac aatgttaaca tggactaatg aagacttaat cttctatcgt 34980

gatatctcac gccgtcctgc tcaatctaca gtagtaaaat acgaccaata tttacgtcat 35040

ggtaacgtag gtcactctcg tttcgttaaa gaaatcggag tagcaccagt atctgaccca 35100

aatatccgtc aaaaaactgt atcaatgaaa tacgtttctg atactaaaaa tatgtcaatt 35160

gcatcaggtt tagtaaataa cattgctgac ccatcacaaa tccttacaga agatgctatc 35220

gcagttgttg caaaaacaat tgagtgggct tcattctacg gtgacgcttc attaacttct 35280

gaagttgaag gtgaaggtct agagtttgat ggtttagcta aattaattga caaaaataac 35340

gtaattaacg ctaaaggtaa tcaattaact gagaaacact taaatgaggc ggcggtacgt 35400

atcggtaaag gtttcggtac agctacagat gcttacatgc ctatcggtgt acacgcagac 35460

ttcgttaact caatcttagg tcgtcaaatg caattaatgc aagacaacag cggtaacgtt 35520

aacactggtt acagcgtaaa tggtttctac tcatctcgtg gattcattaa attacatggt 35580

tctacagtaa tggaaaatga actaatctta gatgaatcat tacaaccatt accaaatgct 35640

ccacaacctg ctaaagttac agctactgtt gaaactaagc aaaaaggtgc ttttgaaaat 35700

gaagaagacc gtgcaggatt atcatataaa gtagtagtta actcagatga cgctcaatca 35760

gctccttctg aagaagtaac agctacagta tctaacgtag acgatggtgt taaactttca 35820

attaatgtta acgctatgta ccaacaacaa ccacaattcg tttctatcta ccgtcaaggt 35880

aaagaaacag gtatgtactt cctaatcaaa cgtgtaccag ttaaagatgc acaagaagac 35940

ggaacaatcg tattcgtaga taagaacgaa acattgcctg aaacagcaga cgtatttgtt 36000

ggtgaaatgt caccacaagt agttcactta ttcgaattac ttccaatgat gaaattacca 36060

ttagctcaaa ttaatgcttc tattacattt gcagtattat ggtatggtgc attagcatta 36120

cgtgctccta aaaaatgggc tcgtattaaa aacgttcgtt atatcgcagt ttaatagaat 36180

aagaaaaact gaatacaaga gaatagggat aaacttaggg tttatccctt ttttattaaa 36240

ataaacttga agggatttaa taaatatgtt atactataag aaactattag ataaaaaaat 36300

ggctactgtt tatggtacag tggagattga caaagatgga gtagttaaag gattaactaa 36360

agagcaagaa aaagaatttg caaatgttcc aggttttgaa tttgaagaag aaaagaaaac 36420

tactagaaaa caatcagctt ctactagtaa agaagaagag cctaaggaag aggaaaagaa 36480

agcctctact agaaaaacta caagtactac tagaaaatct acagcacgta aaacaacagc 36540

caaaaaagat gaaaataagt aaagggtgaa ttaaatggtt aactcaatgt ttggagggga 36600

cttagaccct tatgaaaaat cattaaacta tgaatatcct tatcatccta gtggtaatcc 36660

taaacatata gacgtaagtg agatagataa tttaacatta gctgattatg gatggtcacc 36720

ggatgcagtt aaagcatata tgttcggtat cgtagttcaa aatcctgata caggacagcc 36780

tatgggtgat gagttttata accatatatt agaaagagcg gtaggtaaag ctgaaagagc 36840

attagatata tctatactac ctgacactca acatgagatg agagattatc atgagacaga 36900

gtttaatagt tatatgtttg tacatgctta cagaaaacct atattacagg tagagaactt 36960

acagctacag tttaatggta gaccaatata taaataccct gctaactggt ggaaagtaga 37020

gcatctagca ggacatgttc aattatttcc tacagcactt atgcaaacag gacaatcaat 37080

gtcatatgat gctgtattca atgggtatcc tcaattagca ggtgtatacc cgccatcagg 37140

ggcaacattt gcacctcaaa tgatacgatt agaatatgta tcaggtatgc ttccacgtaa 37200

aaaagcagga agaaataaac cttgggaaat gcctcctgag ttagaacagt tagttataaa 37260

atatgcattg aaagaaatat accaagtatg gggtaactta atcattggtg ccggtattgc 37320

taataaaaca ttagaagtag acggtattac agagacaata ggtactactc aatcagctat 37380

gtatggtgga gctagtgcac agatacttca aataaatgaa gatataaaag aactattaga 37440

tggtttaaga gcttactttg gatataatat gataggatta taaggagggt tagaaaatgg 37500

aaaaaccgta tatgatagga gccaactcta accctaatgt tattaataag tcaacaacat 37560

atactactac aacacaagca gatgaacaag ataaacctaa gtatactact agactagagt 37620

ttgatacgat tgacatgatt aggtttatta atgaccgagg tataaaagta ttatgggaag 37680

aagcatattt ctgtccttgt cttaatcctg atacaggaca tcctagggta gattgcccta 37740

gatgtcatgg taaagggatt gcatatctac ctcctaaaga gactataatg gcaatacagt 37800

ctcaagagaa aggaactaac cagttagata taggtatatt agacacaggt actgcaatag 37860

gtaccactca attagaaaag agaatttcct atagagatag gtttactgtt cctgaggtat 37920

tgatgcctca acaaatgatt tattttgtga ataaagatag aattagaaaa ggtatacctc 37980

tatactacga tgtaaaagaa gtaacttata tagctactca agatggtaca gtctatgaag 38040

aagattatga aattaagaat aacagattgt atttaaatga aaaatatgag aaccatacag 38100

taactttaaa gatacttatg actttaagat atgtagtatc agatatacta aaagaaagtc 38160

gttatcaata tactaagttt aatcaaccta aatcaaaatt tgaaaactta cctcaaaaat 38220

tacttcttaa aagggaagat gttattgtac tacaagaccc ttataaagtt aatgatggca 38280

tagaagaaga cctagaaatt caagtagatg accctaaggc ttcagcatct aatcctagta 38340

atttaggtgg attcttcgga ggtgcattta aataatgcca gttcacggaa agagacctaa 38400

tttatttaaa aataaaaact ataagcaggt aggtaagaga acaattgatg gtatgcgttc 38460

agaagttctt gataaattac aagcaacagc acagcaagta gagaatacta gtattaaacg 38520

tatgcctact tacctacaaa taacagagaa aaagcttgaa aaagaaggag tagtagacct 38580

taaaaaagct tttgctcact catctaaaaa gaaaactagt aaagatggcg gatggtattt 38640

aactgtacca atccgcatca aaactagtag aatgaataac agtacttacc aagatatgag 38700

aactttaaaa gtagataaag gtacaggttc agtctctaag ataactgatt acctagaagg 38760

acgtagaaag aatgtaagcc atccttcaat gaagcctgaa cctatgactc ataatatgac 38820

taaagttaaa agaggaaagc aatcttctta ctttatattt agaactgttt ctagtaagtc 38880

acctgctagt tcttggatac ttaacagaga taaagttaat gaagataact tctctaaaac 38940

aactctaaaa actgttaagc aattaatgaa ctggaagatg aaaaatttaa attaagagga 39000

gggttagtat taaatggcaa taacatcagt tgattcatat ttattatcag aaataaagcc 39060

tagacttaac actgtgctag agaattgtta tattatagat gaagttttaa aagactttga 39120

ttatcaaact agagagagct ttaaagaagc tttctgtggt aagaatgcac aacatgaagt 39180

aacggtagga tttaacttcc caaaatttaa aaataactat gaagctcatt acttgataca 39240

attaggtcaa ggacaagaga caaaaaactc tttagggagt attcagtcat cttactttga 39300

ggcaacagga gataccttag tcgaatcttc tacagcaata agagaagatg ataagttagt 39360

ttttactgtt tctaaaccaa taggagagtt aataaaggta gaagatatag agtttgctaa 39420

atacgataat ctccaagttg aaggtaataa ggtatcattt aagtatcaaa caaatgaaga 39480

ttatgagaac tacaatgcta acattatatt taccgaaaag aaaaatgatt ctaaaggttt 39540

agtaaaagga ttcacagttg aagaacaagt aacagttgta ggtctttcat ttaatgtaga 39600

cgttgcaaga tgtttagatg ctgtactgaa aatgatttta atatctatga gagatagtat 39660

agaagagcaa caaacattcc aattacagaa tttgtctttt ggtgatattg caccaataat 39720

agaagatggt gactcaatga tttttggtag accaacaatt attaagtaca caagttctct 39780

agatttggat tatactatta cacaagatat taataaacta acttttaaag aaagaaagga 39840

ttggaagtag gatggctaga aaaaagacac ctgaaaataa cactcctaaa tttaatggtt 39900

atgttcatat agatacattc cttgatactg caaaaaccct ttttaatatg aaggattcac 39960

aagtagcagg atttaaagct tatatggaag gtagtcatta tttgtttagt gagcaagaat 40020

tcttaccatc attagagaag tatctaggta ggaaattaga tatataataa cattcagata 40080

aggagaatta aatatggcag tagaaccatt cccaagaaga cctattaccc gtcctcatgc 40140

atctattgaa gtagatactt caggtatcgg tggctcagca ggttcaagtg aaaaagtatt 40200

ttgcttaatc ggtcaggctg aaggcggaga accaaataca gtttatgaat tacgtaacta 40260

tgcacaagct aaacgtttat tccgttcagg agaattactt gatgcaatag aattagcatg 40320

gggttctaac cctaactata cagcaggtaa gattttagct atgcgtatag aagatgctaa 40380

acctgcttca gcggaaatcg gtggattaaa agtaacatct aaaatctatg gtaatgttgc 40440

taacaacatt caagtaggat tagaaaagaa tacattaagt gattcattac gtttaagagt 40500

aatcttccaa gatgaccgtt tcaatgaggt ttatgataat atcggtaata tcttcacaat 40560

caagtacaaa ggagaagaag ctaacgcaac tttctctgta gaacatgatg aagaaactca 40620

aaaagcaagt cgtttagtat taaaagttgg agaccaagaa gttaagtcat atgatttaac 40680

tggtggagct tatgactaca ctaatgctat tattacagac attaatcaat tacctgattt 40740

cgaagctaaa ttatcacctt tcggagataa gaacttagaa tctagtaaat tagataaaat 40800

tgaaaatgca aatatcaaag ataaagctgt atatgtaaaa gcagtttttg gtgacttaga 40860

aaaacaaaca gcttacaacg gtatcgtatc tttcgagcaa cttaatgcag aaggagaagt 40920

accaagtaat gtagaggttg aagcaggaga agaatcagct acagtaactg ctacttcacc 40980

tattaaaact attgagccgt ttgagttaac taagttaacg ggcggtacta atggagaacc 41040

acctgctaca tgggcagaca agttagataa atttgcacat gaaggcggat actacattgt 41100

cccattatca tctaaacaat cagttcatgc agaggtagct tcttttgtta aagaacgttc 41160

tgatgcaggg gaaccaatga gagctattgt tggtggagga ttcaatgaat ctaaagaaca 41220

attgttcggt agacaagcat cattatctaa tccacgagta tcattagtag ctaactcagg 41280

tacttttgtt atggatgatg gacgtaaaaa ccacgtacct gcttacatgg tagccgtagc 41340

tctaggtggt cttgcaagtg gtttagaaat tggtgaatca atcacattca aaccactacg 41400

tgtaagttca ttagaccaaa tctatgagtc aatagactta gatgaattaa atgaaaatgg 41460

tattattagt atagagtttg ttcgtaaccg tactaataca ttcttcagaa tcgttgatga 41520

cgtaactaca ttcaatgata aatcagaccc agttaaggct gaaatggctg ttggggaagc 41580

taatgacttc ttagtaagtg agcttaaagt tcaacttgaa gaccaattta ttggtactcg 41640

tactatcaat acaagtgctt caatcattaa agactttatc caatcttact tgggtcgtaa 41700

gaaacgtgat aatgaaattc aagacttccc tgctgaagac gtacaagtta ttgttgaagg 41760

taacgaagca agaatttcaa tgacagttta cccaatcaga agcttcaaga aaatttctgt 41820

tagcttggtt tacaagcaac aaacattaga agcctagtct aggtgatgga gtacctggat 41880

taggtactcc tattaatata atttgaatac tttaggagag tgaatacaga tggcatcaga 41940

agctaaacaa accgtccata ctggtaatac cgtcctactt atgattaaag gtaaaccggt 42000

aggaagagca caatcagcat caggtcaacg tgaatacggt acaactggtg tatacgaaat 42060

cggttctatc atgcctcaag aacacgtata tttacgttat gaaggtacaa ttacagtaga 42120

acgtttacgt atgaaaaaag aaaactttgc agatttagga tatgcttcac ttggtgaaga 42180

aattcttaag aaagatatca ttgatatttt agtggtagat aacttaacga aacaagttat 42240

tatctcatat catggttgct ctgcaaataa ctacaatgaa acttggcaga caaatgaaat 42300

tgtaacagaa gaaatcgagt tcagttacct ttaactaata gaggctatgt ttggtgacaa 42360

gcatagaaaa cactttaaat tgcgtgaaag tcttaaagac tagataacta caacgtaact 42420

cgaaagggta agcgtgaatg ttgagaaatc agaaaaaata tctagtatag tataaggtta 42480

aatcctaagt acagtaaaat agatgatacg caggcaagcc tacaaatgtg ggaagcttca 42540

acgactataa taggtgagtc ttagttacac attaagatta tggtatagtc tactcccttt 42600

aaaatatatc gaaagatagg gtacaaagga cagcatcaga taaagctaga acttaaattt 42660

cttattaaga ccaacaataa aagttggtct tatattttat acttgctttg tctgaggcag 42720

tgtgctataa ttaaaataca aggaggtaat aatatgggaa aaaatcaata tacatttaat 42780

attaaagaaa ataaaaataa atggtatgaa tggtgtaaac tacaaaacgt aaaaccttta 42840

gtagaatatg aaaatgcaca acaaatattt tattttgaat ttcttgaagg taaatttaaa 42900

ggactaatag gaaaaacata ttgggctagt ataaatagag gttctaatat gcgtatgagt 42960

tgtttaacat cagaaagtaa agataaatat ttaaaaaatt taggaaaaag aaaaggtata 43020

gaggtagtag aagactataa gggtggcaga aaattaaaac ataaatttat agttttagaa 43080

ggtaagtacc aaggatgtga agggtatata actttaaatg atttagagaa tttaggtaga 43140

gtagataata gaagtttatc tgaaaaagga aggaaacaat actttgataa acaggcaaga 43200

cttagagatt gtattattct agagtaccct aaagactata gaataaaaac taaagataag 43260

atagtagtaa aagataaaga agggcatgtt cataatatta ttgttcagga ctttttgag 43320

aaatcatctt tattggagtt atcttgtgct agtgaaggag agaaaatagt taaagaaata 43380

cttactaaaa attctataaa atttgaaaaa gaaaaatcat ttagaaacaa agaaggtaaa 43440

gtacaaagat ttgattttta tattaatgaa aataataaag aatatgcaat agagtacaat 43500

ggtgcacagc actacataga ttctacagga tatcttaaag atactttgga aacaacccag 43560

aaaagagata aactaaaaaa agaatacagt aaagataaag gtataaattt attaattatt 43620

ccttacacaa taacagataa gaaagaaatg gaaaaaatta ttttaaattt tttaaacaaa 43680

taacccttga cactccctca agggatatgt tattataata acaggttagg agtaataagt 43740

atgaataata ggcaagctaa actaaaagga tataaccaat ttcattatta tgattttcca 43800

acaactaaag gtaagtttaa agatataatg aaaagaaaat ctagaacaga acttaaaaaa 43860

gatttacaaa aagaaaggaa gtattatctt gacaaataag agaaaaacga taggtaagat 43920

gagtaacaca agagcaacat ggaatattaa tccggtaact aaagttaaaa aagataaaac 43980

aaaatattct agaaaaaata aacataaagg tcttgacaat tataattaac taaggtatat 44040

tattagtata acaaaaaaag gagatgttat aatatgagaa tttatataag taatgactat 44100

aacaaagagc tattagataa atgtttatca gatattaaca aagataaagg taatataaac 44160

tacagtatta attatggtga aggtaacatt aaagaagcag atgtagaaat tattaaacta 44220

gataagaatc tattagaaac agaatcaaga gcatttgctt attcgaagtt tgttgaagat 44280

tgtatatttt tatttcctta taagattgct ttacttagag ggggtaaaat agagttaaga 44340

tttgattgga atgaaatatt ataacaaaaa aaggagatgg atatatgagt acattttggt 44400

cagaaagaag aacaactaat aaagataggc aagttaaaaa acattatact caaatgagta 44460

tgtatgaaag aaagaaatgt gtagagttat tacaagagac aattactgaa aatagaatta 44520

ttaattttac acgacatagt gcaaaaaaag ttaaaggtaa accaacaaca aatataccta 44580

aattaatagg ttttattttt aaaaataagt ttgcctacga aaatatcata gagtacaata 44640

acacagatta taatggtaat attgagagga gaattgttgt taaacatccc aaagttataa 44700

ctgtagaagg aaaacttagc tatcagtttt tgacaattag tcttgaagat gctagagtta 44760

ttacggtgtg gtataacagt gtagatgata cacatagaac actagattta aattattata 44820

gtaaagactt gacaattcaa taaggaggag ttataatggg attaacaata gtaaatggtt 44880

atttctttct atcaagtatt atatttattg tagtaagtat actaaatgga aaaggtacag 44940

ttacaaggga atcactagct atgagtcaag cattagtgat aataacatcc attcaatttt 45000

tagcattttt aattataaat ggcatttatt actcattaaa atatatgtaa taaaaaggag 45060

tacaaatgga aatatacatt gtaatagact taagaggaag cacagaagaa gaaacaagta 45120

tggattttaa agcttttaga aaattacaag atgctataac atatgtagat ggtaatggta 45180

acagggattt acatataatt cctctagaat tagaataaaa gtattgacaa attaaaacta 45240

ataaattata ataaaggtat aacaaattaa aggagaagat ataaaatgtc acaagataaa 45300

ttaagagcaa tttacacaga aatgaaagta gaattacaca aatttcctaa agaggtagat 45360

gtaacaagta aatcaactgc aattgcaatc aatcagattt tagataaatt caaaacatta 45420

acagaacaag caggaaagat tactagaaaa tatttagaag gtcaagaaat attaactatt 45480

gattatgagt actatgattc attacaagaa tactatattt acctacttag aaatagtgaa 45540

aaaattgaac aaagtttaca agaaattact aagcgtacag gtgaatatgt aaagtaattt 45600

tgatttaaaa acaaaatatg atatactatg tttaaagtag taagcctaca ctagtccgtg 45660

ttatattaat attgaatcgg ataagcgtag gctttattaa tatttaaaaa aaggaaggta 45720

tatcatatta tggcagaaga aattaaaaag gaacaagatg tacaagaaac aactaaagaa 45780

gaaaaaaaag atgttagcaa aatgacaccg gaagaaatag ataaattaaa atatcaagac 45840

aagcaagaaa aagaacaagt tattaacaaa gttattaaag gtgttaatga tacttgggaa 45900

aaagaatata actttgaaga attagactta agatttaaag ttaaaattaa attacctaac 45960

gcacgagagc aaggtaatat atttgcgtta cgttctgctt acttaggtgg tatggatatg 46020

taccaaacag accaagtaat tagagcatat caaatgttag ctacattaca ggaagtaggt 46080

attgaagttc ctaaggaatt ccaagaccct gacgatattt ataacttata tcctttaact 46140

gttatgtatg aagattggtt aggattctta aactcctttc gttactaata gtatagaaac 46200

actagataaa gatatagaac gattgggcgg tatggaatca attgttaaac aacctttatc 46260

tagaaatcta tgggctatta tgaaagagtt taatgtttta cctactgagc aaagatttaa 46320

ggacttagat gattatcaga tagagtttat tattgggaat atgaacagag atgtttatga 46380

acataacaaa caacttaaac aagctcaaaa aggtggaaaa ttcgatagtc aatttgaaga 46440

tgatgatagt agttggtgga atgaatctca tgaagacttt gacccagtac ctgatttctt 46500

agatgctgat gatttagcac aacagatgga agctaaatta tccgatagag ataaggaaga 46560

aagagctaag agaaacgatg cagagttaaa tgatgaaaca gaaggactta ctacacaaca 46620

tctagctatg atggaataca tcagacagaa acaacaagaa ttagatgatg aagtaggaaa 46680

tggtaagact agtgaagatg acgctactat atcacaagat agcgttaata aagcactaga 46740

agacctagat gatgactggt atatgtaaag ggtggtaggt gatactacca tccttatttt 46800

tttaaaatgg atggtgaata atgatggcaa tgaatgacga ttatagattg gtcttgtccg 46860

gtgatagttc ggatttagag aatagtctaa aggcaataga actttatatg gattctttag 46920

agtctaagaa tattgatgct cctttagata atttcttaaa aaaattaaaa gtaattgcta 46980

aagaagttaa aaatgtacag aacgcaatgg ataaacaaga tggtaaatct gttatatctt 47040

ctaaagacat ggatgaatct attaaatcca ctcaatctgc tacaaagaat ataaatgaat 47100

taaagaaagc tttagatgac cttcaaaaag agaatatatc taaaggtatt gcacctgacc 47160

ctgaagttga aaaagcatat gctaagatgg gtaaagttgt agatgaaact caagaaaaac 47220

ttgagaaaat gtcttcacaa aaaataggtt ctgatgctag tattcaaaat agaattaagg 47280

aaatgaaaac cttaaatcaa gtaactgaag aatacaataa aataagtaaa gattctagcg 47340

caactaaaga ttatacaaaa cgattaagag ctaatcgtaa tatgactaga ggttacatgg 47400

agcgttcaga aggaacagga cgtttgacat atgaccaagg tgcacgagtt agaagtgaac 47460

taggtaaagt aagttcttat gagagccaaa gaaaacaaaa ccaacgtaat ttgggacaag 47520

caagagaaca atatagcaac tatagaaacc aacaacaaga cttgactaaa cgtagagcta 47580

gcggtcaaat taataaggca caatatgaac aagagttagc ttctattaaa caggaaatga 47640

aagctagaga agaacttata tctaactatg agaaattagg agcagaactt gataaaacag 47700

ttcagtatta taagggttca gttcaaaagg atttccaatc tagagacgta gaccaacaaa 47760

gaggaacatt tggtagaatg gttcaagaac gtttgccatc tattggttct catgctatga 47820

tgggtactac agctatggct acaggtttat acatgaaggg tgcctcacta agtgaaacta 47880

atagacctat ggttacatca ttaggtcaaa attccgataa tatggatata gattctgtaa 47940

gaaatgcata tggagacttg tcaattgata acaaattagg ttataatagt actgacatgt 48000

tgaaaatggc tacttcatat gaagcatcag taggacataa aagtgatgag gacacaatgg 48060

caggaactaa acagcttgct attggaggac gttctttagg cattaaagac caagaagctt 48120

atcaagagtc tatgggtcaa atcatgcata ccggcggagt aaattctgat aacatgaagg 48180

aaatgcaaga tgcattctta ggtggtatta aacagtcagg tatggttggt cgtcaagatg 48240

aacaacttaa agcactaggt tctatagcgg aacaatcagg agaaggaaga actctaacta 48300

aagaccaaat gagtaatctt actgccatgc aatctacttt tgcagagtca ggaagtaaag 48360

gattacaagg tgaacaaggt gccaatgcta ttaacagtat agaccaagga cttaaaaatg 48420

gtatgaatag ttcttatgct cgtatagcaa tgggatgggg aacgcaatac caaggtcttg 48480

aaggtggata tgatttacaa aaacgtatgg atgaaggtat atctaatcct gaaaacttga 48540

cagatatggc tgatatggct actcaaatgg gtggcagtga aaaagaacaa aaatacctat 48600

ttaatagaag tatgaaagaa ataggcgcta acctaactat ggagcaatct gatgaaatat 48660

ttaaggactc taaagaagga aaactgtcta aagaagagtt agctaagaaa gctaagaaaa 48720

tggaaaaaga aggtaaaaaa gaaggagaag ataacgccac tgattataaa gaatctaaat 48780

caggaaaaaa tgaccaaaat aaatctaaga ctgatgataa agcagaagat acttatgata 48840

tggctcaacc actaagagat gctcatagtg ctttagcagg tcttcctgcc cctatatatt 48900

tagctattgg tgctatagga gcatttacag cttcactaat tgcatctgca agtcaatttg 48960

gagcaggtca cttaattggt aaaggagcca aaggacttag aaataaattt ggtagaaata 49020

aaggtggtag ctccggtggt aaccctatgg caggtggaat gcctagtggt ggtggttcac 49080

ctaagggtgg aggctcacct aaaggtgggg gcactcgttc tactggagga aaaatacttg 49140

atagcgctaa aggtcttgga ggattcctag taggtggcgc aggatggaaa ggtatgtttg 49200

gcggggagtc taaaggtaaa ggatttaaac aaacatctaa agaagcctgg tcaggtacta 49260

gaaaagtatt taatagagat aatggtagaa aagccatgga taaatctaaa gatatagcta 49320

aaggtaccgg tagtggtctt aaagatatct ataatgatag tatatttggt aaagaaagaa 49380

gacaaaacct aggagaaaaa gctaaaggtt ttggtggcaa agctaagggt ctctatggta 49440

agtttgctga taagtttggt gacggaggta aaaatggtat cctttcacaa tcaccaaaag 49500

caggtggaag tggcataggg aaacttggaa aacttgcagg tggacttgga aaaggagccg 49560

gagttttagg tgttgctacg tctgccttat cattaatacc tgctttagct tccggagata 49620

gtaaagctat cggcggagga ataggctcta tgggtggagg aatggcaggt gcatcagcag 49680

gagcttctat aggagcttta tttggtggtg taggtgcaat ccctggagct ttaataggtg 49740

gagctatagg ttctttcggt ggaggagctg ttggtgaaaa agtaggagac atggctaaga 49800

aggctaacac taaagaagga tggaacctag gatggactaa tggagataaa gacggtaaga 49860

ataaattcca agattcttta ttaggaaaac ctatatctaa agcatggagt ggtataacag 49920

gtctctttga taatgacgct gaagcatctg aagaaaatag caaagataag aaaaaaggcg 49980

ttaaaggtgt taaaggggat actaagaaga aagaaaaaat gacagcagaa caacttagag 50040

aaaaaaataa ccaatctgaa actaagaacc ttaaaatcta tagtgattta cttgatagag 50100

ctcagaaaat tattgagagt gctaaaggta ttaatataga tggaggaact tctgatagtg 50160

gttctgatag tggaggctct gcatctgatg taggaggaga aggtgcagag aaaatgtata 50220

agttccttaa aggaaaagga ctatctgata accaggtagg agctgttatg gggaacttac 50280

aacaagaatc taaccttgac cctaatgcta agaacccttc aagtggagca tttggtattg 50340

ctcaatggtt aggtgctaga aaaacaggat tagataactt tgctaagtct aaaggtaaaa 50400

aatccagtga tttagatgtt caattagact acctatggaa agaaatgcaa tctgattatg 50460

aaagtaaaaa cctcaagaat gcaggttgga gtaaaggtgg aagtctagaa cagaatacaa 50520

aagcatttgc taccgggttt gaacgtatgg gagcaaatga ggctatgatg ggtactcgtg 50580

ttaacaatgc caaggaattc aagaagaaat atggaggttc cggcggagga ggcggagggg 50640

gcgctatgtc ctctacttac caagaagcta tgagtaaccc tgtattaacc actggttcca 50700

actacagagg ctctaacgat gcttctaatg cttctacaac taacagaata acagttaatg 50760

ttaacgttca aggcggaaat aatcctgaag aaactggaga cattatcgga ggaagaatta 50820

gagaagtttt agacagcaac atggatattt ttgcaaatga acataagaga agttattagt 50880

gattttgtat tgacacaaga gtagtatagt agtatactac tcttatacat ataaaaataa 50940

aaggaagtat gtgtatatga aaagattaag aagacctaag gtaagaatag agatagttac 51000

agatgataat acatttacat taagatttga agatacacgt gactacaatg gtgatgagtt 51060

tggagctaaa cttttaggct ttcaaactaa aaactctatg gaagatgata gttctgtatt 51120

ccaaatcaat atggcaggag atacttactg ggataagtta gttatggcta atgatataat 51180

cagaatattt attacaccta atgatgaccc taatgataaa gaaggtcgtc aagaacgttt 51240

aatacaagta ggtatggtat cacaagtatc aaaagtaggt agctatggta atgaccaaac 51300

tcaatttaga ataacaggtc aatcttttgt aaaacccttt atgaaatttg gattaggtgt 51360

tattcaagag gttcaagctg tattacctga agtaggttgg cttattgatg gtgatgggga 51420

taatgaagta aaatttactg gtagttcggc acatgaagtt atgacaggta ttatccgaag 51480

atttgttcct tatatgaaat ataactatac agaaaaaaca tataatacaa tagatagtta 51540

ccttgattat gatgatttaa gtagttggga tgaatttgaa aatctgacag aagtatctgc 51600

ttttactaat tttgatggct cattaaaaca gttgatggat atggtaacag ctagaccttt 51660

caatgagtta ttctttaaaa actccgaaaa aacaccaggt aaagcacagc ttgttttaag 51720

aaaaactcct tttaatccta ctgagtggag agctttggat atgattaaag tacctactga 51780

agactttatt gaagaggatg tgggtaaaag tgacgtagaa acatactcta tatttacagc 51840

tacacctgca ggtatgttaa aagaacttaa tggtgatgta ttttctaaac cacaatttca 51900

ccctgaattg actgatagat atgggtatac taaatttgaa gtagagaata tctatcttag 51960

tactaaatca ggttcagcta ctgaagactc agattcttcg ggtgatgata atggtactga 52020

aagaggaact tattctaaaa ttatgaaaga tttaagtaac tatggaagag ataatatatc 52080

taaaggtata gataagtata caagtaaatt atcctcaaaa tataaaaact taaaaaagcc 52140

caagctaaaa aaattataga gaagtttgtc aaagaaggaa aagtaacaga aaaagaatat 52200

gaaaagataa caggtaataa ggtagatgat gaattaacat cagataacag accgaagttg 52260

acaaaagata aattaaagag tatactaaaa gagaagttta aaacacaaga tgattttaat 52320

aattctaaaa aaagaaaaaa gctaaaacag atgcacttaa agaattgaca actaaatatc 52380

gttttggtaa taaaacacat gctacaactt tgttagatga atatattaaa tacaaaggag 52440

aaccacctaa tgatgaggct tttgataaat atcttaaagc tattgaaggt gttagtaata 52500

tagctacaga tacaggttca gatgcaagtg atagtccttt agttatgttc tctagaatgc 52560

tatttaactg gtatcatggc aaccctaact tctatgcagg agatattatt gttttaggag 52620

accctaagta tgacctaggt aaaagattat ttattgaaga taagcaacga ggagacactt 52680

gggagttcta tattgaatct gtagaacata aattcgatta taaacaaggg tattatacaa 52740

ctgtaggagt aactagaggt ttaaaagatg ctattctaga agacggtaaa ggtagtcctc 52800

atagatttgc aggactatgg aaccaatcat cagacttcat gggaggtctt atgggtgaag 52860

atacttctaa agaacttaaa gaaaaaggtg tatcagagaa acaaagcagt ggagataaag 52920

acggtggctc tgatagtggt ggcgctcaag atggtggctc tttagattca cttaaaaaat 52980

ataatggcaa acttcctaag catgacccaa gttttgttca acctggtaac cgacattata 53040

agtatcagtg tacatggtat gcttataata gaagaggtca attaggcatt cctgtgcctt 53100

tatgggggga tgccgccgac tggataggcg gtgctaaagg agcaggttat ggagtaggta 53160

gaacacctaa acaaggtgct tgtgttatat ggcaaagagg agtacaagga ggtagtgctc 53220

aatatgggca tgttgctttt gttgagaaag ttttagacgg aggtaaaaaa atatttatct 53280

ccgaacataa ctgggctact cctaatggat atggtactag aacaatagat atgagctcag 53340

ctataggtaa gaatgctcaa ttcatttacg ataagaaata aaggaggata gtctatggca 53400

acagataaag aagctaaaga tgttattgac aagtttatag ataatgtatt taattttgat 53460

gtattaacta tggaaagagt taaagaaaaa gatgaagaaa ttaaaaaaat aactacagat 53520

gatatgtatg aaaaggttgt gtatatacga ccttatgttg gagtaataca aagccttaac 53580

cctcaacatg tacagtatga atcattttct aataatggtt atgatataga ggcagaatta 53640

agtttcagga aagtaagtta tttagttgat aaagggtcta tacctacaga ttctttatct 53700

actttaacag ttcatttagt agaaagaaat caagagctat taatagatta ctttgatgag 53760

atacaagatg tgttgtacgg agaatatatg gaagaagaat atgtattcga tgaagatgta 53820

cccttaagta cgatactagc attagactta aatgataatc ttaaatcctt atcaaatata 53880

aagtatatgt tcaaaggtgc tcctaaagag aatccatttg gaacagataa agatgtttat 53940

atagatactt ataacttatt atactggtta tatttaggtg aagatgaaga gttagcatac 54000

cctatgaata ttaattattt ctttacagag ggtagattct ttactatatt tggtaaaggg 54060

cataagtaca aggtagatgt tagtaaattt atagttggag atatattatt ctttggtaga 54120

agtgatacta atataggtat ttatgtaggt gatggagagt ttatatctat gataggtaaa 54180

tttcctaaag atgaaacacc tataggaaaa tataaacttg atgattactg gaatgaattt 54240

aacggaagag ttatgagatt cgatgaagag gtgtatattt aatggtagta agattccaat 54300

cttccatggg aagaagttta aaaagagtag attcagatga tttaaatgta aaaggattag 54360

ttttagctac agttagtaaa attaattata aatatcaatc agtagaagtt aaagttaaca 54420

acctaacttt gggaagtcgt ataggtgacg atggtagctt agctgtacct tatcctaaat 54480

ctttcatagg aagaacaccg gaaggaagcg tattcggtac aaaacctctt attactgaag 54540

gttctgtagt attaataggg ttcctaaatg atgatataaa tagccctata atcttaagtg 54600

tttacggtga taatgaacaa aataaaatga ttaatacgaa tcctttagat ggaggtaaat 54660

ttgatacaga cagtgtttat aaatatagta gtgcactata tgaaatttta ccatctttaa 54720

attataagta tgatgatgga gaaggtacaa gtattaagac ctataatggt aagtcattct 54780

tctccatgac atcaggtgaa gaagaaaaac ctcaggcaac agatttttac actggaactg 54840

agtatcaaga tttatttact tcttattatg gtaataagac attaattgag cctagaatac 54900

aaaaggctcc taatatgtta tttaaacatc aaggagtttt ttatgatgat ggtacaccgg 54960

ataatcatat aactacttta tttatatctg aaagaggaga tataagagct tcagttttaa 55020

atacagaaac acagaaaaga accacacagg aaatgtcaag tgatgggtct tatagggtta 55080

tcaaacaaga tgacgattta atgttggatg aagctcaagt ttggattgag tatggtatta 55140

gtgaagataa taaattttat attaaaaatg acaagcataa atttgaattt actgatgagg 55200

gaatctatat agatgataag cctatgttag aaaacttaga tgagagtata gcagaggcta 55260

tgaagaattt gaatgaaata caaaaagaac tcgatgatat aaactacctt ctcgagggtg 55320

tgggtaaaga caatttagaa gaattaatag agtctacaaa agagtctata gaagcttcta 55380

aaaaagcaac ttcagatgtc aatagactta caactcagat agcagaagtt agtggtagaa 55440

ctgaaggtat tataacacag ttccaaaaat ttagagatga gacttttaaa gatttttatg 55500

aagatgcttc tactgttatt aatgaagtaa atcagaattt ccctactatg aaaacagatg 55560

ttaatacctt aaagactaaa gttgataacc tagagaaaac tgaaatacca aacattaaaa 55620

ctagattaac agaactagag aacaataata acaatgccga taaaataatc tcagatagag 55680

gagagcatat aggtgctatg atacagttag aagaaaatgt tactgtaccg acaagaaact 55740

atatgccaat accttggagt aaagttactt ataataatgc agagttttgg gattctaata 55800

atcctactcg attagtagta cctaaaggaa taacaaaagt aagagttgca ggtaatgttt 55860

tgtgggactc taacgccaca ggacaacgta tgttgagaat attgaaaaat ggtacttata 55920

gtctagggtt accttataca agagatgtag ctatatctac agcccctcag aacggtacta 55980

gtggagttat tcctgttaaa gaaggagatt actttgagtt tgaagctttc caagactcag 56040

aaggtgacag acaattcaga gcagaccctt atacatggtt tagtattgaa gctatagaat 56100

tagaaactga aactatggag aaagacttta tgcttatagg acatagagga gcaaccggat 56160

acacagatga gcacacgata aaaggatatc aaatggcttt agataaaggt gcagattata 56220

tagaattgga tttacaatta acaaaagata ataagttatt gtgtatgcat gattctacta 56280

tagacagaac aacaacagga acaggtaagg taggagatat gactttatct tatatacaaa 56340

ctaactttac atctcttaat ggtgagccga taccatctct tgatgatgta ttaaatcatt 56400

ttggaacaaa agttaaatat tatatagaaa ctaaacgtcc gtttgatgct aatatggata 56460

aagaattatt aactcaatta aaagcaaaag gattaatagg aatagggtca gagagattcc 56520

aagtaattat tcaatcattt gctagagaat cattaattaa tattcataat caattctcta 56580

atataccttt agcttattta acaagtacat tctctgaaag tgaaatggat gattgtttaa 56640

gttatggttc ttatgctatt gctcctaagt atacaactat aactaaagaa ttagtagatt 56700

tagctcatag taaaggtctt aaagtacacg catggacggt aaacacaaaa gaagaaatgc 56760

aaagcttaat acaaatgggt gtagatggat tctttacaaa ctacttagat gaatataaaa 56820

agatttaata ttaaagacct attaatttag gtctttttt agttgtaatt taaactagtt 56880

cgtgatatat tagtagtatg agatttatat acatactgaa aaggagagga taaaatgcca 56940

caatcagatg gaataagtaa tcttcataga atagctttac gcttccctaa agaaggcggt 57000

ggttatgata tgtatagatt taaagttaac cccgagaact acacaataga ttcaccacaa 57060

cgtacgacag caattaaaac aaaatcagat attgtaatag aagattatgg taaagacata 57120

gaagttatta acttcacagg tacaactggt tttagacctg ttagagaagc agacggatta 57180

aaaacaggta agcagaaaat ggaagagtta caaagtagag ttagtgaata tgctatgcaa 57240

ggtggtagtg gtaatgtaag tggttcttac ttacaatttt ttaactttac agatgatagc 57300

tactataaag ttcatttagc tcctcaaggg ttaaagataa ctaggtctaa agatgaacca 57360

ttacttttta gatatgaaat aacattagta gttattggtt cgttaacaga agcagataga 57420

agtgctgtaa caacagaaga gtttggtaat gttaaaccta atgcttctca aagagtagat 57480

gagggtataa aagaattaga taaaaatgct cgtaaaacga gagatagaaa taatcaagaa 57540

atatctaaaa gagaaaatac aatacctaaa tctacaggag ataatacgaa tgagggtaat 57600

agacttaagc aaagcttccc tagtagttct atatataatc ctagacaatc tactaacgga 57660

ttaaaaggga atattgacaa tatggctctg ataataggtt acggtgatgg aggtgtatct 57720

agctaatgaa taattttata ccacaacctc aaggtctact cagattttta aatgccctag 57780

atgcagattt aacttcttct cacatgaatt tactggatga agaggtatca tttgtatcta 57840

aattttacac accacagcta caattaagtg aattagcaaa aaaagtattg acaaatataa 57900

agacagatga tatacctgta ttagaaagag aatttaatga taatacaatt atccataaag 57960

ctaatgatac attactaaaa gtacaggctc caagaatgta tatgattcta cagtctattg 58020

tgcttgaagc atatgctatt gttaattgct ttgtagaaaa tccaagctct ttaaaatact 58080

taactgaaga agatgttagt ataacacgag aaaatttaaa ttatgtagct gactacttag 58140

gtaactatga tgactacaat agtgttgtct tagacttaag agatttagac ttatgtttta 58200

gtgctataga attacaatta cctctaatta aaaaggaggc taatgtataa tgagatttaa 58260

gaaacacgta gttcaacatg aagaaacgat gcaagcaata gcacagagat actatggtga 58320

tgttagttat tggatagacc tagtagagca taataatcta aagtatccct atttagtaga 58380

aactgatgaa gaaaaaatga aagaccctga acgattggct tctacaggtg atacactgat 58440

tatacctata gaatctgatt taacagatgt atcagcaaaa gaaattaatt ctagagataa 58500

agatgtacta gttgaattag ctttaggaag agatttaaat attactgcag atgaaaagta 58560

ttttaatgaa catggtacta gtgataatat actagcattc agcacaaacg gtaatggaga 58620

tttagatact gtaaaaggca tagataatat gaaacagcaa ttacaggcac gtttattaac 58680

tcctagaggt tctttaatgc tacatcctaa ttatggttca gatttgcata atttatttgg 58740

tcttaatata cctgaacaag ctacattaat agaaatggaa gtattgagaa cattaacatc 58800

agataataga gtaaaatctg ctaatctaat tgattggaaa atacaaggta atgtttattc 58860

aggtcaattt tcagtggaaa taaaatctgt tgaagaatca ataaattttg tcttaggaca 58920

agatgaggaa ggaatttttg ctttatttga ataggaaagg attaaattat gaaaactaga 58980

aaattaacta acatactatc aaaattaata gataagacaa tggcaggtac aagcaagata 59040

acagacttta ctcctggttc agcttcccgt tcattattag aagctgtatc attagagata 59100

gagcaattct atatcctaac aaaagaaaat attgattggg gtatacaaga aggtatcatt 59160

gaagcttttg attttcaaaa aagacaatct aaaagagctt atggtgatgt tactattcaa 59220

ttctaccaac ccttagatat gagaatgtat atacctgcag gaacaacttt tacttcaaca 59280

cgacaagaat atcctcagca atttgaaaca ttagttgatt attatgcaga gcctgattct 59340

actgagattg ttgttgaagt ttattgtaaa gaaacagggg ttgcaggtaa tgttcctgaa 59400

ggaacaatta atactatagc atcaggttct agtttgatta gaagtgttaa taacgagtat 59460

tcttttaata caggaactaa agaagagagc caagaagact ttaagcgcag attccactct 59520

tttgtagaat ctagaggtag agcaactaat aaatcagtaa gatatggtgc attgcagata 59580

cctgatgtag aaggtgttta tgtttatgaa gaaacaggac atattacagt atttgctcat 59640

gatagaaatg gtaatttatc agatacctta aaagaagata taatcgatgc tttacaagac 59700

tatagaccaa gtggtataat gttagatgtt acaggtgtag aaaaagaaga agttaatgtt 59760

tctgctacag taactatatc taataaatct agaattggtg atacattaca aaaacatatc 59820

gaaggtgtta ttagaagcta tttaaataat ctaaaaactt ctgatgactt aataattaca 59880

gaccttattc aagctataat gaatattgat gatgtactaa tatatgatgt gtcatttgat 59940

aacctagatg agaacattat agtaccacca caaggaatta ttagagcagg agaaataaaa 60000

gtagaactaa agtaaagaga ggtgaaactt aagtcgtggc taatttttta aagaatcttc 60060

atccattatt aagaagagat agaaacaaaa aagataatca agaccctaac tttgctctca 60120

tagatgcact caatgaagag atgaatcaag tagagaaaga tgctatagaa agtaaattac 60180

aatcctctct aaagacatct acaagtgaat atttagataa gtttggggat tggtttggag 60240

tttatcgtaa gactgatgag aacgatgatg tttatagagc aagaattata aaatatttac 60300

tcttgaaaag aggaactaat aatgctataa tagatgctat aaaagattat ttaggtagag 60360

atgatattga tgtaagtgta tatgaacctt ttacaaatat tttctatacg aacaaatcac 60420

atttaaatgg tgaagaccac ttaatgggat actattatag atttgctgtt attaatgtct 60480

ctataggtga ttatttccct gtagagatta tagatgtaat taatgaattc aaacctgcag 60540

gtgtaactct gtatgtcact tatgatggag cttctactat tagaggtgga gcaattatta 60600

agtggttaga tgggttacct aaaatagaaa cataccaaga gtttgatagg tttacaggat 60660

acgatgatac attctatggt catattaaca tgaatcaaag taaagatact gataatagta 60720

catcagatat ttttaaaaca aaccatagct taattaatag tttagatgtt ttaacaggtt 60780

cctctagcgt aggtagacag tatgttaact atggatatat aacatcatat gtttataatc 60840

caggtatgac atcttctgta aatcaaataa gcgctagtac agaaggtaga gggcaagaag 60900

tacctactga ctattatatg tatactagta ctaagaataa caatacagta gaacttagta 60960

tgcaaactac ttccggtgtg tcttatttat ataataactt taattttagg gattatatga 61020

gtaaatatag acctcaagta aatttacaat ctgatgaggc tagaagaatt gtatctgatt 61080

atataaaaga attaagtatt gattattatc tcagtgctgt aatacctcct gatgaaagta 61140

tagaaattaa attacaagtt tatgattttt ctattaatag atggcttaca gtatcaatta 61200

ataatttatc tttctatgaa aaaaatatcg gtagcaatat aggatatata aaagattatt 61260

taaacagtga attaaatatg tttactagat tagagataaa cgcaggtaaa agagattcag 61320

tagatattaa agttaattac ttagatttaa tgttttatta ctatgaacga ggtatttata 61380

caataaaacc ttataaagcc ttagtagaaa attatttaga tatatctaga gagacttacg 61440

tagaggcatt taaaatatca tcgttatcta atggagatat tataactaaa acaggttatt 61500

tacctatagg ttatctaaga gtatcaggag acattgataa cttaagtaac catatagaaa 61560

ttattaccat agataataat actaatagta ttacaagtac tcttttagaa gatgactcta 61620

atagtttgat attatcatat ggtaacgtca aaaccaatat acacagtttt gaattaaata 61680

gtgatgcttc aatttcaaat attaaatttg aatactctta ttatggtgat gcttgggaag 61740

aactgacagt attaactgaa atatctgagg gtgaaactat agtacctaat atactaatag 61800

atttatatgg attacagaca gtagattatt ctaatataaa tccaatgtca aaagtatcat 61860

tacgttctat ttggaatgtt aaattaggtg aacttaataa taaagaaggt tctttatcaa 61920

atatgcctaa cgattatttt aatgctgtat ggcaagatat agataaacta tcagatattg 61980

atttaggctc tatgagaatg attaaagaca ctgagggtgg agtatttgat ggagctacag 62040

gtgaaattat taaagctact ttatttaatg ttggtgtata tactgattta gatatgttag 62100

cctacacttt aactaactat actgaaccaa taactttagg ttctagtcga ttaataagtg 62160

aacttaaaga agaactatta acatcagaat catttaatgt cgataataga attaaagtaa 62220

ttgactcaat atctgagcag ttacctaata acaatatatt aagtaactct taccaaacac 62280

aaactattac acagaatgga tttgctaagt ataatttgaa agaacctata gagcagagaa 62340

aacaatacaa tctaagaata catggagatt ttaaagaagg attagaaaga ttagctatag 62400

gtaattctaa tggttcattt aatgaagtat ttgtttaccc tgaaaatatt aaagatggta 62460

tagtagatat tacttacact tctagagatg ataattacgc agaagggaaa caaagactta 62520

ataatgatta tagagtttac gctcaaccat acgatagtga agtagtaaca atttacagtt 62580

tagagttaat aaaagtttaa taaataagtt gacagaaagt taataatatg gtatacttat 62640

aaagtaatat ttagtgggta taccatgtta tattaataaa gaaaacaaca gatgaaagga 62700

attaaaaaat atggcaattg caacgtataa ttctcatgtt gagttagcaa aatatctagt 62760

tagtaaagct gattcagttt acttaacaat tggaaagagc acaccgtggt ctaatgaaac 62820

aaacccaccg caacctgatg aaaatgcaac agtattacag gaggttatag gatacaaaaa 62880

agctactaaa gtaactttag ttagaccttc taaatcacct gaagatgata ataagaattt 62940

aatttcttat ggtaataaat catgggtaga agtaacacct gaaaatgcta aagatgaagg 63000

agctaaatgg gtttacttag aaagcagtat tgttggtgac gaactacctc ttggaacata 63060

tagacaagta ggatttgtta tggacttagt agcaaaaagt ggtattagta aatttaactt 63120

agtacctagt gaagtagaat caactggaac attattattc tttgataata aacaattcca 63180

aaatagaagt gagcaaacaa ctgctaaaga aagatttatt gtagaagttt aaagaaaggg 63240

agataattct aaatggcaat taattttaaa ggttcacctt atttagatag atttgacccg 63300

tctaaagata gaacaaaagt attatttaat cctgatagac ctctacaaca ggcagaatta 63360

aatgaaatgc agtctataga ccaatattat ttaaaaaatc taggagacgc tatttttaaa 63420

gacggagata aacaatcagg tcttggattc acattatctg aagataatgt attgacagta 63480

aatcctggtt atgtatatat caacggtaaa ataagatatt acgataatga cgattcagtt 63540

aaaataactg gcgtaggtaa agaaactatc ggtattaagt taacagaacg tattgttaca 63600

cctgatgaag atgctagcct actagaccaa actagtggag taccaagtta cttctctaaa 63660

ggtgcagata gattagaaga aaagatgtca ttaactgtta atgaccctac atcagcaact 63720

atttatactt tcatggacgg agatttatat atccaatcaa ctaatgctga gatggataaa 63780

atcaataaag tattagctga acgtacttat gatgagtcag gttcatataa agtaaatggt 63840

tttgagttat tctcagaagg taatgctgaa gatgatgacc acgtttctgt agttgtagat 63900

gcaggtaaag cctatgtaaa aggttttaaa gtagataaac ccgtatcaac aagaattagt 63960

gtacctaaat cttatgactt aggaacagca gaaaatgaaa gtactatctt taataagtct 64020

aataattcta ttagtttagc taatagccct gtaaaagaaa ttagacgtgt tacaggtcaa 64080

gtacttattg aaaaagaacg agttacaaga ggagcccaag gtgatggtca agattttctt 64140

tcaaataata cagcatttga aattgtaaaa gtttggactg aaacaagccc tggagttact 64200

acaaaagagt ataaacaagg agaagacttc agattaacag atggtcaaac gattgactgg 64260

tcacctcaag gtcaagaacc ttcaggaggt acttcatact atgtttctta taaatataat 64320

aaacgtatgg aagtcggtaa agattatgaa gtaacaactc aaggagaagg gttaagtaag 64380

aaatggtata ttaattttac acctgaaaat ggtgctaaac ctattgacca aacagtagta 64440

ttagtagatt atacttatta cttggctcgt aaagattcag tgtttattaa taagtatggt 64500

gatattgcaa tattacctgg tgaacctaat attatgagat tagttacacc accattaaac 64560

acagaccctg agaatttaca attaggtaca gttacagtat tacctgattc agatgaagcc 64620

gtatgtattt catttgcaat cactagattg tctatggaag acttacagaa agttaaaaca 64680

agagtagata acttagagta taaccaagca gtaaatgcct tagatgatgg tgctatggaa 64740

ggacagaacc ctctaacatt acgttcagta tttagtgaag gtttcattag tcttgataaa 64800

gcagatatta cccatcctga cttcggaata gtatttagtt ttgaagacgc agaagctact 64860

ctagcttata cagaagccgt taaccaacct aaaattattc ctggagatac aacagctcat 64920

atttggggta gattaatttc agcaccattt actgaggaac gtacaatcta tcaaggtcaa 64980

gcatcagaaa cattaaatgt taacccttat aatatcccta ataagcaagg tgtacttaag 65040

ttaacaccta gtgaggataa ttggattgat actgaaaatg ttacaattac tgagcaaaaa 65100

actaagaaag taactatgaa acgattttgg agacacaatg aaagttacta cggtgagact 65160

gaacactact tgtactctaa tttacaatta gacgcaggtc aaaagtggaa aggtgaaact 65220

tacgcttatg acagagagca tggtcgtaca ggtacattac tagaatcagg cggtcaacgt 65280

actttagaag agatgattga attcattaga attagagatg tatccttcga ggttaaaggt 65340

ctaaacccta atgataataa cttatattta ttatttgatg gtgtaagatg tcctattact 65400

cctgcaactg gttacagaaa aggttctgaa gatgggacta ttatgacaga tgcaaaagga 65460

acagctaaag gtaaatttac tattcctgca ggtattcgtt gtggtaaccg agaagttaca 65520

ctcaagaatg ctaactctac aagtgctaca acttacacag ctcaaggacg taaaaaaatc 65580

gttcaagata ttattattag aactcgtgta acagtaaact tagtagaccc gttagcacaa 65640

tcattccagt atgatgagaa cagaactata tcatcattag gtttatactt tgcttctaaa 65700

ggagataagc aatctaacgt tgttatccaa attagaggta tgggtgacca aggttatcct 65760

aataaaacaa tctatgcaga gacagttatg aatgcagatg atattaaagt atctaataat 65820

gctagtgctg aaactagagt atactttgat gaccctatga tggcagaagg cggtaaagaa 65880

tacgctattg ttattattac tgagaacagt gattatacaa tgtgggtagg tactagaact 65940

aagcctaaga ttgataaacc taatgaggtt atctcaggta atccatatct tcaaggtgtg 66000

ttattcagtt catcaaacgc atcaacatgg actcctcatc aaaactctga ccttaaattt 66060

ggtatctata cttctaaatt taatgaaaca gcaacaattg aattcgaacc aattaaagat 66120

gtatctgcag atagaatagt tcttatgtct acgtacttaa ctcctgagag aacaggatgt 66180

acatgggaaa tgaaattaat tctagatgac atggcatctt ctacaacatt cgaccagttg 66240

aaatgggaac ctattggtaa ctatcaagac ttagatgttt taggtctagc aagacaagtt 66300

aagttaagag caactttcga atctaataga tatatctcac cattaatgag ctctagtgat 66360

ttaacattca ctacattctt aacagagtta acaggttcat atgttggtag agctattgat 66420

atgacagagg ctccttacaa tacagtaaga tttagttatg aagctttctt acctaaaggt 66480

actaaagttg ttcctaagta ttctgcggat gatggaaaaa cttggaaaac atttactaaa 66540

tcccctacaa ctactagagc caataatgag tttacacgct atgtcattga cgagaaagta 66600

aaatcatcag gaacaaatac taaactacaa gttagattag atttatcaac tgaaaatagc 66660

tttttacgtc ctcgtgttcg tagacttatg gttactacta gggatgaata aactagaggg 66720

gttgattgac ccctctttat ttaataagga gagatttata tgcctagaga agttagagac 66780

ccttattctc aagctaaatt atttatacct acagttgagg aaaaatcaat taaggaatta 66840

gaaaaaacat acaaagaaaa aattgatgaa gctactaagt taatcaatga attaaagaaa 66900

gagagaggag aaaaatagat ggcatttaac tacacgcctc ttactgaaac acagaagtta 66960

aaagatatgt atcctaaagt taatgatata ggtaactttt taaaaacaga agttaacctt 67020

agtgatgtaa aacaaatatc acaacctgac tttaataata ttttagcatc tatacctgat 67080

agtggtaact actatgtaac taattcaaaa ggtgctccta gtggagaagc tacggcagga 67140

tttgtaagat tggataaacg aaatgtaaat tattataaaa tttattattc accatatagt 67200

agtaataaaa tgtatatcaa gacttatgct aatggtactg tatatgattg gattagtttt 67260

aaattagatg aaggtaactt atacaatgaa ggtaatactt tgaatgtaaa ggaacttact 67320

gaatctacaa ctcaatatgt aacactagtt aatcctccaa aagagaactt aaatacaggt 67380

tgggttaatt acaaagaaag taaaaatggt gtttcttctt tagtagaatt taacccagtt 67440

aactctacct caactttcaa gatgataaga aagttaccag tacaagaaca aaagcctaac 67500

ttattgaaag atagtttatt tgtttatcct gaaactagct cttcaaatat taaaacagat 67560

aattggaata cacctccttt ttggggatac acagctaata gtggtcgttc aggggttaga 67620

tttagaggag agaatactat acagattgat gatggtagta gcacatatcc tactgcaatg 67680

actaatagat ttaagatggg taatgagctt tctgtaggtg atacaattac tgtatctgta 67740

tatgctaaaa ttaatgaccc tgcattactt aaagataact tagtttactt tgaactagcg 67800

gggtatgata tggtagatag aactgataat ccttatacag gaggacgtag agaaataaca 67860

gcaagtgaga taacaactga gtggaaaaag tactccttca cattcacgat acctgaaaat 67920

acaattggag catcaggcgt taaagttaat tacgtatctt tactcttaag aatgaattgt 67980

tcatctagta aaggtaatgg tgctgtggta tactatgctc tacctaaatt agaaaaatca 68040

tctaaagtta caccgtttat cacacatgca actgatgttc gtaagtatga tgagatttgg 68100

tctaactggc aagaagttat tagtaaagat gaattaaaag gtcactctcc tgtagatata 68160

gaatataatg attactttaa gtaccaatgg tggaaatctg aagttaatga aaagagttta 68220

aaagatttag ctatgacagt acctcaagga tatcatacat tttattgcca aggctctatt 68280

gccgggacac ctaggggacg ttctattaga ggaaccattc aggtagatta tgacaaaggt 68340

gacccctaca gagctaataa gtttgttaaa ttattgttta ctgacacaga aggtatacct 68400

tatacattat actacggagg gtataatcaa ggttggaaac tcttaaagca atcagaaact 68460

tctactttac tatgggaagg tactttagat tttgggtcta cggaagctgt taacttaaat 68520

gactcattag ataattatga tttaattgag gtaacttatt ggactcgttc agcaggacat 68580

ttttctacaa aaagattaga tataaaaaat acatcaaatt tactgtatat tagagatttt 68640

aatatttcaa atgatagtac aggttctagt gtagactttt ttgaagggta ttgcactttt 68700

cctactagaa catcagtaca acctggtatg gtaaaatcta taactttaga cgggtctaca 68760

aatacaacaa aagtagcatc atggaatgaa aaggaacgta taaaggtata caatattatg 68820

ggaattaata gaggataaag aaaggtggaa taaaaaaaac tatggctgtt aaatatgata 68880

taggtaataa tgagatagta ttacatttaa gagaaggtaa atatataaca gggtttacaa 68940

cagtaggagg gtatgataag gagttaggac aagtaaaagt taatagagaa atcttacctg 69000

cttacttctt tgataatttt gcctatgaaa gatacttgta ttatagtaaa cctgaagagg 69060

ttatagagaa taaaaactat gtaccacctc aaatcaataa tggtgatgag gaatctcaac 69120

aaaatactgt acctaaagaa caatatgata gtttaaaaga agaactagaa cttatgagaa 69180

aacaacaaga agctatgatg gaaatgcttc aaaaactctt aggtcaaaag gggtaataat 69240

aaatggcatt aaattttact acaataacgg aaaacaatgt tattaaagac ctgactactc 69300

aggtcaataa cattggggaa gaattaacaa aagaaagaaa tatatttgac attacagatg 69360

atttagttta taattttaat aaatcacaga agattaaact aactgatgat aaaggattaa 69420

ctaaatcgta tggaaacata acagctctta gagatataaa agaaccaggt tactactata 69480

taggcgctag aacattagca acattattag atagacctga tatggagtct cttgatgttg 69540

ttttacatgt agtacctctt gatacttcta gtaaggtagt tcaacattta tatacactat 69600

ctactaacaa taaccaaatt aaaatgttat atagatttgt ctcaggaaac tctagttcag 69660

aatggcaatt tattcaagga ttaccgagta ataaaaatgc tgttatatca ggaactaata 69720

ttctagatat agcttcacca ggtgtttatt ttgttatggg aatgacagga gggatgccta 69780

gtggtgtaga ttcaggtttt ttagatttaa gtgtagatgc taatgacaat agattagcta 69840

gactaactga tgctgaaact ggtaaagaat atactagtat taagaagcct acagaagtat 69900

acacagcttg gaaaaaagaa tttgagccaa aagatatgga gaaatattta ctaagtagta 69960

tcagagacga tggtagtgca tcattcccac tcctagttta tactagtgat aataaaacgt 70020

ttcaacaagc tattatagac catatagata gaacaggtca aacaaccttt actttctacg 70080

ttcaaggtgg tgtatcaggt tcccctatgt ctaatagttg tcgaggtcta ttcatgtcag 70140

atacacctaa cacttctagt ttacatggtg tctataatgc tataggtaca gatggtagaa 70200

atgtaacagg ttcagtggta ggaggtaatt ggacttcacc aaagacatca ccttcccata 70260

aagaattatg gacgggagca caatcattcc tatctgtagg tactactaag aatctagcag 70320

atgatattag taattactct tatgtagagg tttatactaa acataagaca gtagagaaga 70380

ctaaaggtaa tgatgactcg ggtacaattt gccacaagtt ctacttagat ggtagcggta 70440

cttacgtttg ctcaggaact tttgtttcag gagatagaac agatacaaaa ccacctgtta 70500

cagagttcta tagagtaggt gtatctttca aaggttcaac atggacgctt gtagatagtg 70560

cagtacaaaa tagtaaaact caatacgtta caagaattat aggtattaat atgccataga 70620

ctaggataag tttcctagtc ttttttttctt gacttgaaaa ggattctatg gtatactata 70680

actcgtgtaa ggatataagg agattaaaat gagattaaga attaagaact tatataccta 70740

tgtagaattt gaggaggatg ataaatactt aaaagatata tttttaaaga gagttcatac 70800

aactatagga gcaaggcaag aaggttttca gtatagccct gcttacaaaa gaggcagttg 70860

ggatgggtat gtagactttt atgtttatga ggaagataaa ttccctactg gacttttatt 70920

taaaattgag ttattattag gtgagctaca atcaagatat aacttccagt ttgaaacaat 70980

tgatgagcgt gatgaaagtt tcttatctga agaagatatt gatgacgaga taacattgct 71040

tgataataat gtaggtcaaa ttaccttacg agattatcaa tatgaggcag tgtacaacag 71100

cttaacattt tacaatggta ttgctcattt agctactaat ggaggtaaaa ctgaggttgc 71160

tagtggtatt atagaccaac tattacctca attagaaaaa ggtgaaagag tagcattctt 71220

cacaggctct acggagatat tccatcagtc tgcagataga ctacaagaac gtttaaatat 71280

ccctattggt aaagtgggtg caggtaagtt tgatgttaag caggttacag ttgtaatgat 71340

acctacttta aatgcaaacc ttaaagaccc aacacaaggg gtaaaggtta cacctaaaca 71400

aaatattagt aaaaagattg ctcaagagat attaccgaaa tttgaaggcg gtacaaatca 71460

aaaaaaatta ctaaaagtat tacttgataa cacaacacct aaaacaaaag tagaacaaaa 71520

cgtattaagt gccttagaga taatttacca aaatagtaag acagatgcag aagttttatt 71580

aaacttaaga aatcataatg cacattttca aaaaattgtt agagaaaaaa acgaaaagaa 71640

atatgataaa tatcaagata tgagagattt tttagactca gttacagtta tgatagttga 71700

tgaggcacac cattctaaat ctgattcctg gtacaacaat ctaatgacat gtgaaaaagc 71760

tttataccga attgcattaa cagggtctat agataaaaaa gatgaattac tttggatgag 71820

attgcaggct ctattcggta atgttattgc acgaactact aataagtttt taattgatga 71880

aggtcattct gctagaccaa caataaatat tatacctgta gctaatccta atgacataga 71940

tagaattgat gattataggg aagcttatga taaaggtata acaaataatg attttagaaa 72000

taaacttatt gcaaaactaa cagaaaagtg gtataatcaa gataaaggta cattgattat 72060

tgtaaacttc attgaacatg gagacacaat atcagaaatg ttaaatgatt tagatgtaga 72120

gcactacttc ttacatggag aaatagactc tgaaactagg agagaaaaat taaatgatat 72180

gagaagtggt aaacttaaag taatgatagc tacatcactt attgatgagg gtgtagatat 72240

atccggtatt aacgcactaa tattaggtgc aggaggcaag tcattaagac aaacattgca 72300

acgtattggt cgtgctttgc gtaagaaaaa agacgataat acaacacaaa tatttgattt 72360

taatgatatg acaaatagat ttttatatac tcacgctaat gagcgtagga aaatttatga 72420

agaggaagat tttgaaataa aagacttagg aaaataggag ggtaagagat ggcaacaaaa 72480

acacaaagaa agctatacca atatctagag gaaaatgcta cagaaaataa atttcatatt 72540

tctactaaga aagagttagc agattctcta ggtgtttcca tctctgctct atccaataac 72600

cttaaaaagt tagaagaaga aaataaagtc gttactgttt ctaaaagagg aaaaaacggt 72660

ggagtaataa taactttagt tagagagtat gacacagaag aattgaaaga atttaataat 72720

tctacagata atattattac ttccgattta cagtatgcta aggcattaag agaaaagcac 72780

ttcccttctt atagatatga gagaaaagaa caacgtagac gtactaagat agaaatggca 72840

caatacaatg ctattaagga tgagaagaga agaattatag cagatatgaa tttctattca 72900

gaaggtcttc cttacccttc taaagatatt tttaatatgt cttatgaccc ggaaggtttt 72960

tataaagcat acatcttatg taagttatat gaccaatatg ctatttctca tatggatgct 73020

aaacatacaa gtcatcttaa agcaatgagt aaggcaacaa ctaaagatga atatgactac 73080

catcaacata tgtctgaata ctatagaaat aaaatgattc aaaatttacc tagaaatagt 73140

gttagtgata atttctttgg tagtaaaatg tttaatactt tttataattt ttatttaaaa 73200

ataaaagata aaaatattaa tgtatttaaa tatatgaaaa acgtatttaa aaatgtaaca 73260

ttttattacg agaacggtat gcaacctaat ccaatacctt ctcctaactt ctttagttca 73320

gataagtatt ttaaaaacta taataattat attaaaggaa taaaaaaagg cattaacagt 73380

acgaatagac acctaggtga tacagacagc atcattaatt catcagacta tgtgaaaaac 73440

cctgctgtat tacatctaca ccaactatat actacaggat taaattctac tttacatgat 73500

attgatacta tgtttgaaca agccttagac cttgagaatg cttcttatgg attatttgga 73560

gatatgaaac atattatctt actacagtat aattctatga ttgaagaaga aattaagaat 73620

ttacctatag aagagaagga tattattaat aaatatgtaa aacaatgcat aattaataat 73680

tactcaccaa caagtatttc accatctgca agattatcaa tgtttactat gcagaaagag 73740

catatagttt ataataagca attaaataag ggaatcaaga gagaggattt attaccatta 73800

agtctaggag gtatagtgaa taaagattca ttaagtagta tggatataca aaacttagaa 73860

cagaatggca atgaatacct atatatgaga caacatactt caacttatta tatactaaga 73920

atgtttggtg actatttagg gtatgaggta aatttaagag aagtaaaata tattgtagag 73980

aaatataatt taattgataa aataccattg acaaaagagg gtatgttgga ttataataaa 74040

cttatacatt tagtagagga agaggttaat aactatgagt aagaagataa aggagcttat 74100

ccttcataaa tcaatgaagg atatacattt tgcaagagaa gtattagata acttacctaa 74160

gaacttattt tcagcagagt ctgaagacat gggttactta tttacagcca taaagagaac 74220

agcacatatt tccgataaga tgtcaaatga agcattagca attaaagtag aacagcttat 74280

gggtaataac aaggaagatg aggagaaagt aaccaagaca ttaacttact tagaagattt 74340

atataaagta gacgttaatg aaaaagatga atctgttaat tatgaaatag agaagtatat 74400

taaaacagaa atgtcaaaag aagttttagt taaatttatt gcagaaaata aacaagaaga 74460

ctctgataat ctacatgaac ttgtagacaa actaaagcaa atagaagtaa gtgacatctc 74520

aggaggtaat ggggagttta ttgacttctt cgaagataca gaaaagaaac aagaactatt 74580

gagtaattta gctacaaata aattctctac tggatttact tctattgaca accatattga 74640

aggtggtata gcaagaggag aggttggatt aatcatagct cctaccggta gaggtaaatc 74700

attaatggct tcaaacttag ctaagaatta tgttaaaagt ggattaagtg ttttatatat 74760

tgccttagag gaaaaaatgg atagaatggt tttgcgtgct gagcaacaaa tggcaggagc 74820

agaaaagagt caaattgtaa atcaggatat gtctttaaat aataaagttt atgatgcaat 74880

acaaaatcat tatcagaaga atagaaagtt attaggtgac ttttatattt ctaaacatat 74940

gccgggtgaa gttacaccaa accaattaga gcaaattatt gtcaatacaa caattaagaa 75000

agataaaaat attgatgttg ttattattga ctatcctcat ttaatgagaa atccttatgc 75060

taaatatcat tcagaatcag atgcaggcgg aaaattgttt gaagatattc gtagattatc 75120

acagcaatat ggatttgttt gttggacgtt agctcaaact aaccgtggtg cttatggttc 75180

agatgttatt acaagtgagc atgtagaagg ttctcgtaaa attgtcaatg ctgttgaggt 75240

gtctttagca gtaaaccaaa aagatgaaga attcaagagt ggtttcttaa gattatattt 75300

agataaaatt cgtaatagct ctaacacagg agaacgattt gttaatctta aagtagaacc 75360

aactaagatg attgtaagag atgaaacacc tgaagaaaaa caagagcata tacaattgct 75420

atcagataat ggaaaagaag acacaagtaa atttcaaaat aaagataata aaatagaagc 75480

tataaataac acattcggag gattaccggg agtttaattt tttaaaatat accacttgac 75540

attttatatg ttaggtggta taattatttt ataaagaata aaggagagat taataatgaa 75600

atttgtattc tttacagata gtcattttca cctatttact aactatgcta aacctgataa 75660

tgaatttgtg aatgatagat ttaaagaaca gatagaagca ttacagaaag tttttgatat 75720

tgctaaaaaa gaagaagcaa cagttatatt tggtggagat ttattccata aacgtaactc 75780

ggtagatact agagtatata acaaagtatt tagtacattt gccaaaaata atgaggttcc 75840

tgtattatta cttagaggta atcatgatgc tacaactaat tcattatata ctgattcaag 75900

tatagataca tttgagtatc tacctaatgt aaatgtaata aaatcattaa atacaatttt 75960

aaaagataat gttaatattg tgtttactgc ttatggggat gagacgaagg aaataaagac 76020

atacattaat agtaattatg ataaagatat ggtcaatata ctagtaggtc atttaggtgt 76080

agaaggttca ttaactggaa aaggctctca tagattagaa ggggcatttg gataccagga 76140

tttattacct gataaatatg atttcatttt actaggtcat tatcaccgta gacagtattt 76200

ccaaaatccg aatcattttt atggtggctc attaatgcaa caatcatttt ctgatgaaca 76260

agaagctaat ggtgttcatt taatagatac agacaaaatg actacagaat tcattccaat 76320

tcatacacgt agatttatta ctattcaagg agaagatatt cctgataact ttgaacaatt 76380

aatagaggaa gataatttta ttagagttat tggtacagca aatcatgcta aggttttaga 76440

aatggatgac agtatgaaag ataagaatgt tgaagttcaa attaaaaaag agtatactgt 76500

agagaaacgt attgatagtg atgtatctga tgaccctcta acaattgcta gtacctatgc 76560

taaacaatac tcacctgaat cagaacaaga aatccttgaa tgtttgaagg aggttttata 76620

atgaaaaaat atagagaata tctaaataag acagatgcag aaaatttagc agaggattgg 76680

gagaaagtaa ccgaagattt atggaaagtg tttaaagata tgaaacctaa aattaataca 76740

ttagatatca gtaatgtagg aagtaaagat ttagataaaa gtaaacctat actacaattc 76800

caagattcag atggagtaat agagaatatt tgtaatgttg aaggtttaga agatggtcta 76860

agtaaaatga aaaagatttt tgatgatagt aattttgaaa agcattatta caatagagta 76920

gtagaccatg atgggtatta ctggattgat tatggttctc atcattgttt ctttagagtt 76980

acgaaagggg ataagtaatg gttgtattta aacaagtaga agttaataat tttttagcaa 77040

ttaaagaagc tacactagag ttagacaata gaggtttaat tctcattgag ggtgagaata 77100

aatccaatga gtcatttcat tcaaacggct caggtaaatc aactttaata tctgccatta 77160

cttatgcttt atatggtaaa actgaaaaag ggctaaaagc ggatgatgta gtaaataata 77220

ttgagaagaa aaatacgtct gtgaaactta agtttgatat cggggaagat agctatttaa 77280

ttgaacgtta tcgtaaggac aaagagaata agaataaagt aaaattattc gttaatgaaa 77340

aagagattac aggttcaaca aatgacgtta ccgataaaca aatacaagac ttatttggta 77400

ttgagtttaa tacttatgtt aatgccatca tgtatggtca aggtgatatt cctatgttct 77460

ctcaagcaac agataagggt aagaaagaaa ttcttgaatc tattactaag acagatgtat 77520

ataaacaagc gcaagatgta gcaaaagaga aagttaaaga agtagaagaa caacaaaata 77580

atataagaca ggaaatctat aaactaggtt atcagttatc tacaaaagat gagtacttcc 77640

aaagagaaat agaacaatat aatcagtata aagaacaatt ggttcagata gaaaatagta 77700

ataaggaaaa agatagatta agagaacaag aggagaagca aatagaagct caaatagagc 77760

aattagcttc acagatacca acaatacctg aagatgaatt taagcactca gaggagtata 77820

ataaagcctc tcaaagccta gatttacttt ctaataaatt aacggagtta aatcaagtat 77880

actcagaata taataccaaa gaacaagtac taaaatctga aatagctaca ttaagcaata 77940

gtctaaatca gttagatata aatgaccatt gtcctgtttg tggctcccct atagataatt 78000

ctcataaatt aaaagaacag gaaaatatca gcaatcagat tgagaataag aaacaagaga 78060

ttactagtgt attagaaatg aaagatacgt ataaagaagc tattgataaa gtaaaagata 78120

aatcacaaga aattaaagat aaaatgtcac aggaagacca acaagaacga gagcacaata 78180

ataagattaa cagtatcatt caagaggctt ctaggattaa atcagacatt agttcattag 78240

agaataataa aacttattta aaagtgaaat accaacatca atctgttcaa ggattagaga 78300

gagaagaacc aagtaaagaa aaacatgagg aagataaaaa agaattacaa gaatctattg 78360

acaaacatga agagaatata gtacaattag aaactaagaa agggaaatat caacaagctg 78420

tagatgcttt tagtaataaa ggtatacgtt cagtagtgtt agactttatt acaccattct 78480

taaatgagaa agcaaatgag taccttcaaa ctttatcagg ttcagatatt gaaatagagt 78540

tccaaactca agtgaagaat gctaaaggag aactaaaaga taagtttgat gttattgtta 78600

agaataacaa gggtggaggc tcctacaaat ccaattcagc aggagaacaa aaacgtattg 78660

atttagcaat tagttttgca attcaggatt taattatgag taaagatgag atatctacga 78720

acattgcact ttacgatgag tgttttgatg gattagatac tatcggttgt gaaaacgtga 78780

ttaaattatt aaaagataga cttaatacag taggaacgat atttgtaatt actcataata 78840

ccgaacttaa acccctattt gaacaaacaa ttaaaatagt aaaagaaaat ggagtatcaa 78900

aactggagga aaaataatga aattaaagat tttagataaa gataatgcaa cacttaatgt 78960

gtttcatcgt aataaggagc ataaaacgat agataatgta ccgactgcta atttagttga 79020

ttggtaccct ctaagtaatg cttatgaata caagttaagt agaaatggag aatacttaga 79080

attaaaaaga ttacgttcta ctttaccttc atcttatggt ttagatgata ataaccaaga 79140

tattattaga gataataacc atagatgtaa aataggttat tggtacaacc ctgcagtgcg 79200

taaagataat ttaaagatta tagagaaagc taaacaatat ggattacctg ttataacaga 79260

agaatatgat gctaatactg tagagcaagg atttagagat attggagtta tattccaaag 79320

tcttaaaact attgttgtta ctagatatct agaaggtaaa acagaggaag aattaagaat 79380

atttaacatg aaatcagagg aatcacaatt gaatgaagca cttaaagaga gtgatttttc 79440

tgtagactta acttatagtg acttaggaca aatttataat atgttgttat taatgaaaaa 79500

aattagtaaa tagtaaggaa ggatattatg aggtttgaag actttttaac ccaagaatta 79560

ggagaaccaa aagaaaatac tataggtgag ctaagatact gttgtccgtt ttgtggagaa 79620

aaaagttata agttctatgt taagcaagcc ctagactcta gtaatggtca gtatcattgt 79680

aaaaaatgtg atgaaacagg caaccctatt acatttatga agacttatta taacattaca 79740

ggtaagcaag cttttgattt attagagtct aagaatatag atatagagag agccccttta 79800

cttacaacta ataataagga tttaacagaa tcagagaaac ttatattaat gcttagaggt 79860

gtgcaccaag ataaaggaac tactagtatt aaacctcctc gattacctga aggatataaa 79920

ttattaaaag ataatttaaa taataaagag attatacctt ttttaaaata cttaaaaggt 79980

agaggtataa ctttagaaca aatcattaat aacaatatag gctatgttat taatggtagc 80040

ttttataaag ttgacgggga atccaaagta tcattaagga atagtattat atttttact 80100

tatgataaca atggaaacta ccagtactgg aatacaagaa gtatagagaa gaacccttat 80160

attaaatcta ttaatgctcc tgctaaacaa gatgaagtag ggagaaaaga tgtcatattt 80220

aatttgaata tagcaagaaa gaaaaagttc ttagttataa ctgaaggtgt atttgatgct 80280

ttaacctttc atgaatatgg agtagcaaca ttaggtaaac aagtaactga gaatcaaata 80340

aaaaaaataa ttgattacgt tagtatagat acatcaatat atattatgtt agacactgat 80400

gcattagata ataatataga cttagcttat aagttaaaaa cacattttaa taaagtttac 80460

tttgtaccac atggtgatga agatgcaaat gatatgggaa caaggaaagc ttttgagtta 80520

ttaaaacaga accgggtgtt agtaacacct gaaagtatac agagttacaa aatacaacaa 80580

aaacttaaac tttaggcttg accttagaga agttttatgt tatactagta attaagtaat 80640

taataaagga gaaaaaaata atgtcaaata gtaaaaaaga tattttagaa tttgtagatg 80700

aatacattac agctttaaga gttggtaatg agcaacgaca acaccaatta gaagaaatgg 80760

gtaaagaaga aacagcaaca ttaacagatg tagctaaagc tattactaac cttatgttag 80820

gtgttaatga gcagatgaca gacttagaat ataataacga gttaaactta aatattttaa 80880

ttgacgcttt atataaagca gagcttatta atgaagatgt attagactac attcaagaat 80940

caattgataa atcacaagaa gaacctaaaa atgaagaaga aaaaggagaa caagaataat 81000

ggaaaaaaat attagcacac acacaaaagg tattagtcaa gcagacatgg agaaatggat 81060

tgaagctgta gtacaaggaa ctgttgatgg taaacaagtt gatgagaaaa cagctaaaca 81120

attagataga attggttcac gtagtgtttc tttagaagaa gcaactcgta ttgctaaagt 81180

tcttaatgct gtaacagctc aagaggttac aggagacttt aatgatgcat ttaatgcaat 81240

tgacttaatg atgattatca tggaagatga gctaggagta actcaagaaa aagtgggtaa 81300

agctaaagat aaactaaatg aaaaacgaga agcttaccta aaagagaaac aagaagaatt 81360

acgccaaaaa caacaagaag aggcacaaaa agaaactgaa tctgacagca atgagaaagt 81420

aattcagttg aagaaaaatg acgaacagta agaaaaaagg ggatacattc gaacgtaaaa 81480

tagctaaaga attaactgct tggtggggat accaattcaa taggtctcct caatcaggtg 81540

gtgcttcatg gggtaaagat aataatgctg tcggagatat agtagtacct caggaagcta 81600

attttccttt agtagtagaa tgtaaacata gagaagaatg gactatagat aacgttcttt 81660

taaacaacag agagccacat acatggtggg agcaagtcat taatgatagt agcaaggtgg 81720

ataagacacc ttgcttaata tttactagaa acagagctca gagttatgtt gctttacctt 81780

atgatgagaa agtatatgaa gatttgagaa ataatgaata ccctgtcatg agaacagatt 81840

ttattattga taatattaga aaagataaat ttttttatga tgtacttata actaccatga 81900

atgggttgac ctcatttaca ccttcttata ttatatcttg ctacgacaaa aaagatataa 81960

aaccatacaa gaaggtcgag tctaatttat ctgaggtaag taagcatgaa gatgaattga 82020

ttaatgacct tcttagtgat atataaggaa ggtaagataa gtatgacaag taaagaaaga 82080

ccattaatcg tatatttttc aggtacaggg caaacagaaa gattagtaaa taaaattaat 82140

attaataatt catttgaaac atttagggtt aagagtggaa aagagaaagt aaataaacct 82200

tttatactaa taacacctac ttatatgaaa ggtgcaatac ctaaacaaat agaaagattc 82260

ctagaaatta atgggagccc taaagaagtt attggtacag gaaataaaca atggggctct 82320

aatttctgtg gagcaagtaa aaagatttca gagatgttta agattccttt aattgctaaa 82380

gtagagcaat caggacactt taacgagata caaccaatat tagaacactt tagtaataaa 82440

tataaagtag cgtaaaggat gagagatata tggcaacata tggaaaatgg attgagttaa 82500

ataatgaaat aactcaatta gatgacaatg gaaaaaataa actctataaa gaccaagaag 82560

ctttagatga gtatttaaaa tatattgaag acaatacaag aaagtttaat agtgaagtag 82620

aaagaattag agtattgaca aaagaaggaa catatgataa aatatttgac aaggttcctg 82680

atactattat tgatgagatg actaagttag cttacagttt taattttaaa ttccctagtt 82740

tcatggcagg gcaaaagttt tatgaatctt acgcatcaaa acagtatgat gaaaacaaaa 82800

aacctatttt tgttgaagac tatgagcaac ataatgttcg agtagcttta tatttatttc 82860

aaaatgacta tgtaaaggct agagaattac tagtacaact tatggagcaa acattccaac 82920

catctacacc tacgtataac aactcagggc aagctaatag aggtgaacta agttcatgtt 82980

atctatttgt agtagatgat tcaattgagt ctttaaactt tgttgaggat agcgtagcta 83040

atgctagttc taatggtggc ggagttgcaa ttgatttaac tagaattaga cctaaaggag 83100

ctccagtacg taatagacct aattcaagta aaggtgttat tgcttttgct aaagctattg 83160

aacataaagt tagtatttat gaccagggcg gtgtaagaca gggtagtggt gcagtttacc 83220

taaatatatt ccacaatgat atcttggatt tattaagctc taagaaaatc aatgccagtg 83280

agtctgttag actagataaa ttatctattg gtgttacaat ccctaacaaa tttatggagt 83340

tagttaaaga aggtagacct ttctatactt tcgatactta cgacattaat aaagtgtatg 83400

gtaagtattt agatgagcta aacattgatg aatggtatga taagttatta aataatgata 83460

gtatcggtaa agtaaaacat gatgctagag aagttatgac agatattgct aaaacgcaat 83520

tagaatcagg ctacccttat gtattctata ttgataatgc taatgataat cacccattga 83580

aaaacctagg taaagttaaa atgagtaact tatgtacaga aatttcacaa ttacaagagg 83640

tatcagaaat ttatccgtac tcttacagta atcagaatgt tattaataga gatgttgttt 83700

gtacattagg ttctcttaac ttggttaatg tagttgaaaa aggtttattg aatgaatctg 83760

tagatattgg tacaagagca ttaacaaaag ttactgatat tatggattta ccttacttac 83820

ctagtgttca aaaagcaaat gatgatatta gagctatcgg tttaggttca atgaatttac 83880

atggactttt agctaagaat atgattagtt atggttctag agaagcatta gacctagtaa 83940

acagtttata tagtgctatt aacttccagt ctattaagac atctatgtta atggctaaag 84000

aaacaggaaa accatttaaa ggctttgaga agtctgatta cgctacaggt gaatactttg 84060

taagatatat tagagaatcc aatcaaccta agacagataa agctaagaaa gtcttagata 84120

aggtttatat tccaacacaa gatgattggg atgaattagc taaagcagta aaagtacatg 84180

gcttgtataa tggttataga aaagcagaag cacctactca atctatatct tatgtacaga 84240

atgctacaag ttctattatg ccagtcccta gtgctataga gaatagacaa tatggagata 84300

tggagacata ttacccaatg ccttacctaa gtcctataac tcagttcttc tatgaaggag 84360

aaacagctta taagattgac aataaacgta ttattaatac aagcgcagtt gttcagaaac 84420

atacagacca agcagtgtct acaatacttt atgtagagtc agaaatccct actaataaac 84480

tagtatcatt atactattat gcttgggaac aaggattaaa atcattatac tatacacgtt 84540

cacgtaaact ttctgttatt gaatgtgaaa catgttcggt ttagaaagga aatagatatg 84600

gatattacac aaaaagtaaa acaacataat aaaaatgctg tattaaaagc aacaaactgg 84660

aatattgaag atgacggtat gtctgatatt tattgggagc aaggaatctc ccaattttgg 84720

actcctgaag agtttgatgt atcaagagat ttaagttctt ggaatagttt aactgaaagt 84780

gaaaagaaca cttataagaa agtccttgca gggctcacag gtctcgatac aaagcaagga 84840

ggagaaggta tgaacttagt atcctaccat gaaccaagac ccaaatacca agctgtattt 84900

gcgtttatgg gtggtatgga agagatacat gctaaatcct atagtcatat ctttacaaca 84960

ttactaagta ataaagaaac aagctatcta ttagatactt gggtcgaaga aaatgacttt 85020

ttaaaagtaa aagctcagtt tatcggatat tactatgacc aactattaaa acctaaccct 85080

actgtatttg atagatatat ggctaaagta gctagtgcct ttttagaaag tgcactattc 85140

tactcaggat tttattatcc tttacttctt gcaggaagag gtcagatgac acaatcagga 85200

gctattattt ataaaattac tcaagatgaa gcttaccatg gttcagcagt aggattaaca 85260

gctcaatatg attataatct tctaacagaa gaagagaaaa aacaagcaga taaagaaact 85320

tatgaattat tagatattct ttacactaat gaagtagcgt atacacatag tctatatgac 85380

ccactagaat taagtgaaga cgtaattaac tatgttcagt ataattttaa tagagctctt 85440

caaaaccttg gaagagagga ctattttaat cctgaacctt ataaccctat tgtagaaaat 85500

caaactaatg tagacagatt acgaaatgtt gatttcttta gtggtaaagc agactatgaa 85560

aaatctacaa atatcaaaga cattaaagat gaagatttct cattcttaga tagtaaagaa 85620

tacaatactg ccaaggaatt cctataaaaa ggagaaaaga tattatggat agaaaagaag 85680

caatggattt actaagtaaa gcagaaatat tatttaaaaa acatgatgag ttttcatgtg 85740

taagtgatat taatgaccct atgaagttat tcagtagctc taaggatgct aaagctgatg 85800

atacgtctaa gtcttttcag ctagagttta tgcatgatat gaccatgtat actttatctt 85860

atggctcagg acagttaaaa cttattgatt tagcagaagg ttatgaagca caaaaagcta 85920

cagtagttaa ctcatttccc gaaattatta aaacattaga aaaggatgat tcagaagatg 85980

gaaaaaatga atagtttagt agatttaaat acagcaatta gacaaaagaa agatgttatt 86040

gtcatgatta cacaagataa ttgtggtaag tgtgagattt taaaaagtgt aatccctatg 86100

tttcaagagt caggtgacat taaaaaacct atcttaacat taaatctaga tgctgaagat 86160

gtagatagag aaaaagctgt taagttattc gatatcatga gtacaccagt attaattggg 86220

tataaagatg gtcagttagt taaaaagtat gaagaccaag ttacacctat gcaattacaa 86280

gaattagagt cactttaatt tggaatttcc tactatctgt gctatactat aatagtacaa 86340

ggtagtagga ttttttaatg gaaggaagat gacatatcgc aaagaataaa acattaacga 86400

tatataatag tgatagatat tttaatatac acacaaaaga taaagataaa attaatgagg 86460

ctattaaagt cacacatggt aatgaagaag aaattgagaa gaatatggat gaattaatat 86520

ctaagtctag acgatatatc atgagagatg aaaatcatta catgttattt aatgagaagt 86580

ataataatga tagacttata gaaaaagtat gtaaacatgg cggtaaagtt acatactata 86640

ctgattcagt attaccttat tatgttttaa aagacttatc tagtcaccct gactcagaag 86700

ttgtttatcg tatgcgcaat ggttttactg caaaagaagt agataatata gctttatcat 86760

tcatgggtac aaaagttatt attgatattt ctgtagtatt tccttatgta aacccttatg 86820

atattattag aagtttacat gatattaaaa caaatgtaga tgaagttcat ttatcatttc 86880

cacgaatatt agaggtagat gaaaaacaag aaaagtttta tttctttgat ggtgaagctt 86940

atgatttaaa acctgaatat aaagtcgatt ttgcagataa aattagagta tctttatcag 87000

tatggaaaat gtatatctat atcttaacaa gtagtcgtga ttttgaggat gtagacaatg 87060

taattacgaa attaaaacaa caacgaaaga ttaagatata aggtgattat atgagtacag 87120

caaatagaag agatatagca agaaagatat cagagaatac aggttactat atccaagatg 87180

tagaggaaat actaagtgca gagacagatg ctatttctga cttactagaa gaaggatata 87240

ctaaagtaaa gaatcataaa tttatgcaaa tagaagttat tgaaagaaaa ggtaaaaaag 87300

cgtgggatgg tctgaataaa gaatacttcc atttacctaa tagaaaagct ataaaattca 87360

aaccactaaa agaactagaa gaggttattg atagacttaa tgaagaagag aaataattct 87420

cttctttttt tattgacaag gtttaaaata tatggtatag tattattaag ttaaaaaagg 87480

agaggaatta aatgaaagta ttaatcttat ttgaccacat tagagaagag catttttctg 87540

taagtaaaga tgggagtgtg aaatctaatg tactaaatac acctaatgga aaaacactta 87600

agaaattact tgagaagtgt tctaacttaa agagagataa gacaaacaga gattatgata 87660

ttgattttct ctacaatgca gtacctacac ctatcagaaa tgactacggt aaaatcatta 87720

aatatcaaga tgttaaacaa gcagaagtaa agccatacta tgagagaatg aacaatatta 87780

ttattgataa ttcttatgat atggtaattc ctgtaggtaa actaggtgtt aaatacctat 87840

taaatgttac agctatcggt aaagtaagag gagtcccaag taaagtaact attgaaaatg 87900

aaacatcttc tcatgacgtg tgggtattac ctacttacag tattgaatat actaatgtaa 87960

ataaaaatag tgaacgtcat gtagtatcag atttacaaac agttggtaag tttgtagagc 88020

aaggagaaga ggcatttaaa cctaaggaag tatcttacga gttggtagat aacattgaaa 88080

gagtaagaga aatattcaat aaggaagtaa agaacgacaa ttatgatggc gtagatatta 88140

ccgcatggga cttagagact aactcattaa aacctgataa agaaggaagt aaacctttag 88200

tactatctct atcatggaga aacggtcaag gtgtaactat acctttatat aaatcagact 88260

ttaactggga aaatggtcaa gatgatattg atgaagtctt agaattgctt aagaattggt 88320

tagctagtaa agaagacatt aaagtagcac acaacggtaa atgatttgct gttgtaaaat 88380

ccctctcata tcgggcatag ctttaagaag ctgataagag aacctaagtc ctgtaataag 88440

gatagtggta atcccgagcc tacattattg gtgacaatag atggggtgta gagactgagc 88500

tgaggttttg tagaccaagg tgagacatag tgtatcaact taatagaggt ggtacagtga 88560

aaaaagatta tatgacatca gttaaaaata acaaaaaagt atgtagaaga tgtaatgaag 88620

aattagactt atctaatttt aaaacatata aaaagaatga taaaatttat tatcagagta 88680

tgtgtatacc ttgtagaaag gaatacaata aattagataa aactaaaaat actattaaaa 88740

aatgttatga taaaaatgga gataagtatc ggaaacaagg taatgagtat aacacttctg 88800

atagaggaag agaactaaat aaaaagcgtt caagaaaata cagagaaaat aattctttaa 88860

aagctaaagc tagaaactct gtaagaactg cattaagaaa tggttctcta ttaagaccta 88920

gtaaatgttc agagtgtaat aaggaatgta ttcctgaagc tcatcatcct gattataaca 88980

aacctttaga aataaaatgg ttatgtaaat catgtcatga agatacacat cataaaaaat 89040

aatcacacta tgtaaatgag ggacatcaag cccatttagg taactacaaa caaacctaat 89100

ggtaagggct tatgaaggta tagtccgttc tgtatagaaa tatacaggct aaaacgaaat 89160

atgatattaa attcttaatg agtactgaaa actttaaaga ttttgagagt attcaggata 89220

ctaaagtagg ttggtaccta gccgttaccc aggaagttaa agaatcttta agattatctg 89280

atttagctta cgaggttacg gatgtcggag gatatgataa accattagaa gactttaaat 89340

tatggtttgt tactaagtta ttaagattct tctcagataa aattaaagag atacagaaag 89400

aaaataaaaa aattgctaag aaagagtatg atgttaaagc tcctgaatat aaagaatggt 89460

tagagaataa actaaatgaa acagtagtag aactagatga tactgagaag aaatttagag 89520

tcagtgaatt agagaaaaag tatattcaac taggtctttc acctgaaatt gtaaatatga 89580

atttagttat gaataacgat gagtttataa gtattgcaga acaatcacct gagtacatgg 89640

ggttatctga ctacgctaag tcttacacat taaatactgc aattaattta attaatgagt 89700

atagagatgt aaaagatgta gttaatgata ttgatggagg taactttaat tatgattggt 89760

tccctattga gttaatgcat ccatatgctt caggagatac tgatgtatgt agaagaattc 89820

attgtgatgt agttaaaaaa cttaaagaac aagatagacc taaatcaatg catttattag 89880

aagttaatta tccaagactt actaagtctt tagctaggat tgaatcaaat ggtttatatt 89940

gtgacttaga ttatatgaaa gaaaatgatg agtcatacga gtctgagatg gctaaaaatc 90000

atgctacaat gagagagcac tgggctgtta aagaatttga agaataccaa tacaatcttt 90060

accaaatggc gttagaagaa catgagaaaa agccaaaaga tagagataaa gatatccatc 90120

agtatagaga taaatttaaa gatggtaaat ggatgttttc cccaagttcc ggagaccata 90180

aaggtagagt aatttatgat attttaggaa ttcaattacc ttatgataaa gaatatgtta 90240

aggaaaaacc atttaatgct aatgttaaag aagcagacct tacttggcag gactataaaa 90300

cagacaagaa agctattggt tatgcgttag ataatttaga attaaaagat gatgttagag 90360

aacttcttga gttacttaaa tatcatgcta gtatgcagac aaaacgtaat tcatttacta 90420

agaaattacc taatatgatt aataaacaaa aacgaacatt acatggttct ttttctgaga 90480

caggtacaga gacatcaaga ctaagtagta gtaaccctaa cttgcaaaac ttaccggcac 90540

acacatcaga tgtaaacaag tttgattaca aacatccaat taaacgttca tttgtttcta 90600

gatttgaaaa tggagtacta ctgggagccg actatagcgc cctagagatg cgtattattg 90660

gattatttac taaagaccct gatatgctac aatcattctt aaatggggaa gatattcata 90720

aggctactgc aagtattgtt tataataaac cagtagaaga ggtaactaag gaagaacgac 90780

aagcaactaa agcagttaac ttcgggttag ccttcggtga atcacccttc tcatttgcag 90840

gtaaaaataa tatggaagta agtgaagcag aagaaatatt tgaaaagtac ttccaaacaa 90900

aaccaagtgt aaaaacttct attgacaatg tacatgagtt tgtgcaacaa tatggttatg 90960

ttgatacaat gcacggacat agaagattta tccgttcagc ccaatcaaca gataaaaaga 91020

taaaaaatga aggtctaaga cagtcattta acactattat ccaaggttca ggtagtttct 91080

taacaaacat gtctttaact tacttagatg attttatcca atctcgtaac ttaaaatcaa 91140

aagttattgc cacagtacat gatagtatct taattgattg tcctcctgaa gaagctaaaa 91200

ttatggctaa agtgacaatt catattatgg aaaacttacc atttgatttc ttaaaagcag 91260

aaattgatgg aaaagaagta caatacccta ttgaagctga tatggaaatc gggttaaact 91320

ataatgatat ggttgaatat gatgaggaag aaatagatac atttaattct taccaaggtt 91380

atattaagta tatgatgaat ttacagacct tagaagatta taaagagtca ggtaaactaa 91440

cagatgaaca atttgaaaag gctactaacg ttgttaaaag tgaaaaacat atttaccaag 91500

aaatttaata aaagtattga caatatattt aacttatgtt atactatata ggtaataaat 91560

ataaggagga aaaagagtga atacaggaga gattagattt aatcgttcta tggatgaatg 91620

gattataaca agtatgtacc aggatgagct aggtgatatg aatattgttg ttacattcta 91680

taatagagaa gaaaataaac acggttctac agttttaccc acagagtcat ctactggaga 91740

agtaacagag gaattggcaa atcttgaaga agaatatcct ctagctttac ctttaagtag 91800

tatctcagtt aatatttaaa aggaggaact gataaatgga aatacacatt gattccctag 91860

attttacaaa ctttactatt aaagatagaa atgggaactc acaagagttt gatattacag 91920

atgagttaag aattacagag tatacaatac aagaggactt tatgcaacaa tcagctaaat 91980

atgctttttg ggcttctata ttagagaagg taagagcata ttctgaaatg gaacaaagaa 92040

atctagaaac aattggtagt aagctaaacc ttacaattag acaagagtac gaacaacaag 92100

gtaaaaagcc tactaaagat atgattgaat ctagtgttta tattcatgat tcttaccaac 92160

aacaacttaa agttgttgag gcttggaatt ataaagttaa acaacttcaa tatgttgtaa 92220

aagcttttga gacaagaaga gatatgatga ttcaattagg tgcagaatta cgacaaacaa 92280

ataaaaatgg tggaattact aatccatttt cacattaaaa aataaagtaa agaatataat 92340

tgacaaatat aaaaaactat gttataataa ataagtaaat taattaaaag gagaaaagat 92400

aattatggat ttcaatcaat ttattaacaa tgaggcaagc aaattagaaa gcaataacag 92460

ttcttttaac aataatgtag agagctacaa acctaaaaac cctgtactac gtttaggtaa 92520

tattaaagat gcaaacggaa ataaggttgt taaagaaaat gcttttgtac gagtattacc 92580

tcctgcacaa ggaacaaatg ttttctttaa agaatttaga acaacaggta ttaactattc 92640

taagaaagat ggttctcaag gattcacagg attaacatta cctgcagaag aaggttcatc 92700

tgtccttgac ccgtacattc aggactggat aacaaatggt gttcaattta gtagattccc 92760

taataaacca ggagtacgct attacattca tgtgattgaa tactttaata acaatggtca 92820

aattcaacca aaaacggatg ctcaaggaaa tgtaatgatt caacctatgg aattatctaa 92880

cacaggatat aaagaattat tagctaactt aaaagatact atgttaaaac catcacctaa 92940

tgcacctcat agctttatct cagcaaatga agcattctta gttaatattg ttaaagctaa 93000

gaaaggtgaa atgtcatgga aagtaagtgt ttatcctaat gctcctttag gtgcgttacc 93060

gcaaggttgg gaacaacaat tatctgacct agaccaatta gcaaaaccaa cagaagaaca 93120

aaatcctaat tttgttaact tcttaatcaa taatgttaat aacacagagt taagtcatga 93180

taactttaaa tttaaccgtg aaacaaatgt cttaggtgaa gaaccttcag agcctaaaca 93240

agcacctacg caacaagatg tagatagtca aatgccaagt aatatgggag gacaacctaa 93300

tcagcctcag caaggtcaag taggtcagta tgcacaacaa ggtcaaagta atggtcaagg 93360

acagcagtta caaggtacac aacaacctat caataacacg caatttggtc aaggaactcc 93420

ttcaggacaa caaccaagta acacaggttc tgttgattgg gataacttag cgcaacaaca 93480

atcacaacct gattcaaacc cattcaatga ttttgatgtt agcagtgttg atgattcaca 93540

ggtacctttt gagacacaac ctcaaaatac acaacaagca cctgaaccac accaaactac 93600

acaagagcct ccaaaacaaa aacaaacgca aagtattgac gatgtattag gtggtctaga 93660

cttagataac ctataagata tagagtgcct tagagcactc ttttatttga gatataatta 93720

ctaggaggat attaaatggc aagagcaaaa aaaggtaaag aagtagattt aacagattta 93780

aatacaattg atttaggtaa agaattagga ttaacattgc tatcagatac aaacagagca 93840

gatattaaaa acgttatacc tacaatggtt cctcagtatg actatatttt aggtggaggt 93900

attccattag gtcgattaac agaagtttac ggtttaactg gtagtggtaa atctactttt 93960

gcagttcact tatctagaat tgcaacacaa ctaggtgtta tcactatttg gattgatatt 94020

gaaggaacag cagataacaa tcgtatggaa caacttggtg tagatgtttc aaaactattc 94080

tctattcaat caggagaagg tagacttaaa aatacagtag aattatctgt agagcaagta 94140

ggtaaagaat tagaatactg gattgacact ttcaatgaaa agattccagg agtacctatt 94200

gtatttattt gggactcatt aggggctaca agaactcaga aagagattga tggcggtatt 94260

gatgagaagc aaatgggtct caaagcatca gctactcaaa aagtaattaa tgcagtaaca 94320

cctaaactaa atgatacaaa cacagggtta attgttatta accaagcccg tgatgatatg 94380

aacgcaggta tgtatggtga ccctattaaa tctacaggtg gtagagcttt tgaacatagt 94440

gctagtttac gtattaaggt tcataaagca tctcagttaa aacagaagag tgagttaact 94500

ggtaaagatg aataccacgg tcacattatg cgtattgaaa ctaagaaatc taaactatca 94560

cgaccagggc aaaaagctga agcagactta ctatctgatt atatggtagg taaagaagat 94620

gaccctatct tattaaatgg tatcgactta gaacataccg tatataaaga agcagttgaa 94680

agaggtttaa ttactaaagg agcatggaga aactatgtta cattgaatgg tgaggaaatt 94740

aaacttagag atgctgaatg ggttcctgta cttaaagata atagagagtt atatctagaa 94800

ttgtttagta gagtttatgg agaacacttc cctaatggtt actcaccatt acttaataac 94860

aaagtaatcg taactcaatt agaagagtat caagctcttg aaaactacta taaagaatgg 94920

gctacagata ataaacaaga agaacaagag gaagaactaa aaggagaatc tcaagaaaag 94980

gattctgaat aatagatgga taatttaata gataaaaaca tgagtcaggt aaaagaatct 95040

ttggggaacg caaattcctc agatgttctt cctttacctt ataaagatat agcaaagaaa 95100

tttgaagaag taaaagaaaa aggtgaatca attatcattg aagaaggtgg attcccttat 95160

acagattcta cagtgatgta tatagaacat gtaacagata gatgggcagg aggatattcc 95220

ttaattagac atgaaggtga ggaagttaaa gtacctaaga ctatccattt ctctgatata 95280

tatgttaaag ataaatcaca caaagtaaga ataatcttcg agggggctaa tccttatgaa 95340

gaaagctaat aatggtaata gatatgtaat agatatagat ggtatacctg ttgattttga 95400

aagagattta gatagtttac ttaataggta taaaaacctt agatggtctt tatatcatag 95460

atacgcaggg attttatcta atgattttga aagacaagaa ctaagagaat atattgatga 95520

gcaatttatt aaattagtta aagaatataa tattagaagt aaagtggatt ttcctggata 95580

tattaaagct aaactaactt taagagttca aaatagttat gttaagaaga atgaaaaata 95640

taaacgtact gaaattatcg gtaaaaaaga ttatacagta gagtccttaa cagaagattt 95700

aaatgaagac ttcgaggata atcaaattat gagttatgta tttgatgata tagaatttac 95760

agaggttcaa agtgagttac ttaaagaatt acttattaac cctgaaagag aagatgatgc 95820

ctttatcgtt tctcaagtag cggaaaagtt tgatatgaaa agaaaagaag tagcaagtga 95880

gttgacagaa ctcagagact atgttagatt taaaataaat gcataccatg agtactatgc 95940

taagaaagaa ttaaataacc atagagttaa tactgaaaat catatttggg aaaactagtt 96000

acagtgcctt ccttgtgtta tattattatc gagaattcaa taataaagca tagggaaggc 96060

ttttttctat gtcttataga atgctttaaa atagattact aaaataaaga ttggagatta 96120

agcttatggc taaaaagaat gttaatgatg tattacaaca agaatctgtt acagtagcag 96180

ataagtattt acaagttaaa gttaaccgtg acggttatac tcgtacacat gaaggacaat 96240

atgcgtacaa agtagtttca gagggagaag aattattctt ataccctgta caaacagatg 96300

gtaaaggtac attaaatgta atgaagaaat cacctattgc ttacactgat ggagacaata 96360

tccatttcgt agtaaacaca gtagtagacc cttataatca ctcatttatc cgtactgaag 96420

atattaaagg attagataaa ggtaaacaac ttattcaagc tttcttagct ttcgttgaag 96480

accgtttcaa atttggtgtt tataacgtat ttgttgcaaa caacaaagag gatgtattat 96540

ctattgtaga ccctacagat aatgatgcag atgaagttaa agatagttta gagcacgcac 96600

atgaagatgt aattgcggat ttccctgcta gccctgctcg taaggacgtt aaaggcgtag 96660

attcaggaga aggtcaagga gacacttcag aaccatcagc acctaagaac gttcaagtta 96720

ctcctaagga agacggagca gacgtatcag cagaataata tatagataag gatggtaaat 96780

ttggctaagt taaatttata caaaggtaat gagttactaa acagcgtaga aaaaacagaa 96840

ggaaaatcaa caatcacgat tgagaattta gatgctaata cggattaccc taaaggtact 96900

tttaaagtat cattctcaaa tgattcagga gagtcagaga aggtcgatgt tcctcagttt 96960

aagacaaaag caattaaagt tatttcagtt acccttgacg ttgatagttt agaccttaca 97020

gttggagata ctcaccaact atcaacaact atcacgccta gtgaagcatc taacaaaaat 97080

gtgtcatttg aatcagacaa atcaggtgtt gctagcgtaa catcagaaga cttaattgaa 97140

gcagttagtg caggaacagc taatgttact gtaactactg aagatggtag tcacactgat 97200

attgttgctg taacagttaa ggaacctatt cctgaagcac ctgcagacgt aacagttgaa 97260

cctggtgaaa atagcgcaga tattactgta taagaggaca ataaagaatg gaaaagacat 97320

taaaagttta tagtaatggt gaagttgtgg gctctcaagt agctaataac gatggagcta 97380

ctacagtatc tattacaggc ttagaagccg gaaaaactta tgctaaagga gattttaaag 97440

tagcatttgc taatgattca ggtgaatcag aaaaagtaga tgttcctgaa tttacaacta 97500

aaactcctac tgaagaacct tcaggagacg cataataatt aagaccaact aaaaagttgg 97560

tctttttta ttgacaattt ataatatcta tgatacacta tataagaatt aagaaaagga 97620

ggggaaagta atggatattc caacaatatt atttagaaat ccatatgatt atacgaaagt 97680

aaaaaaatta atggaaaaca aagagcagta tattgtagta aagtttgatt ctgtttctgt 97740

tcataattta aatgttcaag gtatgatgaa tgtcatccaa gattacctac acatctatgg 97800

ttacagagtt aaagagtacg gacaagaaaa ttcttctaaa gatgatgaaa gagacgttaa 97860

aggctactta tatgaaagag taggtgagta gggtatggga attatagtaa actccaacca 97920

tattcaatca gacactttat atgagtatga tagctttttt gatattgaga aagtagatac 97980

atttgaagaa ggattgcttt caatacagga tgagccaact gttttagcag gattcatcta 98040

tgatgatatc acatttaata aggtcattaa ttctaattca gatattgatg actatattaa 98100

gaataatgat atttattatg tctctgatat aggattactt cctgatactt ttatcactgt 98160

tgattctgat agaaaatatt attcattatt acaacagata actgagttaa gtaaagaccc 98220

ttttcctaaa tgggtagagg atgatgcaaa aggtttaact aagtattata actttcaaga 98280

ttttgaagat gtatttgatt taaatagttt ttacaaaaaa gaagttgaca tggtaagaga 98340

aaagtgctat aataatggta atgtatattt attatatgag gttctgcctg attataaatt 98400

acctctagct tatagtttac tttcaaacaa ggagcatggt attgttatta tcggttcaca 98460

gacacgttct aataatgata tactgacttt ttatgttaaa ggtatggatg ctaaggcaat 98520

agctagtatg ttcaatgtag aacatgatta tgattctaat attttccata catttgtaaa 98580

cagtcacatt aatattttag gaaatcaaat aactaagttt ataagagaga aaggaagcag 98640

ttatgagtaa ctataaaaca atagaagaag tacaagcagt tattattggg gtattattta 98700

aagatgaagg taaaattata acatctaagt ttaataaaat tactaaagag tttggtttag 98760

atagaatcgg taaagatgac cttaaagaaa ttgtagagga tatccgacaa gacgcttatc 98820

taaatgaact taaaaacaaa gcaattaaag gtaaagtaac gttaggtgat ttaaaagatg 98880

ttgcagataa ccaagtattc gaaggtaata actaccatga agaagtatct acttatgtag 98940

tagctaaaga aaaagaattg tctcacttaa gagaacagcg taagcacaat aggcatactg 99000

catacctca aattatgttt gatgaactta aagaacatat ggttaaggaa ttacaagggg 99060

aaacattagt agaacatcac ggaagtaaag ctaatattaa tgatacagag ctaattgtgt 99120

tactatcaga tttccatatt ggaagtattg tatctgatat gactaatggt aaatatgatt 99180

ttgaagttct taaagcaaga ttaaatcatt ttattaatac aacagttaaa gaaattgaag 99240

atagagaaat ttctaatgta actgtttact ttgttgggga cttagtagaa catattaata 99300

tgagagatgt taaccaagca tttgaaacag agtttacttt agcagaacaa atctctaaag 99360

gtactcgatt acttattgat atcctgaatg tactatctaa tgtagtttca ggagaactaa 99420

gatttggtat tattggtggt aaccatgacc gtatgcaagg taacaagaat cagaagattt 99480

ataatgataa cattgcttat gtagtgttag attctttatt gttattccaa gaacaaggac 99540

tattaaatgg tgtagatatt attgataatc gtgaagatat ttatactatt agagatacct 99600

ttggcggtaa atctattatc attaaccacg gagatgggtt aaaaggtaaa ggtaatcata 99660

tcaataaatt tatcttagat agtcatattg acttattaat tacaggtcat gtacatcatt 99720

tctcagtaaa acaagaagat tttaatagaa tgcacatcgt agcttcatct ccgatgggat 99780

ataataacta tgctaaagag ttacatttat caaaaactaa accttcacag cagttattat 99840

tcataaataa ggaaaataaa gatattgata ttaaaacagt atttttagat taaggatggt 99900

taataaatgg atacaatttt tattataggt gtagcgttta taacttttgc aacatttaac 99960

atagtcttta gattatttga tttatggact acagagaaaa aaatggtaag tcaaggacaa 100020

cctccactaa gtaactttga gtactatcat gtgatagtac cttacttagt aggtgttatt 100080

gttattatac tgagtattat ttttagggat tccttgtatt ccgcacaatc agggttcggt 100140

gttattatta caagctttat ttacatgcta gtttatgtta taattggtct tgtagggtca 100200

tttgtactta caatattcca agctagaaaa gctagacagt atcaaacaca ggaggataat 100260

aatgaagttc aatgatattt atgagcaatt aattaaaaat gatacagtac aaaacattca 100320

tgagtctcaa gatgacaaag gaaatattta tacaatacag tttgataaag gtaatgataa 100380

gtatttattt aatgttatta atgatggatt cttgaaagaa atgacaaatg gtatggtaga 100440

ccatcctgaa ggtcagccat attcagtaag tttaatcaat aaagaaacac ctagtatgtc 100500

agtgaaacaa tatttaacag atgtagaaga tattgtacct actattagaa aaatggaaaa 100560

ggatttctta tagagtcaag tctttacttg actcttttta ctatatatgg tatattaata 100620

tagaggtgac ttaaaaatgg attttaattt tagtgctttt gataatagct cattagcaat 100680

gagaattagt gagggtgtat actatttcaa tgatacgcct tattacttta ttgagcatgt 100740

agaagaagaa atgtctgagt atgttattgt atatgacata catgacagag aggaaaaaga 100800

aaatcctcag aagaaatata gaatagaacc ttaccaacgt acaataccgg gaggaacacc 100860

tcttagtaat ttaattaaga gtatgatgcc tcaacgtaag tatcctaaga aggttacaga 100920

agaccctata tttgtagcta atgttattcc tttaggaaca gatacagtaa caggtaaaac 100980

cggtaaagga ttttttgaaa gagataagga tagaactatc tattctcaaa aggaaccaac 101040

taaagtcgtt catggtcaat acacaggtgt ttttataggt ctaacaagtg ttaagtggaa 101100

tagaacatat acccccttag aaagtgttgt tgagtactac aaaagggtta aaggagatag 101160

gttaaatgtc taatgatgta gttaagttct atgaaaaaga tattaaagac cttatcagaa 101220

ctaaaaaaca catgttcaaa gacgatgaaa taactagtga tataaacgat atacgaatct 101280

ttaatgagaa agtcatttgt caaggtaaat gtagaacaga ttgtttagtg ttagaccgta 101340

atggtacagt aatgggtata gagataaaaa cagaacgaga ctctacacaa agattaaata 101400

accaattaaa atattatagt ctagtatgta agtatgtata tgtaatgtgc catgacaaac 101460

atgtacctaa agtagaacaa atacttaaaa ggtataaaca taatcatgta ggtataatga 101520

gttacattag ttttaaaggc aaacctgttg taggcaaata caaagatgct acaccatcac 101580

cacatagaag cccttatcat acaatgaata tattatggaa gacaaactta atgacaatac 101640

ttagattgat tagagaccct catacgtata gaacagggta tagctataat gctagtggta 101700

gatatagtgg aggggaaggt aatttctccc aaacaactca aagtaaaaga atgaaaaaac 101760

ctgctattat taaccaaata attcattatg taggggtaga taatacttat aaactcttta 101820

caagaggtgt tatctatggt tataataata ggtgggaagt tatagaagaa gatttcttta 101880

atactatgaa gaatggggta agagtaatta atgagcaaag acaaaccaaa tagacgtaaa 101940

gagatacagc atcaacctgt taactttgcc cctacgaata ctttaacagg agctaataat 102000

agtttctttg ctaaaaatcc ttcagagcct aaagatgcaa catctgttat tgaatatcgt 102060

atactattta ttaaaagatt tgataacgta acaagtacag atgtgaaatt acagaaaaag 102120

tatgcactaa atcttattag tgaagcactt gatgttaaag aaacttactt gtctcttaag 102180

caaaaaggaa aaaaaacaga atctattttg catacagata gagtttatta tgttcataga 102240

ggtaaaaaac ttattggaaa gtgtagtatc agagagcaaa gaacatttaa gggtaaacat 102300

ttgatattta tattcaaaac aagacataga gttaaagcag aaaggaaaga taaataatgt 102360

taaaaggatt ttcagaacat gtagacaaac ctacaactag taagacctta tacaagacct 102420

taacaagtgg taaagtagaa ttactaggtg tatcttacga tagtgattac ttcccttcag 102480

gtgttacagt acaatcttac attgaggata taggtaatga agatgagggt ctacagtttg 102540

ttaataaggt aaatgtagta gaatcaatga aacaggctgt agtaggtatg aataatcaat 102600

taggttcttc aggtcttggc tatgtgagaa ctgaacaact taaaaaagag ttggaagaga 102660

ctggactaat gacagattta cttgctagag gtactaactt aacctctact aagaaagtag 102720

atattgtaag tacttttatt gagcctgagg taacatacca aaatattact atagctaaag 102780

atattaaact acgtttgtat aaagtagaag aagaatcacc attaaatggt tacactcata 102840

ttgtatactt acttactaca gaaaaactat atgatggtca aacactcttc ggtatgctct 102900

ctaaaaaaga taagttatct aaaggagata ctgataaatt attagcattc ttcagaaaca 102960

atagtttaat aagtaaaagt gtattttgtg ttaagttatt aagtaaagac tactacttta 103020

atttatataa tacacatgag acagggatat tctttttaga agacacagat gttattacta 103080

ttgcttgtgg tcagtcatat gttaaagtta acactaaaga tattaagtct agttatgtta 103140

aaattgaaga taagactcat aaattaactg agctagtaat taacctaaag ggtgacgaca 103200

cattaactat tttattctag gaaaatgtta taaatatgtg ataattaagt ataaatatac 103260

gttatataag aagttttcat aatgttttta atacagaaac tagttaagtt ttttctactt 103320

gctctagttt ctgtgaaatt atatttatga aaagttaaaa tatcttttag gtaaaggctt 103380

tgtaaatagt taaaaaatat attaaaattt tatacaaagt agttaataaa attatattac 103440

atttatatat tatgaaataa taacagaaat tgtgatatat tatatagtgt aaccttgaaa 103500

cagttgatgt tgtagggttt gtttatgttc gttaaactgg tttcaaaaca tcagttacca 103560

taaataaatg acagttaagg agagctatat aatggctaga aaaaagaatt tacgaaataa 103620

aaacagtgat ataaaagttg ttcctgataa agaaaaagaa agtatattat ctaagctata 103680

ccataataaa ttactacgtt ctaaggtaga taatgcatta gatgaagata tgagttatga 103740

tgatattata gaactatgta aagaatatga tttagaattg tctaaatcag ctattacaag 103800

atacaaaagt aaaagaaaag aagctattga aaatggttgg gatttaggag aattaattga 103860

taaacgtaaa aaaacaagtg taaaagatat taaggaaaaa gaaactccta tattagaaga 103920

ggagcaactt tctccattcg aacaatcaaa acatcacaca caaacaattt atgatgatat 103980

tcaagtacta gatatgatta tttctaaagg tgcaaaagga ttagagtttg tggaaacttt 104040

agaccctgct ttaatgatac gtgcaatgga aactaaagat aagattaccg gaaatcaatt 104100

aaaaggtatg tcatttattg gacttagaga attacaatta aaacaaacag ctcaagatac 104160

agctatgagt gaagtattat tagaatttat acctgaagag aaacatgaag aggtattaca 104220

acgattagaa gaactacaaa atgaattcta caaaaatcta gatttagatg aggaaagtag 104280

aaaattaaaa gaagctcttg atagagtagg ctatacaatt tagatagtga ggttagagta 104340

atggcagatg agattagttt aaatccaata caagatgcta agccaattga cgatatagta 104400

gatatcatga catacttaaa aaacgggaaa gtactgagag ttaaacaaga caaccaagga 104460

gatatccttg ttagaatgag tccagggaaa cacaaattta ctgaagtatc tagagactta 104520

gataaagaat cattctacta taaaagacat tgggttctct ataatgtatc tgttaactct 104580

cttataacat ttgatgttta tctagatgaa gaatattcag aaacaactaa ggttaagtat 104640

cctaaagata ctattgtaga atatacaaga gaagaccaag aaaaagatgt tgctatgatt 104700

aaagaaatac ttacagataa taatggtaat tatttctatg cacttacagg agaaacaatg 104760

ctctttgatg aaaataaatt aaataaagtt aaagattagg gttgacagct tctatagttt 104820

atgatatagt atatgtatac taaaaataaa ggagctaaca attatgttta tttcattaaa 104880

tcaagaagag aaagaattat taactaaaga ggaaagtaaa tacacaccac tagaaacatc 104940

aagagagttt aacacaccta aagaagaatt cattgtaaca agttataacg aaggtaaacc 105000

cttagattac attgcaaaag aagctaaggt aagtatggga ttaatttaca cagttctaaa 105060

ctactataaa gtaggtaagc gtaataagaa atcacctgta gaagaaagaa ttgcacatat 105120

cttaaaagat aaaaacttag tcaaagagat tattaaggat taccaatata tgaatttaca 105180

ggacatttat agtaaatata atcttcataa gaatggttta tattacatct tagatttata 105240

ccatgtagaa agaaaatctg aacttaagga caaagcatta gaagaggata atattgtcgt 105300

tgagtaagta aagaggttat aatatgagaa ataaaaaatc atttcaagag cagttaaatg 105360

acatgcgtaa taaagagaaa tgggtatctg aagaggagtt cactgaagaa gtggctcctt 105420

ctgaagaacc tgaagtagaa gaagaaaaac tatatacttt aaatgagtta aaagagaact 105480

tactagatgc tcaaggatta aaagatgttg tagctgattt tcctgcatct aaagatttat 105540

atgaacctaa taaactatat atttgtacaa taccaaaagg atatcgttct acagaagtac 105600

aaccaggtca atatattggt atcagtacag gattattatc agaatcagaa gattttagtc 105660

atttaagagg tcaaatgcct agaaatcttt atgaaacttc tcatgtttta aaacctttag 105720

tacgtattaa taatacaaat ctcgaatatc aacagcatga gttacttgaa gatattaaag 105780

atgacaagaa gatatacgat gttgaattag aagacctgag attagtaaca ggagaagaaa 105840

tatcccattt agaaattgtc gatagtaagt tttttgaaag tcgtattaat gaaattctag 105900

accgctatac tgaattaacg gattccgatg atttgcttat atactatagt aaattacgag 105960

aattagttgg tagtgacaaa atgatttatt gttcactttt agataaatgt gttaaaatta 106020

tagattaata gttagtctcc tcttatatta taactgtaag aggagacatt tttgtataga 106080

ggtgttaatt atgtcaagaa aagcaagtat attctatata ctagtggtta ttgttttggc 106140

tttttctatt tcatcttatt atatatcttc tttcatgtat cacgacaaag caaagaatga 106200

agtctctact gagttatcaa acacgggaaa gattaaagaa gaaaagaacg tagaatttgt 106260

cggtgactat acacttaaaa aagtggaaaa taataaagct tattttatgg aaacattacc 106320

tacttaccta cccggtagaa caggagataa cagcatagat atgaggtact acaaaacaag 106380

tagatttaaa gaaggggtaa atttcaagct tattagggta tatactgaag atggggaaga 106440

taatccaatt cataagtata ggtttgaagc agtaccaacc aaaaagtaat aaggaggtga 106500

cttaaatgac aacattaatt gtcgtcatct ttattgctat catttattac ttatggaaca 106560

gtgattgagt caagttaatt cttgactctc tttttgtttt atggtatatt aatatataga 106620

aaggagagat taattatgga aatggcagat ttagaaagat tcgatacgtt tgtaagatta 106680

gtttcagatg atgagctttc ggaggagaga gcattagaat taagtgtaga cttattaaat 106740

ccgatactag aaggaggtac agcttaccaa gctaaaaaac gcattagaag taagttcggt 106800

aaaatagaag caaaaaactt taaaagaaat tataaattct tactcaagtc gatagctcaa 106860

atagaccaaa ggagatagga caatgataga aagggaaaag ttagttaaag aaattgaaga 106920

tgctaataga gacatacaat tgaggttaaa agaagtagat gattataagg atagtatacg 106980

ttctaaagga acaagaaact atgtatctac taaggtatta gattcagtta tggtagggct 107040

aattataagt ttctttattc ttgtaatgtt acgtgtactt gaatattttg taacaggtaa 107100

tgctgtttat tcacctttag cacccgcagt tattattatg tttgttttag ccttaggtac 107160

atggaaagta agtaaaatga ataaaatagt atcctatagg ggaactatta agatgtactg 107220

ggaattaagt aatgctgaac agaaccaagc taaggtattt aagtatccta atgatgaagt 107280

agatattgta tcaaaacata acttaagaca aataactttt agtgagatta atatacttca 107340

tcttaaatat atgagatata ataaggcagt agaacagcat actaagttat ctaaagaact 107400

ttttaaaaaa gataaagaaa ctgttgacaa gaataaataa gtgtagtata gtattactaa 107460

aggaggagag atattatggt tatacctagt attaaagcac aaaacaaatt caagaatgaa 107520

ttagagtatt ataagcaagg tcacattagt gaaagtaaaa tgttagaatt agcttttgat 107580

tacattcaag aattagaaca aaataatgaa tacgttacta atttgctaga agaggagaga 107640

tacggtgagt aaatttattg gagtgtactt atttaattta ttagtagtag cactaattta 107700

cacagtagga tttttattct tttatggtgt agctagctta gttattattt taactcatgc 107760

tactattgac ccgttcgtat tagctacttt cttaggaata ggattcttag ttattagaac 107820

tgcacacaga atcatggcac gagtaattaa tgatgcagta gctaaagcta ttaaggataa 107880

agaaaatgaa taaaggggaa tttattatgg ataaaacatt accaaagttt agtgtatatg 107940

aagttattgt aaagactgta attatgacac caacagaagg aagttctgac ctagaatcat 108000

tttacttttc aactagagag ttagcagaaa gatttgttga agaaaataca gtggaaacaa 108060

aaaacggtaa acgtgtatct tttgctgtta aagaacgtaa agtaaatcaa ccaggctaac 108120

attaatttgt tagctttttt tattgacaaa tcattttata tagtgtatag taatattata 108180

cagaaaagga ggaattatta tgaaagtttc agaagaagta aaacagagtt atctagagaa 108240

tagagctaat actaaaatgg ataagataag ttggtctgag ttaaggtcta gtcctttagg 108300

tattacctta ggtgatatta tattttatag tgtggttatt atagataaca ttatagctat 108360

tattttaact ttaaccttaa taggtactat tactgactca attgagagta ctttagccca 108420

aataatcgta gggatgttca taatcattac tatatatgga atcctatcag cgttaatacc 108480

tattctagtt cataaagctg tatcaccggg atggagctat actgaatgga atgaatccta 108540

ttacatcaga ttacctggag aagagaacta caagtactat agtaaatggt atttagattt 108600

attaggagtt aaagaatttt actataagag agacaatgga gaagaagtaa aagaaaaaat 108660

atatcatggg cttttcaagc tgaagtaaaa agacctgaag atgttaacca ctggaaaaac 108720

caattgctta ctaatagacc tttaacaatt ttagaatata aaaaattaaa gaaattagat 108780

aaggaaagtg aaattaggaa acaagaagat ttagaagaat ataaacaata caatagtaat 108840

taaagaggtg gaaagcaatg ataagctcat ttgatagtat actacttgtc atatacatta 108900

ttatagcttt tgcagtagct atggcaatta tctacttagt atttaaaggt atgactattc 108960

tactagataa gctaatgatg ttattattaa gtaaaactac attagatgta gaagcttgct 109020

ctatgataat ggcagtcatc agtacaattg tgtttggaat tattgtactt ttaatatggc 109080

tagcagtaaa taatatttta ctataaggag atttactatg gattttaatg actttataaa 109140

cagtgaatcg gatagggtag gtaagcctaa acaaaagaag aaggtagaga ataagctacc 109200

ttcttctact cctattgaag ataaggaaaa gaaattaaaa gagataagaa agaaatcatt 109260

atatattgat ttaaggagaa aaagaaatga ctaaagaaac aaatgtactt tacaaagata 109320

agtatagaga ttatactata gttgtaagat tagcagggaa tattattgtt actgaagtag 109380

ataagaaaca taaaacagca tttacaccta ttatatttga caatggtgta gaaggcgtag 109440

agcttgtaat gcgtataggt tctgtagagc ttagcatgac agatttacgt gagttcacaa 109500

aggaagtatc tacagctcag aaagctttag aatattttaa taaaaaactt tatattaaag 109560

gcttgacaga tgaagcattt taatatatac taaaagtata aataaaataa agaaaagagg 109620

aatgattatt atgttattag gaattttatg gtttatatgg ggatttgtat cgtactttgt 109680

attgatgttt ggaattgagt tttggaaaga tagatggatg ccaggtgtta tcggagcagg 109740

agctttacta ctattcttat tttggattat gaaatctatt cataatgcta tgacagtagt 109800

atacttgtat taggaggttg tatagatgat tgatatacta gttattcact atgaagaaac 109860

aaataaacgg gttttaaaag aaacaataca aacaatacaa aatcatttaa atgatgaaca 109920

tggtttggtt aagatgacag caacaaaact tagcagagag aatatagaga aaagatttaa 109980

taactataat atagtcattg cagaagatga ccctgataat tcttatcatt acggtgaagc 110040

tgtagaagac gcagatttta ttatagacat accaatttca tatttagata tacatgcagg 110100

aatagaatgg gatgttgata atcctgtaga tatgctagat aggaatcctg attttataga 110160

agctgtaaat aaactaaatg aagacttaat gttataagga ggaaatagaa tgctaaatga 110220

aaaactaaaa aacctggaag atacaaaagt atacatgatt aatagtattg caagtttact 110280

aagcgcaagt acaggaaaat caagtaaagt atttttgat gaaggaacta ttaaaattgt 110340

aagtggtgaa acaaaagcag tagaagttat tgataactta gttcaccctc actcaggacg 110400

tttacctatt aaaacaacag aacgtattgc gctaggtaga ttaacagatt ctttacagtt 110460

tgttatctca gaaatagaag tagttaaaga ccaaattata gatgaagaaa atgaagctta 110520

cattgatttt gtgatggaag actggaactg ggattaatgc ctatggactt attaactatt 110580

gcttctgttg cttttatagc tgtagtcatt attgatttga ttaatgatga tatgagctat 110640

atgcttactg gtactgcaat cttaataaat atttgggcgg gattttatgg atggtttttc 110700

ttactacaag caggtatgtt acttttctta ttattagcta ggaaggttaa agatgataag 110760

gagtcaatac tatattccag tgcttcatta atatgtgcac taggaatgat aataaatctt 110820

ctttcatttt cttaaaaata agtattgaca cctttgtact tttgtattat acttagtata 110880

taacaagtac aggagatgat taatatgagt aaagaaacaa tcagaagaca attttcaaat 110940

gcaattgaga ttatggcaac aactaaagaa tggtggaact tccctaaaag ttttgatacg 111000

aataaagaat ttaaaattaa aacttttaaa aatgatacac ttgtatttga agttagagaa 111060

ggtagtagaa acttaggaag ctttgtagtt tttacaaaca ttgattttga ttatgataaa 111120

ctagaaggaa cttcaacaca atatatgatt aattactttg ctaagaaatt aactaaagat 111180

atgtttaact atcataagtt acaattatag taggaggtgg aaagatgaga gaagagttaa 111240

aacctttaa taggaaacaa gttaatgtta aagggtattt agatgatgtt aagtactcaa 111300

agcgtagaag acataagggt aatcaacatg ggtgtgttaa aatcacagtt actgatgtaa 111360

agattaatgg tatacctatt gaccacgtta acattgaagt tggtatctct ttctatgaaa 111420

aactaaagga gcttcaagga aagagaatcc aatttgtagg cactgtttac aagtatgtta 111480

aacatgctag agggcgcaaa ggtagaatta aaggatttta taaagaggat tatagcgtaa 111540

ctttagataa gaagttacaa aaggaggaaa aataatgact gaatggtatg ctttatgcta 111600

ttatgataaa gtaggtaaaa agaaaatacc taggcaagtt agagcgcaca gagatatttc 111660

agtattagaa gaattaaaag aaagattaga agaaagaaat cctaatacag aatactctat 111720

aaaaacaaca aaagaatttg atgaggagag ataaggatgt taacaccaca acaaaaagat 111780

tcattaaaag aacaacaaaa gaaattaagt aaaaagaaga aataactgtt gacaaatgag 111840

tgtgcatagg ttatacttaa gttaacaaat aaagaggagg tatgacctat gttattcata 111900

atttttattc tagcagtatt ctttgtacta ggatttatta acggatggaa ctcagaagac 111960

taaaaaagga gtggttatag tgaagttaga agataaagta ttagaaagaa ttgattctct 112020

tggaggtaag ttaggtgata ttagccaaca tgcttgggaa gctttagtaa agtaccaaat 112080

tatatatggt attatagacc ttatagtagg tattgtagtt atagcattaa ctttatttt 112140

atggaaggta tttattaatc aacataagaa ggtaaatgat atggatagag atgatgatta 112200

tagtttacta tttgaagatt gtgaagattt atcaggcata ggtttgtttt atgtaatagt 112260

tacatcatta atatcactat ttgcatttat atacttaatc tatggaatac ctatggatat 112320

tataaagata ttaaaccctg aagtatttgc agtaaaagac ttaatagaac aagctaaagg 112380

aggaaattaa tatgaaacaa agagatttcg aatttgaaga ggattttgta ttaacttatg 112440

aatgtgagga ttgcaaacat ttcgaggatt ggggtcatga tgaagagcct gaagaatgca 112500

gtgaatgtgg tagtagtgac ttaattaaca atacaagtca tgaagacact gagtgtgata 112560

tgtgtaaagg atacattgat atgtggcaag atggttatag atacatggga gataataaag 112620

cataccttga aaaagaagat tcaggtttaa tttgtgaaga ttgctatgag aaattagata 112680

tttaataagg aggaatttat atgaataaag cagtagaaca agcaagtaac gcagtaggtc 112740

aaggattttc agccatggta tggcatcaag tattagtagg tctagggttt attttattag 112800

ggttgatatt atccttacta gtttgggtac tagtgaaaaa atttcatgta ccttttaatc 112860

acccaacagc ttttgttgta tattcaatta tgttagttag tattgttgct agttttattt 112920

ggggcggttt acatgtaatt aaccccgagt attacgctat cttagaactt aaaggtttta 112980

taaagtagga ggaattctat gactaaagaa gagttagagc aaagagtaaa agaacttgaa 113040

gcagagaata aagaacttaa aaaacaaata gaacgttttg aagacgaggg aggaaaaaca 113100

aaagatgaat agtagacaaa agaaaatttt aacattaaca gtaagtaact ttttaattct 113160

agccttagat actgtagcac taattagata taaaaaaggt aaaattaaac aagagaatta 113220

taacacaggg caaattacaa gaatgatagc tacaacagct aactcattag gtattcttta 113280

cttagaagag caagagcgta aagaagttaa agatattaaa gtaggtactt ttgaaattgg 113340

agccttaaaa agatttacaa ataataaata aaaaaagttt aagaaaccta ttgacattag 113400

gtttctttta ttatatacta atattataag aaataaggag gttaacttat gaaaggtatt 113460

atcatatttt acaaggaaga gaccaaagag gatttaggat attttcttgg gtttataaac 113520

tttaagctag aaggattatc ttacacaact gaaggtactt tagtagataa tgatgtagta 113580

gttttaaagg ataaccaaat taatgaggat aatttagagc agtttagtat gtcaaacaat 113640

aatttagtta ttggaatact aggtcattca tctctttcag tacgcatcta tgaaaaaggt 113700

attagacaag agtttgatag agtagaagaa tatttagagg agttgagaca ataatgatat 113760

ttatattaat ttttggttta ctatttattt tatctttact aggtattttt atttattcta 113820

tagttttacg aaagaaaaaa caattaatag aagaaagaga atcatttggt atttataata 113880

gaacaaaaga aaaactgggt gatgtaacac gtttagggta tgaggaagat gtatataagt 113940

taatccataa ccaatctaat aaaacaatca tagaggataa aaagagtaaa gttgtagata 114000

caattaaaaa gatgtatgaa ttagaattaa catctgtaga tgtttctaag gtagaaggat 114060

tatctccact tgatacagaa cctatgacaa atatgaaatt actttcatat aagctagata 114120

gagaaggatt atatagttta agtaaattta tttaggagtg atacaatgga atttatagat 114180

aaaaataatg taattaaagc ttatgatata ccaaatgttt atttaaaagg ttatgtatta 114240

caggcatgtg ataaaaatgg agatacaaca gcttatgatg gttatgacca aatacactat 114300

aaagaaggta gagtattaac attccctttt gataaaccat taagaaagat aaatgtacta 114360

tcaggatatt acaaactatt taaaaaggag gacataatat gatttatttt gttagtgatt 114420

tacatttcgg tcatgataat attagagaat tcgaagcacc tacaagaagt cactggaact 114480

cagtagaaga aatgaatgaa ggtttaattg agttgtggaa taatacaatt acaaataacg 114540

atattgttta taacattgga gacttctttt tcaatatgaa accttctaaa gtagaagata 114600

tacttaatag actaaattat aaagagatga tactgattgc aggtaaccat gaccataaga 114660

aacttataaa actatatgaa cgtaatggta ttacagtaaa gtacgcagac atgattaaaa 114720

aggatggtaa gagattttat ctaagccatt atcctacact aataggtaga aaaaacatgt 114780

ttaatattca tggtcatata cactcacaat taatgggtac tgaatatcac atcaatgtag 114840

gttatgatgt agagggtaaa attgcctata gttttgatga tattataagt agagcaggtg 114900

aatataatgg agaaattcaa aggtaaagat ttatataaaa ctagaattag aaaacaaaca 114960

attaaaaatt tagttataaa aacagagaag ctacataata aacacggaaa gtatagacct 115020

attggtcatg tttattatta tccaaaaaca aaagagttta ctttatctaa acctgagcag 115080

aaaatattta tagagtatat gaaggcatta ggttttagtg ttaaacataa gagacgtaag 115140

aaaataatta tagtatacaa gaatgtgtta gatgaatatc ttagtatgta tcaggaagca 115200

attgaaagta cgtgttgaca attaaggtat actatgctat agtatagaaa aggaggttaa 115260

ctgatgaagc attttatttt gattttaggt attgtaattc tagttattgc attaggtatt 115320

gttttacctg catggatttt acaattagta ttatctgcat tcggtgttaa agtaagtatt 115380

tgggtatgta tcgggatatt tattttaatc agtgcagtag gaagtatgtt tagtagaaat 115440

taaaggagga actataaatg gcaaaatatg aatcaaatat caatggagaa aattatattg 115500

caacaccgtc acaagcttta agagaggcat tggcagaatt aattagagaa gaaaagaatt 115560

ttgcagagta tcaaactaag ggtgaggaac agtatgaatc acagttacaa ctaagacact 115620

ttgattcaat gatttctcag tatgaagagg ctattcgagt actagaggat agatattcac 115680

ctcagatttt tattccaaaa gataataagg aggaaaagta attatgaaag cagaatcaat 115740

agcaagattt tttcaggata aggtattaca aatagaaggg tataaagtaa gattcactca 115800

agctagttca tcatatattt tagatataga tactatggat gaatcagtat tgtttttaga 115860

tactgtagtt ttcactctat caggcaagta cttattagat acgcacatta caattaataa 115920

acctgagaca ctaagttcta atgaattata cacagagatt agtaataaac tacaagagat 115980

tgtaggagac caaactaaaa cagatataga gttatcaaaa tactttaagg aggtaaaata 116040

aatgagttca gaagctatta caaatcattt attaaattta aatcaaataa aaattaaaga 116100

atataatatt catgcttaca ttaaaaaatc tgtttgttcc ggtattgaaa atgcagattt 116160

tgaagtaaga ataaactata tagcagacaa agaccctaac tatattagaa ctattaattc 116220

tattattttt gttgattaca gtaaccgtaa tccaaaagaa attttactac agtttaaaga 116280

aaaaattctt tctattgtaa aagaacaggt agagattgat aatgatttta ttgaggctat 116340

taaagatatt aatacaaatc atgaactaga gaaattagaa ccttttatta ataaagaata 116400

ctattctatg tttaagtcat ctattgaaaa agaggtacca gtagctttat catctgaagt 116460

acttaataga tgtacaggta aaacaagcac actagcttat ttagctattg aaaaggattt 116520

acctttaatt gtgtctaaca attctatgat gaaaatgctt aaaaaagatt acccttctgt 116580

taaagtttcg tctgttgaag atttctcaaa ctataatatt aaaggtgaaa ttgtacttat 116640

agatgaagta gatgtagacc agttatatag tgcagataga gtttctgttg atgcactact 116700

agtaggtatc ataaaaaatt aaataaattt gtaaatacct gttgacagca ggtatttttt 116760

atagtatact ttagatgtaa agaaaaagga ggtagtaata tggttggtat tataatttta 116820

attgtcggtt taatattatt tttagctagt ggatataaat tagttttagg taaatattat 116880

gatgacatag atttaaagat gttatttaca atctttggta ttggtgctat actattactt 116940

acaggattta tattataaag gaggaaatta caaatgaact ataaagaagt actagaagtt 117000

attaaaaaga ataagccatg taaggttaga tttactggaa gtattttagc aatcgttaat 117060

aaggaattta atgcagatac tgataaaggt atactacaaa ttgatgtatc aaatattaat 117120

aaaaatgact acattaagtt acaacagtat tgtttagaaa gagatgatta tactgtagca 117180

ggagctattt tattttaagg aggagtaatt atgaattata gagattttat tacggattgt 117240

attagttgtg gttataaagt ccacattagt gttactgaga aaagagttca cattatttca 117300

gaaatgacat cagcatctta tccaaagaaa gaaattaatt tggatgaatt acaagcttat 117360

gtttattata tgaataattt tggaagtcag attacaacgg agggattata aatggaatta 117420

gttattaata ttatagcagt attaattggt atgtatggta tttactttta tgttacaaaa 117480

tttagtactg gtctatcagg tatcttaatt gtactaggta tggctgtagg tctttacttt 117540

tacttagatt acttaaatgt tagagagaat gttattcgat tagtatctgt aatgtttggt 117600

gctttcttat ttagtatcga gatgatttat aataagatta tgtttgaaat taaaaaatct 117660

aagtatgata agactgttag aacgtacaga ggagaccaat aagaatttta ctataaagag 117720

tacttaaaat aggttaagtg ccctatatgg taccttaaaa tggcttagaa ttgaaattaa 117780

ggagatgaaa agttattata gctactaaat atattgtatc tattgaacga tggtaaataa 117840

ggaggagtag ttatgaatgc taggaaagca cgtaagaaca ctaaaaatca taaagactct 117900

agtgtagtaa ctaaggagca acacctaact tatatctata ataagataaa ctacttgatt 117960

gcaaatagta gtagtcaggg taagacatat gtggtaatga acctaagaac aggttatcct 118020

gacgagttct ctttatctaa attaaaatat ctaaaagaaa ttaaacagca ctataaagac 118080

ctaggattta ccgtacaaac tcaagtaaga aagtcacggt ggtcagagaa aagtataatc 118140

aggtactact ttaacttagg ttatatagat agcgtgttag ttcctattat acacattagt 118200

tggtaattac aaggaggaat agttatggat aatccaaact taaataaaaa gacactgaga 118260

gctgtaataa gagaaatgga taaagatata gaagaaagag cagaagcatt aagaagagaa 118320

gagactagat taagtattgc tagggataat agaaaaaggc tttacattga attagagtct 118380

atactagagg aggaataatt atggatttta atttgaaaga ctatgctgta agacctataa 118440

cagacaaaga aggaaatatg gtagtaagaa cagtgtatgt gtgtttaaag agagaataca 118500

gtgattgggt agtagataaa gtatatggta gacaagagag ttctgaaacg tggttaaaat 118560

ttatgcaaga aattagaaac atagagagag caaaactaag agtggagaaa tggcaagtta 118620

attagaataa ttagttaaag gagggaaaga tatgagttta tcagaattat tagagtatca 118680

taaaaatagt ggtaaggaac gagcagagta tataagtgat aatggtaatt gtagagtagc 118740

tattatgcat tatgataaat gggcagttgt aggagattta gagaatgcag tctttacaat 118800

tgagaagtaa tagttatgta cttatttgct aaaataatta ttatatctat tgatgttata 118860

cccttaatgt ctattattgt tgtacagtta attacagatt ataatgatag acattaagta 118920

tcgaatattg ttgactagta agaagaagaa aatattacta ttaagaagtt aaagttaccc 118980

gggaatattg ttgactaaca ataataagaa gaaaaaaata ttattactat taagtacctg 119040

ggaattcttt tacctctccc actcagccta ttacttacta ccgacttccc taactactta 119100

ttctatagtt atagtattca tttattatac aatacttaaa ctatagtatt ctaaccttaa 119160

tctatgctga agcggtatta atctattgtt attatataat aatcttatct aatagtggta 119220

taatctaggt tattacatta gaatgattct aatctagtat tttaatcttt agaccctagg 119280

aaaagtggta ctaaaatata gaaccctata ggtacgggat tcttattttt aaaattacta 119340

aaaagtatta ggttttccct agggtaaagt tttaatgtac ttaaaatcgt aagtagctcc 119400

ttatcattta ggtctgttta attgagaata ttagaagata tccgcttcaa ttacaattaa 119460

gtgttgacaa tcatgaagcg gtatgttata cttagtatat aaattaatag gagatgaatt 119520

aaatgattat accattaatt atactcatga tgaccttcgg tacatttgca ttcagttatg 119580

ttgcacatga tgcatacagg gtagatgaaa aaggtatcat gtatgctatg gtagttggta 119640

ttgtagttat aaatgtaatt ggtttagaaa tgataattgt agaatgttta tagaggagat 119700

gatttaatat gattgatatt tatttacaca gtgaatatga taaagataag ttaaaattta 119760

tccttaaagc aataagggat ttttctccta gagaattaac ctacgatttt aggaatccaa 119820

aagcggatgt tagtatccag gaactactag gagatgacat agacatattt gaatctatag 119880

cattagatta ccctaatgat attaatatcc ttgtaggaga tagtggatac tcgatagttt 119940

atcagaatga ttttcttaca attagtggat tgagtacggc tatgaaggag gtaataggat 120000

gataggattc acaatattaa gtacaataat ggttatctta gttatagcta tgtacactca 120060

ggtgttagta gatatgattc agtcaatcag gtatgataga tttgataagg tacttaacat 120120

agtaacgttt atagttatga cagttgtact agtatcaggt attttaatta tgtttgacat 120180

ttagagctta tttaagaagc ggttaagtag ttaaggataa attggtctag aaatatacta 120240

ccgcttctct atggctcttt aaataggctt agaattgaaa ggagatggaa taatgaaagc 120300

aattgtatat tgtgctaaaa gatatagtaa gcatacactg aagcatattt tagaggaatt 120360

agaagcggag aatagtgact taacatttag tacagaaata tcagatttag gggaagtaga 120420

tattgttgta caacatacta aattaccttt ctcagaacta atggatttgt gtagtaaagt 120480

aagtaaaggg tctgaccgct tctatgtatt tgttggtaat cactcagggt attatataaa 120540

cggtgattta tatatcaacg agataggtaa gtttattaca tctagagaaa ctaatgttat 120600

gatgtagagg aggagatatt atgatagaaa ttagattagt tgaaggctat gataaaagtc 120660

agttgaagtt tatgttaaag aaaattaaga gagtagcacc tagggaatta acttatgata 120720

tagaagcggg gatagattcg gtagatgtta atattgaaga tgtacttcct cataaatcac 120780

cccaggagta tgaaagatat tcaatgttac ttgaagaaga cttatggata gttatacttg 120840

agtcaggtta tatagcttac tgggatggaa agaagtatgg tggtgaagct ttagatgata 120900

ttatatataa tatgtttaaa gggagaggga gactataatg atagaagtat ttttaagtaa 120960

agattatgat aaggatttac tcaaagctta tttagagtat attagaaagt ccgcttcaag 121020

agagttaaag tataatacta accatactaa aggaacggat gttaatattg aaaatattat 121080

tagttatact aatcaagagg ttcatcattt tagctcttac ggtatgtata gagatgactt 121140

atgtgtattc atagataata caagagtatc tgagtatctt aatggtgaac ctgtaggggt 121200

agatacaata tataaatata taaaggagat gtaatggatg tttaaagtat attatacagt 121260

ttatcataga caaagtatga agactattaa ggataagtta gatagaagcg gtttaatcta 121320

tttcttatat gaaacttggt ataaagatat aaataatgta tgtccttcta actataaccc 121380

ggaatttggt agtcttaata aagatataga catagataga ttaattgaag cggttaatga 121440

agaagggata ctacttatta accatggtaa ttatgttaca gtagaagagt ggtaggatgt 121500

tgacaaatca taagtagtgt ggtatgatta aggtagaaat tttacgataa actcgtagga 121560

taaaaccgta ggataaaaaa ggaggataga atatgataga tattgagata aaaatttggg 121620

atgaaaccct taggatgcag gttgaagaag aggatgtact ttccttctta tctaagttta 121680

aaaataaaac aacaggtgat aaagaagaat cttatggagt agggttagat gaatctaaat 121740

ggaaagtaca cccattctat acacgttatg aggtacaccc tgaaggatac gttaggttga 121800

aggatactaa aacacctgta atatttacta agtatagaaa agaacttcac cataaaccac 121860

agtttattag ctctaatata atggatgatg aaggtaagca tacagtagct ctacataagt 121920

tagttgctga tacatttata cctattccat ggtatttaca gggatataac tatacagatt 121980

tatcagtagg cttgaaggat ggagattatg aaaataaaga agcggttaaa gcatataact 122040

tagcttggta tgtaggaagg atacgaggta atgctccaat gattaaactt atggacttag 122100

aagatgatag agtattatac tttgctagta ttcctcaaat agagaacttt attagagata 122160

ataaattaga ccctaaacgt tttaattaca aaactgaata aatgataagt agagagggct 122220

taagtagtcc tcttttattt aggttagaat aattagtaag tagctcctcg taatactaag 122280

tagttcctga ttttttgata tagttgtaag tagtcccctg gtaatccccc cagtttatcc 122340

caaccgcttc aagcagaccg caataagaat ccccaggaat tatattccca gggatttcta 122400

taatttttt atttaattaa gatatgtttc aatatattct tcataaattg cacttgctaa 122460

atcattgtac ccgtcttttt gtttttcctc cattaaccaa ttgtaatcta cacttaaact 122520

gaataaataa tctttttctt ttacatcaat taaatttctt aattcattct caaagatatt 122580

aacttgatac acatagttta ctttttttaa taggttgtgc acctctttat tcaattcttc 122640

tttagttccc tcaaatttaa attccattgt tatcaatcct tttcatttag ttgttaaggt 122700

gtttgattac cttacaaata ctattatatc agattgagga taaattgcaa taggtttttg 122760

aaacttttt aaattctttt tgtgttgact tgatcgacct ataacaacta tttagtaggc 122820

ttttttgaat atgtttttc tgtttcttcc attataaaca aaaaataggc tcataaaact 122880

ttttaaaaga atttgtaaat atgtattgac ttattaatca tatgatagta atataaaggt 122940

acagcaaggg aacagcaaca agatattaga attatataaa aaaattattt aattggagat 123000

gatttaaatg gatgtaaaag aaattgcaaa tactataatg gagttgtggc aaatggacgg 123060

ctacagatgt acagaaccac cattatatga aagcacatta aaccatacac gcacatatac 123120

ggctttaatc gtaagcatta aaggaaacta tgacactgtt caaatgttcc gcaaaacgcc 123180

tataatgagc atgagagggc aagcccaacc ggctagtatg ttagtaaatg taattgatga 123240

tgtgattata atcgtatatg aaaatgttgt ttacggggta cagaataaag aaataaaatt 123300

tattgaagaa atttaaaaat aggggttgca ataccccttа agatgtagta atataataga 123360

tgtaagggat agcaacacac cttaaaaaac tttttaaaaa gttaaaaaaa gtgttgacac 123420

cttacaagat acatgttatt attagtatag aagttaagac aagccacata gcaaataacg 123480

aaattaaata aaaaaattat agaataggat ttgattatta tgacaaacaa aaattactta 123540

tatgaagaag ctcacacagt acaagggaac gaaattacgg ctttcagaat tccaaatgac 123600

gcaaacggca acccacgtta tgtagtgcat ttcatggatt taaatattaa actagcagac 123660

tatgacaaca tcaataaact ttacggattt aataaatatc gtgctaaatg gtttggcggt 123720

ggtgtagtat tccaaagcta taatatagaa gatacattaa attttgcact agataaagtt 123780

aaagaaatag aagcggttaa gaattaaaac cgcttctgaa ttaaataaaa aatttatata 123840

aaaaggatat gataatatga aatttaaaat agaaaaaaat aacagtgata taaaaacttt 123900

atggaattta gctaaaaatg gatatatgag ttatcaaact gtacacaata tatttaaaaa 123960

tgaatcagat gaatttatta tatttaacag taaacaaact tataataaat ttatggaatt 124020

aagatataat agaagtgcaa tccaatagta taaaaaaatt atacaattcc ctgggattaa 124080

attcctaggg atttttattt gttttaattt atataaaaaa attatttaat aaataagtta 124140

gtgtaaaatt gactattgac aaggttgtat tttttatggt ataatgaagt gaagaccttt 124200

tttagtataa aaaaattatt atataaaaaa tttatattaa atggttttaa agcgggtctt 124260

tctcccaacc ttgtcattta tatagcggaa gggttaggct ggttaccgct gttttacttt 124320

ctatatatag aatactatga ataatggtaa ttgtcaacac ctttcagaaa ctttttttac 124380

tttcttttat tattatataa aaaaattata catattttag ggctccactt ccattatata 124440

ataattcggt attaatgtca atagataaat gtaaaaaagt tttttaaatt aatttcatta 124500

aatccattga cttgtgtttc tttctatagt aatatatagg tataccaaca agggaggcaa 124560

tacaaatgct aaaattcaaa tggaaaaaca aaacaattaa atcaactcaa aaaacggata 124620

acattctatt acttattata ggtggtttag ttgcaacaat cacacctaaa cttgtaaact 124680

ggtttttact actacaagat aatataaata ttttttttaag ataactattg acaacctaga 124740

aacaacatgt taatattaag ataacaaata aatcaataaa ggaaatgata aaaatgaaaa 124800

aaatcacaac aactttaaac ttaatcggca tgaaaaataa tgaaaggttt acagaagagt 124860

taaaaaacta ccgtcaagat gttactttct tgaaagcaaa taaaattgta aaatattcaa 124920

aataaggctt gacaacttaa acactacatg ttattattaa ggtacaaggt aagggaagcg 124980

gtcaaccgct tccaacctaa ataaaaaagt ttaaaaaaac tattgacagt cacttgaaac 125040

catgatatta ttaagataac aaaaaacaaa cagaaaagga attgattata atgaaattta 125100

tcaaaactat cgaaaactta ttaactaaag cagaaaacaa agggcaagca attttaaacg 125160

gtcgttatta tgacggatat agaaacggtg agcttgaaga aaaatacgca atcgaaattg 125220

agggaaacaa attagttatg cgtcactggg gaacacaaac aattgagatt gacttaggta 125280

tgaaagaaat tgtttcatac tatggagaaa gcaactcaga ccgtgacagt ttaaacacac 125340

ttgtatattg cttaggaatt gcgccaaact ttagatactt accaagcaaa gacttattta 125400

tttacgaaaa ttaattaaat aaagggcttg acttccaagc cctaccatgt tattattaaa 125460

ttgtaaggta atcaagcaca acgacaaaat aaactgaaaa ggaattgatg aaaatgttca 125520

aattacaaaa taaagtggaa attatcgtac ctaaatatac taatagtggt aaagagattt 125580

caagccctgc aattaaagaa gcggttaaca atgcaactaa aatatgtgga ggttgtacga 125640

taactgaaat caagggacaa tggtggtcag acgatgaaca acgtattatg gaagatgaca 125700

acttaaatct tgagtggtac tatgacaaag gtatgcaaga catgaacgac caacaagggt 125760

tattacaagc cttatcaaag attgctagac aattgattgt attctatgaa caagaggcaa 125820

tcagtataaa aattaatggt acactatata ttatagatta tgaagattta gatttattat 125880

cttatgactt atatgaatta atgtttaaaa attaaataaa aattttatat aaaccgcttc 125940

ggattaaatt cttgaagcgg ttttttatgt aaaatttatg cttgacaaat gtattaaaaa 126000

atgagataat agagtgacaa ctttttttag tataaaaata atattatata aaaaagttat 126060

agagttttta aggctccaag tccattatat caattttact actggttgtc aatactttct 126120

ttttttatat aataatttaa ttatcttaaa gataccgtcc acctccatta tctcaaattt 126180

tgcccccaaa gtcaagaact ttctttcaaa taatttattt aaaaaagttt ataaaaaggg 126240

ttgacttatt ttgtactata gtgtaatata taaagtgtag taaggaagcg gaggaaataa 126300

cctaaaaaaa gaatttaaaa aacttttaaa aaggtgttga caaacttcca aatacatgat 126360

aatattaaga tagttagaaa aacaaaaaac gaaaaggaat tgataattat gaacagatta 126420

gaaatagtaa aagatacggc aatggaatat atccttatga tggataacag tgttatggac 126480

ggcgttatga cacaagagga atacaacgaa gcggttagct ttgaaaaggt gtatgactat 126540

actctatcag aagcaaatca agaatgtaaa ttcttaggtg gtaaggtttt aactttccta 126600

gtacatgaag caatcgaaga atacgcataa aaaaacttaa taaaaggggt tgaatgtcaa 126660

cccctaccat gttaatatta atatatacca aatgagagga attgataatt atgagatacg 126720

aaatcgtaac attagttaat ggagaattat tcatgtttgc aacatttaag aaagcagagg 126780

cagaaaataa atatcaagaa tggtgtgact tgtacggtca agaaaatgtg agcatggaaa 126840

aaaattaaaa taagcggttg acaaactaac cgcttcatgg taatattaaa ctatactaaa 126900

gaaaaggaaa tgattacaat gacaaaaaca atcaaacaat tagaaagcca acttgaaaga 126960

ctagaaagaa aatcagatga gcaactagca aacggatatt atgaagcctt tgaaagaact 127020

tgcgcacaaa ttagagaatt agacctacaa atcgaattaa aaaagaattc agaaactgtt 127080

taaaaaaatt aaataagggg ttgacactta acccccttaga tgttattatt aatacataag 127140

gtaaaacaaa taaaggagga aaacaaaatg atgatttgga tattgatttt tatggtaatc 127200

ccttttgtac ttggattcat taacggttgg aactcagaag aagaaaatta aaaaaagtgt 127260

tgacacttta aaaaatacat gttaatataa atatatacta aagaaaagga attgataaaa 127320

atgaaattat taaacagaga caatgaaatc gtaattagca tagcaacatt agagagcgta 127380

aaacaagcct taatttggga atacatcgac cacatagata ataacatcct agacagtgaa 127440

atctatgacc aagaagcggt tgtcgttact tctaagactc tacaatcaat aaaatttgca 127500

gacactatgg aagacctgca ggaatacatt gcagatatca attggaaatt agtttaaaaa 127560

agttttaaat aactgttgac accttagcaa atagatggta atataagagt ataaagaaaa 127620

acaaaaaaac gaaaaggatt tgattataat gacaaacaca ataaaaggat ttttacaaac 127680

agaagaagca agcacagtta aggacgtagc aactcacgga gtacaaagcg gagcaattgg 127740

cagattaatc tatacatcgg acgtagtaaa attctttgat agacattatt cagatattga 127800

agcggtagta ttagacttct tagaaggctt tacaggtcaa agatactatg acctattaga 127860

ttatgacttg atgagagaac tcgaagagca tgcaaatgta gagtttgaag acgaagacga 127920

atataataat attcaatttg acttagcaga aaatattgct tctgatgaga ttgaaggatt 127980

cgaagacatg gacgaagccg agcaggcgga tgcagttatc gaagctatgg acgatgtaga 128040

attagagata ctagacacgg ataaggtgca gtttgttaac ttagcagttg agattgtagc 128100

acaacaaatg caagaagcat aagaccctgc aggaagcaca cagagacaca cagagaagct 128160

taaccgcttc tctaatataa aactattagg agatgttgaa catgacaatt aaagagatta 128220

taaaccaatt acaagcagta gaaaataagg aacttgaact attcgtatgt gacaaggaag 128280

gaaataacat ttcaattaaa gatattactt tgtttgatag tgaagcggag cacacagaaa 128340

acaacccatt agggattaac tattaggagg tttataattg aacattagag aggttcataa 128400

tgtcgttaag agtgcaaaga gcaaactcct acaggagcag aataatatta ataatgtaat 128460

gatagatgac tacatcacag aagagcttca cagacgcaca cagagaagcg gaacaataca 128520

gatgaacaat aacaccgctt catatagtaa tggctcatat ggtagcttag aagagattag 128580

agaagcttat gacctatctt cattatctac taatgagatt aaagaactgc ttgaaacatt 128640

tgtttaaatt attttatcaa aacgctttac aactatttaa tttgtatgat ataatgaact 128700

taacaaatta aaagaaaagg aaatgatgaa catgagagac ttacaagaaa gaaaaagaga 128760

attgaaaaca ttactattta acttagctat agagaagaac agagcaactg acgagacact 128820

aagaagtgta ttagaagaag cccatcaaga ggtaggaaac caactaagaa aagtaagaaa 128880

agaaattgaa attttagttg aagaaaaaga aagagaattt tggaacgatt tcgactttaa 128940

tggattagac taagagggaa taaaatccct cttttatttt tatcctatta tataattttt 129000

ttatattata cgggggcagg ggtaaaatgc cactcaatgg gggtgggtct atataccccc 129060

atggtctacc caggtactta ttttttgggg aaaattatga aaataaatat tctaaaagtc 129120

aacacccccc tattataagt caacattaca accctaccct ataagtcaac aatttataat 129180

ataaatagat agcccttaaa tataaagtca acatatctaa aataaaaaag ccaccccttt 129240

aggagtgact tagtgtttta atattttatt tcttctccta aaatgagttt gttttgataa 129300

ctacctaatc ttgtatatat cttactatta gggtctgatg aatttatact atttgtgcta 129360

ccataagcta tacaactatc taaccacata tgactacctg atgaagtttg gaaatctttg 129420

ccttggtaac tttcgaaagc ggtacatcct aaattccaag attctgtacc ttcatttaca 129480

tctgcgacat taccgccatc atttctagca taaataccgt ttactcgtat agctttaaga 129540

ccatcatgag ttgtggaacc attatttgat ttagtacctg ctgttccttt ttcgaatcca 129600

ttttctaaag ctgtacaatt aatttcaata actaaaggtt tagagctatc tgcacctata 129660

tgataattaa atccatccat atagttatta ttagctacac tattattgac gataacttct 129720

ttacctccaa caatttctaa accattacca ttgacttggg aagcatagct cagtacacag 129780

ttattaatat atacgctatt gtcttggttt aattcaaacc tagcaggtct agctccaccg 129840

tacagattta aattttcaat ataaaagtca gttggtacac tagatactat taggtgttgg 129900

gatgataata gcggtacaac ttttttgtta ggttctatgg aaccgttatt aacataaact 129960

tttgtaccat cagagtacca agaaaaaagt gtcgtatcta ctttatctaa ggaggtaaca 130020

tttgtaaact ccctatcatt attaaaatct actacccttc taacggcgga acgtgtaaat 130080

tcataagtgc tatctctacc tgatgtttta gtccaagttg gctcatctgc cataaataag 130140

tttacatttg agcccaaacc aataatatta atactcttat tacttattgg tggaagcaat 130200

gtgcctccta ctctaaagta atccccgtca ctaacataaa gtgtatcccc attatttatt 130260

atgccttgag ctttttaaa tgttttaaag ggggttgatt gagaaagacc gtcattagta 130320

tcattaccat tttctccatc aacatagtaa gatttacctc ccctaagttt aaagttctcc 130380

atatttaaag aagtggaaaa cttacctaaa ccatctgtaa aaatattatt gacaagcggg 130440

tggtctttaa ttaagtaatc tacaggagtg aaaacaggta ttttatacga tgtttctttt 130500

ttcatagaaa ttttcatatt atcaatttct ttgattaatc ctttaatgaa ttcctcatta 130560

ttaactgttt gtattttctt agtagaagaa ccatcaaaaa gtagaaactg ttttatattt 130620

acaggtgaag taacttgtct tgtatctatt cttaaactaa ttttgcttga attttccggg 130680

atatttatat tattaattgc aaatgtcgtg tcatttattt tattaagttg agtaattgtt 130740

tgtatatatg aaccatcaga atcttgtatt gaatactcaa atgatgcttt cgggtcaggt 130800

acgtcatctg ttattatttt agcactaaat gttttacctg gtgcaagttt ttcaacagct 130860

ttaactgtgt aaaataacca accatttgaa ttaagtgtaa aagaaccatc ggggttcatg 130920

gtattttccg gtatactgtt tctaattgta atattagaga aatatgtttt atctactgtt 130980

gatgggtata aacgaatgtc ttctccatta tcagggtaca ctattaaact atcttccatt 131040

gttttattta cttcttgtaa attagagtca ctaggattaa caaaaactct caatgaatct 131100

aattgttctt cggtaaatct atcaaaagta aagtctttac ctggttcccc tgttttacct 131160

ggctctcctg gttttcctgg ctctcctggt tttcctggct ctcctggttc acctttaatg 131220

gacttaaccc attcttcttc tgtacctgta aaaccattat ctactgctat atcataagct 131280

gttttaggtt taacagttaa gatgtcttta gcataaaaag taatttcttt gtaagaagat 131340

tctaatgtag taaattcagg aactacagtt ttttccgact catagttatc cccttcccaa 131400

gaaacataaa actccccttg agggtactta gtatgaggtt ttaaatttgg tataataact 131460

gaaccttgct cagtatatac attataacct atggctagta tattgccttc tttatcataa 131520

gcttttaaat gtggcattta taaatctcct attctaatgt gttagtacat ataatatatc 131580

aaattgaata aaagaagagt attagttacc cttctttatg tttatatcgc agtctacgat 131640

attaagttca tgaatagtaa tcatatccat tccatcgaat cctcttgggt ctcctttaat 131700

gaactcttgt tctcctctat aattagtctc ttccctatac ccttcttctt taatacgttt 131760

aattaatttt tccttatttg tatatacatt gtcttctcta aaatgaaaat tatcttcata 131820

aggttcacaa ttatcatgtt ctacttgata tagtttcatt catttgtcct cctttactct 131880

ctataataat catatatttc taagtaaggt gaaaatggtg aatcacctct agtattaata 131940

ataacttcac cttcatgttt acttatctct gtaagctctt ctagactatt aatttctaca 132000

caccatcgtt ctagtgtaaa tggattacct ttttggtcta caagttctag tttctttata 132060

taggcaccct ctataggctt tttattaatg gtgcttgtcc tatctataaa aaattccatt 132120

agttttcctc cttttcataa gaccattcac catattctgc gttaaaatgg gctgtatccg 132180

taccctcgtc ttcatattct acactatacc atgcatcctc ttctgtttct gcatctatat 132240

atcttacttc ctctgtagta ataatacgtt ttactttaaa tctctccata ttagttttcc 132300

tccttatatt ctttataact tttaataaca atcttacaga tacctctatt aacagctaaa 132360

aacaataaaa atgataacag agttataact gctctagtat ctcctgtgaa aggtaatact 132420

ttaaatagta aaacactttc taaaacactt gtagctgtga tagttgttag gtataagata 132480

gttagtaaat aatcttttaa ttttagctta acaaaaggtt ttttattatc ttgagttctt 132540

actataccat atagaattat aaaccattct acagttacga gcatagttat aaagtaatta 132600

tttatgtcta atgcatataa accataaatg atacctgcag gaataccaat aatgaatgct 132660

aaaaatacag agagtataat tagcattata agaagagcta caaggaatcc taagccttgt 132720

tttgagtact ctagtgtatt ctttcctatg gctttaaaga atgttttatt catctgctac 132780

ctccttgtaa tatacagtat ctatatggat aatattgtct ttgaaccata tagatgtatc 132840

acctttgtta gattctaaaa atttaacacc attaaaaaca agacccccga taaaagaatt 132900

taaattagtt ttagtatctt tttgctttat aatagtagaa gtccctgata catcatgaat 132960

ccttataaaa ttaatatctt tttttacttc ctcttcttta tgtttttaa atatcattat 133020

tcttcctcct ttatattctc ttctaatatt tgttttaacg tctgacaatc tttttggtct 133080

aaagtattcc aactttctag attttgtaat tgatagtgaa attcatttac aatttcatcg 133140

aaggcttctg ctttttggta gacttcttgt aactcttcta attctttttc attatcaata 133200

caccagtagt tctcgttgtc agttataata tcttgaattt tatttttata ttcataagcc 133260

attatttatc cctcctcttc tatagaatta ctttccgtaa tagttacctc tagcatgtta 133320

ttgtaatact cattcttttg attgatattg tagtagtcat tatattcatt aaagtctaca 133380

taagtgtatt catttgtatc atcatcataa ataatatcta tagctgtaat atctgagtat 133440

gctgtaatca tttcataagc atttgtatta tccggataag caaaaccaac ttgagatatt 133500

tctttagggt tatcaataag aataccaaaa taagtacatc tacgtgttcg acttatatgt 133560

gaagtaccat agtaatctat accttctgta attccatcta catggaacct ttttacatct 133620

ttaggttcta gtcttacaac atcacaattt tctaatacta aatcaatata ttttatattc 133680

attttaattc tcctctttat ttaaacctat tatatacgca atggactcta acatcttcca 133740

ttactttacc taatagattc tgacctttcc agttgctttc atctaatatc ttagggtcat 133800

ttgctttaat acctacaccc catattttat catagggtga tgcttctacg aaatctttac 133860

gtaaatctgt atctagtatt ttttgtttta agtgtgtagt cataaattta tctttaacca 133920

cttctaccat aatgtcatat ctcaccttat tccattgctc ttcattaaaa ttacgaactt 133980

tacgacctag acttttagca tggttcggat gcttagcatt taatatttct cctgctattt 134040

gccagtcttt aaaatattga gctttacgcc acataaaggc ttgttctgag ttattaaatg 134100

ttcttccttt gtgtttaaat gttattgggt aaaagttaga atagatatct tccttacccc 134160

aaaacataat gtattcttta gtctctttca tattatctct cctttaattc cataatgatg 134220

gtaatacgat tttaaagtta tctagaattt tgttttgtac ctgttcaatc tcgtcctcat 134280

tatcaacatc aaagctatcc attgattcgt ggtagaattg aattaaactt aatatatgct 134340

ttatcatatc tatctgtgtt ctttcttttc cttctatatc agtaaatgta tggtactcca 134400

tatccacatg attactactt tctacaaaag catttaaatc agcatatagt tgaataaaga 134460

aggacatatc atagttccaa tatttaggtt catttctacc taattcttta ttcatttttt 134520

tgtatttttt attctttttt aatccaaaaa cttctttttc aaagtcattt aatttaagtc 134580

ctttaaaata tcttttcttc atgagtttcc ctccaattta ataaaaggta aatctatatc 134640

cctgaataca gcacctacat cacacattaa catgtctcca ttaatttcta cttctccact 134700

gtcagttggt gtatgaccac atacataggt aaaaccatct tttctaggtt gaaagtctct 134760

tgaccatatt aattggtcaa ttgtttgttc ttctacaggc ttccaactaa ccccgcctga 134820

atgagagaat atatacttgt cttctttata gtactttcta caattaacca taagtatttt 134880

aaattttcta tagtcgtctg attctttaag tttctttagt tcacttttaa taaaatcata 134940

attacttctt aggttttctt ctacactact atactttaaa gttaccgtac tcacaccgta 135000

agagttaagt gtttctatac aatatcttga gagccattca atatcataga tacttaatcg 135060

gtctacgttt tccataacat tataaaactc atcatcatgg ttccctaaca gagttactac 135120

attatcatca ttagacatta aatcaaatat atagttaaca acgtcttttg acctttacc 135180

tctatctaca taatccccta aaaatactat tgtttcttta ggttttcttt cattgtttat 135240

tttatccata attgttaata atttttggta ttctccatga atatcgggaa caacgtatat 135300

agccatctaa tctcctcctt attgtatata actatcttac catacttagt aaaaaaagtc 135360

aataaaaaaa cacctattaa tttaataggt gtttatcatt taatgttatt ttaaagtatc 135420

attaccatgt gctaattttt tatcatctat tgcatggtca ttataaatat atttaacctc 135480

tatatactgg tcttcacttt tcagtgcatc tactatagaa gcattattag ttattgagct 135540

tgttctaggg taagtaaatt tttgaccgtc agataaaata atagtaacat caacttcaaa 135600

gttaacaggt agtctgtatc cataatcttc caaataatta ataaagttat taagagaaaa 135660

tggtttatac ttgccatcta aggtatagtc aatatattca tttaatgcat cagtaagttc 135720

tgattctgtt aactccattg tatcataatc tttttcgtta tagaatacta caacattatg 135780

ttgttctata ctagaatctc cgtctttata cttagatata aaaaatccaa tatttccttt 135840

atgctctaaa taatctgctt tcataatttt aaatacttct tctgctatag gttttgctaa 135900

tagtgttacc cattcacctt tttctgcgtc ataaacacta ggtagtacgt ttaccatcat 135960

ttaaatctcc tcttcttaat ttattggttt aaaccacaat ttactcttat cacttggttc 136020

tgtttcacta actacgaaag agttagaatc aatgtttaaa gtattaaaaa caatttcttg 136080

tttgtcttca ttacttttg ttgtaaattc gggaacatct gttaatatag actctttacc 136140

attaatagtc catgatattt taaaagaccc ttggctatac actgtattcg gtgtcagttt 136200

ttcaattata attttagcgg atgcacctgt aatttttct gaagatttta ataatttacc 136260

tttggaatca tataagttta atgttctctc cacaaatttt atctccttta ctatattttg 136320

tacaattaat ataacaaaaa aacacctatt agtttaaata ggtgtccgac agagctcccg 136380

tacttagatt acggttaata atattttacg acaactatat gagaccctct gtcgttgaaa 136440

ctcttgtcac tgcgttattc cacaagatat tttagaaggt agcttgtgga agaagattgt 136500

ttttaaaggt acaattagcg tttttaagcc tattcgatac ccaggacact atgtccgtac 136560

taactattac gtcaataaag gttctacggt ctcaattacc tactctttat tgttaaaact 136620

aaaattaagc ttgagtgctc tagaagccaa aatcaattaa ttaactatag atacggaatg 136680

gagggacact accatccgga gtctacggtc agatacaaag cctctgccgg gcaacatacg 136740

gtatctctcg tacatcaggt tgactagacc tttagagttt ttcactcctt ctcttataac 136800

cagtaactta ggagaaatag gttttactta gtagatatga aacaataaat ccacatacaa 136860

tattaaatca tagtcaagtg attgcacata tgtctaatac ctataagttt tttgctagcc 136920

tggtatatgg actctgcagg attcgaacct acagtcaaac cgttatgagc ggttggcttt 136980

acctttaagc taagagtcct agaaatatcc tgagagagga ctcgaacctc aacgactagg 137040

tagctacatc tagccaatgc cattactcag gattgctagt aacgctaaat agaattataa 137100

cgttaccgta gacctttct acgcttggta gataggtaaa atataatgat ttcaaagtac 137160

ccatatagtt aggctcttat tctcattata aggttaaaaa ggctaactgt gtttagcatt 137220

atataagagg ctttagttaa ctactatact aatagtatac cataaataat acttaatgtc 137280

aagttaattt atcaattgaa tccataattt ttgatgtact tcttatatcc gcttctttac 137340

tgtgtttaag aagatatttt 137360

<210> 561
<211> 155
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 561
Met Lys Lys Ile Tyr Ile Leu Glu Glu Glu Ile Glu Glu Met Asp Tyr
1 5 10 15

Asp Leu Trp Glu Glu Asp Thr Val Tyr Thr Thr Ser Tyr Glu Val Leu
20 25 30

Gly Tyr Thr Asp Ser Leu Glu Asp Ala Glu Tyr Ile Lys Asn Asn Tyr
35 40 45

Gly Thr Ser Asn Pro Ile Phe Ile Asn Glu Tyr Pro Tyr Leu Thr Lys
50 55 60

Asp Lys Leu Ile Glu Glu Gln Arg Tyr Tyr Arg Tyr Asn Ser Ala Ile
65 70 75 80

Glu Leu Lys Arg Val Asp Gly Tyr Phe Glu Val Tyr Glu Ile Asn Asp
85 90 95

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

Asp Cys Pro Phe Ser Ile Asp Met Phe Ser Ser Asp Arg Asn Ser Ile
115 120 125

Phe Ile Glu Phe Met Met Tyr Ser Glu Tyr Asp Asn Lys Lys Asp Thr
130 135 140

Ile Glu Lys Glu Lys Asn Ser Phe Leu Met Lys
145 150 155

<210> 562
<211> 72
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 562
Met Lys Lys Ile Ile Asn Phe Leu Val Asp Tyr Asn Ile Asn Phe Ser
1   5   10   15

Tyr Ser Glu Asp Ser Leu Asn Val Met Gly Asn Ser Tyr Leu Val Asp
            20   25   30

Lys His Gly Thr Gln Asp Tyr Glu Ile Ile Gly Asn Tyr Gly His Ile
        35   40   45

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

Lys Asn Leu Ile Gly Val Trp Glu
65   70

<210> 563
<211> 64
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 563
Met Arg Asp Lys Arg Ile His Ser Glu Leu Leu Tyr Asn Ile Ile Gly
1   5   10   15

Lys His Ile Gln Glu Glu Glu Asn Ile Thr Pro Tyr Ile Glu Ala Ile
            20   25   30

Tyr Val Asp Ile Met Asn Ile Ile Val Val Glu Tyr Thr Phe Tyr Asn
        35   40   45

Glu Asn Gly Thr Arg Met Leu Gly Gln Tyr Pro Ile Gly Glu Val Met
    50   55   60

<210> 564
<211> 245
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 564
Met Asn Leu Glu Lys Ser Phe Leu Leu Ser Thr Ile Glu Phe Gly Ser
1   5   10   15

Thr Tyr Gln Gly Thr Ser Asp Glu Tyr Ser Asp Lys Asp Tyr Met Ser
            20   25   30

Leu Val Val Gln Pro Leu Ser Asp Thr Ile Phe Arg Asn Ser Glu Lys

35 40 45

Ala Ser Lys His Thr Glu Val Ser Arg Tyr Tyr Ala Val Glu Arg Phe
50 55 60

Ile Ser Leu Val Leu Lys Ser Gly Phe Asp Asn Val Leu Asn Leu Cys
65 70 75 80

Ala Gln Leu Glu Gln Ala Lys Asn Thr Arg Phe Asn Lys Thr Val Leu
85 90 95

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

Phe Lys Pro Ile Ala Tyr Ser Val Ile Gly Asn Ile Asn Asn Ile Leu
115 120 125

Lys Lys Glu Glu Leu Ala Gly Lys Asp Leu Val Lys Phe Tyr Thr Phe
130 135 140

Tyr Asn His Leu Glu Tyr Tyr Asn Asp Leu Leu Asp Asp Leu Asp Asn
145 150 155 160

Leu Asn Val Ser Tyr Lys Asp Phe Ala Lys Val Lys Tyr Met Pro Lys
165 170 175

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

Asp Leu Val Thr Lys Val Glu Pro Leu Ile Gln Glu Val Lys Asp Lys
195 200 205

Leu Lys Ser Asn Glu Ser Asn Ile Lys His Tyr Lys Asp Ala Met Glu
210 215 220

Leu Val Glu Lys Ser Leu Lys Asp Lys Thr Val Ser Phe Leu Thr Glu
225 230 235 240

Val Tyr Asn Glu Arg
245

<210> 565
<211> 34
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 565
Met Lys Tyr Ile Leu Gly Leu Ile Thr Leu Gly Val Ile Leu Phe Lys
1 5 10 15

Ile Tyr Glu Tyr Phe Lys Tyr Ile Gln Asp Glu Val Asp Thr Thr Glu
            20   25   30

Asp Ile

<210> 566
<211> 75
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 566
Met Asp Phe Tyr Gln Phe Leu Asn His Glu Asn Val Arg Val Asn Ser
1   5   10   15

Ile Thr Pro Ser Gln Lys Asn Phe Ile Arg Glu Asn Ile Asp Tyr Thr
            20   25   30

Asn Leu Asp Thr Val Asp Ile Asp Phe Met Asn Ser Lys Gln Ala Lys
        35   40   45

Lys Glu Ile Glu Lys Ile Ile Arg Thr Lys Asn Glu Glu Glu Tyr Asp
    50   55   60

Met Ala Met Asp Ala Leu Ser Gly Trp Glu Gly
65   70   75

<210> 567
<211> 128
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 567
Met Phe Gly Lys Ala Pro Glu His Ile Met Glu Ile Ile Asp Lys Glu
1   5   10   15

Asp Asn Ile Leu Gly Glu Asp Leu Thr Leu Asn Ile Asp Tyr Lys Gly
            20   25   30

Ile Asn Leu Thr Val Lys Arg His Pro His Ser Gly His Leu Asn Gly
        35   40   45

Tyr Ile Asn Val Pro Thr Asn Ile Thr Lys Glu Gln Phe Asn Ser Ile
    50   55   60

Glu Asp Cys Ser His Gly Gly Ile Thr Tyr Asp Glu His Glu Gly Asp
65   70   75   80

Tyr Arg Val Leu Gly Phe Asp Cys Ala His Tyr Ser Asp Met Thr Pro
                85   90   95

Tyr Ala Val Ile Ser Phe Ser Asp Ser Tyr Tyr Arg Asp Leu Lys Tyr
100 105 110

Val Leu Asn Thr Leu Lys Asp Met Ala Asp Cys Leu Lys Glu Gly Glu
115 120 125

<210> 568
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 568
Met Glu Lys Val Asn His Glu Phe Leu Ala Glu Leu Ala Lys Ser Asn
1 5 10 15

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

Glu Phe Asp Tyr Asp Gly Phe His Phe Glu Phe Ser Gln Lys Asn Gly
35 40 45

Tyr Trp Gln Trp Lys Tyr Asn Ala Lys
50 55

<210> 569
<211> 160
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 569
Met Ala Asn Glu Lys Glu Leu Ile Arg Met Val Asn Tyr Leu Ile Asp
1 5 10 15

Asn Met Ser Met Trp His Ile Asn Tyr Ala Arg Ala Val Leu Ile Pro
20 25 30

Ser Glu Val Glu Lys Ile Ile Lys Glu His Glu Lys Phe Asp Asp Leu
35 40 45

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

Ile Asp Asp Leu Glu Thr Tyr Asn Gln Ile Met Asn Asn Gln Lys Asp
65 70 75 80

Glu Met Met Ile Gln Glu Ile Asp Ile Tyr Thr Gln Gly Lys Thr Ile
85 90 95

```
Lys Val Asp Asn Lys His Tyr Ser Ser Asn Glu Leu Asn Glu Val Ile
            100                 105                 110

Asn Lys Ile Glu Gln Ser Glu Asp Ile Lys Ile Lys Ser Asn Tyr Lys
        115                 120                 125

Leu Leu Cys Ile Asp Tyr Thr Lys Val Ile Gly Tyr Glu Val Thr Tyr
    130                 135                 140

Ala Ser Ser Tyr Glu Glu Lys Phe Lys Asn Asp Leu Glu Lys Asp Leu
145                 150                 155                 160
```

<210> 570
<211> 180
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 570

```
Met Asp Arg Ile Ile Gly Lys His Asn Leu Thr Gln Asp Leu Arg Leu
1               5                   10                  15

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

Asp Gly Thr Ile Glu Leu Gly Asp Lys Val Thr Glu Gly Ile Val Val
        35                  40                  45

Asp Tyr Lys Gly Asp Phe Thr Gly Asn Thr Ser Gly Leu Val Thr Leu
    50                  55                  60

Asp Ser Ser Glu Glu Glu Leu Ile Ile Gly Glu His Asn Phe Lys Leu
65                  70                  75                  80

Ile Glu Glu Gly Asn Leu Gln Ala Val Tyr Asp Ser Val Ser Lys Asn
                85                  90                  95

Lys Val Glu Ser Leu Ser Glu Asp Tyr Asp Met Tyr Arg Lys Leu Leu
            100                 105                 110

Gly Val Lys Ser Gly Glu Leu Glu Asp Ile Ser Tyr Glu Leu Glu Arg
        115                 120                 125

Leu Ile Met Glu Tyr Asn Lys Lys Val Asp Asn Tyr Asn Gly Leu Leu
    130                 135                 140

Thr Leu Ser Lys Glu Lys Ala Arg Glu Leu Ser Leu Leu Thr Gly Asp
145                 150                 155                 160

Arg Lys Met Ile Pro His Met Lys Asn Lys Arg Leu Glu Leu Gly Thr
                165                 170                 175
```

Glu Ala Asp Phe
            180

<210> 571
<211> 177
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 571
Met Val Tyr Asp Ser Ile Ile Ser Arg Thr Met Ala Val Ser Ile Leu
1   5   10   15

Asn Lys Trp Ile Ala Glu Leu Ile Thr Asp Val Asp Leu Asp Lys Cys
            20   25   30

Lys Phe Thr Glu Glu Glu Tyr Gly Lys Val Val Thr Asn Ser Ile Asn
        35   40   45

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

Glu Leu Tyr Asp Ile Val Cys Thr Glu Leu Ile Asn Pro Ile Lys Asn
65   70   75   80

Asn Thr Glu Glu Glu Lys His Asn Glu Lys Asn Asp Leu Leu Glu His
                85   90   95

Leu Glu Asp Leu Ala Phe Arg His Asp Ile Asp Leu Gly Tyr Val Ser
            100   105   110

Asp Gly Ser Tyr Asn Leu Thr Val Thr His Trp Leu Met Gln Asp Glu
        115   120   125

Phe Thr Asp Val Asn Ile Lys Val Asn Lys Asp Glu Asp Phe Tyr Thr
    130   135   140

Ile Thr Ile Pro Glu Ser Lys Tyr Phe Trp Leu Pro Ile Thr Lys Glu
145   150   155   160

Asn Leu Glu Met Phe Leu Thr Gln Asp Pro Ile Asn Lys Gly Glu Ile
                165   170   175

Glu

<210> 572
<211> 54
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F44/10

<400> 572
Met Lys Asn Leu Ile Lys Phe Leu Ser Met Val Val Val Thr Ile Leu
1   5   10   15

Thr Phe Ser Leu Thr Tyr Val Ile Leu Lys Lys Glu Thr Asn Asn Lys
            20   25   30

Arg Asn Gly Val Ala Pro Phe Asp Phe Ser Leu Glu Asp His Ile His
        35   40   45

Leu Asn Lys Glu Ile Lys
    50

<210> 573
<211> 92
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 573
Met Val Asn Asn Ile Trp Ala Val Val Leu Ser Ile Ile Ile Leu Leu
1   5   10   15

Ile Ile Leu Leu Ile Leu Trp Phe Leu Phe Arg Lys Lys Val Asn Gly
            20   25   30

Gly Ser Ser Lys Asn Val Glu Ile Gln Lys Ala Glu Glu Gly Asn Asp
        35   40   45

Asn Lys Glu Gln Glu Val Glu Glu Ala Gln Tyr Arg Glu Leu Asn Glu
    50   55   60

Glu Glu Lys Glu Lys Asn Glu Asn Ser Ser Lys Asp Tyr Lys Tyr Asp
65   70   75   80

Lys Glu Lys Val Lys Asn Lys Leu Lys Glu Leu Glu
                85   90

<210> 574
<211> 281
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 574
Met Gly Arg Arg Leu Ile Asp Asn Ser Glu Leu Asn Val Ile Lys Tyr
1   5   10   15

Asp Gly Leu Pro Asp Phe Phe Ser Ala Leu Lys Lys Asn Arg Val Ser
            20   25   30

```
Gly Arg Glu Asn Ser Ser Asp Thr Gly Ser Tyr Asp Phe Thr Gly Thr
        35                  40                  45

His Ser Phe Gln Glu Ala Tyr Asn Leu Met Val Lys Gly Asp Arg Glu
    50                  55                  60

Ser Tyr Asp Met Val Val Lys Leu Lys Lys Met Thr Asp Ala Leu Phe
65                  70                  75                  80

Arg Met Asp Lys Ser Val Lys Arg Lys Pro Val Val Ala Pro Glu Gly
                85                  90                  95

Tyr Gln Pro His Val Pro Asn Ala Ile Lys Gly Leu Pro Asn Ser Met
            100                 105                 110

Met Ser Gln Gln Arg Val Lys Ala Glu Lys Lys Val Ile Asp Val Phe
        115                 120                 125

Tyr Asn Ser Ser Ile Ser Trp Met Glu Asp Pro Glu Asn Leu Ala Tyr
    130                 135                 140

Arg Gly Ala Ile Met Leu Ser Ala Ile Gln Thr Leu Glu Thr Lys Gly
145                 150                 155                 160

Tyr Ser Ile Asn Leu Tyr Leu Gly Lys Leu Ser Asn Ser Glu Tyr Glu
                165                 170                 175

Asn Lys Leu Thr Gly Phe Val Val Asn Ile Lys His Ser Tyr Gln Arg
            180                 185                 190

Leu Asn Val Phe Lys Ser Ser Phe Tyr Leu Val Asn Pro Ser Phe Leu
        195                 200                 205

Arg Arg Ile Ser Phe Arg Val Leu Glu Val Glu Pro Asp Met Val Asp
    210                 215                 220

Leu Thr Asn His Gly Tyr Gly Ser Val Val Ser Lys Ser Ser Tyr Gly
225                 230                 235                 240

Asn Lys Leu Thr Glu His Ile Leu Asp Asn Ala Val Ile Phe Asp Ser
                245                 250                 255

Ser Ile Gly Ile Asp Ile Asn Asn Asp Ser Ser Glu Asn Leu Arg Ala
            260                 265                 270

Val Lys Lys Leu Phe Gly Gly Arg Leu
        275                 280
```

<210> 575
<211> 372
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 575
Met Ala Lys Gln Asp Thr Ile Glu Arg Leu Glu Arg Leu Val Glu Gln
1   5   10   15

Gln Met Glu Thr Thr Ala Asp Leu Ala Lys Lys Leu Gly Glu Lys Asn
            20   25   30

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

Gly Thr Glu Ser Arg Glu Ile Ile Ile Thr Asp Val Lys Lys Gln Ile
    50   55   60

Glu Glu Tyr Val Glu Glu Gln Leu Ser Asn Leu Pro Val Lys Ile Glu
65   70   75   80

Leu Gln Gln Glu Gly Lys Thr Ile Lys Asp Ile Ser Gly Ile Phe His
                85   90   95

Tyr Arg Tyr Gln Asp Ile Leu Lys Leu Val Asn Gln Asn Ile Pro Val
            100   105   110

Phe Leu Lys Gly Gly Ala Gly Ser Gly Lys Asn His Val Leu Glu Gln
        115   120   125

Val Ala Glu Ala Leu Asp Leu Asp Phe Tyr Phe Ser Asn Ala Ile Thr
    130   135   140

Gln Glu Phe Lys Leu Thr Gly Phe Ile Asp Ala Asn Gly Lys Phe His
145   150   155   160

Glu Thr Gln Phe Tyr Lys Ala Phe Thr Lys Gly Gly Leu Phe Phe Leu
                165   170   175

Asp Glu Met Asp Ala Ser Ile Pro Glu Val Leu Leu Ile Leu Asn Ser
            180   185   190

Ala Ile Ala Asn Lys Tyr Phe Asp Phe Pro Ile Gly Arg Val Thr Ala
        195   200   205

His Glu Asp Phe Arg Val Val Ser Ala Gly Asn Thr Met Gly Thr Gly
    210   215   220

Ala Asp His Ile Tyr Val Gly Arg Gln Gln Leu Asp Gly Ala Thr Leu
225   230   235   240

Asp Arg Phe Ala Gln Val Glu Phe Asp Tyr Asp Thr Lys Val Glu His
                245   250   255

Gln Leu Ser Ser Asn Glu Asp Leu Val Asn Phe Val Gln Gln Leu Arg
260 265 270

His Glu Asn Asp Glu Lys Gly Leu Pro Tyr Val Phe Ser Met Arg Ala
275 280 285

Ile Ile Asn Gly Ser Lys Leu Asp Gly Val Met Glu Asp Glu Phe Val
290 295 300

Val Glu Ser Ile Ile Phe Lys Ser Val Pro Lys Asp Glu Ile Asn Gln
305 310 315 320

Phe Ile Ser Ser Leu Pro Glu Gly Asn Arg Tyr Thr Glu Ala Thr Arg
325 330 335

Lys Leu Leu Gly Met Gln Gln Glu Pro Lys Gln Glu Pro Arg Lys Ser
340 345 350

Asn Ser Thr Ser Lys Asp Ser Met Asp Phe Asp Thr Ile Met Asp Lys
355 360 365

Leu Gly Leu Glu
370

<210> 576
<211> 108
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 576
Val Ser Lys Arg Thr Asp Asn Phe Ile Tyr Phe Cys Lys Tyr Tyr Phe
1 5 10 15

Ser Glu Tyr Leu Pro Ser Leu Gly Val Glu Val Leu Asn His Asn Glu
20 25 30

Thr Ser His Gly Thr Met Glu Gly Val Arg Lys Tyr Tyr Ile Ala Asn
35 40 45

Ile Leu Tyr Glu Gly Gln Glu Leu Thr Val Thr Ile Asp Leu Glu Glu
50 55 60

Phe Asn Asn Ala Thr Ser Met His Asn Met Leu Glu Ile Met Asn Ser
65 70 75 80

His Thr Tyr Asn Cys Met Phe Met Tyr Asp Met Asp Thr His Gly Thr
85 90 95

Lys Asp Ile Asp Asp Phe Phe Lys Leu Met Tyr Phe

100 105

<210> 577
<211> 138
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 577
Met Asn Ala Lys Glu Phe Met Lys Thr Gln Ala Gln Val Glu Asp Tyr
1 5 10 15

Leu Asp Lys Leu Lys Val Thr Ile Ile Glu Asp Ala Leu Ser Val Ser
20 25 30

Lys Glu Trp Ser Asn Asp Ser Asn Asp Leu Gly Tyr Ala Leu Ser Ser
35 40 45

Leu Gly Glu Ser Ile Gly Leu Leu Glu Asp Tyr Tyr Asn Ile Gln Val
50 55 60

Asp Ala His Leu Pro Glu His Tyr Lys Gly Ser Lys Asp Val Ile Ser
65 70 75 80

Phe Leu Glu Glu His Phe Ser Tyr Asp Gly Phe Val Asp Ser Met Ile
85 90 95

Phe Asn Ile Val Lys Tyr Thr Thr Arg Leu Gly Arg Lys Asp Ala Val
100 105 110

Asp Lys Glu Val Gln Lys Ile Lys Thr Tyr Tyr Val Arg Leu Glu Arg
115 120 125

Asn Ile Lys Tyr Gly Asp Ser Thr Arg Val
130 135

<210> 578
<211> 100
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 578
Met Glu Lys Val Glu Leu Ile Lys Gln Trp Ala Lys Asp Arg Asn Leu
1 5 10 15

Gln Thr Gly Lys Pro Glu Gly Gln Met Leu Lys Leu Leu Glu Glu Ala
20 25 30

Gly Glu Leu Ala Ser Gly Ile Ala Lys Ser Asn Asp His Val Thr Arg
35 40 45

Asp Ser Val Gly Asp Ile Phe Val Val Leu Thr Val Leu Cys Leu Gln
    50   55   60

Leu Asp Ile Asp Ile Glu Glu Cys Ile Asp Met Ala Tyr Asp Glu Ile
65   70   75   80

Lys Glu Arg Lys Gly Lys Leu Ile Asn Gly Val Phe Val Lys Glu Glu
                85   90   95

Asp Leu Lys Lys
            100

<210> 579
<211> 62
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 579
Met Glu Lys Phe Gln Glu Asp Tyr Val Asn Ile Asp Ile Arg Val Lys
1   5   10   15

Ala Tyr Val Arg Val Gly Tyr Arg Tyr Glu Glu Asp Ile Thr Asn Asn
            20   25   30

Leu His Glu Leu Val Glu Asp Asn Leu Asn Val Thr Ser Asp Ser Asp
        35   40   45

Asn Leu Ile Ile Lys Asp Thr Glu Ile Lys Gly Asp Ile Glu
    50   55   60

<210> 580
<211> 53
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 580
Met Val Lys Pro Val Ile Thr Leu Glu Pro Glu Asp Val Lys Val Leu
1   5   10   15

Leu Asp Tyr Leu Ser Phe Leu Glu Asp Asp Met Arg Asn Tyr Glu Gly
            20   25   30

Met Arg Glu Leu Tyr Glu Glu Leu His Lys Lys Tyr Gln Leu Ala Lys
        35   40   45

Gly Asn Tyr Ser Asp
    50

<210> 581

<211> 682
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 581
Met Ala Ile Thr Tyr Lys Gln Lys Gly Leu Thr Glu Gln Glu Ile Ile
1 5 10 15

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

Val Phe Leu Lys Lys Lys Lys Asn Asn Ile Ile Asn Leu Gly Ser Lys
35 40 45

Glu Leu Phe Arg Asp Ile His Asn Ile Phe Ser Phe Asp Thr Ala Thr
50 55 60

Glu Ile His Leu Phe Leu Ala Leu Cys Gly Asn Lys Glu Val Thr Asn
65 70 75 80

Phe Glu Gly Asp Pro Tyr Glu Thr Val Glu Lys Leu Val Glu Gly Val
85 90 95

Ile Gly Asn Asn Lys Gly Arg Asn Tyr Lys Glu Tyr Ile Glu Ala Asp
100 105 110

Arg Gly Glu Arg Lys Asp Phe Pro Leu Tyr Gly Ser Arg Arg Arg Lys
115 120 125

Gln Ile Gln Ser Lys Gly Tyr Val Glu Glu Lys Ile Lys Glu Leu Glu
130 135 140

Asn Glu Asn Arg Leu Trp Gly Tyr Glu Ala Arg Gln Leu Asp Glu Tyr
145 150 155 160

Lys Glu Ala Val Asp Ser Leu Asn Asn Asp Ile Met Asp Val Leu Asp
165 170 175

Gln Gly Lys Tyr Val Leu Ile Asn Ser Ser Ile Ile Val Met Asn Glu
180 185 190

Asp Ile Glu Lys Gly Ser Ser Glu Tyr Tyr Lys Glu Met Ser Asp Ser
195 200 205

Leu Tyr Ser Arg Val Trp Tyr Met His Pro Ser Thr Glu Asn Asn Ser
210 215 220

Ser Phe Gly Leu Lys Val Arg His Ile Arg Asp Lys His Asn Met Gly
225 230 235 240

```
Asn Lys Trp Val Leu Glu Asn Lys Ser Ser Phe Asp Val Lys Thr Gly
                245                 250                 255

Ala Val Lys Val Phe Leu Thr Asp Ser Leu Val Asn Lys Glu Ile Ala
            260                 265                 270

Leu Asn Leu Tyr Lys Asp Asp Ile Ser Lys Ser Glu Tyr Lys Asn Glu
        275                 280                 285

Leu Thr Leu Ser Val Leu Leu Asn Val Ile Leu Lys Asn Tyr Ser Gln
    290                 295                 300

Pro Asn Leu Asn Arg Gly Ile Ile Ile Lys Ile Ile Glu Gln Thr Leu
305                 310                 315                 320

Glu His His Asn Phe Asp Phe Ser Ser Trp Cys Pro Asp Asn Ile Asp
                325                 330                 335

Val Tyr Gly His Ile Asn Tyr Arg Gly Asp Lys Tyr Arg Ile Phe Ile
            340                 345                 350

Gly Glu Asn Ser Thr Ser Asn Tyr Leu Ile Thr Leu Thr Asp Ile Val
        355                 360                 365

Lys Asn Ile Asp Lys Ile Asn Asn Leu Glu Glu Phe Gly Leu Phe Glu
    370                 375                 380

Arg Asn Ala Leu Leu Phe His Ile Pro Lys Asn Pro Lys Trp Lys Val
385                 390                 395                 400

His Glu Ala Phe Asn Leu Thr Lys Gln Thr Tyr Lys Lys Leu Leu Thr
                405                 410                 415

Leu Asn Lys Phe Glu Gln Gly Asn Tyr Leu Arg Phe Ala Asn Thr Leu
            420                 425                 430

Tyr Lys Asn Tyr Asn His Leu His Asn Glu Val Asn Leu His Gln Leu
        435                 440                 445

Phe Asp Asp Thr Phe Leu Met Val Arg Asp Ser Arg Asp Val Thr Asn
    450                 455                 460

Ala Leu Lys Val Lys Pro Ile Val Asn Glu Ile Leu Ser Ile Ser Phe
465                 470                 475                 480

Ala Asn Tyr Lys Lys Met Thr His Tyr Leu Asp Val Asp Ala Gln Asp
                485                 490                 495

Arg Gln Arg Ile Thr Gly Tyr Ala Leu Asp Asn Tyr Tyr Leu Asp Tyr
            500                 505                 510
```

Leu His Asp Leu Ser Ile Leu Ile Arg Glu Gly Tyr Arg Thr Leu Glu
515 520 525

Ser Val Asn Leu Thr Pro Phe Ser Leu Lys Leu Glu His Asp Ile Val
530 535 540

Thr Asp Glu Lys Gln Ser Ile Gln Gln Gln Leu Asp Asp Ala Glu Leu
545 550 555 560

Lys Ala Lys Tyr Asp Asn Lys Leu Glu Lys Ile Ile Asp Lys Thr Tyr
565 570 575

Lys Leu Lys Asp Gly Arg Lys Val Lys Phe Leu Pro Ala Asp Thr Val
580 585 590

Ser Lys Leu Lys Asp Glu Gly Lys Met Leu Ser His Cys Val Gly Gly
595 600 605

Tyr Ala Asn Arg Ile Leu Lys Asn Ser Cys Leu Ile Leu Leu Ala Arg
610 615 620

Leu Glu Glu Asp Leu Asp Asn Ser Trp Phe Thr Val Glu Ile Arg Ile
625 630 635 640

Thr Asp Asn Gly Tyr Val Leu Gly Gln Gln Gln Ser Ile Asp Ala Tyr
645 650 655

Lys Leu Pro Asn Glu Leu Lys Glu Ala Leu Glu Lys Asp Ile Lys Lys
660 665 670

Ile Asn Lys Glu Glu Phe Lys Glu Val Ala
675 680

<210> 582
<211> 87
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 582
Met Ser Ile Glu Lys Lys Glu Glu Ile Ile Ala His Asn Glu Val Val
1 5 10 15

Phe Arg Ser Leu Thr Gln Gly Leu Tyr Val Lys Glu Val Asp Ile Tyr
20 25 30

Ser Asp Val Val Ser Tyr Thr Lys Asp Val Asp Glu Ala Leu Ala Met
35 40 45

Pro Asn Thr Ile Asn Phe Lys Asn Ser Arg Lys Tyr Glu Lys Leu Ile
50 55 60

Arg Asn Leu Asp Leu Glu Pro Leu Asn Lys Ile Gln Lys Val Ile Tyr
65 70 75 80

Glu Thr His Leu Glu Glu Leu
85

<210> 583
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 583
Leu Asn Asp Leu Ile Lys Glu Gly Asn Lys Tyr Tyr His Lys Val Arg
1 5 10 15

Ala Gly Glu Thr Leu Trp Thr Ile Ser Lys Asn Tyr Asp Val Glu Ile
20 25 30

Lys Lys Leu Gln Glu Leu Asn Asn Ile Lys Ser Val Ser Leu Thr Asn
35 40 45

Leu Glu Tyr Val Leu Val Cys Val Glu
50 55

<210> 584
<211> 192
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 584
Met Asp Asn Leu Ser His Tyr Leu Ser Ile Leu Tyr Ala Ile Leu Val
1 5 10 15

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

Val Lys Gly Val Ser Ser Tyr Phe Trp Tyr Leu Ile Val Ala Thr Val
35 40 45

Gly Ile Ser Phe Tyr Asn Leu Leu Leu Thr Asp Ala Thr Met Phe Gln
50 55 60

Val Val Ser Val Gly Leu Asn Leu Thr Leu Gly Ile Val Cys Leu Leu
65 70 75 80

Val Ala Ser Tyr Arg Lys Lys Asp Tyr Phe Ser Ile Pro Phe Ile Ile
85 90 95

Val Phe Ser Leu Leu Leu Phe Leu Leu Ser Asp Phe Thr Ala Leu Thr

100 105 110

Gln Thr Val Ala Thr Ile Thr Ile Ile Leu Ala Tyr Val Thr Gln Ile
115 120 125

Thr Thr Phe Tyr Lys Thr Lys Ser Ala Glu Gly Thr Asn Arg Phe Leu
130 135 140

Phe Leu Ile Ile Gly Leu Gly Leu Ala Ser Leu Ile Val Ser Met Val
145 150 155 160

Leu Thr His Thr Tyr Val His Ile Ile Ala Thr Glu Phe Val Asn Phe
165 170 175

Val Leu Ile Leu Ile Cys Tyr Leu Gln Ala Asn Tyr Tyr Ser Arg Arg
180 185 190

<210> 585
<211> 207
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 585
Met Val Asn Lys Ile Lys Asp Lys Val Ile Tyr Met Gly Gly His Ile
1 5 10 15

Leu Asn Glu Ala Met Val Asp Tyr Arg Asp Lys Gln His Lys Glu Val
20 25 30

Asp Gly Ile Val Gly Val Thr Pro Tyr Ser Pro His Lys Asp Lys Ser
35 40 45

Ile Asn Asp Lys Ala Asn Ala Glu Gln Thr Lys Leu Ala Glu Arg Ile
50 55 60

Leu Thr Asn Asp Phe Lys Ala Met Gln Glu Ser Asp Ile Phe Val Phe
65 70 75 80

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

Leu Gly Met Lys His Gln Ala Gln Glu Thr Ile Lys Gln Leu Lys Glu
100 105 110

Gln Ser Glu Leu Phe Lys Phe Asn Glu Ile Asp Glu Leu Ser Glu Thr
115 120 125

Tyr Asp Ile Leu Gln Gly Gln Ile Gly Glu Gln Glu Tyr Ile Leu Lys
130 135 140

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

Pro Tyr Asn Asp Pro Asp Arg Ala Glu Phe Ser Thr Asn Gln Phe Val
165 170 175

Tyr Gly Met Val Leu Glu Leu Thr Asn Gly Glu Gly Phe Ile Ser Trp
180 185 190

Glu Glu Val Thr Asn Arg Leu Glu Lys Leu Gly Glu Gln Asp Gly
195 200 205

<210> 586
<211> 298
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 586
Met Lys Ser Tyr Thr Lys Val Lys Asn Lys Gly Ile Val Leu Asp Lys
1 5 10 15

Phe Lys Glu Arg Gly Leu Val Val Gln Glu Lys Leu Asp Gly Ser Asn
20 25 30

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

Lys Lys Leu Asn Glu Asn Glu Thr Leu Asn Gly Phe Tyr Asp Trp Val
50 55 60

His Glu Asn Ile Asn Val Arg Asn Thr Tyr Val Ser Ala Leu Glu Lys
65 70 75 80

Tyr Ile Ile Phe Gly Glu Trp Leu Val Lys His Lys Ile Gln Tyr Lys
85 90 95

Glu Glu Phe Tyr Asn Asn Phe Tyr Val Phe Asp Val Tyr Asp Lys Glu
100 105 110

Asn Glu Val Tyr Leu Ser Ile Glu Asp Met Asn Val Ile Ala His His
115 120 125

Leu Gly Leu Lys Thr Val Lys Thr Leu Leu Val Ala Lys Pro Ser His
130 135 140

Tyr Leu Asn Asp Leu Lys Pro Glu Glu Ile Gln Glu Leu Val Gly Lys
145 150 155 160

Ser Asp Met Thr Val Lys Pro Asp Lys Gly Glu Gly Ile Val Ile Lys
165 170 175

```
Tyr Leu Asp Gly Lys Ser Glu Tyr Asp Asp Tyr Phe Lys Leu Val Ser
            180                 185                 190

Asn Glu Phe Lys Glu Phe Ser Arg Gln Lys Met Lys Thr Glu Val Lys
        195                 200                 205

Lys Asn Glu Ser Val Ala Asp Tyr Ala Ile Thr Arg Ala Arg Met Glu
    210                 215                 220

Lys Met Ile Phe Arg Ala Ile Glu Glu Asp Arg Leu Ser Glu Asp Asp
225                 230                 235                 240

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

Phe Val Asp Asp Ile Met Glu Glu Glu Lys Glu Asn Ile Leu Lys Ile
            260                 265                 270

Val Asp Lys Gln Ile Lys Lys Lys Met Pro His Ile Leu Arg Glu Ile
        275                 280                 285

Leu Glu Glu Lys Gly Asp Thr Ile Asp Gly
    290                 295


<210> 587
<211> 74
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 587
Met Asn Tyr Leu Ala Lys Val Phe Ile Asn Asn Asn Trp Leu Val Lys
1               5                   10                  15

Leu Ile Thr Ile Val Leu Leu Thr Leu Phe Leu Ser Gly Leu Val Tyr
            20                  25                  30

Val Ile Ser Ala Ile Ser Leu Phe Leu Ser Thr Val Leu Asn Leu Pro
        35                  40                  45

Gly Leu Val Val Leu Ala Phe Leu Ala Ser Val Ser Leu Ile Leu Phe
    50                  55                  60

Ser Ile Val His Asn Ser Lys Glu Asp Asn
65                  70


<210> 588
<211> 246
<212> PRT
<213> Unknown

<220>
```

<223> Description of Unknown: Bacteriophage F44/10

<400> 588
Met Ala Ile Gln Leu Lys Glu Leu Asp Phe Lys Leu Lys Asp Tyr Pro
1   5   10   15

Asn Val Arg Tyr Asn Met Gly Glu His Leu Ile Phe Asn Glu Phe Leu
            20   25   30

Glu Lys Ala Thr Thr Glu Gln Leu Asp Phe Cys Glu Asp Phe Phe Asn
        35   40   45

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

Thr Met Cys Ser Val Ala Cys Ala Tyr Ala Asp Tyr Leu Asn Lys Asn
65   70   75   80

Arg Lys Leu Val Phe Ile Ile Ser Pro Val Ser Glu Asp Leu Gly Ser
                85   90   95

Arg Pro Gly Asn Gln Thr Glu Lys Glu Met Ala Tyr Phe Met Gly Leu
            100   105   110

His Asp Ala Leu Ile Glu Leu Asn Met Asn Pro Glu Gln Gln Ile Thr
        115   120   125

Glu Met Leu Met Met Glu Asp Asn Val Lys Glu Asp Lys Leu Gly Asp
    130   135   140

Cys Trp Val Ser Gln Ile Ser His Leu Phe Leu Arg Gly Gly Asn Leu
145   150   155   160

Arg Asp Ala Thr Ile Ile Ile Asn Glu Ala Gln Asn Phe Lys Arg Ser
                165   170   175

Glu Leu Lys Lys Val Leu Thr Arg Val His Thr Lys Asn Ser Thr Val
            180   185   190

Ile Val Glu Gly Asn Phe Lys Gln Ile Asp Leu Lys Asn Glu Ser Lys
        195   200   205

Ser Gly Phe Gly Asp Tyr Met Glu Tyr Phe Lys Asn Tyr Glu Gly Ala
    210   215   220

Val Phe His Asn Phe Thr Val Asn Phe Arg Ser Lys Leu Ala Gln Tyr
225   230   235   240

Ala Asp Asn Phe Lys Trp
                245

<210> 589

<211> 204
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 589
Met Lys Lys Ile Asn Ser Val Ile Lys Gly Glu Gly Lys Lys Val Gln
1 5 10 15

Thr Ala Asp Val Arg Lys Ile Ser Tyr Tyr Val Lys Asp Tyr Asn Pro
20 25 30

Cys Met Thr Val Asp Asp Ala Asn Asp Tyr Asn Ala Thr Ser Gln Tyr
35 40 45

Leu Val Ser Asp Asn Gly Lys Phe Ile Ala Lys Tyr Asn Lys Asp Met
50 55 60

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

Thr His Thr Thr Pro Glu Arg Leu Glu Gly Thr Val Phe Thr Ile Glu
85 90 95

Glu Glu Thr Glu Ile Asp Leu Ile Asn Asp Thr Leu Pro Gln Gly Asp
100 105 110

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

Ser Val Leu Asp Ser Val Asn Tyr Leu Ala Asp Asn Asp Trp Asp Ser
130 135 140

Val Asp Asp Ile Ile Tyr Thr Gly Leu Ser Lys Gly Asn Ser Glu Asn
145 150 155 160

Cys Ile Val Asp Phe Asn Tyr Asn Asn Tyr Asp Ile Gly Tyr Asp Asp
165 170 175

Val Glu Asp Glu Asp Val Cys Asp Asn Tyr Pro Glu Cys Glu Cys Ser
180 185 190

Asn Tyr Cys Ser Ser Thr Gly Glu Tyr Ile Gly Asn
195 200

<210> 590
<211> 141
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 590
Met Gln Asp Ser Val Asn Ile Tyr Thr Asp Gly Ser Ser Ser Tyr Asn
1 5 10 15

Lys Gly Lys Val Gly Ser Gly Ala Val Leu Val Ser Lys Glu Gly Asn
20 25 30

Ile Ile Ser Glu Ile Ser Lys Ser Val Asp Lys Pro Gly Leu Ile Lys
35 40 45

Tyr Asn Asn Val Ala Gly Glu Ile Leu Ala Cys Cys Tyr Gly Ile Glu
50 55 60

Glu Ala Ile Lys Leu Gly Tyr Asn Gln Ala Ile Val Tyr Ile Asp Tyr
65 70 75 80

Ile Gly Leu Ile His Trp Tyr Glu Gly Thr Trp Ser Ala Arg Asn Ile
85 90 95

Leu Ser Lys Thr Tyr Ile Asn Met Ile Arg Glu Tyr Gln Lys Val Ile
100 105 110

Asp Ile Asn Phe Val Lys Val Lys Ser His Ser Asn Asp Lys Trp Asn
115 120 125

Asp Tyr Ala Asp Asn Leu Ala Lys Lys Ser Ile Asp Ile
130 135 140

<210> 591
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 591
Met Lys Lys Gly Val Phe Thr Val Ile Ala Asp Gly Phe Lys Phe Asn
1 5 10 15

Val Ile Ala Lys Asp Lys Lys Glu Val Gln Glu His Cys Phe Lys Cys
20 25 30

Phe Asp Phe Asn Tyr Ile Ser Val Ser Phe Cys Arg Glu Val Tyr Ser
35 40 45

Asp Cys Glu Phe Pro Gln Phe Met Glu Asp Tyr Lys Tyr Ala Gly
50 55 60

<210> 592
<211> 213
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F44/10

<400> 592
Met Glu Asn Asn Asn Leu Val Asn Phe Leu Met Thr Thr Asp Asp Ile
1   5   10   15

Asp Asp Thr Ile Glu Met Val Asp Ser Phe Glu Leu Gln Asp Ile Asn
            20   25   30

Lys Val Leu Gly Glu Asp Thr Phe Leu Thr Ile Met Glu Ile Thr Asp
        35   40   45

Ser Leu Pro Asp Asn Gln Tyr Lys Ile Val Leu Leu Ser Ser Leu Asp
    50   55   60

Lys Leu Leu Asn Thr Asp Arg Lys Glu Leu Val Glu Tyr Asp Glu Glu
65   70   75   80

Phe Pro Thr Ile Arg Lys His Asn Val Ser Glu Leu Lys Arg Asp Thr
                85   90   95

Val Asn Ser Val Ile Asp Ser Tyr Met Asn Thr Asn Ile Glu Ile Leu
            100   105   110

Tyr Thr Glu Tyr Pro Thr Ile Ser Asn Tyr Ser Val Val Val Asp Ser
        115   120   125

Val Lys Val Leu Asn Thr Leu Tyr Leu Ile Glu Ser Lys Asn Gly Lys
    130   135   140

Ile Glu Ala Thr Leu Ser Glu Asp Gly Glu Asp Leu His Glu Tyr Ile
145   150   155   160

Ser Glu Glu Gly Tyr Ser Val Thr Asp Ile Leu Asn Lys Phe Asp Asp
                165   170   175

Val Glu Asp Leu Phe Asp Glu Asp Asp Ser Leu Ile Asn Phe Phe Ser
            180   185   190

Asp Ile Asp Glu Gly Lys Asn Lys Thr Ile Lys Ser Phe Ile Glu Leu
        195   200   205

Val Ile Asn Leu Lys
    210

<210> 593
<211> 76
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 593

Met Asp Glu Lys Lys Glu Ser Lys Pro Leu Asn Leu Gln Lys Ile Arg
1   5   10   15

Val Glu Lys Gly His Thr Leu Arg Ser Leu Ala Ser Glu Ile Gly Val
            20   25   30

His Tyr Ser Leu Ile Ser Tyr Trp Glu Tyr Gly Lys Lys Lys Pro Arg
        35   40   45

Ser Ala Asn Leu Met Arg Leu Glu Lys Ala Leu Asn Thr Pro Gly Lys
    50   55   60

Glu Leu Phe Lys Glu Leu Glu Glu Asp Asp Gly Glu
65   70   75

<210> 594
<211> 75
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 594
Met Asn Lys Phe Lys Arg Trp Phe Arg Ile Asn Val Leu Lys Lys Glu
1   5   10   15

Thr Leu Leu Phe Lys Val Tyr Trp Arg Tyr Glu Ser Pro Ser Leu Lys
            20   25   30

Lys Pro His Val Phe His Ile Glu Leu Tyr Ala Lys Ser Lys Ala Glu
        35   40   45

Ala Arg Asn Lys Ser Gln Glu Tyr Ile Leu Lys Asn Ala Lys Glu Ser
    50   55   60

Glu Asp Phe Lys Phe Leu Lys Val Glu Glu Lys
65   70   75

<210> 595
<211> 230
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 595
Met Lys Lys Thr Ile Phe Ala Thr Leu Ala Leu Gly Thr Ala Ile Thr
1   5   10   15

Phe Gly Gly Ile Ala Thr Asn Glu Ala Ser Ala Asp Glu Ile Asp Tyr
            20   25   30

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

```
Lys Pro Ile Gln Glu Gly Asn Tyr Asp Phe Ser Phe Ser Asp Gly Glu
    50                  55                  60

Phe Thr Tyr His Phe Tyr Asn Tyr Asn Gly Asn Phe Gly Tyr Glu Tyr
65                  70                  75                  80

His Ser Gly Ser Thr Gln Val Asp Asn Thr Val Ser Arg Leu Ala Gly
                85                  90                  95

Glu Glu Gln Thr Pro Glu Gln Lys Val Asp Gln Gln Gln Ala Gln Phe
            100                 105                 110

Asp Thr Gln Asn Lys Gln Asp Thr Lys Lys Glu Val Gln Thr Thr Ser
        115                 120                 125

Ala Pro Val Gln Lys Glu Thr Lys Gln Pro Thr Gln Ser Thr Ser Ser
    130                 135                 140

Thr Gly Gly Ser Val Ala Glu Gln Ile Arg Gln Ala Gly Gly Asp Glu
145                 150                 155                 160

Ala Met Ile Glu Ile Ala Met Arg Glu Ser Thr Met Asn Pro Asn Ala
                165                 170                 175

Val Asn Ala Ser Ser Gly Ala Gln Gly Leu Phe Gln Gly Leu Gly Lys
            180                 185                 190

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

Tyr Met Ile Asp Arg Tyr Gly Ser Thr Ser Gly Ala Leu Ala Tyr His
    210                 215                 220

Asn Ala His Asn Ser Tyr
225                 230


<210> 596
<211> 264
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 596
Met Arg Lys Ser Val Val Ile Ser Gly Val Leu Gly Phe Leu Ala Ile
1               5                   10                  15

Ile Gly Phe Ile Ile Leu Leu Met Cys Ile Thr Lys Ile Pro Gln Gly
            20                  25                  30

His Val Gly Val Val Tyr Ser Val Asn Gly Val Lys Glu Asp Thr Lys
```

35 40 45

Ser Pro Gly Trp His Leu Thr Ala Pro Phe Asp Lys Val Asn Lys Tyr
50 55 60

Pro Thr Lys Thr Gln Thr His Lys Tyr Lys Asp Leu Asn Val Ala Thr
65 70 75 80

Ser Asp Gly Lys Asn Leu Gln Met Asp Ile Asp Val Ser Tyr Lys Val
85 90 95

Asp Ala Thr Lys Ala Val Asp Leu Phe Asn Arg Phe Gly Ser Ala Asp
100 105 110

Ile Glu Glu Leu Glu Lys Gly Tyr Leu Arg Ser Arg Val Gln Asp Asn
115 120 125

Val Arg Gln Ala Val Ser Lys Tyr Ser Val Ile Asp Ala Phe Gly Val
130 135 140

Lys Thr Gly Glu Ile Lys Lys Asp Thr Leu Asp Ser Leu Asn Asp Asn
145 150 155 160

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

Lys Ala Asp Lys Asn Thr Gln Lys Ala Ile Asp Ser Arg Val Lys Ala
180 185 190

Asn Gln Glu Leu Glu Arg Thr Lys Val Asp Lys Gln Ile Ala Glu Gln
195 200 205

Asn Ala Lys Lys Lys Glu Val Glu Ala Asn Gly Asp Lys Lys Ala Asn
210 215 220

Glu Ile Arg Glu Ser Ser Leu Ser Asp Lys Ile Leu Arg Gln Gln Leu
225 230 235 240

Ile Glu Lys Trp Asp Gly Lys Gln Pro Ile Gln Ile Gly Gly Asp Gly
245 250 255

Thr Ile Val Asp Val Thr Gly Lys
260

<210> 597
<211> 102
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 597

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

Leu Val Gly Phe Gly Ile Ser Tyr Leu Phe Asp Phe Leu Ser Met Lys
            20   25   30

Glu Lys Lys Ser Asn Ile Arg Lys Gln Tyr Arg Glu Leu Val Arg Gln
        35   40   45

Gly Thr Leu Asp Glu Tyr Gly Leu Glu Gln Tyr Val Lys Tyr Lys Lys
    50   55   60

Gln Phe Leu Asn Asp Arg Arg Gln Ser Ile Val Thr Arg Ala Asp Lys
65   70   75   80

Gln Glu Ile Asp Gln Glu Glu Lys Ala Leu Asn Ser Leu Ile Lys Glu
                85   90   95

Ile Glu Lys Gly Glu Met
            100

<210> 598
<211> 495
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 598
Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr Ala
1   5   10   15

Lys Gly Thr Val Asp Ser Pro Tyr Arg Val Lys Lys Ala Thr Ser Tyr
            20   25   30

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

Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp
    50   55   60

Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile
65   70   75   80

Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu Asn Lys Pro Ser
                85   90   95

Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr
            100   105   110

Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp Gly Gly Asn Thr Ser
        115   120   125

```
Thr Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys
    130                 135                 140

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

Ile Pro Val Lys Ala Gly Thr Thr Val Lys Lys Glu Thr Ala Lys Lys
                165                 170                 175

Ser Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys Ala Thr Leu Lys Val
            180                 185                 190

Ser Lys Asn His Ile Asn Tyr Thr Met Asp Lys Arg Gly Lys Lys Pro
        195                 200                 205

Glu Gly Met Val Ile His Asn Asp Ala Gly Arg Ser Ser Gly Gln Gln
    210                 215                 220

Tyr Glu Asn Ser Leu Ala Asn Ala Gly Tyr Ala Arg Tyr Ala Asn Gly
225                 230                 235                 240

Ile Ala His Tyr Tyr Gly Ser Glu Gly Tyr Val Trp Glu Ala Ile Asp
                245                 250                 255

Ala Lys Asn Gln Ile Ala Trp His Thr Gly Asp Gly Thr Gly Ala Asn
            260                 265                 270

Ser Gly Asn Phe Arg Phe Ala Gly Ile Glu Val Cys Gln Ser Met Ser
        275                 280                 285

Ala Ser Asp Ala Gln Phe Leu Lys Asn Glu Gln Ala Val Phe Gln Phe
    290                 295                 300

Thr Ala Glu Lys Phe Lys Glu Trp Gly Leu Thr Pro Asn Arg Lys Thr
305                 310                 315                 320

Val Arg Leu His Met Glu Phe Val Pro Thr Ala Cys Pro His Arg Ser
                325                 330                 335

Met Val Leu His Thr Gly Phe Asn Pro Val Thr Gln Gly Arg Pro Ser
            340                 345                 350

Gln Ala Ile Met Asn Lys Leu Lys Asp Tyr Phe Ile Lys Gln Ile Lys
        355                 360                 365

Asn Tyr Met Ser Asn Gly Thr Ser Ser Ser Thr Val Val Lys Asp Gly
    370                 375                 380

Lys Thr Ser Ser Ala Ser Thr Pro Ala Thr Arg Pro Val Thr Gly Ser
385                 390                 395                 400
```

```
Trp Lys Lys Asn Gln Phe Gly Thr Trp Tyr Lys Pro Glu Ser Ala Thr
                405                 410                 415

Phe Val Asn Gly Asn Gln Pro Ile Val Thr Arg Ile Gly Ser Pro Phe
            420                 425                 430

Leu Asn Ala Pro Val Gly Gly Asn Leu Pro Ala Gly Ala Thr Ile Val
        435                 440                 445

Tyr Asp Glu Val Cys Ile Gln Ala Gly His Ile Trp Ile Gly Tyr Asn
    450                 455                 460

Ala Tyr Asn Gly Asn Arg Val Tyr Cys Pro Val Arg Thr Cys Gln Gly
465                 470                 475                 480

Val Pro Pro Asn Gln Ile Pro Gly Val Ala Trp Gly Val Phe Lys
                485                 490                 495


<210> 599
<211> 167
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 599
Met Ala Asn Glu Thr Lys Gln Pro Lys Val Val Gly Gly Ile Asn Leu
1               5                   10                  15

Ser Thr Arg Thr Lys Ser Lys Thr Phe Trp Val Ala Ile Ile Ser Ala
            20                  25                  30

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

Ser Ala Gln Ile Glu Gln Gly Val Asn Ile Val Gly Ser Ile Leu Thr
    50                  55                  60

Leu Leu Ala Gly Leu Gly Ile Ile Val Asp Asn Asn Thr Lys Gly Leu
65                  70                  75                  80

Arg Asp Ser Asp Ile Val Gln Thr Asp Tyr Val Lys Pro Arg Asp Ser
                85                  90                  95

Lys Asp Pro Asn Glu Phe Val Gln Trp Gln Thr Asn Ala Asn Asn Ala
            100                 105                 110

Ser Thr Phe Glu Ile Asp Ser Tyr Glu Asn Asn Ala Glu Pro Asp Thr
        115                 120                 125

Asp Asp Ser Asp Glu Val Pro Ala Ile Glu Asp Glu Ile Asp Gly Gly
    130                 135                 140
```

Ser Ala Pro Ser Gln Asp Glu Glu Asp Thr Glu Glu His Gly Lys Val
145 150 155 160

Phe Ala Glu Glu Glu Val Lys
165

<210> 600
<211> 61
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 600
Met Ala Ser Ala Lys Gln Leu Tyr Tyr Thr Glu Ser Leu Val Gly Lys
1 5 10 15

Ala Ile Ile Asn Asn Lys Val Ser Asn Lys Glu Glu Val Trp Asp Lys
20 25 30

Leu Glu Leu Leu Pro Glu Thr Lys Leu Glu Asp Leu Asp Asn Lys Gln
35 40 45

Met Ser Glu Val Ile Lys Lys Leu Asn Gln Ile Asn Glu
50 55 60

<210> 601
<211> 72
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 601
acacccuuag uauaauuagu aguacaaggg ucuccaaaac ccuuagucuu ugugcaaauc 60

aaagagggug ug 72

<210> 602
<211> 73
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 602
gguuucuuag cucagauggu agagcacuag auugaagcuc uaggugucau ugguucaaau 60

ccaauagaaa cca 73

<210> 603
<211> 74
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 603
ggcucauugg uguaacuggu uaacacacug cccugucacg gcagagagua cgaguucgag 60

ucucguaugg gucg 74

<210> 604
<211> 72
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 604
Met Lys Arg Gln Lys Met Phe Tyr Ser Ser Leu Ile Cys Lys Glu Cys
1 5 10 15

Gly Asn Val Phe Lys Val Pro Arg Lys Arg Ala Asn Lys Arg Glu Glu
20 25 30

Gly His Ile Lys Asp Ile Tyr Cys Ile Lys Cys Cys Lys Thr Thr Lys
35 40 45

His Ile Glu Asp Asn Arg Ser Glu Ala Glu Arg Arg Trp Asp Ala Ile
50 55 60

Gln Glu Glu Leu Thr Lys Asp Asn
65 70

<210> 605
<211> 69
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 605
Met Ser Lys His Ile Glu Ile Thr Met Ser Ser Gly Ala Lys Tyr Phe
1 5 10 15

Leu Val Ser Thr Asp Glu Lys Ser Tyr Asn Arg Gln Asp Ile Asp Tyr
20 25 30

Met Leu Arg Gly Met Asp Glu Thr Ser Ile Lys Val Tyr Thr Glu Ser
35 40 45

Ala Ile Thr Ser Pro Gln Val Tyr Ile Asn Pro Asn Arg Ile Glu Ser
50 55 60

Phe Lys Ile Val Phe
65

<210> 606

<211> 110
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 606
Leu Asp Lys Glu Ile Asn Asn Leu Val Ser Gln Val Glu Thr Ile Lys
1   5   10   15

Ser Lys Ile Gln Glu Gly Asn Tyr Ile Asp Arg Gly Thr Phe Lys Asp
            20   25   30

Leu Glu Val Glu Val Ala Glu Leu Arg Lys Met Ile Val Ser Ile Asp
        35   40   45

Lys Asp Val Ala Val Asn Ser Glu Lys Gln Ser Ala Ile Tyr Val Gln
    50   55   60

Leu Glu Arg Leu Asp Glu Lys Ile Ser Glu Leu Ala Gly Ser Thr Lys
65   70   75   80

Thr Lys Asp Thr Lys Lys Lys Asp Thr Thr Glu Lys Val Leu Leu Leu
                85   90   95

Val Leu Gly Ala Ile Leu Ser Phe Val Phe Asn Lys Phe Ala
            100   105   110

<210> 607
<211> 108
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 607
Leu Thr Lys Tyr Lys Asp Ile Leu Lys Leu Glu Phe Lys Asp Ala Leu
1   5   10   15

Ala His Phe Lys Arg Asp Arg Arg Tyr Phe His Val Tyr Arg Ile Asp
            20   25   30

Arg Val Leu Ile Asn Gly Ser Ile Ile Tyr Phe Asp Tyr Tyr Tyr Leu
        35   40   45

Pro Ser Asp Asp Pro Asn Ile Val Ile Lys Glu Leu Asp Leu Gln Ser
    50   55   60

Phe Gly Lys Leu Arg Phe Glu Ile Asp Thr Lys Thr Ser Tyr Gly Lys
65   70   75   80

Val Val Thr Asp Asn Tyr Met Glu Ile Ile Asn Asp Phe Leu Glu Asn
                85   90   95

Tyr Asp Ile His Ser Glu Ser Glu Thr Val Arg Pro
100 105

<210> 608
<211> 128
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 608
Leu Asn Asn Asn Ile Ala Ile Phe Ile Phe Lys Thr Leu Val Ile Ile
1 5 10 15

Ile Phe Leu Leu Leu Ile Leu Ser Val Ile Asn Ser Leu Ser Leu Ile
20 25 30

Tyr Ser Ile Arg Pro Ser Val Val Met Thr Tyr Phe Ile Phe Gly Gly
35 40 45

Ile Val Ser Asn Val Ala Leu Thr Val Thr Asp Lys Phe Leu Leu Lys
50 55 60

Lys Glu Asp Pro Leu Pro Glu Tyr Val Leu Lys Lys Val Glu Ile Asn
65 70 75 80

Asp Lys Glu Ile Arg Ile Ile Lys Lys Ile Ile Glu Ser Asn Tyr Gly
85 90 95

Ile Thr Ala Glu Glu Ile Lys Val Arg Ala Lys Ala Gln Arg Arg Ile
100 105 110

Glu Glu Asp Ser Lys Lys Glu Asp Tyr Asp Glu Asn Lys Glu Arg Asn
115 120 125

<210> 609
<211> 92
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 609
Met Lys Thr Lys Lys Glu Ile Lys Glu Gln Arg Lys Glu Leu Lys Asp
1 5 10 15

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

Ser Pro Ser Arg Ile Cys Ser Leu Cys Gly Gln Gln Leu Ser Gly Met
35 40 45

Asn Tyr Thr Lys Gly Lys Ala Leu Ser Lys Val Asn His Phe His Leu

50 55 60

Gln Tyr Ser Lys Tyr Ile Tyr Phe Asp Ile Cys Ala Asp Ile Asn Asn
65 70 75 80

Cys Tyr Lys Asn Leu Arg Lys Arg Gly Glu Met Asp
85 90

<210> 610
<211> 136
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 610
Leu Ser Ala Glu Asn Ile Arg Asp Ile Ile Asn Lys Lys Lys Leu Glu
1 5 10 15

Glu Glu Asp Thr Arg Lys Tyr Ile Ala Asp Gly Phe Met Asn Gly Ile
20 25 30

Gly Lys Leu Met Tyr Glu Phe Asn Lys Lys Val Asp Asn Lys Glu Ile
35 40 45

Glu Val Lys Asp Pro Asn Asp Leu Tyr Lys Leu Phe Val Ile Phe Ser
50 55 60

Gln Met Gln Asn Met Val Asn Glu Thr Ser Glu Gly Gly Ala Ile Pro
65 70 75 80

Gln Leu Ser Arg Pro Gln Gln Glu Leu Phe Asp Glu Ile Thr Thr Glu
85 90 95

Asp Ser Asn Gly Glu Ser Thr Val Asp Leu Gln Lys Ile Ser Glu Met
100 105 110

Ser Ala Glu Asp Ile Thr Ala Met Ile Ser Glu Lys Glu Lys Val Met
115 120 125

Asn Glu Glu Asn Ser Glu Thr Phe
130 135

<210> 611
<211> 605
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 611
Met Asp Gly Lys Glu Leu Ile Lys Ile Ala Gln Glu Thr Phe Gln Thr
1 5 10 15

```
Glu Lys Ile Thr Arg Glu Gln Ile Asp His Ile Ile Asn Met Leu Asn
            20                  25                  30

Pro Ser Thr Tyr Met Leu Lys Tyr His Thr Leu Arg Gly His Pro Ile
        35                  40                  45

Thr Phe Ser Ile Pro Asn Arg Asp Arg Ser Lys Ala Gln Ala His Arg
    50                  55                  60

Pro Trp Gln Thr Arg Ile Val Asn Asp Thr His Pro Asn Lys Ala Val
65                  70                  75                  80

Ile Lys Ser Arg Gln Leu Gly Leu Ser Glu Met Gly Val Met Glu Met
                85                  90                  95

Val His Phe Ala Asp Met His Ser Tyr Ala Asn Ala Lys Cys Leu Tyr
            100                 105                 110

Thr Phe Pro Thr Asn Glu Gln Met Lys Lys Phe Val Gln Ser Arg Leu
        115                 120                 125

Asn Pro Val Leu Glu Lys Glu Tyr Phe Arg Asp Ile Val Asp Trp Asp
    130                 135                 140

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

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

Leu Ser Leu Asp Glu Tyr Asp Arg Val Asn Leu Leu Ala Glu Ser Ser
            180                 185                 190

Ala Leu Glu Ser Met Ser Ser Ser Pro Phe Lys Ile Val Arg Arg Trp
        195                 200                 205

Ser Thr Pro Ser Val Pro Gly Met Gly Ile His Lys Leu Tyr Gln Gln
    210                 215                 220

Ser Asp Gln Trp Tyr Tyr Gly His Arg Cys Gln His Cys Asp Tyr Leu
225                 230                 235                 240

Asn Glu Met Ser Tyr Asn Asp Tyr Asn Pro Asp Asn Leu Glu Glu Ser
                245                 250                 255

Gly Asn Met Leu Cys Val Asn Pro Glu Gly Val Asp Glu Gln Ala Lys
            260                 265                 270

Thr Val Gln Asn Gly Ser Tyr Gln Phe Val Cys Gln Lys Cys Gly Lys
        275                 280                 285
```

```
Pro Leu Asp Arg Trp Tyr Asn Gly Glu Trp His Cys Lys Tyr Pro Glu
    290                 295                 300

Arg Thr Lys Gly Asn Lys Gly Val Arg Gly Tyr Leu Ile Thr Gln Met
305                 310                 315                 320

Asn Ala Val Trp Ile Ser Ala Asp Glu Leu Lys Glu Lys Glu Met Asn
                325                 330                 335

Thr Glu Ser Lys Gln Ala Phe Tyr Asn Tyr Ile Leu Gly Tyr Pro Phe
            340                 345                 350

Glu Asp Val Lys Leu Arg Val Asn Glu Glu Asp Val Tyr Gly Asn Lys
        355                 360                 365

Ser Pro Ile Ala Glu Thr Gln Leu Met Lys Arg Asp Arg Tyr Ser His
    370                 375                 380

Ile Ala Ile Gly Ile Asp Trp Gly Asn Thr His Trp Ile Thr Val His
385                 390                 395                 400

Gly Met Leu Pro Asn Gly Lys Val Asp Leu Ile Arg Leu Phe Ser Val
                405                 410                 415

Lys Lys Met Thr Arg Pro Asp Leu Val Glu Ala Asp Leu Glu Lys Ile
            420                 425                 430

Ile Trp Glu Ile Ser Lys Tyr Asp Pro Asp Ile Ile Ile Ala Asp Asn
        435                 440                 445

Gly Asp Ser Gly Asn Asn Val Leu Lys Leu Ile Asn His Phe Gly Lys
    450                 455                 460

Asp Lys Val Phe Gly Cys Thr Tyr Lys Ser Ser Pro Lys Ser Thr Gly
465                 470                 475                 480

Gln Leu Arg Pro Glu Phe Asn Glu Asn Asn Asn Arg Val Thr Val Asp
                485                 490                 495

Lys Leu Met Gln Asn Lys Arg Tyr Val Gln Ala Leu Lys Thr Lys Asp
            500                 505                 510

Ile Ser Val Tyr Ser Thr Val Asp Asp Asp Leu Lys Thr Phe Leu Lys
        515                 520                 525

His Trp Gln Asn Val Val Ile Met Asp Glu Glu Asp Glu Lys Thr Gly
    530                 535                 540

Glu Met Tyr Gln Val Ile Lys Arg Lys Gly Asp Asp His Tyr Ala Gln
545                 550                 555                 560
```

```
Ala Ser Val Tyr Ala Tyr Ile Gly Leu Thr Arg Ile Lys Glu Leu Leu
                565                 570                 575


Lys Glu Gly Asn Gly Thr Ser Phe Gly Ser Thr Phe Val Ser Thr Asp
            580                 585                 590


Tyr Asn Gln Glu Gly Asn Lys Gln Phe Tyr Phe Asp Glu
        595                 600                 605


<210> 612
<211> 273
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 612
Met Asn Arg Gly Glu Ile Asp Leu Thr Asp Lys Leu Phe Tyr Gly Thr
1               5                   10                  15


Ile Ser Asn Glu Glu Ile Asn Lys Ser Val Leu Asn Leu Leu Leu Gly
            20                  25                  30


Glu Glu Leu Ser Leu Asp Tyr Val Ser Lys Asn Ser Asp Thr Leu Asp
        35                  40                  45


Val Lys Tyr Glu His Val Tyr Lys Ser Leu Gly Phe Asp Asn Phe Phe
    50                  55                  60


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


Gly Asp Lys Asn Leu Gly Gly Leu Asn Lys Val Lys Arg Thr Val Ile
                85                  90                  95


Arg Asn Gly Lys Glu Met Glu Met Thr Val Tyr Glu Asp Gly Asn Lys
            100                 105                 110


Glu Asn Asp Ser Lys Glu Lys Gln Glu Gly Lys Glu Glu Val Ser Arg
        115                 120                 125


Ser Ala Val Gly Ala Arg Ala Ile Ser Asn Gly Glu Glu Gly Lys Val
    130                 135                 140


Asn Pro Lys Lys Val Ala Asn Ser Leu Ser Asn Leu Ser Lys Lys Gly
145                 150                 155                 160


Val Asp Val Ser His Ile Asn Thr Asn Ser Ser Leu Tyr Lys Glu Phe
                165                 170                 175


Val Asp Asp Asn Gly Asp Thr Leu Gly Ile Thr Ser Phe Lys Arg Thr
            180                 185                 190
```

```
Glu Asn Asp Ile Ile Leu Glu Ser Tyr Ala Ser Ser His Asp Ser Asp
        195                 200                 205

Gly Val Gly Ala Arg Ala Ile Met Glu Leu Leu Arg Leu Ser Ile Lys
    210                 215                 220

Glu Asn Lys Asn Ala Val Val Tyr Asp Ile Glu Leu Pro Glu Ala Val
225                 230                 235                 240

Glu Tyr Leu Lys Thr Leu Gly Phe Lys Pro Asn Lys Asp Gly Tyr Ile
                245                 250                 255

Leu Arg Lys Lys Asp Val Lys Gln Phe Leu Gly Asp Tyr Ser Asp Phe
            260                 265                 270

Ile
```

<210> 613
<211> 60
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 613

```
Val Ile Ile Val Ile Leu Phe Ser Thr Ile Val Ile Tyr Ser Ile Val
1               5                   10                  15

Phe Ile Leu Tyr Ile Val Leu Lys Thr Ile Tyr Ile Lys Ser Asn Met
            20                  25                  30

Ser Arg Ile Asp Asn Thr Thr Glu Leu Leu Lys Ile Leu Gln Glu Asp
        35                  40                  45

Ile Glu Gly Lys Ile Lys Lys Glu Gly Arg Asn Lys
    50                  55                  60
```

<210> 614
<211> 159
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 614

```
Met Thr Leu Glu Glu Asn Lys Leu Thr Leu Glu Glu Ser Ile Thr Pro
1               5                   10                  15

Leu Ser Lys Glu Glu Lys Glu Asp Ser Ile Lys Glu Phe Ser Ser Leu
            20                  25                  30
```

```
Leu Cys Glu Met Val Asn Arg Leu Tyr Lys Ser Tyr Asn Val Phe Arg
        35                  40                  45

Gln Asp Pro Met Asp Glu Thr Gln Arg Leu Asp Gly Ser Leu Met Val
    50                  55                  60

Phe Gln Ser Arg Leu Asn Asp Pro Leu Thr Gly Asp Leu His Asp Lys
65                  70                  75                  80

Met Tyr Lys Leu Ala Phe Ser Lys Arg Ile Asp Ile Phe Glu Ala Asn
                85                  90                  95

Lys Gln Phe Arg Lys Asp Val Glu Ala Gly Lys Ala Ile Glu Leu Gly
            100                 105                 110

Asp Val Ala Ile Ile Asp Thr Ala Leu Ser Asn Ile Leu Ser Gly Asn
        115                 120                 125

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

Lys Glu Arg Ile Arg Lys Glu Glu Glu Glu Lys Leu Asn Asn Leu
145                 150                 155


<210> 615
<211> 108
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 615
Leu Lys Lys Lys Pro Gln Gly Asn Glu Val Ile Ile Thr Ile Ile Thr
1               5                   10                  15

Val Met Ile Ala Val Phe Val Val Ile Met Thr Ile Phe Phe Asn Lys
            20                  25                  30

Tyr Gln Asp Ala Lys Glu Asp Lys Asp Arg Tyr Gln Arg Leu Val Glu
        35                  40                  45

Ile Tyr Lys Lys Ala Asp Asp Asn Asp Gly Glu Thr Lys Lys Lys Tyr
    50                  55                  60

Val Lys Arg Leu Asn Lys Ala Glu Glu Glu Leu Lys Lys Val Lys Lys
65                  70                  75                  80

Lys Gln Ile Ile Lys Ile Ile Ile Arg Ser Gln Val Lys Lys Asp Lys
                85                  90                  95

Lys Lys Ile Lys Lys Leu Glu Arg Lys Tyr Met Met
            100                 105
```

<210> 616
<211> 34
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 616
Val Asp Glu Glu Asp Lys Asn Glu Asp Thr Thr Asp Asp Lys Gln Pro
1   5   10   15

Thr Glu Gln Pro Asp Asp Asn Asn Ile Asp Asn Glu Asp Lys Thr Glu
            20   25   30

Glu Glu

<210> 617
<211> 113
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 617
Met Asn Ile Ile Thr Ser Leu Ser Val Val Phe Thr Cys Leu Ser Leu
1   5   10   15

Leu Thr Leu Met Ile Phe Val His Ser Lys Phe Ser Ser Lys Asn Val
            20   25   30

Phe Val Leu Tyr Val Ile Tyr Ala Ile Ile Gly Ile Gly Thr Tyr Ile
        35   40   45

Val Leu Thr Met Phe Gln Thr Thr Ser Val Leu Ile Lys Asn Asp Val
    50   55   60

Ile Asp Ser Ile Glu Asn Thr Glu His Tyr Ile Gly Phe Asn Asp Pro
65   70   75   80

Ile Ile Ile Phe Thr Ile Ser Phe Ile Gly Ala Ile Leu Gly Gly Ile
                85   90   95

Trp Tyr Lys Met Met Lys Ile Ile Lys Lys Ser Asn Phe Lys Asp Lys
            100   105   110

Lys

<210> 618
<211> 123
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 618
Leu Ile Phe Ser Lys Asp Lys Lys Trp Asp Glu Ala Lys Asp Phe Ile
1   5   10   15

Lys Gly Gln Gly Met Gln Asp Asn Trp Ile Glu Ile Val Asp Tyr Tyr
            20   25   30

Arg Gln Ile Gly Gly Lys His Val Ala Val Phe Ile Ala Leu Asn Lys
        35   40   45

Val Lys Tyr Met Ile Leu Glu Ala Thr Lys Asp Asn Lys Val Ile Leu
    50   55   60

Val Asp Lys Asp Asn Asn Ile Leu Leu Glu Asp Tyr Asp Ile Val Met
65   70   75   80

Glu Ser Lys Lys Met Phe Tyr Tyr Ile Glu Glu Pro Phe Glu Val Lys
                85   90   95

Ile Asn Ile Pro Gln His Ile Arg Asp Val Thr Tyr Asn Asn Thr Val
            100   105   110

Val Leu Thr Thr Val Arg Gly Ser Arg Gly Asp
        115   120

<210> 619
<211> 563
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 619
Leu Ala Asp Leu Phe Lys Gln Phe Arg Leu Gly Lys Asp Tyr Gly Asn
1   5   10   15

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

Ile Lys Lys Ile Glu Gln Asp Asn Lys Glu Tyr Gln Asp Leu Thr Lys
        35   40   45

Ser Leu Tyr Gly Gln Gln Gln Ala Tyr Ala Glu Pro Phe Ile Glu Met
    50   55   60

Met Asp Thr Asn Pro Glu Phe Arg Asp Lys Arg Ser Tyr Met Lys Asn
65   70   75   80

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

```
Leu Asn Ala Ile Ile Leu Thr Arg Ser Asn Gln Val Ala Met Tyr Cys
            100                 105                 110

Gln Pro Ala Arg Tyr Ser Glu Lys Gly Leu Gly Phe Glu Val Arg Leu
        115                 120                 125

Arg Asp Leu Asp Ala Glu Pro Gly Arg Lys Glu Lys Glu Glu Met Lys
    130                 135                 140

Arg Ile Glu Asp Phe Ile Val Asn Thr Gly Lys Asp Lys Asp Val Asp
145                 150                 155                 160

Arg Asp Ser Phe Gln Thr Phe Cys Lys Lys Ile Val Arg Asp Thr Tyr
                165                 170                 175

Ile Tyr Asp Gln Val Asn Phe Glu Lys Val Phe Asn Lys Asn Asn Lys
            180                 185                 190

Thr Lys Leu Glu Lys Phe Ile Ala Val Asp Pro Ser Thr Ile Phe Tyr
        195                 200                 205

Ala Thr Asp Lys Lys Gly Lys Ile Ile Lys Gly Gly Lys Arg Phe Val
    210                 215                 220

Gln Val Val Asp Lys Arg Val Val Ala Ser Phe Thr Ser Arg Glu Leu
225                 230                 235                 240

Ala Met Gly Ile Arg Asn Pro Arg Thr Glu Leu Ser Ser Ser Gly Tyr
                245                 250                 255

Gly Leu Ser Glu Val Glu Ile Ala Met Lys Glu Phe Ile Ala Tyr Asn
            260                 265                 270

Asn Thr Glu Ser Phe Asn Asp Arg Phe Phe Ser His Gly Gly Thr Thr
        275                 280                 285

Arg Gly Ile Leu Gln Ile Arg Ser Asp Gln Gln Gln Ser Gln His Ala
    290                 295                 300

Leu Glu Asn Phe Lys Arg Glu Trp Lys Ser Ser Leu Ser Gly Ile Asn
305                 310                 315                 320

Gly Ser Trp Gln Ile Pro Val Val Met Ala Asp Asp Ile Lys Phe Val
                325                 330                 335

Asn Met Thr Pro Thr Ala Asn Asp Met Gln Phe Glu Lys Trp Leu Asn
            340                 345                 350

Tyr Leu Ile Asn Ile Ile Ser Ala Leu Tyr Gly Ile Asp Pro Ala Glu
        355                 360                 365
```

Ile Gly Phe Pro Asn Arg Gly Gly Ala Thr Gly Ser Lys Gly Gly Ser
370 375 380

Thr Leu Asn Glu Ala Asp Pro Gly Lys Lys Gln Gln Gln Ser Gln Asn
385 390 395 400

Lys Gly Leu Gln Pro Leu Leu Arg Phe Ile Glu Asp Leu Val Asn Arg
405 410 415

His Ile Ile Ser Glu Tyr Gly Asp Lys Tyr Thr Phe Gln Phe Val Gly
420 425 430

Gly Asp Thr Lys Ser Ala Thr Asp Lys Leu Asn Ile Leu Lys Leu Glu
435 440 445

Thr Gln Ile Phe Lys Thr Val Asn Glu Ala Arg Glu Glu Gln Gly Lys
450 455 460

Lys Pro Ile Glu Gly Gly Asp Ile Ile Leu Asp Ala Ser Phe Leu Gln
465 470 475 480

Gly Thr Ala Gln Leu Gln Gln Asp Lys Gln Tyr Asn Asp Gly Lys Gln
485 490 495

Lys Glu Arg Leu Gln Met Met Met Ser Leu Leu Glu Gly Asp Asn Asp
500 505 510

Asp Ser Glu Glu Gly Gln Ser Thr Asp Ser Ser Asn Asp Asp Lys Glu
515 520 525

Ile Gly Thr Asp Ala Gln Ile Lys Gly Asp Asp Asn Val Tyr Arg Thr
530 535 540

Gln Thr Ser Asn Lys Gly Gln Gly Arg Lys Gly Glu Lys Ser Ser Asp
545 550 555 560

Phe Lys His

<210> 620
<211> 257
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 620
Leu Glu Glu Ile Lys Phe Asn Ala Phe Val Pro Met Asp Leu Lys Lys
1 5 10 15

Ser Val Ser Thr Ala Ser Asp Thr Asn Glu Tyr Ser Ile Val Ser Gly
20 25 30

```
Trp Ala Ser Thr Pro Ser Met Asp Leu Gln Asn Asp Ile Val Asn Pro
        35                  40                  45

Lys Gly Ile Asp Ile Glu Tyr Phe Lys Ser Gln Gly Tyr Ile Asn Tyr
    50                  55                  60

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

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

Asp Glu Asn Val Val Lys Met Leu Asp Leu Ala Glu Lys Leu Glu Lys
            100                 105                 110

Ser Gly Ser Gly Arg Arg Leu Gly Phe Ser Ile Glu Gly Ala Val Lys
        115                 120                 125

Lys Arg Asn Ile Asn Asp Asn Arg Val Ile Asp Glu Val Met Ile Thr
    130                 135                 140

Gly Val Ala Leu Val Lys Asn Pro Ala Asn Pro Glu Ala Thr Trp Glu
145                 150                 155                 160

Ser Phe Met Lys Ser Phe Leu Thr Gly His Gly Thr Ser Pro Asp Thr
                165                 170                 175

Gln Val Asp Ala Gly Ala Leu Arg Lys Glu Glu Ile Ala Ser Ser Ile
            180                 185                 190

Thr Asn Leu Ala Tyr Val Thr Lys Ile Lys Asp Leu Lys Glu Phe Asn
        195                 200                 205

Asp Val Trp Asn Gly Val Val Glu Asp Leu Ser Lys Ser Asn Ser Met
    210                 215                 220

Gly Tyr Glu Glu Ser Val Leu Thr Leu Gln Leu Ala Lys Gly Leu Ser
225                 230                 235                 240

Arg Lys Asp Ala Glu Leu Ala Val Met Asp Ile Asn Lys Gln Lys Leu
                245                 250                 255

Glu
```

<210> 621
<211> 316
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F44/10

<400> 621
Met Ser Lys Glu Met Gln Asn Ile Leu Glu Glu Tyr Asp Lys Leu Asn
1   5   10   15

Ala Gln Glu Ala Val Ser Lys Ser Val Glu Asp Asp Glu Lys Asn Thr
            20   25   30

Val Glu Ser Thr Glu Glu Gln Val Ala Glu Thr Thr Glu Glu Pro Ala
        35   40   45

Lys Glu Pro Glu Lys Val Ser Glu Glu Asp Ala Lys Glu Ala Gln Glu
    50   55   60

Gln Gly Glu Lys Val Glu Ser Glu Glu Val Ala Glu Gly Asn Glu Asp
65   70   75   80

Glu Glu Val Glu Lys Ser Ala Lys Glu Ser Lys Asp Pro Val Asp Gln
                85   90   95

Lys Asp Thr Lys Thr Glu Asn Lys Asp Asn Glu Lys Arg Lys Asn Lys
            100   105   110

Lys Asp Lys Lys Glu Asp Ser Asp Asp Glu Asp Lys Asp Thr Asp Asp
        115   120   125

Asp Lys Asp Lys Lys Glu Asp Lys Lys Glu Lys Thr Ser Lys Ser Ile
    130   135   140

Ser Asp Glu Asp Ile Thr Thr Val Phe Lys Ser Ile Leu Thr Ser Phe
145   150   155   160

Glu Asn Leu Asn Lys Glu Lys Glu Asn Phe Ala Thr Lys Glu Asp Leu
                165   170   175

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

Ile Gln Ala Glu Asp Val Ser Lys Ser Val Asp Thr Asp Glu Glu Ala
        195   200   205

Val Glu Lys Ser Val Thr Ser Thr Asn Gly Glu Gln Glu Lys Val Glu
    210   215   220

Gly Tyr Val Ser Lys Ser Val Asp Thr Glu Glu Gln Ala Glu Thr Gly
225   230   235   240

Glu Ala Lys Ser Glu Glu Ala Glu Glu Val Gln Glu Asp Asn Thr Phe
                245   250   255

Lys Gly Leu Ser Gln Glu Glu Arg Thr Lys Phe Met Asp Ser Tyr Lys

260 265 270

Ala Gln Ala Lys Asp Pro Arg Ala Ser Lys His Asp Leu Gln Ser Ala
275 280 285

Tyr Gln Ser Tyr Leu Asn Ile Asn Thr Asp Pro Thr Asn Ala Ser Glu
290 295 300

Lys Asp Ile Lys Thr Val Lys Asp Phe Ala Gln Ile
305 310 315

<210> 622
<211> 463
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 622
Met Thr Ile Glu Lys Asn Leu Ser Asp Val Gln Gln Lys Tyr Ala Asp
1 5 10 15

Gln Phe Gln Glu Asp Val Val Lys Ser Phe Gln Thr Gly Tyr Gly Ile
20 25 30

Thr Pro Asp Thr Gln Ile Asp Ala Gly Ala Leu Arg Arg Glu Ile Leu
35 40 45

Asp Asp Gln Ile Thr Met Leu Thr Trp Thr Asn Glu Asp Leu Ile Phe
50 55 60

Tyr Arg Asp Ile Ser Arg Arg Pro Ala Gln Ser Thr Val Val Lys Tyr
65 70 75 80

Asp Gln Tyr Leu Arg His Gly Asn Val Gly His Ser Arg Phe Val Lys
85 90 95

Glu Ile Gly Val Ala Pro Val Ser Asp Pro Asn Ile Arg Gln Lys Thr
100 105 110

Val Ser Met Lys Tyr Val Ser Asp Thr Lys Asn Met Ser Ile Ala Ser
115 120 125

Gly Leu Val Asn Asn Ile Ala Asp Pro Ser Gln Ile Leu Thr Glu Asp
130 135 140

Ala Ile Ala Val Val Ala Lys Thr Ile Glu Trp Ala Ser Phe Tyr Gly
145 150 155 160

Asp Ala Ser Leu Thr Ser Glu Val Glu Gly Glu Gly Leu Glu Phe Asp
165 170 175

```
Gly Leu Ala Lys Leu Ile Asp Lys Asn Asn Val Ile Asn Ala Lys Gly
            180                 185                 190

Asn Gln Leu Thr Glu Lys His Leu Asn Glu Ala Ala Val Arg Ile Gly
        195                 200                 205

Lys Gly Phe Gly Thr Ala Thr Asp Ala Tyr Met Pro Ile Gly Val His
    210                 215                 220

Ala Asp Phe Val Asn Ser Ile Leu Gly Arg Gln Met Gln Leu Met Gln
225                 230                 235                 240

Asp Asn Ser Gly Asn Val Asn Thr Gly Tyr Ser Val Asn Gly Phe Tyr
                245                 250                 255

Ser Ser Arg Gly Phe Ile Lys Leu His Gly Ser Thr Val Met Glu Asn
            260                 265                 270

Glu Leu Ile Leu Asp Glu Ser Leu Gln Pro Leu Pro Asn Ala Pro Gln
        275                 280                 285

Pro Ala Lys Val Thr Ala Thr Val Glu Thr Lys Gln Lys Gly Ala Phe
    290                 295                 300

Glu Asn Glu Glu Asp Arg Ala Gly Leu Ser Tyr Lys Val Val Val Asn
305                 310                 315                 320

Ser Asp Asp Ala Gln Ser Ala Pro Ser Glu Glu Val Thr Ala Thr Val
                325                 330                 335

Ser Asn Val Asp Asp Gly Val Lys Leu Ser Ile Asn Val Asn Ala Met
            340                 345                 350

Tyr Gln Gln Gln Pro Gln Phe Val Ser Ile Tyr Arg Gln Gly Lys Glu
        355                 360                 365

Thr Gly Met Tyr Phe Leu Ile Lys Arg Val Pro Val Lys Asp Ala Gln
    370                 375                 380

Glu Asp Gly Thr Ile Val Phe Val Asp Lys Asn Glu Thr Leu Pro Glu
385                 390                 395                 400

Thr Ala Asp Val Phe Val Gly Glu Met Ser Pro Gln Val Val His Leu
                405                 410                 415

Phe Glu Leu Leu Pro Met Met Lys Leu Pro Leu Ala Gln Ile Asn Ala
            420                 425                 430

Ser Ile Thr Phe Ala Val Leu Trp Tyr Gly Ala Leu Ala Leu Arg Ala
        435                 440                 445
```

Pro Lys Lys Trp Ala Arg Ile Lys Asn Val Arg Tyr Ile Ala Val
    450   455   460

<210> 623
<211> 98
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 623
Met Leu Tyr Tyr Lys Lys Leu Leu Asp Lys Lys Met Ala Thr Val Tyr
1   5   10   15

Gly Thr Val Glu Ile Asp Lys Asp Gly Val Val Lys Gly Leu Thr Lys
            20   25   30

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

Glu Lys Lys Thr Thr Arg Lys Gln Ser Ala Ser Thr Ser Lys Glu Glu
    50   55   60

Glu Pro Lys Glu Glu Glu Lys Lys Ala Ser Thr Arg Lys Thr Thr Ser
65   70   75   80

Thr Thr Arg Lys Ser Thr Ala Arg Lys Thr Thr Ala Lys Lys Asp Glu
                85   90   95

Asn Lys

<210> 624
<211> 302
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 624
Met Val Asn Ser Met Phe Gly Gly Asp Leu Asp Pro Tyr Glu Lys Ser
1   5   10   15

Leu Asn Tyr Glu Tyr Pro Tyr His Pro Ser Gly Asn Pro Lys His Ile
            20   25   30

Asp Val Ser Glu Ile Asp Asn Leu Thr Leu Ala Asp Tyr Gly Trp Ser
        35   40   45

Pro Asp Ala Val Lys Ala Tyr Met Phe Gly Ile Val Val Gln Asn Pro
    50   55   60

Asp Thr Gly Gln Pro Met Gly Asp Glu Phe Tyr Asn His Ile Leu Glu
65   70   75   80

```
Arg Ala Val Gly Lys Ala Glu Arg Ala Leu Asp Ile Ser Ile Leu Pro
                85                  90                  95

Asp Thr Gln His Glu Met Arg Asp Tyr His Glu Thr Glu Phe Asn Ser
            100                 105                 110

Tyr Met Phe Val His Ala Tyr Arg Lys Pro Ile Leu Gln Val Glu Asn
        115                 120                 125

Leu Gln Leu Gln Phe Asn Gly Arg Pro Ile Tyr Lys Tyr Pro Ala Asn
    130                 135                 140

Trp Trp Lys Val Glu His Leu Ala Gly His Val Gln Leu Phe Pro Thr
145                 150                 155                 160

Ala Leu Met Gln Thr Gly Gln Ser Met Ser Tyr Asp Ala Val Phe Asn
                165                 170                 175

Gly Tyr Pro Gln Leu Ala Gly Val Tyr Pro Pro Ser Gly Ala Thr Phe
            180                 185                 190

Ala Pro Gln Met Ile Arg Leu Glu Tyr Val Ser Gly Met Leu Pro Arg
        195                 200                 205

Lys Lys Ala Gly Arg Asn Lys Pro Trp Glu Met Pro Pro Glu Leu Glu
    210                 215                 220

Gln Leu Val Ile Lys Tyr Ala Leu Lys Glu Ile Tyr Gln Val Trp Gly
225                 230                 235                 240

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

Gly Ile Thr Glu Thr Ile Gly Thr Thr Gln Ser Ala Met Tyr Gly Gly
            260                 265                 270

Ala Ser Ala Gln Ile Leu Gln Ile Asn Glu Asp Ile Lys Glu Leu Leu
        275                 280                 285

Asp Gly Leu Arg Ala Tyr Phe Gly Tyr Asn Met Ile Gly Leu
    290                 295                 300
```

<210> 625
<211> 292
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 625

```
Met Glu Lys Pro Tyr Met Ile Gly Ala Asn Ser Asn Pro Asn Val Ile
```

```
1               5                   10                  15

Asn Lys Ser Thr Thr Tyr Thr Thr Thr Thr Gln Ala Asp Glu Gln Asp
            20                  25                  30

Lys Pro Lys Tyr Thr Thr Arg Leu Glu Phe Asp Thr Ile Asp Met Ile
        35                  40                  45

Arg Phe Ile Asn Asp Arg Gly Ile Lys Val Leu Trp Glu Glu Ala Tyr
    50                  55                  60

Phe Cys Pro Cys Leu Asn Pro Asp Thr Gly His Pro Arg Val Asp Cys
65                  70                  75                  80

Pro Arg Cys His Gly Lys Gly Ile Ala Tyr Leu Pro Pro Lys Glu Thr
                85                  90                  95

Ile Met Ala Ile Gln Ser Gln Glu Lys Gly Thr Asn Gln Leu Asp Ile
            100                 105                 110

Gly Ile Leu Asp Thr Gly Thr Ala Ile Gly Thr Thr Gln Leu Glu Lys
        115                 120                 125

Arg Ile Ser Tyr Arg Asp Arg Phe Thr Val Pro Glu Val Leu Met Pro
    130                 135                 140

Gln Gln Met Ile Tyr Phe Val Asn Lys Asp Arg Ile Arg Lys Gly Ile
145                 150                 155                 160

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

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

Leu Asn Glu Lys Tyr Glu Asn His Thr Val Thr Leu Lys Ile Leu Met
        195                 200                 205

Thr Leu Arg Tyr Val Val Ser Asp Ile Leu Lys Glu Ser Arg Tyr Gln
    210                 215                 220

Tyr Thr Lys Phe Asn Gln Pro Lys Ser Lys Phe Glu Asn Leu Pro Gln
225                 230                 235                 240

Lys Leu Leu Leu Lys Arg Glu Asp Val Ile Val Leu Gln Asp Pro Tyr
                245                 250                 255

Lys Val Asn Asp Gly Ile Glu Glu Asp Leu Glu Ile Gln Val Asp Asp
            260                 265                 270

Pro Lys Ala Ser Ala Ser Asn Pro Ser Asn Leu Gly Gly Phe Phe Gly
```

275 280 285

Gly Ala Phe Lys
290

<210> 626
<211> 206
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 626
Met Pro Val His Gly Lys Arg Pro Asn Leu Phe Lys Asn Lys Asn Tyr
1 5 10 15

Lys Gln Val Gly Lys Arg Thr Ile Asp Gly Met Arg Ser Glu Val Leu
20 25 30

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

Arg Met Pro Thr Tyr Leu Gln Ile Thr Glu Lys Lys Leu Glu Lys Glu
50 55 60

Gly Val Val Asp Leu Lys Lys Ala Phe Ala His Ser Ser Lys Lys Lys
65 70 75 80

Thr Ser Lys Asp Gly Gly Trp Tyr Leu Thr Val Pro Ile Arg Ile Lys
85 90 95

Thr Ser Arg Met Asn Asn Ser Thr Tyr Gln Asp Met Arg Thr Leu Lys
100 105 110

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

Gly Arg Arg Lys Asn Val Ser His Pro Ser Met Lys Pro Glu Pro Met
130 135 140

Thr His Asn Met Thr Lys Val Lys Arg Gly Lys Gln Ser Ser Tyr Phe
145 150 155 160

Ile Phe Arg Thr Val Ser Ser Lys Ser Pro Ala Ser Ser Trp Ile Leu
165 170 175

Asn Arg Asp Lys Val Asn Glu Asp Asn Phe Ser Lys Thr Thr Leu Lys
180 185 190

Thr Val Lys Gln Leu Met Asn Trp Lys Met Lys Asn Leu Asn
195 200 205

<210> 627
<211> 278
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 627
Met Ala Ile Thr Ser Val Asp Ser Tyr Leu Leu Ser Glu Ile Lys Pro
1   5   10   15

Arg Leu Asn Thr Val Leu Glu Asn Cys Tyr Ile Ile Asp Glu Val Leu
            20   25   30

Lys Asp Phe Asp Tyr Gln Thr Arg Glu Ser Phe Lys Glu Ala Phe Cys
        35   40   45

Gly Lys Asn Ala Gln His Glu Val Thr Val Gly Phe Asn Phe Pro Lys
    50   55   60

Phe Lys Asn Asn Tyr Glu Ala His Tyr Leu Ile Gln Leu Gly Gln Gly
65   70   75   80

Gln Glu Thr Lys Asn Ser Leu Gly Ser Ile Gln Ser Ser Tyr Phe Glu
                85   90   95

Ala Thr Gly Asp Thr Leu Val Glu Ser Ser Thr Ala Ile Arg Glu Asp
            100   105   110

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

Val Glu Asp Ile Glu Phe Ala Lys Tyr Asp Asn Leu Gln Val Glu Gly
    130   135   140

Asn Lys Val Ser Phe Lys Tyr Gln Thr Asn Glu Asp Tyr Glu Asn Tyr
145   150   155   160

Asn Ala Asn Ile Ile Phe Thr Glu Lys Lys Asn Asp Ser Lys Gly Leu
                165   170   175

Val Lys Gly Phe Thr Val Glu Glu Gln Val Thr Val Val Gly Leu Ser
            180   185   190

Phe Asn Val Asp Val Ala Arg Cys Leu Asp Ala Val Leu Lys Met Ile
        195   200   205

Leu Ile Ser Met Arg Asp Ser Ile Glu Glu Gln Gln Thr Phe Gln Leu
    210   215   220

Gln Asn Leu Ser Phe Gly Asp Ile Ala Pro Ile Ile Glu Asp Gly Asp
225   230   235   240

Ser Met Ile Phe Gly Arg Pro Thr Ile Ile Lys Tyr Thr Ser Ser Leu
245 250 255

Asp Leu Asp Tyr Thr Ile Thr Gln Asp Ile Asn Lys Leu Thr Phe Lys
260 265 270

Glu Arg Lys Asp Trp Lys
275

<210> 628
<211> 71
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 628
Met Ala Arg Lys Lys Thr Pro Glu Asn Asn Thr Pro Lys Phe Asn Gly
1 5 10 15

Tyr Val His Ile Asp Thr Phe Leu Asp Thr Ala Lys Thr Leu Phe Asn
20 25 30

Met Lys Asp Ser Gln Val Ala Gly Phe Lys Ala Tyr Met Glu Gly Ser
35 40 45

His Tyr Leu Phe Ser Glu Gln Glu Phe Leu Pro Ser Leu Glu Lys Tyr
50 55 60

Leu Gly Arg Lys Leu Asp Ile
65 70

<210> 629
<211> 587
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 629
Met Ala Val Glu Pro Phe Pro Arg Arg Pro Ile Thr Arg Pro His Ala
1 5 10 15

Ser Ile Glu Val Asp Thr Ser Gly Ile Gly Gly Ser Ala Gly Ser Ser
20 25 30

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

Thr Val Tyr Glu Leu Arg Asn Tyr Ala Gln Ala Lys Arg Leu Phe Arg
50 55 60

Ser Gly Glu Leu Leu Asp Ala Ile Glu Leu Ala Trp Gly Ser Asn Pro

65 70 75 80

Asn Tyr Thr Ala Gly Lys Ile Leu Ala Met Arg Ile Glu Asp Ala Lys
85 90 95

Pro Ala Ser Ala Glu Ile Gly Gly Leu Lys Val Thr Ser Lys Ile Tyr
100 105 110

Gly Asn Val Ala Asn Asn Ile Gln Val Gly Leu Glu Lys Asn Thr Leu
115 120 125

Ser Asp Ser Leu Arg Leu Arg Val Ile Phe Gln Asp Asp Arg Phe Asn
130 135 140

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

Glu Glu Ala Asn Ala Thr Phe Ser Val Glu His Asp Glu Glu Thr Gln
165 170 175

Lys Ala Ser Arg Leu Val Leu Lys Val Gly Asp Gln Glu Val Lys Ser
180 185 190

Tyr Asp Leu Thr Gly Gly Ala Tyr Asp Tyr Thr Asn Ala Ile Ile Thr
195 200 205

Asp Ile Asn Gln Leu Pro Asp Phe Glu Ala Lys Leu Ser Pro Phe Gly
210 215 220

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

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

Lys Gln Thr Ala Tyr Asn Gly Ile Val Ser Phe Glu Gln Leu Asn Ala
260 265 270

Glu Gly Glu Val Pro Ser Asn Val Glu Val Glu Ala Gly Glu Glu Ser
275 280 285

Ala Thr Val Thr Ala Thr Ser Pro Ile Lys Thr Ile Glu Pro Phe Glu
290 295 300

Leu Thr Lys Leu Thr Gly Gly Thr Asn Gly Glu Pro Pro Ala Thr Trp
305 310 315 320

Ala Asp Lys Leu Asp Lys Phe Ala His Glu Gly Gly Tyr Tyr Ile Val
325 330 335

Pro Leu Ser Ser Lys Gln Ser Val His Ala Glu Val Ala Ser Phe Val

340 345 350

Lys Glu Arg Ser Asp Ala Gly Glu Pro Met Arg Ala Ile Val Gly Gly
355 360 365

Gly Phe Asn Glu Ser Lys Glu Gln Leu Phe Gly Arg Gln Ala Ser Leu
370 375 380

Ser Asn Pro Arg Val Ser Leu Val Ala Asn Ser Gly Thr Phe Val Met
385 390 395 400

Asp Asp Gly Arg Lys Asn His Val Pro Ala Tyr Met Val Ala Val Ala
405 410 415

Leu Gly Gly Leu Ala Ser Gly Leu Glu Ile Gly Glu Ser Ile Thr Phe
420 425 430

Lys Pro Leu Arg Val Ser Ser Leu Asp Gln Ile Tyr Glu Ser Ile Asp
435 440 445

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

Asn Arg Thr Asn Thr Phe Phe Arg Ile Val Asp Asp Val Thr Thr Phe
465 470 475 480

Asn Asp Lys Ser Asp Pro Val Lys Ala Glu Met Ala Val Gly Glu Ala
485 490 495

Asn Asp Phe Leu Val Ser Glu Leu Lys Val Gln Leu Glu Asp Gln Phe
500 505 510

Ile Gly Thr Arg Thr Ile Asn Thr Ser Ala Ser Ile Ile Lys Asp Phe
515 520 525

Ile Gln Ser Tyr Leu Gly Arg Lys Lys Arg Asp Asn Glu Ile Gln Asp
530 535 540

Phe Pro Ala Glu Asp Val Gln Val Ile Val Glu Gly Asn Glu Ala Arg
545 550 555 560

Ile Ser Met Thr Val Tyr Pro Ile Arg Ser Phe Lys Lys Ile Ser Val
565 570 575

Ser Leu Val Tyr Lys Gln Gln Thr Leu Glu Ala
580 585

<210> 630
<211> 134
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 630
Met Ala Ser Glu Ala Lys Gln Thr Val His Thr Gly Asn Thr Val Leu
1   5   10   15

Leu Met Ile Lys Gly Lys Pro Val Gly Arg Ala Gln Ser Ala Ser Gly
            20   25   30

Gln Arg Glu Tyr Gly Thr Thr Gly Val Tyr Glu Ile Gly Ser Ile Met
        35   40   45

Pro Gln Glu His Val Tyr Leu Arg Tyr Glu Gly Thr Ile Thr Val Glu
    50   55   60

Arg Leu Arg Met Lys Lys Glu Asn Phe Ala Asp Leu Gly Tyr Ala Ser
65   70   75   80

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

Asp Asn Leu Thr Lys Gln Val Ile Ile Ser Tyr His Gly Cys Ser Ala
            100   105   110

Asn Asn Tyr Asn Glu Thr Trp Gln Thr Asn Glu Ile Val Thr Glu Glu
        115   120   125

Ile Glu Phe Ser Tyr Leu
    130

<210> 631
<211> 309
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 631
Met Gly Lys Asn Gln Tyr Thr Phe Asn Ile Lys Glu Asn Lys Asn Lys
1   5   10   15

Trp Tyr Glu Trp Cys Lys Leu Gln Asn Val Lys Pro Leu Val Glu Tyr
            20   25   30

Glu Asn Ala Gln Gln Ile Phe Tyr Phe Glu Phe Leu Glu Gly Lys Phe
        35   40   45

Lys Gly Leu Ile Gly Lys Thr Tyr Trp Ala Ser Ile Asn Arg Gly Ser
    50   55   60

Asn Met Arg Met Ser Cys Leu Thr Ser Glu Ser Lys Asp Lys Tyr Leu
65   70   75   80

```
Lys Asn Leu Gly Lys Arg Lys Gly Ile Glu Val Val Glu Asp Tyr Lys
                85                  90                  95

Gly Gly Arg Lys Leu Lys His Lys Phe Ile Val Leu Glu Gly Lys Tyr
            100                 105                 110

Gln Gly Cys Glu Gly Tyr Ile Thr Leu Asn Asp Leu Glu Asn Leu Gly
        115                 120                 125

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

Asp Lys Gln Ala Arg Leu Arg Asp Cys Ile Ile Leu Glu Tyr Pro Lys
145                 150                 155                 160

Asp Tyr Arg Ile Lys Thr Lys Asp Lys Ile Val Val Lys Asp Lys Glu
                165                 170                 175

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

Leu Leu Glu Leu Ser Cys Ala Ser Glu Gly Glu Lys Ile Val Lys Glu
        195                 200                 205

Ile Leu Thr Lys Asn Ser Ile Lys Phe Glu Lys Glu Lys Ser Phe Arg
    210                 215                 220

Asn Lys Glu Gly Lys Val Gln Arg Phe Asp Phe Tyr Ile Asn Glu Asn
225                 230                 235                 240

Asn Lys Glu Tyr Ala Ile Glu Tyr Asn Gly Ala Gln His Tyr Ile Asp
                245                 250                 255

Ser Thr Gly Tyr Leu Lys Asp Thr Leu Glu Thr Thr Gln Lys Arg Asp
            260                 265                 270

Lys Leu Lys Lys Glu Tyr Ser Lys Asp Lys Gly Ile Asn Leu Leu Ile
        275                 280                 285

Ile Pro Tyr Thr Ile Thr Asp Lys Lys Glu Met Glu Lys Ile Ile Leu
    290                 295                 300

Asn Phe Leu Asn Lys
305


<210> 632
<211> 52
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10
```

<400> 632
Met Asn Asn Arg Gln Ala Lys Leu Lys Gly Tyr Asn Gln Phe His Tyr
1   5   10   15

Tyr Asp Phe Pro Thr Thr Lys Gly Lys Phe Lys Asp Ile Met Lys Arg
            20   25   30

Lys Ser Arg Thr Glu Leu Lys Lys Asp Leu Gln Lys Glu Arg Lys Tyr
        35   40   45

Tyr Leu Asp Lys
    50

<210> 633
<211> 46
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 633
Leu Thr Asn Lys Arg Lys Thr Ile Gly Lys Met Ser Asn Thr Arg Ala
1   5   10   15

Thr Trp Asn Ile Asn Pro Val Thr Lys Val Lys Lys Asp Lys Thr Lys
            20   25   30

Tyr Ser Arg Lys Asn Lys His Lys Gly Leu Asp Asn Tyr Asn
        35   40   45

<210> 634
<211> 96
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 634
Met Arg Ile Tyr Ile Ser Asn Asp Tyr Asn Lys Glu Leu Leu Asp Lys
1   5   10   15

Cys Leu Ser Asp Ile Asn Lys Asp Lys Gly Asn Ile Asn Tyr Ser Ile
            20   25   30

Asn Tyr Gly Glu Gly Asn Ile Lys Glu Ala Asp Val Glu Ile Ile Lys
        35   40   45

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

Lys Phe Val Glu Asp Cys Ile Phe Leu Phe Pro Tyr Lys Ile Ala Leu
65   70   75   80

Leu Arg Gly Gly Lys Ile Glu Leu Arg Phe Asp Trp Asn Glu Ile Leu
85 90 95

<210> 635
<211> 152
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 635
Met Ser Thr Phe Trp Ser Glu Arg Arg Thr Thr Asn Lys Asp Arg Gln
1 5 10 15

Val Lys Lys His Tyr Thr Gln Met Ser Met Tyr Glu Arg Lys Lys Cys
20 25 30

Val Glu Leu Leu Gln Glu Thr Ile Thr Glu Asn Arg Ile Ile Asn Phe
35 40 45

Thr Arg His Ser Ala Lys Lys Val Lys Gly Lys Pro Thr Thr Asn Ile
50 55 60

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

Ile Ile Glu Tyr Asn Asn Thr Asp Tyr Asn Gly Asn Ile Glu Arg Arg
85 90 95

Ile Val Val Lys His Pro Lys Val Ile Thr Val Glu Gly Lys Leu Ser
100 105 110

Tyr Gln Phe Leu Thr Ile Ser Leu Glu Asp Ala Arg Val Ile Thr Val
115 120 125

Trp Tyr Asn Ser Val Asp Asp Thr His Arg Thr Leu Asp Leu Asn Tyr
130 135 140

Tyr Ser Lys Asp Leu Thr Ile Gln
145 150

<210> 636
<211> 64
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 636
Met Gly Leu Thr Ile Val Asn Gly Tyr Phe Phe Leu Ser Ser Ile Ile
1 5 10 15

Phe Ile Val Val Ser Ile Leu Asn Gly Lys Gly Thr Val Thr Arg Glu
20 25 30

Ser Leu Ala Met Ser Gln Ala Leu Val Ile Ile Thr Ser Ile Gln Phe
        35   40   45

Leu Ala Phe Leu Ile Ile Asn Gly Ile Tyr Tyr Ser Leu Lys Tyr Met
    50   55   60

<210> 637
<211> 50
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 637
Met Glu Ile Tyr Ile Val Ile Asp Leu Arg Gly Ser Thr Glu Glu Glu
1   5   10   15

Thr Ser Met Asp Phe Lys Ala Phe Arg Lys Leu Gln Asp Ala Ile Thr
            20   25   30

Tyr Val Asp Gly Asn Gly Asn Arg Asp Leu His Ile Ile Pro Leu Glu
        35   40   45

Leu Glu
    50

<210> 638
<211> 103
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 638
Met Ser Gln Asp Lys Leu Arg Ala Ile Tyr Thr Glu Met Lys Val Glu
1   5   10   15

Leu His Lys Phe Pro Lys Glu Val Asp Val Thr Ser Lys Ser Thr Ala
            20   25   30

Ile Ala Ile Asn Gln Ile Leu Asp Lys Phe Lys Thr Leu Thr Glu Gln
        35   40   45

Ala Gly Lys Ile Thr Arg Lys Tyr Leu Glu Gly Gln Glu Ile Leu Thr
    50   55   60

Ile Asp Tyr Glu Tyr Tyr Asp Ser Leu Gln Glu Tyr Tyr Ile Tyr Leu
65   70   75   80

Leu Arg Asn Ser Glu Lys Ile Glu Gln Ser Leu Gln Glu Ile Thr Lys
                85   90   95

Arg Thr Gly Glu Tyr Val Lys
100

<210> 639
<211> 152
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 639
Met Ala Glu Glu Ile Lys Lys Glu Gln Asp Val Gln Glu Thr Thr Lys
1 5 10 15

Glu Glu Lys Lys Asp Val Ser Lys Met Thr Pro Glu Glu Ile Asp Lys
20 25 30

Leu Lys Tyr Gln Asp Lys Gln Glu Lys Glu Gln Val Ile Asn Lys Val
35 40 45

Ile Lys Gly Val Asn Asp Thr Trp Glu Lys Glu Tyr Asn Phe Glu Glu
50 55 60

Leu Asp Leu Arg Phe Lys Val Lys Ile Lys Leu Pro Asn Ala Arg Glu
65 70 75 80

Gln Gly Asn Ile Phe Ala Leu Arg Ser Ala Tyr Leu Gly Gly Met Asp
85 90 95

Met Tyr Gln Thr Asp Gln Val Ile Arg Ala Tyr Gln Met Leu Ala Thr
100 105 110

Leu Gln Glu Val Gly Ile Glu Val Pro Lys Glu Phe Gln Asp Pro Asp
115 120 125

Asp Ile Tyr Asn Leu Tyr Pro Leu Thr Val Met Tyr Glu Asp Trp Leu
130 135 140

Gly Phe Leu Asn Ser Phe Arg Tyr
145 150

<210> 640
<211> 178
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 640
Met Glu Ser Ile Val Lys Gln Pro Leu Ser Arg Asn Leu Trp Ala Ile
1 5 10 15

Met Lys Glu Phe Asn Val Leu Pro Thr Glu Gln Arg Phe Lys Asp Leu
20 25 30

```
Asp Asp Tyr Gln Ile Glu Phe Ile Ile Gly Asn Met Asn Arg Asp Val
        35                  40                  45

Tyr Glu His Asn Lys Gln Leu Lys Gln Ala Gln Lys Gly Gly Lys Phe
    50                  55                  60

Asp Ser Gln Phe Glu Asp Asp Asp Ser Ser Trp Trp Asn Glu Ser His
65                  70                  75                  80

Glu Asp Phe Asp Pro Val Pro Asp Phe Leu Asp Ala Asp Asp Leu Ala
                85                  90                  95

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

Lys Arg Asn Asp Ala Glu Leu Asn Asp Glu Thr Glu Gly Leu Thr Thr
        115                 120                 125

Gln His Leu Ala Met Met Glu Tyr Ile Arg Gln Lys Gln Gln Glu Leu
    130                 135                 140

Asp Asp Glu Val Gly Asn Gly Lys Thr Ser Glu Asp Asp Ala Thr Ile
145                 150                 155                 160

Ser Gln Asp Ser Val Asn Lys Ala Leu Glu Asp Leu Asp Asp Asp Trp
                165                 170                 175

Tyr Met



<210> 641
<211> 1352
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 641
Met Met Ala Met Asn Asp Asp Tyr Arg Leu Val Leu Ser Gly Asp Ser
1               5                   10                  15

Ser Asp Leu Glu Asn Ser Leu Lys Ala Ile Glu Leu Tyr Met Asp Ser
            20                  25                  30

Leu Glu Ser Lys Asn Ile Asp Ala Pro Leu Asp Asn Phe Leu Lys Lys
        35                  40                  45

Leu Lys Val Ile Ala Lys Glu Val Lys Asn Val Gln Asn Ala Met Asp
    50                  55                  60

Lys Gln Asp Gly Lys Ser Val Ile Ser Ser Lys Asp Met Asp Glu Ser
```

65 70 75 80

Ile Lys Ser Thr Gln Ser Ala Thr Lys Asn Ile Asn Glu Leu Lys Lys
85 90 95

Ala Leu Asp Asp Leu Gln Lys Glu Asn Ile Ser Lys Gly Ile Ala Pro
100 105 110

Asp Pro Glu Val Glu Lys Ala Tyr Ala Lys Met Gly Lys Val Val Asp
115 120 125

Glu Thr Gln Glu Lys Leu Glu Lys Met Ser Ser Gln Lys Ile Gly Ser
130 135 140

Asp Ala Ser Ile Gln Asn Arg Ile Lys Glu Met Lys Thr Leu Asn Gln
145 150 155 160

Val Thr Glu Glu Tyr Asn Lys Ile Ser Lys Asp Ser Ser Ala Thr Lys
165 170 175

Asp Tyr Thr Lys Arg Leu Arg Ala Asn Arg Asn Met Thr Arg Gly Tyr
180 185 190

Met Glu Arg Ser Glu Gly Thr Gly Arg Leu Thr Tyr Asp Gln Gly Ala
195 200 205

Arg Val Arg Ser Glu Leu Gly Lys Val Ser Ser Tyr Glu Ser Gln Arg
210 215 220

Lys Gln Asn Gln Arg Asn Leu Gly Gln Ala Arg Glu Gln Tyr Ser Asn
225 230 235 240

Tyr Arg Asn Gln Gln Gln Asp Leu Thr Lys Arg Arg Ala Ser Gly Gln
245 250 255

Ile Asn Lys Ala Gln Tyr Glu Gln Glu Leu Ala Ser Ile Lys Gln Glu
260 265 270

Met Lys Ala Arg Glu Glu Leu Ile Ser Asn Tyr Glu Lys Leu Gly Ala
275 280 285

Glu Leu Asp Lys Thr Val Gln Tyr Tyr Lys Gly Ser Val Gln Lys Asp
290 295 300

Phe Gln Ser Arg Asp Val Asp Gln Gln Arg Gly Thr Phe Gly Arg Met
305 310 315 320

Val Gln Glu Arg Leu Pro Ser Ile Gly Ser His Ala Met Met Gly Thr
325 330 335

Thr Ala Met Ala Thr Gly Leu Tyr Met Lys Gly Ala Ser Leu Ser Glu

```
            340                 345                 350

Thr Asn Arg Pro Met Val Thr Ser Leu Gly Gln Asn Ser Asp Asn Met
        355                 360                 365

Asp Ile Asp Ser Val Arg Asn Ala Tyr Gly Asp Leu Ser Ile Asp Asn
    370                 375                 380

Lys Leu Gly Tyr Asn Ser Thr Asp Met Leu Lys Met Ala Thr Ser Tyr
385                 390                 395                 400

Glu Ala Ser Val Gly His Lys Ser Asp Glu Asp Thr Met Ala Gly Thr
                405                 410                 415

Lys Gln Leu Ala Ile Gly Gly Arg Ser Leu Gly Ile Lys Asp Gln Glu
            420                 425                 430

Ala Tyr Gln Glu Ser Met Gly Gln Ile Met His Thr Gly Gly Val Asn
        435                 440                 445

Ser Asp Asn Met Lys Glu Met Gln Asp Ala Phe Leu Gly Gly Ile Lys
    450                 455                 460

Gln Ser Gly Met Val Gly Arg Gln Asp Glu Gln Leu Lys Ala Leu Gly
465                 470                 475                 480

Ser Ile Ala Glu Gln Ser Gly Glu Gly Arg Thr Leu Thr Lys Asp Gln
                485                 490                 495

Met Ser Asn Leu Thr Ala Met Gln Ser Thr Phe Ala Glu Ser Gly Ser
            500                 505                 510

Lys Gly Leu Gln Gly Glu Gln Gly Ala Asn Ala Ile Asn Ser Ile Asp
        515                 520                 525

Gln Gly Leu Lys Asn Gly Met Asn Ser Ser Tyr Ala Arg Ile Ala Met
    530                 535                 540

Gly Trp Gly Thr Gln Tyr Gln Gly Leu Glu Gly Gly Tyr Asp Leu Gln
545                 550                 555                 560

Lys Arg Met Asp Glu Gly Ile Ser Asn Pro Glu Asn Leu Thr Asp Met
                565                 570                 575

Ala Asp Met Ala Thr Gln Met Gly Gly Ser Glu Lys Glu Gln Lys Tyr
            580                 585                 590

Leu Phe Asn Arg Ser Met Lys Glu Ile Gly Ala Asn Leu Thr Met Glu
        595                 600                 605

Gln Ser Asp Glu Ile Phe Lys Asp Ser Lys Glu Gly Lys Leu Ser Lys
```

610 615 620

Glu Glu Leu Ala Lys Lys Ala Lys Lys Met Glu Lys Glu Gly Lys Lys
625 630 635 640

Glu Gly Glu Asp Asn Ala Thr Asp Tyr Lys Glu Ser Lys Ser Gly Lys
645 650 655

Asn Asp Gln Asn Lys Ser Lys Thr Asp Asp Lys Ala Glu Asp Thr Tyr
660 665 670

Asp Met Ala Gln Pro Leu Arg Asp Ala His Ser Ala Leu Ala Gly Leu
675 680 685

Pro Ala Pro Ile Tyr Leu Ala Ile Gly Ala Ile Gly Ala Phe Thr Ala
690 695 700

Ser Leu Ile Ala Ser Ala Ser Gln Phe Gly Ala Gly His Leu Ile Gly
705 710 715 720

Lys Gly Ala Lys Gly Leu Arg Asn Lys Phe Gly Arg Asn Lys Gly Gly
725 730 735

Ser Ser Gly Gly Asn Pro Met Ala Gly Gly Met Pro Ser Gly Gly Gly
740 745 750

Ser Pro Lys Gly Gly Gly Ser Pro Lys Gly Gly Gly Thr Arg Ser Thr
755 760 765

Gly Gly Lys Ile Leu Asp Ser Ala Lys Gly Leu Gly Gly Phe Leu Val
770 775 780

Gly Gly Ala Gly Trp Lys Gly Met Phe Gly Gly Glu Ser Lys Gly Lys
785 790 795 800

Gly Phe Lys Gln Thr Ser Lys Glu Ala Trp Ser Gly Thr Arg Lys Val
805 810 815

Phe Asn Arg Asp Asn Gly Arg Lys Ala Met Asp Lys Ser Lys Asp Ile
820 825 830

Ala Lys Gly Thr Gly Ser Gly Leu Lys Asp Ile Tyr Asn Asp Ser Ile
835 840 845

Phe Gly Lys Glu Arg Arg Gln Asn Leu Gly Glu Lys Ala Lys Gly Phe
850 855 860

Gly Gly Lys Ala Lys Gly Leu Tyr Gly Lys Phe Ala Asp Lys Phe Gly
865 870 875 880

Asp Gly Gly Lys Asn Gly Ile Leu Ser Gln Ser Pro Lys Ala Gly Gly

885 890 895

Ser Gly Ile Gly Lys Leu Gly Lys Leu Ala Gly Gly Leu Gly Lys Gly
900 905 910

Ala Gly Val Leu Gly Val Ala Thr Ser Ala Leu Ser Leu Ile Pro Ala
915 920 925

Leu Ala Ser Gly Asp Ser Lys Ala Ile Gly Gly Gly Ile Gly Ser Met
930 935 940

Gly Gly Gly Met Ala Gly Ala Ser Ala Gly Ala Ser Ile Gly Ala Leu
945 950 955 960

Phe Gly Gly Val Gly Ala Ile Pro Gly Ala Leu Ile Gly Gly Ala Ile
965 970 975

Gly Ser Phe Gly Gly Gly Ala Val Gly Glu Lys Val Gly Asp Met Ala
980 985 990

Lys Lys Ala Asn Thr Lys Glu Gly Trp Asn Leu Gly Trp Thr Asn Gly
995 1000 1005

Asp Lys Asp Gly Lys Asn Lys Phe Gln Asp Ser Leu Leu Gly Lys
1010 1015 1020

Pro Ile Ser Lys Ala Trp Ser Gly Ile Thr Gly Leu Phe Asp Asn
1025 1030 1035

Asp Ala Glu Ala Ser Glu Glu Asn Ser Lys Asp Lys Lys Lys Gly
1040 1045 1050

Val Lys Gly Val Lys Gly Asp Thr Lys Lys Lys Glu Lys Met Thr
1055 1060 1065

Ala Glu Gln Leu Arg Glu Lys Asn Asn Gln Ser Glu Thr Lys Asn
1070 1075 1080

Leu Lys Ile Tyr Ser Asp Leu Leu Asp Arg Ala Gln Lys Ile Ile
1085 1090 1095

Glu Ser Ala Lys Gly Ile Asn Ile Asp Gly Gly Thr Ser Asp Ser
1100 1105 1110

Gly Ser Asp Ser Gly Gly Ser Ala Ser Asp Val Gly Gly Glu Gly
1115 1120 1125

Ala Glu Lys Met Tyr Lys Phe Leu Lys Gly Lys Gly Leu Ser Asp
1130 1135 1140

Asn Gln Val Gly Ala Val Met Gly Asn Leu Gln Gln Glu Ser Asn

1145 1150 1155

Leu Asp Pro Asn Ala Lys Asn Pro Ser Ser Gly Ala Phe Gly Ile
1160 1165 1170

Ala Gln Trp Leu Gly Ala Arg Lys Thr Gly Leu Asp Asn Phe Ala
1175 1180 1185

Lys Ser Lys Gly Lys Lys Ser Ser Asp Leu Asp Val Gln Leu Asp
1190 1195 1200

Tyr Leu Trp Lys Glu Met Gln Ser Asp Tyr Glu Ser Lys Asn Leu
1205 1210 1215

Lys Asn Ala Gly Trp Ser Lys Gly Gly Ser Leu Glu Gln Asn Thr
1220 1225 1230

Lys Ala Phe Ala Thr Gly Phe Glu Arg Met Gly Ala Asn Glu Ala
1235 1240 1245

Met Met Gly Thr Arg Val Asn Asn Ala Lys Glu Phe Lys Lys Lys
1250 1255 1260

Tyr Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Ala Met Ser Ser
1265 1270 1275

Thr Tyr Gln Glu Ala Met Ser Asn Pro Val Leu Thr Thr Gly Ser
1280 1285 1290

Asn Tyr Arg Gly Ser Asn Asp Ala Ser Asn Ala Ser Thr Thr Asn
1295 1300 1305

Arg Ile Thr Val Asn Val Asn Val Gln Gly Gly Asn Asn Pro Glu
1310 1315 1320

Glu Thr Gly Asp Ile Ile Gly Gly Arg Ile Arg Glu Val Leu Asp
1325 1330 1335

Ser Asn Met Asp Ile Phe Ala Asn Glu His Lys Arg Ser Tyr
1340 1345 1350

<210> 642
<211> 400
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 642
Met Lys Arg Leu Arg Arg Pro Lys Val Arg Ile Glu Ile Val Thr Asp
1 5 10 15

```
Asp Asn Thr Phe Thr Leu Arg Phe Glu Asp Thr Arg Asp Tyr Asn Gly
            20                  25                  30

Asp Glu Phe Gly Ala Lys Leu Leu Gly Phe Gln Thr Lys Asn Ser Met
        35                  40                  45

Glu Asp Asp Ser Ser Val Phe Gln Ile Asn Met Ala Gly Asp Thr Tyr
    50                  55                  60

Trp Asp Lys Leu Val Met Ala Asn Asp Ile Ile Arg Ile Phe Ile Thr
65                  70                  75                  80

Pro Asn Asp Asp Pro Asn Asp Lys Glu Gly Arg Gln Glu Arg Leu Ile
                85                  90                  95

Gln Val Gly Met Val Ser Gln Val Ser Lys Val Gly Ser Tyr Gly Asn
            100                 105                 110

Asp Gln Thr Gln Phe Arg Ile Thr Gly Gln Ser Phe Val Lys Pro Phe
        115                 120                 125

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

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

Thr Gly Ser Ser Ala His Glu Val Met Thr Gly Ile Ile Arg Arg Phe
                165                 170                 175

Val Pro Tyr Met Lys Tyr Asn Tyr Thr Glu Lys Thr Tyr Asn Thr Ile
            180                 185                 190

Asp Ser Tyr Leu Asp Tyr Asp Asp Leu Ser Ser Trp Asp Glu Phe Glu
        195                 200                 205

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

Gln Leu Met Asp Met Val Thr Ala Arg Pro Phe Asn Glu Leu Phe Phe
225                 230                 235                 240

Lys Asn Ser Glu Lys Thr Pro Gly Lys Ala Gln Leu Val Leu Arg Lys
                245                 250                 255

Thr Pro Phe Asn Pro Thr Glu Trp Arg Ala Leu Asp Met Ile Lys Val
            260                 265                 270

Pro Thr Glu Asp Phe Ile Glu Glu Asp Val Gly Lys Ser Asp Val Glu
        275                 280                 285
```

Thr Tyr Ser Ile Phe Thr Ala Thr Pro Ala Gly Met Leu Lys Glu Leu
290 295 300

Asn Gly Asp Val Phe Ser Lys Pro Gln Phe His Pro Glu Leu Thr Asp
305 310 315 320

Arg Tyr Gly Tyr Thr Lys Phe Glu Val Glu Asn Ile Tyr Leu Ser Thr
325 330 335

Lys Ser Gly Ser Ala Thr Glu Asp Ser Asp Ser Ser Gly Asp Asp Asn
340 345 350

Gly Thr Glu Arg Gly Thr Tyr Ser Lys Ile Met Lys Asp Leu Ser Asn
355 360 365

Tyr Gly Arg Asp Asn Ile Ser Lys Gly Ile Asp Lys Tyr Thr Ser Lys
370 375 380

Leu Ser Ser Lys Tyr Lys Asn Leu Lys Lys Pro Lys Leu Lys Lys Leu
385 390 395 400

<210> 643
<211> 36
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 643
Leu Thr Lys Asp Lys Leu Lys Ser Ile Leu Lys Glu Lys Phe Lys Thr
1 5 10 15

Gln Asp Asp Phe Asn Asn Ser Lys Lys Arg Lys Lys Leu Lys Gln Met
20 25 30

His Leu Lys Asn
35

<210> 644
<211> 338
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 644
Leu Thr Thr Lys Tyr Arg Phe Gly Asn Lys Thr His Ala Thr Thr Leu
1 5 10 15

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

Phe Asp Lys Tyr Leu Lys Ala Ile Glu Gly Val Ser Asn Ile Ala Thr
35 40 45

```
Asp Thr Gly Ser Asp Ala Ser Asp Ser Pro Leu Val Met Phe Ser Arg
    50                  55                  60

Met Leu Phe Asn Trp Tyr His Gly Asn Pro Asn Phe Tyr Ala Gly Asp
65                  70                  75                  80

Ile Ile Val Leu Gly Asp Pro Lys Tyr Asp Leu Gly Lys Arg Leu Phe
                85                  90                  95

Ile Glu Asp Lys Gln Arg Gly Asp Thr Trp Glu Phe Tyr Ile Glu Ser
            100                 105                 110

Val Glu His Lys Phe Asp Tyr Lys Gln Gly Tyr Tyr Thr Thr Val Gly
        115                 120                 125

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

Pro His Arg Phe Ala Gly Leu Trp Asn Gln Ser Ser Asp Phe Met Gly
145                 150                 155                 160

Gly Leu Met Gly Glu Asp Thr Ser Lys Glu Leu Lys Glu Lys Gly Val
                165                 170                 175

Ser Glu Lys Gln Ser Ser Gly Asp Lys Asp Gly Gly Ser Asp Ser Gly
            180                 185                 190

Gly Ala Gln Asp Gly Gly Ser Leu Asp Ser Leu Lys Lys Tyr Asn Gly
        195                 200                 205

Lys Leu Pro Lys His Asp Pro Ser Phe Val Gln Pro Gly Asn Arg His
    210                 215                 220

Tyr Lys Tyr Gln Cys Thr Trp Tyr Ala Tyr Asn Arg Arg Gly Gln Leu
225                 230                 235                 240

Gly Ile Pro Val Pro Leu Trp Gly Asp Ala Ala Asp Trp Ile Gly Gly
                245                 250                 255

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

Cys Val Ile Trp Gln Arg Gly Val Gln Gly Gly Ser Ala Gln Tyr Gly
        275                 280                 285

His Val Ala Phe Val Glu Lys Val Leu Asp Gly Gly Lys Lys Ile Phe
    290                 295                 300

Ile Ser Glu His Asn Trp Ala Thr Pro Asn Gly Tyr Gly Thr Arg Thr
305                 310                 315                 320
```

Ile Asp Met Ser Ser Ala Ile Gly Lys Asn Ala Gln Phe Ile Tyr Asp
325 330 335

Lys Lys

<210> 645
<211> 295
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 645
Met Ala Thr Asp Lys Glu Ala Lys Asp Val Ile Asp Lys Phe Ile Asp
1 5 10 15

Asn Val Phe Asn Phe Asp Val Leu Thr Met Glu Arg Val Lys Glu Lys
20 25 30

Asp Glu Glu Ile Lys Lys Ile Thr Thr Asp Asp Met Tyr Glu Lys Val
35 40 45

Val Tyr Ile Arg Pro Tyr Val Gly Val Ile Gln Ser Leu Asn Pro Gln
50 55 60

His Val Gln Tyr Glu Ser Phe Ser Asn Asn Gly Tyr Asp Ile Glu Ala
65 70 75 80

Glu Leu Ser Phe Arg Lys Val Ser Tyr Leu Val Asp Lys Gly Ser Ile
85 90 95

Pro Thr Asp Ser Leu Ser Thr Leu Thr Val His Leu Val Glu Arg Asn
100 105 110

Gln Glu Leu Leu Ile Asp Tyr Phe Asp Glu Ile Gln Asp Val Leu Tyr
115 120 125

Gly Glu Tyr Met Glu Glu Glu Tyr Val Phe Asp Glu Asp Val Pro Leu
130 135 140

Ser Thr Ile Leu Ala Leu Asp Leu Asn Asp Asn Leu Lys Ser Leu Ser
145 150 155 160

Asn Ile Lys Tyr Met Phe Lys Gly Ala Pro Lys Glu Asn Pro Phe Gly
165 170 175

Thr Asp Lys Asp Val Tyr Ile Asp Thr Tyr Asn Leu Leu Tyr Trp Leu
180 185 190

Tyr Leu Gly Glu Asp Glu Glu Leu Ala Tyr Pro Met Asn Ile Asn Tyr

195 200 205

Phe Phe Thr Glu Gly Arg Phe Phe Thr Ile Phe Gly Lys Gly His Lys
210 215 220

Tyr Lys Val Asp Val Ser Lys Phe Ile Val Gly Asp Ile Leu Phe Phe
225 230 235 240

Gly Arg Ser Asp Thr Asn Ile Gly Ile Tyr Val Gly Asp Gly Glu Phe
245 250 255

Ile Ser Met Ile Gly Lys Phe Pro Lys Asp Glu Thr Pro Ile Gly Lys
260 265 270

Tyr Lys Leu Asp Asp Tyr Trp Asn Glu Phe Asn Gly Arg Val Met Arg
275 280 285

Phe Asp Glu Glu Val Tyr Ile
290 295

<210> 646
<211> 848
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 646
Met Val Val Arg Phe Gln Ser Ser Met Gly Arg Ser Leu Lys Arg Val
1 5 10 15

Asp Ser Asp Asp Leu Asn Val Lys Gly Leu Val Leu Ala Thr Val Ser
20 25 30

Lys Ile Asn Tyr Lys Tyr Gln Ser Val Glu Val Lys Val Asn Asn Leu
35 40 45

Thr Leu Gly Ser Arg Ile Gly Asp Asp Gly Ser Leu Ala Val Pro Tyr
50 55 60

Pro Lys Ser Phe Ile Gly Arg Thr Pro Glu Gly Ser Val Phe Gly Thr
65 70 75 80

Lys Pro Leu Ile Thr Glu Gly Ser Val Val Leu Ile Gly Phe Leu Asn
85 90 95

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

Gln Asn Lys Met Ile Asn Thr Asn Pro Leu Asp Gly Gly Lys Phe Asp
115 120 125

```
Thr Asp Ser Val Tyr Lys Tyr Ser Ser Ala Leu Tyr Glu Ile Leu Pro
    130                 135                 140

Ser Leu Asn Tyr Lys Tyr Asp Asp Gly Glu Gly Thr Ser Ile Lys Thr
145                 150                 155                 160

Tyr Asn Gly Lys Ser Phe Phe Ser Met Thr Ser Gly Glu Glu Glu Lys
                165                 170                 175

Pro Gln Ala Thr Asp Phe Tyr Thr Gly Thr Glu Tyr Gln Asp Leu Phe
            180                 185                 190

Thr Ser Tyr Tyr Gly Asn Lys Thr Leu Ile Glu Pro Arg Ile Gln Lys
        195                 200                 205

Ala Pro Asn Met Leu Phe Lys His Gln Gly Val Phe Tyr Asp Asp Gly
    210                 215                 220

Thr Pro Asp Asn His Ile Thr Thr Leu Phe Ile Ser Glu Arg Gly Asp
225                 230                 235                 240

Ile Arg Ala Ser Val Leu Asn Thr Glu Thr Gln Lys Arg Thr Thr Gln
                245                 250                 255

Glu Met Ser Ser Asp Gly Ser Tyr Arg Val Ile Lys Gln Asp Asp Asp
            260                 265                 270

Leu Met Leu Asp Glu Ala Gln Val Trp Ile Glu Tyr Gly Ile Ser Glu
        275                 280                 285

Asp Asn Lys Phe Tyr Ile Lys Asn Asp Lys His Lys Phe Glu Phe Thr
    290                 295                 300

Asp Glu Gly Ile Tyr Ile Asp Asp Lys Pro Met Leu Glu Asn Leu Asp
305                 310                 315                 320

Glu Ser Ile Ala Glu Ala Met Lys Asn Leu Asn Glu Ile Gln Lys Glu
                325                 330                 335

Leu Asp Asp Ile Asn Tyr Leu Leu Glu Gly Val Gly Lys Asp Asn Leu
            340                 345                 350

Glu Glu Leu Ile Glu Ser Thr Lys Glu Ser Ile Glu Ala Ser Lys Lys
        355                 360                 365

Ala Thr Ser Asp Val Asn Arg Leu Thr Thr Gln Ile Ala Glu Val Ser
    370                 375                 380

Gly Arg Thr Glu Gly Ile Ile Thr Gln Phe Gln Lys Phe Arg Asp Glu
385                 390                 395                 400
```

```
Thr Phe Lys Asp Phe Tyr Glu Asp Ala Ser Thr Val Ile Asn Glu Val
                405                 410                 415

Asn Gln Asn Phe Pro Thr Met Lys Thr Asp Val Asn Thr Leu Lys Thr
            420                 425                 430

Lys Val Asp Asn Leu Glu Lys Thr Glu Ile Pro Asn Ile Lys Thr Arg
        435                 440                 445

Leu Thr Glu Leu Glu Asn Asn Asn Asn Asn Ala Asp Lys Ile Ile Ser
    450                 455                 460

Asp Arg Gly Glu His Ile Gly Ala Met Ile Gln Leu Glu Glu Asn Val
465                 470                 475                 480

Thr Val Pro Thr Arg Asn Tyr Met Pro Ile Pro Trp Ser Lys Val Thr
                485                 490                 495

Tyr Asn Asn Ala Glu Phe Trp Asp Ser Asn Asn Pro Thr Arg Leu Val
            500                 505                 510

Val Pro Lys Gly Ile Thr Lys Val Arg Val Ala Gly Asn Val Leu Trp
        515                 520                 525

Asp Ser Asn Ala Thr Gly Gln Arg Met Leu Arg Ile Leu Lys Asn Gly
    530                 535                 540

Thr Tyr Ser Leu Gly Leu Pro Tyr Thr Arg Asp Val Ala Ile Ser Thr
545                 550                 555                 560

Ala Pro Gln Asn Gly Thr Ser Gly Val Ile Pro Val Lys Glu Gly Asp
                565                 570                 575

Tyr Phe Glu Phe Glu Ala Phe Gln Asp Ser Glu Gly Asp Arg Gln Phe
            580                 585                 590

Arg Ala Asp Pro Tyr Thr Trp Phe Ser Ile Glu Ala Ile Glu Leu Glu
        595                 600                 605

Thr Glu Thr Met Glu Lys Asp Phe Met Leu Ile Gly His Arg Gly Ala
    610                 615                 620

Thr Gly Tyr Thr Asp Glu His Thr Ile Lys Gly Tyr Gln Met Ala Leu
625                 630                 635                 640

Asp Lys Gly Ala Asp Tyr Ile Glu Leu Asp Leu Gln Leu Thr Lys Asp
                645                 650                 655

Asn Lys Leu Leu Cys Met His Asp Ser Thr Ile Asp Arg Thr Thr Thr
            660                 665                 670
```

```
Gly Thr Gly Lys Val Gly Asp Met Thr Leu Ser Tyr Ile Gln Thr Asn
        675                 680                 685

Phe Thr Ser Leu Asn Gly Glu Pro Ile Pro Ser Leu Asp Asp Val Leu
    690                 695                 700

Asn His Phe Gly Thr Lys Val Lys Tyr Tyr Ile Glu Thr Lys Arg Pro
705                 710                 715                 720

Phe Asp Ala Asn Met Asp Lys Glu Leu Leu Thr Gln Leu Lys Ala Lys
                725                 730                 735

Gly Leu Ile Gly Ile Gly Ser Glu Arg Phe Gln Val Ile Ile Gln Ser
            740                 745                 750

Phe Ala Arg Glu Ser Leu Ile Asn Ile His Asn Gln Phe Ser Asn Ile
        755                 760                 765

Pro Leu Ala Tyr Leu Thr Ser Thr Phe Ser Glu Ser Glu Met Asp Asp
    770                 775                 780

Cys Leu Ser Tyr Gly Ser Tyr Ala Ile Ala Pro Lys Tyr Thr Thr Ile
785                 790                 795                 800

Thr Lys Glu Leu Val Asp Leu Ala His Ser Lys Gly Leu Lys Val His
                805                 810                 815

Ala Trp Thr Val Asn Thr Lys Glu Glu Met Gln Ser Leu Ile Gln Met
            820                 825                 830

Gly Val Asp Gly Phe Phe Thr Asn Tyr Leu Asp Glu Tyr Lys Lys Ile
        835                 840                 845

<210> 647
<211> 263
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 647
Met Pro Gln Ser Asp Gly Ile Ser Asn Leu His Arg Ile Ala Leu Arg
1               5                   10                  15

Phe Pro Lys Glu Gly Gly Gly Tyr Asp Met Tyr Arg Phe Lys Val Asn
            20                  25                  30

Pro Glu Asn Tyr Thr Ile Asp Ser Pro Gln Arg Thr Thr Ala Ile Lys
        35                  40                  45

Thr Lys Ser Asp Ile Val Ile Glu Asp Tyr Gly Lys Asp Ile Glu Val
    50                  55                  60
```

```
Ile Asn Phe Thr Gly Thr Thr Gly Phe Arg Pro Val Arg Glu Ala Asp
65                  70                  75                  80

Gly Leu Lys Thr Gly Lys Gln Lys Met Glu Glu Leu Gln Ser Arg Val
                85                  90                  95

Ser Glu Tyr Ala Met Gln Gly Gly Ser Gly Asn Val Ser Gly Ser Tyr
            100                 105                 110

Leu Gln Phe Phe Asn Phe Thr Asp Asp Ser Tyr Tyr Lys Val His Leu
        115                 120                 125

Ala Pro Gln Gly Leu Lys Ile Thr Arg Ser Lys Asp Glu Pro Leu Leu
    130                 135                 140

Phe Arg Tyr Glu Ile Thr Leu Val Val Ile Gly Ser Leu Thr Glu Ala
145                 150                 155                 160

Asp Arg Ser Ala Val Thr Thr Glu Glu Phe Gly Asn Val Lys Pro Asn
                165                 170                 175

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

Arg Lys Thr Arg Asp Arg Asn Asn Gln Glu Ile Ser Lys Arg Glu Asn
        195                 200                 205

Thr Ile Pro Lys Ser Thr Gly Asp Asn Thr Asn Glu Gly Asn Arg Leu
    210                 215                 220

Lys Gln Ser Phe Pro Ser Ser Ser Ile Tyr Asn Pro Arg Gln Ser Thr
225                 230                 235                 240

Asn Gly Leu Lys Gly Asn Ile Asp Asn Met Ala Leu Ile Ile Gly Tyr
                245                 250                 255

Gly Asp Gly Gly Val Ser Ser
            260


<210> 648
<211> 174
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 648
Met Asn Asn Phe Ile Pro Gln Pro Gln Gly Leu Leu Arg Phe Leu Asn
1               5                   10                  15

Ala Leu Asp Ala Asp Leu Thr Ser Ser His Met Asn Leu Leu Asp Glu
            20                  25                  30
```

Glu Val Ser Phe Val Ser Lys Phe Tyr Thr Pro Gln Leu Gln Leu Ser
35 40 45

Glu Leu Ala Lys Lys Val Leu Thr Asn Ile Lys Thr Asp Asp Ile Pro
50 55 60

Val Leu Glu Arg Glu Phe Asn Asp Asn Thr Ile Ile His Lys Ala Asn
65 70 75 80

Asp Thr Leu Leu Lys Val Gln Ala Pro Arg Met Tyr Met Ile Leu Gln
85 90 95

Ser Ile Val Leu Glu Ala Tyr Ala Ile Val Asn Cys Phe Val Glu Asn
100 105 110

Pro Ser Ser Leu Lys Tyr Leu Thr Glu Glu Asp Val Ser Ile Thr Arg
115 120 125

Glu Asn Leu Asn Tyr Val Ala Asp Tyr Leu Gly Asn Tyr Asp Asp Tyr
130 135 140

Asn Ser Val Val Leu Asp Leu Arg Asp Leu Asp Leu Cys Phe Ser Ala
145 150 155 160

Ile Glu Leu Gln Leu Pro Leu Ile Lys Lys Glu Ala Asn Val
165 170

<210> 649
<211> 234
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 649
Met Arg Phe Lys Lys His Val Val Gln His Glu Glu Thr Met Gln Ala
1 5 10 15

Ile Ala Gln Arg Tyr Tyr Gly Asp Val Ser Tyr Trp Ile Asp Leu Val
20 25 30

Glu His Asn Asn Leu Lys Tyr Pro Tyr Leu Val Glu Thr Asp Glu Glu
35 40 45

Lys Met Lys Asp Pro Glu Arg Leu Ala Ser Thr Gly Asp Thr Leu Ile
50 55 60

Ile Pro Ile Glu Ser Asp Leu Thr Asp Val Ser Ala Lys Glu Ile Asn
65 70 75 80

Ser Arg Asp Lys Asp Val Leu Val Glu Leu Ala Leu Gly Arg Asp Leu

85 90 95

Asn Ile Thr Ala Asp Glu Lys Tyr Phe Asn Glu His Gly Thr Ser Asp
100 105 110

Asn Ile Leu Ala Phe Ser Thr Asn Gly Asn Gly Asp Leu Asp Thr Val
115 120 125

Lys Gly Ile Asp Asn Met Lys Gln Gln Leu Gln Ala Arg Leu Leu Thr
130 135 140

Pro Arg Gly Ser Leu Met Leu His Pro Asn Tyr Gly Ser Asp Leu His
145 150 155 160

Asn Leu Phe Gly Leu Asn Ile Pro Glu Gln Ala Thr Leu Ile Glu Met
165 170 175

Glu Val Leu Arg Thr Leu Thr Ser Asp Asn Arg Val Lys Ser Ala Asn
180 185 190

Leu Ile Asp Trp Lys Ile Gln Gly Asn Val Tyr Ser Gly Gln Phe Ser
195 200 205

Val Glu Ile Lys Ser Val Glu Glu Ser Ile Asn Phe Val Leu Gly Gln
210 215 220

Asp Glu Glu Gly Ile Phe Ala Leu Phe Glu
225 230

<210> 650
<211> 348
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 650
Met Lys Thr Arg Lys Leu Thr Asn Ile Leu Ser Lys Leu Ile Asp Lys
1 5 10 15

Thr Met Ala Gly Thr Ser Lys Ile Thr Asp Phe Thr Pro Gly Ser Ala
20 25 30

Ser Arg Ser Leu Leu Glu Ala Val Ser Leu Glu Ile Glu Gln Phe Tyr
35 40 45

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

Glu Ala Phe Asp Phe Gln Lys Arg Gln Ser Lys Arg Ala Tyr Gly Asp
65 70 75 80

```
Val Thr Ile Gln Phe Tyr Gln Pro Leu Asp Met Arg Met Tyr Ile Pro
                85                  90                  95

Ala Gly Thr Thr Phe Thr Ser Thr Arg Gln Glu Tyr Pro Gln Gln Phe
            100                 105                 110

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

Val Glu Val Tyr Cys Lys Glu Thr Gly Val Ala Gly Asn Val Pro Glu
    130                 135                 140

Gly Thr Ile Asn Thr Ile Ala Ser Gly Ser Ser Leu Ile Arg Ser Val
145                 150                 155                 160

Asn Asn Glu Tyr Ser Phe Asn Thr Gly Thr Lys Glu Glu Ser Gln Glu
                165                 170                 175

Asp Phe Lys Arg Arg Phe His Ser Phe Val Glu Ser Arg Gly Arg Ala
            180                 185                 190

Thr Asn Lys Ser Val Arg Tyr Gly Ala Leu Gln Ile Pro Asp Val Glu
        195                 200                 205

Gly Val Tyr Val Tyr Glu Glu Thr Gly His Ile Thr Val Phe Ala His
    210                 215                 220

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

Ala Leu Gln Asp Tyr Arg Pro Ser Gly Ile Met Leu Asp Val Thr Gly
                245                 250                 255

Val Glu Lys Glu Glu Val Asn Val Ser Ala Thr Val Thr Ile Ser Asn
            260                 265                 270

Lys Ser Arg Ile Gly Asp Thr Leu Gln Lys His Ile Glu Gly Val Ile
        275                 280                 285

Arg Ser Tyr Leu Asn Asn Leu Lys Thr Ser Asp Asp Leu Ile Ile Thr
    290                 295                 300

Asp Leu Ile Gln Ala Ile Met Asn Ile Asp Asp Val Leu Ile Tyr Asp
305                 310                 315                 320

Val Ser Phe Asp Asn Leu Asp Glu Asn Ile Ile Val Pro Pro Gln Gly
                325                 330                 335

Ile Ile Arg Ala Gly Glu Ile Lys Val Glu Leu Lys
            340                 345
```

<210> 651
<211> 854
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 651
Val Ala Asn Phe Leu Lys Asn Leu His Pro Leu Leu Arg Arg Asp Arg
1   5   10   15

Asn Lys Lys Asp Asn Gln Asp Pro Asn Phe Ala Leu Ile Asp Ala Leu
            20   25   30

Asn Glu Glu Met Asn Gln Val Glu Lys Asp Ala Ile Glu Ser Lys Leu
        35   40   45

Gln Ser Ser Leu Lys Thr Ser Thr Ser Glu Tyr Leu Asp Lys Phe Gly
    50   55   60

Asp Trp Phe Gly Val Tyr Arg Lys Thr Asp Glu Asn Asp Asp Val Tyr
65   70   75   80

Arg Ala Arg Ile Ile Lys Tyr Leu Leu Leu Lys Arg Gly Thr Asn Asn
                85   90   95

Ala Ile Ile Asp Ala Ile Lys Asp Tyr Leu Gly Arg Asp Asp Ile Asp
            100   105   110

Val Ser Val Tyr Glu Pro Phe Thr Asn Ile Phe Tyr Thr Asn Lys Ser
        115   120   125

His Leu Asn Gly Glu Asp His Leu Met Gly Tyr Tyr Tyr Arg Phe Ala
    130   135   140

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

Val Ile Asn Glu Phe Lys Pro Ala Gly Val Thr Leu Tyr Val Thr Tyr
                165   170   175

Asp Gly Ala Ser Thr Ile Arg Gly Gly Ala Ile Ile Lys Trp Leu Asp
            180   185   190

Gly Leu Pro Lys Ile Glu Thr Tyr Gln Glu Phe Asp Arg Phe Thr Gly
        195   200   205

Tyr Asp Asp Thr Phe Tyr Gly His Ile Asn Met Asn Gln Ser Lys Asp
    210   215   220

Thr Asp Asn Ser Thr Ser Asp Ile Phe Lys Thr Asn His Ser Leu Ile
225   230   235   240

```
Asn Ser Leu Asp Val Leu Thr Gly Ser Ser Ser Val Gly Arg Gln Tyr
                245                 250                 255

Val Asn Tyr Gly Tyr Ile Thr Ser Tyr Val Tyr Asn Pro Gly Met Thr
            260                 265                 270

Ser Ser Val Asn Gln Ile Ser Ala Ser Thr Glu Gly Arg Gly Gln Glu
        275                 280                 285

Val Pro Thr Asp Tyr Tyr Met Tyr Thr Ser Thr Lys Asn Asn Asn Thr
    290                 295                 300

Val Glu Leu Ser Met Gln Thr Thr Ser Gly Val Ser Tyr Leu Tyr Asn
305                 310                 315                 320

Asn Phe Asn Phe Arg Asp Tyr Met Ser Lys Tyr Arg Pro Gln Val Asn
                325                 330                 335

Leu Gln Ser Asp Glu Ala Arg Arg Ile Val Ser Asp Tyr Ile Lys Glu
            340                 345                 350

Leu Ser Ile Asp Tyr Tyr Leu Ser Ala Val Ile Pro Pro Asp Glu Ser
        355                 360                 365

Ile Glu Ile Lys Leu Gln Val Tyr Asp Phe Ser Ile Asn Arg Trp Leu
    370                 375                 380

Thr Val Ser Ile Asn Asn Leu Ser Phe Tyr Glu Lys Asn Ile Gly Ser
385                 390                 395                 400

Asn Ile Gly Tyr Ile Lys Asp Tyr Leu Asn Ser Glu Leu Asn Met Phe
                405                 410                 415

Thr Arg Leu Glu Ile Asn Ala Gly Lys Arg Asp Ser Val Asp Ile Lys
            420                 425                 430

Val Asn Tyr Leu Asp Leu Met Phe Tyr Tyr Tyr Glu Arg Gly Ile Tyr
        435                 440                 445

Thr Ile Lys Pro Tyr Lys Ala Leu Val Glu Asn Tyr Leu Asp Ile Ser
    450                 455                 460

Arg Glu Thr Tyr Val Glu Ala Phe Lys Ile Ser Ser Leu Ser Asn Gly
465                 470                 475                 480

Asp Ile Ile Thr Lys Thr Gly Tyr Leu Pro Ile Gly Tyr Leu Arg Val
                485                 490                 495

Ser Gly Asp Ile Asp Asn Leu Ser Asn His Ile Glu Ile Ile Thr Ile
            500                 505                 510
```

```
Asp Asn Asn Thr Asn Ser Ile Thr Ser Thr Leu Leu Glu Asp Asp Ser
        515                 520                 525

Asn Ser Leu Ile Leu Ser Tyr Gly Asn Val Lys Thr Asn Ile His Ser
    530                 535                 540

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

Ser Tyr Tyr Gly Asp Ala Trp Glu Glu Leu Thr Val Leu Thr Glu Ile
                565                 570                 575

Ser Glu Gly Glu Thr Ile Val Pro Asn Ile Leu Ile Asp Leu Tyr Gly
            580                 585                 590

Leu Gln Thr Val Asp Tyr Ser Asn Ile Asn Pro Met Ser Lys Val Ser
        595                 600                 605

Leu Arg Ser Ile Trp Asn Val Lys Leu Gly Glu Leu Asn Asn Lys Glu
    610                 615                 620

Gly Ser Leu Ser Asn Met Pro Asn Asp Tyr Phe Asn Ala Val Trp Gln
625                 630                 635                 640

Asp Ile Asp Lys Leu Ser Asp Ile Asp Leu Gly Ser Met Arg Met Ile
                645                 650                 655

Lys Asp Thr Glu Gly Gly Val Phe Asp Gly Ala Thr Gly Glu Ile Ile
            660                 665                 670

Lys Ala Thr Leu Phe Asn Val Gly Val Tyr Thr Asp Leu Asp Met Leu
        675                 680                 685

Ala Tyr Thr Leu Thr Asn Tyr Thr Glu Pro Ile Thr Leu Gly Ser Ser
    690                 695                 700

Arg Leu Ile Ser Glu Leu Lys Glu Glu Leu Leu Thr Ser Glu Ser Phe
705                 710                 715                 720

Asn Val Asp Asn Arg Ile Lys Val Ile Asp Ser Ile Ser Glu Gln Leu
                725                 730                 735

Pro Asn Asn Asn Ile Leu Ser Asn Ser Tyr Gln Thr Gln Thr Ile Thr
            740                 745                 750

Gln Asn Gly Phe Ala Lys Tyr Asn Leu Lys Glu Pro Ile Glu Gln Arg
        755                 760                 765

Lys Gln Tyr Asn Leu Arg Ile His Gly Asp Phe Lys Glu Gly Leu Glu
    770                 775                 780
```

```
Arg Leu Ala Ile Gly Asn Ser Asn Gly Ser Phe Asn Glu Val Phe Val
785                 790                 795                 800


Tyr Pro Glu Asn Ile Lys Asp Gly Ile Val Asp Ile Thr Tyr Thr Ser
                805                 810                 815


Arg Asp Asp Asn Tyr Ala Glu Gly Lys Gln Arg Leu Asn Asn Asp Tyr
            820                 825                 830


Arg Val Tyr Ala Gln Pro Tyr Asp Ser Glu Val Val Thr Ile Tyr Ser
        835                 840                 845


Leu Glu Leu Ile Lys Val
    850


<210> 652
<211> 173
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 652
Met Ala Ile Ala Thr Tyr Asn Ser His Val Glu Leu Ala Lys Tyr Leu
1               5                   10                  15


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


Trp Ser Asn Glu Thr Asn Pro Pro Gln Pro Asp Glu Asn Ala Thr Val
        35                  40                  45


Leu Gln Glu Val Ile Gly Tyr Lys Lys Ala Thr Lys Val Thr Leu Val
    50                  55                  60


Arg Pro Ser Lys Ser Pro Glu Asp Asp Asn Lys Asn Leu Ile Ser Tyr
65                  70                  75                  80


Gly Asn Lys Ser Trp Val Glu Val Thr Pro Glu Asn Ala Lys Asp Glu
                85                  90                  95


Gly Ala Lys Trp Val Tyr Leu Glu Ser Ser Ile Val Gly Asp Glu Leu
            100                 105                 110


Pro Leu Gly Thr Tyr Arg Gln Val Gly Phe Val Met Asp Leu Val Ala
        115                 120                 125


Lys Ser Gly Ile Ser Lys Phe Asn Leu Val Pro Ser Glu Val Glu Ser
    130                 135                 140


Thr Gly Thr Leu Leu Phe Phe Asp Asn Lys Gln Phe Gln Asn Arg Ser
145                 150                 155                 160
```

Glu Gln Thr Thr Ala Lys Glu Arg Phe Ile Val Glu Val
165 170

<210> 653
<211> 1152
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 653
Met Ala Ile Asn Phe Lys Gly Ser Pro Tyr Leu Asp Arg Phe Asp Pro
1 5 10 15

Ser Lys Asp Arg Thr Lys Val Leu Phe Asn Pro Asp Arg Pro Leu Gln
20 25 30

Gln Ala Glu Leu Asn Glu Met Gln Ser Ile Asp Gln Tyr Tyr Leu Lys
35 40 45

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

Gly Phe Thr Leu Ser Glu Asp Asn Val Leu Thr Val Asn Pro Gly Tyr
65 70 75 80

Val Tyr Ile Asn Gly Lys Ile Arg Tyr Tyr Asp Asn Asp Asp Ser Val
85 90 95

Lys Ile Thr Gly Val Gly Lys Glu Thr Ile Gly Ile Lys Leu Thr Glu
100 105 110

Arg Ile Val Thr Pro Asp Glu Asp Ala Ser Leu Leu Asp Gln Thr Ser
115 120 125

Gly Val Pro Ser Tyr Phe Ser Lys Gly Ala Asp Arg Leu Glu Glu Lys
130 135 140

Met Ser Leu Thr Val Asn Asp Pro Thr Ser Ala Thr Ile Tyr Thr Phe
145 150 155 160

Met Asp Gly Asp Leu Tyr Ile Gln Ser Thr Asn Ala Glu Met Asp Lys
165 170 175

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

Lys Val Asn Gly Phe Glu Leu Phe Ser Glu Gly Asn Ala Glu Asp Asp
195 200 205

Asp His Val Ser Val Val Val Asp Ala Gly Lys Ala Tyr Val Lys Gly

210 215 220

Phe Lys Val Asp Lys Pro Val Ser Thr Arg Ile Ser Val Pro Lys Ser
225 230 235 240

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

Asn Asn Ser Ile Ser Leu Ala Asn Ser Pro Val Lys Glu Ile Arg Arg
260 265 270

Val Thr Gly Gln Val Leu Ile Glu Lys Glu Arg Val Thr Arg Gly Ala
275 280 285

Gln Gly Asp Gly Gln Asp Phe Leu Ser Asn Asn Thr Ala Phe Glu Ile
290 295 300

Val Lys Val Trp Thr Glu Thr Ser Pro Gly Val Thr Thr Lys Glu Tyr
305 310 315 320

Lys Gln Gly Glu Asp Phe Arg Leu Thr Asp Gly Gln Thr Ile Asp Trp
325 330 335

Ser Pro Gln Gly Gln Glu Pro Ser Gly Gly Thr Ser Tyr Tyr Val Ser
340 345 350

Tyr Lys Tyr Asn Lys Arg Met Glu Val Gly Lys Asp Tyr Glu Val Thr
355 360 365

Thr Gln Gly Glu Gly Leu Ser Lys Lys Trp Tyr Ile Asn Phe Thr Pro
370 375 380

Glu Asn Gly Ala Lys Pro Ile Asp Gln Thr Val Val Leu Val Asp Tyr
385 390 395 400

Thr Tyr Tyr Leu Ala Arg Lys Asp Ser Val Phe Ile Asn Lys Tyr Gly
405 410 415

Asp Ile Ala Ile Leu Pro Gly Glu Pro Asn Ile Met Arg Leu Val Thr
420 425 430

Pro Pro Leu Asn Thr Asp Pro Glu Asn Leu Gln Leu Gly Thr Val Thr
435 440 445

Val Leu Pro Asp Ser Asp Glu Ala Val Cys Ile Ser Phe Ala Ile Thr
450 455 460

Arg Leu Ser Met Glu Asp Leu Gln Lys Val Lys Thr Arg Val Asp Asn
465 470 475 480

Leu Glu Tyr Asn Gln Ala Val Asn Ala Leu Asp Asp Gly Ala Met Glu

485 490 495

Gly Gln Asn Pro Leu Thr Leu Arg Ser Val Phe Ser Glu Gly Phe Ile
500 505 510

Ser Leu Asp Lys Ala Asp Ile Thr His Pro Asp Phe Gly Ile Val Phe
515 520 525

Ser Phe Glu Asp Ala Glu Ala Thr Leu Ala Tyr Thr Glu Ala Val Asn
530 535 540

Gln Pro Lys Ile Ile Pro Gly Asp Thr Thr Ala His Ile Trp Gly Arg
545 550 555 560

Leu Ile Ser Ala Pro Phe Thr Glu Glu Arg Thr Ile Tyr Gln Gly Gln
565 570 575

Ala Ser Glu Thr Leu Asn Val Asn Pro Tyr Asn Ile Pro Asn Lys Gln
580 585 590

Gly Val Leu Lys Leu Thr Pro Ser Glu Asp Asn Trp Ile Asp Thr Glu
595 600 605

Asn Val Thr Ile Thr Glu Gln Lys Thr Lys Lys Val Thr Met Lys Arg
610 615 620

Phe Trp Arg His Asn Glu Ser Tyr Tyr Gly Glu Thr Glu His Tyr Leu
625 630 635 640

Tyr Ser Asn Leu Gln Leu Asp Ala Gly Gln Lys Trp Lys Gly Glu Thr
645 650 655

Tyr Ala Tyr Asp Arg Glu His Gly Arg Thr Gly Thr Leu Leu Glu Ser
660 665 670

Gly Gly Gln Arg Thr Leu Glu Glu Met Ile Glu Phe Ile Arg Ile Arg
675 680 685

Asp Val Ser Phe Glu Val Lys Gly Leu Asn Pro Asn Asp Asn Asn Leu
690 695 700

Tyr Leu Leu Phe Asp Gly Val Arg Cys Pro Ile Thr Pro Ala Thr Gly
705 710 715 720

Tyr Arg Lys Gly Ser Glu Asp Gly Thr Ile Met Thr Asp Ala Lys Gly
725 730 735

Thr Ala Lys Gly Lys Phe Thr Ile Pro Ala Gly Ile Arg Cys Gly Asn
740 745 750

Arg Glu Val Thr Leu Lys Asn Ala Asn Ser Thr Ser Ala Thr Thr Tyr

```
        755                 760                 765

Thr Ala Gln Gly Arg Lys Lys Ile Val Gln Asp Ile Ile Ile Arg Thr
    770                 775                 780

Arg Val Thr Val Asn Leu Val Asp Pro Leu Ala Gln Ser Phe Gln Tyr
785                 790                 795                 800

Asp Glu Asn Arg Thr Ile Ser Ser Leu Gly Leu Tyr Phe Ala Ser Lys
                805                 810                 815

Gly Asp Lys Gln Ser Asn Val Val Ile Gln Ile Arg Gly Met Gly Asp
            820                 825                 830

Gln Gly Tyr Pro Asn Lys Thr Ile Tyr Ala Glu Thr Val Met Asn Ala
        835                 840                 845

Asp Asp Ile Lys Val Ser Asn Asn Ala Ser Ala Glu Thr Arg Val Tyr
    850                 855                 860

Phe Asp Asp Pro Met Met Ala Glu Gly Gly Lys Glu Tyr Ala Ile Val
865                 870                 875                 880

Ile Ile Thr Glu Asn Ser Asp Tyr Thr Met Trp Val Gly Thr Arg Thr
                885                 890                 895

Lys Pro Lys Ile Asp Lys Pro Asn Glu Val Ile Ser Gly Asn Pro Tyr
            900                 905                 910

Leu Gln Gly Val Leu Phe Ser Ser Ser Asn Ala Ser Thr Trp Thr Pro
        915                 920                 925

His Gln Asn Ser Asp Leu Lys Phe Gly Ile Tyr Thr Ser Lys Phe Asn
    930                 935                 940

Glu Thr Ala Thr Ile Glu Phe Glu Pro Ile Lys Asp Val Ser Ala Asp
945                 950                 955                 960

Arg Ile Val Leu Met Ser Thr Tyr Leu Thr Pro Glu Arg Thr Gly Cys
                965                 970                 975

Thr Trp Glu Met Lys Leu Ile Leu Asp Asp Met Ala Ser Ser Thr Thr
            980                 985                 990

Phe Asp Gln Leu Lys Trp Glu Pro  Ile Gly Asn Tyr Gln  Asp Leu Asp
        995                 1000                1005

Val Leu  Gly Leu Ala Arg Gln  Val Lys Leu Arg Ala  Thr Phe Glu
    1010                1015                1020

Ser Asn  Arg Tyr Ile Ser Pro  Leu Met Ser Ser Ser  Asp Leu Thr
```

1025 1030 1035

Phe Thr Thr Phe Leu Thr Glu Leu Thr Gly Ser Tyr Val Gly Arg
1040 1045 1050

Ala Ile Asp Met Thr Glu Ala Pro Tyr Asn Thr Val Arg Phe Ser
1055 1060 1065

Tyr Glu Ala Phe Leu Pro Lys Gly Thr Lys Val Val Pro Lys Tyr
1070 1075 1080

Ser Ala Asp Asp Gly Lys Thr Trp Lys Thr Phe Thr Lys Ser Pro
1085 1090 1095

Thr Thr Thr Arg Ala Asn Asn Glu Phe Thr Arg Tyr Val Ile Asp
1100 1105 1110

Glu Lys Val Lys Ser Ser Gly Thr Asn Thr Lys Leu Gln Val Arg
1115 1120 1125

Leu Asp Leu Ser Thr Glu Asn Ser Phe Leu Arg Pro Arg Val Arg
1130 1135 1140

Arg Leu Met Val Thr Thr Arg Asp Glu
1145 1150

<210> 654
<211> 52
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 654
Met Pro Arg Glu Val Arg Asp Pro Tyr Ser Gln Ala Lys Leu Phe Ile
1 5 10 15

Pro Thr Val Glu Glu Lys Ser Ile Lys Glu Leu Glu Lys Thr Tyr Lys
20 25 30

Glu Lys Ile Asp Glu Ala Thr Lys Leu Ile Asn Glu Leu Lys Lys Glu
35 40 45

Arg Gly Glu Lys
50

<210> 655
<211> 639
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 655

```
Met Ala Phe Asn Tyr Thr Pro Leu Thr Glu Thr Gln Lys Leu Lys Asp
1               5                  10                  15

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

Asn Leu Ser Asp Val Lys Gln Ile Ser Gln Pro Asp Phe Asn Asn Ile
        35                  40                  45

Leu Ala Ser Ile Pro Asp Ser Gly Asn Tyr Tyr Val Thr Asn Ser Lys
    50                  55                  60

Gly Ala Pro Ser Gly Glu Ala Thr Ala Gly Phe Val Arg Leu Asp Lys
65                  70                  75                  80

Arg Asn Val Asn Tyr Tyr Lys Ile Tyr Tyr Ser Pro Tyr Ser Ser Asn
                85                  90                  95

Lys Met Tyr Ile Lys Thr Tyr Ala Asn Gly Thr Val Tyr Asp Trp Ile
            100                 105                 110

Ser Phe Lys Leu Asp Glu Gly Asn Leu Tyr Asn Glu Gly Asn Thr Leu
        115                 120                 125

Asn Val Lys Glu Leu Thr Glu Ser Thr Thr Gln Tyr Val Thr Leu Val
    130                 135                 140

Asn Pro Pro Lys Glu Asn Leu Asn Thr Gly Trp Val Asn Tyr Lys Glu
145                 150                 155                 160

Ser Lys Asn Gly Val Ser Ser Leu Val Glu Phe Asn Pro Val Asn Ser
                165                 170                 175

Thr Ser Thr Phe Lys Met Ile Arg Lys Leu Pro Val Gln Glu Gln Lys
            180                 185                 190

Pro Asn Leu Leu Lys Asp Ser Leu Phe Val Tyr Pro Glu Thr Ser Ser
        195                 200                 205

Ser Asn Ile Lys Thr Asp Asn Trp Asn Thr Pro Pro Phe Trp Gly Tyr
    210                 215                 220

Thr Ala Asn Ser Gly Arg Ser Gly Val Arg Phe Arg Gly Glu Asn Thr
225                 230                 235                 240

Ile Gln Ile Asp Asp Gly Ser Ser Thr Tyr Pro Thr Ala Met Thr Asn
                245                 250                 255

Arg Phe Lys Met Gly Asn Glu Leu Ser Val Gly Asp Thr Ile Thr Val
            260                 265                 270
```

```
Ser Val Tyr Ala Lys Ile Asn Asp Pro Ala Leu Leu Lys Asp Asn Leu
        275                 280                 285

Val Tyr Phe Glu Leu Ala Gly Tyr Asp Met Val Asp Arg Thr Asp Asn
    290                 295                 300

Pro Tyr Thr Gly Gly Arg Arg Glu Ile Thr Ala Ser Glu Ile Thr Thr
305                 310                 315                 320

Glu Trp Lys Lys Tyr Ser Phe Thr Phe Thr Ile Pro Glu Asn Thr Ile
                325                 330                 335

Gly Ala Ser Gly Val Lys Val Asn Tyr Val Ser Leu Leu Leu Arg Met
            340                 345                 350

Asn Cys Ser Ser Ser Lys Gly Asn Gly Ala Val Val Tyr Tyr Ala Leu
        355                 360                 365

Pro Lys Leu Glu Lys Ser Ser Lys Val Thr Pro Phe Ile Thr His Ala
    370                 375                 380

Thr Asp Val Arg Lys Tyr Asp Glu Ile Trp Ser Asn Trp Gln Glu Val
385                 390                 395                 400

Ile Ser Lys Asp Glu Leu Lys Gly His Ser Pro Val Asp Ile Glu Tyr
                405                 410                 415

Asn Asp Tyr Phe Lys Tyr Gln Trp Trp Lys Ser Glu Val Asn Glu Lys
            420                 425                 430

Ser Leu Lys Asp Leu Ala Met Thr Val Pro Gln Gly Tyr His Thr Phe
        435                 440                 445

Tyr Cys Gln Gly Ser Ile Ala Gly Thr Pro Arg Gly Arg Ser Ile Arg
    450                 455                 460

Gly Thr Ile Gln Val Asp Tyr Asp Lys Gly Asp Pro Tyr Arg Ala Asn
465                 470                 475                 480

Lys Phe Val Lys Leu Leu Phe Thr Asp Thr Glu Gly Ile Pro Tyr Thr
                485                 490                 495

Leu Tyr Tyr Gly Gly Tyr Asn Gln Gly Trp Lys Leu Leu Lys Gln Ser
            500                 505                 510

Glu Thr Ser Thr Leu Leu Trp Glu Gly Thr Leu Asp Phe Gly Ser Thr
        515                 520                 525

Glu Ala Val Asn Leu Asn Asp Ser Leu Asp Asn Tyr Asp Leu Ile Glu
    530                 535                 540
```

Val Thr Tyr Trp Thr Arg Ser Ala Gly His Phe Ser Thr Lys Arg Leu
545 550 555 560

Asp Ile Lys Asn Thr Ser Asn Leu Leu Tyr Ile Arg Asp Phe Asn Ile
565 570 575

Ser Asn Asp Ser Thr Gly Ser Ser Val Asp Phe Phe Glu Gly Tyr Cys
580 585 590

Thr Phe Pro Thr Arg Thr Ser Val Gln Pro Gly Met Val Lys Ser Ile
595 600 605

Thr Leu Asp Gly Ser Thr Asn Thr Thr Lys Val Ala Ser Trp Asn Glu
610 615 620

Lys Glu Arg Ile Lys Val Tyr Asn Ile Met Gly Ile Asn Arg Gly
625 630 635

<210> 656
<211> 124
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 656
Met Ala Val Lys Tyr Asp Ile Gly Asn Asn Glu Ile Val Leu His Leu
1 5 10 15

Arg Glu Gly Lys Tyr Ile Thr Gly Phe Thr Thr Val Gly Gly Tyr Asp
20 25 30

Lys Glu Leu Gly Gln Val Lys Val Asn Arg Glu Ile Leu Pro Ala Tyr
35 40 45

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

Glu Glu Val Ile Glu Asn Lys Asn Tyr Val Pro Pro Gln Ile Asn Asn
65 70 75 80

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

Ser Leu Lys Glu Glu Leu Glu Leu Met Arg Lys Gln Gln Glu Ala Met
100 105 110

Met Glu Met Leu Gln Lys Leu Leu Gly Gln Lys Gly
115 120

<210> 657
<211> 458

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 657
Met Ala Leu Asn Phe Thr Thr Ile Thr Glu Asn Asn Val Ile Lys Asp
1 5 10 15

Leu Thr Thr Gln Val Asn Asn Ile Gly Glu Glu Leu Thr Lys Glu Arg
20 25 30

Asn Ile Phe Asp Ile Thr Asp Asp Leu Val Tyr Asn Phe Asn Lys Ser
35 40 45

Gln Lys Ile Lys Leu Thr Asp Asp Lys Gly Leu Thr Lys Ser Tyr Gly
50 55 60

Asn Ile Thr Ala Leu Arg Asp Ile Lys Glu Pro Gly Tyr Tyr Tyr Ile
65 70 75 80

Gly Ala Arg Thr Leu Ala Thr Leu Leu Asp Arg Pro Asp Met Glu Ser
85 90 95

Leu Asp Val Val Leu His Val Val Pro Leu Asp Thr Ser Ser Lys Val
100 105 110

Val Gln His Leu Tyr Thr Leu Ser Thr Asn Asn Asn Gln Ile Lys Met
115 120 125

Leu Tyr Arg Phe Val Ser Gly Asn Ser Ser Ser Glu Trp Gln Phe Ile
130 135 140

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

Leu Asp Ile Ala Ser Pro Gly Val Tyr Phe Val Met Gly Met Thr Gly
165 170 175

Gly Met Pro Ser Gly Val Asp Ser Gly Phe Leu Asp Leu Ser Val Asp
180 185 190

Ala Asn Asp Asn Arg Leu Ala Arg Leu Thr Asp Ala Glu Thr Gly Lys
195 200 205

Glu Tyr Thr Ser Ile Lys Lys Pro Thr Glu Val Tyr Thr Ala Trp Lys
210 215 220

Lys Glu Phe Glu Pro Lys Asp Met Glu Lys Tyr Leu Leu Ser Ser Ile
225 230 235 240

Arg Asp Asp Gly Ser Ala Ser Phe Pro Leu Leu Val Tyr Thr Ser Asp

245 250 255

Asn Lys Thr Phe Gln Gln Ala Ile Ile Asp His Ile Asp Arg Thr Gly
260 265 270

Gln Thr Thr Phe Thr Phe Tyr Val Gln Gly Gly Val Ser Gly Ser Pro
275 280 285

Met Ser Asn Ser Cys Arg Gly Leu Phe Met Ser Asp Thr Pro Asn Thr
290 295 300

Ser Ser Leu His Gly Val Tyr Asn Ala Ile Gly Thr Asp Gly Arg Asn
305 310 315 320

Val Thr Gly Ser Val Val Gly Gly Asn Trp Thr Ser Pro Lys Thr Ser
325 330 335

Pro Ser His Lys Glu Leu Trp Thr Gly Ala Gln Ser Phe Leu Ser Val
340 345 350

Gly Thr Thr Lys Asn Leu Ala Asp Asp Ile Ser Asn Tyr Ser Tyr Val
355 360 365

Glu Val Tyr Thr Lys His Lys Thr Val Glu Lys Thr Lys Gly Asn Asp
370 375 380

Asp Ser Gly Thr Ile Cys His Lys Phe Tyr Leu Asp Gly Ser Gly Thr
385 390 395 400

Tyr Val Cys Ser Gly Thr Phe Val Ser Gly Asp Arg Thr Asp Thr Lys
405 410 415

Pro Pro Val Thr Glu Phe Tyr Arg Val Gly Val Ser Phe Lys Gly Ser
420 425 430

Thr Trp Thr Leu Val Asp Ser Ala Val Gln Asn Ser Lys Thr Gln Tyr
435 440 445

Val Thr Arg Ile Ile Gly Ile Asn Met Pro
450 455

<210> 658
<211> 582
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 658
Met Arg Leu Arg Ile Lys Asn Leu Tyr Thr Tyr Val Glu Phe Glu Glu
1 5 10 15

```
Asp Asp Lys Tyr Leu Lys Asp Ile Phe Leu Lys Arg Val His Thr Thr
            20                  25                  30

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

Gly Ser Trp Asp Gly Tyr Val Asp Phe Tyr Val Tyr Glu Glu Asp Lys
    50                  55                  60

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

Gln Ser Arg Tyr Asn Phe Gln Phe Glu Thr Ile Asp Glu Arg Asp Glu
                85                  90                  95

Ser Phe Leu Ser Glu Glu Asp Ile Asp Asp Glu Ile Thr Leu Leu Asp
            100                 105                 110

Asn Asn Val Gly Gln Ile Thr Leu Arg Asp Tyr Gln Tyr Glu Ala Val
        115                 120                 125

Tyr Asn Ser Leu Thr Phe Tyr Asn Gly Ile Ala His Leu Ala Thr Asn
    130                 135                 140

Gly Gly Lys Thr Glu Val Ala Ser Gly Ile Ile Asp Gln Leu Leu Pro
145                 150                 155                 160

Gln Leu Glu Lys Gly Glu Arg Val Ala Phe Phe Thr Gly Ser Thr Glu
                165                 170                 175

Ile Phe His Gln Ser Ala Asp Arg Leu Gln Glu Arg Leu Asn Ile Pro
            180                 185                 190

Ile Gly Lys Val Gly Ala Gly Lys Phe Asp Val Lys Gln Val Thr Val
        195                 200                 205

Val Met Ile Pro Thr Leu Asn Ala Asn Leu Lys Asp Pro Thr Gln Gly
    210                 215                 220

Val Lys Val Thr Pro Lys Gln Asn Ile Ser Lys Lys Ile Ala Gln Glu
225                 230                 235                 240

Ile Leu Pro Lys Phe Glu Gly Gly Thr Asn Gln Lys Lys Leu Leu Lys
                245                 250                 255

Val Leu Leu Asp Asn Thr Thr Pro Lys Thr Lys Val Glu Gln Asn Val
            260                 265                 270

Leu Ser Ala Leu Glu Ile Ile Tyr Gln Asn Ser Lys Thr Asp Ala Glu
        275                 280                 285
```

```
Val Leu Leu Asn Leu Arg Asn His Asn Ala His Phe Gln Lys Ile Val
    290                 295                 300

Arg Glu Lys Asn Glu Lys Lys Tyr Asp Lys Tyr Gln Asp Met Arg Asp
305                 310                 315                 320

Phe Leu Asp Ser Val Thr Val Met Ile Val Asp Glu Ala His His Ser
                325                 330                 335

Lys Ser Asp Ser Trp Tyr Asn Asn Leu Met Thr Cys Glu Lys Ala Leu
            340                 345                 350

Tyr Arg Ile Ala Leu Thr Gly Ser Ile Asp Lys Lys Asp Glu Leu Leu
        355                 360                 365

Trp Met Arg Leu Gln Ala Leu Phe Gly Asn Val Ile Ala Arg Thr Thr
    370                 375                 380

Asn Lys Phe Leu Ile Asp Glu Gly His Ser Ala Arg Pro Thr Ile Asn
385                 390                 395                 400

Ile Ile Pro Val Ala Asn Pro Asn Asp Ile Asp Arg Ile Asp Asp Tyr
                405                 410                 415

Arg Glu Ala Tyr Asp Lys Gly Ile Thr Asn Asn Asp Phe Arg Asn Lys
            420                 425                 430

Leu Ile Ala Lys Leu Thr Glu Lys Trp Tyr Asn Gln Asp Lys Gly Thr
        435                 440                 445

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

Leu Asn Asp Leu Asp Val Glu His Tyr Phe Leu His Gly Glu Ile Asp
465                 470                 475                 480

Ser Glu Thr Arg Arg Glu Lys Leu Asn Asp Met Arg Ser Gly Lys Leu
                485                 490                 495

Lys Val Met Ile Ala Thr Ser Leu Ile Asp Glu Gly Val Asp Ile Ser
            500                 505                 510

Gly Ile Asn Ala Leu Ile Leu Gly Ala Gly Gly Lys Ser Leu Arg Gln
        515                 520                 525

Thr Leu Gln Arg Ile Gly Arg Ala Leu Arg Lys Lys Lys Asp Asp Asn
    530                 535                 540

Thr Thr Gln Ile Phe Asp Phe Asn Asp Met Thr Asn Arg Phe Leu Tyr
545                 550                 555                 560
```

Thr His Ala Asn Glu Arg Arg Lys Ile Tyr Glu Glu Glu Asp Phe Glu
565 570 575

Ile Lys Asp Leu Gly Lys
580

<210> 659
<211> 537
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 659
Met Ala Thr Lys Thr Gln Arg Lys Leu Tyr Gln Tyr Leu Glu Glu Asn
1 5 10 15

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

Ser Leu Gly Val Ser Ile Ser Ala Leu Ser Asn Asn Leu Lys Lys Leu
35 40 45

Glu Glu Glu Asn Lys Val Val Thr Val Ser Lys Arg Gly Lys Asn Gly
50 55 60

Gly Val Ile Ile Thr Leu Val Arg Glu Tyr Asp Thr Glu Glu Leu Lys
65 70 75 80

Glu Phe Asn Asn Ser Thr Asp Asn Ile Ile Thr Ser Asp Leu Gln Tyr
85 90 95

Ala Lys Ala Leu Arg Glu Lys His Phe Pro Ser Tyr Arg Tyr Glu Arg
100 105 110

Lys Glu Gln Arg Arg Arg Thr Lys Ile Glu Met Ala Gln Tyr Asn Ala
115 120 125

Ile Lys Asp Glu Lys Arg Arg Ile Ile Ala Asp Met Asn Phe Tyr Ser
130 135 140

Glu Gly Leu Pro Tyr Pro Ser Lys Asp Ile Phe Asn Met Ser Tyr Asp
145 150 155 160

Pro Glu Gly Phe Tyr Lys Ala Tyr Ile Leu Cys Lys Leu Tyr Asp Gln
165 170 175

Tyr Ala Ile Ser His Met Asp Ala Lys His Thr Ser His Leu Lys Ala
180 185 190

Met Ser Lys Ala Thr Thr Lys Asp Glu Tyr Asp Tyr His Gln His Met
195 200 205

```
Ser Glu Tyr Tyr Arg Asn Lys Met Ile Gln Asn Leu Pro Arg Asn Ser
    210                 215                 220

Val Ser Asp Asn Phe Phe Gly Ser Lys Met Phe Asn Thr Phe Tyr Asn
225                 230                 235                 240

Phe Tyr Leu Lys Ile Lys Asp Lys Asn Ile Asn Val Phe Lys Tyr Met
                245                 250                 255

Lys Asn Val Phe Lys Asn Val Thr Phe Tyr Tyr Glu Asn Gly Met Gln
            260                 265                 270

Pro Asn Pro Ile Pro Ser Pro Asn Phe Phe Ser Ser Asp Lys Tyr Phe
        275                 280                 285

Lys Asn Tyr Asn Asn Tyr Ile Lys Gly Ile Lys Lys Gly Ile Asn Ser
    290                 295                 300

Thr Asn Arg His Leu Gly Asp Thr Asp Ser Ile Ile Asn Ser Ser Asp
305                 310                 315                 320

Tyr Val Lys Asn Pro Ala Val Leu His Leu His Gln Leu Tyr Thr Thr
                325                 330                 335

Gly Leu Asn Ser Thr Leu His Asp Ile Asp Thr Met Phe Glu Gln Ala
            340                 345                 350

Leu Asp Leu Glu Asn Ala Ser Tyr Gly Leu Phe Gly Asp Met Lys His
        355                 360                 365

Ile Ile Leu Leu Gln Tyr Asn Ser Met Ile Glu Glu Glu Ile Lys Asn
    370                 375                 380

Leu Pro Ile Glu Glu Lys Asp Ile Ile Asn Lys Tyr Val Lys Gln Cys
385                 390                 395                 400

Ile Ile Asn Asn Tyr Ser Pro Thr Ser Ile Ser Pro Ser Ala Arg Leu
                405                 410                 415

Ser Met Phe Thr Met Gln Lys Glu His Ile Val Tyr Asn Lys Gln Leu
            420                 425                 430

Asn Lys Gly Ile Lys Arg Glu Asp Leu Leu Pro Leu Ser Leu Gly Gly
        435                 440                 445

Ile Val Asn Lys Asp Ser Leu Ser Ser Met Asp Ile Gln Asn Leu Glu
    450                 455                 460

Gln Asn Gly Asn Glu Tyr Leu Tyr Met Arg Gln His Thr Ser Thr Tyr
465                 470                 475                 480
```

```
Tyr Ile Leu Arg Met Phe Gly Asp Tyr Leu Gly Tyr Glu Val Asn Leu
                485                 490                 495


Arg Glu Val Lys Tyr Ile Val Glu Lys Tyr Asn Leu Ile Asp Lys Ile
            500                 505                 510


Pro Leu Thr Lys Glu Gly Met Leu Asp Tyr Asn Lys Leu Ile His Leu
        515                 520                 525


Val Glu Glu Glu Val Asn Asn Tyr Glu
    530                 535


<210> 660
<211> 480
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 660
Met Ser Lys Lys Ile Lys Glu Leu Ile Leu His Lys Ser Met Lys Asp
1               5                   10                  15


Ile His Phe Ala Arg Glu Val Leu Asp Asn Leu Pro Lys Asn Leu Phe
            20                  25                  30


Ser Ala Glu Ser Glu Asp Met Gly Tyr Leu Phe Thr Ala Ile Lys Arg
        35                  40                  45


Thr Ala His Ile Ser Asp Lys Met Ser Asn Glu Ala Leu Ala Ile Lys
    50                  55                  60


Val Glu Gln Leu Met Gly Asn Asn Lys Glu Asp Glu Glu Lys Val Thr
65                  70                  75                  80


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


Lys Asp Glu Ser Val Asn Tyr Glu Ile Glu Lys Tyr Ile Lys Thr Glu
            100                 105                 110


Met Ser Lys Glu Val Leu Val Lys Phe Ile Ala Glu Asn Lys Gln Glu
        115                 120                 125


Asp Ser Asp Asn Leu His Glu Leu Val Asp Lys Leu Lys Gln Ile Glu
    130                 135                 140


Val Ser Asp Ile Ser Gly Gly Asn Gly Glu Phe Ile Asp Phe Phe Glu
145                 150                 155                 160


Asp Thr Glu Lys Lys Gln Glu Leu Leu Ser Asn Leu Ala Thr Asn Lys
                165                 170                 175
```

```
Phe Ser Thr Gly Phe Thr Ser Ile Asp Asn His Ile Glu Gly Gly Ile
            180                 185                 190

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

Ser Leu Met Ala Ser Asn Leu Ala Lys Asn Tyr Val Lys Ser Gly Leu
    210                 215                 220

Ser Val Leu Tyr Ile Ala Leu Glu Glu Lys Met Asp Arg Met Val Leu
225                 230                 235                 240

Arg Ala Glu Gln Gln Met Ala Gly Ala Glu Lys Ser Gln Ile Val Asn
                245                 250                 255

Gln Asp Met Ser Leu Asn Asn Lys Val Tyr Asp Ala Ile Gln Asn His
            260                 265                 270

Tyr Gln Lys Asn Arg Lys Leu Leu Gly Asp Phe Tyr Ile Ser Lys His
        275                 280                 285

Met Pro Gly Glu Val Thr Pro Asn Gln Leu Glu Gln Ile Ile Val Asn
    290                 295                 300

Thr Thr Ile Lys Lys Asp Lys Asn Ile Asp Val Val Ile Ile Asp Tyr
305                 310                 315                 320

Pro His Leu Met Arg Asn Pro Tyr Ala Lys Tyr His Ser Glu Ser Asp
                325                 330                 335

Ala Gly Gly Lys Leu Phe Glu Asp Ile Arg Arg Leu Ser Gln Gln Tyr
            340                 345                 350

Gly Phe Val Cys Trp Thr Leu Ala Gln Thr Asn Arg Gly Ala Tyr Gly
        355                 360                 365

Ser Asp Val Ile Thr Ser Glu His Val Glu Gly Ser Arg Lys Ile Val
    370                 375                 380

Asn Ala Val Glu Val Ser Leu Ala Val Asn Gln Lys Asp Glu Glu Phe
385                 390                 395                 400

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

Asn Thr Gly Glu Arg Phe Val Asn Leu Lys Val Glu Pro Thr Lys Met
            420                 425                 430

Ile Val Arg Asp Glu Thr Pro Glu Glu Lys Gln Glu His Ile Gln Leu
        435                 440                 445
```

Leu Ser Asp Asn Gly Lys Glu Asp Thr Ser Lys Phe Gln Asn Lys Asp
450 455 460

Asn Lys Ile Glu Ala Ile Asn Asn Thr Phe Gly Gly Leu Pro Gly Val
465 470 475 480

<210> 661
<211> 341
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 661
Met Lys Phe Val Phe Phe Thr Asp Ser His Phe His Leu Phe Thr Asn
1 5 10 15

Tyr Ala Lys Pro Asp Asn Glu Phe Val Asn Asp Arg Phe Lys Glu Gln
20 25 30

Ile Glu Ala Leu Gln Lys Val Phe Asp Ile Ala Lys Lys Glu Glu Ala
35 40 45

Thr Val Ile Phe Gly Gly Asp Leu Phe His Lys Arg Asn Ser Val Asp
50 55 60

Thr Arg Val Tyr Asn Lys Val Phe Ser Thr Phe Ala Lys Asn Asn Glu
65 70 75 80

Val Pro Val Leu Leu Leu Arg Gly Asn His Asp Ala Thr Thr Asn Ser
85 90 95

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

Asn Val Ile Lys Ser Leu Asn Thr Ile Leu Lys Asp Asn Val Asn Ile
115 120 125

Val Phe Thr Ala Tyr Gly Asp Glu Thr Lys Glu Ile Lys Thr Tyr Ile
130 135 140

Asn Ser Asn Tyr Asp Lys Asp Met Val Asn Ile Leu Val Gly His Leu
145 150 155 160

Gly Val Glu Gly Ser Leu Thr Gly Lys Gly Ser His Arg Leu Glu Gly
165 170 175

Ala Phe Gly Tyr Gln Asp Leu Leu Pro Asp Lys Tyr Asp Phe Ile Leu
180 185 190

Leu Gly His Tyr His Arg Arg Gln Tyr Phe Gln Asn Pro Asn His Phe

195 200 205

Tyr Gly Gly Ser Leu Met Gln Gln Ser Phe Ser Asp Glu Gln Glu Ala
210 215 220

Asn Gly Val His Leu Ile Asp Thr Asp Lys Met Thr Thr Glu Phe Ile
225 230 235 240

Pro Ile His Thr Arg Arg Phe Ile Thr Ile Gln Gly Glu Asp Ile Pro
245 250 255

Asp Asn Phe Glu Gln Leu Ile Glu Glu Asp Asn Phe Ile Arg Val Ile
260 265 270

Gly Thr Ala Asn His Ala Lys Val Leu Glu Met Asp Asp Ser Met Lys
275 280 285

Asp Lys Asn Val Glu Val Gln Ile Lys Lys Glu Tyr Thr Val Glu Lys
290 295 300

Arg Ile Asp Ser Asp Val Ser Asp Asp Pro Leu Thr Ile Ala Ser Thr
305 310 315 320

Tyr Ala Lys Gln Tyr Ser Pro Glu Ser Glu Gln Glu Ile Leu Glu Cys
325 330 335

Leu Lys Glu Val Leu
340

<210> 662
<211> 125
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 662
Met Lys Lys Tyr Arg Glu Tyr Leu Asn Lys Thr Asp Ala Glu Asn Leu
1 5 10 15

Ala Glu Asp Trp Glu Lys Val Thr Glu Asp Leu Trp Lys Val Phe Lys
20 25 30

Asp Met Lys Pro Lys Ile Asn Thr Leu Asp Ile Ser Asn Val Gly Ser
35 40 45

Lys Asp Leu Asp Lys Ser Lys Pro Ile Leu Gln Phe Gln Asp Ser Asp
50 55 60

Gly Val Ile Glu Asn Ile Cys Asn Val Glu Gly Leu Glu Asp Gly Leu
65 70 75 80

Ser Lys Met Lys Lys Ile Phe Asp Asp Ser Asn Phe Glu Lys His Tyr
85 90 95

Tyr Asn Arg Val Val Asp His Asp Gly Tyr Tyr Trp Ile Asp Tyr Gly
100 105 110

Ser His His Cys Phe Phe Arg Val Thr Lys Gly Asp Lys
115 120 125

<210> 663
<211> 639
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 663
Met Val Val Phe Lys Gln Val Glu Val Asn Asn Phe Leu Ala Ile Lys
1 5 10 15

Glu Ala Thr Leu Glu Leu Asp Asn Arg Gly Leu Ile Leu Ile Glu Gly
20 25 30

Glu Asn Lys Ser Asn Glu Ser Phe His Ser Asn Gly Ser Gly Lys Ser
35 40 45

Thr Leu Ile Ser Ala Ile Thr Tyr Ala Leu Tyr Gly Lys Thr Glu Lys
50 55 60

Gly Leu Lys Ala Asp Asp Val Val Asn Asn Ile Glu Lys Lys Asn Thr
65 70 75 80

Ser Val Lys Leu Lys Phe Asp Ile Gly Glu Asp Ser Tyr Leu Ile Glu
85 90 95

Arg Tyr Arg Lys Asp Lys Glu Asn Lys Asn Lys Val Lys Leu Phe Val
100 105 110

Asn Glu Lys Glu Ile Thr Gly Ser Thr Asn Asp Val Thr Asp Lys Gln
115 120 125

Ile Gln Asp Leu Phe Gly Ile Glu Phe Asn Thr Tyr Val Asn Ala Ile
130 135 140

Met Tyr Gly Gln Gly Asp Ile Pro Met Phe Ser Gln Ala Thr Asp Lys
145 150 155 160

Gly Lys Lys Glu Ile Leu Glu Ser Ile Thr Lys Thr Asp Val Tyr Lys
165 170 175

Gln Ala Gln Asp Val Ala Lys Glu Lys Val Lys Glu Val Glu Glu Gln
180 185 190

```
Gln Asn Asn Ile Arg Gln Glu Ile Tyr Lys Leu Gly Tyr Gln Leu Ser
        195                 200                 205

Thr Lys Asp Glu Tyr Phe Gln Arg Glu Ile Glu Gln Tyr Asn Gln Tyr
    210                 215                 220

Lys Glu Gln Leu Val Gln Ile Glu Asn Ser Asn Lys Glu Lys Asp Arg
225                 230                 235                 240

Leu Arg Glu Gln Glu Glu Lys Gln Ile Glu Ala Gln Ile Glu Gln Leu
                245                 250                 255

Ala Ser Gln Ile Pro Thr Ile Pro Glu Asp Glu Phe Lys His Ser Glu
            260                 265                 270

Glu Tyr Asn Lys Ala Ser Gln Ser Leu Asp Leu Leu Ser Asn Lys Leu
        275                 280                 285

Thr Glu Leu Asn Gln Val Tyr Ser Glu Tyr Asn Thr Lys Glu Gln Val
    290                 295                 300

Leu Lys Ser Glu Ile Ala Thr Leu Ser Asn Ser Leu Asn Gln Leu Asp
305                 310                 315                 320

Ile Asn Asp His Cys Pro Val Cys Gly Ser Pro Ile Asp Asn Ser His
                325                 330                 335

Lys Leu Lys Glu Gln Glu Asn Ile Ser Asn Gln Ile Glu Asn Lys Lys
            340                 345                 350

Gln Glu Ile Thr Ser Val Leu Glu Met Lys Asp Thr Tyr Lys Glu Ala
        355                 360                 365

Ile Asp Lys Val Lys Asp Lys Ser Gln Glu Ile Lys Asp Lys Met Ser
    370                 375                 380

Gln Glu Asp Gln Gln Glu Arg Glu His Asn Asn Lys Ile Asn Ser Ile
385                 390                 395                 400

Ile Gln Glu Ala Ser Arg Ile Lys Ser Asp Ile Ser Ser Leu Glu Asn
                405                 410                 415

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

Leu Glu Arg Glu Glu Pro Ser Lys Glu Lys His Glu Glu Asp Lys Lys
        435                 440                 445

Glu Leu Gln Glu Ser Ile Asp Lys His Glu Glu Asn Ile Val Gln Leu
    450                 455                 460
```

```
Glu Thr Lys Lys Gly Lys Tyr Gln Gln Ala Val Asp Ala Phe Ser Asn
465                 470                 475                 480


Lys Gly Ile Arg Ser Val Val Leu Asp Phe Ile Thr Pro Phe Leu Asn
                485                 490                 495


Glu Lys Ala Asn Glu Tyr Leu Gln Thr Leu Ser Gly Ser Asp Ile Glu
            500                 505                 510


Ile Glu Phe Gln Thr Gln Val Lys Asn Ala Lys Gly Glu Leu Lys Asp
        515                 520                 525


Lys Phe Asp Val Ile Val Lys Asn Asn Lys Gly Gly Gly Ser Tyr Lys
    530                 535                 540


Ser Asn Ser Ala Gly Glu Gln Lys Arg Ile Asp Leu Ala Ile Ser Phe
545                 550                 555                 560


Ala Ile Gln Asp Leu Ile Met Ser Lys Asp Glu Ile Ser Thr Asn Ile
                565                 570                 575


Ala Leu Tyr Asp Glu Cys Phe Asp Gly Leu Asp Thr Ile Gly Cys Glu
            580                 585                 590


Asn Val Ile Lys Leu Leu Lys Asp Arg Leu Asn Thr Val Gly Thr Ile
        595                 600                 605


Phe Val Ile Thr His Asn Thr Glu Leu Lys Pro Leu Phe Glu Gln Thr
    610                 615                 620


Ile Lys Ile Val Lys Glu Asn Gly Val Ser Lys Leu Glu Glu Lys
625                 630                 635


<210> 664
<211> 198
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 664
Met Lys Leu Lys Ile Leu Asp Lys Asp Asn Ala Thr Leu Asn Val Phe
1               5                   10                  15


His Arg Asn Lys Glu His Lys Thr Ile Asp Asn Val Pro Thr Ala Asn
            20                  25                  30


Leu Val Asp Trp Tyr Pro Leu Ser Asn Ala Tyr Glu Tyr Lys Leu Ser
        35                  40                  45


Arg Asn Gly Glu Tyr Leu Glu Leu Lys Arg Leu Arg Ser Thr Leu Pro
    50                  55                  60
```

```
Ser Ser Tyr Gly Leu Asp Asp Asn Asn Gln Asp Ile Ile Arg Asp Asn
65                  70                  75                  80

Asn His Arg Cys Lys Ile Gly Tyr Trp Tyr Asn Pro Ala Val Arg Lys
                85                  90                  95

Asp Asn Leu Lys Ile Ile Glu Lys Ala Lys Gln Tyr Gly Leu Pro Val
            100                 105                 110

Ile Thr Glu Glu Tyr Asp Ala Asn Thr Val Glu Gln Gly Phe Arg Asp
        115                 120                 125

Ile Gly Val Ile Phe Gln Ser Leu Lys Thr Ile Val Val Thr Arg Tyr
    130                 135                 140

Leu Glu Gly Lys Thr Glu Glu Glu Leu Arg Ile Phe Asn Met Lys Ser
145                 150                 155                 160

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

Asp Leu Thr Tyr Ser Asp Leu Gly Gln Ile Tyr Asn Met Leu Leu Leu
            180                 185                 190

Met Lys Lys Ile Ser Lys
        195


<210> 665
<211> 355
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 665
Met Arg Phe Glu Asp Phe Leu Thr Gln Glu Leu Gly Glu Pro Lys Glu
1               5                   10                  15

Asn Thr Ile Gly Glu Leu Arg Tyr Cys Cys Pro Phe Cys Gly Glu Lys
            20                  25                  30

Ser Tyr Lys Phe Tyr Val Lys Gln Ala Leu Asp Ser Ser Asn Gly Gln
        35                  40                  45

Tyr His Cys Lys Lys Cys Asp Glu Thr Gly Asn Pro Ile Thr Phe Met
    50                  55                  60

Lys Thr Tyr Tyr Asn Ile Thr Gly Lys Gln Ala Phe Asp Leu Leu Glu
65                  70                  75                  80

Ser Lys Asn Ile Asp Ile Glu Arg Ala Pro Leu Leu Thr Thr Asn Asn
```

85 90 95

Lys Asp Leu Thr Glu Ser Glu Lys Leu Ile Leu Met Leu Arg Gly Val
100 105 110

His Gln Asp Lys Gly Thr Thr Ser Ile Lys Pro Pro Arg Leu Pro Glu
115 120 125

Gly Tyr Lys Leu Leu Lys Asp Asn Leu Asn Asn Lys Glu Ile Ile Pro
130 135 140

Phe Leu Lys Tyr Leu Lys Gly Arg Gly Ile Thr Leu Glu Gln Ile Ile
145 150 155 160

Asn Asn Asn Ile Gly Tyr Val Ile Asn Gly Ser Phe Tyr Lys Val Asp
165 170 175

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

Asp Asn Asn Gly Asn Tyr Gln Tyr Trp Asn Thr Arg Ser Ile Glu Lys
195 200 205

Asn Pro Tyr Ile Lys Ser Ile Asn Ala Pro Ala Lys Gln Asp Glu Val
210 215 220

Gly Arg Lys Asp Val Ile Phe Asn Leu Asn Ile Ala Arg Lys Lys Lys
225 230 235 240

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

Tyr Gly Val Ala Thr Leu Gly Lys Gln Val Thr Glu Asn Gln Ile Lys
260 265 270

Lys Ile Ile Asp Tyr Val Ser Ile Asp Thr Ser Ile Tyr Ile Met Leu
275 280 285

Asp Thr Asp Ala Leu Asp Asn Asn Ile Asp Leu Ala Tyr Lys Leu Lys
290 295 300

Thr His Phe Asn Lys Val Tyr Phe Val Pro His Gly Asp Glu Asp Ala
305 310 315 320

Asn Asp Met Gly Thr Arg Lys Ala Phe Glu Leu Leu Lys Gln Asn Arg
325 330 335

Val Leu Val Thr Pro Glu Ser Ile Gln Ser Tyr Lys Ile Gln Gln Lys
340 345 350

Leu Lys Leu

355

<210> 666
<211> 112
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 666
Met Ser Asn Ser Lys Lys Asp Ile Leu Glu Phe Val Asp Glu Tyr Ile
1 5 10 15

Thr Ala Leu Arg Val Gly Asn Glu Gln Arg Gln His Gln Leu Glu Glu
20 25 30

Met Gly Lys Glu Glu Thr Ala Thr Leu Thr Asp Val Ala Lys Ala Ile
35 40 45

Thr Asn Leu Met Leu Gly Val Asn Glu Gln Met Thr Asp Leu Glu Tyr
50 55 60

Asn Asn Glu Leu Asn Leu Asn Ile Leu Ile Asp Ala Leu Tyr Lys Ala
65 70 75 80

Glu Leu Ile Asn Glu Asp Val Leu Asp Tyr Ile Gln Glu Ser Ile Asp
85 90 95

Lys Ser Gln Glu Glu Pro Lys Asn Glu Glu Glu Lys Gly Glu Gln Glu
100 105 110

<210> 667
<211> 150
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 667
Met Glu Lys Asn Ile Ser Thr His Thr Lys Gly Ile Ser Gln Ala Asp
1 5 10 15

Met Glu Lys Trp Ile Glu Ala Val Val Gln Gly Thr Val Asp Gly Lys
20 25 30

Gln Val Asp Glu Lys Thr Ala Lys Gln Leu Asp Arg Ile Gly Ser Arg
35 40 45

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

Val Thr Ala Gln Glu Val Thr Gly Asp Phe Asn Asp Ala Phe Asn Ala
65 70 75 80

```
Ile Asp Leu Met Met Ile Ile Met Glu Asp Glu Leu Gly Val Thr Gln
                85                  90                  95


Glu Lys Val Gly Lys Ala Lys Asp Lys Leu Asn Glu Lys Arg Glu Ala
            100                 105                 110


Tyr Leu Lys Glu Lys Gln Glu Glu Leu Arg Gln Lys Gln Gln Glu Glu
        115                 120                 125


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


Lys Lys Asn Asp Glu Gln
145                 150


<210> 668
<211> 202
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 668
Met Thr Asn Ser Lys Lys Lys Gly Asp Thr Phe Glu Arg Lys Ile Ala
1               5                   10                  15


Lys Glu Leu Thr Ala Trp Trp Gly Tyr Gln Phe Asn Arg Ser Pro Gln
            20                  25                  30


Ser Gly Gly Ala Ser Trp Gly Lys Asp Asn Asn Ala Val Gly Asp Ile
        35                  40                  45


Val Val Pro Gln Glu Ala Asn Phe Pro Leu Val Val Glu Cys Lys His
    50                  55                  60


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


His Thr Trp Trp Glu Gln Val Ile Asn Asp Ser Ser Lys Val Asp Lys
                85                  90                  95


Thr Pro Cys Leu Ile Phe Thr Arg Asn Arg Ala Gln Ser Tyr Val Ala
            100                 105                 110


Leu Pro Tyr Asp Glu Lys Val Tyr Glu Asp Leu Arg Asn Asn Glu Tyr
        115                 120                 125


Pro Val Met Arg Thr Asp Phe Ile Ile Asp Asn Ile Arg Lys Asp Lys
    130                 135                 140


Phe Phe Tyr Asp Val Leu Ile Thr Thr Met Asn Gly Leu Thr Ser Phe
145                 150                 155                 160
```

```
Thr Pro Ser Tyr Ile Ile Ser Cys Tyr Asp Lys Lys Asp Ile Lys Pro
                165                 170                 175

Tyr Lys Lys Val Glu Ser Asn Leu Ser Glu Val Ser Lys His Glu Asp
            180                 185                 190

Glu Leu Ile Asn Asp Leu Leu Ser Asp Ile
        195                 200
```

<210> 669
<211> 130
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 669

```
Met Thr Ser Lys Glu Arg Pro Leu Ile Val Tyr Phe Ser Gly Thr Gly
1               5                   10                  15

Gln Thr Glu Arg Leu Val Asn Lys Ile Asn Ile Asn Asn Ser Phe Glu
            20                  25                  30

Thr Phe Arg Val Lys Ser Gly Lys Glu Lys Val Asn Lys Pro Phe Ile
        35                  40                  45

Leu Ile Thr Pro Thr Tyr Met Lys Gly Ala Ile Pro Lys Gln Ile Glu
    50                  55                  60

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

Asn Lys Gln Trp Gly Ser Asn Phe Cys Gly Ala Ser Lys Lys Ile Ser
                85                  90                  95

Glu Met Phe Lys Ile Pro Leu Ile Ala Lys Val Glu Gln Ser Gly His
            100                 105                 110

Phe Asn Glu Ile Gln Pro Ile Leu Glu His Phe Ser Asn Lys Tyr Lys
        115                 120                 125

Val Ala
    130
```

<210> 670
<211> 704
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 670

```
Met Ala Thr Tyr Gly Lys Trp Ile Glu Leu Asn Asn Glu Ile Thr Gln
1               5                  10                  15

Leu Asp Asp Asn Gly Lys Asn Lys Leu Tyr Lys Asp Gln Glu Ala Leu
            20                  25                  30

Asp Glu Tyr Leu Lys Tyr Ile Glu Asp Asn Thr Arg Lys Phe Asn Ser
        35                  40                  45

Glu Val Glu Arg Ile Arg Val Leu Thr Lys Glu Gly Thr Tyr Asp Lys
    50                  55                  60

Ile Phe Asp Lys Val Pro Asp Thr Ile Ile Asp Glu Met Thr Lys Leu
65                  70                  75                  80

Ala Tyr Ser Phe Asn Phe Lys Phe Pro Ser Phe Met Ala Gly Gln Lys
                85                  90                  95

Phe Tyr Glu Ser Tyr Ala Ser Lys Gln Tyr Asp Glu Asn Lys Lys Pro
            100                 105                 110

Ile Phe Val Glu Asp Tyr Glu Gln His Asn Val Arg Val Ala Leu Tyr
        115                 120                 125

Leu Phe Gln Asn Asp Tyr Val Lys Ala Arg Glu Leu Leu Val Gln Leu
    130                 135                 140

Met Glu Gln Thr Phe Gln Pro Ser Thr Pro Thr Tyr Asn Asn Ser Gly
145                 150                 155                 160

Gln Ala Asn Arg Gly Glu Leu Ser Ser Cys Tyr Leu Phe Val Val Asp
                165                 170                 175

Asp Ser Ile Glu Ser Leu Asn Phe Val Glu Asp Ser Val Ala Asn Ala
            180                 185                 190

Ser Ser Asn Gly Gly Gly Val Ala Ile Asp Leu Thr Arg Ile Arg Pro
        195                 200                 205

Lys Gly Ala Pro Val Arg Asn Arg Pro Asn Ser Ser Lys Gly Val Ile
    210                 215                 220

Ala Phe Ala Lys Ala Ile Glu His Lys Val Ser Ile Tyr Asp Gln Gly
225                 230                 235                 240

Gly Val Arg Gln Gly Ser Gly Ala Val Tyr Leu Asn Ile Phe His Asn
                245                 250                 255

Asp Ile Leu Asp Leu Leu Ser Ser Lys Lys Ile Asn Ala Ser Glu Ser
            260                 265                 270
```

```
Val Arg Leu Asp Lys Leu Ser Ile Gly Val Thr Ile Pro Asn Lys Phe
        275                 280                 285

Met Glu Leu Val Lys Glu Gly Arg Pro Phe Tyr Thr Phe Asp Thr Tyr
    290                 295                 300

Asp Ile Asn Lys Val Tyr Gly Lys Tyr Leu Asp Glu Leu Asn Ile Asp
305                 310                 315                 320

Glu Trp Tyr Asp Lys Leu Leu Asn Asn Asp Ser Ile Gly Lys Val Lys
                325                 330                 335

His Asp Ala Arg Glu Val Met Thr Asp Ile Ala Lys Thr Gln Leu Glu
            340                 345                 350

Ser Gly Tyr Pro Tyr Val Phe Tyr Ile Asp Asn Ala Asn Asp Asn His
        355                 360                 365

Pro Leu Lys Asn Leu Gly Lys Val Lys Met Ser Asn Leu Cys Thr Glu
    370                 375                 380

Ile Ser Gln Leu Gln Glu Val Ser Glu Ile Tyr Pro Tyr Ser Tyr Ser
385                 390                 395                 400

Asn Gln Asn Val Ile Asn Arg Asp Val Val Cys Thr Leu Gly Ser Leu
                405                 410                 415

Asn Leu Val Asn Val Val Glu Lys Gly Leu Leu Asn Glu Ser Val Asp
            420                 425                 430

Ile Gly Thr Arg Ala Leu Thr Lys Val Thr Asp Ile Met Asp Leu Pro
        435                 440                 445

Tyr Leu Pro Ser Val Gln Lys Ala Asn Asp Asp Ile Arg Ala Ile Gly
    450                 455                 460

Leu Gly Ser Met Asn Leu His Gly Leu Leu Ala Lys Asn Met Ile Ser
465                 470                 475                 480

Tyr Gly Ser Arg Glu Ala Leu Asp Leu Val Asn Ser Leu Tyr Ser Ala
                485                 490                 495

Ile Asn Phe Gln Ser Ile Lys Thr Ser Met Leu Met Ala Lys Glu Thr
            500                 505                 510

Gly Lys Pro Phe Lys Gly Phe Glu Lys Ser Asp Tyr Ala Thr Gly Glu
        515                 520                 525

Tyr Phe Val Arg Tyr Ile Arg Glu Ser Asn Gln Pro Lys Thr Asp Lys
    530                 535                 540
```

Ala Lys Lys Val Leu Asp Lys Val Tyr Ile Pro Thr Gln Asp Asp Trp
545 550 555 560

Asp Glu Leu Ala Lys Ala Val Lys Val His Gly Leu Tyr Asn Gly Tyr
565 570 575

Arg Lys Ala Glu Ala Pro Thr Gln Ser Ile Ser Tyr Val Gln Asn Ala
580 585 590

Thr Ser Ser Ile Met Pro Val Pro Ser Ala Ile Glu Asn Arg Gln Tyr
595 600 605

Gly Asp Met Glu Thr Tyr Tyr Pro Met Pro Tyr Leu Ser Pro Ile Thr
610 615 620

Gln Phe Phe Tyr Glu Gly Glu Thr Ala Tyr Lys Ile Asp Asn Lys Arg
625 630 635 640

Ile Ile Asn Thr Ser Ala Val Val Gln Lys His Thr Asp Gln Ala Val
645 650 655

Ser Thr Ile Leu Tyr Val Glu Ser Glu Ile Pro Thr Asn Lys Leu Val
660 665 670

Ser Leu Tyr Tyr Tyr Ala Trp Glu Gln Gly Leu Lys Ser Leu Tyr Tyr
675 680 685

Thr Arg Ser Arg Lys Leu Ser Val Ile Glu Cys Glu Thr Cys Ser Val
690 695 700

<210> 671
<211> 349
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 671
Met Asp Ile Thr Gln Lys Val Lys Gln His Asn Lys Asn Ala Val Leu
1 5 10 15

Lys Ala Thr Asn Trp Asn Ile Glu Asp Asp Gly Met Ser Asp Ile Tyr
20 25 30

Trp Glu Gln Gly Ile Ser Gln Phe Trp Thr Pro Glu Glu Phe Asp Val
35 40 45

Ser Arg Asp Leu Ser Ser Trp Asn Ser Leu Thr Glu Ser Glu Lys Asn
50 55 60

Thr Tyr Lys Lys Val Leu Ala Gly Leu Thr Gly Leu Asp Thr Lys Gln
65 70 75 80

```
Gly Gly Glu Gly Met Asn Leu Val Ser Tyr His Glu Pro Arg Pro Lys
                85                  90                  95

Tyr Gln Ala Val Phe Ala Phe Met Gly Gly Met Glu Glu Ile His Ala
            100                 105                 110

Lys Ser Tyr Ser His Ile Phe Thr Thr Leu Leu Ser Asn Lys Glu Thr
        115                 120                 125

Ser Tyr Leu Leu Asp Thr Trp Val Glu Glu Asn Asp Phe Leu Lys Val
    130                 135                 140

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

Pro Thr Val Phe Asp Arg Tyr Met Ala Lys Val Ala Ser Ala Phe Leu
                165                 170                 175

Glu Ser Ala Leu Phe Tyr Ser Gly Phe Tyr Tyr Pro Leu Leu Leu Ala
            180                 185                 190

Gly Arg Gly Gln Met Thr Gln Ser Gly Ala Ile Ile Tyr Lys Ile Thr
        195                 200                 205

Gln Asp Glu Ala Tyr His Gly Ser Ala Val Gly Leu Thr Ala Gln Tyr
    210                 215                 220

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

Thr Tyr Glu Leu Leu Asp Ile Leu Tyr Thr Asn Glu Val Ala Tyr Thr
                245                 250                 255

His Ser Leu Tyr Asp Pro Leu Glu Leu Ser Glu Asp Val Ile Asn Tyr
            260                 265                 270

Val Gln Tyr Asn Phe Asn Arg Ala Leu Gln Asn Leu Gly Arg Glu Asp
        275                 280                 285

Tyr Phe Asn Pro Glu Pro Tyr Asn Pro Ile Val Glu Asn Gln Thr Asn
    290                 295                 300

Val Asp Arg Leu Arg Asn Val Asp Phe Phe Ser Gly Lys Ala Asp Tyr
305                 310                 315                 320

Glu Lys Ser Thr Asn Ile Lys Asp Ile Lys Asp Glu Asp Phe Ser Phe
                325                 330                 335

Leu Asp Ser Lys Glu Tyr Asn Thr Ala Lys Glu Phe Leu
            340                 345
```

<210> 672
<211> 109
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 672
Met Asp Arg Lys Glu Ala Met Asp Leu Leu Ser Lys Ala Glu Ile Leu
1 5 10 15

Phe Lys Lys His Asp Glu Phe Ser Cys Val Ser Asp Ile Asn Asp Pro
20 25 30

Met Lys Leu Phe Ser Ser Ser Lys Asp Ala Lys Ala Asp Asp Thr Ser
35 40 45

Lys Ser Phe Gln Leu Glu Phe Met His Asp Met Thr Met Tyr Thr Leu
50 55 60

Ser Tyr Gly Ser Gly Gln Leu Lys Leu Ile Asp Leu Ala Glu Gly Tyr
65 70 75 80

Glu Ala Gln Lys Ala Thr Val Val Asn Ser Phe Pro Glu Ile Ile Lys
85 90 95

Thr Leu Glu Lys Asp Asp Ser Glu Asp Gly Lys Asn Glu
100 105

<210> 673
<211> 106
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 673
Met Glu Lys Met Asn Ser Leu Val Asp Leu Asn Thr Ala Ile Arg Gln
1 5 10 15

Lys Lys Asp Val Ile Val Met Ile Thr Gln Asp Asn Cys Gly Lys Cys
20 25 30

Glu Ile Leu Lys Ser Val Ile Pro Met Phe Gln Glu Ser Gly Asp Ile
35 40 45

Lys Lys Pro Ile Leu Thr Leu Asn Leu Asp Ala Glu Asp Val Asp Arg
50 55 60

Glu Lys Ala Val Lys Leu Phe Asp Ile Met Ser Thr Pro Val Leu Ile
65 70 75 80

Gly Tyr Lys Asp Gly Gln Leu Val Lys Lys Tyr Glu Asp Gln Val Thr

85 90 95

Pro Met Gln Leu Gln Glu Leu Glu Ser Leu
100 105

<210> 674
<211> 198
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 674
Met Asp Glu Leu Ile Ser Lys Ser Arg Arg Tyr Ile Met Arg Asp Glu
1 5 10 15

Asn His Tyr Met Leu Phe Asn Glu Lys Tyr Asn Asn Asp Arg Leu Ile
20 25 30

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

Val Leu Pro Tyr Tyr Val Leu Lys Asp Leu Ser Ser His Pro Asp Ser
50 55 60

Glu Val Val Tyr Arg Met Arg Asn Gly Phe Thr Ala Lys Glu Val Asp
65 70 75 80

Asn Ile Ala Leu Ser Phe Met Gly Thr Lys Val Ile Ile Asp Ile Ser
85 90 95

Val Val Phe Pro Tyr Val Asn Pro Tyr Asp Ile Ile Arg Ser Leu His
100 105 110

Asp Ile Lys Thr Asn Val Asp Glu Val His Leu Ser Phe Pro Arg Ile
115 120 125

Leu Glu Val Asp Glu Lys Gln Glu Lys Phe Tyr Phe Phe Asp Gly Glu
130 135 140

Ala Tyr Asp Leu Lys Pro Glu Tyr Lys Val Asp Phe Ala Asp Lys Ile
145 150 155 160

Arg Val Ser Leu Ser Val Trp Lys Met Tyr Ile Tyr Ile Leu Thr Ser
165 170 175

Ser Arg Asp Phe Glu Asp Val Asp Asn Val Ile Thr Lys Leu Lys Gln
180 185 190

Gln Arg Lys Ile Lys Ile
195

<210> 675
<211> 101
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 675
Met Ser Thr Ala Asn Arg Arg Asp Ile Ala Arg Lys Ile Ser Glu Asn
1   5   10   15

Thr Gly Tyr Tyr Ile Gln Asp Val Glu Glu Ile Leu Ser Ala Glu Thr
            20   25   30

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

His Lys Phe Met Gln Ile Glu Val Ile Glu Arg Lys Gly Lys Lys Ala
    50   55   60

Trp Asp Gly Leu Asn Lys Glu Tyr Phe His Leu Pro Asn Arg Lys Ala
65   70   75   80

Ile Lys Phe Lys Pro Leu Lys Glu Leu Glu Glu Val Ile Asp Arg Leu
                85   90   95

Asn Glu Glu Glu Lys
            100

<210> 676
<211> 290
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 676
Met Lys Val Leu Ile Leu Phe Asp His Ile Arg Glu Glu His Phe Ser
1   5   10   15

Val Ser Lys Asp Gly Ser Val Lys Ser Asn Val Leu Asn Thr Pro Asn
            20   25   30

Gly Lys Thr Leu Lys Lys Leu Leu Glu Lys Cys Ser Asn Leu Lys Arg
        35   40   45

Asp Lys Thr Asn Arg Asp Tyr Asp Ile Asp Phe Leu Tyr Asn Ala Val
    50   55   60

Pro Thr Pro Ile Arg Asn Asp Tyr Gly Lys Ile Ile Lys Tyr Gln Asp
65   70   75   80

Val Lys Gln Ala Glu Val Lys Pro Tyr Tyr Glu Arg Met Asn Asn Ile
                85   90   95

```
Ile Ile Asp Asn Ser Tyr Asp Met Val Ile Pro Val Gly Lys Leu Gly
            100                 105                 110

Val Lys Tyr Leu Leu Asn Val Thr Ala Ile Gly Lys Val Arg Gly Val
        115                 120                 125

Pro Ser Lys Val Thr Ile Glu Asn Glu Thr Ser Ser His Asp Val Trp
    130                 135                 140

Val Leu Pro Thr Tyr Ser Ile Glu Tyr Thr Asn Val Asn Lys Asn Ser
145                 150                 155                 160

Glu Arg His Val Val Ser Asp Leu Gln Thr Val Gly Lys Phe Val Glu
                165                 170                 175

Gln Gly Glu Glu Ala Phe Lys Pro Lys Glu Val Ser Tyr Glu Leu Val
            180                 185                 190

Asp Asn Ile Glu Arg Val Arg Glu Ile Phe Asn Lys Glu Val Lys Asn
        195                 200                 205

Asp Asn Tyr Asp Gly Val Asp Ile Thr Ala Trp Asp Leu Glu Thr Asn
    210                 215                 220

Ser Leu Lys Pro Asp Lys Glu Gly Ser Lys Pro Leu Val Leu Ser Leu
225                 230                 235                 240

Ser Trp Arg Asn Gly Gln Gly Val Thr Ile Pro Leu Tyr Lys Ser Asp
                245                 250                 255

Phe Asn Trp Glu Asn Gly Gln Asp Asp Ile Asp Glu Val Leu Glu Leu
            260                 265                 270

Leu Lys Asn Trp Leu Ala Ser Lys Glu Asp Ile Lys Val Ala His Asn
        275                 280                 285

Gly Lys
    290


<210> 677
<211> 170
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 677
Val Tyr Gln Leu Asn Arg Gly Gly Thr Val Lys Lys Asp Tyr Met Thr
1               5                   10                  15

Ser Val Lys Asn Asn Lys Lys Val Cys Arg Arg Cys Asn Glu Glu Leu
```

20 25 30

Asp Leu Ser Asn Phe Lys Thr Tyr Lys Lys Asn Asp Lys Ile Tyr Tyr
35 40 45

Gln Ser Met Cys Ile Pro Cys Arg Lys Glu Tyr Asn Lys Leu Asp Lys
50 55 60

Thr Lys Asn Thr Ile Lys Lys Cys Tyr Asp Lys Asn Gly Asp Lys Tyr
65 70 75 80

Arg Lys Gln Gly Asn Glu Tyr Asn Thr Ser Asp Arg Gly Arg Glu Leu
85 90 95

Asn Lys Lys Arg Ser Arg Lys Tyr Arg Glu Asn Asn Ser Leu Lys Ala
100 105 110

Lys Ala Arg Asn Ser Val Arg Thr Ala Leu Arg Asn Gly Ser Leu Leu
115 120 125

Arg Pro Ser Lys Cys Ser Glu Cys Asn Lys Glu Cys Ile Pro Glu Ala
130 135 140

His His Pro Asp Tyr Asn Lys Pro Leu Glu Ile Lys Trp Leu Cys Lys
145 150 155 160

Ser Cys His Glu Asp Thr His His Lys Lys
165 170

<210> 678
<211> 776
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 678
Met Ser Thr Glu Asn Phe Lys Asp Phe Glu Ser Ile Gln Asp Thr Lys
1 5 10 15

Val Gly Trp Tyr Leu Ala Val Thr Gln Glu Val Lys Glu Ser Leu Arg
20 25 30

Leu Ser Asp Leu Ala Tyr Glu Val Thr Asp Val Gly Gly Tyr Asp Lys
35 40 45

Pro Leu Glu Asp Phe Lys Leu Trp Phe Val Thr Lys Leu Leu Arg Phe
50 55 60

Phe Ser Asp Lys Ile Lys Glu Ile Gln Lys Glu Asn Lys Lys Ile Ala
65 70 75 80

```
Lys Lys Glu Tyr Asp Val Lys Ala Pro Glu Tyr Lys Glu Trp Leu Glu
                85                  90                  95

Asn Lys Leu Asn Glu Thr Val Val Glu Leu Asp Asp Thr Glu Lys Lys
            100                 105                 110

Phe Arg Val Ser Glu Leu Glu Lys Lys Tyr Ile Gln Leu Gly Leu Ser
        115                 120                 125

Pro Glu Ile Val Asn Met Asn Leu Val Met Asn Asn Asp Glu Phe Ile
    130                 135                 140

Ser Ile Ala Glu Gln Ser Pro Glu Tyr Met Gly Leu Ser Asp Tyr Ala
145                 150                 155                 160

Lys Ser Tyr Thr Leu Asn Thr Ala Ile Asn Leu Ile Asn Glu Tyr Arg
                165                 170                 175

Asp Val Lys Asp Val Val Asn Asp Ile Asp Gly Gly Asn Phe Asn Tyr
            180                 185                 190

Asp Trp Phe Pro Ile Glu Leu Met His Pro Tyr Ala Ser Gly Asp Thr
        195                 200                 205

Asp Val Cys Arg Arg Ile His Cys Asp Val Val Lys Lys Leu Lys Glu
    210                 215                 220

Gln Asp Arg Pro Lys Ser Met His Leu Leu Glu Val Asn Tyr Pro Arg
225                 230                 235                 240

Leu Thr Lys Ser Leu Ala Arg Ile Glu Ser Asn Gly Leu Tyr Cys Asp
                245                 250                 255

Leu Asp Tyr Met Lys Glu Asn Asp Glu Ser Tyr Glu Ser Glu Met Ala
            260                 265                 270

Lys Asn His Ala Thr Met Arg Glu His Trp Ala Val Lys Glu Phe Glu
        275                 280                 285

Glu Tyr Gln Tyr Asn Leu Tyr Gln Met Ala Leu Glu Glu His Glu Lys
    290                 295                 300

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

Lys Asp Gly Lys Trp Met Phe Ser Pro Ser Ser Gly Asp His Lys Gly
                325                 330                 335

Arg Val Ile Tyr Asp Ile Leu Gly Ile Gln Leu Pro Tyr Asp Lys Glu
            340                 345                 350
```

```
Tyr Val Lys Glu Lys Pro Phe Asn Ala Asn Val Lys Glu Ala Asp Leu
        355                 360                 365

Thr Trp Gln Asp Tyr Lys Thr Asp Lys Lys Ala Ile Gly Tyr Ala Leu
    370                 375                 380

Asp Asn Leu Glu Leu Lys Asp Asp Val Arg Glu Leu Leu Glu Leu Leu
385                 390                 395                 400

Lys Tyr His Ala Ser Met Gln Thr Lys Arg Asn Ser Phe Thr Lys Lys
                405                 410                 415

Leu Pro Asn Met Ile Asn Lys Gln Lys Arg Thr Leu His Gly Ser Phe
            420                 425                 430

Ser Glu Thr Gly Thr Glu Thr Ser Arg Leu Ser Ser Ser Asn Pro Asn
        435                 440                 445

Leu Gln Asn Leu Pro Ala His Thr Ser Asp Val Asn Lys Phe Asp Tyr
    450                 455                 460

Lys His Pro Ile Lys Arg Ser Phe Val Ser Arg Phe Glu Asn Gly Val
465                 470                 475                 480

Leu Leu Gly Ala Asp Tyr Ser Ala Leu Glu Met Arg Ile Ile Gly Leu
                485                 490                 495

Phe Thr Lys Asp Pro Asp Met Leu Gln Ser Phe Leu Asn Gly Glu Asp
            500                 505                 510

Ile His Lys Ala Thr Ala Ser Ile Val Tyr Asn Lys Pro Val Glu Glu
        515                 520                 525

Val Thr Lys Glu Glu Arg Gln Ala Thr Lys Ala Val Asn Phe Gly Leu
    530                 535                 540

Ala Phe Gly Glu Ser Pro Phe Ser Phe Ala Gly Lys Asn Asn Met Glu
545                 550                 555                 560

Val Ser Glu Ala Glu Glu Ile Phe Glu Lys Tyr Phe Gln Thr Lys Pro
                565                 570                 575

Ser Val Lys Thr Ser Ile Asp Asn Val His Glu Phe Val Gln Gln Tyr
            580                 585                 590

Gly Tyr Val Asp Thr Met His Gly His Arg Arg Phe Ile Arg Ser Ala
        595                 600                 605

Gln Ser Thr Asp Lys Lys Ile Lys Asn Glu Gly Leu Arg Gln Ser Phe
    610                 615                 620
```

```
Asn Thr Ile Ile Gln Gly Ser Gly Ser Phe Leu Thr Asn Met Ser Leu
625                 630                 635                 640

Thr Tyr Leu Asp Asp Phe Ile Gln Ser Arg Asn Leu Lys Ser Lys Val
                645                 650                 655

Ile Ala Thr Val His Asp Ser Ile Leu Ile Asp Cys Pro Pro Glu Glu
            660                 665                 670

Ala Lys Ile Met Ala Lys Val Thr Ile His Ile Met Glu Asn Leu Pro
        675                 680                 685

Phe Asp Phe Leu Lys Ala Glu Ile Asp Gly Lys Glu Val Gln Tyr Pro
    690                 695                 700

Ile Glu Ala Asp Met Glu Ile Gly Leu Asn Tyr Asn Asp Met Val Glu
705                 710                 715                 720

Tyr Asp Glu Glu Glu Ile Asp Thr Phe Asn Ser Tyr Gln Gly Tyr Ile
                725                 730                 735

Lys Tyr Met Met Asn Leu Gln Thr Leu Glu Asp Tyr Lys Glu Ser Gly
            740                 745                 750

Lys Leu Thr Asp Glu Gln Phe Glu Lys Ala Thr Asn Val Val Lys Ser
        755                 760                 765

Glu Lys His Ile Tyr Gln Glu Ile
    770                 775


<210> 679
<211> 80
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 679
Val Asn Thr Gly Glu Ile Arg Phe Asn Arg Ser Met Asp Glu Trp Ile
1               5                   10                  15

Ile Thr Ser Met Tyr Gln Asp Glu Leu Gly Asp Met Asn Ile Val Val
            20                  25                  30

Thr Phe Tyr Asn Arg Glu Glu Asn Lys His Gly Ser Thr Val Leu Pro
        35                  40                  45

Thr Glu Ser Ser Thr Gly Glu Val Thr Glu Glu Leu Ala Asn Leu Glu
    50                  55                  60

Glu Glu Tyr Pro Leu Ala Leu Pro Leu Ser Ser Ile Ser Val Asn Ile
65                  70                  75                  80
```

<210> 680
<211> 160
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 680
Met Glu Ile His Ile Asp Ser Leu Asp Phe Thr Asn Phe Thr Ile Lys
1 5 10 15

Asp Arg Asn Gly Asn Ser Gln Glu Phe Asp Ile Thr Asp Glu Leu Arg
20 25 30

Ile Thr Glu Tyr Thr Ile Gln Glu Asp Phe Met Gln Gln Ser Ala Lys
35 40 45

Tyr Ala Phe Trp Ala Ser Ile Leu Glu Lys Val Arg Ala Tyr Ser Glu
50 55 60

Met Glu Gln Arg Asn Leu Glu Thr Ile Gly Ser Lys Leu Asn Leu Thr
65 70 75 80

Ile Arg Gln Glu Tyr Glu Gln Gln Gly Lys Lys Pro Thr Lys Asp Met
85 90 95

Ile Glu Ser Ser Val Tyr Ile His Asp Ser Tyr Gln Gln Gln Leu Lys
100 105 110

Val Val Glu Ala Trp Asn Tyr Lys Val Lys Gln Leu Gln Tyr Val Val
115 120 125

Lys Ala Phe Glu Thr Arg Arg Asp Met Met Ile Gln Leu Gly Ala Glu
130 135 140

Leu Arg Gln Thr Asn Lys Asn Gly Gly Ile Thr Asn Pro Phe Ser His
145 150 155 160

<210> 681
<211> 423
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 681
Met Asp Phe Asn Gln Phe Ile Asn Asn Glu Ala Ser Lys Leu Glu Ser
1 5 10 15

Asn Asn Ser Ser Phe Asn Asn Asn Val Glu Ser Tyr Lys Pro Lys Asn
20 25 30

Pro Val Leu Arg Leu Gly Asn Ile Lys Asp Ala Asn Gly Asn Lys Val

35 40 45

Val Lys Glu Asn Ala Phe Val Arg Val Leu Pro Pro Ala Gln Gly Thr
50 55 60

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

Lys Asp Gly Ser Gln Gly Phe Thr Gly Leu Thr Leu Pro Ala Glu Glu
85 90 95

Gly Ser Ser Val Leu Asp Pro Tyr Ile Gln Asp Trp Ile Thr Asn Gly
100 105 110

Val Gln Phe Ser Arg Phe Pro Asn Lys Pro Gly Val Arg Tyr Tyr Ile
115 120 125

His Val Ile Glu Tyr Phe Asn Asn Asn Gly Gln Ile Gln Pro Lys Thr
130 135 140

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

Gly Tyr Lys Glu Leu Leu Ala Asn Leu Lys Asp Thr Met Leu Lys Pro
165 170 175

Ser Pro Asn Ala Pro His Ser Phe Ile Ser Ala Asn Glu Ala Phe Leu
180 185 190

Val Asn Ile Val Lys Ala Lys Lys Gly Glu Met Ser Trp Lys Val Ser
195 200 205

Val Tyr Pro Asn Ala Pro Leu Gly Ala Leu Pro Gln Gly Trp Glu Gln
210 215 220

Gln Leu Ser Asp Leu Asp Gln Leu Ala Lys Pro Thr Glu Glu Gln Asn
225 230 235 240

Pro Asn Phe Val Asn Phe Leu Ile Asn Asn Val Asn Asn Thr Glu Leu
245 250 255

Ser His Asp Asn Phe Lys Phe Asn Arg Glu Thr Asn Val Leu Gly Glu
260 265 270

Glu Pro Ser Glu Pro Lys Gln Ala Pro Thr Gln Gln Asp Val Asp Ser
275 280 285

Gln Met Pro Ser Asn Met Gly Gly Gln Pro Asn Gln Pro Gln Gln Gly
290 295 300

Gln Val Gly Gln Tyr Ala Gln Gln Gly Gln Ser Asn Gly Gln Gly Gln

305 310 315 320

Gln Leu Gln Gly Thr Gln Gln Pro Ile Asn Asn Thr Gln Phe Gly Gln
325 330 335

Gly Thr Pro Ser Gly Gln Gln Pro Ser Asn Thr Gly Ser Val Asp Trp
340 345 350

Asp Asn Leu Ala Gln Gln Gln Ser Gln Pro Asp Ser Asn Pro Phe Asn
355 360 365

Asp Phe Asp Val Ser Ser Val Asp Asp Ser Gln Val Pro Phe Glu Thr
370 375 380

Gln Pro Gln Asn Thr Gln Gln Ala Pro Glu Pro His Gln Thr Thr Gln
385 390 395 400

Glu Pro Pro Lys Gln Lys Gln Thr Gln Ser Ile Asp Asp Val Leu Gly
405 410 415

Gly Leu Asp Leu Asp Asn Leu
420

<210> 682
<211> 418
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 682
Met Ala Arg Ala Lys Lys Gly Lys Glu Val Asp Leu Thr Asp Leu Asn
1 5 10 15

Thr Ile Asp Leu Gly Lys Glu Leu Gly Leu Thr Leu Leu Ser Asp Thr
20 25 30

Asn Arg Ala Asp Ile Lys Asn Val Ile Pro Thr Met Val Pro Gln Tyr
35 40 45

Asp Tyr Ile Leu Gly Gly Gly Ile Pro Leu Gly Arg Leu Thr Glu Val
50 55 60

Tyr Gly Leu Thr Gly Ser Gly Lys Ser Thr Phe Ala Val His Leu Ser
65 70 75 80

Arg Ile Ala Thr Gln Leu Gly Val Ile Thr Ile Trp Ile Asp Ile Glu
85 90 95

Gly Thr Ala Asp Asn Asn Arg Met Glu Gln Leu Gly Val Asp Val Ser
100 105 110

```
Lys Leu Phe Ser Ile Gln Ser Gly Glu Gly Arg Leu Lys Asn Thr Val
        115                 120                 125

Glu Leu Ser Val Glu Gln Val Gly Lys Glu Leu Glu Tyr Trp Ile Asp
    130                 135                 140

Thr Phe Asn Glu Lys Ile Pro Gly Val Pro Ile Val Phe Ile Trp Asp
145                 150                 155                 160

Ser Leu Gly Ala Thr Arg Thr Gln Lys Glu Ile Asp Gly Gly Ile Asp
                165                 170                 175

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

Ala Val Thr Pro Lys Leu Asn Asp Thr Asn Thr Gly Leu Ile Val Ile
        195                 200                 205

Asn Gln Ala Arg Asp Asp Met Asn Ala Gly Met Tyr Gly Asp Pro Ile
    210                 215                 220

Lys Ser Thr Gly Gly Arg Ala Phe Glu His Ser Ala Ser Leu Arg Ile
225                 230                 235                 240

Lys Val His Lys Ala Ser Gln Leu Lys Gln Lys Ser Glu Leu Thr Gly
                245                 250                 255

Lys Asp Glu Tyr His Gly His Ile Met Arg Ile Glu Thr Lys Lys Ser
            260                 265                 270

Lys Leu Ser Arg Pro Gly Gln Lys Ala Glu Ala Asp Leu Leu Ser Asp
        275                 280                 285

Tyr Met Val Gly Lys Glu Asp Asp Pro Ile Leu Leu Asn Gly Ile Asp
    290                 295                 300

Leu Glu His Thr Val Tyr Lys Glu Ala Val Glu Arg Gly Leu Ile Thr
305                 310                 315                 320

Lys Gly Ala Trp Arg Asn Tyr Val Thr Leu Asn Gly Glu Glu Ile Lys
                325                 330                 335

Leu Arg Asp Ala Glu Trp Val Pro Val Leu Lys Asp Asn Arg Glu Leu
            340                 345                 350

Tyr Leu Glu Leu Phe Ser Arg Val Tyr Gly Glu His Phe Pro Asn Gly
        355                 360                 365

Tyr Ser Pro Leu Leu Asn Asn Lys Val Ile Val Thr Gln Leu Glu Glu
    370                 375                 380
```

Tyr Gln Ala Leu Glu Asn Tyr Tyr Lys Glu Trp Ala Thr Asp Asn Lys
385 390 395 400

Gln Glu Glu Gln Glu Glu Glu Leu Lys Gly Glu Ser Gln Glu Lys Asp
405 410 415

Ser Glu

<210> 683
<211> 117
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 683
Met Asp Asn Leu Ile Asp Lys Asn Met Ser Gln Val Lys Glu Ser Leu
1 5 10 15

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

Ala Lys Lys Phe Glu Glu Val Lys Glu Lys Gly Glu Ser Ile Ile Ile
35 40 45

Glu Glu Gly Gly Phe Pro Tyr Thr Asp Ser Thr Val Met Tyr Ile Glu
50 55 60

His Val Thr Asp Arg Trp Ala Gly Gly Tyr Ser Leu Ile Arg His Glu
65 70 75 80

Gly Glu Glu Val Lys Val Pro Lys Thr Ile His Phe Ser Asp Ile Tyr
85 90 95

Val Lys Asp Lys Ser His Lys Val Arg Ile Ile Phe Glu Gly Ala Asn
100 105 110

Pro Tyr Glu Glu Ser
115

<210> 684
<211> 220
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 684
Met Lys Lys Ala Asn Asn Gly Asn Arg Tyr Val Ile Asp Ile Asp Gly
1 5 10 15

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

Lys Asn Leu Arg Trp Ser Leu Tyr His Arg Tyr Ala Gly Ile Leu Ser
35 40 45

Asn Asp Phe Glu Arg Gln Glu Leu Arg Glu Tyr Ile Asp Glu Gln Phe
50 55 60

Ile Lys Leu Val Lys Glu Tyr Asn Ile Arg Ser Lys Val Asp Phe Pro
65 70 75 80

Gly Tyr Ile Lys Ala Lys Leu Thr Leu Arg Val Gln Asn Ser Tyr Val
85 90 95

Lys Lys Asn Glu Lys Tyr Lys Arg Thr Glu Ile Ile Gly Lys Lys Asp
100 105 110

Tyr Thr Val Glu Ser Leu Thr Glu Asp Leu Asn Glu Asp Phe Glu Asp
115 120 125

Asn Gln Ile Met Ser Tyr Val Phe Asp Asp Ile Glu Phe Thr Glu Val
130 135 140

Gln Ser Glu Leu Leu Lys Glu Leu Leu Ile Asn Pro Glu Arg Glu Asp
145 150 155 160

Asp Ala Phe Ile Val Ser Gln Val Ala Glu Lys Phe Asp Met Lys Arg
165 170 175

Lys Glu Val Ala Ser Glu Leu Thr Glu Leu Arg Asp Tyr Val Arg Phe
180 185 190

Lys Ile Asn Ala Tyr His Glu Tyr Tyr Ala Lys Lys Glu Leu Asn Asn
195 200 205

His Arg Val Asn Thr Glu Asn His Ile Trp Glu Asn
210 215 220

<210> 685
<211> 210
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 685
Met Ala Lys Lys Asn Val Asn Asp Val Leu Gln Gln Glu Ser Val Thr
1 5 10 15

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

Arg Thr His Glu Gly Gln Tyr Ala Tyr Lys Val Val Ser Glu Gly Glu

35 40 45

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

Val Met Lys Lys Ser Pro Ile Ala Tyr Thr Asp Gly Asp Asn Ile His
65 70 75 80

Phe Val Val Asn Thr Val Val Asp Pro Tyr Asn His Ser Phe Ile Arg
85 90 95

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

Phe Leu Ala Phe Val Glu Asp Arg Phe Lys Phe Gly Val Tyr Asn Val
115 120 125

Phe Val Ala Asn Asn Lys Glu Asp Val Leu Ser Ile Val Asp Pro Thr
130 135 140

Asp Asn Asp Ala Asp Glu Val Lys Asp Ser Leu Glu His Ala His Glu
145 150 155 160

Asp Val Ile Ala Asp Phe Pro Ala Ser Pro Ala Arg Lys Asp Val Lys
165 170 175

Gly Val Asp Ser Gly Glu Gly Gln Gly Asp Thr Ser Glu Pro Ser Ala
180 185 190

Pro Lys Asn Val Gln Val Thr Pro Lys Glu Asp Gly Ala Asp Val Ser
195 200 205

Ala Glu
210

<210> 686
<211> 170
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 686
Leu Ala Lys Leu Asn Leu Tyr Lys Gly Asn Glu Leu Leu Asn Ser Val
1 5 10 15

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

Asn Thr Asp Tyr Pro Lys Gly Thr Phe Lys Val Ser Phe Ser Asn Asp
35 40 45

Ser Gly Glu Ser Glu Lys Val Asp Val Pro Gln Phe Lys Thr Lys Ala
    50   55   60

Ile Lys Val Ile Ser Val Thr Leu Asp Val Asp Ser Leu Asp Leu Thr
65   70   75   80

Val Gly Asp Thr His Gln Leu Ser Thr Thr Ile Thr Pro Ser Glu Ala
                85   90   95

Ser Asn Lys Asn Val Ser Phe Glu Ser Asp Lys Ser Gly Val Ala Ser
            100   105   110

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

Val Thr Val Thr Thr Glu Asp Gly Ser His Thr Asp Ile Val Ala Val
    130   135   140

Thr Val Lys Glu Pro Ile Pro Glu Ala Pro Ala Asp Val Thr Val Glu
145   150   155   160

Pro Gly Glu Asn Ser Ala Asp Ile Thr Val
                165   170

<210> 687
<211> 75
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 687
Met Glu Lys Thr Leu Lys Val Tyr Ser Asn Gly Glu Val Val Gly Ser
1   5   10   15

Gln Val Ala Asn Asn Asp Gly Ala Thr Thr Val Ser Ile Thr Gly Leu
            20   25   30

Glu Ala Gly Lys Thr Tyr Ala Lys Gly Asp Phe Lys Val Ala Phe Ala
        35   40   45

Asn Asp Ser Gly Glu Ser Glu Lys Val Asp Val Pro Glu Phe Thr Thr
    50   55   60

Lys Thr Pro Thr Glu Glu Pro Ser Gly Asp Ala
65   70   75

<210> 688
<211> 86
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 688
Met Asp Ile Pro Thr Ile Leu Phe Arg Asn Pro Tyr Asp Tyr Thr Lys
1   5   10   15

Val Lys Lys Leu Met Glu Asn Lys Glu Gln Tyr Ile Val Val Lys Phe
            20   25   30

Asp Ser Val Ser Val His Asn Leu Asn Val Gln Gly Met Met Asn Val
        35   40   45

Ile Gln Asp Tyr Leu His Ile Tyr Gly Tyr Arg Val Lys Glu Tyr Gly
    50   55   60

Gln Glu Asn Ser Ser Lys Asp Asp Glu Arg Asp Val Lys Gly Tyr Leu
65   70   75   80

Tyr Glu Arg Val Gly Glu
                85

<210> 689
<211> 251
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 689
Met Gly Ile Ile Val Asn Ser Asn His Ile Gln Ser Asp Thr Leu Tyr
1   5   10   15

Glu Tyr Asp Ser Phe Phe Asp Ile Glu Lys Val Asp Thr Phe Glu Glu
            20   25   30

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

Tyr Asp Asp Ile Thr Phe Asn Lys Val Ile Asn Ser Asn Ser Asp Ile
    50   55   60

Asp Asp Tyr Ile Lys Asn Asn Asp Ile Tyr Tyr Val Ser Asp Ile Gly
65   70   75   80

Leu Leu Pro Asp Thr Phe Ile Thr Val Asp Ser Asp Arg Lys Tyr Tyr
                85   90   95

Ser Leu Leu Gln Gln Ile Thr Glu Leu Ser Lys Asp Pro Phe Pro Lys
            100   105   110

Trp Val Glu Asp Asp Ala Lys Gly Leu Thr Lys Tyr Tyr Asn Phe Gln
        115   120   125

Asp Phe Glu Asp Val Phe Asp Leu Asn Ser Phe Tyr Lys Lys Glu Val

130 135 140

Asp Met Val Arg Glu Lys Cys Tyr Asn Asn Gly Asn Val Tyr Leu Leu
145 150 155 160

Tyr Glu Val Leu Pro Asp Tyr Lys Leu Pro Leu Ala Tyr Ser Leu Leu
165 170 175

Ser Asn Lys Glu His Gly Ile Val Ile Ile Gly Ser Gln Thr Arg Ser
180 185 190

Asn Asn Asp Ile Leu Thr Phe Tyr Val Lys Gly Met Asp Ala Lys Ala
195 200 205

Ile Ala Ser Met Phe Asn Val Glu His Asp Tyr Asp Ser Asn Ile Phe
210 215 220

His Thr Phe Val Asn Ser His Ile Asn Ile Leu Gly Asn Gln Ile Thr
225 230 235 240

Lys Phe Ile Arg Glu Lys Gly Ser Ser Tyr Glu
245 250

<210> 690
<211> 416
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 690
Met Ser Asn Tyr Lys Thr Ile Glu Glu Val Gln Ala Val Ile Ile Gly
1 5 10 15

Val Leu Phe Lys Asp Glu Gly Lys Ile Ile Thr Ser Lys Phe Asn Lys
20 25 30

Ile Thr Lys Glu Phe Gly Leu Asp Arg Ile Gly Lys Asp Asp Leu Lys
35 40 45

Glu Ile Val Glu Asp Ile Arg Gln Asp Ala Tyr Leu Asn Glu Leu Lys
50 55 60

Asn Lys Ala Ile Lys Gly Lys Val Thr Leu Gly Asp Leu Lys Asp Val
65 70 75 80

Ala Asp Asn Gln Val Phe Glu Gly Asn Asn Tyr His Glu Glu Val Ser
85 90 95

Thr Tyr Val Val Ala Lys Glu Lys Glu Leu Ser His Leu Arg Glu Gln
100 105 110

```
Arg Lys His Asn Arg His Thr Ala Tyr Pro Gln Ile Met Phe Asp Glu
        115                 120                 125

Leu Lys Glu His Met Val Lys Glu Leu Gln Gly Glu Thr Leu Val Glu
    130                 135                 140

His His Gly Ser Lys Ala Asn Ile Asn Asp Thr Glu Leu Ile Val Leu
145                 150                 155                 160

Leu Ser Asp Phe His Ile Gly Ser Ile Val Ser Asp Met Thr Asn Gly
                165                 170                 175

Lys Tyr Asp Phe Glu Val Leu Lys Ala Arg Leu Asn His Phe Ile Asn
            180                 185                 190

Thr Thr Val Lys Glu Ile Glu Asp Arg Glu Ile Ser Asn Val Thr Val
        195                 200                 205

Tyr Phe Val Gly Asp Leu Val Glu His Ile Asn Met Arg Asp Val Asn
    210                 215                 220

Gln Ala Phe Glu Thr Glu Phe Thr Leu Ala Glu Gln Ile Ser Lys Gly
225                 230                 235                 240

Thr Arg Leu Leu Ile Asp Ile Leu Asn Val Leu Ser Asn Val Val Ser
                245                 250                 255

Gly Glu Leu Arg Phe Gly Ile Ile Gly Gly Asn His Asp Arg Met Gln
            260                 265                 270

Gly Asn Lys Asn Gln Lys Ile Tyr Asn Asp Asn Ile Ala Tyr Val Val
        275                 280                 285

Leu Asp Ser Leu Leu Leu Phe Gln Glu Gln Gly Leu Leu Asn Gly Val
    290                 295                 300

Asp Ile Ile Asp Asn Arg Glu Asp Ile Tyr Thr Ile Arg Asp Thr Phe
305                 310                 315                 320

Gly Gly Lys Ser Ile Ile Ile Asn His Gly Asp Gly Leu Lys Gly Lys
                325                 330                 335

Gly Asn His Ile Asn Lys Phe Ile Leu Asp Ser His Ile Asp Leu Leu
            340                 345                 350

Ile Thr Gly His Val His His Phe Ser Val Lys Gln Glu Asp Phe Asn
        355                 360                 365

Arg Met His Ile Val Ala Ser Ser Pro Met Gly Tyr Asn Asn Tyr Ala
    370                 375                 380
```

Lys Glu Leu His Leu Ser Lys Thr Lys Pro Ser Gln Gln Leu Leu Phe
385 390 395 400

Ile Asn Lys Glu Asn Lys Asp Ile Asp Ile Lys Thr Val Phe Leu Asp
405 410 415

<210> 691
<211> 122
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 691
Met Asp Thr Ile Phe Ile Ile Gly Val Ala Phe Ile Thr Phe Ala Thr
1 5 10 15

Phe Asn Ile Val Phe Arg Leu Phe Asp Leu Trp Thr Thr Glu Lys Lys
20 25 30

Met Val Ser Gln Gly Gln Pro Pro Leu Ser Asn Phe Glu Tyr Tyr His
35 40 45

Val Ile Val Pro Tyr Leu Val Gly Val Ile Val Ile Ile Leu Ser Ile
50 55 60

Ile Phe Arg Asp Ser Leu Tyr Ser Ala Gln Ser Gly Phe Gly Val Ile
65 70 75 80

Ile Thr Ser Phe Ile Tyr Met Leu Val Tyr Val Ile Ile Gly Leu Val
85 90 95

Gly Ser Phe Val Leu Thr Ile Phe Gln Ala Arg Lys Ala Arg Gln Tyr
100 105 110

Gln Thr Gln Glu Asp Asn Asn Glu Val Gln
115 120

<210> 692
<211> 103
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 692
Met Lys Phe Asn Asp Ile Tyr Glu Gln Leu Ile Lys Asn Asp Thr Val
1 5 10 15

Gln Asn Ile His Glu Ser Gln Asp Asp Lys Gly Asn Ile Tyr Thr Ile
20 25 30

Gln Phe Asp Lys Gly Asn Asp Lys Tyr Leu Phe Asn Val Ile Asn Asp
35 40 45

Gly Phe Leu Lys Glu Met Thr Asn Gly Met Val Asp His Pro Glu Gly
50 55 60

Gln Pro Tyr Ser Val Ser Leu Ile Asn Lys Glu Thr Pro Ser Met Ser
65 70 75 80

Val Lys Gln Tyr Leu Thr Asp Val Glu Asp Ile Val Pro Thr Ile Arg
85 90 95

Lys Met Glu Lys Asp Phe Leu
100

<210> 693
<211> 178
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 693
Met Asp Phe Asn Phe Ser Ala Phe Asp Asn Ser Ser Leu Ala Met Arg
1 5 10 15

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

Glu His Val Glu Glu Glu Met Ser Glu Tyr Val Ile Val Tyr Asp Ile
35 40 45

His Asp Arg Glu Glu Lys Glu Asn Pro Gln Lys Lys Tyr Arg Ile Glu
50 55 60

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

Lys Ser Met Met Pro Gln Arg Lys Tyr Pro Lys Lys Val Thr Glu Asp
85 90 95

Pro Ile Phe Val Ala Asn Val Ile Pro Leu Gly Thr Asp Thr Val Thr
100 105 110

Gly Lys Thr Gly Lys Gly Phe Phe Glu Arg Asp Lys Asp Arg Thr Ile
115 120 125

Tyr Ser Gln Lys Glu Pro Thr Lys Val Val His Gly Gln Tyr Thr Gly
130 135 140

Val Phe Ile Gly Leu Thr Ser Val Lys Trp Asn Arg Thr Tyr Thr Pro
145 150 155 160

Leu Glu Ser Val Val Glu Tyr Tyr Lys Arg Val Lys Gly Asp Arg Leu

165 170 175

Asn Val

<210> 694
<211> 255
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 694
Met Ser Asn Asp Val Val Lys Phe Tyr Glu Lys Asp Ile Lys Asp Leu
1 5 10 15

Ile Arg Thr Lys Lys His Met Phe Lys Asp Asp Glu Ile Thr Ser Asp
20 25 30

Ile Asn Asp Ile Arg Ile Phe Asn Glu Lys Val Ile Cys Gln Gly Lys
35 40 45

Cys Arg Thr Asp Cys Leu Val Leu Asp Arg Asn Gly Thr Val Met Gly
50 55 60

Ile Glu Ile Lys Thr Glu Arg Asp Ser Thr Gln Arg Leu Asn Asn Gln
65 70 75 80

Leu Lys Tyr Tyr Ser Leu Val Cys Lys Tyr Val Tyr Val Met Cys His
85 90 95

Asp Lys His Val Pro Lys Val Glu Gln Ile Leu Lys Arg Tyr Lys His
100 105 110

Asn His Val Gly Ile Met Ser Tyr Ile Ser Phe Lys Gly Lys Pro Val
115 120 125

Val Gly Lys Tyr Lys Asp Ala Thr Pro Ser Pro His Arg Ser Pro Tyr
130 135 140

His Thr Met Asn Ile Leu Trp Lys Thr Asn Leu Met Thr Ile Leu Arg
145 150 155 160

Leu Ile Arg Asp Pro His Thr Tyr Arg Thr Gly Tyr Ser Tyr Asn Ala
165 170 175

Ser Gly Arg Tyr Ser Gly Gly Glu Gly Asn Phe Ser Gln Thr Thr Gln
180 185 190

Ser Lys Arg Met Lys Lys Pro Ala Ile Ile Asn Gln Ile Ile His Tyr
195 200 205

Val Gly Val Asp Asn Thr Tyr Lys Leu Phe Thr Arg Gly Val Ile Tyr
    210   215   220

Gly Tyr Asn Asn Arg Trp Glu Val Ile Glu Glu Asp Phe Phe Asn Thr
225   230   235   240

Met Lys Asn Gly Val Arg Val Ile Asn Glu Gln Arg Gln Thr Lys
                245   250   255

<210> 695
<211> 148
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 695
Met Ser Lys Asp Lys Pro Asn Arg Arg Lys Glu Ile Gln His Gln Pro
1   5   10   15

Val Asn Phe Ala Pro Thr Asn Thr Leu Thr Gly Ala Asn Asn Ser Phe
            20   25   30

Phe Ala Lys Asn Pro Ser Glu Pro Lys Asp Ala Thr Ser Val Ile Glu
        35   40   45

Tyr Arg Ile Leu Phe Ile Lys Arg Phe Asp Asn Val Thr Ser Thr Asp
    50   55   60

Val Lys Leu Gln Lys Lys Tyr Ala Leu Asn Leu Ile Ser Glu Ala Leu
65   70   75   80

Asp Val Lys Glu Thr Tyr Leu Ser Leu Lys Gln Lys Gly Lys Lys Thr
                85   90   95

Glu Ser Ile Leu His Thr Asp Arg Val Tyr Tyr Val His Arg Gly Lys
            100   105   110

Lys Leu Ile Gly Lys Cys Ser Ile Arg Glu Gln Arg Thr Phe Lys Gly
        115   120   125

Lys His Leu Ile Phe Ile Phe Lys Thr Arg His Arg Val Lys Ala Glu
    130   135   140

Arg Lys Asp Lys
145

<210> 696
<211> 287
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 696
Met Leu Lys Gly Phe Ser Glu His Val Asp Lys Pro Thr Thr Ser Lys
1   5   10   15

Thr Leu Tyr Lys Thr Leu Thr Ser Gly Lys Val Glu Leu Leu Gly Val
            20   25   30

Ser Tyr Asp Ser Asp Tyr Phe Pro Ser Gly Val Thr Val Gln Ser Tyr
        35   40   45

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

Val Asn Val Val Glu Ser Met Lys Gln Ala Val Val Gly Met Asn Asn
65   70   75   80

Gln Leu Gly Ser Ser Gly Leu Gly Tyr Val Arg Thr Glu Gln Leu Lys
                85   90   95

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

Thr Asn Leu Thr Ser Thr Lys Lys Val Asp Ile Val Ser Thr Phe Ile
        115   120   125

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

Leu Arg Leu Tyr Lys Val Glu Glu Glu Ser Pro Leu Asn Gly Tyr Thr
145   150   155   160

His Ile Val Tyr Leu Leu Thr Thr Glu Lys Leu Tyr Asp Gly Gln Thr
                165   170   175

Leu Phe Gly Met Leu Ser Lys Lys Asp Lys Leu Ser Lys Gly Asp Thr
            180   185   190

Asp Lys Leu Leu Ala Phe Phe Arg Asn Asn Ser Leu Ile Ser Lys Ser
        195   200   205

Val Phe Cys Val Lys Leu Leu Ser Lys Asp Tyr Tyr Phe Asn Leu Tyr
    210   215   220

Asn Thr His Glu Thr Gly Ile Phe Phe Leu Glu Asp Thr Asp Val Ile
225   230   235   240

Thr Ile Ala Cys Gly Gln Ser Tyr Val Lys Val Asn Thr Lys Asp Ile
                245   250   255

Lys Ser Ser Tyr Val Lys Ile Glu Asp Lys Thr His Lys Leu Thr Glu
            260   265   270

Leu Val Ile Asn Leu Lys Gly Asp Asp Thr Leu Thr Ile Leu Phe
275 280 285

<210> 697
<211> 243
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 697
Met Ala Arg Lys Lys Asn Leu Arg Asn Lys Asn Ser Asp Ile Lys Val
1 5 10 15

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

Lys Leu Leu Arg Ser Lys Val Asp Asn Ala Leu Asp Glu Asp Met Ser
35 40 45

Tyr Asp Asp Ile Ile Glu Leu Cys Lys Glu Tyr Asp Leu Glu Leu Ser
50 55 60

Lys Ser Ala Ile Thr Arg Tyr Lys Ser Lys Arg Lys Glu Ala Ile Glu
65 70 75 80

Asn Gly Trp Asp Leu Gly Glu Leu Ile Asp Lys Arg Lys Lys Thr Ser
85 90 95

Val Lys Asp Ile Lys Glu Lys Glu Thr Pro Ile Leu Glu Glu Glu Gln
100 105 110

Leu Ser Pro Phe Glu Gln Ser Lys His His Thr Gln Thr Ile Tyr Asp
115 120 125

Asp Ile Gln Val Leu Asp Met Ile Ile Ser Lys Gly Ala Lys Gly Leu
130 135 140

Glu Phe Val Glu Thr Leu Asp Pro Ala Leu Met Ile Arg Ala Met Glu
145 150 155 160

Thr Lys Asp Lys Ile Thr Gly Asn Gln Leu Lys Gly Met Ser Phe Ile
165 170 175

Gly Leu Arg Glu Leu Gln Leu Lys Gln Thr Ala Gln Asp Thr Ala Met
180 185 190

Ser Glu Val Leu Leu Glu Phe Ile Pro Glu Glu Lys His Glu Glu Val
195 200 205

Leu Gln Arg Leu Glu Glu Leu Gln Asn Glu Phe Tyr Lys Asn Leu Asp

210 215 220

Leu Asp Glu Glu Ser Arg Lys Leu Lys Glu Ala Leu Asp Arg Val Gly
225 230 235 240

Tyr Thr Ile

<210> 698
<211> 152
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 698
Met Ala Asp Glu Ile Ser Leu Asn Pro Ile Gln Asp Ala Lys Pro Ile
1 5 10 15

Asp Asp Ile Val Asp Ile Met Thr Tyr Leu Lys Asn Gly Lys Val Leu
20 25 30

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

Gly Lys His Lys Phe Thr Glu Val Ser Arg Asp Leu Asp Lys Glu Ser
50 55 60

Phe Tyr Tyr Lys Arg His Trp Val Leu Tyr Asn Val Ser Val Asn Ser
65 70 75 80

Leu Ile Thr Phe Asp Val Tyr Leu Asp Glu Glu Tyr Ser Glu Thr Thr
85 90 95

Lys Val Lys Tyr Pro Lys Asp Thr Ile Val Glu Tyr Thr Arg Glu Asp
100 105 110

Gln Glu Lys Asp Val Ala Met Ile Lys Glu Ile Leu Thr Asp Asn Asn
115 120 125

Gly Asn Tyr Phe Tyr Ala Leu Thr Gly Glu Thr Met Leu Phe Asp Glu
130 135 140

Asn Lys Leu Asn Lys Val Lys Asp
145 150

<210> 699
<211> 147
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 699
Met Phe Ile Ser Leu Asn Gln Glu Glu Lys Glu Leu Leu Thr Lys Glu
1 5 10 15

Glu Ser Lys Tyr Thr Pro Leu Glu Thr Ser Arg Glu Phe Asn Thr Pro
20 25 30

Lys Glu Glu Phe Ile Val Thr Ser Tyr Asn Glu Gly Lys Pro Leu Asp
35 40 45

Tyr Ile Ala Lys Glu Ala Lys Val Ser Met Gly Leu Ile Tyr Thr Val
50 55 60

Leu Asn Tyr Tyr Lys Val Gly Lys Arg Asn Lys Lys Ser Pro Val Glu
65 70 75 80

Glu Arg Ile Ala His Ile Leu Lys Asp Lys Asn Leu Val Lys Glu Ile
85 90 95

Ile Lys Asp Tyr Gln Tyr Met Asn Leu Gln Asp Ile Tyr Ser Lys Tyr
100 105 110

Asn Leu His Lys Asn Gly Leu Tyr Tyr Ile Leu Asp Leu Tyr His Val
115 120 125

Glu Arg Lys Ser Glu Leu Lys Asp Lys Ala Leu Glu Glu Asp Asn Ile
130 135 140

Val Val Glu
145

<210> 700
<211> 234
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 700
Met Arg Asn Lys Lys Ser Phe Gln Glu Gln Leu Asn Asp Met Arg Asn
1 5 10 15

Lys Glu Lys Trp Val Ser Glu Glu Glu Phe Thr Glu Glu Val Ala Pro
20 25 30

Ser Glu Glu Pro Glu Val Glu Glu Glu Lys Leu Tyr Thr Leu Asn Glu
35 40 45

Leu Lys Glu Asn Leu Leu Asp Ala Gln Gly Leu Lys Asp Val Val Ala
50 55 60

Asp Phe Pro Ala Ser Lys Asp Leu Tyr Glu Pro Asn Lys Leu Tyr Ile
65 70 75 80

```
Cys Thr Ile Pro Lys Gly Tyr Arg Ser Thr Glu Val Gln Pro Gly Gln
                85                  90                  95

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

His Leu Arg Gly Gln Met Pro Arg Asn Leu Tyr Glu Thr Ser His Val
        115                 120                 125

Leu Lys Pro Leu Val Arg Ile Asn Asn Thr Asn Leu Glu Tyr Gln Gln
    130                 135                 140

His Glu Leu Leu Glu Asp Ile Lys Asp Asp Lys Lys Ile Tyr Asp Val
145                 150                 155                 160

Glu Leu Glu Asp Leu Arg Leu Val Thr Gly Glu Glu Ile Ser His Leu
                165                 170                 175

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

Asp Arg Tyr Thr Glu Leu Thr Asp Ser Asp Asp Leu Leu Ile Tyr Tyr
        195                 200                 205

Ser Lys Leu Arg Glu Leu Val Gly Ser Asp Lys Met Ile Tyr Cys Ser
    210                 215                 220

Leu Leu Asp Lys Cys Val Lys Ile Ile Asp
225                 230


<210> 701
<211> 132
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 701
Met Ser Arg Lys Ala Ser Ile Phe Tyr Ile Leu Val Val Ile Val Leu
1               5                   10                  15

Ala Phe Ser Ile Ser Ser Tyr Tyr Ile Ser Ser Phe Met Tyr His Asp
            20                  25                  30

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

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

Val Glu Asn Asn Lys Ala Tyr Phe Met Glu Thr Leu Pro Thr Tyr Leu
```

65 70 75 80

Pro Gly Arg Thr Gly Asp Asn Ser Ile Asp Met Arg Tyr Tyr Lys Thr
85 90 95

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

Glu Asp Gly Glu Asp Asn Pro Ile His Lys Tyr Arg Phe Glu Ala Val
115 120 125

Pro Thr Lys Lys
130

<210> 702
<211> 80
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 702
Met Glu Met Ala Asp Leu Glu Arg Phe Asp Thr Phe Val Arg Leu Val
1 5 10 15

Ser Asp Asp Glu Leu Ser Glu Glu Arg Ala Leu Glu Leu Ser Val Asp
20 25 30

Leu Leu Asn Pro Ile Leu Glu Gly Gly Thr Ala Tyr Gln Ala Lys Lys
35 40 45

Arg Ile Arg Ser Lys Phe Gly Lys Ile Glu Ala Lys Asn Phe Lys Arg
50 55 60

Asn Tyr Lys Phe Leu Leu Lys Ser Ile Ala Gln Ile Asp Gln Arg Arg
65 70 75 80

<210> 703
<211> 185
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 703
Met Ile Glu Arg Glu Lys Leu Val Lys Glu Ile Glu Asp Ala Asn Arg
1 5 10 15

Asp Ile Gln Leu Arg Leu Lys Glu Val Asp Asp Tyr Lys Asp Ser Ile
20 25 30

Arg Ser Lys Gly Thr Arg Asn Tyr Val Ser Thr Lys Val Leu Asp Ser
35 40 45

Val Met Val Gly Leu Ile Ile Ser Phe Phe Ile Leu Val Met Leu Arg
50 55 60

Val Leu Glu Tyr Phe Val Thr Gly Asn Ala Val Tyr Ser Pro Leu Ala
65 70 75 80

Pro Ala Val Ile Ile Met Phe Val Leu Ala Leu Gly Thr Trp Lys Val
85 90 95

Ser Lys Met Asn Lys Ile Val Ser Tyr Arg Gly Thr Ile Lys Met Tyr
100 105 110

Trp Glu Leu Ser Asn Ala Glu Gln Asn Gln Ala Lys Val Phe Lys Tyr
115 120 125

Pro Asn Asp Glu Val Asp Ile Val Ser Lys His Asn Leu Arg Gln Ile
130 135 140

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

Lys Ala Val Glu Gln His Thr Lys Leu Ser Lys Glu Leu Phe Lys Lys
165 170 175

Asp Lys Glu Thr Val Asp Lys Asn Lys
180 185

<210> 704
<211> 58
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 704
Met Val Ile Pro Ser Ile Lys Ala Gln Asn Lys Phe Lys Asn Glu Leu
1 5 10 15

Glu Tyr Tyr Lys Gln Gly His Ile Ser Glu Ser Lys Met Leu Glu Leu
20 25 30

Ala Phe Asp Tyr Ile Gln Glu Leu Glu Gln Asn Asn Glu Tyr Val Thr
35 40 45

Asn Leu Leu Glu Glu Glu Arg Tyr Gly Glu
50 55

<210> 705
<211> 82
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F44/10

<400> 705
Val Ser Lys Phe Ile Gly Val Tyr Leu Phe Asn Leu Leu Val Val Ala
1   5   10   15

Leu Ile Tyr Thr Val Gly Phe Leu Phe Phe Tyr Gly Val Ala Ser Leu
            20   25   30

Val Ile Ile Leu Thr His Ala Thr Ile Asp Pro Phe Val Leu Ala Thr
        35   40   45

Phe Leu Gly Ile Gly Phe Leu Val Ile Arg Thr Ala His Arg Ile Met
    50   55   60

Ala Arg Val Ile Asn Asp Ala Val Ala Lys Ala Ile Lys Asp Lys Glu
65   70   75   80

Asn Glu

<210> 706
<211> 77
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 706
Met Asn Lys Gly Glu Phe Ile Met Asp Lys Thr Leu Pro Lys Phe Ser
1   5   10   15

Val Tyr Glu Val Ile Val Lys Thr Val Ile Met Thr Pro Thr Glu Gly
            20   25   30

Ser Ser Asp Leu Glu Ser Phe Tyr Phe Ser Thr Arg Glu Leu Ala Glu
        35   40   45

Arg Phe Val Glu Glu Asn Thr Val Glu Thr Lys Asn Gly Lys Arg Val
    50   55   60

Ser Phe Ala Val Lys Glu Arg Lys Val Asn Gln Pro Gly
65   70   75

<210> 707
<211> 162
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 707
Met Lys Val Ser Glu Glu Val Lys Gln Ser Tyr Leu Glu Asn Arg Ala
1   5   10   15

Asn Thr Lys Met Asp Lys Ile Ser Trp Ser Glu Leu Arg Ser Ser Pro
20 25 30

Leu Gly Ile Thr Leu Gly Asp Ile Ile Phe Tyr Ser Val Val Ile Ile
35 40 45

Asp Asn Ile Ile Ala Ile Ile Leu Thr Leu Thr Leu Ile Gly Thr Ile
50 55 60

Thr Asp Ser Ile Glu Ser Thr Leu Ala Gln Ile Ile Val Gly Met Phe
65 70 75 80

Ile Ile Ile Thr Ile Tyr Gly Ile Leu Ser Ala Leu Ile Pro Ile Leu
85 90 95

Val His Lys Ala Val Ser Pro Gly Trp Ser Tyr Thr Glu Trp Asn Glu
100 105 110

Ser Tyr Tyr Ile Arg Leu Pro Gly Glu Glu Asn Tyr Lys Tyr Tyr Ser
115 120 125

Lys Trp Tyr Leu Asp Leu Leu Gly Val Lys Glu Phe Tyr Tyr Lys Arg
130 135 140

Asp Asn Gly Glu Glu Val Lys Glu Lys Ile Tyr His Gly Leu Phe Lys
145 150 155 160

Leu Lys

<210> 708
<211> 39
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 708
Leu Leu Thr Asn Arg Pro Leu Thr Ile Leu Glu Tyr Lys Lys Leu Lys
1 5 10 15

Lys Leu Asp Lys Glu Ser Glu Ile Arg Lys Gln Glu Asp Leu Glu Glu
20 25 30

Tyr Lys Gln Tyr Asn Ser Asn
35

<210> 709
<211> 82
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F44/10

<400> 709
Met Ile Ser Ser Phe Asp Ser Ile Leu Leu Val Ile Tyr Ile Ile Ile
1   5   10   15

Ala Phe Ala Val Ala Met Ala Ile Ile Tyr Leu Val Phe Lys Gly Met
            20   25   30

Thr Ile Leu Leu Asp Lys Leu Met Met Leu Leu Leu Ser Lys Thr Thr
        35   40   45

Leu Asp Val Glu Ala Cys Ser Met Ile Met Ala Val Ile Ser Thr Ile
    50   55   60

Val Phe Gly Ile Ile Val Leu Leu Ile Trp Leu Ala Val Asn Asn Ile
65   70   75   80

Leu Leu

<210> 710
<211> 58
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 710
Met Asp Phe Asn Asp Phe Ile Asn Ser Glu Ser Asp Arg Val Gly Lys
1   5   10   15

Pro Lys Gln Lys Lys Lys Val Glu Asn Lys Leu Pro Ser Ser Thr Pro
            20   25   30

Ile Glu Asp Lys Glu Lys Lys Leu Lys Glu Ile Arg Lys Lys Ser Leu
        35   40   45

Tyr Ile Asp Leu Arg Arg Lys Arg Asn Asp
    50   55

<210> 711
<211> 98
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 711
Met Thr Lys Glu Thr Asn Val Leu Tyr Lys Asp Lys Tyr Arg Asp Tyr
1   5   10   15

Thr Ile Val Val Arg Leu Ala Gly Asn Ile Ile Val Thr Glu Val Asp
            20   25   30

Lys Lys His Lys Thr Ala Phe Thr Pro Ile Ile Phe Asp Asn Gly Val
35 40 45

Glu Gly Val Glu Leu Val Met Arg Ile Gly Ser Val Glu Leu Ser Met
50 55 60

Thr Asp Leu Arg Glu Phe Thr Lys Glu Val Ser Thr Ala Gln Lys Ala
65 70 75 80

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

Ala Phe

<210> 712
<211> 60
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 712
Met Leu Leu Gly Ile Leu Trp Phe Ile Trp Gly Phe Val Ser Tyr Phe
1 5 10 15

Val Leu Met Phe Gly Ile Glu Phe Trp Lys Asp Arg Trp Met Pro Gly
20 25 30

Val Ile Gly Ala Gly Ala Leu Leu Leu Phe Leu Phe Trp Ile Met Lys
35 40 45

Ser Ile His Asn Ala Met Thr Val Val Tyr Leu Tyr
50 55 60

<210> 713
<211> 123
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 713
Met Ile Asp Ile Leu Val Ile His Tyr Glu Glu Thr Asn Lys Arg Val
1 5 10 15

Leu Lys Glu Thr Ile Gln Thr Ile Gln Asn His Leu Asn Asp Glu His
20 25 30

Gly Leu Val Lys Met Thr Ala Thr Lys Leu Ser Arg Glu Asn Ile Glu
35 40 45

Lys Arg Phe Asn Asn Tyr Asn Ile Val Ile Ala Glu Asp Asp Pro Asp

50 55 60

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

Asp Ile Pro Ile Ser Tyr Leu Asp Ile His Ala Gly Ile Glu Trp Asp
85 90 95

Val Asp Asn Pro Val Asp Met Leu Asp Arg Asn Pro Asp Phe Ile Glu
100 105 110

Ala Val Asn Lys Leu Asn Glu Asp Leu Met Leu
115 120

<210> 714
<211> 115
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 714
Met Leu Asn Glu Lys Leu Lys Asn Leu Glu Asp Thr Lys Val Tyr Met
1 5 10 15

Ile Asn Ser Ile Ala Ser Leu Leu Ser Ala Ser Thr Gly Lys Ser Ser
20 25 30

Lys Val Phe Phe Asp Glu Gly Thr Ile Lys Ile Val Ser Gly Glu Thr
35 40 45

Lys Ala Val Glu Val Ile Asp Asn Leu Val His Pro His Ser Gly Arg
50 55 60

Leu Pro Ile Lys Thr Thr Glu Arg Ile Ala Leu Gly Arg Leu Thr Asp
65 70 75 80

Ser Leu Gln Phe Val Ile Ser Glu Ile Glu Val Val Lys Asp Gln Ile
85 90 95

Ile Asp Glu Glu Asn Glu Ala Tyr Ile Asp Phe Val Met Glu Asp Trp
100 105 110

Asn Trp Asp
115

<210> 715
<211> 92
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 715
Met Pro Met Asp Leu Leu Thr Ile Ala Ser Val Ala Phe Ile Ala Val
1   5   10   15

Val Ile Ile Asp Leu Ile Asn Asp Asp Met Ser Tyr Met Leu Thr Gly
            20   25   30

Thr Ala Ile Leu Ile Asn Ile Trp Ala Gly Phe Tyr Gly Trp Phe Phe
        35   40   45

Leu Leu Gln Ala Gly Met Leu Leu Phe Leu Leu Leu Ala Arg Lys Val
    50   55   60

Lys Asp Asp Lys Glu Ser Ile Leu Tyr Ser Ser Ala Ser Leu Ile Cys
65   70   75   80

Ala Leu Gly Met Ile Ile Asn Leu Leu Ser Phe Ser
                85   90

<210> 716
<211> 101
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 716
Met Ser Lys Glu Thr Ile Arg Arg Gln Phe Ser Asn Ala Ile Glu Ile
1   5   10   15

Met Ala Thr Thr Lys Glu Trp Trp Asn Phe Pro Lys Ser Phe Asp Thr
            20   25   30

Asn Lys Glu Phe Lys Ile Lys Thr Phe Lys Asn Asp Thr Leu Val Phe
        35   40   45

Glu Val Arg Glu Gly Ser Arg Asn Leu Gly Ser Phe Val Val Phe Thr
    50   55   60

Asn Ile Asp Phe Asp Tyr Asp Lys Leu Glu Gly Thr Ser Thr Gln Tyr
65   70   75   80

Met Ile Asn Tyr Phe Ala Lys Lys Leu Thr Lys Asp Met Phe Asn Tyr
                85   90   95

His Lys Leu Gln Leu
            100

<210> 717
<211> 116
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F44/10

<400> 717
Met Arg Glu Glu Leu Lys Pro Phe Asn Arg Lys Gln Val Asn Val Lys
1   5   10   15

Gly Tyr Leu Asp Asp Val Lys Tyr Ser Lys Arg Arg Arg His Lys Gly
            20   25   30

Asn Gln His Gly Cys Val Lys Ile Thr Val Thr Asp Val Lys Ile Asn
        35   40   45

Gly Ile Pro Ile Asp His Val Asn Ile Glu Val Gly Ile Ser Phe Tyr
    50   55   60

Glu Lys Leu Lys Glu Leu Gln Gly Lys Arg Ile Gln Phe Val Gly Thr
65   70   75   80

Val Tyr Lys Tyr Val Lys His Ala Arg Gly Arg Lys Gly Arg Ile Lys
                85   90   95

Gly Phe Tyr Lys Glu Asp Tyr Ser Val Thr Leu Asp Lys Lys Leu Gln
            100   105   110

Lys Glu Glu Lys
        115

<210> 718
<211> 59
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 718
Met Thr Glu Trp Tyr Ala Leu Cys Tyr Tyr Asp Lys Val Gly Lys Lys
1   5   10   15

Lys Ile Pro Arg Gln Val Arg Ala His Arg Asp Ile Ser Val Leu Glu
            20   25   30

Glu Leu Lys Glu Arg Leu Glu Glu Arg Asn Pro Asn Thr Glu Tyr Ser
        35   40   45

Ile Lys Thr Thr Lys Glu Phe Asp Glu Glu Arg
    50   55

<210> 719
<211> 136
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 719
Val Lys Leu Glu Asp Lys Val Leu Glu Arg Ile Asp Ser Leu Gly Gly
1 5 10 15

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

Gln Ile Ile Tyr Gly Ile Ile Asp Leu Ile Val Gly Ile Val Val Ile
35 40 45

Ala Leu Thr Leu Phe Leu Trp Lys Val Phe Ile Asn Gln His Lys Lys
50 55 60

Val Asn Asp Met Asp Arg Asp Asp Asp Tyr Ser Leu Leu Phe Glu Asp
65 70 75 80

Cys Glu Asp Leu Ser Gly Ile Gly Leu Phe Tyr Val Ile Val Thr Ser
85 90 95

Leu Ile Ser Leu Phe Ala Phe Ile Tyr Leu Ile Tyr Gly Ile Pro Met
100 105 110

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

Ile Glu Gln Ala Lys Gly Gly Asn
130 135

<210> 720
<211> 97
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 720
Met Lys Gln Arg Asp Phe Glu Phe Glu Glu Asp Phe Val Leu Thr Tyr
1 5 10 15

Glu Cys Glu Asp Cys Lys His Phe Glu Asp Trp Gly His Asp Glu Glu
20 25 30

Pro Glu Glu Cys Ser Glu Cys Gly Ser Ser Asp Leu Ile Asn Asn Thr
35 40 45

Ser His Glu Asp Thr Glu Cys Asp Met Cys Lys Gly Tyr Ile Asp Met
50 55 60

Trp Gln Asp Gly Tyr Arg Tyr Met Gly Asp Asn Lys Ala Tyr Leu Glu
65 70 75 80

Lys Glu Asp Ser Gly Leu Ile Cys Glu Asp Cys Tyr Glu Lys Leu Asp
85 90 95

Ile

<210> 721
<211> 95
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 721
Met Asn Lys Ala Val Glu Gln Ala Ser Asn Ala Val Gly Gln Gly Phe
1 5 10 15

Ser Ala Met Val Trp His Gln Val Leu Val Gly Leu Gly Phe Ile Leu
20 25 30

Leu Gly Leu Ile Leu Ser Leu Leu Val Trp Val Leu Val Lys Lys Phe
35 40 45

His Val Pro Phe Asn His Pro Thr Ala Phe Val Val Tyr Ser Ile Met
50 55 60

Leu Val Ser Ile Val Ala Ser Phe Ile Trp Gly Gly Leu His Val Ile
65 70 75 80

Asn Pro Glu Tyr Tyr Ala Ile Leu Glu Leu Lys Gly Phe Ile Lys
85 90 95

<210> 722
<211> 37
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 722
Met Thr Lys Glu Glu Leu Glu Gln Arg Val Lys Glu Leu Glu Ala Glu
1 5 10 15

Asn Lys Glu Leu Lys Lys Gln Ile Glu Arg Phe Glu Asp Glu Gly Gly
20 25 30

Lys Thr Lys Asp Glu
35

<210> 723
<211> 88
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 723
Met Asn Ser Arg Gln Lys Lys Ile Leu Thr Leu Thr Val Ser Asn Phe
1 5 10 15

Leu Ile Leu Ala Leu Asp Thr Val Ala Leu Ile Arg Tyr Lys Lys Gly
20 25 30

Lys Ile Lys Gln Glu Asn Tyr Asn Thr Gly Gln Ile Thr Arg Met Ile
35 40 45

Ala Thr Thr Ala Asn Ser Leu Gly Ile Leu Tyr Leu Glu Glu Gln Glu
50 55 60

Arg Lys Glu Val Lys Asp Ile Lys Val Gly Thr Phe Glu Ile Gly Ala
65 70 75 80

Leu Lys Arg Phe Thr Asn Asn Lys
85

<210> 724
<211> 101
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 724
Met Lys Gly Ile Ile Ile Phe Tyr Lys Glu Glu Thr Lys Glu Asp Leu
1 5 10 15

Gly Tyr Phe Leu Gly Phe Ile Asn Phe Lys Leu Glu Gly Leu Ser Tyr
20 25 30

Thr Thr Glu Gly Thr Leu Val Asp Asn Asp Val Val Val Leu Lys Asp
35 40 45

Asn Gln Ile Asn Glu Asp Asn Leu Glu Gln Phe Ser Met Ser Asn Asn
50 55 60

Asn Leu Val Ile Gly Ile Leu Gly His Ser Ser Leu Ser Val Arg Ile
65 70 75 80

Tyr Glu Lys Gly Ile Arg Gln Glu Phe Asp Arg Val Glu Glu Tyr Leu
85 90 95

Glu Glu Leu Arg Gln
100

<210> 725
<211> 133
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F44/10

<400> 725
Met Ile Phe Ile Leu Ile Phe Gly Leu Leu Phe Ile Leu Ser Leu Leu
1   5   10   15

Gly Ile Phe Ile Tyr Ser Ile Val Leu Arg Lys Lys Lys Gln Leu Ile
            20   25   30

Glu Glu Arg Glu Ser Phe Gly Ile Tyr Asn Arg Thr Lys Glu Lys Leu
        35   40   45

Gly Asp Val Thr Arg Leu Gly Tyr Glu Glu Asp Val Tyr Lys Leu Ile
    50   55   60

His Asn Gln Ser Asn Lys Thr Ile Ile Glu Asp Lys Lys Ser Lys Val
65   70   75   80

Val Asp Thr Ile Lys Lys Met Tyr Glu Leu Glu Leu Thr Ser Val Asp
                85   90   95

Val Ser Lys Val Glu Gly Leu Ser Pro Leu Asp Thr Glu Pro Met Thr
            100   105   110

Asn Met Lys Leu Leu Ser Tyr Lys Leu Asp Arg Glu Gly Leu Tyr Ser
        115   120   125

Leu Ser Lys Phe Ile
    130

<210> 726
<211> 78
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 726
Met Glu Phe Ile Asp Lys Asn Asn Val Ile Lys Ala Tyr Asp Ile Pro
1   5   10   15

Asn Val Tyr Leu Lys Gly Tyr Val Leu Gln Ala Cys Asp Lys Asn Gly
            20   25   30

Asp Thr Thr Ala Tyr Asp Gly Tyr Asp Gln Ile His Tyr Lys Glu Gly
        35   40   45

Arg Val Leu Thr Phe Pro Phe Asp Lys Pro Leu Arg Lys Ile Asn Val
    50   55   60

Leu Ser Gly Tyr Tyr Lys Leu Phe Lys Lys Glu Asp Ile Ile
65   70   75

<210> 727
<211> 175
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 727
Met Ile Tyr Phe Val Ser Asp Leu His Phe Gly His Asp Asn Ile Arg
1   5   10   15

Glu Phe Glu Ala Pro Thr Arg Ser His Trp Asn Ser Val Glu Glu Met
            20   25   30

Asn Glu Gly Leu Ile Glu Leu Trp Asn Asn Thr Ile Thr Asn Asn Asp
        35   40   45

Ile Val Tyr Asn Ile Gly Asp Phe Phe Phe Asn Met Lys Pro Ser Lys
    50   55   60

Val Glu Asp Ile Leu Asn Arg Leu Asn Tyr Lys Glu Met Ile Leu Ile
65   70   75   80

Ala Gly Asn His Asp His Lys Lys Leu Ile Lys Leu Tyr Glu Arg Asn
                85   90   95

Gly Ile Thr Val Lys Tyr Ala Asp Met Ile Lys Lys Asp Gly Lys Arg
            100   105   110

Phe Tyr Leu Ser His Tyr Pro Thr Leu Ile Gly Arg Lys Asn Met Phe
        115   120   125

Asn Ile His Gly His Ile His Ser Gln Leu Met Gly Thr Glu Tyr His
    130   135   140

Ile Asn Val Gly Tyr Asp Val Glu Gly Lys Ile Ala Tyr Ser Phe Asp
145   150   155   160

Asp Ile Ile Ser Arg Ala Gly Glu Tyr Asn Gly Glu Ile Gln Arg
                165   170   175

<210> 728
<211> 103
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 728
Met Glu Lys Phe Lys Gly Lys Asp Leu Tyr Lys Thr Arg Ile Arg Lys
1   5   10   15

Gln Thr Ile Lys Asn Leu Val Ile Lys Thr Glu Lys Leu His Asn Lys
            20   25   30

```
His Gly Lys Tyr Arg Pro Ile Gly His Val Tyr Tyr Tyr Pro Lys Thr
        35                  40                  45

Lys Glu Phe Thr Leu Ser Lys Pro Glu Gln Lys Ile Phe Ile Glu Tyr
    50                  55                  60

Met Lys Ala Leu Gly Phe Ser Val Lys His Lys Arg Arg Lys Lys Ile
65                  70                  75                  80

Ile Ile Val Tyr Lys Asn Val Leu Asp Glu Tyr Leu Ser Met Tyr Gln
                85                  90                  95

Glu Ala Ile Glu Ser Thr Cys
            100
```

<210> 729
<211> 59
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 729

```
Met Lys His Phe Ile Leu Ile Leu Gly Ile Val Ile Leu Val Ile Ala
1               5                   10                  15

Leu Gly Ile Val Leu Pro Ala Trp Ile Leu Gln Leu Val Leu Ser Ala
            20                  25                  30

Phe Gly Val Lys Val Ser Ile Trp Val Cys Ile Gly Ile Phe Ile Leu
        35                  40                  45

Ile Ser Ala Val Gly Ser Met Phe Ser Arg Asn
    50                  55
```

<210> 730
<211> 87
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 730

```
Met Ala Lys Tyr Glu Ser Asn Ile Asn Gly Glu Asn Tyr Ile Ala Thr
1               5                   10                  15

Pro Ser Gln Ala Leu Arg Glu Ala Leu Ala Glu Leu Ile Arg Glu Glu
            20                  25                  30

Lys Asn Phe Ala Glu Tyr Gln Thr Lys Gly Glu Glu Gln Tyr Glu Ser
        35                  40                  45
```

Gln Leu Gln Leu Arg His Phe Asp Ser Met Ile Ser Gln Tyr Glu Glu
    50   55   60

Ala Ile Arg Val Leu Glu Asp Arg Tyr Ser Pro Gln Ile Phe Ile Pro
65   70   75   80

Lys Asp Asn Lys Glu Glu Lys
                85

<210> 731
<211> 105
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 731
Met Lys Ala Glu Ser Ile Ala Arg Phe Phe Gln Asp Lys Val Leu Gln
1   5   10   15

Ile Glu Gly Tyr Lys Val Arg Phe Thr Gln Ala Ser Ser Ser Tyr Ile
            20   25   30

Leu Asp Ile Asp Thr Met Asp Glu Ser Val Leu Phe Leu Asp Thr Val
        35   40   45

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

Asn Lys Pro Glu Thr Leu Ser Ser Asn Glu Leu Tyr Thr Glu Ile Ser
65   70   75   80

Asn Lys Leu Gln Glu Ile Val Gly Asp Gln Thr Lys Thr Asp Ile Glu
                85   90   95

Leu Ser Lys Tyr Phe Lys Glu Val Lys
            100   105

<210> 732
<211> 226
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 732
Met Ser Ser Glu Ala Ile Thr Asn His Leu Leu Asn Leu Asn Gln Ile
1   5   10   15

Lys Ile Lys Glu Tyr Asn Ile His Ala Tyr Ile Lys Lys Ser Val Cys
            20   25   30

Ser Gly Ile Glu Asn Ala Asp Phe Glu Val Arg Ile Asn Tyr Ile Ala
        35   40   45

```
Asp Lys Asp Pro Asn Tyr Ile Arg Thr Ile Asn Ser Ile Ile Phe Val
    50                  55                  60

Asp Tyr Ser Asn Arg Asn Pro Lys Glu Ile Leu Leu Gln Phe Lys Glu
65                  70                  75                  80

Lys Ile Leu Ser Ile Val Lys Glu Gln Val Glu Ile Asp Asn Asp Phe
                85                  90                  95

Ile Glu Ala Ile Lys Asp Ile Asn Thr Asn His Glu Leu Glu Lys Leu
            100                 105                 110

Glu Pro Phe Ile Asn Lys Glu Tyr Tyr Ser Met Phe Lys Ser Ser Ile
        115                 120                 125

Glu Lys Glu Val Pro Val Ala Leu Ser Ser Glu Val Leu Asn Arg Cys
    130                 135                 140

Thr Gly Lys Thr Ser Thr Leu Ala Tyr Leu Ala Ile Glu Lys Asp Leu
145                 150                 155                 160

Pro Leu Ile Val Ser Asn Asn Ser Met Met Lys Met Leu Lys Lys Asp
                165                 170                 175

Tyr Pro Ser Val Lys Val Ser Ser Val Glu Asp Phe Ser Asn Tyr Asn
            180                 185                 190

Ile Lys Gly Glu Ile Val Leu Ile Asp Glu Val Asp Val Asp Gln Leu
        195                 200                 205

Tyr Ser Ala Asp Arg Val Ser Val Asp Ala Leu Leu Val Gly Ile Ile
    210                 215                 220

Lys Asn
225


<210> 733
<211> 52
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 733
Met Val Gly Ile Ile Ile Leu Ile Val Gly Leu Ile Leu Phe Leu Ala
1               5                   10                  15

Ser Gly Tyr Lys Leu Val Leu Gly Lys Tyr Tyr Asp Asp Ile Asp Leu
            20                  25                  30

Lys Met Leu Phe Thr Ile Phe Gly Ile Gly Ala Ile Leu Leu Leu Thr
```

35 40 45

Gly Phe Ile Leu
50

<210> 734
<211> 74
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 734
Met Asn Tyr Lys Glu Val Leu Glu Val Ile Lys Lys Asn Lys Pro Cys
1 5 10 15

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

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

Asn Lys Asn Asp Tyr Ile Lys Leu Gln Gln Tyr Cys Leu Glu Arg Asp
50 55 60

Asp Tyr Thr Val Ala Gly Ala Ile Leu Phe
65 70

<210> 735
<211> 66
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 735
Met Asn Tyr Arg Asp Phe Ile Thr Asp Cys Ile Ser Cys Gly Tyr Lys
1 5 10 15

Val His Ile Ser Val Thr Glu Lys Arg Val His Ile Ile Ser Glu Met
20 25 30

Thr Ser Ala Ser Tyr Pro Lys Lys Glu Ile Asn Leu Asp Glu Leu Gln
35 40 45

Ala Tyr Val Tyr Tyr Met Asn Asn Phe Gly Ser Gln Ile Thr Thr Glu
50 55 60

Gly Leu
65

<210> 736
<211> 96
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 736
Met Glu Leu Val Ile Asn Ile Ile Ala Val Leu Ile Gly Met Tyr Gly
1   5   10   15

Ile Tyr Phe Tyr Val Thr Lys Phe Ser Thr Gly Leu Ser Gly Ile Leu
            20   25   30

Ile Val Leu Gly Met Ala Val Gly Leu Tyr Phe Tyr Leu Asp Tyr Leu
        35   40   45

Asn Val Arg Glu Asn Val Ile Arg Leu Val Ser Val Met Phe Gly Ala
    50   55   60

Phe Leu Phe Ser Ile Glu Met Ile Tyr Asn Lys Ile Met Phe Glu Ile
65   70   75   80

Lys Lys Ser Lys Tyr Asp Lys Thr Val Arg Thr Tyr Arg Gly Asp Gln
                85   90   95

<210> 737
<211> 117
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 737
Met Asn Ala Arg Lys Ala Arg Lys Asn Thr Lys Asn His Lys Asp Ser
1   5   10   15

Ser Val Val Thr Lys Glu Gln His Leu Thr Tyr Ile Tyr Asn Lys Ile
            20   25   30

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

Met Asn Leu Arg Thr Gly Tyr Pro Asp Glu Phe Ser Leu Ser Lys Leu
    50   55   60

Lys Tyr Leu Lys Glu Ile Lys Gln His Tyr Lys Asp Leu Gly Phe Thr
65   70   75   80

Val Gln Thr Gln Val Arg Lys Ser Arg Trp Ser Glu Lys Ser Ile Ile
                85   90   95

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

Ile His Ile Ser Trp

115

<210> 738
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 738
Met Asp Asn Pro Asn Leu Asn Lys Lys Thr Leu Arg Ala Val Ile Arg
1 5 10 15

Glu Met Asp Lys Asp Ile Glu Glu Arg Ala Glu Ala Leu Arg Arg Glu
20 25 30

Glu Thr Arg Leu Ser Ile Ala Arg Asp Asn Arg Lys Arg Leu Tyr Ile
35 40 45

Glu Leu Glu Ser Ile Leu Glu Glu Glu
50 55

<210> 739
<211> 74
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 739
Met Asp Phe Asn Leu Lys Asp Tyr Ala Val Arg Pro Ile Thr Asp Lys
1 5 10 15

Glu Gly Asn Met Val Val Arg Thr Val Tyr Val Cys Leu Lys Arg Glu
20 25 30

Tyr Ser Asp Trp Val Val Asp Lys Val Tyr Gly Arg Gln Glu Ser Ser
35 40 45

Glu Thr Trp Leu Lys Phe Met Gln Glu Ile Arg Asn Ile Glu Arg Ala
50 55 60

Lys Leu Arg Val Glu Lys Trp Gln Val Asn
65 70

<210> 740
<211> 52
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 740
Met Ser Leu Ser Glu Leu Leu Glu Tyr His Lys Asn Ser Gly Lys Glu
1 5 10 15

Arg Ala Glu Tyr Ile Ser Asp Asn Gly Asn Cys Arg Val Ala Ile Met
            20   25   30

His Tyr Asp Lys Trp Ala Val Val Gly Asp Leu Glu Asn Ala Val Phe
        35   40   45

Thr Ile Glu Lys
    50

<210> 741
<211> 33
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 741
Met Tyr Leu Phe Ala Lys Ile Ile Ile Ile Ser Ile Asp Val Ile Pro
1   5   10   15

Leu Met Ser Ile Ile Val Val Gln Leu Ile Thr Asp Tyr Asn Asp Arg
            20   25   30

His

<210> 742
<211> 56
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 742
Met Ile Ile Pro Leu Ile Ile Leu Met Met Thr Phe Gly Thr Phe Ala
1   5   10   15

Phe Ser Tyr Val Ala His Asp Ala Tyr Arg Val Asp Glu Lys Gly Ile
            20   25   30

Met Tyr Ala Met Val Val Gly Ile Val Val Ile Asn Val Ile Gly Leu
        35   40   45

Glu Met Ile Ile Val Glu Cys Leu
    50   55

<210> 743
<211> 97
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 743
Met Ile Asp Ile Tyr Leu His Ser Glu Tyr Asp Lys Asp Lys Leu Lys
1   5   10   15

Phe Ile Leu Lys Ala Ile Arg Asp Phe Ser Pro Arg Glu Leu Thr Tyr
            20   25   30

Asp Phe Arg Asn Pro Lys Ala Asp Val Ser Ile Gln Glu Leu Leu Gly
        35   40   45

Asp Asp Ile Asp Ile Phe Glu Ser Ile Ala Leu Asp Tyr Pro Asn Asp
    50   55   60

Ile Asn Ile Leu Val Gly Asp Ser Gly Tyr Ser Ile Val Tyr Gln Asn
65   70   75   80

Asp Phe Leu Thr Ile Ser Gly Leu Ser Thr Ala Met Lys Glu Val Ile
                85   90   95

Gly

<210> 744
<211> 61
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 744
Met Ile Gly Phe Thr Ile Leu Ser Thr Ile Met Val Ile Leu Val Ile
1   5   10   15

Ala Met Tyr Thr Gln Val Leu Val Asp Met Ile Gln Ser Ile Arg Tyr
            20   25   30

Asp Arg Phe Asp Lys Val Leu Asn Ile Val Thr Phe Ile Val Met Thr
        35   40   45

Val Val Leu Val Ser Gly Ile Leu Ile Met Phe Asp Ile
    50   55   60

<210> 745
<211> 104
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 745
Met Lys Ala Ile Val Tyr Cys Ala Lys Arg Tyr Ser Lys His Thr Leu
1   5   10   15

Lys His Ile Leu Glu Glu Leu Glu Ala Glu Asn Ser Asp Leu Thr Phe

20 25 30

Ser Thr Glu Ile Ser Asp Leu Gly Glu Val Asp Ile Val Val Gln His
35 40 45

Thr Lys Leu Pro Phe Ser Glu Leu Met Asp Leu Cys Ser Lys Val Ser
50 55 60

Lys Gly Ser Asp Arg Phe Tyr Val Phe Val Gly Asn His Ser Gly Tyr
65 70 75 80

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

Ser Arg Glu Thr Asn Val Met Met
100

<210> 746
<211> 105
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 746
Met Ile Glu Ile Arg Leu Val Glu Gly Tyr Asp Lys Ser Gln Leu Lys
1 5 10 15

Phe Met Leu Lys Lys Ile Lys Arg Val Ala Pro Arg Glu Leu Thr Tyr
20 25 30

Asp Ile Glu Ala Gly Ile Asp Ser Val Asp Val Asn Ile Glu Asp Val
35 40 45

Leu Pro His Lys Ser Pro Gln Glu Tyr Glu Arg Tyr Ser Met Leu Leu
50 55 60

Glu Glu Asp Leu Trp Ile Val Ile Leu Glu Ser Gly Tyr Ile Ala Tyr
65 70 75 80

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

Asn Met Phe Lys Gly Arg Gly Arg Leu
100 105

<210> 747
<211> 98
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 747
Met Ile Glu Val Phe Leu Ser Lys Asp Tyr Asp Lys Asp Leu Leu Lys
1 5 10 15

Ala Tyr Leu Glu Tyr Ile Arg Lys Ser Ala Ser Arg Glu Leu Lys Tyr
20 25 30

Asn Thr Asn His Thr Lys Gly Thr Asp Val Asn Ile Glu Asn Ile Ile
35 40 45

Ser Tyr Thr Asn Gln Glu Val His His Phe Ser Ser Tyr Gly Met Tyr
50 55 60

Arg Asp Asp Leu Cys Val Phe Ile Asp Asn Thr Arg Val Ser Glu Tyr
65 70 75 80

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

Glu Met

<210> 748
<211> 85
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 748
Met Phe Lys Val Tyr Tyr Thr Val Tyr His Arg Gln Ser Met Lys Thr
1 5 10 15

Ile Lys Asp Lys Leu Asp Arg Ser Gly Leu Ile Tyr Phe Leu Tyr Glu
20 25 30

Thr Trp Tyr Lys Asp Ile Asn Asn Val Cys Pro Ser Asn Tyr Asn Pro
35 40 45

Glu Phe Gly Ser Leu Asn Lys Asp Ile Asp Ile Asp Arg Leu Ile Glu
50 55 60

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

Thr Val Glu Glu Trp
85

<210> 749
<211> 202
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F44/10

<400> 749
Met Ile Asp Ile Glu Ile Lys Ile Trp Asp Glu Thr Leu Arg Met Gln
1   5   10   15

Val Glu Glu Glu Asp Val Leu Ser Phe Leu Ser Lys Phe Lys Asn Lys
            20   25   30

Thr Thr Gly Asp Lys Glu Glu Ser Tyr Gly Val Gly Leu Asp Glu Ser
        35   40   45

Lys Trp Lys Val His Pro Phe Tyr Thr Arg Tyr Glu Val His Pro Glu
    50   55   60

Gly Tyr Val Arg Leu Lys Asp Thr Lys Thr Pro Val Ile Phe Thr Lys
65   70   75   80

Tyr Arg Lys Glu Leu His His Lys Pro Gln Phe Ile Ser Ser Asn Ile
                85   90   95

Met Asp Asp Glu Gly Lys His Thr Val Ala Leu His Lys Leu Val Ala
            100   105   110

Asp Thr Phe Ile Pro Ile Pro Trp Tyr Leu Gln Gly Tyr Asn Tyr Thr
        115   120   125

Asp Leu Ser Val Gly Leu Lys Asp Gly Asp Tyr Glu Asn Lys Glu Ala
    130   135   140

Val Lys Ala Tyr Asn Leu Ala Trp Tyr Val Gly Arg Ile Arg Gly Asn
145   150   155   160

Ala Pro Met Ile Lys Leu Met Asp Leu Glu Asp Asp Arg Val Leu Tyr
                165   170   175

Phe Ala Ser Ile Pro Gln Ile Glu Asn Phe Ile Arg Asp Asn Lys Leu
            180   185   190

Asp Pro Lys Arg Phe Asn Tyr Lys Thr Glu
        195   200

<210> 750
<211> 84
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 750
Met Glu Phe Lys Phe Glu Gly Thr Lys Glu Glu Leu Asn Lys Glu Val
1   5   10   15

His Asn Leu Leu Lys Lys Val Asn Tyr Val Tyr Gln Val Asn Ile Phe
            20   25   30

Glu Asn Glu Leu Arg Asn Leu Ile Asp Val Lys Glu Lys Asp Tyr Leu
        35   40   45

Phe Ser Leu Ser Val Asp Tyr Asn Trp Leu Met Glu Glu Lys Gln Lys
    50   55   60

Asp Gly Tyr Asn Asp Leu Ala Ser Ala Ile Tyr Glu Glu Tyr Ile Glu
65   70   75   80

Thr Tyr Leu Asn

<210> 751
<211> 102
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 751
Met Asp Val Lys Glu Ile Ala Asn Thr Ile Met Glu Leu Trp Gln Met
1   5   10   15

Asp Gly Tyr Arg Cys Thr Glu Pro Pro Leu Tyr Glu Ser Thr Leu Asn
            20   25   30

His Thr Arg Thr Tyr Thr Ala Leu Ile Val Ser Ile Lys Gly Asn Tyr
        35   40   45

Asp Thr Val Gln Met Phe Arg Lys Thr Pro Ile Met Ser Met Arg Gly
    50   55   60

Gln Ala Gln Pro Ala Ser Met Leu Val Asn Val Ile Asp Asp Val Ile
65   70   75   80

Ile Ile Val Tyr Glu Asn Val Val Tyr Gly Val Gln Asn Lys Glu Ile
                85   90   95

Lys Phe Ile Glu Glu Ile
            100

<210> 752
<211> 95
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 752
Met Thr Asn Lys Asn Tyr Leu Tyr Glu Glu Ala His Thr Val Gln Gly
1   5   10   15

```
Asn Glu Ile Thr Ala Phe Arg Ile Pro Asn Asp Ala Asn Gly Asn Pro
            20                  25                  30

Arg Tyr Val Val His Phe Met Asp Leu Asn Ile Lys Leu Ala Asp Tyr
        35                  40                  45

Asp Asn Ile Asn Lys Leu Tyr Gly Phe Asn Lys Tyr Arg Ala Lys Trp
    50                  55                  60

Phe Gly Gly Gly Val Val Phe Gln Ser Tyr Asn Ile Glu Asp Thr Leu
65                  70                  75                  80

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

<210> 753
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 753

```
Met Lys Phe Lys Ile Glu Lys Asn Asn Ser Asp Ile Lys Thr Leu Trp
1               5                   10                  15

Asn Leu Ala Lys Asn Gly Tyr Met Ser Tyr Gln Thr Val His Asn Ile
            20                  25                  30

Phe Lys Asn Glu Ser Asp Glu Phe Ile Ile Phe Asn Ser Lys Gln Thr
        35                  40                  45

Tyr Asn Lys Phe Met Glu Leu Arg Tyr Asn Arg Ser Ala Ile Gln
    50                  55                  60
```

<210> 754
<211> 52
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 754

```
Met Leu Lys Phe Lys Trp Lys Asn Lys Thr Ile Lys Ser Thr Gln Lys
1               5                   10                  15

Thr Asp Asn Ile Leu Leu Leu Ile Ile Gly Gly Leu Val Ala Thr Ile
            20                  25                  30

Thr Pro Lys Leu Val Asn Trp Phe Leu Leu Leu Gln Asp Asn Ile Asn
        35                  40                  45
```

Ile Phe Leu Arg
    50

<210> 755
<211> 43
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 755
Met Lys Lys Ile Thr Thr Thr Leu Asn Leu Ile Gly Met Lys Asn Asn
1   5   10   15

Glu Arg Phe Thr Glu Glu Leu Lys Asn Tyr Arg Gln Asp Val Thr Phe
            20   25   30

Leu Lys Ala Asn Lys Ile Val Lys Tyr Ser Lys
        35   40

<210> 756
<211> 107
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 756
Met Lys Phe Ile Lys Thr Ile Glu Asn Leu Leu Thr Lys Ala Glu Asn
1   5   10   15

Lys Gly Gln Ala Ile Leu Asn Gly Arg Tyr Tyr Asp Gly Tyr Arg Asn
            20   25   30

Gly Glu Leu Glu Glu Lys Tyr Ala Ile Glu Ile Glu Gly Asn Lys Leu
        35   40   45

Val Met Arg His Trp Gly Thr Gln Thr Ile Glu Ile Asp Leu Gly Met
    50   55   60

Lys Glu Ile Val Ser Tyr Tyr Gly Glu Ser Asn Ser Asp Arg Asp Ser
65   70   75   80

Leu Asn Thr Leu Val Tyr Cys Leu Gly Ile Ala Pro Asn Phe Arg Tyr
                85   90   95

Leu Pro Ser Lys Asp Leu Phe Ile Tyr Glu Asn
            100   105

<210> 757
<211> 133
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F44/10

<400> 757
Met Phe Lys Leu Gln Asn Lys Val Glu Ile Ile Val Pro Lys Tyr Thr
1   5   10   15

Asn Ser Gly Lys Glu Ile Ser Ser Pro Ala Ile Lys Glu Ala Val Asn
            20   25   30

Asn Ala Thr Lys Ile Cys Gly Gly Cys Thr Ile Thr Glu Ile Lys Gly
        35   40   45

Gln Trp Trp Ser Asp Asp Glu Gln Arg Ile Met Glu Asp Asp Asn Leu
    50   55   60

Asn Leu Glu Trp Tyr Tyr Asp Lys Gly Met Gln Asp Met Asn Asp Gln
65   70   75   80

Gln Gly Leu Leu Gln Ala Leu Ser Lys Ile Ala Arg Gln Leu Ile Val
                85   90   95

Phe Tyr Glu Gln Glu Ala Ile Ser Ile Lys Ile Asn Gly Thr Leu Tyr
            100   105   110

Ile Ile Asp Tyr Glu Asp Leu Asp Leu Leu Ser Tyr Asp Leu Tyr Glu
        115   120   125

Leu Met Phe Lys Asn
    130

<210> 758
<211> 73
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 758
Met Asn Arg Leu Glu Ile Val Lys Asp Thr Ala Met Glu Tyr Ile Leu
1   5   10   15

Met Met Asp Asn Ser Val Met Asp Gly Val Met Thr Gln Glu Glu Tyr
            20   25   30

Asn Glu Ala Val Ser Phe Glu Lys Val Tyr Asp Tyr Thr Leu Ser Glu
        35   40   45

Ala Asn Gln Glu Cys Lys Phe Leu Gly Gly Lys Val Leu Thr Phe Leu
    50   55   60

Val His Glu Ala Ile Glu Glu Tyr Ala
65   70

<210> 759
<211> 45
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 759
Met Arg Tyr Glu Ile Val Thr Leu Val Asn Gly Glu Leu Phe Met Phe
1   5   10   15

Ala Thr Phe Lys Lys Ala Glu Ala Glu Asn Lys Tyr Gln Glu Trp Cys
            20   25   30

Asp Leu Tyr Gly Gln Glu Asn Val Ser Met Glu Lys Asn
        35   40   45

<210> 760
<211> 54
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 760
Met Thr Lys Thr Ile Lys Gln Leu Glu Ser Gln Leu Glu Arg Leu Glu
1   5   10   15

Arg Lys Ser Asp Glu Gln Leu Ala Asn Gly Tyr Tyr Glu Ala Phe Glu
            20   25   30

Arg Thr Cys Ala Gln Ile Arg Glu Leu Asp Leu Gln Ile Glu Leu Lys
        35   40   45

Lys Asn Ser Glu Thr Val
    50

<210> 761
<211> 78
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 761
Met Lys Leu Leu Asn Arg Asp Asn Glu Ile Val Ile Ser Ile Ala Thr
1   5   10   15

Leu Glu Ser Val Lys Gln Ala Leu Ile Trp Glu Tyr Ile Asp His Ile
            20   25   30

Asp Asn Asn Ile Leu Asp Ser Glu Ile Tyr Asp Gln Glu Ala Val Val
        35   40   45

Val Thr Ser Lys Thr Leu Gln Ser Ile Lys Phe Ala Asp Thr Met Glu

50 55 60

Asp Leu Gln Glu Tyr Ile Ala Asp Ile Asn Trp Lys Leu Val
65 70 75

<210> 762
<211> 157
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 762
Met Thr Asn Thr Ile Lys Gly Phe Leu Gln Thr Glu Glu Ala Ser Thr
1 5 10 15

Val Lys Asp Val Ala Thr His Gly Val Gln Ser Gly Ala Ile Gly Arg
20 25 30

Leu Ile Tyr Thr Ser Asp Val Val Lys Phe Phe Asp Arg His Tyr Ser
35 40 45

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

Arg Tyr Tyr Asp Leu Leu Asp Tyr Asp Leu Met Arg Glu Leu Glu Glu
65 70 75 80

His Ala Asn Val Glu Phe Glu Asp Glu Asp Glu Tyr Asn Asn Ile Gln
85 90 95

Phe Asp Leu Ala Glu Asn Ile Ala Ser Asp Glu Ile Glu Gly Phe Glu
100 105 110

Asp Met Asp Glu Ala Glu Gln Ala Asp Ala Val Ile Glu Ala Met Asp
115 120 125

Asp Val Glu Leu Glu Ile Leu Asp Thr Asp Lys Val Gln Phe Val Asn
130 135 140

Leu Ala Val Glu Ile Val Ala Gln Gln Met Gln Glu Ala
145 150 155

<210> 763
<211> 54
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 763
Met Thr Ile Lys Glu Ile Ile Asn Gln Leu Gln Ala Val Glu Asn Lys
1 5 10 15

Glu Leu Glu Leu Phe Val Cys Asp Lys Glu Gly Asn Asn Ile Ser Ile
            20   25   30

Lys Asp Ile Thr Leu Phe Asp Ser Glu Ala Glu His Thr Glu Asn Asn
        35   40   45

Pro Leu Gly Ile Asn Tyr
    50

<210> 764
<211> 89
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 764
Leu Asn Ile Arg Glu Val His Asn Val Val Lys Ser Ala Lys Ser Lys
1   5   10   15

Leu Leu Gln Glu Gln Asn Asn Ile Asn Asn Val Met Ile Asp Asp Tyr
            20   25   30

Ile Thr Glu Glu Leu His Arg Arg Thr Gln Arg Ser Gly Thr Ile Gln
        35   40   45

Met Asn Asn Asn Thr Ala Ser Tyr Ser Asn Gly Ser Tyr Gly Ser Leu
    50   55   60

Glu Glu Ile Arg Glu Ala Tyr Asp Leu Ser Ser Leu Ser Thr Asn Glu
65   70   75   80

Ile Lys Glu Leu Leu Glu Thr Phe Val
                85

<210> 765
<211> 73
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 765
Met Arg Asp Leu Gln Glu Arg Lys Arg Glu Leu Lys Thr Leu Leu Phe
1   5   10   15

Asn Leu Ala Ile Glu Lys Asn Arg Ala Thr Asp Glu Thr Leu Arg Ser
            20   25   30

Val Leu Glu Glu Ala His Gln Glu Val Gly Asn Gln Leu Arg Lys Val
        35   40   45

Arg Lys Glu Ile Glu Ile Leu Val Glu Glu Lys Glu Arg Glu Phe Trp

50 55 60

Asn Asp Phe Asp Phe Asn Gly Leu Asp
65 70

<210> 766
<211> 759
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 766
Met Pro His Leu Lys Ala Tyr Asp Lys Glu Gly Asn Ile Leu Ala Ile
1 5 10 15

Gly Tyr Asn Val Tyr Thr Glu Gln Gly Ser Val Ile Ile Pro Asn Leu
20 25 30

Lys Pro His Thr Lys Tyr Pro Gln Gly Glu Phe Tyr Val Ser Trp Glu
35 40 45

Gly Asp Asn Tyr Glu Ser Glu Lys Thr Val Val Pro Glu Phe Thr Thr
50 55 60

Leu Glu Ser Ser Tyr Lys Glu Ile Thr Phe Tyr Ala Lys Asp Ile Leu
65 70 75 80

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

Thr Gly Thr Glu Glu Glu Trp Val Lys Ser Ile Lys Gly Glu Pro Gly
100 105 110

Glu Pro Gly Lys Pro Gly Glu Pro Gly Lys Pro Gly Glu Pro Gly Lys
115 120 125

Thr Gly Glu Pro Gly Lys Asp Phe Thr Phe Asp Arg Phe Thr Glu Glu
130 135 140

Gln Leu Asp Ser Leu Arg Val Phe Val Asn Pro Ser Asp Ser Asn Leu
145 150 155 160

Gln Glu Val Asn Lys Thr Met Glu Asp Ser Leu Ile Val Tyr Pro Asp
165 170 175

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

Phe Ser Asn Ile Thr Ile Arg Asn Ser Ile Pro Glu Asn Thr Met Asn
195 200 205

```
Pro Asp Gly Ser Phe Thr Leu Asn Ser Asn Gly Trp Leu Phe Tyr Thr
    210                 215                 220

Val Lys Ala Val Glu Lys Leu Ala Pro Gly Lys Thr Phe Ser Ala Lys
225                 230                 235                 240

Ile Ile Thr Asp Asp Val Pro Asp Pro Lys Ala Ser Phe Glu Tyr Ser
                245                 250                 255

Ile Gln Asp Ser Asp Gly Ser Tyr Ile Gln Thr Ile Thr Gln Leu Asn
            260                 265                 270

Lys Ile Asn Asp Thr Thr Phe Ala Ile Asn Asn Ile Asn Ile Pro Glu
        275                 280                 285

Asn Ser Ser Lys Ile Ser Leu Arg Ile Asp Thr Arg Gln Val Thr Ser
    290                 295                 300

Pro Val Asn Ile Lys Gln Phe Leu Leu Phe Asp Gly Ser Ser Thr Lys
305                 310                 315                 320

Lys Ile Gln Thr Val Asn Asn Glu Glu Phe Ile Lys Gly Leu Ile Lys
                325                 330                 335

Glu Ile Asp Asn Met Lys Ile Ser Met Lys Lys Glu Thr Ser Tyr Lys
            340                 345                 350

Ile Pro Val Phe Thr Pro Val Asp Tyr Leu Ile Lys Asp His Pro Leu
        355                 360                 365

Val Asn Asn Ile Phe Thr Asp Gly Leu Gly Lys Phe Ser Thr Ser Leu
    370                 375                 380

Asn Met Glu Asn Phe Lys Leu Arg Gly Gly Lys Ser Tyr Tyr Val Asp
385                 390                 395                 400

Gly Glu Asn Gly Asn Asp Thr Asn Asp Gly Leu Ser Gln Ser Thr Pro
                405                 410                 415

Phe Lys Thr Phe Lys Lys Ala Gln Gly Ile Ile Asn Asn Gly Asp Thr
            420                 425                 430

Leu Tyr Val Ser Asp Gly Asp Tyr Phe Arg Val Gly Gly Thr Leu Leu
        435                 440                 445

Pro Pro Ile Ser Asn Lys Ser Ile Asn Ile Ile Gly Leu Gly Ser Asn
    450                 455                 460

Val Asn Leu Phe Met Ala Asp Glu Pro Thr Trp Thr Lys Thr Ser Gly
465                 470                 475                 480
```

```
Arg Asp Ser Thr Tyr Glu Phe Thr Arg Ser Ala Val Arg Arg Val Val
                485                 490                 495

Asp Phe Asn Asn Asp Arg Glu Phe Thr Asn Val Thr Ser Leu Asp Lys
            500                 505                 510

Val Asp Thr Thr Leu Phe Ser Trp Tyr Ser Asp Gly Thr Lys Val Tyr
        515                 520                 525

Val Asn Asn Gly Ser Ile Glu Pro Asn Lys Lys Val Val Pro Leu Leu
    530                 535                 540

Ser Ser Gln His Leu Ile Val Ser Ser Val Pro Thr Asp Phe Tyr Ile
545                 550                 555                 560

Glu Asn Leu Asn Leu Tyr Gly Gly Ala Arg Pro Ala Arg Phe Glu Leu
                565                 570                 575

Asn Gln Asp Asn Ser Val Tyr Ile Asn Asn Cys Val Leu Ser Tyr Ala
            580                 585                 590

Ser Gln Val Asn Gly Asn Gly Leu Glu Ile Val Gly Gly Lys Glu Val
        595                 600                 605

Ile Val Asn Asn Ser Val Ala Asn Asn Asn Tyr Met Asp Gly Phe Asn
    610                 615                 620

Tyr His Ile Gly Ala Asp Ser Ser Lys Pro Leu Val Ile Glu Ile Asn
625                 630                 635                 640

Cys Thr Ala Leu Glu Asn Gly Phe Glu Lys Gly Thr Ala Gly Thr Lys
                645                 650                 655

Ser Asn Asn Gly Ser Thr Thr His Asp Gly Leu Lys Ala Ile Arg Val
            660                 665                 670

Asn Gly Ile Tyr Ala Arg Asn Asp Gly Gly Asn Val Ala Asp Val Asn
        675                 680                 685

Glu Gly Thr Glu Ser Trp Asn Leu Gly Cys Thr Ala Phe Glu Ser Tyr
    690                 695                 700

Gln Gly Lys Asp Phe Gln Thr Ser Ser Gly Ser His Met Trp Leu Asp
705                 710                 715                 720

Ser Cys Ile Ala Tyr Gly Ser Thr Asn Ser Ile Asn Ser Ser Asp Pro
                725                 730                 735

Asn Ser Lys Ile Tyr Thr Arg Leu Gly Ser Tyr Gln Asn Lys Leu Ile
            740                 745                 750
```

Leu Gly Glu Glu Ile Lys Tyr
        755

<210> 767
<211> 85
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 767
Met Lys Leu Tyr Gln Val Glu His Asp Asn Cys Glu Pro Tyr Glu Asp
1   5   10   15

Asn Phe His Phe Arg Glu Asp Asn Val Tyr Thr Asn Lys Glu Lys Leu
            20   25   30

Ile Lys Arg Ile Lys Glu Glu Gly Tyr Arg Glu Glu Thr Asn Tyr Arg
        35   40   45

Gly Glu Gln Glu Phe Ile Lys Gly Asp Pro Arg Gly Phe Asp Gly Met
    50   55   60

Asp Met Ile Thr Ile His Glu Leu Asn Ile Val Asp Cys Asp Ile Asn
65   70   75   80

Ile Lys Lys Gly Asn
                85

<210> 768
<211> 81
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 768
Met Glu Phe Phe Ile Asp Arg Thr Ser Thr Ile Asn Lys Lys Pro Ile
1   5   10   15

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

Pro Phe Thr Leu Glu Arg Trp Cys Val Glu Ile Asn Ser Leu Glu Glu
        35   40   45

Leu Thr Glu Ile Ser Lys His Glu Gly Glu Val Ile Ile Asn Thr Arg
    50   55   60

Gly Asp Ser Pro Phe Ser Pro Tyr Leu Glu Ile Tyr Asp Tyr Tyr Arg
65   70   75   80

Glu

<210> 769
<211> 56
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 769
Met Glu Arg Phe Lys Val Lys Arg Ile Ile Thr Thr Glu Glu Val Arg
1   5   10   15

Tyr Ile Asp Ala Glu Thr Glu Glu Asp Ala Trp Tyr Ser Val Glu Tyr
            20   25   30

Glu Asp Glu Gly Thr Asp Thr Ala His Phe Asn Ala Glu Tyr Gly Glu
        35   40   45

Trp Ser Tyr Glu Lys Glu Glu Asn
    50   55

<210> 770
<211> 160
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 770
Met Asn Lys Thr Phe Phe Lys Ala Ile Gly Lys Asn Thr Leu Glu Tyr
1   5   10   15

Ser Lys Gln Gly Leu Gly Phe Leu Val Ala Leu Leu Ile Met Leu Ile
            20   25   30

Ile Leu Ser Val Phe Leu Ala Phe Ile Ile Gly Ile Pro Ala Gly Ile
        35   40   45

Ile Tyr Gly Leu Tyr Ala Leu Asp Ile Asn Asn Tyr Phe Ile Thr Met
    50   55   60

Leu Val Thr Val Glu Trp Phe Ile Ile Leu Tyr Gly Ile Val Arg Thr
65   70   75   80

Gln Asp Asn Lys Lys Pro Phe Val Lys Leu Lys Leu Lys Asp Tyr Leu
                85   90   95

Leu Thr Ile Leu Tyr Leu Thr Thr Ile Thr Ala Thr Ser Val Leu Glu
            100   105   110

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

Val Ile Thr Leu Leu Ser Phe Leu Leu Phe Leu Ala Val Asn Arg Gly
    130   135   140

Ile Cys Lys Ile Val Ile Lys Ser Tyr Lys Glu Tyr Lys Glu Glu Asn
145   150   155   160

<210> 771
<211> 83
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 771
Met Ile Phe Lys Lys His Lys Glu Glu Glu Val Lys Lys Asp Ile Asn
1   5   10   15

Phe Ile Arg Ile His Asp Val Ser Gly Thr Ser Thr Ile Ile Lys Gln
            20   25   30

Lys Asp Thr Lys Thr Asn Leu Asn Ser Phe Ile Gly Gly Leu Val Phe
        35   40   45

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

Phe Lys Asp Asn Ile Ile His Ile Asp Thr Val Tyr Tyr Lys Glu Val
65   70   75   80

Ala Asp Glu

<210> 772
<211> 81
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 772
Met Ala Tyr Glu Tyr Lys Asn Lys Ile Gln Asp Ile Ile Thr Asp Asn
1   5   10   15

Glu Asn Tyr Trp Cys Ile Asp Asn Glu Lys Glu Leu Glu Glu Leu Gln
            20   25   30

Glu Val Tyr Gln Lys Ala Glu Ala Phe Asp Glu Ile Val Asn Glu Phe
        35   40   45

His Tyr Gln Leu Gln Asn Leu Glu Ser Trp Asn Thr Leu Asp Gln Lys
    50   55   60

Asp Cys Gln Thr Leu Lys Gln Ile Leu Glu Glu Asn Ile Lys Glu Glu
65   70   75   80

Glu

<210> 773
<211> 138
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 773
Met Asn Ile Lys Tyr Ile Asp Leu Val Leu Glu Asn Cys Asp Val Val
1 5 10 15

Arg Leu Glu Pro Lys Asp Val Lys Arg Phe His Val Asp Gly Ile Thr
20 25 30

Glu Gly Ile Asp Tyr Tyr Gly Thr Ser His Ile Ser Arg Thr Arg Arg
35 40 45

Cys Thr Tyr Phe Gly Ile Leu Ile Asp Asn Pro Lys Glu Ile Ser Gln
50 55 60

Val Gly Phe Ala Tyr Pro Asp Asn Thr Asn Ala Tyr Glu Met Ile Thr
65 70 75 80

Ala Tyr Ser Asp Ile Thr Ala Ile Asp Ile Ile Tyr Asp Asp Asp Thr
85 90 95

Asn Glu Tyr Thr Tyr Val Asp Phe Asn Glu Tyr Asn Asp Tyr Tyr Asn
100 105 110

Ile Asn Gln Lys Asn Glu Tyr Tyr Asn Asn Met Leu Glu Val Thr Ile
115 120 125

Thr Glu Ser Asn Ser Ile Glu Glu Glu Gly
130 135

<210> 774
<211> 164
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 774
Met Lys Glu Thr Lys Glu Tyr Ile Met Phe Trp Gly Lys Glu Asp Ile
1 5 10 15

Tyr Ser Asn Phe Tyr Pro Ile Thr Phe Lys His Lys Gly Arg Thr Phe
20 25 30

Asn Asn Ser Glu Gln Ala Phe Met Trp Arg Lys Ala Gln Tyr Phe Lys
35 40 45

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

Ala Lys Ser Leu Gly Arg Lys Val Arg Asn Phe Asn Glu Glu Gln Trp
65 70 75 80

Asn Lys Val Arg Tyr Asp Ile Met Val Glu Val Val Lys Asp Lys Phe
85 90 95

Met Thr Thr His Leu Lys Gln Lys Ile Leu Asp Thr Asp Leu Arg Lys
100 105 110

Asp Phe Val Glu Ala Ser Pro Tyr Asp Lys Ile Trp Gly Val Gly Ile
115 120 125

Lys Ala Asn Asp Pro Lys Ile Leu Asp Glu Ser Asn Trp Lys Gly Gln
130 135 140

Asn Leu Leu Gly Lys Val Met Glu Asp Val Arg Val His Cys Val Tyr
145 150 155 160

Asn Arg Phe Lys

<210> 775
<211> 132
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 775
Met Lys Lys Arg Tyr Phe Lys Gly Leu Lys Leu Asn Asp Phe Glu Lys
1 5 10 15

Glu Val Phe Gly Leu Lys Lys Asn Lys Lys Tyr Lys Lys Met Asn Lys
20 25 30

Glu Leu Gly Arg Asn Glu Pro Lys Tyr Trp Asn Tyr Asp Met Ser Phe
35 40 45

Phe Ile Gln Leu Tyr Ala Asp Leu Asn Ala Phe Val Glu Ser Ser Asn
50 55 60

His Val Asp Met Glu Tyr His Thr Phe Thr Asp Ile Glu Gly Lys Glu
65 70 75 80

Arg Thr Gln Ile Asp Met Ile Lys His Ile Leu Ser Leu Ile Gln Phe
85 90 95

Tyr His Glu Ser Met Asp Ser Phe Asp Val Asp Asn Glu Asp Glu Ile
100 105 110

Glu Gln Val Gln Asn Lys Ile Leu Asp Asn Phe Lys Ile Val Leu Pro
115 120 125

Ser Leu Trp Asn
130

<210> 776
<211> 235
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 776
Met Ala Ile Tyr Val Val Pro Asp Ile His Gly Glu Tyr Gln Lys Leu
1 5 10 15

Leu Thr Ile Met Asp Lys Ile Asn Asn Glu Arg Lys Pro Lys Glu Thr
20 25 30

Ile Val Phe Leu Gly Asp Tyr Val Asp Arg Gly Lys Arg Ser Lys Asp
35 40 45

Val Val Asn Tyr Ile Phe Asp Leu Met Ser Asn Asp Asp Asn Val Val
50 55 60

Thr Leu Leu Gly Asn His Asp Asp Glu Phe Tyr Asn Val Met Glu Asn
65 70 75 80

Val Asp Arg Leu Ser Ile Tyr Asp Ile Glu Trp Leu Ser Arg Tyr Cys
85 90 95

Ile Glu Thr Leu Asn Ser Tyr Gly Val Ser Thr Val Thr Leu Lys Tyr
100 105 110

Ser Ser Val Glu Glu Asn Leu Arg Ser Asn Tyr Asp Phe Ile Lys Ser
115 120 125

Glu Leu Lys Lys Leu Lys Glu Ser Asp Asp Tyr Arg Lys Phe Lys Ile
130 135 140

Leu Met Val Asn Cys Arg Lys Tyr Tyr Lys Glu Asp Lys Tyr Ile Phe
145 150 155 160

Ser His Ser Gly Gly Val Ser Trp Lys Pro Val Glu Glu Gln Thr Ile
165 170 175

Asp Gln Leu Ile Trp Ser Arg Asp Phe Gln Pro Arg Lys Asp Gly Phe
180 185 190

```
Thr Tyr Val Cys Gly His Thr Pro Thr Asp Ser Gly Glu Val Glu Ile
        195                 200                 205


Asn Gly Asp Met Leu Met Cys Asp Val Gly Ala Val Phe Arg Asp Ile
    210                 215                 220


Asp Leu Pro Phe Ile Lys Leu Glu Gly Asn Ser
225                 230                 235


<210> 777
<211> 183
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 777
Met Val Asn Val Leu Pro Ser Val Tyr Asp Ala Glu Lys Gly Glu Trp
1               5                   10                  15


Val Thr Leu Leu Ala Lys Pro Ile Ala Glu Glu Val Phe Lys Ile Met
            20                  25                  30


Lys Ala Asp Tyr Leu Glu His Lys Gly Asn Ile Gly Phe Phe Ile Ser
        35                  40                  45


Lys Tyr Lys Asp Gly Asp Ser Ser Ile Glu Gln His Asn Val Val Val
    50                  55                  60


Phe Tyr Asn Glu Lys Asp Tyr Asp Thr Met Glu Leu Thr Glu Ser Glu
65                  70                  75                  80


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


Tyr Lys Pro Phe Ser Leu Asn Asn Phe Ile Asn Tyr Leu Glu Asp Tyr
            100                 105                 110


Gly Tyr Arg Leu Pro Val Asn Phe Glu Val Asp Val Thr Ile Ile Leu
        115                 120                 125


Ser Asp Gly Gln Lys Phe Thr Tyr Pro Arg Thr Ser Ser Ile Thr Asn
    130                 135                 140


Asn Ala Ser Ile Val Asp Ala Leu Lys Ser Glu Asp Gln Tyr Ile Glu
145                 150                 155                 160


Val Lys Tyr Ile Tyr Asn Asp His Ala Ile Asp Asp Lys Lys Leu Ala
                165                 170                 175


His Gly Asn Asp Thr Leu Lys
```

180

<210> 778
<211> 105
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 778
Val Glu Arg Thr Leu Asn Leu Tyr Asp Ser Lys Gly Lys Leu Leu Lys
1 5 10 15

Ser Ser Glu Lys Ile Thr Gly Ala Ser Ala Lys Ile Ile Ile Glu Lys
20 25 30

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

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

Thr Lys Ser Asn Glu Asp Lys Gln Glu Ile Val Phe Asn Thr Leu Asn
65 70 75 80

Ile Asp Ser Asn Ser Phe Val Val Ser Glu Thr Glu Pro Ser Asp Lys
85 90 95

Ser Lys Leu Trp Phe Lys Pro Ile Asn
100 105

<210> 779
<211> 39
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 779
ggacucuuag cuuaaaggua aagccaaccg cucauaacg 39

<210> 780
<211> 26
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F44/10

<400> 780
Lys Tyr Leu Leu Lys His Ser Lys Glu Ala Asp Ile Arg Ser Thr Ser
1 5 10 15

Lys Ile Met Asp Ser Ile Asp Lys Leu Thr
20 25

<210> 781
<211> 166679
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 781
cgttagcacc tttataaccg atggtgaagt aatcctgacg agcatactgg tcgatgtata 60

cacggtagcg accacccaga acaccagcaa atactgcttt agtggtgtcg gtattataac 120

cacgacccag accctgagct gccggagata cgttggtatc aacagctgcc agtacgttaa 180

ctacgttacg ggaagcgata atgaagttac cttcaccgcg accggtctga cgagcgattt 240

cagcggattc tttgtcaatc tggaacagca gagctttaaa gctttcacct gcccaacgag 300

caccgcggat atcaatcggg tcttggaagt cgaatacacc agctttagaa ccaacagtct 360

gggtcatacc agatttacca acctgagcgg agtagttaat ccagtcaaca acttcacggt 420

tgatttccag cataatttcg gtagccagga ttgaactcaa ttcagcatca gcgtccatac 480

cgtgaacagc acggaggtcc tgagccagtt cgatggaata ctgtgctttc agctgacgag 540

atttcgcttc gatagtttgt ttatcgatac ggaagcccat ttcattccac gggttatctt 600

tagaaccgtt aaatgcttct tgcagttcag caacggaagt agccatacct tcggcgattt 660

ctacaacttt accagcttcc agagcagcag taactgcagc gtccagttta gcagcatcgg 720

tagcaccagc gtctacagtg aaatcttcaa caacctgcag atgagcacga ccggtctgtg 780

cgaaatcgtg aacaacgata tcaccaacag tcagagcagc accagcttta actgcttcaa 840

acttctcggt tgcaccctga ccagagaaca ttgcatccgg agcgtacatc ggatggaaag 900

cttctttagc accagcagcc agagggtctt tgccgtaaac agcgcggaga gcgaatacct 960

gaccggttgg gttagacatc ggctgtacac cacagatatc gaaagcaatc aggttaggga 1020

tagcacgacg aaccataccc ataactgccg ggccaatctg ggttacagca ccagaggtct 1080

gaccagctgc gatgttctgt gcatcataac cgtggtcacc gccaatttct gcttcagaca 1140

ggaaagaacc aaatgcttca gcgatttttt catcgcggta ttctggagcc tgattaatat 1200

cagcttcctg gttttcaaaa atcttagcga tcagagcttt tttgctagcg ccaacaattt 1260

ccggcagagc ttcgttctca agcagcggct gccatttttc gataagttta ttctttttca 1320

tgtgttgtat aacctttaa attaagaaag acgagccgct tgggccacat aagcatccat 1380

aacggatggg gttttagtcg caggagtttc ttctactgct tcagttgtga agtttaaacc 1440

gtctgcttct ttgtcgatag tatttatatc ggcagattcc gttacagact gctctacaga 1500

accctgcacc atttcaacaa tagctttcag cttagttgaa aatgcgtcag aataatccat 1560

gccctctgtc agagaaacta ctttctcttt ttgggtatca gtcagttcac gggttgcttc 1620

ttggatagca tactcacgtt gggcataatt gatatactca tcgcgcttag aaacttcttc 1680

aaataaacga gcagtttctg ctttttgctc agcaagttct tcttccatct cagctactac 1740

gtctactgat tcttcaggaa ttacaacgtt gtgctcaaca aacagctctt tcataccgac 1800

aaacatggat tcaaacaggt cagctttaat accgcggtca accgccagct ggttttctgc 1860

catccattct gcagcgatat ggtcaaagta tttagaagca gcttctttca gctcttcgcg 1920

agcttcttct ttagcttttt ctttttcttc ttctactttt tcttctgctt tctcagcaat 1980

cttttcaatg tgagattctg ccagagctac ggcgtgtttt ttgactgttg cttcgaatac 2040

agtgctgaag ttagctttag cttccggaga aagctgaact gattcgaaaa tactgtcaag 2100

agcgacggaa gcatcgatag ttttagcttc ggtcattaaa agttctttaa gcatttttga 2160

tgtcctgtgt taagttacat aattatttat aacgctttta acttctctgc gagagccata 2220

aaagcatcat cagcactatt ggcaacttgt gccgaggtat tttccgaaat ttgtttcggt 2280

tgtacccatg catccggagc actaggaccc caaactgcgt ctacaccaac agtcaggcga 2340

aagccttctt gtacgatgtt atatcctttt cctgagtctt ttaaagaacc gagcccgcgg 2400

cttgatacac caggaatcca accagcacgg atgttagcgg ctaatttatc acctggaccg 2460

tggtctcctt cgatgattct tgcacgccca taaacatcgt tgcctttcca ccacatatct 2520

tcgataatga ttgcggcttg catcgggtca acatttgcgc gaggtggatg gtttaattct 2580

cctagagcct gacgagtagc aacctgttcc ttaatataac gacttaccgc agtctcaaga 2640

atgcgttttg gataaagacg tttattacgg tttactactt ctgcctgcat aaaaacacct 2700

tcaatataca gaccaggttt taagccagat tcattttcgc cttcaacgat aatagattct 2760

agcatgggtt taccatcaat tacatcgccc ggttgacccc aatgctcaat taaaagttgt 2820

tcattgaggt tttccattaa cttagcccca gagcctgacg gcgtttaagt gctttcttac 2880

gtttacgtaa tccacgagtt tgagccgatg gattagcacg ttttgatttt actgctttac 2940

gcgcgatttg acggcgttta gctttagaaa gtccagttgt ttggaacgcg ttacgctcac 3000

gtgttttacg atccttagta cgtgtaatag tacctttaga atcaacatgt ttaacgataa 3060

attcatttag ttgtagagat tcattgattg aacctaaagc aattgctaaa tcaggctcag 3120

aaacaacaag attctctaca attttattta tatcatcttt agagagcgct gcggacaact 3180

tatcaaaacg cgcctgggct tcaggaagaa gagcttcgac agtgtcgata actaattcat 3240

gattttcagg cagtataagc attactcgtc ctcttcgtcg tcttcgtctt tatcagactt 3300

atcttcgtct tcgtcgtctt catcttcgtc ctcatcgggc tcttcaccct caatcatgac 3360

agacgctgcg ataaattttt tgcgctcttc aattaaacca gatgtccgtt cagccataat 3420

tgcaccaaaa gctttttgg ctgctacgag gtctctggat tcaattgcgg aaatataatt 3480

ttccattaga aatcctcttc attttcttgg tcttggaagc gagcctcttt agactctaat 3540

tcaatttgct tggcttcttg ttcaatttct tcatctgaca tctgaaggaa gtctttcatt 3600

gctgtcttat gagaaatata cttgccgata aacggttcag ccattgtgag catattgatt 3660

ctacgctcca taacttcagc atctttcaac tcggtgaaat atgaatcttt atggaacaca 3720

atcttaatat tatttatttc gtcttcccac tcatctttag acaaaacttt tttaagaatt 3780

agattagtgc gaagtggatc aagcataatc tcttcgaatt tatgctgtaa tctacgaata 3840

aatttagcaa aatcaagctc atcgcgagta attgctgtgc cagcatcaaa ctgcacaccg 3900

ccttgattat ttgcatccgg catgcgcgaa agaggaactc gcaatgccat gtataacgct 3960

gttctaaagt aacggacgtc atccatatca ctcatacctg acataccagg aagagtatct 4020

acttcagtaa ctgctttacc atctctacgc tgcaaccaat agtcttctgt cattgacata 4080

ttatgttgct gatttttaat cttaccggtt gatgcatcat atacaacgcg atttttcatc 4140

gtgttcataa tatgttgcat atgagctgcc gctttacgag aaggcatatt accagtgtca 4200

atgtaaaaca cacgacggtc aggagcacga gtaatacgat aaattaccaa cgcatcttct 4260

aatagcttta actggttggc gggtttaacg gctcggtgta aataaccgat gatgttttga 4320

cctgaacaat caactagtcc agaatgtgca tatacgatag catcgcgtgg aattttaatt 4380

ttcgttccgg cggaatataa tctgccatct gcataataac tttctttgcc agtatcgtaa 4440

atgaaatact ctttgtaccc cttaacgatt ttagtaccag cgtcatcagc agtaacgatt 4500

tcacggatga attgtaagtt gcgcgggtca agacgtctca gttcctgaat tccgtctttc 4560

attttcttgg tgttgacgat tttatggaag aatattcttg agtcaacata ccaacggcgg 4620

aaatggtcag cgccctttcg ctcgaaatta aggcatgtta aaactgtatt aaactcttca 4680

agaatgcggt ctttaattgc ttgactgaag tcagtagaat ctaaatcaag agaaactact 4740

ggatgaccgt cttcgtatac aactgcgtca gaaactattt cttcaacagc attgtcaact 4800

tcgtagttat tcattaaact acgataagtg ttgattaaat cagcagttgt tttcattcca 4860

ggttcattgg aaccaaacat catttggttg aatgaattgt actggatttc gttttcgttt 4920

gattcaactt cacgagctcc atcatcaaat tttggagcag tgattgactc taggtcattg 4980

ttgatttgtt gcttatattc agcttcgtcg cgtttttccc acggagcgaa taagtccaaa 5040

atatgaaagg ccattggagt ctccgaaatt atctataagt atatttatat cgaagataaa 5100

catgctttat gatatctcat aattgcacta cgtgttgact ccactccgca tactggacaa 5160

gtcattcgtg gctggtttat ctttttcct ttgttagggt gctcttttcc gaacatagga 5220

tttctttcac ccgacattgc tttagaatgg tcaggtcgtt ttcttccgga taatttaata 5280

gagtgatctg gacgttttat tcctaaccgc tgatgacgtt gtttttcttt agactcttca 5340

ctcatttttc ttcctttagt tgacatccca aagaaaccgt ttggttgtgc taaagccata 5400

tttatatacg aactggattt aactacgtcg tattttattt gcaactcaag ttcagcttta 5460

gaagcttcct ctcgagtttc atatgtgttt aatatccggg ttttgaataa atgaggatta 5520

tcatgttgct cactcttcca gaggtcttta tatttcttgg atttaactga gccatgataa 5580

ttttcatcaa taattcgtga tacactagta gaaccgatgt agcgacgggg aagtttattc 5640

cccgtgtata ttgtcaaata agtacagaac attaatacct ccacttcgtt gttagaggta 5700

tttattcagc attattccca ccaatcgata gcaaaggtag tttcaaacgt ttctatctca 5760

ttattcgaat cccaatccat ctgtacttca ccaacgttag ttggccacag accagtaatg 5820

gtgtgttcat ttgtgatagt tttgccatca cgactaaact ggcgtaccgt agcaaccttt 5880

ttgtaatcgg ctggagtcat accagagata tcattgcctt gagcgtgggc ctgagcctgc 5940

caagcaataa ttgccttacg tacttcgtgt ttatcatcgt tatagatggt aacagtccag 6000

tcgtcataag tacggtcacc agcgacgtta atcttacggt tcatgtaccc gactggaact 6060

ttttctacga tacctgccgg catcggtgct gctttacatt tgaaactgaa gttacgaccc 6120

agataaggaa tttctacctc aaacaggtta ggacgcgcaa agtcaccaga ttcaaacgca 6180

cgagtgatgt ctgttaattc catcgttgtt tcctatagat atttatatag cctctcgatt 6240

gactacatca tcgtagaggc tattaaagtg tgcggtaata taatttatca tctaaagatt 6300

agatgacccc agaatgtcct ggggttcata ttactgtggt ccgattaact catcgaaatc 6360

tgcaccagtt gccgtagcaa cgaagttcag agtgatatag ttaattgaac gtgccggctt 6420

gatgtagaag ctcgctacaa actcgttgcg gtcgataact gctggagtgt tattcgtggt 6480

atcacataca actcggaagt catatacacc acccagagct ttaatacctg cgaggtattg 6540

gctggtttcc atacggaaag aactacgggt aaagttatcg tttaattcaa acagctgcca 6600

cttagaagaa tcaccgatgt tgttcttcag catgttaaac aagcgacgaa cgttaattcg 6660

gtcaaacggt gttggaacag tggttgcagt cttatcaccg aacagaatga aaccttcacc 6720

tgtaccttga ccagtcactg ggttaatacc tgcttggtac atgcggtcac gatgtgcctg 6780

acgcggttca attgccaatt tgatgcaatt taaaatctga ccacgacgat atccagctgg 6840

tgacatccaa ggctgagcaa tatcatcagt acgagcacac aggcctgcaa tatcagcagc 6900

taacggaacc caacggttta cgtcgttata tttatcatac tgatatttat agttaccatc 6960

aattgctgcg tacgtagtat tgatgttcat gttagcagaa tcataagttc catcgccttg 7020

gcgccagtcg attaaattat caacagcacg agtcagagga atatttacaa tcgttgacct 7080

tggaggcgaa atgagtgcta agcagtcttg acgctcatct gcaatagacg aaacgtgttt 7140

ttgtactgta cttgcgattt catcggtttc accagcacaa gcaccagcaa tcagaaggtt 7200

tacacgcaat gcttcacggt caccaaataa atcccagcct tgaattaaat cgccagccgt 7260

aactgattca ttagctgaaa ccccaccacc cagacgaata acgccggaaa atccttcagg 7320

ccatccttgc gcagtagcaa atacatagcg tgaagaaccc ttggagaaat aatcgtccat 7380

aaagatgttg tttccgtaga tatctttatc ttggcggctt gttgataaca ccgctgattc 7440

aactacagca ccatctctac gaacaatgat agcgtactga gtatcggtct gaggaccata 7500

tccaaatacg gcttttgcgg ttgatgcacg ctgtccacca ctcggataaa tcgtcagttg 7560

ttcgccttta tcaaaagcgg cttttgatac aatttcaatt tccagttggt ttccgagctc 7620

gccaggatac gcagctacaa ttccaggcat tttatattgc gcaagcgcag tctggaattc 7680

agtttttgtc atttcttcat gggcagtttc atgttcagtc agtagaactg tagactcaga 7740

aataatttta cctaaagtaa tgacagcgga aacaccagaa ctctgtgaag taatggtagt 7800

tgtccacgaa gaccctaaat caggatattg attaatgctt tttgcatatg caataatctt 7860

cgatgtcgga atgaacaccg acttaatttt tccgtcacta tctacttcag taactgaacc 7920

ggtgtcatct acggtttggt ctgcatattt aaccgtaatt ttatcaccaa cttcatagtt 7980

actaccagca gtagtgatag tccattcaat attatcaacc aatggagatg cgtttttagc 8040

agcttcacgg ttaactacac ggacggtgcg tagatcatta ccatattgca gaaagttcat 8100

tgctgacata aagtaatcag cagtttggtt attagggccg ccaaacatat caaccagttc 8160

aacttcatta gtgatttgag taacttgata tgcaggaccc cattggaact tcccgacaat 8220

tgcggcacga cctgtagcgt taagtactac cgtgctctgt acgctcgttt ctttgagctc 8280

aattccagga gagactaaag gcatgatata tcctcaatgt tgtttgcttt ttattattta 8340

tacaaatgaa agaccatgtt cttgaggcgc atattctgcg ctattcacgg cgtcaacgaa 8400

cactacagga gcgtaatcgt cgttcatatc ttctaattcg cgtttaaaaa cttcagatgc 8460

taaacgcatt tcatctttat ccacgaaatc agcaaatttt tgctgtgttg ttaaccatgc 8520

gaaaattacg agtgacataa ttaaatcgtc atgatatcca tcttctgccg cccaggatac 8580

tcctttctca gagaaagtac gaaattcttg aacagtagca cgatggtgaa taatgagttt 8640

atctttttcg ataaggtctt ttagtgcaga acatccaacg gcttttgacc ttttcgtctg 8700

tttcattcct aaatcaacta ttgaatcgca aatgacattc tcatattcta aatccatata 8760

aagactcttc gctacagaaa cacctgtaga gttaagttct atatagatcg gagcttcgtt 8820

gtactccatt agatatttaa taactatatc cgggaggatt aagtgagaaa ttgtattaga 8880

atgtaatact ccaacttgtt cccattcaga tgtagtaacg tcaataatat ttagtgcatg 8940

gtaatcctga ccgcgtcctt cagcagagtc aagagttgca atatatttgt ggtctgcttc 9000

cgcttcttta aatttataaa acccgtgcga gtcaggagta acttcaatcc aatccatatt 9060

ggcaagtttc ataccggaaa tgagagtacc ggatgtgcca tgaaattccg cacagtgctc 9120

ttgtttaaac tgttcaagag aagaagcact gatagtttga agtgaccatt gccacccatc 9180

atcaaacata tcttcgtcgt tatatagacg ttctttaacc gagttccaaa ttgcagtata 9240

aggcgtaaag ccggatttac cttcaacagc tgcagtccaa atatcataga agtggtttaa 9300

tccacttggt gtagtcgtga taataatttt agaacgacga cctgatgaaa taacaggttg 9360

gatagcaagc catgcatcta tgaagtttgg aataaacgca cattcgtcaa tgtaaatcat 9420

tgcaaatgag ttaccacgaa cggcatcagg actcgaagcg tatgccccaa tagatgagcc 9480

attatctaat tcgattgagc ctttgttcca ttcaacaata ccaggctgaa gaaagtcagg 9540

aagtaattca attgcttgct tagtacggtc gagaacttcc gcagacattg agcctttatg 9600

cgcaagaata cctactgctt tatccttatt aaaacacacg aagtgcgcaa gaaagattgc 9660

tactacagta gttttaccga gctgacgact gaggttacaa caagtcatac gtttggctgc 9720

catgatttcc agcatgtccc tctggtaatc acgaagctgg actttaatgg taccatagtc 9780

aatgtgagta attgcacagt aggtctctgc gaagtacaca atatcgtctc ggcatttctt 9840

ccattctgca actatttcac gggttagttg cattttaata tttgctcgtt taaggtttgg 9900

caatcccata tagcgggtgc gcttattatt tttgtcctta aacgtttgga aatgagctgg 9960

gtcttcacct tgcaaacgaa ttttaactat cccatgcaac ttaagatagt cttcaaattt 10020

ctcaggatac cacttatcat cccattgcga tttaaagaaa cgaactccgt tttcaatttt 10080

cgtttccatt tcagacgggt gacgaataac cgtcagtttc ccgtcattta aaggatgggc 10140

atcactcaga acgttaaacg gttgagtctg ttccatttac tattttctct cgagcttctt 10200

gtgcttcata ggcatcaccg aattcatcca tcatatcagc ggtagaccct acaaagactg 10260

ttgcattttg aatattcatt ccttgctgag gattagctcc ctttccggtg ccaacctgct 10320

cagaagtaat gtctttcatt tctttatgaa gcttaagaat ttctttgttg gttgtagtca 10380

tctgacccat aagagttgca aatacttcca tatgtctagg agaatcagca ttcttagcag 10440

tttccaaaaa tattttagct gcgtccatta acatctgttg ttggaagtgc atgttcttgc 10500

gaacaaccga ataatcatct tcgaggtcag gtttacggtc atttggatta gatttaactt 10560

caactaattc aagtttttca taaactggaa tttcttgtcc ttctattcca ggaattcctt 10620

cgatgtctaa taatttagcc atatctaatt gtaattcact catttttcac ctctcggtcc 10680

aggagcctcc ggatttaccg gaataggaat atcgtgagaa taagtttgtt tactagaacc 10740

atcccaattt tcgtgttgaa catctcgtgg agtgacttcg ctatctactg attcaaagtt 10800

tccttctgga gttaactcct tgctgttagc gaagaaatct aaataaatgg ttctaatttc 10860

gccatcaatt tcagctacag gcggatacaa ccagccattg acttcaaaca tcagcgacca 10920

ttctaatcta cggcgagtga tattatctcc atcaacagct tcatcctgag aaaatgactg 10980

taatacaatt ctaacatcac gattaaagct tgtgtctttg tcgtaaagct cagttatagt 11040

cgtgttaaaa tgcggctgaa aataaggaac gatttgctcg atgatttgat acatatcatc 11100

ttgattgcgt gtataaattc ccaattcaaa aatcatctta atcggagtag gattatactg 11160

agatgtaatt tttgaagggg ttttatatga tttggttcta ttcaactgtg atgttttata 11220

catcgcattg tattgcatat caaccaagtg caaattcatt cttggcaaaa cagtttctat 11280

ctttgcttta ttctcggtag actgaatagc agtccatttt ccgagttgag aaaggaactt 11340

ttcctttgaa gcataagtga taggtacttt aatatatttt agtccagtgt cttcacgcca 11400

acgagcaatt tgtacatgag aaaataaatc tccaagcaat acaatgtatc ggcgtaagga 11460

cgaattatac caatgtccaa acatgatttc tcctaaggga cccaaaggtc ccatctttat 11520

tttatttatt cgaagaaccc gtcatcaaac gaatctgctt taggagggga ctcaagtcct 11580

cttccgttat taacataata cggatgaaca tattcagagg cttctttatt gatttcatca 11640

ctttctgcgt attgtatatc agaaatatca gcaagagcat ctatattttt gattggttct 11700

aaatcaagct cagaaaattc aggaatatta atgccttcat tacgttgcaa ttctggctga 11760

agctgctcac cagaataaat gtatttttgt gcagtaatct tgcgttgaac attttgacct 11820

aactgataaa atggatcgta tggctgaacc cagttaattt cgaataatga gttatccata 11880

ggaaaataaa ttaggtcacc ggcttttggt tcagaattat tagtttgatg cttgaatagg 11940

ttgggattaa tagtcaaatt gacttcatca ttaaccatca taccaaattt actaaagaat 12000

gtgttatcgc cagaatatcc ttcaaatgaa tctaaataag cagcaaattt ccaagctttg 12060

gtgaatttac ttgatgggtc ttctccaaaa agcaaatcag gattgttata ttcacgagga 12120

aggaaataaa actcaattcc tctcatttga atagcctcag ccgataaagc atctgctaac 12180

gtttggctat ttctgtgatt ataaaaattc acataaggat tgagaatttc agtctcatta 12240

gttttattat atcctcgata atcttcgagt ttagcgaaga gcctagaatc aaatgtagac 12300

atcttttacc ccaacagaat aggacaaccc gggtcaagta aatcaagttc ctctcggagc 12360

ctctcgattt cttcttgggc ctctacctta agtgtttgac catcaactgt aactccacct 12420

gccaattgca gaccctgatg tttaaaaaga atttcacccc acagcttttt agttaatgct 12480

gtagcataat cttttaccca acgattatta tatgcgcctt ctctatttgt attaccttca 12540

ccagcatatt gaccattatt acgaaggtca ggattctgat atctatctcc taatccccaa 12600

tgatcagcag tttgcggccc agcaaatccg tatcctgctg tattgcctac catcgcatct 12660

gtattcataa atgatttggt ccagcattca cagacaatga tgtcaccctt catgaagttg 12720

cccattactt taagcatttc attatcagag ttataccaat aatccgggag aggagcaagt 12780

aaatcttgca tcattgacca gtaagtcatc aattgagtaa aatagccaag gtcagcacca 12840

aacgcatttg gcccatagct tttattacag cttgacccca ttccgccatt aattcctgcc 12900

attcccatta gaaagtcggt aaaccatggg tatgtcgcat taccatccat tgaagttaat 12960

gaacctacat ttgttctaac aatttgggtg acagcaaata cattacggcc gcgcaaatca 13020

aatacgccgt tcaaaaatct tgcgttgtca gcttcgtctt ttccaatata aaaaacttga 13080

taacctttat tcaatccgtt aaagtggtat tcaccataca actctaatgc tcgttgaata 13140

caatcataaa tttggtcttc agttacttct acattaatta ccggcgctcc tagacgtcga 13200

agtatagcgt ctttaagcgt ttttgggttg tacgtgttgt atgacatatg aactcctctt 13260

tatattccta tttatacgaa aaagggaccc gaaggtccct tttgttatac agctggatga 13320

atagtaatat ccaaagattt aattttaaca agaacctgtg attcttctga agcagctcta 13380

tacacgattt tgattgcatc accagatgaa aactcaatga gtttcttggt tttaatcaac 13440

tgttcgcccg ttacagcctt aacaccgagc ccgtaggaaa acacctcgat gttattaacg 13500

agaataacaa ttttcacgcc tttatctgaa tcagaagctt cgataaccgt atcagtttct 13560

acgcaaaata cgccatcgtc atcaacaaca atgtcatcga caatacgaat gccagcattg 13620

aatggagcag cgaccaatga gttaggattt accaatgcat cagaacttaa atcaacagtg 13680

aaatcttctt tactgaattc acctattgat gaaggttttt taaaccattc gccctgttta 13740

cggaggtatg ctccagcttg ttctacgtca gtaactgcag tcacgaattt atcttgcaat 13800

tctactacag tagcgtatac accatcacgt tgaactgggt tttctgacga aaagtcacca 13860

ttcatttgag tctgtaatgt aaatacagaa ccctttaacc cttcattgtt attgccaagt 13920

tctacttgaa tgtcctgaat agcagactgt tgagagtttt gcataccttc aacattggtc 13980

attctcgcta aaattgaccc aggaggaatc ggctgctcgc taggaacaat accaacctgt 14040

tggtttatcc atgctacttg accctgaagc cctgatgaag tatcacgtcc tacaacatca 14100

gaaatgtacc cttggtcagt tgaaagagaa ctaatttttc cttcaatagt atcaggctta 14160

tcagaagacc ctaaacgagc atcaatatta ttgacacgag gaactaaccc ggtttgtgca 14220

aagttaagtg ttgcgtcaac tatacgataa tcgttttcta atctagtagt acgagctcca 14280

atttttactg gattggtaaa atcaatggct tggttaatag caaagatttc attattagct 14340

gcggaaatag catcagcgtt attcacaagc cttgcataaa ttgaagctga cgtagctccg 14400

gatttaggac caacttcttt acgcaggtcg tttacttcaa tagtcagaga acctacgtct 14460

gaatcattgt atgcatcctc tagcgcctga atacgctcgt catgttttac tatagctgac 14520

gcattattga tgattcggta tttcatacca gaacccggag agtcttgctt cggctgtccg 14580

ttaatatctt gcccaggata cgcaccaatt tcacgtttaa cccaaactat attatcacga 14640

actgttctgt aatagtcatc tttactagaa tcataaacac ctacatcctc ttcgagaaaa 14700

tcaaggtcag ttcgaagttt ttcggtgtct tcttctaatt taagaatttg tccatcatgc 14760

ttttcaatat tctttttatt gatataaacc tgctcaatgg cgtcagaaga acctgtaatt 14820

tctaacgatt ttttgatttg gtctacatct acttgaatat tttctacagc agttccaacg 14880

ttgttcaaat cgttatgtac ctgaacaacg tttttctgga tttgaacaga agctctattc 14940

agttctccat catttccata gcgggttgaa gccccattaa gaggctctgt atttttatc 15000

cagttaattc tctgttgaaa atcgtctgga attccgtcta cgaacggaag cgaatctact 15060

agtttggtca tattgttcct tacggtctat ttgtacagaa tgtaagcatg cagtcataaa 15120

atataatacg actgtcttct gttggtctta tttgaacagt ggcatttgga ggaatgttat 15180

tgaagaaaaa gttgctagat gcgtaagctt caaatctcca tgaatgacca tttcgtccgc 15240

ctttagtatt ttcgatgtta agagtaagtt caccgcccca ttgggaaccg ttaactatta 15300

caacaaatct gaaaatacga ttgtcatatc cgtcgttgtt acgctcaaat tttacattaa 15360

catttagagc taatctacta gaagcttccc atggtgcatt acatgtaaac gttgcacctc 15420

gactaatcca agattgacct tcaacccaag taacattacc tactctggtt ccagctggca 15480

tgtaacgccc gtcagattct tgtcttgtat aacaattaat atcattgtta gtaatcgtta 15540

tgtcattgtc aagagttttt ccgtttattc tacgggtttt aaagactgca tctgttgcag 15600

ccgctgccaa tgaagcatca gtagttggag aacctgataa tctggttaat ccatatttat 15660

ccttggtgga ttttagcgct tgaagacttt ttggagtaac agccaaattg ttagaagtag 15720

ctgaagccac atctgagtct ttagcaaatt ttactatacc aaatacgctg tcagacgctt 15780

ttgatgccat gaaggttttt ggagttactg cgtatccatc gtgaacagca cctgctgcta 15840

cctgggcttg ggttgcgaca cgaactaatc ccaagttgct ttctgtcgca gaggtataac 15900

taggaggact gacactgaac tttccaatca tttctacaac acgcttagga gttactgcgg 15960

tagtttcgtc agttcctgct tgcgcttgag ccgcagtagt taacctaaca gttccatcta 16020

cgttttcttg ggctttcaca gttttaaaca catgaccgag agccgccgcg gtaatagttc 16080

tatttcctgc ggttaatgct gcggcttcag tattagtagc ataccgtgtt aagccaagaa 16140

ctgttgtagt tgcttcagga cgggtaactg tggattttaa tgtagcagga gttaccgcag 16200

cattaccaat agttccagca tcaacttcag cctgtgttgc tgtgcgaatt acaccggcta 16260

ctgtaggaga tgctacaggt aatccggtat cagttcttgc ccagctacca atcagctcta 16320

acgctgattg gacgtctttt atagcaacag gccattgtgt atttgttggg tcaaatatcg 16380

tatatttggc caaatcactg tagtgattat agttattctg ggccattatc ccatccttct 16440

aaaatagtgg aaagtaaatg tgttcgcgcc gaaggtttta gattcgttgc cgatagcatc 16500

ccattgccca taacctgctt tagctggtga agtaatagta aattcaacag ttaaaccata 16560

ctttttatat gtttcaaaat tatggttctg ataatctaaa tgaataatat caacatactg 16620

tggtgttgcc ggcgattgag taacctgttg aacaaccttt ccaacagctt ctaattcttt 16680

tactttatca taccaacgtg ttgctactgc tgcaaagtca tcaccgtttg caattctaat 16740

tggtaagcca agaatatgaa ttattactgg gtcaccgaca gagccgtctt cttttggctc 16800

taacgcaacg acacctgaaa aagtagcacg cgtaatttgc tgtgcgggct gtggagatat 16860

tccagtgtca ttgcaaataa tagttccaat ttctgctgac tgcaatgaca tcaaatcatt 16920

aatagcagct tcagtatttg gataccaaac ccctaaatcc atttgttcaa aggttaggct 16980

ccctatagga gccgtatttc ctaccgcaat attttgcggg tcaacgcgat attctgaaaa 17040

agcagctaat cttgaattaa ctttagctcc ttcacgagtt ttagtttcaa tcgtcatttt 17100

aacctaccct aatccaacga taaacggtga ttgttggctg aattttagtg atgtcatttg 17160

gaactacacc gttgtttacc gcaacagtgt cttcacggta tttagaataa cctggtccct 17220

gcgcgtctgg gtctaattga catccaccga taactacgct tccatgttca gggtctgaaa 17280

ttagaacttt atctcttgac attagttcag gaatgtgttc ttttcctaac gtaaatgtca 17340

aatctccaac cgttccacct gctgttaatg atggctgacc attttcgttt aagttattgt 17400

tgttacgcga aaaataagga tcagatgaat cattattcca accagcagta acacggcctt 17460

gtgaataaag cttccacacc ccaaatccca tatagtcagc agggtttgcg tggttgtgag 17520

cgttttcata aatcgtgcca atcggataaa ttacgtcaaa aaatgctgca atattattga 17580

ctttaatcat aatatcgtca gcaaccggac gcatattttt ctgattaggt tcatcataat 17640

ttgtgtattc aatgcgattt tttagagtta ctaattgctc agcattcata tacacttggt 17700

cggtttctgc catgatatcg tcaatatcca tagtagtacc gatgttatta ttgaaccaac 17760

ggacggtaag aaggtcttta tcttcaaacg cctcaccaaa aataatagct tcgacgttag 17820

taccagttga gtcaaattcc agtctatagt cttggttaga atttacccat tgaccaccat 17880

tgtttataca gtcttctgcg tatccacctt ccgcaccttc acaataaaat aaaggaagac 17940

ctgcagttcc agcttcgagt aattcctttc cgttcaacga aatttcaagc gaattgggat 18000

tcacacccac acctggaagt acacccatat catctagagt gattcttcga agagcagtaa 18060

ggttatctac tataattgac ccaggaatcg tctgggatgt agtctgggct gaatctcgta 18120

tctggatagc caacttgttg tatgaagacc gataaacacc aattccatct aggaaggttt 18180

caaatgttat tacttcccct tcaacacatg gaacttttaa acgaatgtct ttaccgttta 18240

attctaccaa ttgacctgct actgttccag gagaaccgta atcagcattg gctttatcca 18300

taacgctggt ttcaccgtaa tataaaatat taccacgacg atatacatta agcgagtctt 18360

cgttatattc tacgccatca aaaatgttaa gaaagtcagt ctgacccgca gtagcaataa 18420

ttgatttttt cgctacagta cttaagttac cattagttag cttatctaca gttttatttt 18480

caatatattc ccagcggcca ggggcgcaat aaaccaattc caaatcttgg aagttagtat 18540

tgaaaatttt aggagaagct gaacccttta atgtatcgcc ttgagcagga ataactgtga 18600

ttgggcttaa tcgccaggtt gaccaaacat cacgaagttt aataactttg ttatagtcgt 18660

tggctgtacc ctttggaagc tgaacgttaa ctcttgctgc ctgggtatta atagcaaagg 18720

cctgaccaaa cttagcattt aaagtagttc cagtagggct agctttaaaa gttttccatg 18780

cacctgctgc gaatggaact gaaccatcac ctaactctga atataaatca tcaaagttgt 18840

tattaatttt aagaccacct ttacggaggt aatcaccaga cccatcatct actgattggc 18900

ctactatcaa attttgtttc attattgaga tacccctacg gtctgtgtag caataacttt 18960

aactgccaaa cgtgcgtttc cataagatgt tgaagctgtg catattaaat ctttctgcgc 19020

gttaatagag tatgaaatag aatacatctt ttcattttca gatgattcac cacttcttaa 19080

cactgcatat tcagtgtcaa atactcttcc gtttggcgct gatgaagtaa tagtcgggtc 19140

aatcataagc atgacttcag atgattgcct tttgatggtt tgaccacctg gatttgcgct 19200

gaagcttaat agcaatttaa cagtagagta atcatcatta tatccaagtc gaatattaat 19260

aggagaactc gttaaattat atgtagcttc taacggcgaa tatgtgctgc caaacatact 19320

tgaaattgaa taatcccaaa cagcagcacc gttagctttt acctcaacac accacaattc 19380

aattctacat cttggtgtgt tgataatcaa ttctcgcgat ccgtctttaa atgcatctgc 19440

tacgccttcg ccgtttgttg ttatttttat ggatctagct tttgatgctg agccattact 19500

atttacaacg aatacagctt ctcccgcttt acctttttgaa agacgtattt gaactgcgcc 19560

ttctgaacaa tcagcatcta tgcatgaccc cattggaact gtccctgcag agttagcatc 19620

tccaaatttt atcttttggt aatagcttgt tgcatgaatt ttttggttca atgctccgcc 19680

gccagctgca aataatcgtt ggtcggcgaa ggcgttgtaa atggcgtcga agttatcatt 19740

aattttcaca ccgccatcat acagaatgtc gccggtagaa gcattaccaa tctcaccgac 19800

gtcaattatt tttttaccct tatctgtata cataggttaa cctcatatca aagtatagtc 19860

ttatttatat aaaatgggga gccaaaggct ccccataatt aaaactcgaa aattaagttt 19920

aattcttccg tttggtccat tgaacgaata ataggttgcc gattttccat gtaaatcatt 19980

tcacctgact gtctttcaag accagaagca ctataccagc ctttttcagc cttaacatta 20040

ggtgaatttg gcattggctt aacttcaagc ggattagtta taattgacag ctgtctaaat 20100

ccagtatttc ccggaagact gaactccgga aaataaaccg catcaagata cgctttaaac 20160

ctgatagtat tgcatttcat gcgataaatc aaattaaagt cgttttgttg ccaagttaag 20220

ttgttttgaa atccccaacg ggctggagat tcttcaatct cttctggcca aggaactacg 20280

atatattcat ttgtacatct gttaattgat acgtcggctg gaatttcata tagatattcc 20340

caaagatatc catcgcccaa atcgacggta ccatttgcat caccacgacc tcgaggagct 20400

gaaccagaaa tagtggatgg tgtccattta cccccaagct taatacattc ttctttgctt 20460

gtaagattgc caattgaaca cattccatcc tttggaacat caatacatct atataccatc 20520

catccaaatc cagcatcagt tctgttatat ggcgcagagt tagcaacaac gatatcgcca 20580

attagaaatg tgcgtgggtt aggatatctt gtatctcccc agtctcttct tggaacaaca 20640

cagtcaagca ttgatgattc aattttgacc gcgcccatca tatttgtcca aacatcaact 20700

accccatctc cattatcagc gggatatgga ggtgcaaatc cgggttcaga ttcgttatct 20760

gaccacggag tgcttttgcc aaatgaaaca tacagtgtgt tttggtccgt tcccggacca 20820

atcgatttat aaaatgtgta catcttttca gttctaaact tagatgtaat gatagcacga 20880

taaatcgtgc tacgcgttga acttgctctt gttgaattac tcatcaattt ttacctgtgt 20940

cggattttca ggatcgcgag gattacctgc atcgtcttta agacgttggt taactaaatc 21000

gcgataatta gcaaacgtta ctgctgattg gtcaaacgta ggacttaacg gtttacgtcg 21060

ttgtccaggg ttttgtccag cgataatgct gttattattt tcttgattgt agttagcagg 21120

taacgggaaa ggttcaccag cttgagcacg tgaagaatac ctaggctcat tggttattgg 21180

gtctctttct attgtatcat ctgaagcgat aatagcaact ctatcaggat aaactgatgg 21240

cagtcctgca tcccatttat agttcttgag tttatttatg atagtctcaa catgcttcat 21300

atttaagcca ctattgataa acattgtcag caatgttata ccaatgaaac cgaaacctac 21360

cggatgaaca aaccttaata catcgtcgcg gaaacgagaa gtaggaagct gagacttaat 21420

tttcataaca tagtaagaac ggctgcggtt tatataatca atgttattac tcagcatatc 21480

ctttccacga acaccttgaa ctataatacc ctcaaagtcc gtacgctctg atttaatttc 21540

ctggccttca atgaaccgtc ctgataagtt atgaatagta atacgccata acagacgacc 21600

atcccggtat tctctctcga tataagtcac attactacga ccggaagcag tataaatcgt 21660

acgaccaact aaatcgtcag aaatatttgt actttcaaca ataatgtcat attcggtagt 21720

gttctttgac tcaatatcga tttcaacatc ttcattataa agaagtttaa acaagaattt 21780

gtatgagtct tcaattcctt tggtagcata gaaatcattc ttacgggctt caaagaaacg 21840

gacaacagca tcgcgagcgt ctttactcag ataaatattg cgtttataaa cttctgacca 21900

caggtattcc catgcatttt cttcacgagg atatttgttc ttaacaagat taacgagact 21960

gttgtaatgc gttccatttc cgtctgaaag gaattggaga tagtacttac aaaattgctc 22020

aaaattacta tcttgtagca agtaactatc cggcatcatt ttagtaagat acggacgcaa 22080

atctgggtca cgtaagcctg gagtatgttc aggtgtccag tcttcttccc gtgtttggtt 22140

ctgcagaaac gctttaaaca ttacatcagt cggtttccag ttaagcgtta cctggtcacg 22200

aacacgataa tcaaatgcgt aatagcctat cagttttccg tctggttcgt gaaacatgat 22260

gccagaagca tactgcaaaa atccattaaa tgaaactgga gggcaataaa acgttgcgtc 22320

acctttatcc cacacttccg aaagaacacg ctcggtagtt ccctgcgccg ctgcatctac 22380

tctttttga taaagaatat cattataaat gacaactgca tggtcagctg tacttatcca 22440

gcatctgtta ccttcacgag ccatccagac aaaccaaggc tcagcataaa acctcatcgg 22500

tccaggaaca aatgtttccc atcttgaaaa ttcatctgct ctgaaactca tcatgtgata 22560

atgcttatca gagtgatact gaattggatt aacattttta actgcagtag aaattagttc 22620

tggatatttc gtctcaagtt caatatcctg ggtgtactct gttgtcttaa aattagctga 22680

tgaaaagaat atttcctttc cgtcagttga catagacgtc cataaatgct ctatacgacg 22740

tttttcttca tctgtattac cgaatacacg tttccatgta tttgtgtctt cttgataaac 22800

atagacgcct ttagtagcag aatccacaac attccgcggg tctgttgggt ctaatcctaa 22860

ggttttaact tctccggtaa taagagcgaa gattttgcct ccgacagaat ccattttaaa 22920

gcatacagat ttaggattgc ctgttatatg agatgcttct ttttcgaaca ctttttcacc 22980

aaatgtaggg cttaaagggt cagtgtctat tggagcatct tttaatttaa ctctgcgtac 23040

tgtatccttt gcaactacat ataagtggtc atcattgcat gtaaaggctt ctgcatattt 23100

ggtaacatca gcaggtagtg atgcatatgt accaaataac tctacttcaa atcccagttt 23160

taactggtct cccaatttag caaatgtaac ttcgttatcg ctaaatttaa cctcatttga 23220

tgaccagcgt acgtcagatg attttcttcc gtaaaagatt ttatcatagc ctaaaacata 23280

tgatgtggta cttgattgat aaattaccac tctagaaacc ggatttccta cacggtcatt 23340

aaataactga acgtattgcc agttctgtcc tttatcgttt gatactttaa ccatatgttg 23400

gaatctttca aacagataca aaattccgtc tatttctcct agcatggttc tatttttatc 23460

aacacagact gcttcaatag gtccctgaat ttcatgatat ccagattcgc ctactacgaa 23520

attttcaata gctgacaaat gagaatattc aggactaaat tgaaaagact cagtcatcaa 23580

agatgccatc atggcagatg tgttgaagtt aacatacgac atgttattta aagaaaactt 23640

ctgcttaatg aattctttca ctaaactgaa ttcttgcata tgctcaaacg tgtacgcgtt 23700

ttcttcaaaa gtttggaact cttctgtttc aacccattca gacggttcaa atcctgctga 23760

cgtagtttga acacgcattt tataataggt aagcggttca atacgatttt gttcgaacca 23820

atcattatcc gcggtataac ccagtgaaga ccaactcaaa ttatcagcgg ggataatttc 23880

ccccgctctg tttcgagttt cggccagttc tacaaaatag tagaagtttg caccaacgtc 23940

atcccaacga atattgacct gattcgcaga tagcttatga attcgtaagc tggtgacgaa 24000

cggtgcaatt gtcattgagt aataggctcc aatttaatag ttgtgtattg aggacgaagg 24060

tcattctcaa atacgataag tgttccatcg cgggcgaaga cgatatcctg ggtaggagta 24120

gaataaagct caatactttg gtcttcaaac tgaagaggat cggctccaat ggctccaaga 24180

ctccagtaaa tgttatcacc ataataatct acttcaccga ttttatacca gcgagttctt 24240

tcgccgatgg tagttctatc aaaatcgttt tcagtatatg gctggatatg agtattctct 24300

ttaatatcac ctggtttaaa tggtccaata accatatttc ctttgccatt tttatctggg 24360

tcagttccaa cgatattaac tgaatacggt tcagcagttg gggtaacagt aaagaccaaa 24420

tcaccagaac gtaacgtccg cggagtaata gtattatagt atttaatacc tgcgctagga 24480

agagtgaaat agttgacaat ttcacgaacc atctgaatat ccacagaaga accgatgatt 24540

gagtggtcag tgtcatcaat gtaagtcaac aacttagatt tactgaaatt tttgttgaac 24600

atttcaactt catcaacgta atatctatta atcgagtcta taatttttga ctgtaaccac 24660

tgctctgatt cttgcaactt attcaatgca taagaagctt taatattatg acgaatgaat 24720

aagtaatctg ggctcattac cgaaggggta atcggagcaa gacagaaagg ttttagataa 24780

tcctgaatgt cttcccgttg aaccgcagtt aactgcaacc cagattttgg tttgattgcg 24840

ataaatgcat atccgggttt gtcctgatca gtaaagcatt gtactgcttg tacgatagaa 24900

ccaaagcgtg aactaacgaa tgattcatag tcagttttag acacgcatcg catttgagat 24960

tcgcgcttaa tctgtgcgag ctcacgaata cgctcgatgt cttcaggttc accaccgcca 25020

tcagcgccaa cataatcagg agaatctgac cagttttcaa tgattctatt tactacgata 25080

tattgcagag tatccgcata actaaattca gtcgcgccat tagcagcttc accgtcagta 25140

cgaatatatt caataacgac ttgcgcaccc ttagtaggct tcaatccacc gatgaagttg 25200

ctttcaagaa ctcctcctgc cacagatgct tctgccacac cctcaccaaa gaagaattct 25260

gtatttccat cgacagtttc acgcatataa taaattgttg aaatagacga agcatgaacc 25320

attgatcggt ctgtccagtt agtccattca gcgccatcca cccacagctt aacttgcttg 25380

cggtcaattg attgatcgcg aataacaata ggtttcttcg ggtcatatga caactgagta 25440

cgaataatac gtccctgcgc caaattgaca ataggccaat atttttggtc attatcacga 25500

atagccacaa cgttttcagt aacaacgaag ttatatgggt tggctttatc ggattttgag 25560

tatgctaaaa atttagttcc tcgtggaatt acaactctca acgtgctgct cgggttcatg 25620

tgagttacct caagcataat agatgcagta gccgctgatt tggaacttgg caaatacccg 25680

ttttgctgag ctgcttgaac aacggaactt ctcaagttag ctgttccaat aaagctttcg 25740

tataaagcag tattactaaa ttgctgtatg taaagcgtgt tatatgctaa taagtctaat 25800

agcacgttta aacgcgaacc agcaaaatca aagtcctgaa actcttttg accgctaagc 25860

cagttaataa gctgattttt aatttcgtcg aatgttgctc cagtaaatgc gtctgggata 25920

gcgtttgcag tacgcgttaa ctgataattt aagggttctt taatagccat tagtgtatga 25980

ataccttga acttgattgc gcgacagtgt cgccacaaga aattggatcg gccatttgaa 26040

cagctttttt gcctgttaca aataccttgg atgtgcgagg ttgaacaact cctccatgcg 26100

tatcatgagg gtcaaccgtc ttggtgtgtg gggtaattga gtcgccatca actaataccg 26160

ctattccacc agtgaatact ttactttgtg tagcatttac ttctgtcgga ggatacgcac 26220

tatgcccggc agttaagcat ttattaaatg atagtccagc catttaattc cccgcatata 26280

cataagcacg aagttggtcg ccccatctac tccagttgcc tttaacggtt tgagagtaaa 26340

tcttttgctt tttatgttct gttatgattg gagcgctaga acctccggat gaacctccag 26400

acgattcttc tgtcactgta tatattatct caactgtata ggtaaatgtc ttctctagtg 26460

ttctgggggc tttccataga tacaaatcag cagttttggg attaggtaaa tcctcccacg 26520

ctgaagcgga ctttagctca tcaccttcac ggtatttaag cacatcgttt ccaaaagtaa 26580

aaactgagtt ataattacct ttataatgag tttcagacac agagatatca gatactggtt 26640

gatagtcgat aatatttatt gattttaatg tttcgttagt agataattga gcagtaaagt 26700

actgctcaac atattcacct tctattactt cacgtaacgt tgtattaata ggaagtatat 26760

cagccatgat taacctacat caattcgtga accatcaaca gtgtattgac cttgggcgat 26820

tgagctcata gaagccattg tttcagtcca agccccacca acattccaat tcacagtacc 26880

tgctacttgc caagttaaat taccaccgac ggtcacgtcg tggttgccat ctactttagt 26940

agtggcatca ccattgactt ggatatcagc atttccttca acgactatct taatgttacc 27000

cttgacaaaa atagtaccat tgccttcaat cgttttagtt tcatttccac gtacgtaaag 27060

cgtgttatcg ccatcaattt gctgtcgacg attatacatg ttataatagg tctcgttccc 27120

tccaacgtta accttcttat caccagagat taaaatattt ccatcaccct gagtcatgtc 27180

atataaatca gctacagttt ttctggtacg acgtccatca ggagcaactt cttcatatga 27240

accggttgga tgaacaatac gatagcgttc atagccaggc gtatcatcaa attcttggat 27300

atggcctgat tctgtttcca tcgtatgtac atatggatat tgaccattat atgaagactc 27360

aggttctttg aaaagaattc ttgaatcctc tggggtccac gggtcttcag gattaccacc 27420

agacttcggt tctacataag ccgcagacag gttttttcct tctggctttg gagcaggaac 27480

tccatatgat tccatattac ctgttagaat aatcatggaa acacgagaag cacgaccttt 27540

tgtctggtta aaccacacgg agtttcttgc ttcagtatag gctgttttcc aatcaccaat 27600

gagcatggca tcaagcattt taccaaattt tgctaatcca cctacaccca tttgaaaact 27660

catattttct aaagccattt gccttgattt gttgacttta gcatataccg gtcctacgcg 27720

tgaattcgtt ttaatatcag aaagcatttt atcacgatct ttcttaaata gtgcaactgc 27780

ttcgtccatt gtaatgatac cgggatttcc tgtaacagta cgaccaacct gattagataa 27840

agttttatta atgacagaca tatcacgtac tttttgtgcc atgataaggt gtccaatacc 27900

tacagtagga tatccttctg tatcccaata gactttcaat ctaagacctt catccctatt 27960

aagcatatct gttattgtaa ttgcaggatt tgggtcttca ggaatatcgc ttaggtcagc 28020

atcgtcagga ttaatgccaa tatccaagtt tctatcttgg atgatgtttg gtatagcact 28080

atacccagtt tcatcgcctt gaactagtgg gttggtatct gacccaacct gtctaggata 28140

ttgacctgtg gggtcagaaa aaccttccgt gtagtttggc ttagtttttc tgtgcgcaga 28200

atatgttcct attactaatc ctgctgtttt gaattcatca agccataagc caaataccga 28260

tgttccttcc accattccag ttatagacga gccaactccg gaaattccag ctgagtttgt 28320

aggctgaatc actgacatcc aaggaaggtc ttcggtagga agaccggtta tagctccttg 28380

taccttttca aacggatgaa gcccgtaaac acgtactcgc actcttcctt gctttaacgg 28440

gtcttgtctg tcttcaacaa caccagtaaa ccattttaat gaatcgttca tttcaatcat 28500

aaaacttctc cgatggtagt ctgggatttg tatcggcctg attcgtattc gctgtcaggt 28560

gctttttcca tttctcgtat aatatcagaa agaaatgcct caatatcact aggattgata 28620

atgtttattt ggcgcagttt ttcattttct atgatagagt cttcataaat gtcaacacca 28680

gccaaagcac cagtatattg aggatactga tgattaaagt ccccttttatc ataccaaaca 28740

cctgaatttt caggatattg ctcgagattg taatagcgat tgccatacgc atccacgtga 28800

tagagtattt ggtctccacc tacatctgca tatttttgct gcgcaaattg atagcatgca 28860

tcttgggttt taatccaatc tctgaatggg tcatatacat tattacacat taaaagaatc 28920

cagtacagct gactatttcc ataaagaata tatgctaatt cttctggtct aggagctcca 28980

cttatgtaat atgtttgtaa aagatagttt tctgccacag tgtcaaaata tttgcgataa 29040

ttacgaaata tgtcagcggt tgggatagct tttgccttag caccttttac ggtctttgca 29100

gaataatcta tcggactaaa aaatgagaag agcatagttt atcctcttat aaatattaat 29160

aacagtattt ataaggaggc cactatggca tattccggca aattcatgcc gcagaatctc 29220

cacaaatata aaggcgactt cagaaagatt acttatcgtt ctacgtggga acagtacatg 29280

atgagatggc ttgacaatca tccagatgta gttcaatgga acagcgaaga ggtagtcatt 29340

ccatacttta gtaatgcaga tggaaagaaa cgccggtatt tcatggattt ctgggctaag 29400

ttttctaatg gtcaacagtt ctttttgaa gttaagccga agaaagaaac tagacctccg 29460

gtcaaaccca caaagttgac gacatcagcg aagaaacggt acattgatga aatttacaca 29520

tggtctgtaa acgttgataa gtggaaagca gctcaagcta ctgccagtaa aatgggtata 29580

gaatttaggt taattaccga agattcactt aaaaaattag gatggaaagg ctgatggcta 29640

tatttgaatt tatcactgaa gctgcagaat cgcctaaagc taaatcccgt agtgaaaatc 29700

aatgggtagc attaggagtt gaatactctg ctgctcgtaa aaaaggcatg acatcaaaat 29760

catttgctga aagtaaagga ataaatcctg ctacgttcag taaagctatg gctcgtcatg 29820

catcaagaat taaaacggca attaaagtag cagaaattga gaaaaaacct gctaacaaaa 29880

tgaccaaaca agagcgtgct cttgtgatgg taaattcatt tcgaagctct atcaaagata 29940

aaattcgtaa tgaaggcgca gcagtaaaca ataaatctgc taaatggttt gcagaaacta 30000

taaagaaaaa tatacgtggt cattctgtaa ccaagcctca acctggaaag ctatatgctt 30060

acatgtatga cgctaagcac aaagacactc ttccattctg ggataaattt cctttgatag 30120

tttatcttgg tcttggaaag caaggtacaa ccacattgat gtatgggtta aaccttcact 30180

acattccgcc aaaggctcgt cagcagtttt tagaagaact tctgaaacag tatgctaata 30240

cgccagtgat atctaataag accagattaa agataaactg gagccaggtt aaaggatttg 30300

ctggcgctga caaaatgatt aaagcatata ttcctggtaa tataaagggt gctttaattg 30360

agataaaacc ggctgattgg gcgaatgtag tcatgttacc actgcagcag ttcatgtcga 30420

aaggcaaacg ctactctgct acttctgtat ggaaatcata atgtctactg gactgtttaa 30480

tcaaactaac acaactaact ttatattaga ggtccctgac gggggcctca cccaagcgtt 30540

taaagctaat cttcaaacag ctgtagttcc tggaattcat attcctgcta ctgatactgt 30600

gggttcgccg caaggcatgc accgtgctaa attgcctggg tctacctttg aatttgacgc 30660

tgttcctgtt agatttttag tagacgaaaa ccttgattca tgggtacaaa tgtacaaatg 30720

gatgttaagc tgtcaaaact acattgaccg agacaagtct ggatggaata acggcggtga 30780

aggatttcct ggtgcagttt taatgcatgt tcttgataac gataaacatg atatagtatt 30840

aactgtccgc tacatcggag gttgggtgag tgatttatct gaaattgagt attctttaac 30900

cgaagaatcc gacccagcaa tggtatgtgt agcaactttg cagtacaaat acattgaagt 30960

tgaaaaagat ggtataataa ttactggtag accttctgtc aatgatactc gcgaatccca 31020

gtatcaacag aaagttatgg gaatgcatcc ttctatgagg taataatttg aagcttttat 31080

ttttgattgg taaaaaacgt agtggcaaag atacaactgc tgactacatt atggataact 31140

ataacgcaac aaagcatcag ttagcaggtc caattaaaga tgctttggct gatgcaatgc 31200

ttactgagtg gtatcgcgat acgtctcgtg agtttccgcg cattactcgg tctatgattg 31260

agggcattga ttacgatcgc gaacaagatt taaatctgtc tactaaagac gtgattcgta 31320

tcatggcgaa tgcgattgaa tatgttcatc atgatttgcc tttacctggc gtggtttatg 31380

ataacaaacg taaaatactt gacggcgata cgatggaagt catccgtaaa gttgtaataa 31440

ataaacctgt tgagccatgg tcaattcgtc gtctcatgca gacccttggg actgacattg 31500

tctgtgataa gctcgatcgc atgtattggg taaaacgatt cactttggtt atggctgata 31560

cttttggtga ttatgattat ttcattgtcc cagatactcg tcaagaccat gaacttgatg 31620

tagccagggc gatgggtgct acagttattc atgtagttcg tcctgagcaa gaaggttcta 31680

aaaaagatac tcacgtcaca gagcgtggac ttccgattcg cgaaggcgat atcgtaataa 31740

ctaacgacgg ttctctagaa gaactttatt caaaaatcaa cactatatta ggaattcaaa 31800

atgactactg aacaactgca agcccaagtc gatactctga aagttcgtgt atttgacctg 31860

tctgaaacta tccaaggcct ttctgctctg cgtgcacaat atgaagaagt actgcagaag 31920

ctgattgctg tatccggcgt tgaaattggc gaagacggcc aggttaaact tgatgacctg 31980

gttgcaaaaa tcgaagcaca gttcgcagaa gaaactactg aagaatctga gtgatgaaat 32040

tcagtgattt tagcactggc ttatatgtag ctgctaaatt ctctgagaaa actcttgatg 32100

ctattgagga ccttcagcgt gaattgaagg tccctaatcc tgtacctcgt cataagattc 32160

atacgacgat atgctattca agagttcatg ttccatacgt ttgtgcttca ggaagttttg 32220

aagttgctac atcaggtaaa cttgaagtat gggacacaca agacggacgt acgctagttc 32280

ttaagctaga ttcagaatac ttaaaattcc gtcaccaata tgcaagagct ttgggagcaa 32340

ctcatgattt cccagattac tcaccgcaca ttactctcag ctacaatgta ggtccagctc 32400

acttcgaggg tgaagttcaa gtacctgtag tgcttgatag agagtaccaa gagccactaa 32460

aactgaactg gtcagaggac cttaaatgaa gtcataccaa gaatttttaa tggaaactga 32520

ggctcttttg gagtctactc tgccagatta catgattgta aaaagcttta atgtaaaaaa 32580

tggctacgta attaaatttc ctatcgctag tgtcaagcct ggtgctgaca tgtcaaatga 32640

tgctggcatt agtgttaaag ttaatgtaca gtttattaat tacaactctg ctaaaaagtc 32700

gtatgatgct aaaatgactt tttccggtgg cgaaaaggta gttaaaaaca ttaagttaga 32760

ttacgatgaa tccgcagaaa gtgtcaagaa acgctttggt gataaactgg taaaatctat 32820

catggttcat ccaactttca aacgcgattt cacggaactt tataaataaa aagttgttta 32880

ctttcctcga gggctatgat actatagccc tatcaaaaca aatgaggata aaacatgaaa 32940

cgctgtgaac tgataagaaa tgttgcttct gctatttgcc ttactgctgt gggcactagc 33000

attttcggtg ccatctttat gggtgcaaaa gaaataatgg ttgtgttagt agctgcattt 33060

cttatgggtt caatttcatt tattatggat aaaatttctc atgaaaaaga ttaaacaatg 33120

gtttgttaag acctatgatt taggccgtga agaagtaact aagtatgatt atgttacttt 33180

gggtgtagga ctaggtgcac tactggcagc attgcattca tcattacttg ccattgcagt 33240

gcttcttatt ttggctcact acagctggaa acgtaagtaa tgtatgcact tttaacttgg 33300

tctaattatt atcctgctcc tggctctgac caaatcagag gtgtttactc tacagtagaa 33360

gaatgctatg aagccctcca gggaacgtat caggactatt ttgagatact gaactctcgg 33420

tttgagaccg ttgctaaagg ttcaactgaa gcatacaaag attaattgtg aggaaattgt 33480

gatgaatatc agagctgcat ttaatacttt ctaccaagag aattataagc ttctttccca 33540

tgaatactat gatgcacaag gcgttccaat tcctagtgat ttagttacgc ctaagcatgt 33600

caaaaccgat tctcttgaca atgaaattca acctggtgat ttggtatcat actattgtgg 33660

cgggtcactt tctgcagcaa gcgttggtat tttgctagga tttacgccta aaggttatcg 33720

tgtggttcct ttccatacaa gtccaattcc tgagcaccgg gtattgctct ctcatatgga 33780

ttcaccgcat agggtattcc tggttaaatc aaagagctca ccgattgtgt aatatgcttt 33840

aggttttctt tgttattatt aatctatcaa ctgctctgat taatttcagg gcagtataaa 33900

taaaattacc caatggggag ttagaccgta ggggtagcgg gacagactgt aaatctgttg 33960

ctcaaaaggc tcgagtggtt cgactccatt actccccacc aaatttaagg gatactagct 34020

cagttggtta gagcaccgga cttttaatcc gggtgtacga agttcgaatc ttcggtgtcc 34080

caccaaattc gggtcgttgg ctgagagggt aagcgacgga ctgttaatcc gtgtcagaaa 34140

tgactaggca ggttcgatac ctgcacggcc cgccaaatga agaagtcaga agacgttctg 34200

ataaatcgtc ggcatagaat tccctggcat ggcgtttgta ttaaggagta tgatttcatc 34260

ctgcttaata cttgttcatg ttataatttc ttacggcgtt gaaagttcgc tttcagggat 34320

acatcttaga acagagtgct aaacaagatt catctggtac caaggtgatg agagtcctgt 34380

tccccttgc ttcggcatag tgccagagta tctctgaaag cgaattatag tgctgtagtc 34440

gagatggtta agacactccc ctgtcacggg agagatcgcg ggttcgacac ccgtcagcac 34500

tgccaaatac gagagcaaca tgaaagatta tgaaaagtac cgcatgcaaa aagtgcatgc 34560

caaataaaga ggtattgaat ttaaattgac atttgatgaa tggttatcat ggtggaaagc 34620

tactggcaaa tatcatttgc ggggtagagc atcagataac tattgcatgt gtcgtaaagg 34680

agatgttgga ccatattctt tagataacat ctattgcgca actaatgcgc aaaacgctaa 34740

agacgctggc gctaacggaa gaataatatc tactggtttt actggacata accattctga 34800

tgaaacaaaa ataaaaatat cagaaaacca tgcacacaag ttaaatgcag acgaaatttc 34860

tttgcgaata gacctgtata attctataga ttttacacag cgtggtgcac tagtaaaatt 34920

tgcaaataaa cttggaatta gtcatactca agctagaaag ttcataaata agtttataaa 34980

gtaacgtggc agttcttgaa gatgagtttg agtcctgtaa gataatgccg aggacgaagc 35040

ggtttgttcc cacggaataa gctctatatt cgtaagatta tatctttagc gtgttctaca 35100

tcaagctact tgttagtact tcaagaaccc ggataaatgc ggagtaactt cagttggtag 35160

aatgttgggc tcatatcccg acacgcgcag gttcgagtcc tgcctccgcc tccaaacaat 35220

tgaatcatag ccaagttggt aaggcagtag gttttgatcc tacgatccct ggttcgagtc 35280

caggtggttc agccaaatta atattcattc aacgcgatgt gtaggcagaa gtcatgaacc 35340

tgctttagct accgtatgaa gtcctcatga tggatggagt gaatattgat gtggtcgtag 35400

ttcagttggt agaacccgag gttgtgatcc tcgatgtcac ggattcgaat tccgtcggcc 35460

accccaacaa tgaaggaatg gtggaaaaat acacggcccg caaaacgctg tggctgtcgc 35520

taagcgaatt gtgtctataa tggcacttcc ttcaccaatt aatggagagt agcgctagtg 35580

gtagcaaacc ggacttgaaa tccgggccac cggaaacggt gagggttcaa ctcctttact 35640

ctccgccaaa tttatgaaag ttaaacgctg cccatagcag tggtacatca acaattagat 35700

gattagcttt ccatgggagt atagctcatt tggtagagct ctcgaccgat aatcgagcgg 35760

tgactggttc gagtccagtt actcccacca aataacaggt tcttagtata atggctatta 35820

tgctgggctc caaacccagt gatgagggtt cgattccttc agggcctgcc aaatttgcat 35880

ccatcgtata gcggatatta tgtctggctt ccacccagaa gatgggagtt cgattctccc 35940

tggatgctcc aaattactcc gtatagctca gcctggtaga gcgctccatt tgggatggag 36000

aggtcgaatg ttcgagtcat tctatggaga ccaaattaac ggtatgacac aatacaagat 36060

ggtgtaagct gagtagcggg attgcagtct cgttcagata tgctatcgag tatgggtgat 36120

atattaaaca cacggattct gcaaagtcca tgtgactcgg ttcgagaccg ggcataccgt 36180

ccaatcactt gccattgaga attatattat gaaatattac ggcttcaaaa catcccattt 36240

cgggaaagca tatcgtacag aaaacattga tagacgtcga gcatattacg aatcactgca 36300

taaagcagga cgttctcgtg cacgacaaga aggccaaaaa caagcgaagg aaatagaatg 36360

aatattttta ttggtgttgc aaataacgta aatgctatta cggtgaaatt acaatggaat 36420

cgtccaacta attttgcttt aggattatgt aaatctgaac gtgatttaat gcttcatgct 36480

gattttgcat acacttttga tgaacgcaaa ggtatgtggg tatggattaa atgcagatac 36540

gaagcattaa tcaaatatga gtacttcagt gagcgtgata ttcaagaagt tattgcttat 36600

cattctggct gtaaagtaag taaactgcgt caagttattc cgtttactaa tgcttcaaat 36660

gtagaagagc taattactga ttttaaacga atttatcagg cgaaatatga tgaaagattc 36720

taaaggtcga gacgtacaag ttggtgatat cgttttctat ggagaacgta catacaataa 36780

aggcggtcgt ggttctatgc gctgtggtcg tattactgat attgcttcag gattggctaa 36840

agtagataac gactacgttg caatgcgaag caaatcattc gttaaggttt ctcctatgtt 36900

cgcaacaatg tgggaaaacg gaacgatttt cgagatttaa tgctacaaga ataacctgtt 36960

attattacta catcaaaaca aacaaggaaa aagaatgaaa cgtatcgcac tgattgttga 37020

ccaagaagct atgttcgctg ctaccggtaa atttcatccg gtgagtaaat ttgttgctcg 37080

cagcgagaaa atcgttggtc tggtagaaac tgtcgcaggt gatgtaattg tttctattaa 37140

aacgtctgaa atttctccag tagttaaagt agcagttgaa aatgacttct gggaagtagc 37200

tgattttatg tgtgagtaat tctgcctagc aggtggataa gcccgacaag gcgccctctt 37260

cggagggctt ttataaaagt cataagattt ctataaaggc cctgtagctc aattggtaga 37320

gcgttcccct cataagggat tggttgcatg ttcgagtctt tgccagggtc accaaattaa 37380

tgaggaaaat attatgatgc gattagttaa agtagttgta gaagaatctg aatacatggg 37440

cgatagccga atgattgaag aattcgttac tgttgaggca gattctgaat ctgaaatcgt 37500

tgataaagtt tatcgtcatt ttgataatat gtctgattcg tatggcacaa tgtatagcat 37560

ttatcgttta gatgtaatag tacatatcaa ctgaggaaat tgaaatgcat attagatttg 37620

gacaagttat tcctaaaggc ttagcaatgg caattaccac ttgggaaaac gatgctgatc 37680

ggtattctac ccaaatggtt tatggcttag aaaaagaaga gattaatcaa gtaattcacg 37740

ttcttgaatg gttctcttct aatggtcggc gtggtgaata ccttggaaat aatgattaca 37800

accatgaagc aattcttgaa aagcttcata ctgaacagaa gtatgtaact cctgaatttt 37860

ccaagaaatt ctttggcgtt gatgttcctg catatgattg cacagacgaa gagtttgatg 37920

cttatttaga taaccactat tcttgttcaa atgaagttat gtatgctatt caggcttggt 37980

tgggtaatcc aattgaatat gattatgatt tcatgcgagt atttgagaaa gtagaaatct 38040

ttgacattaa agaagaaatt cgtattcctg atgctccagt tgcattccat gttggaatta 38100

cgtataaaca aaaagaaagt ccattaaaag ttgattggtt gaaatacgtg aaggaaaagt 38160

aatggatatt ggttcaggca gttcatatcc atcatgtgct ttgagcaact ttgctcctca 38220

taaatttatc tatgatggcg tagaatgtgc ctcaatggag ggattcttgc agtccctcaa 38280

attttcttcg cctgaaatgc aagcacatgt atgtacacta gtcggaaagt ccgctaaatt 38340

taaaggtaag aagaaacgtt ggtggccaac tcaaacactt tattggaaag gcgtgccaat 38400

ccatcgtgct tcagaagcgt atcagaattt actgacagga gcatacgatg cacttagtaa 38460

aaatgaagga ttcagaaaag ctttggctgc tacccggaat gctacgctca ctcacagtat 38520

gggtaaaaat aaaatttctg aaacgatttt gactgaacgc gaattctgta atcaacttta 38580

tcgtttgaga aatgctataa ataatcagta atataattat cttgttcagt gttgaaatcg 38640

gtagacatgg tgacgggcac cttttgagct cgcatattgc atcatatgct ggcgatggtg 38700

gtaaatcgcc gacggaatca gtcgtgcagg ttcgagtcct gcctgaacaa atatttgcgt 38760

cgatgttgga attggtagac aaaggagact taaaatctcc cgggattaaa cccgtacgag 38820

ttcgagtctc gttcgacgca ccaaagccct tatagtgtaa tggatagcac acgatcgttc 38880

taaggtcggt agtccgggtt cgagtcctgg tgggggtacc acgccgattt agctcagttg 38940

gtagagcgct tcacttgtaa tgaagatgcc gcgggttcga ctcctgcaat cggcaccaaa 39000

ttcgaaggga aacttgcgta taccctcgtt gagtcgtcag atagaagaga atggttcgtc 39060

cattgccgca agtcggttgt tccctgtcgc aagcataacc tcctgacgct atacttcttt 39120

ggatgagact gatgcctccg agtccaaaga aatgaatttc gcaggtcatc tgccagtggg 39180

tgatgctgtc gattattaga gccctgtctt cggacggggc tttttagtat aaatagtaat 39240

ttaatcggca ctaaggattt ttttgcaatg aaatttaaag atttttttaac cgaagaagag 39300

ctttttgaag cagctcctgg ccgcatgact aaatcgaaat ggcgtgacgc tctggtattg 39360

gttccacgtg gtgaacgcca tgattttagc aaatttgcgg cttctgtgga aaagatttat 39420

ggtattggga ttagcgatcc taaagactat gctaaggtag cagctgcctt tgaaagttta 39480

ggcggaaagg ttactacacc tgcacgtgga gcttctccgg cacaagcacc ggccgcaaaa 39540

ccggctccgg ttaaagcgaa acctaaaaat attcctggcc ttaaaattag tggagaccat 39600

ggagacatca ttggttcagg tgaactgttt aaagctattg ataaagctct tccactagta 39660

agagataatg gtcctcttta taaagcagtt caattctatt tcgataatct gtggaagtat 39720

cgtgaatccc aaggtgctaa accttctgca cgtgaaactc agcatatcgg tgaagtgaaa 39780

acacttttag ctaaactgaa tcatcacctt gttgaactca gtcgtcagac agaattatcg 39840

tacaatgtat aataaaatgt aatcctacag ccctagaatt catctagggc atttttgtat 39900

cctcggctgt ataaatccat tctatcttcc agaaagttcc tccagatgcc ctaaaaattt 39960

ttgcacaaag ttgtttactt cctctatcaa ctcggttact atagctccat caaaacaaaa 40020

cagagtaacg gagaataaaa tgtctaaatt caactttatc caaattgaac gtggttataa 40080

caattacggt actcctgatc gttatcgcgc gatttggatt aaaggtgaac atgaacacgc 40140

agtgttcaat gtagcagaaa ctcgtgaact taaagatttg attaagcatg ttcgtaaaga 40200

ttggcctgct gttgaagagt actacgttcg agtttaccat gaagaagctc ctaccgaaac 40260

tgttcaaatt aaattcgcaa aaactgctag tgctttaacc aaacgaattg aagctgtaat 40320

taactgctaa taattttggg gagttataat gaactcccca cctactgagg aaataaaatg 40380

tctattctga aaaaacttgt tgaattcatc cgttctaaat tcggtacctt tgttgcacag 40440

aacacttctg ttgaagacca gtatacgatg gcagcaaacc gtattattga tgaaatcact 40500

aaactgcgta ccacgcatgt taaatcagta aatgaagaaa agcgtctgct gaaacttgct 40560

gatgaaaaag accaagcggg tgcttctaaa gagcgtgaaa ttcgtcgctt gatggcagaa 40620

ggtatgaatg tagaaaccca tgctaaactg ggtcttctgt atcgtcgtac tgctaaggct 40680

ttacgtgata aagctgccga atataaagaa atgcgggccc aaattgaaga aaccgtagtt 40740

aagcttgatg accaacgtct tgatttggca gtgaaactcg aatacatccg tgagacccgt 40800

aatgcttctg ctctgggtat tacctctgct gacgacgtga ttgaaatcgc agaactcgct 40860

aaagtagatg tacaagacat catgatgaaa gttgaaacct tcagcggtac tcagcctggt 40920

attgaaacca ccactgctga tgtccaggaa tatctggaaa gtctgaagta attttaccgg 40980

ggccttcggg ccccctaact tggataataa aatgttatat gaatgcgctg gagatattcc 41040

aatggcaaca cctcaaatta aagaattaat tgcagcagga ttcccaacag aaatcactga 41100

tattcttgga aaatttgctt atcctgatac tcggcctgaa aattggaaaa ctcgctataa 41160

cgggtataac accacagttt taccgcgggc tatcgttctt aaagactatt ccaagctgaa 41220

aaacttaatt tctaatattt cgtctatttc cgacggagtt aagcttgtgg atatttttgc 41280

acttcggtac ggaatctact cttttaacga ttctccatca aatttaaaat cagcccgtac 41340

taatgccggt gaatactcta cttctggttc aacaacgtac accatagtta ttgagattat 41400

tcataataaa aatagctatc gtcttggtat taacctagtt aaatatgtga catctcagga 41460

tgattatagc aattatttaa attactgtgt taatgaattg ccatcaaagg ttatgagtat 41520

gtttgactct aacaacatgg taggcaaaca attaatcatt gatgaattta tcaaatactg 41580

ccgtgagagg gtgcagaaat gagtaactta tatctgccaa gtgaacctcc cgtttataat 41640

tatgtctata aatttgatca gattgattat gcccttgttc ctggtattgg tgcaactgtc 41700

ggcgcaatgt gtacctttgc cgcgattgat atcatgcatt taactgatat tacaccggca 41760

gtgttattcg gaattctgct tgcatggtgg ggaactagtt tgctcatcat gggattaatt 41820

gaatgttccc gatgggttaa atggtctcgc aataattata agcgtaaagc tgaatggaaa 41880

gaacagtgca agaatttaac tcttgaatgg aatcgcaaaa agtcgtttga gtttattaaa 41940

gaggtgagaa gaaaatgaat gaatataaac ccgacggatt ttggaatcaa gatgggctcg 42000

cgccaggttt tggaattgtg acatggcttt tatattgtgc tttcgtaatt gttggaggga 42060

cattctttgg attgaacgtc tcagagttta tgattatgct tttattttta ggtgttttcg 42120

cattcagcct catgtggatg ctaattatcg cgttgattaa ttgctgtaca tttttagctt 42180

accgaatgaa atacaagaag tggaaagaaa aagaagattt caacacctgg attaggagct 42240

gcagaaaatg attaaaactt gctaccgtgg aatgattaaa agcgatgagc ctgggtattt 42300

cttcctattt ctgcttattt ggttttcatt atcagccttt gttggatttg gaacattctg 42360

ggggttctac ttcttttctc cagtatttgg cgatgcgtta tattacatag gctggatgtc 42420

aggtgttgga acttggtttg caatacttgc ccggtggttg caattcgttt cccagcggca 42480

gaggggtgta ttcgataagc ccaaagtaaa gaaagaaaaa tctaaagatg actctcgtag 42540

tgaaacttta tcctggatta aggagatgaa ataatggctg ttgcagtgca tgtaaaattt 42600

gaaaatggtg atactcgcct tctgtgttac agtgataatg aatcactgag cggtatcgag 42660

atttcactca aagaagaact gcttggtatt aatggaccta tctgtgattt ctcggtagaa 42720

ggttcggata attgtaatga tgatttggag tctatggtct atactgccat ggaagatatt 42780

cttgaagaaa gttggaacga atgccaatga aagagctcag tgcaggaatt ttattcttta 42840

ccgatgacaa acggctttta atgggtcgta tgacaaatac atatgtccag ggcagaggct 42900

ctagatggga tattccaaaa ggacatgttg agcctggtga aacaccaaaa gaagctgcta 42960

ttcgcgaatg caaggaagag actggattta ctgagtttga ccaagacctc ttatatgacc 43020

ttggacgaca tgattatgca agcaataagg atatccatct gtttggatat atgctccctg 43080

taagcccaga aatgttcaga aattgccgtt gtacagctta ccataaagat gaaaatggaa 43140

ttaattttcc tgaaatcgat gcatttgctt taattaaacc aagccagtgg aaatatgtga 43200

tgggaccaag tttatacaaa atcatgacgc aaatgtatag cacagctcag tgaggttatt 43260

atggaagaag ccgttgaatt aggcattcca cacatttata aacatgagct acgatttatt 43320

cacgatggaa aatggattag catatttcat cctagggata aaatgtcgcg tatactaatg 43380

aaatcacggt atgtcttcag tgatagtgag tatataaaat cagcatatta tatagcagaa 43440

cagctatatc cgggatttag tgaattgccc gaggacgata aaagagatta tgtgtggtgg 43500

aaagataaat ggacaccata cgagaagtgt agccttgagt tattcatagc caagtgcagg 43560

gccaaataaa tactcctata aattaatagg aggtccttat ggatattttt ggcatgttgc 43620

gtattgatga aggatacgac agcaaaattt ataaagatag cgaagggtat tggactatcg 43680

gtattggtca cttactgact aaagacccgt caaaatcttt ggctatttct aatctggaca 43740

aactggtagg tcgttctacc ggtggccaaa ttactcaggc tgaggcagaa gtaatttttg 43800

ccaaagatgt tgagaaggca attaaaggta ttgttgctaa tgctacatta agcccggtat 43860

ataatatatt agatgatgtt cgtagagctg ctctgattaa catggtattc caaatgggtg 43920

tgtctggtgt agccgggttc ccagcttcaa tgaagttatt actcgctaaa aaatgggatg 43980

ctgctgccaa ggaacttgca aattcacgtt ggtatcgtca gacacctaat cgtgctcgtc 44040

gtgtaattga aactatgcgg accggaactt gggccgctta tcaaggaaaa taaatgaaaa 44100

cctatcaaga atttttaaat gaatcccgtt tagcaacagt tggcgtaatg actgaatctg 44160

ttggaagtaa tcttctgaaa tttaaaaaag gtcagaagat gacagccacg ctagaagatg 44220

gcacagaaat tgaaatggac gttgttggat ataactacgt agtagacggc aagttatata 44280

ataagagcca tgctaagttt gattcattcg atgattttgt ctcttcggtt gaagatgaat 44340

cttctcgcaa agcagtagca tctggcgatg cacgctcttt aatggcccat ggacatatgc 44400

gtattaagtc taagcagaac aaacctggtg aagataactt tgcattagta ggttatcagt 44460

ctggtaaaac ttctaacggt taccagcgta cggttaccat gtacatgcgt aatggtaaaa 44520

ttgcattcgt aaacgatcgc ggcgctattc gttacgctaa atcaattaag taagcaattt 44580

cctaataaag ccgaacacga cctctcctca tgaacgtcga gtcctctgag tgaagtagct 44640

tttcctacct gtaataaggt cgagcgcaag tgcggtaagg ggtttacata gtgtgtcgat 44700

ggattaaaca tgtgccaagg aatggcccca tttaatttaa aacttttacc tttctggatt 44760

taaaaatgaa aacttataaa gaatttatca ctgaagcgcg agtgagtgca ggtaaattag 44820

aagccgctat aaataaaaag gcccattcat ttcatgattt gtcagataaa gaccgtaaga 44880

aacttgtaag cctttatatt gacaaagagc gtattctcgc tcttcctggc gctaatgaag 44940

gtaaacaggc caagcctttg aatgctgtcg aaaagaaaat tgataacttt gcttctaaat 45000

tcggtatgtc tatggatgac cttcagcaag cggctatcga agcagctaaa gtaattaaag 45060

gtaaataaca gtttactttc tcctagaatt gtgatagtat attcatattt acatttaaac 45120

aacattggaa taacctggac ctcatgattc tatgagggat tcccgcctac ctgtaataag 45180

gtcgagccca agtgtggcaa tgccagttac ataaggtatc ggaatggact cactccatgc 45240

gccaaggaat ggccccatta aaagagagct tatgaaatac ttaacaccaa tttatttgac 45300

cctgatgcat gctttcaaag acgctgcaga cagacgatta aataatccca actacagttt 45360

ttatgaaccg tcttgcctta tgcgagagta cggtaccctt cgtctagatg gtggaagaca 45420

aaccggaaag accgcagcct tatgccaatt cgctaccgat tggttgcttg aagatggttc 45480

ggttataatc ttatctactc gatacacaca atcatctgaa ctgatggaag gtattctacg 45540

agaatataat tcatcgcatt taattaataa attaccggct aacgagatag ctaaatcaat 45600

tgttccgatg acaatcaggg aatttctatc caatgattcc tcttataagt ttagaggaag 45660

aaagcttgga agagcattaa ttatcattga agaaccaatg aaagttcccg atatgatgaa 45720

gttctatgat atgtaccagg aagctatcag atggtctatg cctaatgata ccttaccttt 45780

atttttcgtg ataggaatgc aatgatgaca cagacagaaa ttgttgatat gattacagtg 45840

atggaaaata caggatttgc cgatatgaag caattaataa caatggttac ggctggcaac 45900

ctgcttgagt acaagcgcta caagtttctg tctggcccgt tcaaaggcgc agaattcatt 45960

tctaatgctc ctaacacgaa gtggatgaat cgctatccta attttagaat tgagtttata 46020

tctggtaagc taaaaggcgt gattagttca agcttaatca catatgacca acgcattcaa 46080

gagaaaacaa tgcaatggct gaaattgtta taaggtgtcc tccacaccta gttgagagct 46140

tctgtgaatg gttcagtaat tctggtgagc aagattttta tgaagctcac cagaatggaa 46200

cttggaatga aacaaccaaa cagtgggaag aagctacaac gtatataggc actcgcggat 46260

atggagttaa cgagcctatt gaaattgtgg aatacgataa agaaactgat gaagaagtta 46320

cttatcatga agataaaata acttatctag aagcagctgc aaagtttcat tcagacgaat 46380

ggaataaaat gagtgtaatt accgcataca tgcgtggttg gaataaagaa tctaattaag 46440

aggaaatatg aaagcatatc aaattcttga aggtgaactt aaaggcacca tttacatcga 46500

agatggtgat gacgcacgag taatcgtttc aaaagttctt aaagaagata ctattacgga 46560

tgctgaaact ttttatggct acaaggctcg tgaagtagaa attgaatacc agccaacggt 46620

aaaaattgaa ggcggtcagc acctgaacgt taacgtgctg cgtcgcgaaa ccctgctgga 46680

cgcggttgag catccggaaa aatacccgca gctgaccatt cgtgtttccg gctacgctgt 46740

acgcttcaac tccctgacgc cggaacagca gcgcgacgtt atcgcccgta ctttcacaga 46800

ggcactataa tggcaattga agatatcaaa ggatataagc cacataccga tgaaaaaatt 46860

ggtaaagtga atgctattaa agacgcggaa attcgtcttg gattaatttt caaagcgtta 46920

gaagaagaac atgttgaaaa gtacatgaat ttagatgtta gcacaatgag cgacaaagaa 46980

tttgatttag cacatgagcg tattactcaa attcgcaacg cgattcaaca cttgaaggaa 47040

gcttctatgt gggcatgtcg ttcagtgttt caaccagaag aaaaatatta aaaagtagtt 47100

tactttcctt acgggccatg atactatggc cctacaaaca aaggagaatg aactatgtca 47160

actaacccag aagtattcat ccgcagaact aaactacgtc gtaagtttga ggaagcattt 47220

cgctctttga atttatcagt tcgtgcccga gctaaagctg agggcaaaga gcctttcttc 47280

actaagtact ctgatcattt gttggaccgt gctatccaac gtgaaattga tgaagagtat 47340

gtattctctg ttctttccaa aattcctaat catcttaaag aaattaatga attcttagca 47400

atgccttggc ttccaattga cccaaaggac attgatgaaa acattgagta taagccaatg 47460

cggttagaaa ttacggatgg aaatctgtgg ctagggttta ctatggatat tccaagacca 47520

ggaaaaggac ctagtataaa gtgtcgtatg gcattcgtta atgataaacg tttgaaaggt 47580

aaaatcagca caaaagttat acacattaat tgaggtaaac atgaaaaaag cgcttatcgg 47640

tctaatggcc ttatgttcaa cggcctttgg gtctgagcca actttcagta atgttcaact 47700

tgacaacttg cattacgcat ataattttgg tgaacaatat caaaaatccg gaaaagaaaa 47760

atctccgcat aaccgatatg ataataacgg cttaggatat ataatggctg ctatatcatg 47820

gaaagaatct tcggcaggag ccaatttaaa agcaggaaag gggcatcatt cttatggggt 47880

atttcaaaat tacttgccta cggttaaagc cagagctaaa ttagagggca aaaaccttag 47940

tgattctgaa ataagaaaaa tgcttaaatc tagacagaat tccgcggaat gggcatatat 48000

tgagctttca tattggttaa atatacataa cggcaatatg cgaaaagctc ttgctagtta 48060

taatgcagga tggaatgtca aaaggggaaa ctcttatgcg tcagatgtcc tagagaaagc 48120

taatttctta aaaaaacata aaatgctaca tacaaaggtg gaataatggt aaagtacgcc 48180

gcgcttcttg gattggtatt ggcattctct gctaatgctg aaaattcaat gacagattca 48240

cttcgtatcg ctaaaacatt ttgcaatacg aactctgaat gtgttgatat attagcgctt 48300

gaattagatt cagcattcag cgatggagta aaagattcac gtagcccggc tcagtggaca 48360

acactaataa atcgtaaggc taagagcatg aaagatttat gtgtcaatgc tcctaacgaa 48420

aatatatgtt taatgtatcg tgaccaatta atggctcgtt atatgtcagg actatcgtca 48480

aaatgaaaaa agcggctatt ttattatgct gcgcattttc agttaatgcc tgggaaaaac 48540

tcccaggcta tcctgaaact gtacttgcag cacagggtac taaaatagaa agcaatggcc 48600

cattcaagaa caacattgaa atagcatttg ttcctagcag cagaaaattg ctaatgtcat 48660

tttataatta tcaagataaa gatgaccagg tgatagttcc acttgtcgaa tataatgctc 48720

gtggatgtgg aatgcagagc gatggcgttt ctgttgatgg agtaatgcat cctaaagaac 48780

aaggagtgct gaaccctatc cttaattgta acaatgctat atttttaaga gtatacaata 48840

atcttaatga atatgcaaca tataaaattc cataggtgaa taaatgatta ctggatatat 48900

taagggcaat attgtagaac tattcatgaa gcatgaatgc gatatcgctc atgggtgtaa 48960

ttgctttact acaatgggtg ctggtgtagc aggacaactt gctaaagcat atcctccaat 49020

tctcgatatt gacatcgatg aagaccgtta ttatgacaat aatttagcca agcttggaac 49080

tcatacacga gccattcaca aaaaaggcac tgcatattgc tataatctgt atactcagta 49140

tgctccaggt ccaaacgttg attacggcgc aatttttaat gcattccatg aactaaattc 49200

tggtcgtatt gtttataatc gtcctctata cattccaaaa attggagctg gtattgctgg 49260

cggtgattgg gaactaattg agaaattaat caatttagca acacctgata ttgacattat 49320

ggtggtagaa tatgaagaag ctaaaagcta aatccgtctt gtagaggtaa atagatgatt 49380

actgaagagc aaaaaactaa actgtggcag ttgattgacg attatgcagg tgccgagcaa 49440

gtagtagcta ttagtgccat ttacggaaat ggtctacctg aagaatacga tgaactcatt 49500

cgttctaaga atgctatttc tgattttatg gagacacttt aatggcacag ctttatttca 49560

actacgcgag catgaatgca ggcaaatcag ctaaccttct tacagcagct cataactata 49620

aagaacgcgg catgggaact ctcattctga aacctgctat tgatactcgg gattcggcaa 49680

cggaagttac ttctcgtatt ggtctacgtc atgaagctaa tacagtagac gaatctattg 49740

acatacttga atttttcaag tgggcacaaa cacaacgtga tattcattgt gtatttgtag 49800

atgaagcaca attcttgact gctgaacatg ttcttcagct atgtaaaatc gttgacttgt 49860

atgatgttcc agtaatggca tatgggcttc gcactgattt tcgcggcgag ttattcgaag 49920

gttctaaagc tcttctttct gtagccgata aacttgttga gctcaagggc gtttgccact 49980

gtggacgtaa ggctacaatg gtagctcgta ttgacgaaaa cggaaatgct attaccgatg 50040

gtgaagtagt agaacttggt ggtgaagaca aatacgtttc tctttgtcgt aaacactggt 50100

gcgaactggt aggtgtttat aatgaagcca agaacgtata acactatcct gatgctagtt 50160

ttaagtatgt tattcatttg gatgggtgta gcagcatcta ttcaaagcga tagacgagaa 50220

gaacttcaaa atcgtcttga ttctggatgc aaagtattag ctcagggtaa agactttatt 50280

gctaatacaa atgggtgtta tattaaatat gagtagccta tttgctatag cgggtgtata 50340

gtactagtac tcgtgattgg gtttttacta tacgtaatat ttctttcgtt attggtttaa 50400

tatgaaaaaa tatgtgatgt gctatcgttg tcttcatgta tatgattaca acactgctcc 50460

aaagactgct accaagcgtc ttaaaaccaa agaacctgaa tgtccaaaat gtaaatgcaa 50520

ggtcatctat tcatgaatat taaatttttc aaatcaggat tttactatcg ttgaggtaat 50580

ttaacttaac gaggtaataa tgtctagaac aattcgccgt aaaggctggc atgtagtaaa 50640

atcttccaaa tggaacgatc agaataataa cgaatttgct tatattaaaa gctataacga 50700

atacgttaaa actcagaaag ataaagaaaa ccagcagaaa tatgttgaac tgcgtatttc 50760

tgaaaacagt gaaagaccgt tagaggccaa gaaactgatc gctaaatcaa agcgcgatgg 50820

attctggaaa actctacgtt ggacccgtta tgctatgccg gttccgcgtt tatttcataa 50880

agccgaaatt aaacgtgcat tgaagtatga tgaagaatat aactgggacg aagctggtgc 50940

tagaaccatt gagcaaggca tctgcgaatg gctttgggat taagtaacac atacttatat 51000

aaatactatt actaactgat gaggtgtata tgcagcattt aagtgaaaag caacttcgta 51060

atcttactgt agagcagctg gacgaacttc gtcgtgagat tgggcatggt atttcgcacc 51120

ttcaggaaga aattcgtcaa catagttcaa aagcagatta tacccgtaaa cgtacgctgg 51180

aaaaatacct caaagaagtt aaggctgtac ttcagcacaa acgtaatact ggacaaaaat 51240

aataggaggc cgtatggcct ttaatcacat ttgcttagcc ctggtgttgg gctgcgggat 51300

ttcattccca gctgcatcac acgacgacat ttcagattat aattcgtatg ttgagggagc 51360

tctacaagtt tatgctaaat ttaaggagcc tagtaagcaa gagtctgaac agttctatgc 51420

tttcgtacaa agtaaatgga agagcgagtc ttgttctaaa gattgcgatt ctttaggacg 51480

ttcagcaggt gaagaatacg ctaaccgtat gaggatacaa ttcgataatg aagttcaatg 51540

attttgtaaa ggacggtaaa cttactccgc aggatgaatt catcggttta cttatggtgt 51600

ctcaagcgta ttttcattca gcgcattttg ataccaaatc gtatgccaga cataaagcgt 51660

atgaagtttt ctttaacgag attccagatt tgatagatgc ttttggtgag cagtggttag 51720

gattctcagg taagagttat acaccggctt taccatcgca gaaagagctg ccaaaggaca 51780

ccattgaaat gctagacttc attctggcta aggccgatgg tatctacaag tccgttcctg 51840

ccgccctcca aagtgttctg gatgacatta caggcctatg ctacaagact aagtatttgt 51900

tatcattgca gtaataccct ccgcctcctt cgggaggcat tttcttttca aaaagttgtt 51960

tacttccctt cattacatga tactatagac atatcaacaa ccaaacgaga aaaacattat 52020

gattaagtta actaccgagc ttcaacctgg aaaaatcttt tatcacgtgt gtggtgttaa 52080

tcgcacagaa actaaacccg gcgaaataac gcgttacatt gttgcttcag gcacatatga 52140

tgtagaactt ggtcttagtg gtgtatattc acgtaaatct cctttcttcc aagtgatttg 52200

tgaatatgaa aactatgctg gccaaactga aagctattca actgaacggt ctgcccatga 52260

tatgggtata ttcaagccag gtgaaaagcg ttcggttcat aatcttaatc gtgggttttg 52320

gacgcgtgaa gaagctgaac agttcatcaa agagctccaa gaaaataagt tcagcgatcc 52380

agatgatcaa gcatatgcag acagactgac cccttctgaa gatttccgcc gtcaacaaga 52440

atttatggat tcttatcttg acagttgtga ttatgattac tacgactttg atgatggcga 52500

agaatgagaa acgttttact tatcatctac attgtggtac aataccagca tccgatgttt 52560

acatataatt tggtgcaaat gattctggag agtttgaaat gaatggatgg ggcccatcag 52620

atgacggatt tgcaactcgc gaagctacaa tagcagacgg gattgaatgg gcccgtcttc 52680

agaaacaact ccaagaacag cgggaatccg aagagttctg tgttgattgt gatgaggaaa 52740

tcccagtagc tcgtcgtctg ttggttaaag gctgtcaacg gtgtgtagaa tgtcaaggaa 52800

agtgggatac agtaatgact tctgcttata atcgccgtgg ttcaaaagat tcacaattga 52860

ggtaattatg gaaagtattc ttgatagtac caatttagat aatccgtaca gcgatgtgca 52920

tgtaaaggtt gtgaattcgt attttactaa aaagttgagt cgtgtcgtgc taaaacaagg 52980

taatgatata attcatcttg atactaaaca aattgattca ttaattcaat tcttgataga 53040

ggcaaaagat ggcgagtaaa ttagtatggg acggaaaacc ccgtaaaggc gatgcagtaa 53100

ttgaagatga aagcccgcat gttattgatt tgtatcttac ggtattccac acgtatgaac 53160

ataatactat catcgaaatt gaacgtgacg gagattgtgt agctattgat aaaagcgacg 53220

ctattgaact ggtcaaatat cttaccgcaa tgattccaac tatgaaacag gataacttat 53280

aatgaatatc aataaaaatt cttggcattt caaaatgaac ctatggttta aatctggcaa 53340

tatatggaaa atgccaaaaa ctctatgtgg atacttttgg accacagtac ttcatattct 53400

gttctcttca gcaattgcta tattcattgg ttctgttgca tggatgttcg gttggccgct 53460

tatagcgcag acgggtattc tcgcttggat aggtgttagt ttatccgcct tttggctaaa 53520

tgttgtagca gtaccagttg gtgcagtgtt tatagcaaca tttgtgcttg cgtttgtagc 53580

aatagtgttt ggatttattt tcggtttaga aaaatttaaa gaataccgta aaaataaaca 53640

atttacgaag aaacttgctc gagtaaaagc tggtcttccg gcagaatccg aaccgttagt 53700

attcatccag tatttaaaag ctcgtaaacg gaaagtttgc ccaatgattg attatgtaga 53760

aggtaaaact agtgaagaat gatcaagttt atatcgtgaa cggccgaaag gccgtctttc 53820

gtgctaaaac tgaacgtggt ataatttcta cataccctat tgccgaattt acttttgaag 53880

atggcgagca gattaaaatt aaatatgttc cgttatctca gacgtaccga ttcatcggcg 53940

gcgaaattga tttagacatt tattatgaag gtggcgtatg gaaattgaaa tcgtaacaac 54000

caaaaagaaa ctctctatga gcttgcttaa gcagatgaaa atggcaagct cttctgaaat 54060

caaattcgca atgtttgacc gagttcatcg tgttcttgga tatgttaatg cctttaaatg 54120

gaacaaaatg gatatccaag tagcaatcat taacactggg aacgattggg cattagttcc 54180

tatgtatgat acacatgtta ttaaaaccgc ccggcgcgaa ccacatccag acggtcaaga 54240

atatcatttc catgacgtag tatactacca tactatgcag aaaatcggga atgttcatcg 54300

caattctaag aagagtactg ataaagaaca tgttgaagcc tgtgctaaag cctcaaatga 54360

tttgattaaa ttcgctaaag ggaatcatat ttacttatga aaacaatcgt aaaatcttat 54420

tttggttcac atctgtatgg tacttcaact cccgagtcag atgtggattt taaagaaatc 54480

tttgtacctc atccgcgtga tattctaatg tgtcaggcga tgaaccacac caattgtaat 54540

actaacaaca gcgcaaccaa aaatacgaaa gacgacgtcg accatgagct gttcagctta 54600

aagtatttct tcaagctcgc tgctgacggt gaaactgtcg cgttggatat gctgcatact 54660

ccaccggaat tggtagttgc atctgacctt cctgaagtat ggaaattcat tcaagacaac 54720

cgagctcgtt tctataccac tgacatgaaa gcttatctcg gatatgtccg taagcaagca 54780

ggtaagtatg gtgttaaggg ttctcgttta gctgacctgc ataaagtcct ggatgttatc 54840

agagatgttc ctgaatggaa atatgacgat cgtcctcagc agaagggtat caatgagcgt 54900

tggaaagtac aggatatcgc agagaaactt cctctcggtg aattcctcga atggaccacc 54960

ttcgttgacc acaaatcagg cgagcagaag ttttataacg ttctgggtcg taaattccag 55020

acgactatca ctatcaaaga gatgaagtat tcccttgaga agcttgatgc tgaatacggt 55080

gaacgtgctc gtaaggcaga agctaacgaa ggcgttgact ggaaagcact gagtcatgct 55140

cttcgtgcag gtctgcagct tcaggaaatc tatatgactg gtgaccttca attccctctg 55200

acccatgcta aaatggtcaa gatggtcaaa gcaggtgagt taccgttcaa agaagtacag 55260

gagcttctcg agtctgtagt agatgaagta gaaattctag ctcatactgc tgaaaagaac 55320

ggaatgccta agaaagtaga catgaagttc tgggacgatt tcgtcgagaa ggtttatctt 55380

gaaaaccaca attcttacta caaatgatac aatgaaggtc ttcttgaatt atggaagacc 55440

tcataaaggt agacggtggt atttggaagc agtttgcaga gagactggtc gtagagaaaa 55500

tgctaaattc tctgctcgac caactcgaaa acaaatccac caatttatgt catgggccgg 55560

agaaactctc cggttctcac tttactgggc tgaaatatga ttttactttg gagcgtagta 55620

gtgccaatcg ttgttgcaat aatttacttt atcgtgggtt ggtctgtctg taaacatcta 55680

atcaaaaacg gaactattga gaaggtagga gagtattggt tctatctcat cttttggttc 55740

cctgctttta ttgttggagc gattatcatg ttcttccgct gggcaggtaa acttccaaag 55800

cgtatcgcag aaaacgctat caacaagcac gcataactga ggagccttcg ggctcctctt 55860

tttgtttcaa aagaatgcat aaagtagtat acaaactcgc gggctggtga tactatagac 55920

ctgtaccacc caaacagata cattggagaa taaaatgaaa actttagaaa tcgtcgtaaa 55980

caacattgat aaagccttta agctgctga agcccacggt gtagaatttg aaccaatgat 56040

ggtgggagaa gcgttctcta agcttgctat catccgtggt gaaactgaca acttgattga 56100

ttttgtggat gacttctatc tcggttcaaa ggtccgtcct tactacatca atgaaatttt 56160

agaaaaataa ttaaaaagta gtttactttg gagctgtaga atgatactat agctccatca 56220

aaacaaaaca gagtaacgga gaataaaatg tcaactatca ccatcaagaa agggatttac 56280

ttcggcaaag agatttcagg tacttatgag ttactcggtg agtggttccc ggatagctta 56340

agtgctgaag attctcgcca gggtgatggt aaagtctttg ttgaactgaa tggcaaaaag 56400

cgtggtgttt gggtattcaa agatgatatc acaattgacg gagtagctgc taaaattgaa 56460

gttgttgaat ccgttgatga aatgaaagag cgtatcaaga aacgctttaa cgttatggga 56520

ttaatgacta acggtttaat ccacgggaac attcgttctc tgattatctc cggagcagca 56580

ggtatcggta agacttactc tttggataaa gcattacaac atgctcatga tactaacgct 56640

attgattaca aatcagtgaa cggtaaaatc tcaggaattg gtttatactg ccgtctttgg 56700

gaatcacgtg aagcaaattc agttctgctt attgatgatg tagatgtatt ctctgatatg 56760

gacattctta accttctgaa agctgctttg gattcagggg agaaacgtaa agtatgctgg 56820

agcactgcat cttctttctt ggaagataaa ggaattccta atgagtttga gtttgaaggt 56880

actgtggtct ttatcactaa cgttgatatt gaccgtgaat tagagcgcgg ttctaaactt 56940

gctccgcatc ttcaagcctt ggtatcacgt tcggtttatc ttgaccttgg tgttcacact 57000

aatgaagaga ttatggttcg tgttcaagat gtaataatga ctacttctat gttacagaac 57060

cgtgggttaa gaaattctga agttattgaa gttttggaat ttatgaaaga taacgtaaat 57120

cgtctgcgta acgtatctct ccgtactgct ctttatatcg gtgatttcgt tgcgactgac 57180

cgtaaaaatt ggcggacaat cgctgaagta acaatgctga aataatttaa acgggaggag 57240

aaatcctccc taactgagga aaatataatg gctactttaa tttctaatga tgtaaaacgt 57300

gttttgttta aaggcggaat gtatatcgtt gatactccta aaggtgatac ctcttcctgg 57360

actattaacg agtggattaa ttacattgat gaaaacggag cgtgggtaca atgagtttag 57420

cagctattaa agatattgaa tgttggttaa acgatattaa agtatatccg cctggtcata 57480

tctttgcagg taaacccaag ggtaaagcag agaaagcttg tgaagcaatc tgtgaaaaac 57540

tttataagtt taattttggc gataagaaaa atgtattagc tgaagtccat tcttcttatc 57600

atgaattacg tgtaatggta aacgtatttc gtgctcctcc attcattgag ctcaggaaag 57660

aatacgctaa taaagtattt gatactttcc ttgcaaatgt gcaggatgca gtaaagcatt 57720

tagacgaaat gcataaacaa caccaagatt taaatgccta ttataagcct tggcgtaaat 57780

cataccaaga gcttaaaaat cgtattgaac ttattcgtta tgaggtgcta aaatgaaaaa 57840

ctgggtaatg acggaaagtg aagcctatgc agcgtatgtt tcaccagacg atcgtcgtag 57900

tgagttgttt ggttattatg gttcatattg cgttgccgaa gaagcagtta aggggcagtc 57960

ttggtggggc tcagatggta cagttaatcg taagccaacg gaactaatta cattcaccga 58020

tgaaaatggc gaatcatgga cttttcctaa aagcgctgct attagtgttc aggaagaaac 58080

acctgaagct aagcgtaaac ggttggaaaa aattaaagaa tccgctttgg ctaaattaaa 58140

tcctgatgaa cgcgaggcgc tcggattatg agtaaagaat ttagtactac tcgtatggta 58200

gatgcttttg gatatccgtg caacggttat cgtgaattta ttcacccgga agttgaaaat 58260

caatttaaag aagtcgtaag aaatattttg ctcaatgcat ttaaaactca aggaactaac 58320

ccgagagatt taggcattta tcttgaagaa gccatcagag acgtacaaaa gagcgtatcg 58380

gctaaacttc attgggctga agaaaatatt gcttggtcaa acaagaaacg ttctgattta 58440

aattggcccg ctgatcgtga acaaatcgtc aattatgcta aagggtaacc catgtttaat 58500

actatagtgt ctatacatgc gtattacgaa gggcagttaa atgctgcccg aaccaagtat 58560

aagcgaggaa tggaggaatc tgtggaatgc cttaaagata ttcagacatt tgcccagaag 58620

acccagaacc tcatcttgat ggaccgtaaa caggtctcat tggctgaaga gctaaaagcc 58680

tctaagatga ttatagaaga caataggaaa caccaactga aattgcttaa acggcgacaa 58740

caccagtcgc catggtttaa cagtgatttc cgatcttttt aagggccttc gggccctttt 58800

gttgtttaca tcttagaaaa gccatgataa gatagcttcc gttaactaat gaggagattg 58860

aaatgaaagc acctacttgg aacgaacttc aagaaatgtt caatactgaa gaagcttttg 58920

gaactatttc tgaaatggtt gagaatttag tagattctcc ttcagaagat aatcttctgt 58980

gtttagcaca gttcatcatt gaaacttaca tagagaatca gaaatgacag tatacgtaga 59040

tgtcttgatg aatcatggtt ggaaaatgag aggtcatcaa gtaaagaact gccacatgtt 59100

tagcgacaat cttgatgagt tgcatgctat ggcagaagcc atcggaatga aacgttcttg 59160

gttccaggat aagcgagttc cacactatga tttgcgtgat gttcgtcgca agcaagcagt 59220

tgctctagga gcagtagaag tatctcgtag agacgcagtt ctgctttgga gaaaattttt 59280

cacaaagtag tttactttcg gcgaggctgt tgataagatg gtctcgtcaa ccaaactgga 59340

gaataaaatg aaaactttaa ccgagattat ctctgcactt gttgaagaaa atcgtgtagc 59400

ccgccaagca caccgagcga aagttgaaaa acgcgccgag gagttgaatg ctggatgggc 59460

gaagacccgc ttcggtcgtg aatactttga taaagtggta gctcctactt ggggcaaaga 59520

tgatcgtcct catgctccct ttgatggtta tctttgggaa aatgaattag gtgaagttga 59580

agcttatcac gcaggcagtt acttgccgta tgttacagaa ttggattcac tggataagcc 59640

tgagtatacc ggtgaccacg gttggtggaa aatccgctta actcaagaag agtacaaaga 59700

acttcgggag tatggttatc ctcttgaagt acgcattcca tataaagagt ggaaattgca 59760

agatggcaca aatgttgtta tggcagaagt tagagctcat aagagcatct tagaggctat 59820

ccaggaacat tcaaaagagg tctttgataa tatattcaat gagctgaata agaataaagg 59880

ggatgcaccg gaaggacgag tgaccgtctc tggtacagta acgtcagtaa aagtttatga 59940

agactattac ggcgtacaat gtaagatgat ggttgtgctt gagaatggag ctacggttta 60000

cggctccctt ccaaaaagta ttccgtttga atacagaggc aaagtacagt ttactgctac 60060

atttgaatta gcgaaagatg ataaaactca tgctttctat aagcgtccaa gcaaagttat 60120

tatgcttgat gaatagttgt tgtataatgg gttcagggag attttgagat actctttgag 60180

cccagtccaa aatagaggaa aagataatga ataagaatga attaaagatg tttgtagaag 60240

ctgaatttaa taagttgaaa gataaaactc tcacgaagcg tgagaaacat gttaaggtgt 60300

tatcagcttt acatgattta aatccaaggg cttatgatgt agcaattgct ggtaacgtag 60360

ctcgtcgtgt gctaaatagc atggcatcac atgaagccaa ttatgctggt tttgttgtag 60420

aaaacattcg tcgttctcgc tggttaggtg caatgtcagc agagaaacag ctcaaaaagt 60480

ttgctatcgg caatgctaaa atttacggtc agcgttatag ctttgcggca ggggcgttta 60540

aaactgaaga aagacatgac cgtagcgctg ctcaaatctt ctgttctgaa tttaatgcaa 60600

acctgcgccg tattcttaat cgttcaattt gcttgcttaa aggcgatgac cgcgtgaaat 60660

accaggcatc ttctactagt tctagaaatc ctaagggtgt ttcatttatt cgtgccgaag 60720

aacttgacaa tgtaactgta cgaattcata ttaatagcca tttatccagc ggaaagtatc 60780

cggctcgggc gcttttagcg caagttcgta ctgcattaga tcatatggat gtagttaaaa 60840

aatcatgctg taaacagcag ggtgaaaact catctgttct tgaagtacat ttggacccat 60900

ttaagatttt tcctaaaaca ttgagcacca ccccagttat tgatgaagat gtagcacata 60960

tgtatctcaa tgttgttaag cctcttccgt taacaccagt aaatcatatt gaaatcgcta 61020

agaatagtat tactgccgaa atggaatcgg ttaagcgatt tattgacaca aaagaagctg 61080

aattggctaa gcatgaattg acgatggcag atttggttaa atcgcttaac gaatacaaag 61140

agcgttatga atctctcgag tatgcccgga gcttactgtg aaaaatcaat taaaagaaga 61200

catggtcgtt gatgataacg accttgaaat tgagtttgag tatccacctg tacctgaatt 61260

taaaattgac tgggacgcct gtcttgaaat ggtagaccgt cgagaagctg cagctaaaca 61320

agttgtgcct tgcgaaaaat gtggtagtat tcaagtacag cttgtcgatt ggacaaccga 61380

tattctgaaa atgaaatgcc ggacttgtaa acacagattt gagagaaaat taaaatgatt 61440

actaaaacta ttactggtgc taatactaag ttttttgtcg agtatgctaa taacctcata 61500

aaagacaaaa actttgataa catcattgca gatatgattc ttgacgcata cgaaagtggc 61560

atcgacccta tgcagcttaa agaatatctt cgagcgacaa tggattttac agttcttaac 61620

atgatgctta gaactgatac tgaattcaat gaaatgattg ctcgtcgtaa tgaaggcaag 61680

ttcaatttga ctgatgatga agtattagca tgcgctgctc acgaagcttg gaagaaggtg 61740

attaaatgaa aacaactggc gcgctttgga aagaatttta taacgatgaa gccttctggg 61800

aaggctatta tcatgatgac actttaatac tctttgatga tgttgaagta gaagaatatg 61860

aagacccttc gcctgatgcg gtagtaaaaa ttgaaagcgg atatgtttac aaaaccgatg 61920

atgattcctt cacttcccat gatttgagtc ttgaaacttt ctttaaacgt tggaaaaaga 61980

aacagaccac tcgcactatg gtagtcactg ttgataaaga tgacttcgcc aaagtatttg 62040

aaactatctc taatattcct ggagtgaaaa aggtaaaatg attgacatta aattagatac 62100

ttatgcagta cgccagttat tcccagaagg tacagcagcc cgtgctcaac tgcaacagtc 62160

agtaatcaat aacatcgtta aagaaatggt gttaaaagat tcacagaata agctgaagca 62220

agcagtacaa tctgaagtta atattgctgc tgtgactatt ccagatgtcc gagcagaagt 62280

taagaagcaa gttcagcaga tgttccatac tcgcggttgg aatgatatgt ctgctaaaga 62340

agaaatgtca cagatgatgc gtaacgctgc ccaatcatgc gctaaaaatg ctattgatga 62400

tatggttcgt caaactattg atgacgctgt taagcaagct gaaggtcgta ttaagatgtc 62460

tattgaaaga gctaatctcc gaattcaaga aatcattgtt aatgcaatga ataaaaattt 62520

cgctgatcaa attaacgctg ccattgctgc taaattggca gaacacttcc cggtaactgc 62580

taatggataa aattgatttt agcaaattaa atataccacg tatgggaatt cctgatgata 62640

ttgccaagca attagctagc gttcaaccaa tgccagataa ttgcatcaaa gatattttcg 62700

atgcgttaga tggtaaaaca ttagttataa ctactaaggc tgaaaatggc tcgtaaacga 62760

tatatggaag aagccgaacg agtaatgcta ctcatgtatt cggtttatta taatgagact 62820

ggtcaaatag ttgatagttc taaactcaaa ggagctatga ctcgtggccg aggttttgca 62880

caagcagcta ttgataaaga aattatttct cgccttggaa ttaagtatag ctccaagatg 62940

tatctccatc ctggctggaa ccaagttcaa gctcaagtat ttaaggaaat agaagaagat 63000

gttcacagtt tttggctacg acagcaacat ccataagtgt gtattttgcg ataatgcaaa 63060

gcgtctgctc gatgttaaga aacaagagta tgcattcatt aatgtaatgc cagaaaaagg 63120

cgtatttgat gaagtggtta tcagtgattt gcttcgtcgt ttaggtcgtg aatcacaggt 63180

tggattaact atgcctcaga tttttgctcc tgacggtaca catatcggcg gttttgatga 63240

actccgtaaa ttcaaattca atgcatgatt atcgtggaac cctccttcgg gagggtgata 63300

ttgtagccct ttattatggc tatggcggat tagaaaccgg tgagattaaa caaatcaaaa 63360

atcatcgagc aaaggtagag gtaacttact ctaatggagt taaggttatg tctaaatgga 63420

aatacggtga gtgtatggtg aaattatgat tagcatgagg aagagttatg agttatgata 63480

ttggtgattt aaaagctccg tgcacggtaa caatttcagc agaagagttc atccgcttgc 63540

aagctattga agaactgttg tgggaaattg aatgtgcgct tccgtctggt ttagaaagct 63600

ggattgatga tgaagaccta caaaaactgc gaggttaaaa tgactaacgc tgaattagta 63660

aaagaaatca agcatatcgc tggtgtcact ggcgaatggg acgacaacta tgatttcgaa 63720

tatccgccta atgcaccaga cgatgatgca gaagaaatct ttgttttagt agaagatgat 63780

gaatggacac aggaccataa gtatcaaagc cgttctcaga tttggtatta cccagctcgc 63840

ggcgtccatt tcatggtatc agagtctcgt tcaggttcat atcataccga ttggtattat 63900

aatcctcctg aagtagatat cgtcactcgt cacgagaaag tagttactcg tactgaagtt 63960

gaatggcgta ttgaatacga ttctgttaat gattccgctc cggcaccatg caaagcagca 64020

aaggcataaa accttggtac acggctcgat gggaaactgt cgagccagag gaagatgcta 64080

ttcctgaaga agattataat acttctgaac ctaccattaa cgaactactt gattatgagg 64140

acaaagtgaa tggaacttat tggtaagcag tttgaagtta tagaaaatga tgatgaatta 64200

actgaacaat ttccccagtt tgttcctgga tttaaatttc aggttatcaa tgcagttaat 64260

gaagatgacc ttgaaacatg tggcattaca gcagtaattg atttgctcac aaataaaatc 64320

atcacaatta atgacccaac tccattcggt gaatcttggt tctggtgctt ctatagtgaa 64380

gataccatgc accaaattaa agaaatcggc caaggtgaag acgttccaaa tatttctgaa 64440

attaaactcg accattttca tggaaaaatt gttccaatta ccaaagctct ttatgctttc 64500

gcaggtcaag aaaattgtga ttctgaagaa tacgatttaa tgcagaaagc agctgattat 64560

atcgtcgcct tggaaactcg tcttggagtt caatatgtct aaatcatgcg taaccaaaac 64620

tattacagta aaaattttgg atttttgtga tattcatcgt attgcaaggg aaatcttacg 64680

tagtcatgga tataaaattg gtgacattat taaattcagt aatggatatt atgacgatga 64740

catcggtgga atggcttggc caaaaatgag tattattcac aaagaaacta attcatatat 64800

tgagttcaat gcggatgatt atgaaggcat ctatgctttc tgtacttctt tctgcataaa 64860

agagtctaat cataacatct atagtagtta ctcgttaatt taactataaa tactcttatc 64920

taatcgctga ggtaagagta tgttattaac cggtaagtta tataaagaag aaaaagaaaa 64980

actatatcag gcacagaacg gattatgtcc ttgctgcaaa cgtcctttag atgaggatat 65040

tcaaaagaat cacctcgacc atgaccatgc gttagaaggt gacaatgcag gaaaggtcag 65100

aggcttgctc tgtaacctgt gtaatgcggc agaaggccaa atgaagcata agttcaaccg 65160

ctctggttta aaaggtcaag atattgacta cctcgaatgg ttagagaatt tgctggttta 65220

tctccgccag aatcgtaaag acagtaatat tcacccgcaa tatgttgccg atatggctaa 65280

acgcttttca cgtcttggta aacctgagat gattgctgaa atggaattgc atgggtttac 65340

atacgaggaa agtgatggaa aatcacaact tgcttcaaaa tacaagaagc agcttcgtaa 65400

gagtttaaaa tgaatatcga attagaaatc cagggactta ttaataaaac caacaaggac 65460

ctcttaaacg agaatgctaa caaagattct cgtgtttttc ctacccaacg tgacctgatg 65520

gctggtatcg tatctaaaca tatcgccaat caggtcattc ctttctctgt aatggaagca 65580

cacaaagaag gtgttatcca ttttcatgat atggactaca gtccagcttt gcctttcacc 65640

aactgctgtt tggtagattt gaaaggtatg ttgcagaatg gctttaaact tggtaacgct 65700

caaattgaaa ctcctaagag tattggagta gctactgcta tcatggcgca aatcactgca 65760

caagtagcat ctcaccaata tggtggaact acttttgcta atgtcgattt agttctggct 65820

ccttatgtag agaagacatt cgctaaacat gtacgtgatg ctcgcaaata tcaagtagca 65880

ttagtaaaag attatgctat ttcaaaaaca gaaaaagacg tatttgatgc tttccaggcg 65940

tatgaatatg aagtgaatac tttgttcagt tcaaatggcc aaactccatt tgtgactatc 66000

acatttggta tgggaacgtc atgggaagaa aaattaattc aacgagctat tcttgataat 66060

cgtattcgtg gattaggacg tgatggaatt actccaatct ttccaaagct tgtgatgttt 66120

gtagaagaag gcattaatct acgcaaagaa gacccgaact atgatattaa gcagcttgca 66180

ttagaatgcg cagctaaacg catgtatcct gatatcatca gtgctagaaa taatagagca 66240

attacaggtt cagaaactcc tgtatctcca atgggctgta gaagtttcct tggtgcttgg 66300

agagactctt ctggcaaacc cgttcttgac ggccgtaata atctaggggt agtaacattg 66360

aacctcccta ggatagctct ggatgcaaat tataaaagtt cagatgatag taataaactg 66420

ttcaaactac tggatgaacg tcttgatatt tgtaaagaag ctcttttaac tagaattaaa 66480

tcccttgaag gtgttactgc gtcagttgct cctattcttt accaggaagg tgcttttggt 66540

gtgcgtatga aacctgatga tgaaattctt gagctattca aaaatggacg tagttcaatt 66600

tcattaggat atattggcat tcacgaattt gatatgctta cttttaaagg aagcggtaaa 66660

ctcgtcctga agtacatcaa cactaagcta aacaagtgga cggaagaaac cgggtatgcc 66720

tttagtttgt attctactcc ggctgaaagt ctgtgctatc gtttctgtaa gattgaccaa 66780

gccaagtttg gtgatgttaa gggcgtaact gataaaggct ggtacactaa tagtttccat 66840

gtgtcagtag aagaaaacct gtcgcctttt gaaaagattg accgtgaagc accatatcat 66900

tccattgcta aaggtggtca tatttcttat gttgaactgc ctgacatgaa gcgtaacctt 66960

gaaggtcttg aagtggtatg ggactatgct atcgagaagt tggattattt tggtgttaat 67020

atgccagtag ataaatgtct ttcttgcggt tctactcatg agatgacacc tactgaaaac 67080

ggattcactt gctcaatttg cggtgaaact gatccaaaga aaatgaatac aattcgtagg 67140

acttgcggct atcttggtaa tccttctgag cgtgggttca atcttggtaa gaacaaagaa 67200

attatgcata gggtaaaaca tgttagagaa accaatgaag caagttgatt ggaaccaact 67260

tagcgaatgg ggattgattt ggaaaatcaa caaagaggtt ctgcacccgc ttggaattgc 67320

tataacccgt gaccccgaaa gtggattatc ggctggggct attcaaactg atgagccctg 67380

gaaatatgat gcagaagtag aagcacgtaa tgaggtaagg ttcaatgaat ttcgacagaa 67440

tctacccttc tgactttgtg aatggccctg gatgcagggt cgttcttttt gtcacagggt 67500

gtttgcataa atgtgaaggg tgttataata aatctacttg gaatgctcgt aacggacagc 67560

tattcactat gaatactgtt aaagaaattg catctcactt aagcaaatcg tatatccaag 67620

gccttacctt aaccggtggt gacccacttt atccacagaa ccgagaagag atttcaaatt 67680

tagtttcttg ggttaaagca agatttccgg agaaagatat ctggatgtgg acaggatata 67740

agtttgaaga tatcaaagat ttagatttgc tacaacacat cgatgttata attgatggga 67800

aatatgagaa atcactgcca actactaaaa actggcgcgg ttctgacaac caaagactct 67860

gggtaagaaa tggttctacc tggacacatg attgaggaaa tttatatgct gacttacaaa 67920

attatgttta ctctgaacca catggctact gaactgtttg gaccggaatt tctggctatg 67980

acagcgttca tcttaactat ttaaggaaaa ttatgaaatt tattaatgct attcgtaaat 68040

ttatttctaa cgttatcgct ttggttgcat taacggcagg tgctttcgta gcaattccgt 68100

ttattgttct tattatcatc gcagattgga ttaatcctac caagaaagat gaaaagttat 68160

ctaatgaaga atttcagaaa cgagttaaca ctctgactgc taaactccaa caggtcatga 68220

aatgatagaa atctatggca tccctgaaga agtttggaga tgccctggat gtaaagcagt 68280

tcgtgacttg ctcgataagc tgcaacttcc gtatgagttc tataacgtaa tcaatgaggt 68340

agacggtcaa ccggtttatg accgtccgtt gattgagtca cttgctaaac gcatcgggtg 68400

ctatccatcg cttgctattc ggtatcctgt catttttatg gataacgtta agcagtatga 68460

cattccaaca ttcaaaacca atcttattgc tgctgggcat gacccagata tcatagaaga 68520

ttaaccggtt cctttctaag gtcatcttga ccaccttctg tatatttcta tacccttcat 68580

ttagaggttc ctgtgggacc tctcttttat tttaaatcca tttcacaaag ttgtttacaa 68640

gctagctgat gagtgatact atagctctat caacggataa cagcataccg tttaactcga 68700

gaggaaaata tgaactggtt aaattggcaa gaagctctag aagctatgag taaaggctgt 68760

aaagtaaagc atgtgcattt tactgatgac gaatacttct tgatgaagaa caaagtcatc 68820

tgtgacgaaa atggatatga tatgactcgc tggtacaagg gtgagtcttg gcaaaacgaa 68880

cattggtaca tcgcatgaaa acttttgctg taggtgatat cgtccgtacc agaatttggg 68940

atgggcttca atttgaagta gttgtctacg tcggttcaga tggagttcta cttcaccgaa 69000

ttaacaatct gattaagtgg caccttgaac gcttcgtgaa atatcatgaa ttcaatagct 69060

accactgtac tgtagctccg gttgctagta aagaatacta cgatatgctc gaagagttaa 69120

aatctctcaa agattgattt gctacaggag atttgattta aaatctcctc tgtcaagaca 69180

atcactactg aggaaaataa catgtcccaa gcaattaaaa acgcactgaa cgctttcgca 69240

tactataaag tttctgcaat gctggaagaa ggacgttgtg taactccgtc tttgcttgat 69300

cagtgggaag ttgagcttca cggtacgatg aaagaagaag gacaaaaaat tggtaaagca 69360

cgcatccgtg aattagtggt tgcttatctt ctgtctgaat ttggtattaa agcctttggt 69420

gtagaaccca tcgtagttgg tgttggtgaa atttctgaat ccgctattcg caaaatgaaa 69480

aaccaacgca agaaaggttt tcgtgatgtg aaagcggtta aggcggcaaa atgaaactaa 69540

atcaaaacgg atgtccttct cgcgtacgat tttgcattct agaattacga tctaacattg 69600

tcgttattga cgaatacacc acgattgtag gtgtacaaca atatcttgat agacgttttg 69660

atacacgaac ccatatgaaa tatggatttc caggcaaatg taaattttat ccaatgagtg 69720

ctgatcatca atctgtagta aatgatgaat acaagtgggc agaaggtctt actttaaaag 69780

aacttgagga atatcttgat gcgtaaagtt attctataca cagaaatttt taccagccgt 69840

tgggtgtttg acagtgtcag aatttcaaac gcttcaaaag aagatgttcg taacgctcag 69900

cgattagcat acgatgaagc tggaaaatca ccagcatttg taaaaattga gtatatcatt 69960

actgattctg ctttaattca taatgtatca gaatcagtat taaagaagtt ctgcgttgat 70020

cgcatcaata aaggaacttc aatggaatat tttctattag cgagagaact gaaatggtag 70080

aagaacaaat tgcagaaatc ggtttactcg gatggttcgt gtctaaaact aaagacggca 70140

gaaacttgat tgaaactcca gaaggagaat tcattattga agaagatttt gacgcgtttt 70200

ggatttatga acgctctgga gagaatgaat acacatccgt ggatgctttc tctaaatttg 70260

aagatgctat tgactcggtg aaagcatggc taaagtaaac caaattatga ttgtagtaga 70320

aggcattggc ggatttacta tagattctta tatgggtgtt tggtttgaca atgaagaggg 70380

catgtattgg gaaacgcatg cctctatgtt aaatgaaact cattatgaaa gtttatactc 70440

ttcattcatg gaaatgatgc atgaagtaga tgaatctgat tggtttgaac ttagtttggt 70500

tgagttcaaa cgtatcatgg aacagctgtt ccaatgctat cgtattatga agggtgaact 70560

atgaaaattc aattgactct tacacatgaa aatattaaag gtgtgttctg tcttgaaaat 70620

agccaaataa cttttgcaca agatggaacg tactggtatg ctgaatcaga tgatatcgct 70680

ggttatggaa tggaacgtgt atttgaagat tttgaagccg tcattgatgt tccattagat 70740

ttcacgtata acgattttta tcgtatcatg atgaaattaa ttgcatgcgc tgaattgatt 70800

aagtaatgct ttaatcctct cgcttcccaa atttgttata atagatatta ttaattgaag 70860

cgaagaggca atatgagtaa ttatgtaaat aacaaggagt tgtataaatc aatctgttca 70920

tggaaagaga agtgtcggga gtctgaagct gctggcggtc ctcgagtagt aaaacagaac 70980

gatacgatcg gccttgctat tatgctgatc gcagaaggtc tgagtaagcg tttcaacttt 71040

tcaggataca cccaatcctg gaagcaagaa atgatttcag acgggattga agccgcaatt 71100

aaaggcttaa tcaacttcga tgaaactaag tatgataacc cgcatgcgta tataacccaa 71160

gcttgtttca atgcattcgt tcagcgtatc aaaaaagaac gcaaagaaat ggcaaagaaa 71220

tacagctatt ttgtccacaa cgtgtatgat tcacgggacg atgatatggt tgcgttagca 71280

gatgaaacct ttattcagga catctacgat aaaatgacgc agtatgaatc caccgcttat 71340

aaggcgccag ggtctgctaa aaagagcgaa cctacaagtg atggacctaa tctggaattt 71400

ttatatgagg ctgaagatta acctcgacgg gtttttagaa gatgtgcaag acctagacgc 71460

tatcccttat ttgctaaaga tgtatttaag ggaggtgctt gatcttgata ttcacattga 71520

cccgaaaaat ccacatgacg ctgatttcag atcagattct gctataattg aacatagtta 71580

taattggact gatactgaat tcacatttga aataaattac catccaaagg aataacatga 71640

acaatattac ccaggaagag cgcgacgaac tgcagcagaa actaatggaa gcggcagaag 71700

aacaagctat tgctcgagcc aacaaaattg ttcgtaaaaa ccgtcgtgaa attgagcgat 71760

taaaagctca tgctggagac gcggtattag acaacaattt ccctgcttac aagtatgcta 71820

ttgaaaaact gcgtactatt ttaaaacaac cttttaccga tgagattatt ctcacctgtt 71880

ggaatacctc tcgtaaatct gtttgggaca ttctaaatgc tggtacaagt aaaatttaaa 71940

cgtgttcgta aagacgcagg atttactttg aacactgcta ctggaacaat ggcagtaaaa 72000

gtagcagata atcaatatcg cgtgttaggc tctaccgaag gatgtaagct aatagataag 72060

aactctcttg tctgggttga caccttccaa gttaaacggt ggtatgaatg gtaaatgaag 72120

agaattggga tgtatgacga atttgatggg ttctaatcct gggcatgatt ggcctgaagg 72180

aaattacgcg tgtcggtgta gtaattgttc agaacgttat acaggaccaa agcgtagtta 72240

cttctgctat aaatgcgata ccgccaggag agaagcaccc gctcccgatt atgaagcaat 72300

tcgtaatgct aagatagata tgctcaagcg ctttgaagaa gctaagcgta tatgcgaagc 72360

agcgggttat gttgtgtata agaaaattta aagggcttcg gccctttgc tttattacgg 72420

gaatggtaaa atatccaaaa ttaacaacaa aggtcaatat atgaagatta atattttaat 72480

ggctcgcgga cttgagggat gcggcgtaac caagttcagt ctcgagcatc gtgagtggtt 72540

agtaaaacat ggccatgaag taaatatcat ttacgctaaa gataaagcgt ttactcgtaa 72600

tagagcacat agctataaag atgtaactat tcctgtgtct ctggcagatg actacgataa 72660

gactttatct ctgcttaatg catgtgacat tcttatcatt aactcagtac ctgctgtcaa 72720

cgctccagaa gcagcgattg ataactataa gaagctcata gagaacatta aacctgaagt 72780

tcgggtagtc gtatatcaac atgaccatag agcattgtca cttcgtagaa atgctggtct 72840

tgaagaaacc gttaagcgtg ctgatgtact gtttagtcat agctcaaacg gcgattttaa 72900

taccgtgcta atggaagaat attttccaag cggcgggttg agtttctttg atgattctga 72960

ctcagctcct ccggtttata actttcaacc tgctatgaac atcaaagcaa ttcgtgataa 73020

gtattggaaa gacttctctg ccattgattt tgatatccat cgttggattg gtcgtactac 73080

tacgtggaaa ggctatttct tgatgtttga ctttcatgaa agtcatctgc gtcccgcagg 73140

caaaacgact atcttggaag ggttagaacg cagtcctgcg tttattaaca tcaaagaacg 73200

ctatgaaatt gactattgcc gtcattatca tcaggttaaa actgggccag gtctgaatcc 73260

tcaagttctt gaccgatatg ttaactctga aatgcttgag cgtatgtctc aatctggatt 73320

tggctatcag ctgtcacgtc ttccggataa attccttgag cgttcgttgg aatatactca 73380

tttggaatta ggtgcatgtg gtactattcc tgtgttccat aaagccaccg gtgatgcttt 73440

gaaattccga gttgatggaa agccattgac ttctcatgat tctggcattc tgtggttgaa 73500

tgatgaaaat aaaaatgaag tctttgaacg aatgaaacat ctgtcatctg accagaagct 73560

ctatgataaa gagcgaaata aagcatttga attcctggta gaacaccaag attctgagca 73620

ttgctttaaa gaacaatttg agttaatgac aaaataagta atgggccttc gggccctttt 73680

tgctattcat ggaataatat aaaattaaac tctactagag aggttatatg aaaattattc 73740

actcaggcga ttggcattta ggtgtccgcg cagatgaccc gtgggtacag gatgtacaac 73800

gacacggaat taagcagcat attgattatg ccaaaaagca tggaattaaa actatcattc 73860

aatacggtga tatttttgat gttcgtaaag ctatcactca taagacaatg gaatttgctc 73920

gtgaaattgc agagtctctt gagaaagaag gaattaactt aattacgatc gtcggaaatc 73980

atgacatgca ctacaagaat acgttgacgc ctaatgcatc aaccgaagtt cttggtaagt 74040

ataagcatat tactgttatt gaaaagcccg tgactatgga ttttgatggg actttgattg 74100

acttgtgtcc atggatgtgt gaagagaaca catcagaaat catgaagcat atcaaagaat 74160

cgtctgctga atactgcatt ggtcattggg agcttaatgg cttttatttt tataaaggaa 74220

tgaaatctca tgggctggaa ccagatttcc tcaaaaagta caaacaagta tggtctgggc 74280

acttccacac catatcaagc gcagcaaacg ttaagtacat cggaacgcct tggacgctta 74340

cagcgggtga cgagaacgac ccacgcggct tctgggttca agacactgaa ttatcaacct 74400

ttgatttcgt ccctaatgaa atcacttggc acagaaaact gatttatcct gtcacagggc 74460

aagttgattt tgaagagttc agaaatcttg cagtgcgaat tattatcact gcggtcgatg 74520

aagaccttcc taagtttgaa tcagaacttg aaaaggtagt acatgaatta agaactgttt 74580

ctaaagttga caactcggtt gagtctgaag atggcgaaga agtagaagtt aaaagcttat 74640

tggatttaat ggaagaatat atccaagcac ttgaagacct gtccgcagat gatatcaaag 74700

ccttaaaggt tatgtctaaa cagttataca ttgaggcaca aaatcagtga agacttttaa 74760

actaaatcgt gtcaagtata agaatataat gtcagttggc caagcggcca ttgacattca 74820

acttgataaa tgtcaaaaga ccttaatcac aggtaagaat ggtggtggca aaagtactat 74880

gcttgaagct attacttttg ccttatttgg taaaccattc cgtgatatta agaaaggtca 74940

attaattaac tcattcaata agaaggactc tgtagtagaa ctgtggatgg agtatgacgg 75000

tcatagtttc tacattaaac gtggacaaaa accgaatgtc tttgagattt tacgagatgg 75060

caataagctt gatgaagccg caagttcaaa ggattttcaa tcctactttg aaagcctcat 75120

cggcatgtca tacacatcgt ttaagcagat tgtcgtatta ggaacggcag gatatactcc 75180

gttcatgggg ttatcaactg ctaatagacg aaagctcgtt gaagatttgc ttgaagtgtc 75240

tcttttagct gatatggaca aactgaacaa gacacagata agagaaatca atcagcaaat 75300

ccaggttaat gatgttcagc gtgaagcatt gactaatgaa attaaaactc accatgagta 75360

tgcagaaaag cagaagaaac tttctggtga taacgttgct cgcctgcagg cgatgtatga 75420

tgaacaggtc aatgaagccc gtgggtataa agcagaatta gaaactcttc agagagaact 75480

gcttgagtta gtaattggag acgacccagc agagtcaatc caagaagttc aaggtaaaac 75540

atttaaaatt cggtctaaaa ttgaatcata ttcaaaggtt cttgggctgt atgataaagg 75600

tggtcattgc ccaacgtgct tgcaggattt gcattctaat gacactctaa tcactaagat 75660

taatcatcat gttgaagaat gtaataccat tcttggtgag ttaaagacgc gccagagtga 75720

actggatgaa ctagctcgcg agtataacac ggtccgggct cgcgctagag atatcaaaac 75780

ccaaatgggt agtttaaagc aaatgactat cactgctgtg gaaaaggcac gtcgtattaa 75840

agcagctatt gataaagcat ctcaggagtt tattgataac tcagacaaga ttaaactgct 75900

acaagaagaa ttagataaaa ttatcctcgt caaaactaat ttggttatgg aaaaatatcg 75960

tcgtggtatt ttaactgaaa tgctgaaaga ctccggtatt aaaggagcta tcatcaagaa 76020

gtacatcccg atgttcaata agcaaattaa cagctaccta aaaattatgg aagctgatta 76080

ttcgttcaca ctgaacgaag agttctctga aacgattaaa tcacgtggac gagaagagtt 76140

tagttatgcc tcgtttagtc agggtgaaaa agccagaatt gatatagcat tactattcac 76200

gtggcgtgat attgctgaaa aagtttctgg tgttaaaata aactgtctgt tccttgatga 76260

agtttatgat tcggctaccg acgcagaagg tgttaaggca ataactgcta ttcttaataa 76320

gatggtagat gccaatgtgt ttattatttc tcaccgtgac cacgacccgc aggcatatgg 76380

ccaacacctt caaatgaaga aggtcggacg attcacggtg atggaatgaa tgagtttact 76440

acgggccaac atctgttggc ctttcctgaa ttaaagcgtt atgtgttagt taatttattt 76500

tctgatgaac gtcatcttgt aactgaagaa atgttacgag atgcttttac gggaaatgaa 76560

tataatagag tcatgtccaa caggaatccc ggttggatgg ttgaagatta ctacgattaa 76620

ggtaaatata atgattaatt ttgttgatgt gaaagatatc caggttaaaa acgtacgtgc 76680

agattccaac ccgaataacc aaaatcgtat tcgtaaatct tgggttctgg ctctaactga 76740

agaaactaaa caggctatca aagataagat taaagattct gaagctcgct ttgctttcta 76800

taaatctatc gatgatgaag tcgcagaaaa atggattgaa ctgatgcgta agcattacaa 76860

tgaatcaatc aaggctggtg ctaaaattgt tactgatcgt cacggtggcg aacgtctaga 76920

aaatgattac tgtgtagatg ctgatgagca actcgttgcg gcaggtcaga ttgttgcaga 76980

agaattaact gctacattcg cagcttgata taattatcct gaacttaatt aaaaggtatt 77040

gaaatgaaat tctctaaaga aactctgaac attctgaaaa atttctccac catcaactct 77100

ggtatcatgc tgaaacctgg caattttatc atgactcgtg ctgttaatgg tacgacttat 77160

gctgaagcaa caatttctga taccatcgat actgatgtag caatttatga cctgaacagt 77220

ttcctgagca ttctgtcttt ggttggtgat gatgcagata ttatcatgca ggaagatggt 77280

aatctggcaa ttaaagatgc tcgctcaact atcttctggc cagcagctga cccgagcaca 77340

atcgtgttcc cgactaaacc aatcccattc ccggtggcaa acgtaattat cgattttaaa 77400

ggtgaagacc tgcaacagct gatgcgagta tctcgtggca tgcagattga cacaattgct 77460

atcaccaatg ttgatggtaa aattgttctg cgtggttata acaaagtaga agatgctgca 77520

ctgacccgtc cgaagtattc tctgacactc ggtgattatg aaggtgaggg taacttcaac 77580

tttatcatca acatgagcaa tatgaagatg actatcggcg attataaact gatgctgtgg 77640

gcaaaaatga atggctccaa gaaacagact gccgcaaaat ttgaaggtgc atcagcctct 77700

tatgtagtag caatggaagc agacagtacc tttgattttg agtaataact tcggggcttc 77760

ggccccatct ttaatctgaa tgaggaaata taaatgaaat tgacagtaaa cgaagcagac 77820

ttcatgtggg aacagaaata tcgtccaggt actatttctg agtgtgtact tcctgctgaa 77880

gataaagaaa ttttttcagc tttagtagct aaaggaaaaa ttcctcattt aattctccat 77940

agcacttctc ctggtactgg taagactaca gtagctaaag cattatgtaa tgacattaat 78000

gctgaaatga tgttcgtgaa tggttctgac tgtaagattg atttcgttcg tggaccgtta 78060

actgcatttg caagttctgc ttctattgca ggcaagcaga aaattatcgt tattgatgaa 78120

tttgaccgtg caggtcttgc agaatctcaa cgacatctgc gttcattcat ggaagcgtat 78180

agcacaaact gtactattat cattactgca aacaatcttg atggtatcat taaacctctt 78240

cagtctcgtt gccgtgtaat taattttggt aaaccatctc catctgatgt taagccaatg 78300

caaatcgaga tgctcaagcg ttgtctcgca atttgtgaaa acgaaggcgt ggtagttgaa 78360

gataagaaag ttgtagctgc tttggtcaaa aagaattttc cagaattccg taagaccatt 78420

aacatgcttg accattattc ttctaagggt gtgattgatg caggtatctt gtctatcgtt 78480

ctgaatgacc gtggttcaat tgaagatgtc atcgaagcta ttaaaactaa gaacatcaaa 78540

gaactccgtg ctcttgcccc gaaatatgca gcagactata cttggttcgt agataaactt 78600

tcttcggaac tgtatacaat ggttactggc ccaagcatta tccgaatgta tgaaatcatt 78660

ggtgaaaata accagtatca tggcatagca gcttcgattg aattacactt ggtttatatg 78720

cttattcaac ttgttgtaga gatgcagtgg aaatgatgag tttatttgaa gatgatgatc 78780

agtataacga gcaccaaata gcgtggttag gtaaagactg gacgaaagtc caggaattat 78840

ctgattcata taaagaaaaa gcagaaaatc aattcttcac aattattggg tctattaacg 78900

aaaagcaaga gcatttgaat atctcgacga tggattattc aaaattcatg gttgaaaacg 78960

ctctttctca acaccctgac tgtatgcctt cggtttatgt tatgaacctt gttggtcaag 79020

ggttatctga ccaagcacac tataactata tgatggcctc tgttcctaga ggtcgtcggt 79080

atggtaaatg ggctaagtta acagaaaaca tccaggatgc attgattctt caagttataa 79140

tgacatatta caaggtcaat gcgattgacg ctaggatgta tagagagacc ctggaagcta 79200

aaaacaagct taaacctgct ctcaagaaaa tgaaaggtct tgtgactgat gaattggtca 79260

agacaatcac gaaaaacgtg aaagaacaga aaaatcttaa gaaaacagca ttggaatggt 79320

aaagatgatt gaaattacac tgaaacagcc tgaagacttc ctgaaagtta aagaaactct 79380

gacccgtatg ggaattgcta ataacaaaga taaggtacta tatcaaagct gccacattct 79440

tcagaaacaa ggtcgttact atattgttca ttttaaagaa atgttgaagc ttgatggccg 79500

ccctgttact attgatttgg aagatgaaat tcgtcgagac tcaatcgcac aactacttgc 79560

tgactggggt ctactgagta ttaatcgtgg tcaaactctt gctcagatgc agaataactt 79620

ccgggtcatt acgttcaagc agaaacatga atggacctta aaatctaaat atacgattgg 79680

tgcataatga cagaccaaga attttacgac aaacttaaaa atatcaggat tactgctcct 79740

gaatggttca gtcttcctat tgatgaacaa attcagtatc aggtaaaaga aactttagaa 79800

aaatatcctg gccgaaaagt tatgatgtgc ttcacatatg ataagaatcg agttcctcga 79860

attcagaagc aagtaattga agtttaagaa aaggccttcg ggccttttac tttataaaac 79920

tcggagtata attatcccac ctaaagacta ataactcggt ctataaacaa aggaaaccca 79980

tgaaagaatt ttatattagc gttgaatctc taggcaatga cattgtagaa cgttatatcg 80040

attctactgg tgaggaacgc atgcgtcgtg ttccgtattc tcctgtgatg tttagtcatt 80100

gcatggaaga aacaaagtac aaagatatct acggcaagta ttgcaagaaa aatacattcc 80160

caactatgaa agatgcccgc gattggatgc gtcgtatgga agatatggga atggaagcaa 80220

tgggtatgga tgatttcaaa ctcgcgtata tcagtgatac ttacggttca gaaatcgtct 80280

ataataaaaa attcatccga attgcaaact gtgacattga ggttactgca tctcaattcc 80340

cagacccaat gaaagcagaa tatgaaattg acgctatcac tcattatgat tcggttgatg 80400

acaagttcta cgtatttgat ttactgcatt ctctttatgg ttctgtttcc gagtgggaca 80460

agaaacttgc tgctcgttta gattctgaag gcggtgatga agttccacaa catattcttg 80520

accgcgtagt atatatgccg ttcaattcag aaaaagaaat gatgcttgag tacatcaatc 80580

tttgggaaca gaaatgccca gcaatcttta ctggatggaa cattgaagga tttgatattc 80640

cgtacatcat gaatcgtgtg aaacagattc ttggtgagcg tgcgatgaaa cggttctctc 80700

ctctgaataa agtttcatct aagattatca caaacatgta tggtgataaa gaaatttatt 80760

ctatcatggg tgtgactatt cttgattaca tggatttgta taagaaattt agtttcacga 80820

accaaccgac gtataagttg gatttcattg cttattatga aaccaagaaa ggtaaattag 80880

catatgacgg tccgatcaat aaattgcgtg aaactaacca ccaacggtat atttcgtata 80940

acatcatcga cgttgaatca gtacaagcga ttgatgctgt tcgtggattt attgacctgg 81000

ctatctcgat gtcttattat gcgaagatgc catatcaagg tgtaatgagt ccaattaaaa 81060

catgggacgc aatcatcttt aacagtctga aagaacaaga caaggttatt ccgcaaagtc 81120

gttctcatgt taaacagtca tatcctggtg cgtatgttaa ggaaccagtt cctgctgcat 81180

atcgctatat catgtcgttt gacttgacat ctctgtatcc gtcaatcatc cgacaagtta 81240

atatttcacc agaaaccatc gttggacagt ttaaacttca tccgttgggt gagtacatta 81300

acaagactgc tcctcgtccg tctgatgaat attcatgttc accaaatggt tggatgtatc 81360

gtaaagatgt agatggtgtc attccagttg aaatcgcgaa ggtattttat cagcgtaaag 81420

agtggaaaaa taaaatgatg ggtgccaaac gaaatcaaga actgattaaa aaggttctga 81480

atgataagaa gtttggaact atcgataaat tcgcagaagt taatgtctat gaagatttct 81540

ctgatgatat gaaagcagaa ctgctgacat ataccgaaga gtgtcttgac aaactgatgt 81600

ttgaatgtaa acacgctgaa atcttgggta acactaacca gttaaaccgt aagattctga 81660

tcaactcact ttatggtgca ttgggtaaca tttacttccg ttattatgat ttgcgcaacg 81720

catcagcaat cacattgttt ggtcaaatgg caattcaatg gattgaacgt aaagttaatg 81780

aatacctcaa caaggtatgt ggcaccgaag gacattcgtt tgtagtagct ggtgatactg 81840

actcaattta cgtttgtgtt gataaggtta tcgagaaggt aggtcttgag cgtttcaaag 81900

aaactaacga tttggtcgaa ttcctgaacc aattcggcaa gaagaaaatg gaaccatgga 81960

ttgaccaatc atatcgtgag atgtgtgaat acatgaacaa caaagaacat ttaatgttca 82020

tggaccgtga agctatttct tgtcctccgt tggggtcaaa cggcattggc ggattctgga 82080

aagcgaagaa acgatatgct ctgaacgtgt atgatatgga aggtactcga tatgcagaac 82140

ctcatctgaa aatcatgggt atggaaactc agcaaagttc tacgccaact gctgttcaga 82200

atgcattgga agaatctatt cggcgtatgc tgcaggaagg tgaagaatct ttacagcaat 82260

attataagca gtttgagtct gaatatcgtg aacttgatta taaagtaatc gccgaagtta 82320

agactgcaaa caacatcggt aagtatgatg acggtgcagg atatccagat aaaggtacac 82380

catatcacgt taaaggtgct ttggcatata accgagcaac cgcaggattt gaaggtataa 82440

caccaatcat ggaaggtgag aaagtgatgg tcatcccgct gcgtgaaggt aacccgtacg 82500

gtgagaaatg catggcatgg ccatcgggca ctgagctgcc acaagaaatc cgacaggaag 82560

ttctagtgtg gcttgaccac agtgttctgt tccaaaaatc gttcgttaaa cctctgacgg 82620

gtatgtctga agcggcaggg ttagactatg aagagaaatc gtctcttctt gacatgttcg 82680

atttttaaaa aagttgttta ctttaccaca aggatgtggt actatagctc tcgaaataac 82740

atactgagga gattacaatg aaatcgttac ttgctgttat tgttgctctc acgctgactg 82800

gttgtcaaat gccacaaggt gatatcgtcc cggcttcttc tgttgggcag gtgcgagcaa 82860

ttggcggtac tgtaggatac tatcgtgcta gcaaccaggt ctctgctgaa tcgctcgcgg 82920

ttgagcgtcg gttggcgaaa gaaaaagcta atcctaatcg tcagctgtct gcgatggaac 82980

ttgacatgat tgagcagaat aagcatgaac tggaagaaat taagcgtctg cgtaaaactc 83040

aaaaagaacg tacgtgcact gctcaagcgg cagcagtgaa tgaccagatt cgtttaactg 83100

attttgctaa cggcggattg agttataatg agcataaaca acgtatggag cagttaaaat 83160

ctctccaaaa tcacatctac aacaaatgca tgtctaactg aggagattaa catggaagca 83220

gtatttggtt taatcattct tttcttcatc tatttttgc cgacctttgt agcttgcagt 83280

cgtaagcata aatcacgggg tggaatcttt atcacaaatc tagtattcgg ttggtccatt 83340

atcggttggt taattgcgct gatttggtct gcttctaacg cacagcagaa tacaattatt 83400

atccagcaag ttaaataaga ggtctcatga ttgtaactcc aatgacagta caagatatcc 83460

gtcaagaatt cgctgatgct ttgctcaaca aagaatttgt gattgataag acgggtgtga 83520

agactattga aatcgtaggt gcatcattta ttgcagatga aaacctaatt tttggcgcag 83580

ttaatgatgg atacattgct cgtgaacttg agtggtataa atctcaaagt ttattcgtta 83640

aagatattcc gggtgaaacc ccagctattt ggaaagcaat tgcatccaaa cacggcgaga 83700

ttaattctaa ctatggctgg gcagtttggt caacacaaaa ctattcacag tttgctaact 83760

gtgcgaaaga acttatcaat aatcctgatt ctcgccgcgg aattatgatt tatacacgac 83820

ctcaaatgca gtatgatttt gagcgcgatg gcatgagtga tttcatgtgt actaacaatg 83880

ttcagtatct gattcgtgat aatcgtgtgc atgctgtggt aaacatgcgt tcgaatgatg 83940

tcgtctttgg atatcgtaat gactatgcat ggcagctcta tgttttggaa cagttaacca 84000

aacttctgaa tgcatcaggt aaaaattatt cagttggtga cattatttgg aacgtcgggt 84060

ctttgcacgt atattctcga catttctatc tcgtagataa ttatgctcac acgggtgaaa 84120

ctcacatcgc aaagaaagac tataaaggtg aatggaaatg attcagtttg taattccaag 84180

ttataagcgc gccggggcag ttactgccct gactatgttt cctgaaggtt atgttccaca 84240

tcttgtagta cgtgaatcag aaaaagaagc atacgaaact tggcacggtc atgctgctaa 84300

aatcgttact gtccccgatg atgtcgatgg aattgcggga actcgccgtc tgattactga 84360

aatgtatgca gggcaacgaa tttggatgct tgatgatgat acgaccattc atctgactga 84420

aattcgtgaa cgcgacgatc gccgggttcc acttggtgtc ggcgaggcaa tgagtcaaga 84480

ggtatttgat gatatggtca aatacgtcga gactgccatg gattgtggtt attatcacgg 84540

tcatgctcgc ttaccgattt tcaaaatcac atcaagctgg ggtcattatc gtgagaatag 84600

ctttgggttc accaatactt tctatgattt gactaaactt accgcagaag acattggcta 84660

cggaattatt gaccttaacg aagatgctta tgcttttcta aaattaatta acatgggtca 84720

tcctcatctg gctctgttta agtacctcgt taaatctggt aaggtgcagt cacctggtgg 84780

ttgttctaca cagcgtgata ctgctcgcca gaatagagcc cttgaacagc tgcatgctgc 84840

tttcccaaat caagcccgtt ggaaatctaa agacggtgaa agacgtggtt tattcggtga 84900

tgacgaacca ctaaaatcaa ttcgtatgtg tattaacact cgagtgaaat cccaggcctt 84960

ccatgaattt ggtaaggtag aaccatatct gtgagggcga aagccctcca aggacctctt 85020

atgaacatct atgataaatc tgatgtagct ggtaacatat tcaaggctga agaattcaga 85080

tgcttcgtat gtaaatctga tgagtttgtt catgaaggaa ctactggctc agatggaatg 85140

cattgctggt ggcacggcat gtgtgttgga tgtaaaatac actacgaaat agatatggaa 85200

acagtggttt ataacaccaa gaagaaatgg aacttctgtt aatagcttca agaacaaagt 85260

aatataatta ctctatcctt taacctgtga gaaaaatata atggagactt atggaatata 85320

atgaatgtct gacttaaaat ctcgcctgat taaagcatcc acttctaaaa tgacagcaga 85380

actgactaaa tcaaaattct ttaacgagaa agatgtagtt agaaccaaaa ttccgatgct 85440

taatatcgca atcagtggag cgttggatgg tggtatgcag tccgggttga ctatcttcgc 85500

aggtccatct aaacacttca aatctaacat gtctctgaca atggttagtg cttatcttaa 85560

taagtatcct gatgcggtct gcttgttcta tgattcagaa tttggtatca ctccagctta 85620

tctgaaatct atgggtgttg accctgaccg tgtaattcat acaccggttc agtcggttga 85680

acaattaaaa atcgatatgg ttaaccagct tgaagctatt gagcgtggtg aaaaagtcat 85740

cgtgtttatc gactctattg gtaacatggc gtctaaaaag gaaaccgaag atgctttgaa 85800

cgagaaatct gttgcagata tgactcgtgc gaaaagtctg aagtcgctct tccgtatcgt 85860

aactccttac ttctctatta agaacattcc ttgtgtagcg gttaaccaca caatcgagac 85920

tatcgagatg ttcagtaaga cggtaatgac aggtggtaca ggtcctatgt attctgcgga 85980

tactgtattc atcatcggta aacgtcaaat taaagatggt tctgagcttg agggatatca 86040

gtttgtcctg aacgctgaga aatcgcgtac tgtcaaagag aaaagtaagt tcttcatcga 86100

tgttaaattc gatggtggta tcgatccata tagtggtctg cttgatatgg ctctagatat 86160

cgggtttgtg gttaaaccga aaaatggatg gtatgcacga gaattcctgg atgttgaaac 86220

cggtgagatg attcgtgaag aaaaatcctg gcgggcaaaa gatacgagca gtacggaatt 86280

ttggggtcct ctgtttaagc atgagccatt ccgtgacgct atcaaagccc ggtatcagtt 86340

gggtgctatt gattcaaacg ctgcggttga tgaagcggta gcagaaatga ttaactcaaa 86400

agtttcaact aaggttgatg gtgttaaact tcctgagagt ggttcagtat cagctgctga 86460

agttgaagat gaattagaga acttcatgaa tgaagactga gtttgattta gaatctgaac 86520

tcgagaaatt tgaacaagaa tctccctcgg aagagggaga cttcgagcgt caagaacgag 86580

tgttcaagaa aagccatgaa ataatccaag aagctatgaa gactgttatc caagaaattg 86640

tgataaaatt aaatggtcaa tcacacttgg tttatgttca taaattaaat atttctcctt 86700

cgggggaagt aactattgag ttcagtacac catctgaagc tcataaggat gaactttatc 86760

ctcatgtgga agcttgtgtt aaacaacaaa tccagagtgc attaaagacc aagaaaaaat 86820

cattatggaa aatcttttaa gaggttaaag tggtagaaac aatcttagct aatctgattt 86880

acaaccaggc tttctttacg aaggtttggc catatatgga caaagagtac ttcgagcaag 86940

gacctgctca gacggtgttt aacataatta agaaacacgt taatgaatac acagcaattc 87000

cttcaaagac tgcgttatgt gtagcactgg ataattcgtc tataactgaa acggaacatg 87060

aaggtgcaaa gaaacttatt gataagttat ctgatgctcc tgaagatttg aattggttag 87120

ttaaggaaac agagaagtac gttcaagaaa aggctatgta caacgcaacg tctcgaatta 87180

ttgaaattca gactaatgcc cagcttgagc caaataaacg cgataagcgt cttcctgata 87240

ttggggctat tcctgatatc atgcgtgaag cgttatcagt atcgtttgat agctatattg 87300

gccatgattg gatggaagat tatgaagctc gttggttatc ataccagaat aaagctcgta 87360

aagttccgtt taaacttagc attctgaaca aaattactaa aggtggtgcc gagactggta 87420

cactgaacgt attgatggct ggcgtcaacg ttggtaaatc attaggatta tgttcattgg 87480

ctgcagacta tcttcagatg gggcataacg tcctttatat ttccatggaa atggccgaag 87540

aagtttgcgc taaacgtatt gatgctaact tgcttgatgt atcacttgat gatattgacg 87600

atggatgtgt atcatacgct gaatataaag gcaagatgga aaaatggcgt agttctagta 87660

ctcttggtcg tttaatcatt aaacagtatc cgactggtgg cgctaacgct aatacattcc 87720

gagctcttct gaatgagttg aaactcaaga agaactttaa accgactgtt atcatcattg 87780

actatcttgg tatttgtgct tcttgccgta ttcgtcaata tactgaaaac agttacacgt 87840

tagttaaagc tattgcagaa gaacttcgtg cattggctgt agaatctgaa actgttcttt 87900

ggaccgcagc tcaggtaggt cgttcagcgt gggatgcttc tgatatggac atgagtgata 87960

ttgcagaatc tgcgggtcta cctgctacgg cagactttat gctggctgtg attgaaaccc 88020

ctgaacttgc tcagatgaag cagcaattaa ttaagcagat taaatcacgt tacggtgata 88080

agaacatcaa caataagttc tctatgggtg tacataaggc taatcagcgt tgggtagaaa 88140

ttgagcagca aaacgaccca actaagccta atccaagcaa taccgtccga gaaggtgccg 88200

gtgcacagaa ccgtgtagcc gaatctaatc gtcaagaacg agtatcacgt tctaagcttg 88260

atgctctagc agaagagttg aaattctagg gtaaatttta tgatttttgt gtttagcgta 88320

attcgcgacc aatcaggtcg ctcctttgtg gtgacggcgt ctgatagcgt ccatcgtgga 88380

gtcatagctt acaacaaagc agatttatct tcatatgact atggtgaagt taaggcatat 88440

aatgacgaag gtatctgggt taactctgcg atataccttc caaccaagaa tttgacatcc 88500

gacgaagtcc tcgaaaaatt attcaaaaga tagtttactt ttaagtttgg ccatgttatt 88560

atggccttac tgaaacaaac tgaggaaaac aaaatgaaaa agattgtact tgctttaatc 88620

ttcgcagtat caagttgctc tgctgttccc gctctggcga actatgacaa agacctctgc 88680

gaatggtcaa tgactgcaga tgaaaaagat gttgctgagc agattcgtgc tgatgtaggt 88740

catatcattg ataacactga cccaagcaag atgaaagaag ttcaggcaga aatctccaat 88800

gatggcgcag caattaaact gaactatgct ctgtactgcg atgctaattt tgataacttc 88860

acaattgcaa gctggattct cggatgatta catacgtatt agtaatggct ataatgactg 88920

gtgccggcgg tgtttctact gaaaagttat cattcacagg aatgaacgag tcttcgctgg 88980

ctcagaaatg tgaagatgcg ggaaaacaat ttactggcat caaagccgat tccgggttcg 89040

gttcaccatc agtctacact acgtacaagt gtattcgtat tgatggtgga aataataaat 89100

agtttggagg ctctatgaaa acatttaaag agtttgttaa acttaatgag gaaatggttg 89160

ctggcgatgc cggcggtaat cctcagaaca ttgcatcagg cactacttcg ggcgcagtag 89220

taaataaagg cccagaaact ctcccaaaga aaaagcgaga taaatcaaaa cctgaaacgt 89280

gatacaatgg ccttattagt ttaaggccag aggaatataa tatgtcatgg gttgataacg 89340

aattcgctat ccgcgcaata tctcacctac ctaagtttag acacgttact acatcttcaa 89400

catttaagtt aaactgccgt tgcccaattt gtggtgactc acagaaagat atcaataaag 89460

cccgattctg gatttttgat gcgggtcaag gattacgctg ccattgcttc aactgtgagt 89520

ataacaagtg gctatcacaa tatcttaaag ataatgaacc cgatctctat cgagagtatc 89580

ttcttgagaa aagaaaggag caggtctttg ataagccaaa gaccgtagaa ccgtctgaga 89640

aaattaatgc aaaactcccc gtaatagaaa aacttaattt ctgtgagcga ttagatagac 89700

ttcctaagga acatccgata gttaaatacg tgactgccag atgtattcca agcacttctt 89760

ggaaaaggtt atggtttact aaccaatggc cttctcttgt taactccgtt aatccaggaa 89820

cctataagaa tgagacgaac gaaccacgtt tggttattcc tatcttcaac aagaaaggag 89880

agattgagtc gtttcaagga cgagcactac gaaaaaatgc tccacaaaaa tacatcacaa 89940

tcaaagccca tgaacacgcg accaaaattt atggtctcga cactattgat gagtcaaaac 90000

tcgtattcgt catggaagga ccaatagatt cgttgttcat tgataacgct attgcaatca 90060

ctggcgggtc tttagattta gctcaagttc catgccatga taaccgagcg tggattatgg 90120

accatgaacc tcgtcatccc gatacaatta agcgtatgaa acgtttagta gatgctggtg 90180

aaaaggtagt tttctgggat aagtcgcctt ggaaaagcaa agatataaat gatatgatta 90240

tgaaagaggg ggcaactgct tctgaaataa cggattatat taatcaaaat atatcgcaag 90300

gtttaatggc taaattacgt cttgacaaat atgcgaagat ataggggcca aagcccctta 90360

aattaaagca atcctccagt cataataaac gacacaactt tttctaacgg cattggagga 90420

agaactagcc cgtgtgtgct agctaatgga actaccacat aattccatgc agctaaagca 90480

gcagtggcga ttccgacgta aagatatctt ccaaatcctc ctttgtcttt acattctcgt 90540

ttcacttcag acatgaatcc tcctgctatt tatgttaagt gatataatat ttatctaatt 90600

taattgaaag gaaaaataat atgccacatt tcaacgaatg tagtcaactg atcgctggtg 90660

cagataaagc tgaagctcga tacgcaggta tcgtacgcaa agttggtggt gaccctctgc 90720

aagtaatgct tgatatgcaa aaatctcttc aggttcgtct tgcaaatgac aagcctggta 90780

ctaacatgca tcctgatgaa ttggcccaag ccggtgatat cgtgcagtgg ctgcgtaacc 90840

aaaaagatta cattgatgac gaattccgcg aattgctgac gtctcttggc ggtatgagta 90900

atggtgaaaa ggcagctagt gctgtgtgga aaccatggaa atctgaccac gtcaaaatgc 90960

aggaaactta tatcaaagac ctgtctgata aagaccagct tgaaatcaaa tttgaaatga 91020

ttgatatcct gcactttgtt ctgaatatgt ttatggcgct tggtctggat tctgaagaaa 91080

tctttaagct gtattatctg aaaaacgccg agaactttgc tcgccaagac agtggttact 91140

gatggccaaa agaatatcta agcgtcgttt aaaaattatc agaaaacaaa aagaaagggc 91200

cttagtattg gcccttcgag aagaaatcac tcgagaaatt gataaagaaa tattaaaggc 91260

gcttacagca gctatataaa tactcctgta aactaaatag gagattaaaa tggcttacgt 91320

aaacatcaaa acttttgacc atacaactgc tgatggtgaa gttaaaggta cagaagtatc 91380

tgtagctttt aaggtgtatt ctgattcaca tcgcattgct aacgcacagt atcagatttt 91440

cccatctgaa aaagctgctt attcaacagt agttgatgat gctgcaactt gggcaaccac 91500

caacgctaaa atgtttgaag ctgttccatc tgatgcagaa gtataaaaat taaggactcc 91560

tccgggagtc cttttatgct atactgggaa tagtatatta ttcctactaa ctgaggagaa 91620

gaaaatgata tgttatacta agccctggta tcaatcgtca ttaaagaagt ctcattttga 91680

ttgttggtac agaggtgtaa gagctgcagc gttattactc aaagctgcgc cggctttaat 91740

taaagcaaat gataagtggt ttgaagacaa caacatgact gaaggagctc tttgtggcaa 91800

acgcaaaaat ctataacgca aaaatctata aagtaagctt acaacgcgca gttcaatcaa 91860

gaagtgatgc aaatggagtt ttgcgtctag accaagatag aatttttact gttgctctat 91920

acagtacgtt cgacaaagat ttcaaagacc tagttaataa attcgaagcg tttggttggt 91980

gtccttctga agattatggc attattaaga ctgcccatgt ctttgacgta gatacagttc 92040

caggaagtcc tgttgctata ctacgtgctc tccacttgaa aggatacact aatgtatgtc 92100

atgaaactag cttatatgaa tacgaaaatg acataatttc aagaggcaaa aagattatca 92160

ttgatagcac agattctcta atagaattta ctaagttagt ttggttgtat atgggcgcag 92220

attttatcaa actgactcca agcccgctgt tgcaaaaagc ggctgatgga tataacagca 92280

gtagttgtct gtatcgcaat aatgagtggt tcatgtgatg gatttgtttg aaatgatgga 92340

agagcctcag gaagaggttc aagttcatcc agtgatttct aaggacatca aagacgaata 92400

ccgtataatt atacagaagt atggtattaa agccccagaa gctcttctag atgaactagc 92460

ttcaatctgg tctgacccgc cgccctggtc tccgtgggca aaataatttc acaaagtagt 92520

ttactcttcc aaaagccatg ataagatacc tctcgtaacc aaaaaatgga gaatatcatg 92580

gctatttcat taaacccatc tatttcagta aaattatcaa aggttattcc tatcgaaaaa 92640

cccattcgtt ccattgatgt tcttaacttc gcgcgagaaa gcaaaggatt acctttatat 92700

gatttaagcg tgtgggaagc attagccaat cgttttgact gcaaagaaca gtcaattcta 92760

tggcaatgca tgaacaataa gattggcgaa gaatttcata agaaacttga ctctatcgtt 92820

agacgtcatc aaattgataa tagtgacatt ctctatagag gtctatcatg ccgcgagtct 92880

aaagcctttt atgacgccct tattaaagga gagaaatttg gctttggaaa ggttgcgtca 92940

ttcacaacag atgaaacgat cgccagagag tttgcaggca aatggcatta ctcgaccttt 93000

gtagtcattg aagtcaataa ttgccatcaa tcatttgatt atcataccaa catgaaatcg 93060

cttttaatta ctgcaccaga ttctgaattc atgcgtccaa atgatgtgat tgataacatt 93120

gctcagcgca gaagcgctga catcgagatg attgataaag aacaagaaag gatgctaccg 93180

atgggaacta agttcaaagt ggtgggtcat aacaaagttg aaaaatctgg tttacttatg 93240

gactacttta gtgttactat agcttagtca actagtgatt atctagaact agggacctag 93300

acccattata ccgtccgtaa gacgaaagca tttttgagga aaacatgatg aaatttactg 93360

ctgaaaccgc taagatttat actcgcctga ttacaacttt aggttctgcc cagcgtcgga 93420

acaaggagtt caatcttacc cctgagtatc tgtttaacat catgcaacag actcattgcg 93480

catactcggg tgaaaagttt ggaaccgtca aaggaaacca tcctgacagc atgacgcttg 93540

aacgctggaa taatgacttg ggatatgtaa tggggaatgt tattcctgtc aagcaaaagt 93600

ataatacttt gcgtggaaat aatacgattg aaggccttga gcgaaaagcg aatgaaatcg 93660

cagcacgcat agttcgttct tcagattctg ttaagccaac aagtgataaa gaagcttctc 93720

gtttggaaaa gattcgtgag tatgaaaaaa ctataacatc aattaaaact aacttacaca 93780

atcgtgaaaa tcatctttct caatttgtgc aaaaagaaaa gaatggaact gcaacctcgg 93840

ctgatttaga acttattaat gcattgagaa ctcgtatcag cggtggtaag tctgaattag 93900

ctaaagttga gcgtaagtta tctgctattt tagcgtcagt tccgaatcgt ccgtcagatg 93960

ctgaaatccg tgtacaatca atacggttaa ttgttagctc acttcgtcgg ttagaagaat 94020

gctcaatgtt agataagtta aaattgaaaa aaggtcttcc attgactgct tccttcttcc 94080

aacttttgag aggtaaaatg taatgcaaca ctatggatat gtagtagcgt ataaggataa 94140

agacggattt gaccatccag tcacaactga tatgtatgat ggagaacgat gtgtagtctt 94200

cactaatgaa gaatcagcca ataaagcacg gattcgtaca atgtcggttt taacagacaa 94260

attggcaaag gggaatttta ctgggaaaag caaaaccaaa gggatgcttt ggtggaaaac 94320

aactgagcta gtgtatgaac cacttagcga tgttgagcgt gaaaaactca aagcaaaaat 94380

taaaaatcta catgtagtga gggtaaaagt ggcatgatta cgtttgacca attaaaagaa 94440

agtcaaaaag cgatttttaa taaagtcatt gaaatggtca aacaaggagc taaaggtcaa 94500

catattacga ttaatggacc cgccggtaca ggtaaaacaa ctttaaccaa atttatcatt 94560

gacgctttga tttctcaggg tatctctgga attgcattgg cagcacctac gcatggggcc 94620

aaaaaggttt tatctaagct cagcggaatg caagccagta ctattcatag tcttctgaaa 94680

attaacccga cgacatatga agaaaacgtt ctgtttgagc aaaagaaagt tccggatatg 94740

gcatctattc gagttcttat ctgtgatgaa gcttcaatgt atgaccgtaa gctgtttaag 94800

attttgatgg caactattcc tgcctggtgt attgtcattg ccattggtga taaggctcaa 94860

atacgtccgg tagaacctgg aagtaatgaa cctgcactga gtccattctt cactcataaa 94920

gatttcttac aacttcattt gaccgaggtg atgcggagta atgctccaat cattgaagtt 94980

gctactgaaa tcagaaacgg tgggtggatt cgtgactgtg tagttgatgg tcatggcgtc 95040

cgtggtttta ctaaaggaac cgcccttaaa gattttatgc taaattattt taatttagtt 95100

aaaacaccag aagatttatt tgaaaacaga atgcttgcat tcactaataa atctgtggat 95160

aaattgaacg aaataatcag acgcagaatc tatgaaactg aacgaccatt cgtagtaggt 95220

gagattgttg ttatgcaaga acctcttacc aaggaactta aatttgaagg gaagaaattc 95280

agcgaaattc ttttcaataa tggtcagttt gttcgcatat tagatgcaat tgaaaccacg 95340

tcatttttag gtgccagagg tgttccaggt gaatatctgg ttcgtcattg ggtattagat 95400

attgaaacct atggcgacga tgaagagtac gctagagaga aaatctgtgt catctcatcc 95460

gaagaagaaa tgaataagtt tcaattcttc ttggcaaaaa cagcggatac atataagaac 95520

tggaataaag gcggtaaagc accttggtct gaattctggg atgctaagcg caagtttcat 95580

aaagtgaaag cattaccagc ttcgactttc cataaggccc agggcatctc aattgacaga 95640

agcttcattt atactccatg cattcacatg gcagatgctt ctctcgcgca acagttatta 95700

tatgttggta ctactcgtgg tcgctatgat gtattctatg tgtgaggtaa tatgtttgaa 95760

ttgaaattag aagaccttca aacaatgatt gttggcttac aagaatctaa gtttgaagca 95820

ccagataatg ttaagcgtgc tattaacatt aaaattgata tagttctgaa tgagcttcgt 95880

gatatagcag ataatgctaa tgctattact tggttcacag gatatgaccc aaaggtgtat 95940

ctgagcgaat atattggttg ccagttacgc gaaattaaat ttatgctaga ggctcaaaat 96000

ggctaaagac tttattattg attttgaaac attcggaaat gtgtcaagct cttctgtgat 96060

tgaccttgct ctaatcacat ttgattctga ccccgaagtt ttggaaagct tcgatgaatt 96120

ggttaaacgt ggtcatcgta ttaagtttga ccttaaatcc cagaaaggtc atcggttgtt 96180

tggtaagtct actcttgagt ggtggaagaa acaatcagct gaggcccgtg ctaacctggc 96240

ctcaacgcca gacgatttat cagtaattgc tggaattaaa gaagctcagc aatatctgat 96300

tgataatgga attcacccat gggattcctt tggctggtgt cgtggacaga gctttgactt 96360

tccaattttt gttgattgtc ttcgcgatgt tcaacgagcc caaggaattt ccgaagaaga 96420

aattgataca tttaaagaag aaccatgtaa gttctggaat cagcgtgata ttcgtaccgc 96480

gattgaatca ctgcttctta cccgcgggct gacaactacc cctcttccaa agggtactct 96540

caacgggttt attgcgcatg atagtatcca tgactgtgct aaagatattc taatgcttaa 96600

atatgctcaa cgctatgctc taggcctaag cgaagcacca agtccagaag ataccgatcc 96660

actgagttta cctaaggggc gtggctaatg gaagagtttg agttcgatga aaactttgaa 96720

gagtggttca accgggaaat cctcccgaaa atctctccaa cgatggttct ggtggccaag 96780

gctttgatgg ctaaaggctg ggacgcaggg tatatgttcg gcgtcgatgt tgggtgtgaa 96840

atttctcacc gatagctatt tactttatga aagagccgtt atataatggc tctacattaa 96900

caaactgaga gaaacatgat gaaaaatttg gttgtaggcg aaaacgttaa agtaattggt 96960

ggtaagcata tcggtaaaga aggcgtaatt gttggaatct ttaaccgttc taacaaaatg 97020

tcttcatatt tgcttcaatt ggaaaatgaa gacaaagccg tgtattcgct gcaaaaattc 97080

gtagttgctc tagaatcgcg cgatttgctt gattctatgt ttaacgaaag ctatctgcgc 97140

aagtgggtac atgtgaattc acttgacaat gttattaccc aatcggtgag ttctactaat 97200

tcagccacta atctgtcgct gcataaaaat gttcttgtca ctgatgagtg ggaagaagac 97260

ggtaaaaccc tagtaaacgt agtgtttcaa ggcaactatg cagttctgcc taaagccgat 97320

gtagagccga cagaatcgca acgtcaaggt ttagtataaa aagttgttta ctttgccaca 97380

aggatgtggt actattatct tatcaactac tgaggagaat aacatgaaaa ctgaaaacac 97440

cgtaaaaatt actgccgaag cttttgaaga cattctgttc aacccggact taatcgtcgt 97500

tcagaaagag aaaaccttcg gtaaagaaga gcattggacc tggttgtatg tattcgcgaa 97560

ccatggtgat atcgtcccag ttcgtacctt tgctcgtgta attacagttg atggcccaga 97620

atacatggag attgtgtaat gaattttaaa gaaggcgtac agtacaaatt cgtcaatgat 97680

gaagcggaag aagaattttc ttcacgttat gaggttaatg aagactttgt gtatgaactc 97740

tatgaaaatg gcgggagttt tactgttact aaagttgacc gccaaaataa tagagtatca 97800

ggaattatgt gggctaatgg cacagaatgt gatgaagtcg gcggtgaaga ccttgtaatt 97860

tttgatagcg aattcaaata ctttactgaa gttggaactt ccgcgaatgt aattccaacc 97920

gatttggtta tgaatctttc tattcataac cgtggtcaag caatcgctgc tattgcagca 97980

ctgcagagtg catatcaatg ttaaatttag ctcctatttt tgaagcatca aaactgtctt 98040

atcctattcc taaccgtagc attgggaatg tcatgctgca actttcttca gaaactggag 98100

aaatgtgtga ttggattaat cgtccatggc ggcagaaaga agagtttgaa ggtgagtgcg 98160

cagatgttat taactgtgta gtagatgcac tttggctgca tttcagaaat cgtcataaaa 98220

atgataccca tgtatcagat gatgaaatct ccatgatggt tactcgtgca ctaaatgagc 98280

aaatcatggt caaaacacaa aaatggaagg atgctgttaa tgccaatgta tgattacaag 98340

tgtgaagtct gtggaaaaaa gatagaaatt atgcgtaaaa tttcccatcg tgactatact 98400

gttaactgct ttaaccctaa gtgtgaaggt caaatgaagc gggtggtttc tgctccggca 98460

gttcactacg atggattaaa gagtggtgat tattgatggg aactaaagca cgcattacca 98520

tgaaacccgg agaaatccgg gttattaaag taggtaatat aacttatagg gttaaattga 98580

aatgaaaaag attttaatta cagcgcttgc cttcatgatg attggatgca ctgacgctga 98640

taacgcaact cgagtattag aaaatgcagg attcactgaa gttgatatca ctggatacaa 98700

atttttctca tgttcagaag atgattttca gcataccggg ttcaaagcgg tcggtcctac 98760

cggaaagacg gttaaaggta cagtgtgttc tgggattttc ttgaagaata gtactattcg 98820

ttttgaataa aaaggacctt cgggtccttt agttgtttac acgaatagtc ttctgcggta 98880

ttatagactt ataaactact ggagaataaa acatgaaata catcatctta actttaatcg 98940

cattagttat ctcaattgga gttctggttt ccttagcaga ttctacggaa tcttctaatg 99000

aagttcagaa aagctcaatt ggtattggtg tgaatggaca agttggtgtt aagatttcag 99060

ataatctttg tgttaatcct tctactggtg ctgctgaagt atgcttttaa aatgtattga 99120

tataatgcct ccactaactg aggaaatgta atgattaaga acgaaattaa aattctgagt 99180

gaccgagaac atatcattaa gcgcagcgga atgtacatcg gtagttctgc gtgtgaggca 99240

catgaccgtt ttctttttgg taaattccaa tcagtaaagt atgttcctgg tattattaag 99300

cttattgatg aaatcattga taactctgtt gatgaagcaa ttcgtacaaa ttttaaacat 99360

gccaataaaa tttccgttga tatcaaggga aataagatta tcgtaactga taatggtcgt 99420

ggtcttccac aggctccggt agtaactcct gaaggagaaa ctattccagg cccagtcgcc 99480

gcatggactc gtcctcgtgc gggtggtaac tttggcgatg atgctgagcg taaaactggt 99540

ggtatgaacg gtgtcggttc tgcattaact aacatctttt cagtatcttt cactggtgca 99600

acatgtgatg gtaaaaatga aatcattgtc cgttgttcta atggctcaga aaatatctcc 99660

tgggaagaac atccagcaaa agacaaagaa ttcatcaaag ataagactgg tactgtagta 99720

tcattcattc cagatttcag tcactttgaa agcacaggat tgactgatgt tgaccaatca 99780

atcattcacg atcgtctgat gacattagca gtagtttatc ctgatattga attcaaattc 99840

atgggtaaac gtgttcaagg taagtttaaa gcttacgccc agatgtatga tgaaaatgcg 99900

gtagtgcagg attctgatac ttgtgctatt gctattggtc gctcagatga tgggttccgc 99960

cagctttcat atgttaataa cattcacacc aaaaatggtg gtactcacgt tgacctagtt 100020

cttgatgaac tgagcaatga acttattcca gcattaaaac gcaagtacaa actagaagtt 100080

aataaagcac gaattaaaga gtgtctgact gtcattatgt ttattcgtga catgtctaac 100140

atgcgatttg attctcagac taaagagcgt ttgacttctc cttggggcga aattcgtagt 100200

catattgata ttgattacaa gaaacttgct aacgctatta tgaaatctga agatattcat 100260

atgccgatta ttgaggcgat gttagctcgt aaacttgctg cagagaaagc tgcagaaact 100320

aaagccgcca agaaagcgca gaaagctaaa gtagctaagc acatcaaagc caacaaatat 100380

ggtaaagatg ctgacaccac tttattcttg accgaaggtg attctgcgat tggttatcta 100440

ctcacaactc gcgaccgtga acttcatggt ggatatcctc tacgtggtaa gttcatgaat 100500

acatggggaa tgtctgctgc agatgctatg aagaacaagg aagtatttga catttgtgca 100560

atcaccggtt tgacgattgg tgagcctgct gaaaatacta actaccgaaa tattgctatc 100620

atgaccgatg cggatgttga tggtgttggt tcaattttcc caagtctttt agcgtttttc 100680

agtaattggc ctgaactgtt tgaacaaggt agaatccgct ttgtgaaaac tccggttatt 100740

attctcacca aaggtaaaga acaacgttgg ttctattctc ttggcgaata tgaagaccat 100800

aaagatgatt tcaaaggttg gaaacttcgt tatattaaag gtcttggttc tcttgaagaa 100860

gatgaatatg aacgtgttat tcaagacccg gtttatgatg tagtatctct tcctgaaaac 100920

tggaaagaac tgtttgaatt aattatgggt aatgatgctg ctccacgtaa gacctggatg 100980

agtgaataaa tagtacgggt aatattgccc tgctatagaa ggaattacta tgcaacgtta 101040

ttggattact ttggtctcag gcgattacgg atacatgttt gccgaaaaga aacctctccc 101100

tggtacttgg gttactatct gggtggaaaa ctcggatggt tctaaacatg aggtgtatgg 101160

ccgcgttagc agagtgcatt aatcccgagg ggcttcggcc cctcttttct gaggaaatta 101220

ttatgaagtc aactatcatt tcaatactcc gcactgaggc actaaaatac tcagtcgacc 101280

cctccaatga ataccaagaa cttttaatca aacggttatt aaattctata gctgaccgtt 101340

tggaaagtaa ccagagtgtc cctattaatc acagcctttt tgctatgaaa gtgatacgct 101400

ttttacgtcc tgatattaaa attgctgaca tggtcaaagt gattaaatcg tcaggagcag 101460

taaaatgcta aagaaaagtt atgttccaaa taaagaatta tttgatgatg ctatatatcg 101520

agagtatcgt atcatccaac gtttctttga tatccaagca gcagaggaat tcaaagaccg 101580

ctttaaacaa atcagtgata aaatttttac aactaacacc gctactgctg aagagctcct 101640

tgaagtagca gaaatcatta aacgacacaa ttgataggaa taaaatgaaa attaaatgtg 101700

atgatgaagt aattattggt tcttctgacg ctgaggattc aacgtttacc attaaagctt 101760

caggtaaagc ttttgacatc ttgtcaaaca aactctataa gtataaagtt cgtgcggttg 101820

ttcgtgaact ttctactaac tgtgatgatg ctcataaact gaacggtaat gaaaatcgtc 101880

cattttacat caaagcacca actcgtcttg acccgcgctt tgtaattcgt gattatggtc 101940

caggtcttaa tcataatgac atgatgacga tgtacaaaac gttctttgaa tctacaaaga 102000

ataatagtaa tgatttcatc ggtgctcttg gtcttggttc taaatcgcct ttaagctata 102060

caagtacatt taacgtagta tcatatcata atggtaaagc caccggttat actgtcatga 102120

aaaaccgcgg tgaacctact attcgtccga tgtttgtcga tgatatgaaa gaagacgaag 102180

aaactggtct tgaaattaca gttccggtta aagtagaaga tattgatacc tggcactatg 102240

aaatcgcata tattttgcgt acatttggtg ctgtacctcc aaaggtagat tctcttcgcc 102300

gtgaaattga atatttccca gtagataaaa ctgattggtt tagcgttaat agctcttacg 102360

aaagttatgg cctgtatgca gtttatggaa aaatcgtata tcctatcagc ggtgtagatg 102420

ttaaggcaga ttggctgctt aatcgctatg gtaaggttta tgttcatttc ccactgggtg 102480

aattggatat cactccatct cgtgaagagc tttctcttga cgaagaaaca attgctaata 102540

tccagaagcg tgtgaatgct cttgaagaag aggtaattac cgcagatatt aaagcgtttg 102600

aagcgtatga atctgaccgt gaattcctgc gtgagttcaa taagctgagt tctaaggaac 102660

gctctattct tcagagccgc ggtattacca ttgggaaccg cgatattaaa caagtagttg 102720

cgaagtataa tcttgataaa attcgttcat actatgtaga taacgaagta tcagtttatg 102780

tttcatgcga tgaacctgct cgtcgtaaag tgtcaagcag ttcttggcat cgtcataacc 102840

aagtaaacat ttctgatatt tgcggggttg atagaactaa agcgtttgtt cttattgacg 102900

ataaagcggg taagcgtatt gctacggttc gtgctctgtg taaatctggg ttagttccaa 102960

tctgggcaca cattactgta atcaaagaca atgaagatga attacatgtc attgatgagc 103020

tgaagaaaat catggatact gatgaagttg tagtattccg tgtgtctgaa cttgaagccc 103080

agagaaaagc tcttcctgat tacgacactg gtccaaaaga gaaacgtcct aaatcaccaa 103140

atgtttctct gcattggatt gataaagacg ggtactggga agaagaccgt cagactttat 103200

tatcatctga aattactgag cttgaaggtt atgctatcgg tcgcaatcgt gatgaaatcc 103260

acactttccc agataatgtt tggtggtgga atatgagcat cacagatatg cgttctttgg 103320

cagaagcatg tggaattaag aaattctatg caattcgtcc gagtgctatg aaagccgcgg 103380

ccaaagctga tggattgctt tcatttgacc ggtttattat tgaccaatac atcaagtgta 103440

ttgataaggt agactacgac cagtacatgc catcaaatgc tactggaaac cgtatctgtg 103500

gaaatattgc gcattacgat aaattgaatt tcttgtcgag taagtttact gcgtctggaa 103560

tgaaaaatcc gttcctgaca aaactaaaca aaatcgctaa agtttgtcgt acaagtaaaa 103620

tcaaagatga aaatgatgaa aacaatgatt tagctttatg taataaaatt tataataaac 103680

tgtctagtga tgctgagaca atcttctata aaaagattga acagtttaaa gatgattatc 103740

ctgtcatcgc aagtgtcttg gatacttggc ggactgacag caaactcgtc gatgatatcg 103800

taaaaatcat ggagctcctt gatggagctt ctactcaaaa ttctgaaaat aaaggtgaat 103860

aaatggctgt tacctgtctg tctgaaatcc aaaaagatgc aatcgttaaa aacttcaaaa 103920

acggtctgta cactaagaaa gagctcgccg agaattatgg tgtttcccgt gacactattc 103980

ggcgtgtttt taaagagcgt gaagctcgag ctgccgcggc agctgttcct gctaaagtag 104040

aagctccagt tgagcgtgaa tttaaatggg cagcaagttc caaattcatt tcaattactg 104100

aaggccgtac tacttataac gctgatagcc aacatcccgg gtttaaatct gcactgcaga 104160

aacttgtaga tggtgatatc gctggtgcta ttgaccacat taacctggaa caaggcatca 104220

agaaattcgt tcagggtaac gtccgaattg aagatggtac tttgttctat aaagatatcg 104280

agctgaaatc tggtctgact gagcgtatcg ttcgagctat ggaagatggc gaagacttta 104340

aacgttatct gcctttcctg gaaaacctga tgctgaaccc gtctcgtcgt gcagtttatc 104400

gtctgtttga tttcctgaac gcaaacgata tcgacatcac tgatgatggc cacttcattg 104460

gttggaaagt agttcgttcc aattacttcg attgtgcttc aaacacattt gataactctc 104520

cgggtaaaac tgttacgatg ccgcgtaacc aggtagatga agatgatcag cgtacttgtt 104580

ccacaggtct gcatgtctgc tctaaatctt acatcggtca cttcggtagt ggttccgatc 104640

gtatcgtttc agttaaagtt catccgcgtg atgtagtatc tatcccggtt gattacaacg 104700

atgctaaaat gcgtacatgt ggttatgtag tacttgaaga tgtaaccgat cgttggggtt 104760

cagaacttcg ctaattataa ggagccttcg ggctcctctt ttattatggg tgaaacatga 104820

ttaatccatt taacgtatct cattctaaag ttgttaatct tcgtggtact catcatgctg 104880

ctacggtatt ttgccatcat gtagttaaac atgaaggtga tgttcactat gcttggttgc 104940

actgtgatga actcgtagaa cttggtgatg attttgttgt ggaaccagac acatgtaacc 105000

acgacgatcg tgtttatttt ggtgaattac atatcagagg aatttatggc attgatgaac 105060

aaagccctgc agagattgaa ccaactccgg acatttaccc tagatttgaa taagctaagg 105120

ggtgaagcaa aagtaaaaat cattgatact gccagatata gcttagatat cgatccatct 105180

caagatagaa ttgacgttct taaacgatgc agaattgcta taccggcaga gtatgtggta 105240

gcggattttc ttgatggata cgtgaacgat caagttgttg accataataa caacgaccca 105300

tatgaatggg cctgggacgt attagctcat ccacactacc aaggtgttag ggttgaagtt 105360

aaaacacact ttgttcatga ccgagcaaat cataagccat ggattaatgt tacaactggt 105420

aaagacggtc cattcccaga tggaagtgga ataaatctag ggcccatgtt taaacataaa 105480

gtcgcagact gtataattat attcgttgca gaagaagtgt cccagaatgt catacggtac 105540

acaccaatgt ttgccggcgg tatcgaacag ctcatggaag tagtaaaacc ttcacgtgtt 105600

ggagctggcg ggtatatcat gcacaaattt taaaaagttg tttacttccg ggattggcca 105660

tgatactatg gccctacaaa ctgaacggga gtaaaacatg agttacttag agctaaaatc 105720

acttcgagcc aaacgcggaa atgcttctat taaagctgag cttttgaaag agtatagaat 105780

tctcgaatct atgaattggc attatgctat cattgcttgt gataatggcg attcaactta 105840

cggtggattg tatcccaatg gagccgctgc tgcccgtgat gagcataaag ataaagttaa 105900

agccttagaa gaaaaaattc gtaacttgtg catttaacgg tttactttcc tgttcttcgg 105960

tgatactata atcttgttag ctaaactgga gaacaaaaat gaaaaagtta cttacgattt 106020

tgaagaacac ctttgtagta ttctgcctta tcgttacttt cattggtgtt ttcgcatggg 106080

atttagttaa cgtttggatt aatgctttca tctgaggaaa atataatgat tcgtagtagt 106140

tttgatcgtc gctttaactt aatgagaact gttgttctgt cctttatcgt tgcggtagcg 106200

cttggaattg ttgctatatt cgggttcgga atttattttg ctattcaagc ggtagatatt 106260

attcagaccg atggccttaa atctttagta gaaaccgtat gggaaggtca aaaatgaaac 106320

gacacatcgt gtatcgtctg ttggcttcgg gtcttcttgc attttgggtt ggtatcgtga 106380

cagtggtagt agtattttgg taataagagg ggcttcggcc ccttatcgga gaataaactt 106440

taatcaactg aggaaattaa catgcgtaat attatgactt ttgctgatct cgataacgct 106500

ggtgcagaac tgatcggttc tattcgtaac ggtgattggg cagcaggtgc tccatctcgt 106560

gaaattactg agcgtgaagg attttatttc ctgatgttca atgatggcaa agcaggttat 106620

atcggtgcat ctgctcgttt ctttgtagct aaacaacgtt caaaggcagg atttgagagt 106680

gttctttctc atatccgttc tggacgttct cagttgggtc gtacccttcg ttcaaactgt 106740

gtaacatacg gtgtgttctg gattcctgcc aataaaatga aaccgctcac caccggttat 106800

ggcaaaggtc aacttgcact ggcgtttact cgtcagcatt caagcgccgc gcagacctac 106860

tctgaactga atcgtattct gaatgataac ttcatcttta ctttgcagaa atactaatga 106920

gaaccttctt cgtgatgggc tatgtgtttc tgatggccct aatgatttgc tcaggaacat 106980

tcatgtggta tggccttgtg cctaccacta aagtaatcgg aagcattgcg ttcactgcag 107040

catttattat gtttgagcgc atttgtaaaa ttgtaggagt ttacaaatga ttaaaggaat 107100

tgctggcgga atttgggctg ctctatgcgt atcgacattg actaccggtg aaacttctgt 107160

tatttcgcag gcgttagcgc aaggaacttt atcaattatt cttattatag cagccttttc 107220

caatgattaa gaaaattttg attggagcgg ctttagtagc cgctttgctt ttaattttgt 107280

actatggaat gatttacggg atgatttata ttgtgctttt catttccgat gttatagtac 107340

aaatcggctc actaatttgg taggtacaat ggatattttt gacactctat taaaacaagc 107400

aggttctatc gatgatttgg ctaaggcatc aaatcttcgt catcgcgatt tgaaatctat 107460

cattgataat gaagcaaaag agtatgcgat ttacactgta gaaaaccgtg ctattccgaa 107520

cttgattgat gggtttaaac ctgtacagcg ttttgttatt gctcgggctc ttgatttagc 107580

tcgtggtaat aaagaaaaat tccataagct tgcgtctgtc gccggtggtg tagctgattt 107640

aggatatcat catggcgaaa cctctgctca agatgctggt gcattgatgg caaacacatg 107700

gaataacaac tatcctctgt tagatggaca aggtaacttc ggttcgcgtc tggttcaatc 107760

tgctgcggca agtcgttata ttttctgccg gatttctgac aacttccgta aaatctacaa 107820

agacacagaa atcgctccgg tgcataaaga caaagaacat gttccacctg cgtattatct 107880

tccggtaatt ccgactgttc ttctgaatgg cgttcgcggt attgcaacag gttattcaac 107940

ttctattctt ccgcatagtt ttgaatctgt tttggaatgc actaaagcag cacttcgtgg 108000

cgaaatgatg gaacctgaag tacagtttcc taaatttaac ggaaaaatcg ttcaaacaga 108060

agacggttct gttgagctgc acggcgtgta taaagaaact tcacggaact caatctatat 108120

cagtgaaatt ccatacaagt ttgaacgagc ttcttacgtt gaaaaagtac ttgacccgtt 108180

ggaagatgca ggatatatca catatgatga tgactgttct aagactggct ttggctttaa 108240

ggttaaattc cgtaaagact atgctttaag cgaagaccct gagcagcgtc atgctaaaat 108300

catgaaggat tttaaactca ttgagaaaat gagtcaatac attgtggtca tcgatgagaa 108360

tggtaagctg aacgacaagt tcaaaacttc cggtgagctg attcgtcatt ttgtagaagt 108420

ccgtaagaca ttcactgcca aacgaatcga gcataaaatc gctgaaacta agcaggcgtt 108480

taatcttgct caggcaaaag ctcaatttat caaagaggtt atcgcaggta acatcgttat 108540

ccaaggtaaa actcgcaagc aactgactaa agaaattgaa caaaatgaac tattcaaaga 108600

ccattctgaa aaactcgttt caatgaacat ctatcacatc actgatgatg aagcgaagaa 108660

acttgctcag gaagcaaaac gcctagcaca agaggttaag tactgggaaa agacaactcc 108720

tgaagccgag tatctgaaag acctggaaga actatgatag aattttattt aattataggt 108780

tctgtaattg ccgtattagg tttagtttta ttgctcctca gttaatctag ggaacctgga 108840

ggtcatctcc aggtccttcc atataaatct atatccctcc aaaatccttc cttagaatgc 108900

cccaaattat tttcacaaag ttgtttacat gcttactcgg ttgtggtatt atagcaatat 108960

caaaacaaca cggagtaaaa caaaatgatt acatcattaa aatctgatat caaaaacatt 109020

ctttatattt ccactcaagc cgatggcact cgactgagcc actatgtcaa aggtaacatt 109080

gtggtgctcg atgagttcga agttaatcgc gagtatccta tgcgtcaggt aattcaagca 109140

agtaactatg aagacggtga agagtatcaa gtcgttcttt gtgtatatga tgatttctgg 109200

gtgcttaaac ttgagaatgg cgataagttc ttgatcttta acgtataaca tttttactgc 109260

tctttgaaga aaatttttca gagagcagaa taaaatggtt tacaactgct ttaaaccatg 109320

gtattatagt ctcataccaa acaaactgaa taaaacatca tggagaatca caatgtctaa 109380

agtaacttac atcatcaaag cttccgaaga tgctctgaac gaaaaaactg ctgctatcct 109440

ggttcaggta gctaaaaagg atttcatcac ttcttctgaa ctgcgtgaaa tccttgaaga 109500

aaccatgaac gcaagttctg ttaactcaaa catcggcgtt ctgattaaga aaggtctcat 109560

cgagaaatct ggtgacggtt taatcatcac tggtgaagca caggacatca tctctaaagc 109620

ggcagttatc tatgcagaag agaacaagcc tgaacttctt aagaaacgca atactcgtaa 109680

agctcgtcct ctgactgaag atatgaatga gcacaaagac ctgatgatga aacttctcgg 109740

tgagatggaa gatatcttgc ctttgaaaga actgactgtt taccgcagta actatatcgc 109800

agttctggaa aaacgtacct tcggtattcg tagtcttgaa gttaacaaca aaggtacttt 109860

ccgcatcttc ggttacaaga tttctgaaga gcatcagaaa cacttcactg acctcggaat 109920

gtcttgccgt gtagctgcaa caggcaatac ttacttagat atcgcccgta ctgctgaaaa 109980

cattgaaacc atcatccgct ctattaagga actgtaatgg aactttggga aattatatat 110040

gaagatgatg tgaatatcag aggcagcatc ttcattaagg ccctggacaa atatcacgcg 110100

attgaattgt ttgaacagtt acagcaacaa acttatatca atgaatcgcg ttatttaatt 110160

aaactcgcaa tgtttttggt ggaataatga acaagtttaa agtattgaat gagcttcagc 110220

gttgtgttga aaaggttaac ttgaatgcta atatcccaac tgattgttgg gatgtatggt 110280

tccgtggaca ctttatcgga tacattgata agaaattcac aaaatgctat gctatctaca 110340

atgcagatgg taaacatatc atggatgtag ataattacca aaaggccctt gctaaatttg 110400

ttccattagc ggaagctgtt aactcaatgg aatggttaga gaaaatacag ggtgaacctg 110460

ttattcgcca gattggtatt cgtgaaaaga aaagtttgtg gcagaaaatt aaaggattct 110520

ttaaatgagc aagttttccg aacaaatgaa taaatttgtt gatgcttctc gtcacggtgc 110580

tctaattaat gaaccagaag aagttagtat tcctgaaatt tgctttaaag tagctgattg 110640

gtgggatgga cgattacttc aacgccgtat cgtttgtgca gcaaatcgtt ttgaattgaa 110700

atctggtgga acaattgtgg ttccaggcac tcgccattat tctgttgata tggcgaacgt 110760

tctagatatg ttccgtgaca aactggtttc tgaccatgtc catggagaca atcaaggatt 110820

tgtcgaccag tggggtgagt acttcacacg tgaagaagca ttaatcatcg ctacacatgc 110880

aggtcaagtt aatacagttc gtcctaaatc aggacccgcc aatgaattat tctcagagga 110940

tttatactaa tgattagtac attaaagaat aacattacgc ttttaaaaat tcaacgtaaa 111000

tcgcttcagc gctcattaga aatgatggac gataattggg gtacatatac caatgaagcc 111060

gggtttaaaa tggcagatag caaattcatg aaaactctca tggataagga atacatctgc 111120

ccgtttagcc atccatttaa tggcggtgct aagccatttc ttgctgaaat gtacaaaata 111180

atgacagaag aaatgattaa agatattgac tattacatca aggaacttga atgcaaggaa 111240

gataaagtgt gagagcaata agcgccaagg cagattactt caatagctta aatcgttcag 111300

aaaaggctca aattaaacgg tttatcttgg aattgggata tgtgcatgcc ggagatttaa 111360

aagcacatat ccaagaatgt ggtattgcta agcgttttga tattacacgc aactgcttaa 111420

atgaggtaat tgcacatgta caacccagta gcgaagaatg actttaacaa aggaggcgcg 111480

cataaagata aaaagcgtgc tgctaaagaa tcaaaacgta agcaaaaaca taaaggtaaa 111540

gacaatgcgc attctgaata attctaaatg tactacttta accattattt gtgatgacct 111600

agaagctctc cataaaaaat taggggacca ttctggatta gtagcagata tccattctga 111660

actaatggaa gacctccaga atgctggata tggggactgg atggtacatg attggaataa 111720

tggtaccttt actgtagcta ttattgctaa cgttgaacct gaagaagttc ttgaacaatt 111780

tcagaaatgc gttgatgctt atgatattgg agattatcta tgaatactga aactttacgc 111840

agagaagatg aagccaaggc atatcataaa cgtgttgaat tactttcagc aattaaagta 111900

gaatacactt tacaagttag gcttaaagtt cttaactctt gggctaatga cttagaagta 111960

aaacatttag aacaagcagt aatgtttacg tttactcagg aagcttctaa accgtttagt 112020

ctatcagcag atttccacac gtatggaatt attactatta aagcaaagga tagaggtgac 112080

attataagtg gagttgagta tattgaaagc attttaggta atcgcggaga ggttgtttta 112140

gcatgagtca taacttagaa tctgtcattg aatcacaaag atatctcgaa gcgttaatga 112200

ataaaatcgc gcttggaagt ctaatcgact tgtcctttca ggaggcaatg gacgtatgtc 112260

actggatgaa tcgtagggtt cgtccaattg gaaaggaatg gtatttaacg gctaaagtaa 112320

aagatggtcg ctacgggctc tggatgtcct ctggtgctga gtatatcact accaaggaag 112380

atttgaattc tcgttgggaa ttggcataaa ctggtttaca acgtggtatc aagatgatac 112440

tataatcaca taatccatta tgttgtagga aaaataatga ctaagtttga aattgtccaa 112500

gaaattgtta ccgttgcttc tattctgact aagttcaatg ctgaacatat catggagaag 112560

cgagatgaat ttattgcgtt cttgaacgaa attggaatca agaacgagca ggggcgtcag 112620

ttaaatcaga gcaacttccg taaaatggtt tctgagttaa ctgacgaaga gaagagaatt 112680

ctcgttgaag aatacaacga gggatttgag tctatctatc gaacaatggc tatgcatagt 112740

aataagtaat cacttagctc ttcctagagc tctaaccgcc tgaccacata tcgatgttag 112800

tctttcgtta gataatgcag gtttggaatt gtaccagtac atttcaacag ttccagcata 112860

aacattgtct aaattgaaat acggacagct aaacatgtac gatatttcag gtggttttct 112920

ttttgtcggt aagaaaacaa attccttatc cgtccaaaaa tatctacccg ataaatgcgt 112980

gctatattca gcagacgttt tgtcgattgg atatcctccc aggtttttag aatctaccgt 113040

gctaggtaaa gtcccctcat aagcaattaa gtctacgaag tagttcaagt ttttaggtct 113100

gaacgtaaag accgcagaaa aatctgcacc acttgagata tgtactatct ggagttgttc 113160

gagtgctgta ttatcaaatc gggtatccct atccttttga accagtttat catacttgtc 113220

atatgtacta tcgacgtaag cagtaataag actatctgac ttataaccag caaacgccaa 113280

caatgctaaa agtatgacaa caaaaacacg ggaaaagaga actcttcccg tggctccatc 113340

tttgaataat agctcgagca acccaagaaa catatcaaaa aatggtattg attgtttgct 113400

tgccatattg ctctccttac agagctattt attgctatct tctagttata agaccttgcc 113460

agtattggtc agttctgtca ctaaaccagt ttttaagctt attagcttcg tcatttgaag 113520

ctatttgata gtttcttaca tctccatcca ttttacctgg agtaaaatca aaggtagtgc 113580

catctgacat cattacccga agatttattg cgtcgccatt tcttattccc aaggttgtac 113640

cttgagggtc accgttccaa tagttaaccc caccttgtcc agatacagac acaaataaag 113700

taacctcttt accttcgaag ttaccttgta ctgtattttt ggttgtcggt ttagggctcc 113760

agttccagcc accaacttgc catgaacctc tatagtaaat attgttccag ttacgatatt 113820

gcactgttaa actaaagtta aaaacacttc gtcctatcat attagacatc cagaaaggtg 113880

ttcctagtct taatttggct ccggcttggg ccatccacgg ctcgccggtt tcagccttcg 113940

cggaacttcc aacccatggt cctgttactg ccatgatatc tccttaaaga tggggccgaa 114000

gccccatgca ttatttagat ttaagttctt caatttccgc tttaaggcct ttaacctcag 114060

cagaaagctc tttaacagat tcaacaagaa gtgcaattac tgagttgtaa ttcagacgca 114120

ataatccgcc gtccgcttca atatcttgag taactgcttc cggaagaact tcttgaactt 114180

cttgagcaat caacccagca gaacgagtag taccgccaga agtattatga agctcataag 114240

tattaccgct taaggtctct acttttcca aagcgttttc aataacttta atatcagatt 114300

tagctctacg gtcagaacga atctcaacgt tatcaaatga accattgcga gtacagatga 114360

agtcaccgcc agctctgaaa tagaaactgt catctcgacc gaatccatta acattaatga 114420

tagcttggtg gaagttacca acatattctt ggaaatacag agaggcataa gcaccattac 114480

taaatctgct tactaaccca gcggtattgt tatatgtgcc attgggttgt cctgcaggat 114540

aattagtagt gctgctaatt ccgttatagt tagaaatggc tcctgggaat tgacatgaac 114600

cacttgccca gaaattccat actggtccag aagcaccgcc ggctcttata ctaacattac 114660

caggctcatc agcccaaaga agacctttt ctgtaccatc tgctttacgg aagaacacat 114720

ggctattacc ggtgttctga acgttaacag aagtggatac actgaactct tgattaaacc 114780

tagcctttcc atcaacagtt aaaaccccat taacggcagc atctccggta gtccatagag 114840

aagtagtttt cagttgatta cctgtaacta ttaatgtacc agttacagta ccacctgcta 114900

atggaagata agtatcgcca gcattactaa tagcagaagc aaccttatca tcaacatatt 114960

tcttgttggt taggtgcgag ttatcagtag gagcttgacc tgcaataaca aacttaccag 115020

aagcgacgtt gatgtttcca tcagcattaa tcacaccgct gaagcgggaa ttgcctttaa 115080

ctatcaagtc tgagttcaag ttagtattac ttgttactgt aagctgcctg ttaatttggg 115140

catttccgta aacagtttgg tttccgctag catcaacttt gaatatatcg ctaaacgtgt 115200

cagcaggatt aatttggttg ttggtatttg cagataccat aacggtaaat gagttagatt 115260

taccgatggc catttttcct ggcataccgt ttttcttgac taaaccaata tcagagtttt 115320

tgccaagaac gatcattctg ttatcttcag aaacgttcaa gttgcctgtg attttcgagt 115380

tctgggcctc gaactcacca ccgacagtca ttttaccttt ttggtcaata actgtagctt 115440

ggttggaatc atcgccgtta ggtcttaaat gaagagcttg acctgttttt gcgtagataa 115500

caaaagcacc agagtcgttt gaacgaatac ccgggccata ggaccactca agcagaggct 115560

cagaaccgtt agctttaact ctaatctcag acccagaaga atcaccgaat ggtctaaaag 115620

caatatattt cgctgatgct gcggctgtag cagaagctga catgatcaat gcaccagtac 115680

taccaccttg ggcttcacga actactgcgc catttttaaa tgtgatagtt ggatcacttg 115740

ttccgacgcc attaacaact aaccagccga acttcacact ctgtccttca ccaacaccga 115800

ggttattacg agcagcagcc acagaagttg ctccggtacc gcccaagttg attggttgaa 115860

cccctgcaac aacctctttc catgcagacc atgtgccgtt ttggcagtat ctaacatatg 115920

tgccttcaac attaccgttc tttgtagtaa aggtctgctt acacgtccaa tcactgtcag 115980

aaattttacg caaagacaga acttcaagaa caaagttacc atcagatgta ggtttattag 116040

atatattaga accaccacca gatgatacac atttatacag ctgacgagta cctaaatcac 116100

tgcctttaat aaccatgttg ttaaggtcat tagtcttatc agtaatatta attgcatctt 116160

cagtaccgcg atatgtctga ttaaaaacca aatccccttc tacatcaagg ccatcaggct 116220

taactcggat gtacttgctg ggagctggag tagcaactgc atcttgataa ccaaactgca 116280

cgtatccttc aggagtaatt ttaagcattg ctacggcagc gccagagcca actttacgtg 116340

caagggtcaa tctgctatac ttatctgagt tctctgaacc taaatcaacc attgatccat 116400

tagggttttc gacttttaag ttagcgttaa tagtcaagtt accggtcatg gtatcaccag 116460

tcttgcttac ttgcttacta tcaccagtgg tgatatcatt tttaatagaa gtcaaatagt 116520

tgttaaggtt accgccaaac attgaaccag aggtaatatt cccgtctttg gttagcattg 116580

ctgctccacc aactttaact gctacaggaa catcaaggcg gccatcagaa cggaagctaa 116640

aatcaccggc agaaacatca ccagtagttt ttgcacgaat attaatctga cccaagtccg 116700

cggtattcgg agttgcccaa attacaccac gctcattacc tcctgttcta aaccatacat 116760

gagcgtttcc gcttcctgcg ttaacatata ctgatgcagt accagtgccg gaagcatgta 116820

aattaggaac agttaaatca ccagtcatgg tatcgccggc tttcttaact tgagtatcgt 116880

ttgtcagatt accaagtccg acatcagcct tagatggttt gtttgctgtg ccgtagagaa 116940

cattagaatt tactcttcca cttgctaaac cgctatcgtt tatagcaaat actctgacgt 117000

tgccagttgc ataatctata ttaagcgcag acattgtatc gccagttcta gaaaagaatc 117060

ctgcgccatg ggagtaataa ggagccccgg tataaccact cgctacgttg gctctaaatg 117120

ttgtaccacc aagagcctta aggcgagtca ttaaatcaac atcagaagta atatctacta 117180

gtgattttcc gttaccgcca ataccaaagg caccaacttc catcacattt ccgctggatt 117240

caccaacatc acgaacagcc gcagttctaa gacctaggtt atttctagca tctcctacgt 117300

tagtagcacc tgtaccacca cggttaaccg gaagagtacc ggtagtatcg ctgaaatctg 117360

gttttgagat actatcaaaa acctgtttca ttgaaacaag aatgcttcca gatggtgtag 117420

tagcaccagt atcttggcca gtttcataga taattacttt accgctatct tggccgttgt 117480

attcagcagt gtttagcact gtaacataaa gtccatttcc gtatcgagga actttagcgt 117540

aaaaatcaaa tgaagcctct gaatctgtag cagcatcatt tttaacaacg taatactctg 117600

gaacgtttcc tttattagga gaaccaatcc tgcgccattc aacccagtta tctaaattgc 117660

tagtgctcca ggatgttaaa ttgcgaccag ataacgtgat aaaatcaaca taatgccttc 117720

cgtgtccaga atcaatgcca ccagtaatca ttaaatctaa ctgcgaagat gcatctcctg 117780

ggtgtttaat tgtagctact ttaacccagc gcggagttcc agcggttgca gcagaaatta 117840

cgtattgcca tgcctgacgg ttgttttcta cattcgtcag aagagtaccg gatttaccag 117900

gacctcttcc gttcatggcg taataaacct gtgaatttct gaatgtcaga ttactgtcat 117960

tggttaattg aagaacacct acgcctcgtt ggtttttaat gtaagcgtcg ttagagccta 118020

cacccatttc aaggacaagt gtgcttccat tgttaatttt aacagtttta ttagtggata 118080

atcttaaatc accaggaaga gtggtattac ccgagccgtc aagcaagacc agttttcggg 118140

cttcaacgtt gccgcttccg cgttgtacga attgaatagt ttcagcgcca tcgtcaatag 118200

taccgatttc aagaataccg ctattgcttg taccacctgc accgatgtac cagccatcgt 118260

tagtagcgca tttgccgacg atatgacgca ctattgctcc gcttaaatca gtggcttcaa 118320

aattgatagc tttattcgga gaaatagtaa cgttgtcttt taatgtagta attccatcaa 118380

cattaagatt acctgcagta tctaagaaag gaacaccttt acctgcaagc tgaacaacgt 118440

tatcggcttc atctttagtg taaatggcaa gagtacgccc gtgtgtattc aacacgattt 118500

cgccacgggc tacgatatct gcacctggtg ctttattctc tgtgctagtt cttttaaatt 118560

gtatttgttt taagttttga tcggccatgg ctacctctta gtatgtgcca aaatctattg 118620

ttaccccgcg tgaaataacc tgatctaatc taggagcata ttcaccggat gttgctttat 118680

ttactataac tacgccagcg ttagctctaa gtacaccggt catggtgtcg ccagctttct 118740

tgactgctgc gttagctacg ttgctaacag tatttattag ctcatcgaca tagtctttgc 118800

gtgttaagtg tgaatttgct gttggagctg cagccgcaac agaaacttga ttgttagaag 118860

tgattccacc tttagtagta atattaccag atcgtaaatc gaatgcgata gttattccgt 118920

ttgaaccaga attagattca aatcccaagc cccaccaagt ttttattttg gcattgacac 118980

catttaaagt ggctccatca actccgccat ttacgagttc catgcccccg gagccagtag 119040

tttgaactct taaacctgtt tcaaacgtta ctgttctaga gtaacttccg ccattagctt 119100

ttgacacaaa gtcgttatct gcggcttgtg gtttatctat ctcagtataa acctttttac 119160

ctctataagt tagggagttt cctgccggca caagaggaaa agtacccgcg tgccaaatag 119220

gatttccgcc aactgttgaa cctgctttta aatcggccat agtttatcct cttatatatt 119280

ttctatttat acgaaaaaag gaagcccgaa ggcttcctta gtctgatgtt tctctgaacg 119340

attgaactgg aataacaccg ctcggatcga cttttgaatt tggaagttcc ataatcatag 119400

tagttcctcc ttcaacgcct ttattcattc ttataccatt cacaccaaac tcctgaataa 119460

cactattcaa ttgttcgcca tgagaagttt gaacaaatac gaggtttttg attttagagt 119520

caccaactac agacgttttt ggatatcgcg ataccacgat agtaaatcca tcagcgtctg 119580

taggaacagc ggtaaatctt tcaaatctta accatctatc agctccattt tttggaactt 119640

ctaatgatac gtttgaagat aataaagatg tacccttgaa ccaccgcaag ctagctctag 119700

tagtagaacc agcatcaaga aggcttttag atgcatacat atcacatact aaaaataccg 119760

aatccccagg agatagtcca taatcagcta ttttgcttat agattcattt tgtactggat 119820

atcgtttata ttcatatcca gtagaatccg agtattcatt ggtatcttca atagaacgat 119880

aaggacaccc agtatatcct acatctccta cattgtcata taccgtatct actttagccc 119940

ttgaatcttc tttaaccttt ccgtcattcc cataaaatga ctcaattaat atacgtcctt 120000

ttgctgctcc gagcactcct acataagcag agtttggaaa tgatttggaa aaatcagaac 120060

ctggccaaga tgcagaccac ttatttttaa accatctgtc tattaacggg ctggattgaa 120120

atcgttcatg cgtcattata atatacaatc ctgaagttaa tccatttgca tattctacaa 120180

acgctttgtt attagcgttg ttgtcatcag tggtaacgtc aaacgtttta aagttaataa 120240

atctgtcacc attaacttga acaacattaa tccccctccg taaggaggag gtcatatcaa 120300

aggcaccgtt aatattcaat tctggcttat tcggaacagc attagaatgt gtagcataag 120360

cttttagcca atacttcaca gagtttgcct cagagaggat tcgtgtttcc acgaaatcct 120420

caccaaaggc tgccattaaa attggatcag ccattaatca cctacccatt caaatttgag 120480

agtttggttt ggacggtctg gccagatttt aactggacca agcttaatcc attccaaaac 120540

ttcaagggtt ttaacctgag ttgatactga gcttggagct ccgatatcag ctgcagttgg 120600

aggagtagca gacgtgaaca ctcgcatcca atcatcaaac ttattaaggt ttggattata 120660

aatcctcatc cacacagtat gcgcgaaacg cttatcagca gtttcggttg ttggaggata 120720

aggtgtccaa agctgataag tgttgtttgt agttacacca acctgagtta aaacaccgcc 120780

agcagcagtt ttttcttcat atccggtcac tactaaagtg cttgggttag cagggtcaat 120840

cggtgttctg attggaacca tataaccacg aagacctttc aatttagtag cgtctttaat 120900

ttcagcagtc caagaacctt gtcgcaatac agtatcatta gtcggcacat accacgattc 120960

agaacctgta atgacgatag ccgaactatt tatgttaaga ttgccggtca tggtatcacc 121020

agctttcttg acataacgac catcagctaa tcttgcgtag tttttggtag ttaaaatcgg 121080

atacgagtta gtattatctc gagcaaaaat ttgcgtatca gcgtcacgag tatcaataaa 121140

cgcagagtga gacctagcac caataatagc attttgggtt tcaatagtta atagaaccgt 121200

atcttttacc ataacagttc cgccaactat tgtatttcca gaagacctca gagttttagt 121260

tgatacttca ttaggaacat ccagcgtgcc gtttccacca aatgtgtagg tctggcttgc 121320

agcagtagtt cctgttccgt ttttgacacg aacttttaaa tttccagctg aagctgtttg 121380

ggtttctgca taaattatac cgcgttcagt tccatctcta ttttgaaaac gaacatgcgc 121440

atttccagtg tcagcagttg gagaaatttt tacttcgcca ccattagcgt ataaaatatt 121500

ctggacagaa atgttgttat taaacacagt atcctggcta aatgtccaag ctccagaaat 121560

tgtctgcgct atatcgcgac gagcatattt gtctggggtt tgaccaccta gcattccggt 121620

gtcatacgct ttaccaagac gaggcaagta atgtttcaac gtgaggttca attcatacgg 121680

agacactgcg acgcccttag aggcataccc gttatccgga agagttgagc cattggtatc 121740

attacctttc cacgttccat cgcctgtaga tagcctgacg gtccctctaa cgctgtctgt 121800

agcttgccat gactctgtta cctgaatagt ttgtttcaag taagcaggag gaacaattct 121860

atcacttaat gtgcctgcat caacttgcgc ctgtgtagca tactgagcaa gaccgatagc 121920

tccttcggtt gctgttttcg cgtgcaacgt ggcagcagta actattttct tggcgtcggt 121980

gccggttctg acctcagcag cagttgcaag agtagttgta cctctttgag aagtacttgc 122040

ttcctgtatg ttgatggtat aatggtccca gaggttccca gtaatagtta agccagaact 122100

agtattaact tggatacgac tagtattagc aaatttatcg aacagtaatt tagggtttac 122160

cattactgta cttgaagtac cagcttcaaa ttcaccctgg gcaccaggtg tcgcgaagcg 122220

agcaatacca gtacgatcgt tagttgctgt acggtcattt aatgttttag gtgtaactgc 122280

tttattagtc acgccaccag cattaacttc tgtctgtgta gctatttgga ttaaaccaat 122340

tgctccatca gtagcaactt ttttatgcaa agattctggt gtaacaaccg taggaatatt 122400

tgaagaagca ggagttccgt ttctaacttc gctatcactt gctaaccaaa ctattcctga 122460

ctgatttaca gtagctttat actcacgaag agtttttgga gtaactgcat ttttgtaatc 122520

agaatgatcg aatataccgg tgccagcaga agaacgatca gcagttgtgt taggagcacc 122580

accagttttt actaactgaa taacacctaa ccgtgaatcc gacgtagtac gataaagcaa 122640

cttcttagga gtaacaattg taaaatcgtc tgttcctgca tccattttag cattagacgc 122700

aatttcagct aaacctctac gagtttcagt agcagatctt tcgttaagct ttttaggagt 122760

aacgattacg ttatccaagt aagaagcagt tgttgcctga ttaacttcgc cggaagttgc 122820

aattcttgct ataccagtct gagtttcagt agaacgacgt ccatttaaag tttctggagt 122880

aattgctaat tctttttctg gatttgactc cgcgttggct tgagcttgcg tagcaagagc 122940

aataacacct aatcgtgctc tggtagtatt gtctttagca tcaacacgtt ctacagtagg 123000

gtcagattca gttacaatcc aatagctttt tccggatgct ttatcttcaa tatatgcaag 123060

ctcaagaaca ggaacatatg acgtagttcc attaaaggta atcgagcttg attgaaccca 123120

tgctgcatca ggtggatact ctgagcgttt tggaaactgc agtaaattca aattactagc 123180

gatggtatca ccatcagaag ctttaattac tactgtctgt cctttacgca tataattcat 123240

tgcgattttg acagtatccc caacagctac gtcagtaggt aaagtaatgt taattgtttt 123300

aactgtacta ttatctgcgc caaatacaga aatatgctca ttaggcatta aagtaacgtc 123360

agaagtaatt attcttacac gtgtacgtaa atcattttca aagatgcgcc atattttgtc 123420

aatagcgtca tacaccaaaa atccactacc tgaagtacgt acttgaattt ccgtttgtcc 123480

aggagtccca attgagatag ttgggtcaaa cgtacgcaca gtcatatggt taatcggcga 123540

tgtaccatca aggtcagtaa aattaatgat atcgtttgaa ttagcgaaca acggcagagt 123600

aataaaaatc tctgagttgg aagtataacg acgaactacg ttatcacctg actgtacctg 123660

ggttggaaca atcccgttcg gaactaccat tttagcagta tcgccaaaat cggttaaact 123720

agcacgccat gcaccattac taaacgtaag cataatttgt gaatacggac gagtaagtct 123780

tacctcacgc agacgcgatt caccaaatac gatagacgca ccagtatctt gtgctttaat 123840

taagattccg ttatagccag gacgacctcc aatatcacga actacaatgg tatcgccttc 123900

gtctggtgct aacggaagaa gtagtgtagc attaccggca gcgttcgagt caacgttgat 123960

gaactgacca gattgaattt caaactctcc tttacggacg gtataaatcc agttcgggtc 124020

aacacgtaaa gaagtccaat tggcctgatt aaattctccg gctggttttg gaatatcttt 124080

gtttgcaatc caaatgcgtc gtccataagt cacagcaaaa tcggtgagat acccacgcgt 124140

cgggtcatat ttttggatag tattttcttg aataacgtac tcgacagaga cgccgtcggt 124200

tttaacgttg cggtcagcga gtgccacatt tataacttta tttccgccgg catccaaacc 124260

gttagttgca cggaaatgtt gtttcagtaa atcgctcata gagtctccta tggggttatg 124320

cttcattata gaagtattta taatggctgt actaactaat tgaacgaggt tcaaatgtct 124380

gatttaaatt gcttattcgc cgaagaagac caagtaaaag aaggtgtcat tctgattgac 124440

ttgtcgcaaa tcgcaatggc gacaattctt catacgtata aagaaggaga taaactaacc 124500

actcctatgg ttcgtcatct tattctttct actttaaaat ttaatgcttt taagtggaag 124560

aaagatgggt acactaaaat tgtcatttgt gttgataacg cagttaatgg atattggcgc 124620

cgagatgtag cgtactacta taaaaagaac cgtgctaaag cccgcgaaga atcaaattgg 124680

gattgggaag gttactttga aggtcttcgt actgtaattg atgaatttaa gcagtatatg 124740

ccttattacg tcattgatat tgataaagca gaagctgatg atagtattgc tgtactgacc 124800

aaaaagttca gtctcgaagg ccatccagtc atgattgttt cttcggatgg tgactttact 124860

caattgcata agtatcctaa tgttaagcaa tggtcaccaa tgcagaagaa attagtgaaa 124920

tctaaaaccg gctctcctgc tttagattgc atggttaaaa ttattaaggg tgataagaaa 124980

gataacgtag cttctattaa agttcgttca gatttttggt acacccatgt tgatggcgag 125040

cgtactcctt caacgaaaat gacgtttgtt gaagagtgtc ttgatgctgg cgaaaacatc 125100

aaagatttgc ttaccgaaga acagtataag cgtttcttag aaaaccgagt gttaatcgat 125160

tttgattata tccgtgaaga cattgttgct aacattttag attgttataa taattatcaa 125220

ctaccgggtc gtggtaaaat ttatagctac tttgttaaat ccggtctgtc taaattaatg 125280

aaagaaataa acaactttta aggtgaatat aatggctaag aaagaaaaag agcaagtagt 125340

atttgatgaa gcagtacacg gacaggctct gcgagatatg attaaggaag cctcaggtaa 125400

taagctaaaa gcagaaagct atcttgagct taacaaagac attaaagacc gcgccaagaa 125460

agaacttggc gtagaaggca aattatttaa tcagctgctt gccctgttcc ataaaggtac 125520

acgcgatcgt tttgaaactg aaaaagatga agtggtagaa gcttatgact ctattttcgc 125580

ttaaagatga gggggacaca tccccctccg aatccattaa ccagctgcta gataagcaag 125640

ctaatggatt tgctatcgaa tctatggtaa cagaacttgg aatggggtat ctcgaggcaa 125700

cgacacaatg gctagaagaa aattctattc ctgagggaaa cttcagtaga tatattccac 125760

ctgcaatcat agaaaaaatt atgtcagaag cattagaaga aaatatgctt cgaccatcat 125820

ttagtcaaac acataaaacg aatagtctgg atttttttatt atgattcgtc tacgcatgcc 125880

ccaaaacaat aatagatacg ttaacggtaa gagcgtttat cttttatatt taatgctcaa 125940

acaacacttt gccggtcgtt atgatgttgt taagtataat tgggtcatgc gtgtctctga 126000

taaagcttat caaaagcgca gagacaaata cttctttgag aaacttgccg agaagtatac 126060

gctaaaggaa ttgactctga tattcatgag caatcttgta gctaatcaag atgcttggat 126120

tggtgatatc agtgacgctg atgcgttgat attctatcgt gaatacatcg gtaagttgaa 126180

gcaaatcaaa actacattct ctgaagatgt aaagaatatt tactactttg ctaagaaagt 126240

taatgtagat aagcttcatg atatttttga atataatgag aaagtcggaa catcttatgt 126300

gttcaaactt cttcagtcaa acgttatatc tttcgagaca ttcatcatgc ttgactcgtt 126360

tttagatata ataaatacac atgatactgc aacggataac ttagtttgga gtaattactc 126420

cactaaatta aaagcttata aaaaactttt aaacgttgac ggtgctgaag ctaagaaact 126480

ctttattagc ataatcaaat cttgtaaaga aattagtata taattaatct atcgtccagt 126540

tgcaaggacc catgttgcaa caacaactgt taaattaaaa aggtaatcat atgttcaagc 126600

gtaaaaatcc tgctcaactt caacaacaac tggctggtct gaaaggtggt tcttctttct 126660

ctaatgaaga taaaaacgaa tggaaactga agaccgataa tgctggtaat ggtcaagcag 126720

taattcgctt cctgcctggt aaagatgaaa actctctacc gtttgtaaaa ctgatcaatc 126780

acggtttcaa acatgctggt aaatggtaca tcgaaaattg tacttctacc cacggtgatt 126840

ttgattcttg cccggtttgt gctcatctga gcaaaaacga ttcttataac agcaacccag 126900

ctgaatataa actgctgaaa cgtaaaactt ctttctggtc taacatcctg gttattaaag 126960

acccggctaa cccagaaaac gaaggtaaag tatttaaatt ccgtttcggt cagaaaatta 127020

tggacaaaat caacgcgatg gttgaagtcg atgttgatat gggtgaaact ccggttgatg 127080

taacttgtgt gtatgaaggt gcaaacttcg tcatgaaagt taagaaagtc ggtggtttcc 127140

agaactatga tgaatgtaaa ttccttggtc agtccgagat tgcaaacatc aatgatgaag 127200

aaactcagaa attcctgacc gaaaatatgg ctgacctcag cgaaattgtg gctccatctc 127260

agtttaaatc gtttgaagtt aacgaagcta aatttaaaca gattatgggt acagcagctc 127320

ttggtggtgc cgcggcaaaa gcagcagctc aagccgataa aattggtgat gacctggatt 127380

cctttgacaa agacctgtct gattttgaat ccaaaccgac ctcttctcgt tccgcagacg 127440

atatcatggg cgatgctggt gacagtgttg gcgatgacga tctgaatgat attttgaacg 127500

acctctaata taaagggacc ttcgggtccc tttttcttta tccctccaaa aatattttca 127560

caaaattgtt tacaagccag ttgatgagtg atactatatc tacatcgaaa caaaacgagt 127620

agaggaaaac atcatgggta aattaaacat tgatatcgtg gcagaacctt acatcaataa 127680

atcaggattt tgtactgatt taatttttga agatggttca cgtttttatg acactgacca 127740

tggtattgat tttgatttag ttatcaaaga aggccctggt ggtggttggc caaatattga 127800

cctccgcggt tctaaagaag cagttcgtgc ttggttagaa gcaaacgagt gggaagatat 127860

tgatttgatg atggaagact ggaaagagta attacctttg gggacttcgg tccccacttt 127920

gaggaaatga taatggcaca ggttactgta gaaatatatg attatgaaca cttcattgaa 127980

accattgaaa aatacggttt gattgaagtt agtaacaagt ctgccccatg gggaggaaac 128040

gaaatcactg tagaaggtga tactcctacc ctatggttat ggcttgaaca agaatatttt 128100

cctggcatgg atgatgaatg ccgtgaagat acattaacga cttttagcgg gtaaattatg 128160

aaactgaaca cagaatatcg cattatccca agtcttgctg ccgagtggga cctttcatct 128220

agcggaaatc gccggatgcg cttgatgatt gaagaacatg gtggttcgtt ctttcctact 128280

aaaatgctcg acgaagataa tagtttcatc acagaagtaa aatttaaaga tggaacaact 128340

gctgacgctg aaggatttgg agatgcatac tttgaaatat ctgattatga attcaaatac 128400

ttcgaaccag tatatgaaat tggtagtgca atccaacctg gtcctactcg cttggacttg 128460

atcgttaccc cagaaaatgc agaagaaatg attgacttga tcaaaaaagt tttcaaaaag 128520

tagtttacac ggagctatgc ttgtgatagt atagctccat aatctactgg agaataaaaa 128580

tgaaacttca acgtcaaagc attaaacttg gttctgaata tcgtggtaaa tggaatttct 128640

gcatttgcga taaaaaccca gaagaattag agcgtgttga agaagtactg tgccaaatgg 128700

aagctccatt cactatgggt ggtgaaactg tctattggaa tgattactgt gataactgcc 128760

catgctatga agatgggtat ggctcaggct tctggattcc agttgaagat gttgaagaat 128820

tcaaaaaagc atttaaactt gctaaggcca agaaatgatt gaggctgaat tagtagtttt 128880

gttaatttct gttactgtcg cttttattag cggcgttata ttaggattat ttttatatgt 128940

ctaaatttag tgtaacggga tatcctcgcg ttaatattcg ctgccagttt gatgaaattc 129000

ctggagtaac tcatattgag ctcgtatttg accctcattc gcgatgcaat caggtttcag 129060

gtaaaattga ttcagcgtat ggcgaatttt taattaatga ccaagttgtg gtttcagcta 129120

tttctggtga acaagcaggt tcgttgtata ttctgaaaag ggaagtattt gaggaaattt 129180

cagaagccat aaaagaaggg tttaaaactc ttcagagcat gattaaagct agtgagtaca 129240

agtcatgtgg attttaactg actgggattg taagtactgt ggcggtagct tatggcaatt 129300

aggtggccgg tgttttaagt gtggaatgag gcaaggttaa tggaaaattt cgcagtagat 129360

gattacgatg atttgatttg gtgggacggc cgtgaatggg taactatctg cgcaatgtcc 129420

aatatcgata gcgctatcaa acgtctccaa gagcttcaac agaagtggga agacggtaat 129480

gttgaacggg ttgaatttta ttgaggttta aatgattcaa atagtttatg cctttgctcc 129540

tacaaaaact gtagacggca aaaatgaaaa tgctttcggt ttaggcgatg gtcttccatg 129600

gaaacatatt tcccaggaca tgaaaaactt tgctaatcgt actcgagata ctatcttgat 129660

ttgcggagca aagactttta tgagttttcc tgaacctctt cctgggcgta agacaatcgt 129720

tgtccaagac atgagtcgtg cgttggcaac tgctaaaaat ggcttctttg cagatgctta 129780

tgtaagtgaa ttagaattta tcggtttctt gggtggtgac attatggccg ctcatacttc 129840

ttacaacagt actatcactt ttaatagaga ccttaattat tctatcatag gtggtgccgg 129900

aatcatccag aaggcatatc catacgcgga tagggttatc caaacaatca ttagaaaaag 129960

tcatagagtg aattctgatg tcactctacc tgctgaattt gtaacagctc ctacttggcc 130020

agaatcagga ttcattacta aagaaaatca ctggtatcat attgatgaag tgactaacat 130080

ttcagaggtg gtctatgagc gcaaactatg atatcactca gctatcagaa gacaaagtcc 130140

aaaagaggtg gaaaagattt ccatttaagc atggtattca tcttctagtt ttcagttata 130200

atggtcttag cacttataac ggttcaacta cagtatataa ccgaaatgga aatataccta 130260

ttgaaattga acgtgattat aagaagatgt tcatcggaat gtcacacggt aatgtgacgg 130320

ttaatgatga tgtagtgtct attattgggc gatttgaaaa gcgtggtgat cagcttttct 130380

ttacacctct tcaggaaaaa tttaatgcgt gaataccaag aattaattaa agacattttt 130440

gaaaacggct atgagacgga tgaccgtact ggtaccggta ctattgcaaa gtttggtact 130500

caacaccggt ttgatttaca agaaggattt ccggcagtaa ctaccaagcg tcttgcgtgg 130560

aaagcgtgca ttgcggagct gatttggttc atgtgtgggt ctactaatgt gcatgaatta 130620

cgtcttattc agcatgactc attactagaa ggtaaaactg tctgggacga caactatgaa 130680

aaccaggcaa aagacatggg gtattccggt ggtgagctag gtcctgtgta tggtaagcaa 130740

tggcgtgatt tcatgggtgt tgaccaactg aaattgatca ttgatcgtat caagcaactt 130800

ccatatgacc gtcgtcagat tgtgactgct tggaacccgg ttgatttgga taagatggca 130860

ttgccaccat gtcatttgct gtatcaattt aacgttcgtc aggggcatct tgacctccaa 130920

tggtatcagc gttctgtaga tgtattcctt ggcctcccct tcaatattgc gtcatatgca 130980

gcattggttc atatcattgc taaaatgaca aatcttaaac ctgggcattt ggtattcact 131040

ggtggtaaca ctcatattta cctgaaccat attgagcaat gtaaagaaat cttgcgtcga 131100

gagccaaaag agttgtgtga acttgaaatt gcattcccag atacgtatga aacttggcag 131160

actagttctc agattcgttg gttagaacaa tttgcacgtc ctcatcattt tgaactagtt 131220

gggtataaat cccatccaac aattaagggg aaaatggcta tatgaatatt cgatttgttc 131280

gtaaaggaca tcagtctaaa accgtattag gagaaatgca ggacgcattc tctagtgatt 131340

tgcctgaggt taatgacacg atagtttttg acggaaccga acaacgtgtt ttatctgtca 131400

ttaaatcata tgaatggtct attggcaaaa cacaattaat ctgctggttt gaagttgata 131460

taacatgaag atatgtcggg tggttaataa ataccattcc gacttcgatg taaatatcca 131520

acgtggaaca atgtggggaa attacgtcgg taaagattgc gataatcgtc ctgatgctat 131580

tgcggcattt aaggacgatt ttattgctaa gattcggaac ggagaaataa agcgagagca 131640

cttagaaact ttaagaggaa tgagattagg atgcacctgc aaaccgcttc cttgccatgg 131700

tgatataata gctcttgtag tgaataaact ttttaaagat acatttgaat tagaggactt 131760

atgcaagtaa ttaagagctc aggtgttagt caagaatttg acatgcagaa aatcattaaa 131820

gtcctcgaat gggcgtgcga aggaactaaa gtagacccat acgagttgta tgaaattatt 131880

aaatctcatc tgcgtgatgg catgagcact gcagatatcc agaagactat cgttaaggta 131940

gcggcgaata gcatttctat tgatgagcca gattatcaat atgtagcatc caatgcagca 132000

atgtttgaaa tccgtaaacg tgtttatgga cagtttgaac cgcctgcatt tattgaccac 132060

atttcacgtt gtgttaacgc aaataagtac gataaagaaa ttctaagtaa gtggtctgca 132120

gaagaaatta ctttgcttga ttcttatatt aagcatgagc gtgatttcac tatgacttat 132180

gctggaacaa tgcagcttat cgagaagtat ctcgtaaaag accgtcatac tggtgaattg 132240

tatgaaactc cacagtttgc ctttatgctg atcggtatgt gcttgcacca agatgatggc 132300

gaaaatcgtt tagcaaacgt tattcgtttc tatgatgcag tttctactaa aaagatttca 132360

ttgccaacac caattatgtc tggtgttcgt actccgacac gccagttcag ttcatgcgtg 132420

gttattgaag gtggtgacag tcttaattca attaacgaag ctgctgcgtc aattacgaaa 132480

tacatcagta agcgtgcagg tattggtatt aatgcaggca tgattcgcgc agagggttca 132540

aaaattggat ttggtgaagt caaacatact ggagttattc ctttctggaa acacttccag 132600

acagcagtta aatcctgctc ccaaggtgga gtccgtggtg gcgcggcgac actgtactat 132660

ccaatctggc acttggaagt tgaaaacctc ctcgtactta agaacaacaa aggtgtagat 132720

gaaaaccgta ttcgtcattt agattatggt gttcagatta ataacctaat gattgaacgc 132780

ttgattaaga atgattacat cactctgttt agtcccgatg tatgtcttgg cgcgctgtac 132840

acagaatact tccgtgatgc acaagcgttc cgtactttat acgaagagct ggaaaagaac 132900

ccagatataa gaaagaaacg tattaaagcc cgtgaactgt ttgagttgtt ccttactgag 132960

cgtgctggta ctgctcgaat ttacccgtac atggtagata acgttggtga atatggtcct 133020

tttattcgtg atgtggctac ggttaagcaa tcaaacctct gcctcgaaat tgcgttacca 133080

acttcggatg ttggccaaga agatggcgaa atcgcgctgt gtacactcgc agcattcgtg 133140

ctcgacaact tcaactggca agaccaagaa gaagttaacg aaatcgcaga agtaatggta 133200

agagctttgg ataacctttt ggattaccaa gattatccag tagacaaagc gttaaaagca 133260

aaagaccgca gagcattagg tgttggcatt actaactatg cagcttggtt agcaagtaac 133320

tttgcttcat acgcagatgc taatgatatt actcacgaaa tgatggaacg tattcaatat 133380

gcactcatca aagcctcagt taaacttgct agcgaaaaag gtccgtgcgc gctttacaaa 133440

gaaacacgat atggacgtgg cgaactgcct attgactggt acaataaacg aattgaccaa 133500

ctcgcagctc caaactatgt ctgtgactgg gaactcctgc gagaagacct caagcgatac 133560

ggtatccgaa attcaacgtt atctgcgctt atgccatgcg aatcgtctag tcaggtatca 133620

aactctacca acggtattga accaccacgt ggaccagtgt cagttaaaga atcaaaagaa 133680

ggaagcttca accaagtcgt tccaaatgtt gaacacaatg cttcccttta tgattatgcc 133740

tggcagctcg cgaaacaggg taataagcct tatctgaacc aggttctgat tatgcagaaa 133800

tttgtagacc aaagcatctc tgctaatact tattacgacc cggcgaattt ccctaaaggt 133860

aaagttgaaa tgtcggtaat gatggacgac ttgctttatt tctggtactt tggcggtaag 133920

actctttact atcataacac ccgtgatggt tccggtaacg atgatatgat tcaagactct 133980

gctgactgcg cggcctgtaa attataatga attatcaaaa cgtatataat agtttaatct 134040

cccgggctag agcccgggaa tctttattag gatataaaga gactcatcat ataattccta 134100

gatgcatagg aggttctgat gataaagaaa acttagttga attaacaggt agagaacatt 134160

ttatagcgca ctggctttta tgtaaaatat atgaagcgcc gggattaaag aaagcctttg 134220

gtttaatgtg tttgaccggt aaaaatcgct catataaagt ttcctctcaa ttgtatgaat 134280

taggcaaacg gcgtttatct gaagctgcta caggacgtaa agcttctata gaaaccagag 134340

aaaagataag caaatctctt aaaggaaggg aatttaccga agagcattta gccaacatga 134400

gaaagcctaa aactgaagaa accaaaaaga atatagctgc tgctaaagtg ggcgtgctta 134460

atcctatgta tggtaaaatt tctccaacaa gagatgttcc ccatactaaa gaaacccgtg 134520

atgtgatttc tttgagaact aagcaaggta cagagtatcc accttgtcca cattgcggca 134580

agaaagttaa taaaggtaat gctcttcgtt ggcattatga taaatgtaaa tttaaggacc 134640

ctaaatgagt acagttttta ataaagaacc cgtagacatt atgaacgaac cgatgttctt 134700

aggctctggt ctaggaatcg ctcgttatga tgtccaacgg cacaaagtat ttgaagaact 134760

tattgagaag tctttatcat ttttctggcg tcctgaagaa gttaacgtta tgatggaccg 134820

tggtcagttt gaaaaactcc cagaacacca gcgtaatatc ttcactgata acttgaagta 134880

ccaatctctt cttgattcaa ttcaaggacg agctccagca gcagttttat ctgcacttat 134940

ttctgaccca agcctagata cttggaacca gacttggacg ttcagtgaaa ctattcacag 135000

ccgttcgtac acgcatatca tgcgtaacct ttatgtagac ccagctaaaa tctttgatga 135060

aatcgttctt gacgaagcaa tcatgaaacg cgctgagtca attggtgttt actatgatga 135120

tgttatagcg aagactcgcg catgggaaaa tgccaaaaat cgctgcttta atcaagataa 135180

tatcgaaatt aaagaagcta aacgtgattt aatgaaatct ctttatcttt gcttacatgt 135240

tattaacgca ttagaagcta ttcgtttcta tgttagtttt gcatgtacct tcaacttcca 135300

taaaaatatg gaaatcatgg aaggtaatgc taaaatcatg aagttcattg ctcgcgatga 135360

acaacttcat ctgaagggca cacagtacat tctgcgtcaa cttcaaactg gaactgatgg 135420

cgaagaatgg gttgagattg ctaaagagtg tgaacaagaa gcaattgaaa tcttcatgga 135480

agttaaccgc caagaaaaag attgggctat tcatcttttc cgcaatggtg gtcttccggg 135540

tctgaatgtt aaaattcttc atgacttcat tgactatctg actgtatctc gtatgcgtag 135600

ttgtggtctt ccttgtccga ttactgatgc accaactcgt catcctattc cttggattcg 135660

cgaatatctt aactctgatg cagtccaatc tgctcctcag gaagttgaga taagttctta 135720

tctggtagct cagattgaca atgatgtcac tgatgatgtt ctaattggat ttaaaaggta 135780

cttataagga aaggggcttc ggcccctctt tattatgaat gatattgcta acgagttttc 135840

ttttataaaa tatgttcaac ttgagttaga accagatttc agtattaaac ctgttttggt 135900

agcaaacaag ttgaatgtag tttatgccat cgcagttgat gatgaactag tttacattgg 135960

taagactaaa aatcttcgta aacgtataaa ttattataga actgctatta atcggaaaga 136020

ccaaacctct gattcggcta aatctgccaa gatttttgaa gcactaatgg ctggcaaaaa 136080

agtagagttc tatgctcgtc agtgttttaa tcttttgatt aataatgaac ttggcgagat 136140

gtcaatatcc actatggact tggaagaacc gatgtttatt aaaaagttca atcctccatg 136200

gaacacacaa cataaggtaa agaaatgtta gagctatata aaaatttaat gaatctatgt 136260

gaaagctcag aagttgcaaa attcttttat aaagatttta ccggtcctat ggatggtaag 136320

ttcagagtgt tttcatacca ctatgcaagc tacagtgagt ggttaaaacc tgatgctctt 136380

gagtgccgcg gtatcatgtt tgagatggat ggcgataccc caattcgaat tgcttcgcgt 136440

ccgatggaaa aattcttcaa tttgaatgaa aacccactaa cgatgggaat tgatattagt 136500

gatgtagaat acattatgga taaggctgat ggttctctag tatcatctta tgtcgatgat 136560

gggtatctat accttaagtc aaaaacatct ctctacagtg accaggcaag acaagcttca 136620

gctttgctta acagtgaaga atattcttcg cttcatcagg ttattcttga gctagcgcta 136680

gatggttata cggtaaacat ggaatttgtt tcacctaata atcgcgttgt tttagcatat 136740

caggagccac agctgtttgt gttaaacgtc cgtaataaca caactggcga gtatattaaa 136800

tatgatgatt tgtacgctaa tgctaagatt cgtccttatt taattaatgc ttacggaatt 136860

tctgatccca caacttgggt tgaaggtgtt cgtgaacttg aaggcgtaga agggtacatt 136920

gcagttctaa acactgggca gagatttaag gttaaaaccg aatggtattc tgctcttcat 136980

cacactaaag actcaataac gtcaaatgaa agactgtttg cgtctgtcgt atctgcaaat 137040

tccgacgatt tgcgttctct ttttgctgga gatgaataca caattaagaa aatttctgcg 137100

tttgagcaag cttatctaga ttacctcgga aagtcacttg agctgtgtca gtcattctat 137160

gatgaataca gaggtcgtgc tcgtaaagat tatgctattg ctgctcagaa agcaacggtt 137220

aatcagcgcc atctttttgg tgttatcatg aacatgtacg aaggaactgt agatgtagat 137280

aaactgctta aagacctcga aagggtgttc ttgaagtact gggcaggata tgttccaaaa 137340

gagtacgaaa aggaaattga aatttccgaa gaataattgt ttacatcctc atcagggtgt 137400

gataccatag acttacacca actgatgagg ataatgaaat ggatatgcaa gcaattactt 137460

tagatatggt tgttaacaaa tacggtactc attctgacgg gatttttgtg tggaatggta 137520

ccaagaaagt gggattcgtc actgatctac gtacccatat ggctcgcaag gaagctgctc 137580

gtaagaagca aaaagagtac actaatcgtg tgaacgagca gcgtgccgaa gcccttcctg 137640

aagccgtaga tgaaatgatt gatttcctag ataatcatct cgcgaagtat ggtgcagagg 137700

tgttcaagaa catcacccag ccaaacgttc atgctaacgg gtgcaaatgc tatgtaatcg 137760

ttgacccgat ttatggtaag catcgtcttg gtattatgca tcgtgagctg aattattctg 137820

agatggcaga atatgtagaa gcgtgcttca agtgttctcc ttcggaaagt tctgatcgtc 137880

acatcctcat ttcgggatta tcccgtgatg atatcgtaga ggttatcctt aaactatgct 137940

caaaataaac acaacttggt tgttgattgg agtgttagca ttatccgcag gaggattgaa 138000

atatctttcg tggcgggtag aaaatcttaa agctgacctc aaagtcgtcc aagatgaatc 138060

tgatcgacaa gcaaaagaaa tagaaaatat tggtgtttct ataaaaaatc tgcagacaac 138120

atataaaggc tatcaggaaa accgagcagc tcgtgatact tctaacgcta agatgaataa 138180

agattctaag cgtggaaacg tagttgcagc caaacctgga ttagttgaaa aacagattaa 138240

tgcaagcttc aataagtttg cagaagatat ccaggaggct accagatgaa acgaagtcta 138300

ttagccatgt gtattatcag cttattagct ggatgctctt ctagtgcccc agatgttccg 138360

gttttacatc ctgagtggcc agatccaatt caaaaatggg aaggacattg ggaagtaaaa 138420

gtaattgacg gtaaagcctg ggttggtatg ccgtttgaag agtcgcaaga atatcgtatc 138480

tggatgaatg acattttacg atatactaaa gatgctaatg gaatgatatg ttattatcgt 138540

tctgaactta aagaacctcg ttgcgttaag taaactaaac aagaggaaaa tattatggaa 138600

ccgtcacatt tttattctta ctttgtaaaa gacgcatcgc atcttttatc gattaaaaat 138660

acacagctca gaaatatgct agctgttggg tcgtgccagt taactcctct tgctaagaaa 138720

gctactgtta taccggaaaa tatttctaat ggatatgttt atacagtccg tgttagtgtg 138780

cctggcgctt taaaagaaag attgtttgag cttaatgacc aaacacgaat ttcgtttgat 138840

gtgtggttta aactattcat ggtagaattc atgtatcctg atttcttgaa gtttgttcag 138900

cgtaaagagg cattgaagga agcaatttct gaattggaag atgcctcaat tgaatttggt 138960

aaggcactcc aatttgtaga aagtggcggt gtagagcaag atgctgttaa cgggtttttg 139020

aagaaatatg gaaagcgccg ctcattggcg catcgtaatc tttctaaaat ggtgatgtag 139080

tgaatcaaga acagtatgaa acacttaaag gattaattgc tgaaaatgaa ttggcgtgca 139140

tcgtgtttgg acgcgcagct gaaaattatg acaaaaatga tatactgtca atgaataagc 139200

cattgcgagc aattaaagaa aaatatcgtg ctaattgggg tgaaaagtct aaggctcttc 139260

atgattttat tgacactctt aaggacgtat aatgaaaaaa ttggttttga cacaggggc 139320

tccaggctct ggtaaaacaa cctgggctaa cgaatacgta gcagctaatc caggttggta 139380

tgttttgtct cgtgatgatt tgcgtgaagg catctttggc cttgataagc gtaatgatta 139440

caaatattct aagcttcgtg agaagtccgt atctgtatgc cagttttcta tggcgaagac 139500

tctactcgag atggaaacca ctaaaggtgt catcattgct gatactaacc ttaatccaac 139560

gactatcaag aagtggcaag agttggcata tgaaattgat ggtgtcaagt gggaaattaa 139620

acgctttgac gttccttgga ctgaactagt taagcgtaac ctctatcgtg gcgcgaatgc 139680

agttcctatt gaagtgctcc gtagcttcta ctctaagatg catccgtatg atttgtacat 139740

tccagatgaa tcattgccaa aagcagttat ctttgacctt gatggcacgt tagcagataa 139800

caatcatcgt tctccttatg acttggccaa atgtggtaaa gaccatccaa aggaaatggt 139860

aattgaattt cttaaaatgc ttcgtaacaa aggatataaa attcttactg tttctggtag 139920

agagtctgga actaaagaag accctacagt ttatcaacgt attacgaaga aatggctgtt 139980

ggaccatgtt ggcgaaacag gcgaacactt ccaacgtaag caaggcgatt cacgcaaaga 140040

cgatgtggta aaagaagaaa tcttctggga ccgaattgct gatcgttata atgtaaaact 140100

tgcagtagat gacagggcgc aggtagttga aatgtggcgt cgtatcggtg ttgaatgctg 140160

gcaagtagcc cacggtgatt tttagaggaa agtataatgt ttccaaagta ttctgaagta 140220

gtaaaagtat catttacgca agttgttgct aatcatttaa cagatgagtt tactccggct 140280

gaagtagcca aaatgcatgc agagttttta tctgccatga atgcacttat tccaaatggc 140340

gaagttgtta aattttcaat tgaccgtcta ggcggttcgt ctgaaattaa aatttcttgt 140400

ggcgaaggtg aacacgactg gtttatcgtt ggaattattg ctaattttga aacccaacag 140460

gttgagactt atgttgtctg acgctaaatt ttcacatgat gaatttattt cgaaggttaa 140520

aatcttcgca caggaagtag caaaccgggt tcctggaagt aaagtgactc tccgacgaga 140580

gtcatccttt aactatgttg atgcttatat cattacagtt aataatggaa agagcaatca 140640

acatactcaa ttggctttaa ctggaacagg ccaagttgaa atgactaaca ttttaggaca 140700

tatctaatga ctttacgtga agcggtagaa gctcttttaa ttgaacatgc tcgtggcatt 140760

aaagcagaaa tcagcccaaa tggtattcgg ctgatcagtg ctgttattgg ttctgaccaa 140820

ggtgtttggt caattccacg cgaagaatat gatgctattt tgtacagtaa cgttaatgtc 140880

aaggaaggac aacctatgta tggttatgtc ttctctgact cgcttgaacg aggaaaccat 140940

ccgtttccag atggcacagg cattcgtact tctcgagtag agagttttgc ttctcctacc 141000

gacgagttaa aattggttaa aacaaataac acaacttatc tggtgattta aatgaaagcg 141060

tcgacggtac tacaaattgc gtatctcgta tctcaagagt caaaatgctg ctcgtggaaa 141120

gtcggcgcag taattgaaaa gaacggacga attatttcta ctggctataa cggttcacct 141180

tctggtggtg tgaactgttg tgaccatgca gcagaacaag gttggattgg tgaaattcct 141240

tacaaatcta cgggattgcg tcaagacgga ttccaagtca aaaaagtcgg attgctcaaa 141300

gaacatcgag cagcccactc tgcatggtct aaagtcaatg aaatccatgc tgagcttaat 141360

gctattcttt ttgctgcccg gaacggcagt agtattgatg gagcaacaat gtatgtcaca 141420

ctgtctccat gtccagattg tgcaaaagcc atcgctcagt ctggtattaa aaaattagta 141480

tactgtgaaa catacgacaa gaacgaacct ggctgggacg atattcttcg ttctgctgga 141540

atcgaggtgt tcaatgttcc aaaacgtaat ttggataagt tgaattggta taacattaaa 141600

gaattctgtg gaattgaata atgaaactta gaattgttga aattaataaa cttaacctaa 141660

gtggtgatgt tgttatatca tactcagtag aacgccggta ttggtttaaa tggaaaccat 141720

tagcaacatt taaatttgaa gatcaagcag ttcgattatt aaaagaatta tccaagcgca 141780

aatctgtaat tatcaaaact attaaagaga catcaaaatg aaactgacta ctgaacaaaa 141840

catccatatt cgtgaaactc tgaaggctgt gctgagcatg ggcgaatccc agattgtgtt 141900

tgaaaaagct gatggcacta ttcgtactct gcgctgtact cgtgataaag acattattcc 141960

atctgatttg gtagaaagca ctactaaatc tgctcgagca gaaagcacta cttcacttcc 142020

agtatatgat accgagaaag aaggttggcg ctcatttgcc tttgataaac tgatctcggt 142080

aaatggtatg aaagttgagc atctgctgca gatgatcggt aagtaatttg ctttaaactg 142140

accatgttaa tataactaca tggtcaaaca ataaaggtaa cacatggaac ttccaattaa 142200

agctctaggc gagtatgtaa ttctcgtatc tgaacctgca cagcaaggtg atgaaattgt 142260

ttctccttct ggtattattc ttggtaaaga agaacaagga caactgccgg atatgtgtga 142320

aatctattct atcggtgatg atgtaccgaa aggatttgtc gaggtcggtg atttgactcc 142380

gttgcctgtt ggtaatatca gaaacgtacc tcatccgtta gtagcagcag gtgtgaagaa 142440

acccaaagaa attcggcaga agtttgtgac ttgtcattat aagtcccttg catgcgtata 142500

taaataataa tatgaattgg gcgtcggaca attagttacc cgagcaattc tacgtggtgg 142560

atgcccgagc taaacctcgg ttaccgtcca ccaaatttta acctcatttg aggaacgatt 142620

caatgaacaa acaacttact aaagctctgg aactccaacg taatgcatgg aattccggtc 142680

acgaaaacta cggtgcttca atcgatatct atgcagaagc actggaagtt ctgaaagggt 142740

ttaaacacct gaacccagca caagctgaat ttcgtgatac tttagaagcg atggacgaac 142800

tgaagtatgc taagcatctt ggttctgctg ctcgcaaagc tgttcgccac tttgtggtaa 142860

cgctgaagta atttgtacgc ccaccatgtg tacgcatggg taacgtatga tgtggacgtt 142920

gttggttatc cccacgtaaa acatccgaaa ccaacggtga tttgctacca aagtgcagct 142980

agaaataaac ggcaagtgca tgctaccccg aggcgatggc caatcgggag tacgcctcaa 143040

ggcctataca tccatcggtg tatatcttat ccccgataaa tcggacccgg aacctttaag 143100

ctaacggtgt gcaacagata agagtttaaa cgtacccctt gagggctttc gggagctaca 143160

accgaaagaa ctgtcgaaag aagttgaacc tcggaagaac gtgctcccat gtatttctcc 143220

aaaatggaag atgataaaat ggctaaacaa gctaaagcaa aaactgcagt aaaagaagtt 143280

gttggtacct ctaaacgcgc tggctacaag cgtgggtcga acaagcgtat caatcagacg 143340

gttgagaaaa tcatgcgtcg agctcgtgcg gttcttcgcg atgatgcttc tcgttttggt 143400

aagccgaaag cataagttca gggactcctt cgggagtccc ttttttattt tccacagaat 143460

gaaaaaagtt gtttacttct aggctcaaca aggttactat agacctgtac cacccaaacg 143520

gacaacggag aataaaatga acttcactaa cttcaaccgc aaatacgtac agaacaatgc 143580

ctgggacgtc tctactactt tgctgtggga acacaacaac ggcacagtgg ctcaaatcga 143640

tatgtactgg gaagataact acgtattttt cagctttgaa aatggtccta ctctggatat 143700

tcagttcaac ggttctgaaa tcaaagttgg attccatgat gaagttcgta aacgtgattt 143760

atcttcacat ccgtcttgga acacaaatcg tcagctgctt gttaaaattt atctgcgcca 143820

catcctcggt cgtaaaacaa ccgaagaaca acgtgaagca atctgggata tcgtttcaaa 143880

cgaaataaag ttttaactaa ctcggggctt cggccccact attgaggaaa tgataatgga 143940

aaaaggtaaa ttctataagc ttaaaaagac tccaagcttg tctccaggcg ctcttatcaa 144000

gggtgttttt gagcaaatcg gtaataatcc aattaaaatt accagaacct ttaaatatgc 144060

ggaaaacact ggattagttg aatttgaaat cattaagccc gatggggaat acaaacgcgt 144120

tagtatagat gaagttcgct tttctcgcat gtggtgtatt attactaatc aagagtttca 144180

gcattatttt gaagaaacca cccacaaaga acctgaaccg aagaccgatg acggaagcaa 144240

tgattggggt gtttggacct caaataaagg aaatgatacc tacaaaggtg gattaacaaa 144300

ggaagaagct gttaatcttg caaaagtaca acgcctgaat gcaactaaag acacaaaagt 144360

tgtaatcatg caacctttg ctgtccctgt ggttcacgtt aatattcgcc cgttttaaga 144420

ggaaattgaa atgattgtat cagctttcta tgattcacga aagaaaaaag ttgaaaccat 144480

tatcagcgat acccgcgatg gtacacctgc taataaaaat ggtgtgaaag catacattga 144540

taagtattgc cctcctgaat ttcgtatgat tgacggtgta gattctctga gcattaacat 144600

tataaatgct aaaattgaat ttattaatga aactgtgcca attgggtatt ctgacggtga 144660

tggctcaaat gctaaaatgc cgaaagaaaa attcataact aaattttgag gaaatcaaca 144720

tgattgtatc cgtgcctaaa tctaaagatg gtatttttc ttgcggcttg aaaaaccacc 144780

caatggttga tatcatgtca gctaacgtta aacaacacac cgttgagtat gaaattgatg 144840

ctccggattt ctttgaattg cctgaatggg cagtgaggct tgatgcatga aatatcatat 144900

cttcaataca gtaagattag caaatggaat tcctggagtt gtatgtgata cggctccagc 144960

cattaaagcc tactcggttg aaccttggta tgaagttaat tgggttgatg gcaatcgttc 145020

aatccatgca gaatccgagc tttatccaat tactcaatta agggctgcta acgacgatgt 145080

ctattaatcc tcacttcggt catatggttg cccgacgtat caccagggaa atgctaaaga 145140

ctgctgagta ttataatata gaattaattg atatagaacc ctcggacgct ccagggttaa 145200

tctggttcaa tttcaccggt gccgcaaata gcgtcgccaa atttaaacaa gcattgagga 145260

atttccccga atgtcaaaac cagtaatcgc aaccgatgtt gatggaatca tcgttaagtg 145320

gcaaagtggt ctgccttact ttgcccaaaa atataacctt ccggtagagc atatccttga 145380

tatgatgact actgaaaaat tcattaaacc cgctgagctg tttgattgtg aagaagacct 145440

ggctgttaag cttcttctga aatataacaa cagtgatttt attcgttatc tggcgccgta 145500

tgcggatgct ttagctacag ttaataagct caaagaaaaa tacgattttg tcgctatcac 145560

ggctcttggt aattcagtag atgctaacct taatcgtcgt ttcaatctga atgctttgtt 145620

ccctgatgca tttacagaaa tcatggtctg cgattatgat gaatctaaag atgctttact 145680

ggaaaaggct aaagtaaaat acggcgatcg catcgtctgc tatgtagatg atttgcctaa 145740

acatattgct gcggccagca aagtatttga agacactgaa acccgtgtgt tctatatgcc 145800

tcgtggtgag cgagagggtt cagtgactgc tcctggaatt atggttgaag attggcatca 145860

aattgtaact tgcctggaat ctttggaatc tgttaagaaa ccgcagaagt ctctttctag 145920

attgtgggaa gaagctatca aagaccaaat tcgtaaagag caacatcctt ttaattggcc 145980

tccacggcaa gttccaggag attggtggaa acaacctatc attccgttta gtcctagtcc 146040

gcatgttcct cctggaaacg actggtggaa taacggtcgt attacatgtg ataaccacca 146100

aattaattgc taacacactg ggtatggtat aatagccata ccctaggagg aaatatgttt 146160

gtagttcata ctaaggtagg taaacgttgg ttatcatgtg attatggcca tgttaatcag 146220

ttttatcgtt ggaatccaat ttggcgtgaa gcaaaggcgt gcccgatttg gaatgaatgc 146280

atcaataacg ggtttgttta tatcgatgga ttaacttatc atcgtagcgt aagcgaactt 146340

tcaaaagaat taggtgaata atgatttttg atatcatcaa agcgattgaa gatgctaagg 146400

gttctaaagc caaaacccaa attctcattg acaataaaga taacgttgat ttaaaacgag 146460

cttatctgct ggcgtattcc gggcgattta agttctttat taagaaagtt ccagaatata 146520

ctcccgttaa atatccaaat gttccttcaa agacgttttc tgatggtcta gattacctcc 146580

aagacattct ggcagcacga gtacttactg gtaatatggc aatccagggg ctagtagatt 146640

tgctctctaa gatgaacgag ggtgatgcta gtgtactggt ccgtgtactt cttaaggata 146700

tgcgttgcgg cgcttcaggt tctattgcta acaaggtatg gaagaagtta attcctgaga 146760

tgccacagat gttagcatca gcttattctg agaaagcgct atcgtatatt aagttccctg 146820

catttgctca gcttaaagcc gatggagccc ggtgcttcgc tgaaatccgc ggagatgatt 146880

tagatgatgt aactcttctt actcgttccg gtaatgaata cctgggtcta gataaactta 146940

agcgtcaact tatcgagatg accaaagaag cccgagaacg ccatcctaat ggtgtgatga 147000

ttgatggcga gttggtatat catgtcgaag tgaaagaaga agaaaacgac ctgtttgata 147060

tgtttaaaga gcctgagctt cctgaactaa gtaaagctaa ggaattccaa cagacggctc 147120

gtacagaatc aaacggcttg gctaataagg ccattaaagg aacaatctct gccgaagaag 147180

cagaaggcat gagattccaa gtttgggatt atgttccgct tgatgtagta tattccgaag 147240

gtaaagttcc tggatttgct tatgatgtac gcttccgtgc actggaaatg atgagcaaag 147300

gctatgacaa gattattcta attgaaaatc atgtcgtaca caacatccat gaagctcgtg 147360

ctatctataa gacatatgta gaccaaggtc tcgaaggtat tatccttaag aatatcggtg 147420

cttattggga agataagcgt tctaagaacc tcgttaaatt taaagaggtt atcactgtag 147480

atttgaaatg tgtcggttcg tacgagcata gaaaacaacc tggtaaaatg ggcggcttga 147540

tgttcgtatc agaatgtggt cgtattcgtg ttaacgctgg gtcaggtctt aaagataagc 147600

ccgaagaact gcacgagctt gaccgtactc atctatggaa aattagagat tctcttccag 147660

gaactatctg ggaacttgaa tgtaatggtt gggtaactgc tgaaggtcgt gatgatggta 147720

cggtaggatt gttcttgcct atcattaaac agcgcagata tgataaagaa gtggctaata 147780

cattcgaagc cgcatttggc gtgaacttta cagaggcaac aggaataaaa tgaaagtatt 147840

atacgaagta attgctaaaa ctgatgatgg gcgaggaggt atttccgtcc ataccgaagt 147900

tcttgatttt gataatatcg atgtattcaa aaacttcaaa gaaaacattg aagagtatga 147960

gtctgtaaat ggattacagg tttggcgtac tgccacaata attaattaaa ggccttcggg 148020

ccttttttcg tataaataga ataaacaaac gaggatatgt catggaactt ttaaatgaag 148080

ttttcgatga agagaatagc aaaatctatc ctgtcgagaa cgttaaacca aaactaaagg 148140

tgcctcaggt atttctgatt aaggtgccgg gtaataacaa tctaatgatt cgcttagtac 148200

atgggtcagg tcaaggtgat gcagttaaga atatcaaaat gggtgataaa ttcattcagg 148260

tatatgtttt ctctgtgtca gaaaaaggta atattggagc cctcaagggt gggttaggac 148320

aagacccgat tggtgctatc aatacaatct ttgaaactgt caacaaagta gttaaacaaa 148380

ttaaagccga tgcagtaatg ttccgcttta atccaaagaa aatgcaagga caagataaag 148440

ctattcaacg cattcttgct cggttgatta ctactcgcac cggtggtcgg ttcaatctaa 148500

tgaaagatat ggcttactat aaaggtaagt atgcttattc cattatggtt cacaaaggta 148560

agaagcttga agagattgaa ggaattcctg aaatttcaga tgagttatac acaaaggttg 148620

aatccaaagt aggtgaaatt tatgtgtcta aagaaaccgg cgaaagcgtt accaaagccg 148680

aagcattggc taattctatt ggcgaaaaag aagacaagaa atctgaactc gctgtaatga 148740

gtaaaatgaa agtgtctcga aaagatttaa tccgagcaca gtacggcaaa tttgtttcat 148800

atgttgatga agattggcca gaaaataaac gcgaacgttg gtacgaatta actactaaca 148860

ctccagtact aaacgcagaa ggcgatacgg tagacctcca aaaagatatc aaagccggat 148920

tagaaaaatc aattcctttt tatgttgatg atatcaagca ctatcgtgtt cgtggcggat 148980

atggaagtaa ttttggcgat gcagttgaga gattatttgt aggccaaatg tcgagaatgc 149040

atgacgactg gaaggttttc attccttcgg gttcagacaa aatgaaaatc gctgaacaac 149100

gaatttcaga cgttgctgac gttattgctc aagctaaaaa tcctgcatct atggaaacaa 149160

tgcgtaaaat cgttgaagta gctactcgtg gatttgatat gcctccagct gacgatttcg 149220

gagctttgcg tcaataccaa aatcttgtca attatatgat atccgcttat gtgtcaattg 149280

ttggcgattc tatatccaaa gcaattgaat ataaccgtga aatgcaatct cgtttaagcg 149340

aagaagaaag agatgcaata catcattact gtggttctgg ttattcattt gttaataact 149400

atcttattgg tatggaaagc ttaggcgatc cgattattga caagaaaatt cgtccgctcg 149460

attctgcctt tgaaaaaggt ttgcgtcttg aaccaggcac tcttttgtat cgtggtcagc 149520

gaggaaaata tgaagacttt aaagataaca ttgagtctaa aatgttttat ttccagaact 149580

atgtttctac ttcgttaagt ccaattatct ttggtgctta ttcaaatgct ggtgattcat 149640

taatgccaga cgcacctagt tctgatttag aaaacaaaga aacaactgct aatgcggtat 149700

cttctgttat tggaacagac aacttggaaa gagttgatag aggcgaggaa gttgcctatg 149760

gcgatgagtt taagtttgga ttcgttattc atggggctga taaagttaag gtagttatcc 149820

caggtgtctt gtcaagcttt agcgatgagg ctgaagttat tcttcctcgc gggttggcaa 149880

tgaaagtcaa caaagtatgg ggaactcctt ttagaaatgg agttggtgta gcgaataaca 149940

agacattcat ggtagaaatg acggtagttc cgccagagca aatcgatgaa tccgttcatc 150000

tctatgatgg tgacatcttg atggaacaag gaaaagtgga acctcttgaa gaaagcaagt 150060

tcaaaggctt tttaaatgag atttactttt cgccagaccg ttctacagat aaggttagct 150120

acacacgtac catggagcta ctggctggtg ctatcaacct ggatggtatc ccagaaaaac 150180

ttgcataaag ttgtttactt atcacaagga cgtgatacta tagacttaca caaaccaatg 150240

aggaaattga tatgaaacac gtattccgct ttaacggtat tgaatggtct gctgatgtta 150300

aagatgcaga gaagttcaat gaagaagttc ttatcatgct tgaagggttt aacgaaggta 150360

ctccgacggt tcttattcaa gatatcttcc gtaagccaac tgaaccatcg tttgttgaag 150420

cggttctaaa cggtaaagca gaaggtatta ttccggtcaa agtagtttgg actactaaag 150480

aaatgaaact tcttcgtact gagccagggt ttattggctg cattgcataa aacaaagggg 150540

ccataaggcc cctaaattat tctgcttgtt gaagtagtga tattagaaat tccaccacct 150600

gccccgccta aacgagacaa tcttgaagca gacgtactca agccctgatt tggattaatc 150660

gtctcaattt tctgaatagt tttatcttct aaccaatcca ttgcggcttg ttttccgact 150720

gaacctgttt gcatgctgcg ataagcaaac gtgacatcaa acacagctat tgtgttttct 150780

ccatcgtaag taaattcggg agctccacat gctacaggca tagcccctga gaacaggcat 150840

acagtatgtg gtaatccatt tctagcatga aggttaactt ggatatcaca ttctacgtct 150900

tgtggcaatc ctcgcagacc agtcaccggg tcttcaactg catttaccca atcttgcatt 150960

gctctatagt tgcttgcttc tgggtccatc ctaaatgaaa gaaccaacgg ctccatatct 151020

cttccagtga tttttatgtt aggagcgtta tggaacttat ccatttcata tgacagtcta 151080

ttctctggta ttttagcaga atacaccatc aagcctgctg tcggaaatgc catgttaaag 151140

aaatcaagca gataagtacc tactgtgaat tcacctaaca acgactgtac aacacgctgt 151200

gtcattgcgc caatcataaa tgtattcaca cctgatttgc gaacaacctg tcgagttcct 151260

tgtgtcacta tggttgttat accctgattg aattcacctg gtgtcaatcc aagccaattt 151320

ccatctaaac ccatattatt atacagctct ccgccaaagt cgtttagaag agcctgggtt 151380

ttactagagg gtacagtagc gaatacaaca gagaacatat tagttctctg gaaatcgatg 151440

tcagcagctt gactcttaaa ttcttcgaga gtaaacatta ttcaatacct ccgatataaa 151500

cgttccctct attaagagta agtatttcac gcatagtaat ttcaagcgta aacgtgcttg 151560

gaaggttagg agcgattgct aacccattaa aatgaccgtt cggtgtttta tcaaagcgga 151620

tgctctgaat ttggcacgga ccaaatatat cctctctacc atccattgat gtagaatatc 151680

caaaattacg aacagtccaa atcgttgggt tagaaactac aataacattg cttaaaaacg 151740

atgttatttg ctcaaacaca gtgttttcta ctttagctcc atccggtgct gccgatttaa 151800

gtgttccttt ataccattca tcaatagcag ctttaacttc ttttgcatat gatgaattcc 151860

ccgtcacacc gtaagaatag tagttaaaaa tttcatagat gcgaataatt tgtataaggt 151920

catctgcaga cctaggagtt aaatcccaag taaacacttt cgttctatta tcaggtccgg 151980

catacatact acgggcagtg ttataaattt gctcaccgtt atcggccatt aatccctgcg 152040

ttaaagattc tatcgaccca aacaccgcag tagaagccac gttgcttaat acaccagtag 152100

cagtaccgct gccgcgagta acaagagaat cgccaacatc attaaattta tggctaaccg 152160

aatcaacgtc tgacttagac cgtggtaata gaatattagc taccggcgca gtacttgtag 152220

tagaacttga tgaattagcc agtgctgaca ttggtgaatc gaatacagac gataacatta 152280

catctcgtct aaatgaacgc aaatcaggag tagttcttcc tttaaaatca tatgctgtga 152340

ataataatcc gttacgatac aagtcatgta ctctcatatc ttgtgcggaa tcgtttccgg 152400

ctgagcgttc ggccggaaac tgcgccacct tagtggtagg cgcattcgtc agtttagatt 152460

taccttggga aattcgagtt cctgattttt tgatgttttc aaggccatcg gccagttctt 152520

caaaaatcat tgtttttcct taagaggttt tcatagcgcc ttgcattcca ggagcagctg 152580

ttgaagtctg tggaggcgtt ctataaacgt atgtgctatt cttatttaca gcggtattaa 152640

cctgaatagg ttgcgactgt gtattagatt cacgtgtacg agctgcttca cgactatctg 152700

cggcggcttt aatagaagca gactgcttaa cctcaggctg ttctgttgca ggtatagctt 152760

cggcagttgg agcaggttct gatattttag aatcaagaag cttttgcaat tggtctaatt 152820

caacctttaa atcttttgca acttctggag ataatttctc caattcttta tatctggtgg 152880

ttgtgctttg tactgcatcc ttagcagagt ctaatcgagt ggaatcagat gcatcagttt 152940

tttcaacata tgcttttgta cgcttgagtt ctgcctcagc attattacga gctgtgatga 153000

ttttgaggcg ttcgtcttct ggcaagtctg catacgctga ctgctttttc tctccgctca 153060

gcaatttatt atattcatcg tcatcaatct gaccggtgaa ttttggaat ttagcagaaa 153120

gctttctttt ccattcaggt tgttcgtcat attctctttc ttgacggtca acatattttg 153180

ctctcatttt agcatcttct tcatctagtt ctgccccagt aacagtttga aatctgtcta 153240

aagcagcgcc ttcaatgtta tctgccgaat cgttaaatcc taatgcgcgt aacattccag 153300

cgagaagctt actcattccg agcataatag tttctccgag cttgtcaatt acatcaacca 153360

agccagaacc aatggcttta gctaatccgc cccaatcccc tttgacgaat gattttacta 153420

tttcattcga catctcgctt attgctgtta atagcggacc ccattctttg gcttgcttgt 153480

taaattcaac aaagttcttt tcgaacagtt tagtccaata attaaaatga actttaatta 153540

aatctataag cattatcacg cccaaaacca tggcggcagt tttcgccatt tgagccaaag 153600

cgctaacagt atagctaaat agcatgctgc taattttatc tgttaatgaa atagtttttc 153660

caaaaccaga tttaacactt ttaattaatt ctccaaattt taggccaaga aacttttttat 153720

tcttatcctc agtttctttg ttaggttctt ttctttcctc ttgctcttct gtgttaggaa 153780

agaaatccgc gtcaggacgt ctatcatcct gtggaggaat aagcctttcg agtaattcct 153840

ctagcggctg ctgaaccgga gcatcaggta cttgttccgt tattgtttct aacgatgttc 153900

cagtaccagt cttttggaca tcttgctgaa catcatgctt tttagataac aagtcggcaa 153960

gtttcgtgag cttatcatta attaacgatg ctgtatcatt tagtttagag acagcatctg 154020

ttgtgcgttc tgaagcttca gcagttaatt caacaccagc tgaaacatct tctactgatt 154080

tgataatttc atttgattta gtttctatta catccgaaat caaatcagta gacgcttgtt 154140

ggtcgtctaa gcgacgacca atatcttcta gcgtattaat ctgagcatca gcttgagact 154200

cagccttttt ctgtggagcc gagtcagcaa taactcttct acgcattgaa ttcatttctg 154260

atttcttagt cattcaaata tttccattac gttaagcatg cctttgattg gtccttcagg 154320

tccatcaatg gctatagtgt ttactaagtc atcagcccac tttgttacaa aagctggaag 154380

cttcataaag tttatatcca ttggttttcc atctactgat tcaagaaatt cgcttaaaat 154440

tgaatctact gaacctagtt tggaataacg aggaggagct ctgaatttga attctttacc 154500

atctaaccgc tgagttaatc gttggcaaat gtaaacttta ttcaaatcgt aggtaaaatc 154560

atctttaaca accgtttctt ttattcggtt gttaaatgct aataaatgta gtacaacgat 154620

atcggattcg gctgccgtta atcctgggca aattgaatct aaaagaagat tcatgttttc 154680

gtctggtccc ttaacatctt tcatcagatt atggtgcttt aatccaagtt ttggaattga 154740

tatcgtcttt tcgtttatta ctattttctt aataggaaga atcacgttta agttcatttt 154800

tcaccttaat caaatctaca ggttcaaggg cagagccatt tgtgaacata tataagttag 154860

ttatagatgt gttatttgat atttcatgga taacttcatc tacataaaag tcagttctga 154920

actggtcctt taaatcaaca aaattgattt tcattccagg agttagttca aaattaccgt 154980

aacatttagt ttgagcatac ccgtcatatt gagccatcgt agaaatgcgt agtgcttctt 155040

catagccatt tctaaaaatc atgtcagaat atccgcctga cctattaatg aatacgctgt 155100

tttggccttc tccattaata attcgggtaa catctttgtc cacaaacgag tgtgcataaa 155160

atgttgcgtt tttcatggga tttctattat atctgtttga tttaacaagc cattcaaaat 155220

cccatgccaa tggatatttt aatcctgctg caaactgacc tattgtttga ggagctccaa 155280

acatgaatac atttgggttc tgggatatca ttgattcata atccatcatg ttaatcccag 155340

tgatatcttc ccatgcaaaa ataaattggt cgttatcagt agaaatgcct acgtttctaa 155400

cgtatcgcaa gtaatctttg agagtactag tccatggaac tcgtgggacg taggcgttaa 155460

ttccgttgat aggaggagca atcaatggtt ggtcaacata catcgcgcct atcatttctt 155520

ttatagtttc atatgcagaa ctaaaaaacg ctctactgaa cttgagattc attatgtcat 155580

gcagcgttcc aagctgaagg gtgataatgc tatcaccttt atcatcaaca ccgactgtaa 155640

agtgtttaat tccgtaaatt cgagtttgcg ttcttgatgt gttactgttt gcaacagata 155700

tttgaactag ttcatcaccg ttcatacgcg tgtgcatatt tttcgaatca taaaactgaa 155760

gtagaccctc attagtcccg cgtaatgaat ctctcattgt taatgtaata aatgtagctg 155820

ctaattcaac gaatctatta gctagccacg catcatatcc agaatataat tttatgctta 155880

tattaggata tcctaatctt tgtgctgtca tgatttaagg tccttttcaa taagcgataa 155940

ggttatgcca cgttctatag gcagcatttt cattatagaa ttcaaatcgt atttaccctg 156000

agaaaccaat ctatggttaa tctgataaaa tgtgaaaatc tcgtcaggat gtagcaatag 156060

cttaaaaata tcgacaatgt tatcatattt taatattgtc gtggtatcac agcatgatgt 156120

ttttaattca aaattaaagg gcttcatctg tgataaaatc ttttccaagg tttcaacatc 156180

tatagcatcg ataacggtca atttattgct atcgctcaat tcattccatg cgtattcccc 156240

agatgaatcc ttcacagata taatgttatc taaaatcatt ttacctgtat cgtcaattat 156300

ttctatgggt tttttgaact tgagcgttaa tccagcaacc tctacttttg gatttaccaa 156360

tggaggttgg ttaagattaa aaagatactg cttatatttt ccgcattttg ggcacttcat 156420

tctgacaggt attttggttt taccaatact tgaaagaaat accttaagaa atatataagg 156480

acgatactcg gcaggatggt catgaaaata atcatccatt aattctgcta taagttgttt 156540

ttgttcttct tcagacttgg tgttcatgtc gtttctaacc aataaaaggt ctctataatc 156600

ttctactgta aatggcttaa aacgttggac accatctggt aattcgcatc taactatatt 156660

ggccataagg taatcctctt tatactattt ataaataatt gaataagagg agtggatatg 156720

aacatcacat acaaatttga aacaagaata aatggcaaga atatccagtg ccgagctttt 156780

acactagaag aatacgctaa tttaattgca gcgaagaaaa acggcacaat cgatgaatgc 156840

attaaagcat tgctcagaga atgcactaat gccactgaat taaacaaaca ggaatcggaa 156900

ttacttatag ttatactctg ggcccatagt attggcgagg ttaatcacga ggtgacctgg 156960

aattgcacct gcgggcgtaa aattcctgtg ccattaaatt atacacacgc gcaaatcgat 157020

cctccagaag acctctggta tgacttaaag ggatttaaaa taaagttcaa gtatccgagt 157080

ctttttgacg attcagacat tccaatgatg atatcaaaat gcatagatta tatcgtggtt 157140

ggaaatgagc agatttactt taatgattta aacgatgcag aaatcgatga tttatattct 157200

gctattacaa ccgaagatgt agttaacatc aaaaatatgc tattgaagcc gcaggttcaa 157260

ttagcagttc ccattacttg tgaatgcgga atttctcaca ttcatgtaat taaggggctt 157320

aaagaattct ttaagattat gtcatgagca atatcgataa attatattct gaccttgacc 157380

cagagatgcg acttgcttgg gatactgatg tgtcaaaaac ggtaggagca cgatcggtta 157440

aaaatagcct tcttggaata ataaccacca gaaaggggtc tcggccattt gacccagcgt 157500

ttggctgtga tatcacaaac gaattatttg aaaacatgac tccattaact ggtgatacga 157560

taaagcgtaa tatagtctct gccgtgcgta attatgagcc taggattaat cgtctatcgg 157620

ttgatgtgct tccgttatat gacgataatg ctataattgt tacggtgcag ttttctatag 157680

tagacgaccc tgatacgcta gagcgtatac gcatacagat gcgtagtaat gctaactcta 157740

gcagtagagt ataatgggac tagtccttcc aaagaaacag tagagtggag atagaatgag 157800

attagaagaa ttacaggatg aattggataa tgatttgatt atcgaccaga ctaaactaca 157860

gtatgaagcg gctaataacc ctgttctgta tggtaaatgg gtgcgtaagc actcgacttg 157920

tcgaaaagaa atgttaagat tagatgccct caaaaagcaa aatcttaaag cacgattgga 157980

ttattacact ggccgtggag aggttggtgg tgaagtatgc atggatgtat atgaaaaatc 158040

agaaatgaaa actgttttaa gcgctgataa agaaatcttg ggtgtagata ctaaattgca 158100

atattgggga attcttttgg agttctgtag cgatgcaatg gatgctatca agtcacgagg 158160

ttttagcatt aagcacatta ttgaccttcg tcagtttgaa gctggcgcgt aataaataaa 158220

cttgtaaact aaggagacaa tcatgtcgaa tacggtatgt gtcgtctgta aaggaccaat 158280

cgatgaagca ttggttgtcc aaacagacaa aggcccggtt catcccggag cttgctataa 158340

ttatgcgatt gaattgcctg tcactgaaga cacagaagag caattacaag aaacgcagct 158400

tttaatttag tctagtgttg atgtagccaa ttggctttgc cccttccttt cggttggggc 158460

ttttttatat cagaagtctt cgtcttcgtc atcttcagaa tcagcttcaa gagcctgtct 158520

acgccccgcc aaagcatccc gcacaatgat gtcatcagaa tcagcaagag tagtttcttt 158580

agagcgctta tcgtaatact tctcgagttc tttcagacca tctaaggttt ggcaagcatt 158640

aattttactc atgaagttat cgatagtagc ctcacgaatt gtggcttcgt aaatatcttc 158700

aaatttaatc atagatttac cgttttcatt acgtagttaa atttttcatc agcatatcgt 158760

tgaatacgct ctaatgcatg ttttaagcaa tagtttaaat gtgtgtattt ctttttagca 158820

ttggctgact tcggctttac gcccaggtca tcaatgatat cccacactgt agccaaagat 158880

ttatctttat gcttacgaag aacacgacca atagtttgga gtacgataat cttcgattta 158940

actggatggg ctaaaattac atgatgcagg tttttaacag aaatacctgt agaaaataca 159000

ccgtagcttg cgacgataat aattcccttt ccgttttctg ccatagcctt taaagcatta 159060

cgtgtttcgg tattaacttc gcctgacaca taatatacat gctcatgacc cgcagcttta 159120

atcatctcga acagctcttt accatgagct acatgtttaa acatcacaaa ggcattttcg 159180

tcacgcgctg caagtttagt agcaagatta gcaatccaac gatttctttt cttaacattg 159240

gtgatgaatt taatttcttc ttgatacgtt ttgcctttta aagcgtttgc ggctgcatct 159300

gggtatctta agaagattgt attaatttta agctcagtta cttgtccatc ttccattaac 159360

ttagaagttg atactggacg gaagatttca ccaaacatac caacatattg catgatatta 159420

gctttgccgt ctttaagaga accagacagt ccgtacttaa acatgcaatt tgtaagacct 159480

gcaatgattg ttgaaattga ctttcctgtt gcaagatgac attcatcatt catcatcatg 159540

ccgaattgag aaaaccattc tttaggctgc ttaacagcgg tctgccaggt agatacataa 159600

actaatgcat tcgaatcacg agcagtacca cctcgaatac ccagcatagc attgcgagga 159660

aataaacgat aatcacaaaa atcatcaatc atctggtcaa ctaacgctgt ggtaggaacg 159720

atgataagaa ccttgccttc gtaattttct acataatatc gagcaagtaa tgcctggata 159780

agagacttac cagcagatgt tggaagatta agaattctac gccgattaac tagaccttca 159840

tatacagcat ctttctgata ccagtgaggt tcaatcttag ttaatcctga ataaatttct 159900

ttagttgata accaattatc aaaatcctcc cgcgaaagag tttcttgctc gaatatagct 159960

ggatcgaaat aaaccttata tccgaattgg tcagcgaatt ttctgatttg gccaacaaga 160020

ccaaacggta agagacgatt ataatctagc agacgaattc gtccatccca atgtccatag 160080

cgatatttcg ggttgaatct gtatccatcg gcttcgaagc taaaatagtc tctgagttca 160140

tagaaaatcg agtcatcaca ctcaatatga acatgactaa aatctttaaa tttgacttgg 160200

atgtcgtgca ctgtactatc ctcagttata aatacaatca tatttataca ttacatgagg 160260

cacacccaat gctagataaa gactatatta aagaaattca ggcactcgat aaaaaagaag 160320

ctaaagataa gctcgacgag tatgcccaaa ctttcggtat taaactgaaa aagacccgtt 160380

catttgacaa tatggttgct gacttagaaa aagaactggc taaattggcc aatgagccta 160440

tgccagaaga taatgatggg ctgtcaattg ctgatttaat tcaagcagat gatgaaattg 160500

agggtaaagc agtatttaaa gatgaagcgt ctgatgaggc aaaactactg tttgacgctc 160560

cagttaatgt tggtattaaa attcatgata ttgacccagg tttttataaa gaaaccccta 160620

aggtaaatga cccagggttt gaagtaaaaa caccttctat caatgataaa ggattttatg 160680

ctgaagctcc tattggagac agcgttattc atatagatga tgaaggacaa gttaccaata 160740

ttccggttag tatcacggac cctgaagaat tctccaaagc aatggacaaa gtagttaaaa 160800

ttattaaaac agacgaaatc attgagcttc ctgaaaactt tagtccaaat atgcaattgc 160860

taggtaagaa cccaggatat attactcttc catggtggat ttaccaatgg attaaagata 160920

acccagattg gaaatctcgg ccaacgtcgt ttgaacaccc atcagcacac cagacactgt 160980

ttagtttaat ctattacatc aaaagaaacg ggtctgttat gattcgtgaa acacgtaatt 161040

cttcatttgt aactttaaaa taaggaacac ctatggctta tagcgtatct attgctcctt 161100

tggctgcttc ggcagtcatt ggagcaacaa ccaattttac tgcaacaact tctggagccg 161160

cagctgaagg cacagaaacg tttgtatgga cagtaaatgg cgtaaaacaa tcttctgtca 161220

ctgcagctat gaattatgtc actgcaggac ctgccggtag taagactgtt aaagtagttg 161280

ctactgttac cccagcagag ggtgaggtag aaaccgctga agcagaaact actttgacag 161340

ttaagaacaa aactatgcct gcgattactt taactttgag cccgacttct gtttctaaag 161400

aaattggaca atcacaagta gtcacggctg atgttactgg cgcaccgtca ggagcaagca 161460

ttgcttatgt ttggaaacgt ggctcttctg ttatttccgg tcaaactggt aaaacaatta 161520

ccttaactga atcaacggaa accagctaca cactgaattg tgaagtgacg gtttctgctc 161580

cagactataa taatggaact gcaactaaag gtattgctgt tgcttttact aaaaagacca 161640

tgagtggtgt ttcagttact ttgagcccaa cttctgtttc taaagaaatt ggccagtctc 161700

aggtagttac ggctaacgtt gttggtgctc cagaaggggc aagtattgct tatgtctgga 161760

agcgtggtac tgtcgttatt gaaggtcaga ctgctaaaac gattaccata actgagtcag 161820

cagaggctaa ttatactctg aattgtgaag caacagtttc tgcaccagat tacaatccag 161880

tgactgtaag caaaggtgct agcgtaacca tcactaaaaa gacaatgagt ggtgtttcag 161940

ttactttgac tcctgaatct attacagtcg agcaggggtc tgatgcatct tttaaagccg 162000

acgttatcgg ttctccagaa ggtgcatccg gaacttattc atggaccaaa gacggttccc 162060

ctgttgaagg ttcaactagt actttagtga ttgacacgtc tgatataggg tctcaagtga 162120

ttggggtttc tgttgaggtt tccgcagaag attataactc agtcacagta actacaactg 162180

gtaatgtaac tattaccaaa agggtagctc ctactcctaa cggagagctt ccgtatattc 162240

atcctctgcc gttccgtgaa acagcttata tctggtgcgg ttggtgggta atggatgaaa 162300

tccagcgaat gactgttgag ggcaaagatt ggaaactcga cgaccctgac agcgattatt 162360

acctacaccg atatactctg gctaaaatgc tagacgatta tccagaagtc gatgtacaag 162420

aatctagaaa tggatacatt gttcatcgta ctgcgctgga agcaggtatt atctatcctt 162480

aatattcggg agccttcggg ctccctttt gctattcata gactggttta atatgtcttc 162540

atcacataga tgaggttatt atgaaagcaa tacaagctca cttgatgcat gaaagtggta 162600

aagatttcca agaaattgcg agagcattag atatcactcc agcggaagct gctaaattgt 162660

gggtctcagt tgagaaagca cacgaacggt ttaagcaaaa agaaaaagtc gtatatcgga 162720

aacgcttaac aaacgttggt ataaaatctc gtcataagaa acttgttaaa cacatgagga 162780

ctttatgatg tctaaagtag acccaattgt agtagaacga tttgaagaaa tgctttctaa 162840

gaaatttacg ccagctgcta atggggtaaa tgtctggttg tttgcatcta aatttgttag 162900

taaaatgatg gctgttcaga gttcttacta ctataaaagt ggtgcacgta aaataacgga 162960

tttgattaat gaacggtatg gaaaaattga ttggatgctg atggataaag atattccatt 163020

agtacttgag gttggaagca aaagtcaatt tgaaatcatg ctaactaaaa gcggatatat 163080

catgtatcgc ttcgtgccga gcggttatta attgctttaa aaatcgatgt ggtataatgg 163140

gctcagggga aatcctctga taccattatc cttatcccaa gatagatgga ctcctggttt 163200

tatattattt attgagagaa aaattatgaa ccttgcagat agaatggcta atacagctat 163260

taatgttgct acagaagaat tgagtgcagc aaaagaagaa gtattaaccc agattgagaa 163320

aaccgcttta gcgggtaagc gtgagctaat tatgtatcct agcagtttag ttaagaaaca 163380

tatcacaaac gttcttaatt atttgcatga tgaaggattt gttacaaatt ataccagtgc 163440

ccagcgtaat ggtgatactg actttatgaa aatcacattc taaggaaatt ataatgtttg 163500

caaaatattc tagtctcgag aaccattaca acaataagtt catcgagaag attcgtggtg 163560

ctggttttga tatgcatact gttgagtggg tggctcgtga gaaaattcat ggcactaact 163620

tcagtgtgat tattacccct accgaaattg ttccggctaa gcgtactggt cctattttag 163680

aaggtgaaag cttctttggt catgagatta tcatgaagaa gtacaaggat tctttcgtta 163740

agatgcagaa catgctgaac accatggatt tagtatctgt tcaaatcttc ggtgaatttg 163800

ctggcggtgg tattcagaaa ggcgtagatt atggtgataa agatttctac gtgtttgata 163860

tcctgtcgga ttccggtaac gaaaaagttt attgggacga ttatgtagta gaatcgtttg 163920

ctactggtct tggtcttaaa ttagctccac tgcttggtcg tggttcattc gctgagctat 163980

ctcagtatgt aaatgacttt aaatctattg tcaattacta taatgaactt gttgacacga 164040

ctgaccttga acatgcaaat aaacatgtgt tcggtccaca ggcttcttct gaaaccggtg 164100

tagctgaagg ctatgttctt aaaccggtta atcctaaatt ctttaataac ggtacccgtg 164160

tagctattaa gtgtaagaat tctaagttca gcgagaaagc taaatctgat aagcctatta 164220

aagctaaggt tgaactcact gatactgata agcgtgttct ggaaatcttt tccgagtatg 164280

taacctggaa ccgtgtaagt aacgttctgt ctcatattgg tactgtaact gccaaagatt 164340

ttggtcgagt tatgggactg actatgaaag atatcattaa cgaagcagct cgtgaaggtc 164400

atgacatgct attcgctgat aatccttctg ctgttaagaa agaactgact actttaattc 164460

aaaacactat tcgtagcaaa tggcatgagg ttttagaata atgaggctgg cgctgattgg 164520

ttcaagagaa gcgccacgca gagttctgag tctaatgact ataatcggtc aacgcctctc 164580

ggaagagggg catttttcat attcaggtgg agctccgggt tcagatgaag cgtggttggc 164640

gaaatacgat aggtcaaatt cttgtaggat tattccttat tctggctttt gtggccatgt 164700

tcctgataca ggtgttgttg tatggtctga attatcaaac gaagccaaaa tcaaaagcat 164760

cattaaggcg agagaagtta cgtcgtactg ggatgaatgc tcgaagatag tacagacact 164820

atttgcacgg aattctatgc aggtattggg cctagaatgc actgagcctg tagataaggt 164880

attatattgg gcgcctgaaa aaagatgtgg gagtgtatct ggagggacga gagtagctgt 164940

tgatatagcc cgtagacatg gaatagaatg cgtcaacctc tatgataaga atgtgtttaa 165000

atccctcgag gaggaatact ccccgaggtt tgacatattt agtttataac aaaaagggga 165060

gccgaagctc cccataaatt agtccgcaat aagcttaggt aacttaacac cgagcagtac 165120

agacatctta cttcttcctg ccatcttatc catatccgca gcattaatca cacgagcttc 165180

gtcctcgtcc aatcctacag tatatgggtt aactgacaat gcatatcgta ccagtaaagc 165240

aacagaaggc tgcaagctag ctgggtcaac aataacttta aatgcaccaa catgctcagg 165300

gtcgtctaaa tccaagcctt cggtatatgg cgcataaaat aaagaaccta cagtttcctt 165360

cccaccaaat tctgccttaa caccaacaat aacgtaatca accggactgt tagtatcaca 165420

ataaagaggt aaaccgttat tcagcatacc gtatgcgttt tccggaatac ttccatcatt 165480

cttctgtgtt aaccaaccgg aagctgcaag caccgcagca caacgagtag atgctactgc 165540

ataagtacca gaataagaag tattacgttg aactgctgaa ttcatttcac aaatgaaacg 165600

atacagagta cgaccttgtt ccggagcaga atcttgttta gttaaatcta atacaccctt 165660

atcggataca ccagctactt taaaccgaga agaaaccgta atcaatgatt gcaagatgtc 165720

tttattaatg tcttctgcca tttcagtagc aagtaaatca tcaataagtt ctggagcatc 165780

gaacccatta gcttctaaat cttgagctaa ttctaccgtt aaatctgttt taagcttacg 165840

tgatttaacc tgggtctgcc atttatcaat tttaaaactg gcttcggtga ttgggtctga 165900

atcgggtcct tcaaattttt cagtgactgc agcatctgac aacatacgaa tattattagc 165960

tgctactgct tcagacacaa ttccaaattc atcggtttct gctgtatcgg taaacgggct 166020

atctttaagt actttaaaga ccacattctg atatttgaac atatcgtctt tattgaatga 166080

gtctttattt gccatagtga gttcttcaat tgactcacgt tctggcgccc cgatttgacc 166140

tgcataagtt gcacccgtat taaacgtcag gtcaccatta gggttaagat atttgatacc 166200

atatagcgct gctacaggct gtttagtacg ctgtgtagca acaagatcgg tatagattaa 166260

tttagtagtt gcgcgcgtta atgcaacgag attagggcga ccaattaagt tgctactcgt 166320

tgtagttgac tcgcgcagaa gttcgttgat tttagccatt gcgctttcct ctgtggattt 166380

ataagtttat ttatatccat taaaacaact aaagggagcc cgaaggctcc cttattggta 166440

ttagatacct ttaacccata cacgacggaa gtaagcattc ttaccaacag agttgacgat 166500

agaaggcata ccagaggtaa tacgaccttt cggctgttga gcagcagaat cggcgaacgg 166560

gttaataccg ataccgtaac gggttttgaa ccccatgacc ggttggaagt tcttcggatc 166620

ggaaccacgc agcggggtca gtgcaacata cggagcatag tagataccag catccattt 166679

<210> 782
<211> 440
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 782

```
Met Lys Lys Asn Lys Leu Ile Glu Lys Trp Gln Pro Leu Leu Glu Asn
1               5                  10                  15

Glu Ala Leu Pro Glu Ile Val Gly Ala Ser Lys Lys Ala Leu Ile Ala
            20                  25                  30

Lys Ile Phe Glu Asn Gln Glu Ala Asp Ile Asn Gln Ala Pro Glu Tyr
        35                  40                  45

Arg Asp Glu Lys Ile Ala Glu Ala Phe Gly Ser Phe Leu Ser Glu Ala
    50                  55                  60

Glu Ile Gly Gly Asp His Gly Tyr Asp Ala Gln Asn Ile Ala Ala Gly
65                  70                  75                  80

Gln Thr Ser Gly Ala Val Thr Gln Ile Gly Pro Ala Val Met Gly Met
                85                  90                  95

Val Arg Arg Ala Ile Pro Asn Leu Ile Ala Phe Asp Ile Cys Gly Val
            100                 105                 110

Gln Pro Met Ser Asn Pro Thr Gly Gln Val Phe Ala Leu Arg Ala Val
        115                 120                 125

Tyr Gly Lys Asp Pro Leu Ala Ala Gly Ala Lys Glu Ala Phe His Pro
    130                 135                 140

Met Tyr Ala Pro Asp Ala Met Phe Ser Gly Gln Gly Ala Thr Glu Lys
145                 150                 155                 160

Phe Glu Ala Val Lys Ala Gly Ala Ala Leu Thr Val Gly Asp Ile Val
                165                 170                 175

Val His Asp Phe Ala Gln Thr Gly Arg Ala His Leu Gln Val Val Glu
            180                 185                 190

Asp Phe Thr Val Asp Ala Gly Ala Thr Asp Ala Ala Lys Leu Asp Ala
        195                 200                 205

Ala Val Thr Ala Ala Leu Glu Ala Gly Lys Val Val Glu Ile Ala Glu
    210                 215                 220

Gly Met Ala Thr Ser Val Ala Glu Leu Gln Glu Ala Phe Asn Gly Ser
225                 230                 235                 240

Lys Asp Asn Pro Trp Asn Glu Met Gly Phe Arg Ile Asp Lys Gln Thr
                245                 250                 255

Ile Glu Ala Lys Ser Arg Gln Leu Lys Ala Gln Tyr Ser Ile Glu Leu
            260                 265                 270
```

```
Ala Gln Asp Leu Arg Ala Val His Gly Met Asp Ala Asp Ala Glu Leu
        275                 280                 285


Ser Ser Ile Leu Ala Thr Glu Ile Met Leu Glu Ile Asn Arg Glu Val
    290                 295                 300


Val Asp Trp Ile Asn Tyr Ser Ala Gln Val Gly Lys Ser Gly Met Thr
305                 310                 315                 320


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


Asp Ile Arg Gly Ala Arg Trp Ala Gly Glu Ser Phe Lys Ala Leu Leu
            340                 345                 350


Phe Gln Ile Asp Lys Glu Ser Ala Glu Ile Ala Arg Gln Thr Gly Arg
        355                 360                 365


Gly Glu Gly Asn Phe Ile Ile Ala Ser Arg Asn Val Val Asn Val Leu
    370                 375                 380


Ala Ala Val Asp Thr Asn Val Ser Pro Ala Ala Gln Gly Leu Gly Arg
385                 390                 395                 400


Gly Tyr Asn Thr Asp Thr Thr Lys Ala Val Phe Ala Gly Val Leu Gly
                405                 410                 415


Gly Arg Tyr Arg Val Tyr Ile Asp Gln Tyr Ala Arg Gln Asp Tyr Phe
            420                 425                 430


Thr Ile Gly Tyr Lys Gly Ala Asn
        435                 440


<210> 783
<211> 270
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 783
Met Leu Lys Glu Leu Leu Met Thr Glu Ala Lys Thr Ile Asp Ala Ser
1               5                   10                  15


Val Ala Leu Asp Ser Ile Phe Glu Ser Val Gln Leu Ser Pro Glu Ala
            20                  25                  30


Lys Ala Asn Phe Ser Thr Val Phe Glu Ala Thr Val Lys Lys His Ala
        35                  40                  45


Val Ala Leu Ala Glu Ser His Ile Glu Lys Ile Ala Glu Lys Ala Glu
    50                  55                  60
```

```
Glu Lys Val Glu Glu Glu Lys Glu Lys Ala Lys Glu Glu Ala Arg Glu
65                  70                  75                  80

Glu Leu Lys Glu Ala Ala Ser Lys Tyr Phe Asp His Ile Ala Ala Glu
                85                  90                  95

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

Leu Phe Glu Ser Met Phe Val Gly Met Lys Glu Leu Phe Val Glu His
        115                 120                 125

Asn Val Val Ile Pro Glu Glu Ser Val Asp Val Val Ala Glu Met Glu
    130                 135                 140

Glu Glu Leu Ala Glu Gln Lys Ala Glu Thr Ala Arg Leu Phe Glu Glu
145                 150                 155                 160

Val Ser Lys Arg Asp Glu Tyr Ile Asn Tyr Ala Gln Arg Glu Tyr Ala
                165                 170                 175

Ile Gln Glu Ala Thr Arg Glu Leu Thr Asp Thr Gln Lys Glu Lys Val
            180                 185                 190

Val Ser Leu Thr Glu Gly Met Asp Tyr Ser Asp Ala Phe Ser Thr Lys
        195                 200                 205

Leu Lys Ala Ile Val Glu Met Val Gln Gly Ser Val Glu Gln Ser Val
    210                 215                 220

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

Asn Phe Thr Thr Glu Ala Val Glu Glu Thr Pro Ala Thr Lys Thr Pro
                245                 250                 255

Ser Val Met Asp Ala Tyr Val Ala Gln Ala Ala Arg Leu Ser
            260                 265                 270


<210> 784
<211> 216
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 784
Met Glu Asn Leu Asn Glu Gln Leu Leu Ile Glu His Trp Gly Gln Pro
1               5                   10                  15

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

```
Gly Glu Asn Glu Ser Gly Leu Lys Pro Gly Leu Tyr Ile Glu Gly Val
        35                  40                  45

Phe Met Gln Ala Glu Val Val Asn Arg Asn Lys Arg Leu Tyr Pro Lys
    50                  55                  60

Arg Ile Leu Glu Thr Ala Val Ser Arg Tyr Ile Lys Glu Gln Val Ala
65                  70                  75                  80

Thr Arg Gln Ala Leu Gly Glu Leu Asn His Pro Pro Arg Ala Asn Val
                85                  90                  95

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

Asn Asp Val Tyr Gly Arg Ala Arg Ile Ile Glu Gly Asp His Gly Pro
        115                 120                 125

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

Ser Ser Arg Gly Leu Gly Ser Leu Lys Asp Ser Gly Lys Gly Tyr Asn
145                 150                 155                 160

Ile Val Gln Glu Gly Phe Arg Leu Thr Val Gly Val Asp Ala Val Trp
                165                 170                 175

Gly Pro Ser Ala Pro Asp Ala Trp Val Gln Pro Lys Gln Ile Ser Glu
            180                 185                 190

Asn Thr Ser Ala Gln Val Ala Asn Ser Ala Asp Asp Ala Phe Met Ala
        195                 200                 205

Leu Ala Glu Lys Leu Lys Ala Leu
    210                 215


<210> 785
<211> 141
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 785
Met Leu Ile Leu Pro Glu Asn His Glu Leu Val Ile Asp Thr Val Glu
1               5                   10                  15

Ala Leu Leu Pro Glu Ala Gln Ala Arg Phe Asp Lys Leu Ser Ala Ala
            20                  25                  30

Leu Ser Lys Asp Asp Ile Asn Lys Ile Val Glu Asn Leu Val Val Ser
```

35 40 45

Glu Pro Asp Leu Ala Ile Ala Leu Gly Ser Ile Asn Glu Ser Leu Gln
50 55 60

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

Arg Thr Lys Asp Arg Lys Thr Arg Glu Arg Asn Ala Phe Gln Thr Thr
85 90 95

Gly Leu Ser Lys Ala Lys Arg Arg Gln Ile Ala Arg Lys Ala Val Lys
100 105 110

Ser Lys Arg Ala Asn Pro Ser Ala Gln Thr Arg Gly Leu Arg Lys Arg
115 120 125

Lys Lys Ala Leu Lys Arg Arg Gln Ala Leu Gly Leu Ser
130 135 140

<210> 786
<211> 74
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 786
Met Glu Asn Tyr Ile Ser Ala Ile Glu Ser Arg Asp Leu Val Ala Ala
1 5 10 15

Lys Lys Ala Phe Gly Ala Ile Met Ala Glu Arg Thr Ser Gly Leu Ile
20 25 30

Glu Glu Arg Lys Lys Phe Ile Ala Ala Ser Val Met Ile Glu Gly Glu
35 40 45

Glu Pro Asp Glu Asp Glu Asp Glu Asp Asp Glu Asp Glu Asp Lys Ser
50 55 60

Asp Lys Asp Glu Asp Asp Glu Glu Asp Glu
65 70

<210> 787
<211> 522
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 787
Met Ala Phe His Ile Leu Asp Leu Phe Ala Pro Trp Glu Lys Arg Asp
1 5 10 15

```
Glu Ala Glu Tyr Lys Gln Gln Ile Asn Asn Asp Leu Glu Ser Ile Thr
            20                  25                  30

Ala Pro Lys Phe Asp Asp Gly Ala Arg Glu Val Glu Ser Asn Glu Asn
        35                  40                  45

Glu Ile Gln Tyr Asn Ser Phe Asn Gln Met Met Phe Gly Ser Asn Glu
    50                  55                  60

Pro Gly Met Lys Thr Thr Ala Asp Leu Ile Asn Thr Tyr Arg Ser Leu
65                  70                  75                  80

Met Asn Asn Tyr Glu Val Asp Asn Ala Val Glu Glu Ile Val Ser Asp
                85                  90                  95

Ala Val Val Tyr Glu Asp Gly His Pro Val Val Ser Leu Asp Leu Asp
            100                 105                 110

Ser Thr Asp Phe Ser Gln Ala Ile Lys Asp Arg Ile Leu Glu Glu Phe
        115                 120                 125

Asn Thr Val Leu Thr Cys Leu Asn Phe Glu Arg Lys Gly Ala Asp His
    130                 135                 140

Phe Arg Arg Trp Tyr Val Asp Ser Arg Ile Phe Phe His Lys Ile Val
145                 150                 155                 160

Asn Thr Lys Lys Met Lys Asp Gly Ile Gln Glu Leu Arg Arg Leu Asp
                165                 170                 175

Pro Arg Asn Leu Gln Phe Ile Arg Glu Ile Val Thr Ala Asp Asp Ala
            180                 185                 190

Gly Thr Lys Ile Val Lys Gly Tyr Lys Glu Tyr Phe Ile Tyr Asp Thr
        195                 200                 205

Gly Lys Glu Ser Tyr Tyr Ala Asp Gly Arg Leu Tyr Ser Ala Gly Thr
    210                 215                 220

Lys Ile Lys Ile Pro Arg Asp Ala Ile Val Tyr Ala His Ser Gly Leu
225                 230                 235                 240

Val Asp Cys Ser Gly Gln Asn Ile Ile Gly Tyr Leu His Arg Ala Val
                245                 250                 255

Lys Pro Ala Asn Gln Leu Lys Leu Leu Glu Asp Ala Leu Val Ile Tyr
            260                 265                 270

Arg Ile Thr Arg Ala Pro Asp Arg Arg Val Phe Tyr Ile Asp Thr Gly
        275                 280                 285
```

```
Asn Met Pro Ser Arg Lys Ala Ala Ala His Met Gln His Ile Met Asn
    290                 295                 300

Thr Met Lys Asn Arg Val Val Tyr Asp Ala Ser Thr Gly Lys Ile Lys
305                 310                 315                 320

Asn Gln Gln His Asn Met Ser Met Thr Glu Asp Tyr Trp Leu Gln Arg
                325                 330                 335

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

Gly Met Ser Asp Met Asp Asp Val Arg Tyr Phe Arg Thr Ala Leu Tyr
        355                 360                 365

Met Ala Leu Arg Val Pro Leu Ser Arg Met Pro Asp Ala Asn Asn Gln
    370                 375                 380

Gly Gly Val Gln Phe Asp Ala Gly Thr Ala Ile Thr Arg Asp Glu Leu
385                 390                 395                 400

Asp Phe Ala Lys Phe Ile Arg Arg Leu Gln His Lys Phe Glu Glu Ile
                405                 410                 415

Met Leu Asp Pro Leu Arg Thr Asn Leu Ile Leu Lys Lys Val Leu Ser
            420                 425                 430

Lys Asp Glu Trp Glu Asp Glu Ile Asn Asn Ile Lys Ile Val Phe His
        435                 440                 445

Lys Asp Ser Tyr Phe Thr Glu Leu Lys Asp Ala Glu Val Met Glu Arg
    450                 455                 460

Arg Ile Asn Met Leu Thr Met Ala Glu Pro Phe Ile Gly Lys Tyr Ile
465                 470                 475                 480

Ser His Lys Thr Ala Met Lys Asp Phe Leu Gln Met Ser Asp Glu Glu
                485                 490                 495

Ile Glu Gln Glu Ala Lys Gln Ile Glu Leu Glu Ser Lys Glu Ala Arg
            500                 505                 510

Phe Gln Asp Gln Glu Asn Glu Glu Asp Phe
        515                 520
```

<210> 788
<211> 195
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

sequence

<400> 788
Met Phe Cys Thr Tyr Leu Thr Ile Tyr Thr Gly Asn Lys Leu Pro Arg
1 5 10 15

Arg Tyr Ile Gly Ser Thr Ser Val Ser Arg Ile Ile Asp Glu Asn Tyr
20 25 30

His Gly Ser Val Lys Ser Lys Lys Tyr Lys Asp Leu Trp Lys Ser Glu
35 40 45

Gln His Asp Asn Pro His Leu Phe Lys Thr Arg Ile Leu Asn Thr Tyr
50 55 60

Glu Thr Arg Glu Glu Ala Ser Lys Ala Glu Leu Glu Leu Gln Ile Lys
65 70 75 80

Tyr Asp Val Val Lys Ser Ser Ser Tyr Ile Asn Met Ala Leu Ala Gln
85 90 95

Pro Asn Gly Phe Phe Gly Met Ser Thr Lys Gly Arg Lys Met Ser Glu
100 105 110

Glu Ser Lys Glu Lys Gln Arg His Gln Arg Leu Gly Ile Lys Arg Pro
115 120 125

Asp His Ser Ile Lys Leu Ser Gly Arg Lys Arg Pro Asp His Ser Lys
130 135 140

Ala Met Ser Gly Glu Arg Asn Pro Met Phe Gly Lys Glu His Pro Asn
145 150 155 160

Lys Gly Lys Lys Ile Asn Gln Pro Arg Met Thr Cys Pro Val Cys Gly
165 170 175

Val Glu Ser Thr Arg Ser Ala Ile Met Arg Tyr His Lys Ala Cys Leu
180 185 190

Ser Ser Ile
195

<210> 789
<211> 163
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 789
Met Glu Leu Thr Asp Ile Thr Arg Ala Phe Glu Ser Gly Asp Phe Ala
1 5 10 15

Arg Pro Asn Leu Phe Glu Val Glu Ile Pro Tyr Leu Gly Arg Asn Phe
20 25 30

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

Val Pro Val Gly Tyr Met Asn Arg Lys Ile Asn Val Ala Gly Asp Arg
50 55 60

Thr Tyr Asp Asp Trp Thr Val Thr Ile Tyr Asn Asp Asp Lys His Glu
65 70 75 80

Val Arg Lys Ala Ile Ile Ala Trp Gln Ala Gln Ala His Ala Gln Gly
85 90 95

Asn Asp Ile Ser Gly Met Thr Pro Ala Asp Tyr Lys Lys Val Ala Thr
100 105 110

Val Arg Gln Phe Ser Arg Asp Gly Lys Thr Ile Thr Asn Glu His Thr
115 120 125

Ile Thr Gly Leu Trp Pro Thr Asn Val Gly Glu Val Gln Met Asp Trp
130 135 140

Asp Ser Asn Asn Glu Ile Glu Thr Phe Glu Thr Thr Phe Ala Ile Asp
145 150 155 160

Trp Trp Glu

<210> 790
<211> 657
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 790
Met Pro Leu Val Ser Pro Gly Ile Glu Leu Lys Glu Thr Ser Val Gln
1 5 10 15

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

Phe Gln Trp Gly Pro Ala Tyr Gln Val Thr Gln Ile Thr Asn Glu Val
35 40 45

Glu Leu Val Asp Met Phe Gly Gly Pro Asn Asn Gln Thr Ala Asp Tyr
50 55 60

Phe Met Ser Ala Met Asn Phe Leu Gln Tyr Gly Asn Asp Leu Arg Thr
65 70 75 80

```
Val Arg Val Val Asn Arg Glu Ala Ala Lys Asn Ala Ser Pro Leu Val
                85                  90                  95

Asp Asn Ile Glu Trp Thr Ile Thr Thr Ala Gly Ser Asn Tyr Glu Val
            100                 105                 110

Gly Asp Lys Ile Thr Val Lys Tyr Ala Asp Gln Thr Val Asp Asp Thr
        115                 120                 125

Gly Ser Val Thr Glu Val Asp Ser Asp Gly Lys Ile Lys Ser Val Phe
    130                 135                 140

Ile Pro Thr Ser Lys Ile Ile Ala Tyr Ala Lys Ser Ile Asn Gln Tyr
145                 150                 155                 160

Pro Asp Leu Gly Ser Ser Trp Thr Thr Thr Ile Thr Ser Gln Ser Ser
                165                 170                 175

Gly Val Ser Ala Val Ile Thr Leu Gly Lys Ile Ile Ser Glu Ser Thr
            180                 185                 190

Val Leu Leu Thr Glu His Glu Thr Ala His Glu Glu Met Thr Lys Thr
        195                 200                 205

Glu Phe Gln Thr Ala Leu Ala Gln Tyr Lys Met Pro Gly Ile Val Ala
    210                 215                 220

Ala Tyr Pro Gly Glu Leu Gly Asn Gln Leu Glu Ile Glu Ile Val Ser
225                 230                 235                 240

Lys Ala Ala Phe Asp Lys Gly Glu Gln Leu Thr Ile Tyr Pro Ser Gly
                245                 250                 255

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

Thr Asp Thr Gln Tyr Ala Ile Ile Val Arg Arg Asp Gly Ala Val Val
        275                 280                 285

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

Asn Asn Ile Phe Met Asp Asp Tyr Phe Ser Lys Gly Ser Ser Arg Tyr
305                 310                 315                 320

Val Phe Ala Thr Ala Gln Gly Trp Pro Glu Gly Phe Ser Gly Val Ile
                325                 330                 335

Arg Leu Gly Gly Gly Val Ser Ala Asn Glu Ser Val Thr Ala Gly Asp
            340                 345                 350
```

```
Leu Ile Gln Gly Trp Asp Leu Phe Gly Asp Arg Glu Ala Leu Arg Val
        355                 360                 365

Asn Leu Leu Ile Ala Gly Ala Cys Ala Gly Glu Thr Asp Glu Ile Ala
    370                 375                 380

Ser Thr Val Gln Lys His Val Ser Ser Ile Ala Asp Glu Arg Gln Asp
385                 390                 395                 400

Cys Leu Ala Leu Ile Ser Pro Pro Arg Ser Thr Ile Val Asn Ile Pro
                405                 410                 415

Leu Thr Arg Ala Val Asp Asn Leu Ile Asp Trp Arg Gln Gly Asp Gly
            420                 425                 430

Thr Tyr Asp Ser Ala Asn Met Asn Ile Asn Thr Thr Tyr Ala Ala Ile
        435                 440                 445

Asp Gly Asn Tyr Lys Tyr Gln Tyr Asp Lys Tyr Asn Asp Val Asn Arg
    450                 455                 460

Trp Val Pro Leu Ala Ala Asp Ile Ala Gly Leu Cys Ala Arg Thr Asp
465                 470                 475                 480

Asp Ile Ala Gln Pro Trp Met Ser Pro Ala Gly Tyr Arg Arg Gly Gln
                485                 490                 495

Ile Leu Asn Cys Ile Lys Leu Ala Ile Glu Pro Arg Gln Ala His Arg
            500                 505                 510

Asp Arg Met Tyr Gln Ala Gly Ile Asn Pro Val Thr Gly Gln Gly Thr
        515                 520                 525

Gly Glu Gly Phe Ile Leu Phe Gly Asp Lys Thr Ala Thr Thr Val Pro
    530                 535                 540

Thr Pro Phe Asp Arg Ile Asn Val Arg Arg Leu Phe Asn Met Leu Lys
545                 550                 555                 560

Asn Asn Ile Gly Asp Ser Ser Lys Trp Gln Leu Phe Glu Leu Asn Asp
                565                 570                 575

Asn Phe Thr Arg Ser Ser Phe Arg Met Glu Thr Ser Gln Tyr Leu Ala
            580                 585                 590

Gly Ile Lys Ala Leu Gly Gly Val Tyr Asp Phe Arg Val Val Cys Asp
        595                 600                 605

Thr Thr Asn Asn Thr Pro Ala Val Ile Asp Arg Asn Glu Phe Val Ala
    610                 615                 620
```

Ser Phe Tyr Ile Lys Pro Ala Arg Ser Ile Asn Tyr Ile Thr Leu Asn
625 630 635 640

Phe Val Ala Thr Ala Thr Gly Ala Asp Phe Asp Glu Leu Ile Gly Pro
645 650 655

Gln

<210> 791
<211> 612
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 791
Met Glu Gln Thr Gln Pro Phe Asn Val Leu Ser Asp Ala His Pro Leu
1 5 10 15

Asn Asp Gly Lys Leu Thr Val Ile Arg His Pro Ser Glu Met Glu Thr
20 25 30

Lys Ile Glu Asn Gly Val Arg Phe Phe Lys Ser Gln Trp Asp Asp Lys
35 40 45

Trp Tyr Pro Glu Lys Phe Glu Asp Tyr Leu Lys Leu His Gly Ile Val
50 55 60

Lys Ile Arg Leu Gln Gly Glu Asp Pro Ala His Phe Gln Thr Phe Lys
65 70 75 80

Asp Lys Asn Asn Lys Arg Thr Arg Tyr Met Gly Leu Pro Asn Leu Lys
85 90 95

Arg Ala Asn Ile Lys Met Gln Leu Thr Arg Glu Ile Val Ala Glu Trp
100 105 110

Lys Lys Cys Arg Asp Asp Ile Val Tyr Phe Ala Glu Thr Tyr Cys Ala
115 120 125

Ile Thr His Ile Asp Tyr Gly Thr Ile Lys Val Gln Leu Arg Asp Tyr
130 135 140

Gln Arg Asp Met Leu Glu Ile Met Ala Ala Lys Arg Met Thr Cys Cys
145 150 155 160

Asn Leu Ser Arg Gln Leu Gly Lys Thr Thr Val Val Ala Ile Phe Leu
165 170 175

Ala His Phe Val Cys Phe Asn Lys Asp Lys Ala Val Gly Ile Leu Ala
180 185 190

```
His Lys Gly Ser Met Ser Ala Glu Val Leu Asp Arg Thr Lys Gln Ala
        195                 200                 205

Ile Glu Leu Leu Pro Asp Phe Leu Gln Pro Gly Ile Val Glu Trp Asn
    210                 215                 220

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

Ser Ser Pro Asp Ala Val Arg Gly Asn Ser Phe Ala Met Ile Tyr Ile
                245                 250                 255

Asp Glu Cys Ala Phe Ile Pro Asn Phe Ile Asp Ala Trp Leu Ala Ile
            260                 265                 270

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

Thr Pro Ser Gly Leu Asn His Phe Tyr Asp Ile Trp Thr Ala Ala Val
    290                 295                 300

Glu Gly Lys Ser Gly Phe Thr Pro Tyr Thr Ala Ile Trp Asn Ser Val
305                 310                 315                 320

Lys Glu Arg Leu Tyr Asn Asp Glu Asp Met Phe Asp Asp Gly Trp Gln
                325                 330                 335

Trp Ser Leu Gln Thr Ile Ser Ala Ser Ser Leu Glu Gln Phe Lys Gln
            340                 345                 350

Glu His Cys Ala Glu Phe His Gly Thr Ser Gly Thr Leu Ile Ser Gly
        355                 360                 365

Met Lys Leu Ala Asn Met Asp Trp Ile Glu Val Thr Pro Asp Ser His
    370                 375                 380

Gly Phe Tyr Lys Phe Lys Glu Ala Glu Ala Asp His Lys Tyr Ile Ala
385                 390                 395                 400

Thr Leu Asp Ser Ala Glu Gly Arg Gly Gln Asp Tyr His Ala Leu Asn
                405                 410                 415

Ile Ile Asp Val Thr Thr Ser Glu Trp Glu Gln Val Gly Val Leu His
            420                 425                 430

Ser Asn Thr Ile Ser His Leu Ile Leu Pro Asp Ile Val Ile Lys Tyr
        435                 440                 445

Leu Met Glu Tyr Asn Glu Ala Pro Ile Tyr Ile Glu Leu Asn Ser Thr
    450                 455                 460
```

```
Gly Val Ser Val Ala Lys Ser Leu Tyr Met Asp Leu Glu Tyr Glu Asn
465                 470                 475                 480


Val Ile Cys Asp Ser Ile Val Asp Leu Gly Met Lys Gln Thr Lys Arg
                485                 490                 495


Ser Lys Ala Val Gly Cys Ser Ala Leu Lys Asp Leu Ile Glu Lys Asp
            500                 505                 510


Lys Leu Ile Ile His His Arg Ala Thr Val Gln Glu Phe Arg Thr Phe
        515                 520                 525


Ser Glu Lys Gly Val Ser Trp Ala Ala Glu Asp Gly Tyr His Asp Asp
    530                 535                 540


Leu Ile Met Ser Leu Val Ile Phe Ala Trp Leu Thr Thr Gln Gln Lys
545                 550                 555                 560


Phe Ala Asp Phe Val Asp Lys Asp Glu Met Arg Leu Ala Ser Glu Val
                565                 570                 575


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


Phe Val Asp Ala Val Asn Ser Ala Glu Tyr Ala Pro Gln Glu His Gly
        595                 600                 605


Leu Ser Phe Val
    610


<210> 792
<211> 169
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 792
Met Ser Glu Leu Gln Leu Asp Met Ala Lys Leu Leu Asp Ile Glu Gly
1               5                   10                  15


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


Leu Val Glu Val Lys Ser Asn Pro Asn Asp Arg Lys Pro Asp Leu Glu
        35                  40                  45


Asp Asp Tyr Ser Val Val Arg Lys Asn Met His Phe Gln Gln Gln Met
    50                  55                  60


Leu Met Asp Ala Ala Lys Ile Phe Leu Glu Thr Ala Lys Asn Ala Asp
```

65 70 75 80

Ser Pro Arg His Met Glu Val Phe Ala Thr Leu Met Gly Gln Met Thr
85 90 95

Thr Thr Asn Lys Glu Ile Leu Lys Leu His Lys Glu Met Lys Asp Ile
100 105 110

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

Met Asn Ile Gln Asn Ala Thr Val Phe Val Gly Ser Thr Ala Asp Met
130 135 140

Met Asp Glu Phe Gly Asp Ala Tyr Glu Ala Gln Glu Ala Arg Glu Lys
145 150 155 160

Ile Val Asn Gly Thr Asp Ser Thr Val
165

<210> 793
<211> 274
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 793
Met Phe Gly His Trp Tyr Asn Ser Ser Leu Arg Arg Tyr Ile Val Leu
1 5 10 15

Leu Gly Asp Leu Phe Ser His Val Gln Ile Ala Arg Trp Arg Glu Asp
20 25 30

Thr Gly Leu Lys Tyr Ile Lys Val Pro Ile Thr Tyr Ala Ser Lys Glu
35 40 45

Lys Phe Leu Ser Gln Leu Gly Lys Trp Thr Ala Ile Gln Ser Thr Glu
50 55 60

Asn Lys Ala Lys Ile Glu Thr Val Leu Pro Arg Met Asn Leu His Leu
65 70 75 80

Val Asp Met Gln Tyr Asn Ala Met Tyr Lys Thr Ser Gln Leu Asn Arg
85 90 95

Thr Lys Ser Tyr Lys Thr Pro Ser Lys Ile Thr Ser Gln Tyr Asn Pro
100 105 110

Thr Pro Ile Lys Met Ile Phe Glu Leu Gly Ile Tyr Thr Arg Asn Gln
115 120 125

```
Asp Asp Met Tyr Gln Ile Ile Glu Gln Ile Val Pro Tyr Phe Gln Pro
    130                 135                 140

His Phe Asn Thr Thr Ile Thr Glu Leu Tyr Asp Lys Asp Thr Ser Phe
145                 150                 155                 160

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

Val Asp Gly Asp Asn Ile Thr Arg Arg Arg Leu Glu Trp Ser Leu Met
            180                 185                 190

Phe Glu Val Asn Gly Trp Leu Tyr Pro Pro Val Ala Glu Ile Asp Gly
        195                 200                 205

Glu Ile Arg Thr Ile Tyr Leu Asp Phe Phe Ala Asn Ser Lys Glu Leu
    210                 215                 220

Thr Pro Glu Gly Asn Phe Glu Ser Val Asp Ser Glu Val Thr Pro Arg
225                 230                 235                 240

Asp Val Gln His Glu Asn Trp Asp Gly Ser Ser Lys Gln Thr Tyr Ser
                245                 250                 255

His Asp Ile Pro Ile Pro Val Asn Pro Glu Ala Pro Gly Pro Arg Gly
            260                 265                 270

Glu Lys
```

<210> 794
<211> 258
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 794

```
Met Ser Thr Phe Asp Ser Arg Leu Phe Ala Lys Leu Glu Asp Tyr Arg
1               5                   10                  15

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

Phe Tyr Asn His Arg Asn Ser Gln Thr Leu Ala Asp Ala Leu Ser Ala
        35                  40                  45

Glu Ala Ile Gln Met Arg Gly Ile Glu Phe Tyr Phe Leu Pro Arg Glu
    50                  55                  60

Tyr Asn Asn Pro Asp Leu Leu Phe Gly Glu Asp Pro Ser Ser Lys Phe
65                  70                  75                  80
```

Thr Lys Ala Trp Lys Phe Ala Ala Tyr Leu Asp Ser Phe Glu Gly Tyr
85 90 95

Ser Gly Asp Asn Thr Phe Phe Ser Lys Phe Gly Met Met Val Asn Asp
100 105 110

Glu Val Asn Leu Thr Ile Asn Pro Asn Leu Phe Lys His Gln Thr Asn
115 120 125

Asn Ser Glu Pro Lys Ala Gly Asp Leu Ile Tyr Phe Pro Met Asp Asn
130 135 140

Ser Leu Phe Glu Ile Asn Trp Val Gln Pro Tyr Asp Pro Phe Tyr Gln
145 150 155 160

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

Ser Gly Glu Gln Leu Gln Pro Glu Leu Gln Arg Asn Glu Gly Ile Asn
180 185 190

Ile Pro Glu Phe Ser Glu Leu Asp Leu Glu Pro Ile Lys Asn Ile Asp
195 200 205

Ala Leu Ala Asp Ile Ser Asp Ile Gln Tyr Ala Glu Ser Asp Glu Ile
210 215 220

Asn Lys Glu Ala Ser Glu Tyr Val His Pro Tyr Tyr Val Asn Asn Gly
225 230 235 240

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

Phe Glu

<210> 795
<211> 313
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 795
Met Ser Tyr Asn Thr Tyr Asn Pro Lys Thr Leu Lys Asp Ala Ile Leu
1 5 10 15

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

Ile Tyr Asp Cys Ile Gln Arg Ala Leu Glu Leu Tyr Gly Glu Tyr His
35 40 45

```
Phe Asn Gly Leu Asn Lys Gly Tyr Gln Val Phe Tyr Ile Gly Lys Asp
    50                  55                  60

Glu Ala Asp Asn Ala Arg Phe Leu Asn Gly Val Phe Asp Leu Arg Gly
65                  70                  75                  80

Arg Asn Val Phe Ala Val Thr Gln Ile Val Arg Thr Asn Val Gly Ser
                85                  90                  95

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

Leu Met Gly Met Ala Gly Ile Asn Gly Gly Met Gly Ser Ser Cys Asn
        115                 120                 125

Lys Ser Tyr Gly Pro Asn Ala Phe Gly Ala Asp Leu Gly Tyr Phe Thr
    130                 135                 140

Gln Leu Met Thr Tyr Trp Ser Met Met Gln Asp Leu Leu Ala Pro Leu
145                 150                 155                 160

Pro Asp Tyr Trp Tyr Asn Ser Asp Asn Glu Met Leu Lys Val Met Gly
                165                 170                 175

Asn Phe Met Lys Gly Asp Ile Ile Val Cys Glu Cys Trp Thr Lys Ser
            180                 185                 190

Phe Met Asn Thr Asp Ala Met Val Gly Asn Thr Ala Gly Tyr Gly Phe
        195                 200                 205

Ala Gly Pro Gln Thr Ala Asp His Trp Gly Leu Gly Asp Arg Tyr Gln
    210                 215                 220

Asn Pro Asp Leu Arg Asn Asn Gly Gln Tyr Ala Gly Glu Gly Asn Thr
225                 230                 235                 240

Asn Arg Glu Gly Ala Tyr Asn Asn Arg Trp Val Lys Asp Tyr Ala Thr
                245                 250                 255

Ala Leu Thr Lys Lys Leu Trp Gly Glu Ile Leu Phe Lys His Gln Gly
            260                 265                 270

Leu Gln Leu Ala Gly Gly Val Thr Val Asp Gly Gln Thr Leu Lys Val
        275                 280                 285

Glu Ala Gln Glu Glu Ile Glu Arg Leu Arg Glu Glu Leu Asp Leu Leu
    290                 295                 300

Asp Pro Gly Cys Pro Ile Leu Leu Gly
305                 310
```

<210> 796
<211> 588
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 796
Met Thr Lys Leu Val Asp Ser Leu Pro Phe Val Asp Gly Ile Pro Asp
1   5   10   15

Asp Phe Gln Gln Arg Ile Asn Trp Ile Lys Asn Thr Glu Pro Leu Asn
            20   25   30

Gly Ala Ser Thr Arg Tyr Gly Asn Asp Gly Glu Leu Asn Arg Ala Ser
        35   40   45

Val Gln Ile Gln Lys Asn Val Val Gln Val His Asn Asp Leu Asn Asn
    50   55   60

Val Gly Thr Ala Val Glu Asn Ile Gln Val Asp Val Asp Gln Ile Lys
65   70   75   80

Lys Ser Leu Glu Ile Thr Gly Ser Ser Asp Ala Ile Glu Gln Val Tyr
                85   90   95

Ile Asn Lys Lys Asn Ile Glu Lys His Asp Gly Gln Ile Leu Lys Leu
            100   105   110

Glu Glu Asp Thr Glu Lys Leu Arg Thr Asp Leu Asp Phe Leu Glu Glu
        115   120   125

Asp Val Gly Val Tyr Asp Ser Ser Lys Asp Asp Tyr Tyr Arg Thr Val
    130   135   140

Arg Asp Asn Ile Val Trp Val Lys Arg Glu Ile Gly Ala Tyr Pro Gly
145   150   155   160

Gln Asp Ile Asn Gly Gln Pro Lys Gln Asp Ser Pro Gly Ser Gly Met
                165   170   175

Lys Tyr Arg Ile Ile Asn Asn Ala Ser Ala Ile Val Lys His Asp Glu
            180   185   190

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

Leu Thr Ile Glu Val Asn Asp Leu Arg Lys Glu Val Gly Pro Lys Ser
    210   215   220

Gly Ala Thr Ser Ala Ser Ile Tyr Ala Arg Leu Val Asn Asn Ala Asp

225 230 235 240

Ala Ile Ser Ala Ala Asn Asn Glu Ile Phe Ala Ile Asn Gln Ala Ile
245 250 255

Asp Phe Thr Asn Pro Val Lys Ile Gly Ala Arg Thr Thr Arg Leu Glu
260 265 270

Asn Asp Tyr Arg Ile Val Asp Ala Thr Leu Asn Phe Ala Gln Thr Gly
275 280 285

Leu Val Pro Arg Val Asn Asn Ile Asp Ala Arg Leu Gly Ser Ser Asp
290 295 300

Lys Pro Asp Thr Ile Glu Gly Lys Ile Ser Ser Leu Ser Thr Asp Gln
305 310 315 320

Gly Tyr Ile Ser Asp Val Val Gly Arg Asp Thr Ser Ser Gly Leu Gln
325 330 335

Gly Gln Val Ala Trp Ile Asn Gln Gln Val Gly Ile Val Pro Ser Glu
340 345 350

Gln Pro Ile Pro Pro Gly Ser Ile Leu Ala Arg Met Thr Asn Val Glu
355 360 365

Gly Met Gln Asn Ser Gln Gln Ser Ala Ile Gln Asp Ile Gln Val Glu
370 375 380

Leu Gly Asn Asn Asn Glu Gly Leu Lys Gly Ser Val Phe Thr Leu Gln
385 390 395 400

Thr Gln Met Asn Gly Asp Phe Ser Ser Glu Asn Pro Val Gln Arg Asp
405 410 415

Gly Val Tyr Ala Thr Val Val Glu Leu Gln Asp Lys Phe Val Thr Ala
420 425 430

Val Thr Asp Val Glu Gln Ala Gly Ala Tyr Leu Arg Lys Gln Gly Glu
435 440 445

Trp Phe Lys Lys Pro Ser Ser Ile Gly Glu Phe Ser Lys Glu Asp Phe
450 455 460

Thr Val Asp Leu Ser Ser Asp Ala Leu Val Asn Pro Asn Ser Leu Val
465 470 475 480

Ala Ala Pro Phe Asn Ala Gly Ile Arg Ile Val Asp Asp Ile Val Val
485 490 495

Asp Asp Asp Gly Val Phe Cys Val Glu Thr Asp Thr Val Ile Glu Ala

500 505 510

Ser Asp Ser Asp Lys Gly Val Lys Ile Val Ile Leu Val Asn Asn Ile
515 520 525

Glu Val Phe Ser Tyr Gly Leu Gly Val Lys Ala Val Thr Gly Glu Gln
530 535 540

Leu Ile Lys Thr Lys Lys Leu Ile Glu Phe Ser Ser Gly Asp Ala Ile
545 550 555 560

Lys Ile Val Tyr Arg Ala Ala Ser Glu Glu Ser Gln Val Leu Val Lys
565 570 575

Ile Lys Ser Leu Asp Ile Thr Ile His Pro Ala Val
580 585

<210> 797
<211> 448
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 797
Met Ala Gln Asn Asn Tyr Asn His Tyr Ser Asp Leu Ala Lys Tyr Thr
1 5 10 15

Ile Phe Asp Pro Thr Asn Thr Gln Trp Pro Val Ala Ile Lys Asp Val
20 25 30

Gln Ser Ala Leu Glu Leu Ile Gly Ser Trp Ala Arg Thr Asp Thr Gly
35 40 45

Leu Pro Val Ala Ser Pro Thr Val Ala Gly Val Ile Arg Thr Ala Thr
50 55 60

Gln Ala Glu Val Asp Ala Gly Thr Ile Gly Asn Ala Ala Val Thr Pro
65 70 75 80

Ala Thr Leu Lys Ser Thr Val Thr Arg Pro Glu Ala Thr Thr Thr Val
85 90 95

Leu Gly Leu Thr Arg Tyr Ala Thr Asn Thr Glu Ala Ala Ala Leu Thr
100 105 110

Ala Gly Asn Arg Thr Ile Thr Ala Ala Ala Leu Gly His Val Phe Lys
115 120 125

Thr Val Lys Ala Gln Glu Asn Val Asp Gly Thr Val Arg Leu Thr Thr
130 135 140

```
Ala Ala Gln Ala Gln Ala Gly Thr Asp Glu Thr Thr Ala Val Thr Pro
145                 150                 155                 160

Lys Arg Val Val Glu Met Ile Gly Lys Phe Ser Val Ser Pro Pro Ser
                165                 170                 175

Tyr Thr Ser Ala Thr Glu Ser Asn Leu Gly Leu Val Arg Val Ala Thr
            180                 185                 190

Gln Ala Gln Val Ala Ala Gly Ala Val His Asp Gly Tyr Ala Val Thr
        195                 200                 205

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

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

Leu Ala Val Thr Pro Lys Ser Leu Gln Ala Leu Lys Ser Thr Lys Asp
                245                 250                 255

Lys Tyr Gly Leu Thr Arg Leu Ser Gly Ser Pro Thr Thr Asp Ala Ser
            260                 265                 270

Leu Ala Ala Ala Ala Thr Asp Ala Val Phe Lys Thr Arg Arg Ile Asn
        275                 280                 285

Gly Lys Thr Leu Asp Asn Asp Ile Thr Ile Thr Asn Asn Asp Ile Asn
    290                 295                 300

Cys Tyr Thr Arg Gln Glu Ser Asp Gly Arg Tyr Met Pro Ala Gly Thr
305                 310                 315                 320

Arg Val Gly Asn Val Thr Trp Val Glu Gly Gln Ser Trp Ile Ser Arg
                325                 330                 335

Gly Ala Thr Phe Thr Cys Asn Ala Pro Trp Glu Ala Ser Ser Arg Leu
            340                 345                 350

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

Asn Arg Ile Phe Arg Phe Val Val Ile Val Asn Gly Ser Gln Trp Gly
    370                 375                 380

Gly Glu Leu Thr Leu Asn Ile Glu Asn Thr Lys Gly Gly Arg Asn Gly
385                 390                 395                 400

His Ser Trp Arg Phe Glu Ala Tyr Ala Ser Ser Asn Phe Phe Phe Asn
                405                 410                 415
```

Asn Ile Pro Pro Asn Ala Thr Val Gln Ile Arg Pro Thr Glu Asp Ser
420 425 430

Arg Ile Ile Phe Tyr Asp Cys Met Leu Thr Phe Cys Thr Asn Arg Pro
435 440 445

<210> 798
<211> 223
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 798
Met Thr Ile Glu Thr Lys Thr Arg Glu Gly Ala Lys Val Asn Ser Arg
1 5 10 15

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

Gly Asn Thr Ala Pro Ile Gly Ser Leu Thr Phe Glu Gln Met Asp Leu
35 40 45

Gly Val Trp Tyr Pro Asn Thr Glu Ala Ala Ile Asn Asp Leu Met Ser
50 55 60

Leu Gln Ser Ala Glu Ile Gly Thr Ile Ile Cys Asn Asp Thr Gly Ile
65 70 75 80

Ser Pro Gln Pro Ala Gln Gln Ile Thr Arg Ala Thr Phe Ser Gly Val
85 90 95

Val Ala Leu Glu Pro Lys Glu Asp Gly Ser Val Gly Asp Pro Val Ile
100 105 110

Ile His Ile Leu Gly Leu Pro Ile Arg Ile Ala Asn Gly Asp Asp Phe
115 120 125

Ala Ala Val Ala Thr Arg Trp Tyr Asp Lys Val Lys Glu Leu Glu Ala
130 135 140

Val Gly Lys Val Val Gln Gln Val Thr Gln Ser Pro Ala Thr Pro Gln
145 150 155 160

Tyr Val Asp Ile Ile His Leu Asp Tyr Gln Asn His Asn Phe Glu Thr
165 170 175

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

Lys Ala Gly Tyr Gly Gln Trp Asp Ala Ile Gly Asn Glu Ser Lys Thr
195 200 205

```
Phe Gly Ala Asn Thr Phe Thr Phe His Tyr Phe Arg Arg Met Gly
    210                 215                 220


<210> 799
<211> 607
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 799
Met Lys Gln Asn Leu Ile Val Gly Gln Ser Val Asp Asp Gly Ser Gly
1               5                   10                  15


Asp Tyr Leu Arg Lys Gly Gly Leu Lys Ile Asn Asn Asn Phe Asp Asp
            20                  25                  30


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


Trp Lys Thr Phe Lys Ala Ser Pro Thr Gly Thr Thr Leu Asn Ala Lys
    50                  55                  60


Phe Gly Gln Ala Phe Ala Ile Asn Thr Gln Ala Ala Arg Val Asn Val
65                  70                  75                  80


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


Arg Asp Val Trp Ser Thr Trp Arg Leu Ser Pro Ile Thr Val Ile Pro
            100                 105                 110


Ala Gln Gly Asp Thr Leu Lys Gly Ser Ala Ser Pro Lys Ile Phe Asn
        115                 120                 125


Thr Asn Phe Gln Asp Leu Glu Leu Val Tyr Cys Ala Pro Gly Arg Trp
    130                 135                 140


Glu Tyr Ile Glu Asn Lys Thr Val Asp Lys Leu Thr Asn Gly Asn Leu
145                 150                 155                 160


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


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


Val Tyr Arg Arg Gly Asn Ile Leu Tyr Tyr Gly Glu Thr Ser Val Met
        195                 200                 205


Asp Lys Ala Asn Ala Asp Tyr Gly Ser Pro Gly Thr Val Ala Gly Gln
    210                 215                 220
```

```
Leu Val Glu Leu Asn Gly Lys Asp Ile Arg Leu Lys Val Pro Cys Val
225                 230                 235                 240

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

Tyr Arg Ser Ser Tyr Asn Lys Leu Ala Ile Gln Ile Arg Asp Ser Ala
            260                 265                 270

Gln Thr Thr Ser Gln Thr Ile Pro Gly Ser Ile Ile Val Asp Asn Leu
        275                 280                 285

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

Val Gly Val Asn Pro Asn Ser Leu Glu Ile Ser Leu Asn Gly Lys Glu
305                 310                 315                 320

Leu Leu Glu Ala Gly Thr Ala Gly Leu Pro Leu Phe Tyr Cys Glu Gly
                325                 330                 335

Ala Glu Gly Gly Tyr Ala Glu Asp Cys Ile Asn Asn Gly Gly Gln Trp
            340                 345                 350

Val Asn Ser Asn Gln Asp Tyr Arg Leu Glu Phe Asp Ser Thr Gly Thr
        355                 360                 365

Asn Val Glu Ala Ile Ile Phe Gly Glu Ala Phe Glu Asp Lys Asp Leu
    370                 375                 380

Leu Thr Val Arg Trp Phe Asn Asn Asn Ile Gly Thr Thr Met Asp Ile
385                 390                 395                 400

Asp Asp Ile Met Ala Glu Thr Asp Gln Val Tyr Met Asn Ala Glu Gln
                405                 410                 415

Leu Val Thr Leu Lys Asn Arg Ile Glu Tyr Thr Asn Tyr Asp Glu Pro
            420                 425                 430

Asn Gln Lys Asn Met Arg Pro Val Ala Asp Asp Ile Met Ile Lys Val
        435                 440                 445

Asn Asn Ile Ala Ala Phe Phe Asp Val Ile Tyr Pro Ile Gly Thr Ile
    450                 455                 460

Tyr Glu Asn Ala His Asn His Ala Asn Pro Ala Asp Tyr Met Gly Phe
465                 470                 475                 480

Gly Val Trp Lys Leu Tyr Ser Gln Gly Arg Val Thr Ala Gly Trp Asn
                485                 490                 495
```

```
Asn Asp Ser Ser Asp Pro Tyr Phe Ser Arg Asn Asn Asn Asn Leu Asn
            500                 505                 510

Glu Asn Gly Gln Pro Ser Leu Thr Ala Gly Gly Thr Val Gly Asp Leu
        515                 520                 525

Thr Phe Thr Leu Gly Lys Glu His Ile Pro Glu Leu Met Ser Arg Asp
    530                 535                 540

Lys Val Leu Ile Ser Asp Pro Glu His Gly Ser Val Val Ile Gly Gly
545                 550                 555                 560

Cys Gln Leu Asp Pro Asp Ala Gln Gly Pro Gly Tyr Ser Lys Tyr Arg
                565                 570                 575

Glu Asp Thr Val Ala Val Asn Asn Gly Val Val Pro Asn Asp Ile Thr
            580                 585                 590

Lys Ile Gln Pro Thr Ile Thr Val Tyr Arg Trp Ile Arg Val Gly
        595                 600                 605


<210> 800
<211> 303
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 800
Met Tyr Thr Asp Lys Gly Lys Lys Ile Ile Asp Val Gly Glu Ile Gly
1               5                   10                  15

Asn Ala Ser Thr Gly Asp Ile Leu Tyr Asp Gly Gly Val Lys Ile Asn
            20                  25                  30

Asp Asn Phe Asp Ala Ile Tyr Asn Ala Phe Ala Asp Gln Arg Leu Phe
        35                  40                  45

Ala Ala Gly Gly Gly Ala Leu Asn Gln Lys Ile His Ala Thr Ser Tyr
    50                  55                  60

Tyr Gln Lys Ile Lys Phe Gly Asp Ala Asn Ser Ala Gly Thr Val Pro
65                  70                  75                  80

Met Gly Ser Cys Ile Asp Ala Asp Cys Ser Glu Gly Ala Val Gln Ile
                85                  90                  95

Arg Leu Ser Lys Gly Lys Ala Gly Glu Ala Val Phe Val Val Asn Ser
            100                 105                 110

Asn Gly Ser Ala Ser Lys Ala Arg Ser Ile Lys Ile Thr Thr Asn Gly
```

115 120 125

Glu Gly Val Ala Asp Ala Phe Lys Asp Gly Ser Arg Glu Leu Ile Ile
130 135 140

Asn Thr Pro Arg Cys Arg Ile Glu Leu Trp Cys Val Glu Val Lys Ala
145 150 155 160

Asn Gly Ala Ala Val Trp Asp Tyr Ser Ile Ser Ser Met Phe Gly Ser
165 170 175

Thr Tyr Ser Pro Leu Glu Ala Thr Tyr Asn Leu Thr Ser Ser Pro Ile
180 185 190

Asn Ile Arg Leu Gly Tyr Asn Asp Asp Tyr Ser Thr Val Lys Leu Leu
195 200 205

Leu Ser Phe Ser Ala Asn Pro Gly Gly Gln Thr Ile Lys Arg Gln Ser
210 215 220

Ser Glu Val Met Leu Met Ile Asp Pro Thr Ile Thr Ser Ser Ala Pro
225 230 235 240

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

Ser Ser Glu Asn Glu Lys Met Tyr Ser Ile Ser Tyr Ser Ile Asn Ala
260 265 270

Gln Lys Asp Leu Ile Cys Thr Ala Ser Thr Ser Tyr Gly Asn Ala Arg
275 280 285

Leu Ala Val Lys Val Ile Ala Thr Gln Thr Val Gly Val Ser Gln
290 295 300

<210> 801
<211> 341
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 801
Met Ser Asn Ser Thr Arg Ala Ser Ser Thr Arg Ser Thr Ile Tyr Arg
1 5 10 15

Ala Ile Ile Thr Ser Lys Phe Arg Thr Glu Lys Met Tyr Thr Phe Tyr
20 25 30

Lys Ser Ile Gly Pro Gly Thr Asp Gln Asn Thr Leu Tyr Val Ser Phe
35 40 45

```
Gly Lys Ser Thr Pro Trp Ser Asp Asn Glu Ser Glu Pro Gly Phe Ala
    50                  55                  60

Pro Pro Tyr Pro Ala Asp Asn Gly Asp Gly Val Val Asp Val Trp Thr
65                  70                  75                  80

Asn Met Met Gly Ala Val Lys Ile Glu Ser Ser Met Leu Asp Cys Val
                85                  90                  95

Val Pro Arg Arg Asp Trp Gly Asp Thr Arg Tyr Pro Asn Pro Arg Thr
            100                 105                 110

Phe Leu Ile Gly Asp Ile Val Val Ala Asn Ser Ala Pro Tyr Asn Arg
        115                 120                 125

Thr Asp Ala Gly Phe Gly Trp Met Val Tyr Arg Cys Ile Asp Val Pro
    130                 135                 140

Lys Asp Gly Met Cys Ser Ile Gly Asn Leu Thr Ser Lys Glu Glu Cys
145                 150                 155                 160

Ile Lys Leu Gly Gly Lys Trp Thr Pro Ser Thr Ile Ser Gly Ser Ala
                165                 170                 175

Pro Arg Gly Arg Gly Asp Ala Asn Gly Thr Val Asp Leu Gly Asp Gly
            180                 185                 190

Tyr Leu Trp Glu Tyr Leu Tyr Glu Ile Pro Ala Asp Val Ser Ile Asn
        195                 200                 205

Arg Cys Thr Asn Glu Tyr Ile Val Val Pro Trp Pro Glu Glu Ile Glu
    210                 215                 220

Glu Ser Pro Ala Arg Trp Gly Phe Gln Asn Asn Leu Thr Trp Gln Gln
225                 230                 235                 240

Asn Asp Phe Asn Leu Ile Tyr Arg Met Lys Cys Asn Thr Ile Arg Phe
                245                 250                 255

Lys Ala Tyr Leu Asp Ala Val Tyr Phe Pro Glu Phe Ser Leu Pro Gly
            260                 265                 270

Asn Thr Gly Phe Arg Gln Leu Ser Ile Ile Thr Asn Pro Leu Glu Val
        275                 280                 285

Lys Pro Met Pro Asn Ser Pro Asn Val Lys Ala Glu Lys Gly Trp Tyr
    290                 295                 300

Ser Ala Ser Gly Leu Glu Arg Gln Ser Gly Glu Met Ile Tyr Met Glu
305                 310                 315                 320
```

Asn Arg Gln Pro Ile Ile Arg Ser Met Asp Gln Thr Glu Glu Leu Asn
325 330 335

Leu Ile Phe Glu Phe
340

<210> 802
<211> 1032
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 802
Met Thr Ile Ala Pro Phe Val Thr Ser Leu Arg Ile His Lys Leu Ser
1 5 10 15

Ala Asn Gln Val Asn Ile Arg Trp Asp Asp Val Gly Ala Asn Phe Tyr
20 25 30

Tyr Phe Val Glu Leu Ala Glu Thr Arg Asn Arg Ala Gly Glu Ile Ile
35 40 45

Pro Ala Asp Asn Leu Ser Trp Ser Ser Leu Gly Tyr Thr Ala Asp Asn
50 55 60

Asp Trp Phe Glu Gln Asn Arg Ile Glu Pro Leu Thr Tyr Tyr Lys Met
65 70 75 80

Arg Val Gln Thr Thr Ser Ala Gly Phe Glu Pro Ser Glu Trp Val Glu
85 90 95

Thr Glu Glu Phe Gln Thr Phe Glu Glu Asn Ala Tyr Thr Phe Glu His
100 105 110

Met Gln Glu Phe Ser Leu Val Lys Glu Phe Ile Lys Gln Lys Phe Ser
115 120 125

Leu Asn Asn Met Ser Tyr Val Asn Phe Asn Thr Ser Ala Met Met Ala
130 135 140

Ser Leu Met Thr Glu Ser Phe Gln Phe Ser Pro Glu Tyr Ser His Leu
145 150 155 160

Ser Ala Ile Glu Asn Phe Val Val Gly Glu Ser Gly Tyr His Glu Ile
165 170 175

Gln Gly Pro Ile Glu Ala Val Cys Val Asp Lys Asn Arg Thr Met Leu
180 185 190

Gly Glu Ile Asp Gly Ile Leu Tyr Leu Phe Glu Arg Phe Gln His Met
195 200 205

```
Val Lys Val Ser Asn Asp Lys Gly Gln Asn Trp Gln Tyr Val Gln Leu
    210                 215                 220

Phe Asn Asp Arg Val Gly Asn Pro Val Ser Arg Val Val Ile Tyr Gln
225                 230                 235                 240

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

Arg Lys Ser Ser Asp Val Arg Trp Ser Ser Asn Glu Val Lys Phe Ser
            260                 265                 270

Asp Asn Glu Val Thr Phe Ala Lys Leu Gly Asp Gln Leu Lys Leu Gly
        275                 280                 285

Phe Glu Val Glu Leu Phe Gly Thr Tyr Ala Ser Leu Pro Ala Asp Val
    290                 295                 300

Thr Lys Tyr Ala Glu Ala Phe Thr Cys Asn Asp Asp His Leu Tyr Val
305                 310                 315                 320

Val Ala Lys Asp Thr Val Arg Arg Val Lys Leu Lys Asp Ala Pro Ile
                325                 330                 335

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

Glu Ala Ser His Ile Thr Gly Asn Pro Lys Ser Val Cys Phe Lys Met
        355                 360                 365

Asp Ser Val Gly Gly Lys Ile Phe Ala Leu Ile Thr Gly Glu Val Lys
    370                 375                 380

Thr Leu Gly Leu Asp Pro Thr Asp Pro Arg Asn Val Val Asp Ser Ala
385                 390                 395                 400

Thr Lys Gly Val Tyr Val Tyr Gln Glu Asp Thr Asn Thr Trp Lys Arg
                405                 410                 415

Val Phe Gly Asn Thr Asp Glu Glu Lys Arg Arg Ile Glu His Leu Trp
            420                 425                 430

Thr Ser Met Ser Thr Asp Gly Lys Glu Ile Phe Phe Ser Ser Ala Asn
        435                 440                 445

Phe Lys Thr Thr Glu Tyr Thr Gln Asp Ile Glu Leu Glu Thr Lys Tyr
    450                 455                 460

Pro Glu Leu Ile Ser Thr Ala Val Lys Asn Val Asn Pro Ile Gln Tyr
465                 470                 475                 480
```

```
His Ser Asp Lys His Tyr His Met Met Ser Phe Arg Ala Asp Glu Phe
                485                 490                 495

Ser Arg Trp Glu Thr Phe Val Pro Gly Pro Met Arg Phe Tyr Ala Glu
            500                 505                 510

Pro Trp Phe Val Trp Met Ala Arg Glu Gly Asn Arg Cys Trp Ile Ser
        515                 520                 525

Thr Ala Asp His Ala Val Val Ile Tyr Asn Asp Ile Leu Tyr Gln Lys
    530                 535                 540

Arg Val Asp Ala Ala Ala Gln Gly Thr Thr Glu Arg Val Leu Ser Glu
545                 550                 555                 560

Val Trp Asp Lys Gly Asp Ala Thr Phe Tyr Cys Pro Pro Val Ser Phe
                565                 570                 575

Asn Gly Phe Leu Gln Tyr Ala Ser Gly Ile Met Phe His Glu Pro Asp
            580                 585                 590

Gly Lys Leu Ile Gly Tyr Tyr Ala Phe Asp Tyr Arg Val Arg Asp Gln
        595                 600                 605

Val Thr Leu Asn Trp Lys Pro Thr Asp Val Met Phe Lys Ala Phe Leu
    610                 615                 620

Gln Asn Gln Thr Arg Glu Glu Asp Trp Thr Pro Glu His Thr Pro Gly
625                 630                 635                 640

Leu Arg Asp Pro Asp Leu Arg Pro Tyr Leu Thr Lys Met Met Pro Asp
                645                 650                 655

Ser Tyr Leu Leu Gln Asp Ser Asn Phe Glu Gln Phe Cys Lys Tyr Tyr
            660                 665                 670

Leu Gln Phe Leu Ser Asp Gly Asn Gly Thr His Tyr Asn Ser Leu Val
        675                 680                 685

Asn Leu Val Lys Asn Lys Tyr Pro Arg Glu Glu Asn Ala Trp Glu Tyr
    690                 695                 700

Leu Trp Ser Glu Val Tyr Lys Arg Asn Ile Tyr Leu Ser Lys Asp Ala
705                 710                 715                 720

Arg Asp Ala Val Val Arg Phe Phe Glu Ala Arg Lys Asn Asp Phe Tyr
                725                 730                 735

Ala Thr Lys Gly Ile Glu Asp Ser Tyr Lys Phe Leu Phe Lys Leu Leu
            740                 745                 750
```

```
Tyr Asn Glu Asp Val Glu Ile Asp Ile Glu Ser Lys Asn Thr Thr Glu
        755                 760                 765

Tyr Asp Ile Ile Val Glu Ser Thr Asn Ile Ser Asp Asp Leu Val Gly
    770                 775                 780

Arg Thr Ile Tyr Thr Ala Ser Gly Arg Ser Asn Val Thr Tyr Ile Glu
785                 790                 795                 800

Arg Glu Tyr Arg Asp Gly Arg Leu Leu Trp Arg Ile Thr Ile His Asn
                805                 810                 815

Leu Ser Gly Arg Phe Ile Glu Gly Gln Glu Ile Lys Ser Glu Arg Thr
            820                 825                 830

Asp Phe Glu Gly Ile Ile Val Gln Gly Val Arg Gly Lys Asp Met Leu
        835                 840                 845

Ser Asn Asn Ile Asp Tyr Ile Asn Arg Ser Arg Ser Tyr Tyr Val Met
    850                 855                 860

Lys Ile Lys Ser Gln Leu Pro Thr Ser Arg Phe Arg Asp Asp Val Leu
865                 870                 875                 880

Arg Phe Val His Pro Val Gly Phe Gly Phe Ile Gly Ile Thr Leu Leu
                885                 890                 895

Thr Met Phe Ile Asn Ser Gly Leu Asn Met Lys His Val Glu Thr Ile
            900                 905                 910

Ile Asn Lys Leu Lys Asn Tyr Lys Trp Asp Ala Gly Leu Pro Ser Val
        915                 920                 925

Tyr Pro Asp Arg Val Ala Ile Ile Ala Ser Asp Asp Thr Ile Glu Arg
    930                 935                 940

Asp Pro Ile Thr Asn Glu Pro Arg Tyr Ser Ser Arg Ala Gln Ala Gly
945                 950                 955                 960

Glu Pro Phe Pro Leu Pro Ala Asn Tyr Asn Gln Glu Asn Asn Asn Ser
                965                 970                 975

Ile Ile Ala Gly Gln Asn Pro Gly Gln Arg Arg Lys Pro Leu Ser Pro
            980                 985                 990

Thr Phe Asp Gln Ser Ala Val Thr  Phe Ala Asn Tyr Arg  Asp Leu Val
        995                 1000                1005

Asn Gln  Arg Leu Lys Asp Asp  Ala Gly Asn Pro Arg  Asp Pro Glu
    1010                1015                1020
```

Asn Pro Thr Gln Val Lys Ile Asp Glu
1025 1030

<210> 803
<211> 652
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 803
Met Ala Ile Lys Glu Pro Leu Asn Tyr Gln Leu Thr Arg Thr Ala Asn
1 5 10 15

Ala Ile Pro Asp Ala Phe Thr Gly Ala Thr Phe Asp Glu Ile Lys Asn
20 25 30

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

Phe Ala Gly Ser Arg Leu Asn Val Leu Leu Asp Leu Leu Ala Tyr Asn
50 55 60

Thr Leu Tyr Ile Gln Gln Phe Ser Asn Thr Ala Leu Tyr Glu Ser Phe
65 70 75 80

Ile Gly Thr Ala Asn Leu Arg Ser Ser Val Val Gln Ala Ala Gln Gln
85 90 95

Asn Gly Tyr Leu Pro Ser Ser Lys Ser Ala Ala Thr Ala Ser Ile Met
100 105 110

Leu Glu Val Thr His Met Asn Pro Ser Ser Thr Leu Arg Val Val Ile
115 120 125

Pro Arg Gly Thr Lys Phe Leu Ala Tyr Ser Lys Ser Asp Lys Ala Asn
130 135 140

Pro Tyr Asn Phe Val Val Thr Glu Asn Val Val Ala Ile Arg Asp Asn
145 150 155 160

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

Arg Thr Gln Leu Ser Tyr Asp Pro Lys Lys Pro Ile Val Ile Arg Asp
180 185 190

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

Trp Thr Asn Trp Thr Asp Arg Ser Met Val His Ala Ser Ser Ile Ser
210 215 220

```
Thr Ile Tyr Tyr Met Arg Glu Thr Val Asp Gly Asn Thr Glu Phe Phe
225                 230                 235                 240

Phe Gly Glu Gly Val Ala Glu Ala Ser Val Ala Gly Gly Val Leu Glu
                245                 250                 255

Ser Asn Phe Ile Gly Gly Leu Lys Pro Thr Lys Gly Ala Gln Val Val
            260                 265                 270

Ile Glu Tyr Ile Arg Thr Asp Gly Glu Ala Ala Asn Gly Ala Thr Glu
        275                 280                 285

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

Glu Asn Trp Ser Asp Ser Pro Asp Tyr Val Gly Ala Asp Gly Gly Gly
305                 310                 315                 320

Glu Pro Glu Asp Ile Glu Arg Ile Arg Glu Leu Ala Gln Ile Lys Arg
                325                 330                 335

Glu Ser Gln Met Arg Cys Val Ser Lys Thr Asp Tyr Glu Ser Phe Val
            340                 345                 350

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

Gln Asp Lys Pro Gly Tyr Ala Phe Ile Ala Ile Lys Pro Lys Ser Gly
    370                 375                 380

Leu Gln Leu Thr Ala Val Gln Arg Glu Asp Ile Gln Asp Tyr Leu Lys
385                 390                 395                 400

Pro Phe Cys Leu Ala Pro Ile Thr Pro Ser Val Met Ser Pro Asp Tyr
                405                 410                 415

Leu Phe Ile Arg His Asn Ile Lys Ala Ser Tyr Ala Leu Asn Lys Leu
            420                 425                 430

Gln Glu Ser Glu Gln Trp Leu Gln Ser Lys Ile Ile Asp Ser Ile Asn
        435                 440                 445

Arg Tyr Tyr Val Asp Glu Val Glu Met Phe Asn Lys Asn Phe Ser Lys
    450                 455                 460

Ser Lys Leu Leu Thr Tyr Ile Asp Asp Thr Asp His Ser Ile Ile Gly
465                 470                 475                 480

Ser Ser Val Asp Ile Gln Met Val Arg Glu Ile Val Asn Tyr Phe Thr
                485                 490                 495
```

Leu Pro Ser Ala Gly Ile Lys Tyr Tyr Asn Thr Ile Thr Pro Arg Thr
500 505 510

Leu Arg Ser Gly Asp Leu Val Phe Thr Val Thr Pro Thr Ala Glu Pro
515 520 525

Tyr Ser Val Asn Ile Val Gly Thr Asp Pro Asp Lys Asn Gly Lys Gly
530 535 540

Asn Met Val Ile Gly Pro Phe Lys Pro Gly Asp Ile Lys Glu Asn Thr
545 550 555 560

His Ile Gln Pro Tyr Thr Glu Asn Asp Phe Asp Arg Thr Thr Ile Gly
565 570 575

Glu Arg Thr Arg Trp Tyr Lys Ile Gly Glu Val Asp Tyr Tyr Gly Asp
580 585 590

Asn Ile Tyr Trp Ser Leu Gly Ala Ile Gly Ala Asp Pro Leu Gln Phe
595 600 605

Glu Asp Gln Ser Ile Glu Leu Tyr Ser Thr Pro Thr Gln Asp Ile Val
610 615 620

Phe Ala Arg Asp Gly Thr Leu Ile Val Phe Glu Asn Asp Leu Arg Pro
625 630 635 640

Gln Tyr Thr Thr Ile Lys Leu Glu Pro Ile Thr Gln
645 650

<210> 804
<211> 97
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 804
Met Ala Gly Leu Ser Phe Asn Lys Cys Leu Thr Ala Gly His Ser Ala
1 5 10 15

Tyr Pro Pro Thr Glu Val Asn Ala Thr Gln Ser Lys Val Phe Thr Gly
20 25 30

Gly Ile Ala Val Leu Val Asp Gly Asp Ser Ile Thr Pro His Thr Lys
35 40 45

Thr Val Asp Pro His Asp Thr His Gly Gly Val Val Gln Pro Arg Thr
50 55 60

Ser Lys Val Phe Val Thr Gly Lys Lys Ala Val Gln Met Ala Asp Pro

65 70 75 80

Ile Ser Cys Gly Asp Thr Val Ala Gln Ser Ser Ser Lys Val Phe Ile
85 90 95

His

<210> 805
<211> 167
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 805
Met Ala Asp Ile Leu Pro Ile Asn Thr Thr Leu Arg Glu Val Ile Glu
1 5 10 15

Gly Glu Tyr Val Glu Gln Tyr Phe Thr Ala Gln Leu Ser Thr Asn Glu
20 25 30

Thr Leu Lys Ser Ile Asn Ile Ile Asp Tyr Gln Pro Val Ser Asp Ile
35 40 45

Ser Val Ser Glu Thr His Tyr Lys Gly Asn Tyr Asn Ser Val Phe Thr
50 55 60

Phe Gly Asn Asp Val Leu Lys Tyr Arg Glu Gly Asp Glu Leu Lys Ser
65 70 75 80

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

Leu Trp Lys Ala Pro Arg Thr Leu Glu Lys Thr Phe Thr Tyr Thr Val
100 105 110

Glu Ile Ile Tyr Thr Val Thr Glu Glu Ser Ser Gly Gly Ser Ser Gly
115 120 125

Gly Ser Ser Ala Pro Ile Ile Thr Glu His Lys Lys Gln Lys Ile Tyr
130 135 140

Ser Gln Thr Val Lys Gly Asn Trp Ser Arg Trp Gly Asp Gln Leu Arg
145 150 155 160

Ala Tyr Val Tyr Ala Gly Asn
165

<210> 806
<211> 576
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 806

```
Met Ile Glu Met Asn Asp Ser Leu Lys Trp Phe Thr Gly Val Val Glu
1               5                  10                  15

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

Gly Leu His Pro Phe Glu Lys Val Gln Gly Ala Ile Thr Gly Leu Pro
        35                  40                  45

Thr Glu Asp Leu Pro Trp Met Ser Val Ile Gln Pro Thr Asn Ser Ala
    50                  55                  60

Gly Ile Ser Gly Val Gly Ser Ser Ile Thr Gly Met Val Glu Gly Thr
65                  70                  75                  80

Ser Val Phe Gly Leu Trp Leu Asp Glu Phe Lys Thr Ala Gly Leu Val
                85                  90                  95

Ile Gly Thr Tyr Ser Ala His Arg Lys Thr Lys Pro Asn Tyr Thr Glu
            100                 105                 110

Gly Phe Ser Asp Pro Thr Gly Gln Tyr Pro Arg Gln Val Gly Ser Asp
        115                 120                 125

Thr Asn Pro Leu Val Gln Gly Asp Glu Thr Gly Tyr Ser Ala Ile Pro
    130                 135                 140

Asn Ile Ile Gln Asp Arg Asn Leu Asp Ile Gly Ile Asn Pro Asp Asp
145                 150                 155                 160

Ala Asp Leu Ser Asp Ile Pro Glu Asp Pro Asn Pro Ala Ile Thr Ile
                165                 170                 175

Thr Asp Met Leu Asn Arg Asp Glu Gly Leu Arg Leu Lys Val Tyr Trp
            180                 185                 190

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

Gln Lys Val Arg Asp Met Ser Val Ile Asn Lys Thr Leu Ser Asn Gln
    210                 215                 220

Val Gly Arg Thr Val Thr Gly Asn Pro Gly Ile Ile Thr Met Asp Glu
225                 230                 235                 240

Ala Val Ala Leu Phe Lys Lys Asp Arg Asp Lys Met Leu Ser Asp Ile
                245                 250                 255
```

```
Lys Thr Asn Ser Arg Val Gly Pro Val Tyr Ala Lys Val Asn Lys Ser
            260                 265                 270

Arg Gln Met Ala Leu Glu Asn Met Ser Phe Gln Met Gly Val Gly Gly
        275                 280                 285

Leu Ala Lys Phe Gly Lys Met Leu Asp Ala Met Leu Ile Gly Asp Trp
    290                 295                 300

Lys Thr Ala Tyr Thr Glu Ala Arg Asn Ser Val Trp Phe Asn Gln Thr
305                 310                 315                 320

Lys Gly Arg Ala Ser Arg Val Ser Met Ile Ile Leu Thr Gly Asn Met
                325                 330                 335

Glu Ser Tyr Gly Val Pro Ala Pro Lys Pro Glu Gly Lys Asn Leu Ser
            340                 345                 350

Ala Ala Tyr Val Glu Pro Lys Ser Gly Gly Asn Pro Glu Asp Pro Trp
        355                 360                 365

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

Asn Gly Gln Tyr Pro Tyr Val His Thr Met Glu Thr Glu Ser Gly His
385                 390                 395                 400

Ile Gln Glu Phe Asp Asp Thr Pro Gly Tyr Glu Arg Tyr Arg Ile Val
                405                 410                 415

His Pro Thr Gly Ser Tyr Glu Glu Val Ala Pro Asp Gly Arg Arg Thr
            420                 425                 430

Arg Lys Thr Val Ala Asp Leu Tyr Asp Met Thr Gln Gly Asp Gly Asn
        435                 440                 445

Ile Leu Ile Ser Gly Asp Lys Lys Val Asn Val Gly Gly Asn Glu Thr
    450                 455                 460

Tyr Tyr Asn Met Tyr Asn Arg Arg Gln Gln Ile Asp Gly Asp Asn Thr
465                 470                 475                 480

Leu Tyr Val Arg Gly Asn Glu Thr Lys Thr Ile Glu Gly Asn Gly Thr
                485                 490                 495

Ile Phe Val Lys Gly Asn Ile Lys Ile Val Val Glu Gly Asn Ala Asp
            500                 505                 510

Ile Gln Val Asn Gly Asp Ala Thr Thr Lys Val Asp Gly Asn His Asp
        515                 520                 525
```

Val Thr Val Gly Gly Asn Leu Thr Trp Gln Val Ala Gly Thr Val Asn
530 535 540

Trp Asn Val Gly Gly Ala Trp Thr Glu Thr Met Ala Ser Met Ser Ser
545 550 555 560

Ile Ala Gln Gly Gln Tyr Thr Val Asp Gly Ser Arg Ile Asp Val Gly
565 570 575

<210> 807
<211> 212
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 807
Met Leu Phe Ser Phe Phe Ser Pro Ile Asp Tyr Ser Ala Lys Thr Val
1 5 10 15

Lys Gly Ala Lys Ala Lys Ala Ile Pro Thr Ala Asp Ile Phe Arg Asn
20 25 30

Tyr Arg Lys Tyr Phe Asp Thr Val Ala Glu Asn Tyr Leu Leu Gln Thr
35 40 45

Tyr Tyr Ile Ser Gly Ala Pro Arg Pro Glu Glu Leu Ala Tyr Ile Leu
50 55 60

Tyr Gly Asn Ser Gln Leu Tyr Trp Ile Leu Leu Met Cys Asn Asn Val
65 70 75 80

Tyr Asp Pro Phe Arg Asp Trp Ile Lys Thr Gln Asp Ala Cys Tyr Gln
85 90 95

Phe Ala Gln Gln Lys Tyr Ala Asp Val Gly Gly Asp Gln Ile Leu Tyr
100 105 110

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

Glu Asn Ser Gly Val Trp Tyr Asp Lys Gly Asp Phe Asn His Gln Tyr
130 135 140

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

Ile Ile Glu Asn Glu Lys Leu Arg Gln Ile Asn Ile Ile Asn Pro Ser
165 170 175

Asp Ile Glu Ala Phe Leu Ser Asp Ile Ile Arg Glu Met Glu Lys Ala
180 185 190

Pro Asp Ser Glu Tyr Glu Ser Gly Arg Tyr Lys Ser Gln Thr Thr Ile
195 200 205

Gly Glu Val Leu
210

<210> 808
<211> 149
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 808
Met Ala Tyr Ser Gly Lys Phe Met Pro Gln Asn Leu His Lys Tyr Lys
1 5 10 15

Gly Asp Phe Arg Lys Ile Thr Tyr Arg Ser Thr Trp Glu Gln Tyr Met
20 25 30

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

Glu Val Val Ile Pro Tyr Phe Ser Asn Ala Asp Gly Lys Lys Arg Arg
50 55 60

Tyr Phe Met Asp Phe Trp Ala Lys Phe Ser Asn Gly Gln Gln Phe Phe
65 70 75 80

Phe Glu Val Lys Pro Lys Lys Glu Thr Arg Pro Pro Val Lys Pro Thr
85 90 95

Lys Leu Thr Thr Ser Ala Lys Lys Arg Tyr Ile Asp Glu Ile Tyr Thr
100 105 110

Trp Ser Val Asn Val Asp Lys Trp Lys Ala Ala Gln Ala Thr Ala Ser
115 120 125

Lys Met Gly Ile Glu Phe Arg Leu Ile Thr Glu Asp Ser Leu Lys Lys
130 135 140

Leu Gly Trp Lys Gly
145

<210> 809
<211> 275
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 809

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

Lys Ser Arg Ser Glu Asn Gln Trp Val Ala Leu Gly Val Glu Tyr Ser
            20                  25                  30

Ala Ala Arg Lys Lys Gly Met Thr Ser Lys Ser Phe Ala Glu Ser Lys
        35                  40                  45

Gly Ile Asn Pro Ala Thr Phe Ser Lys Ala Met Ala Arg His Ala Ser
    50                  55                  60

Arg Ile Lys Thr Ala Ile Lys Val Ala Glu Ile Glu Lys Lys Pro Ala
65                  70                  75                  80

Asn Lys Met Thr Lys Gln Glu Arg Ala Leu Val Met Val Asn Ser Phe
                85                  90                  95

Arg Ser Ser Ile Lys Asp Lys Ile Arg Asn Glu Gly Ala Ala Val Asn
            100                 105                 110

Asn Lys Ser Ala Lys Trp Phe Ala Glu Thr Ile Lys Lys Asn Ile Arg
        115                 120                 125

Gly His Ser Val Thr Lys Pro Gln Pro Gly Lys Leu Tyr Ala Tyr Met
    130                 135                 140

Tyr Asp Ala Lys His Lys Asp Thr Leu Pro Phe Trp Asp Lys Phe Pro
145                 150                 155                 160

Leu Ile Val Tyr Leu Gly Leu Gly Lys Gln Gly Thr Thr Thr Leu Met
                165                 170                 175

Tyr Gly Leu Asn Leu His Tyr Ile Pro Pro Lys Ala Arg Gln Gln Phe
            180                 185                 190

Leu Glu Glu Leu Leu Lys Gln Tyr Ala Asn Thr Pro Val Ile Ser Asn
        195                 200                 205

Lys Thr Arg Leu Lys Ile Asn Trp Ser Gln Val Lys Gly Phe Ala Gly
    210                 215                 220

Ala Asp Lys Met Ile Lys Ala Tyr Ile Pro Gly Asn Ile Lys Gly Ala
225                 230                 235                 240

Leu Ile Glu Ile Lys Pro Ala Asp Trp Ala Asn Val Val Met Leu Pro
                245                 250                 255

Leu Gln Gln Phe Met Ser Lys Gly Lys Arg Tyr Ser Ala Thr Ser Val
            260                 265                 270
```

Trp Lys Ser
        275

<210> 810
<211> 200
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 810
Met Ser Thr Gly Leu Phe Asn Gln Thr Asn Thr Thr Asn Phe Ile Leu
1   5   10   15

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

Thr Ala Val Val Pro Gly Ile His Ile Pro Ala Thr Asp Thr Val Gly
        35   40   45

Ser Pro Gln Gly Met His Arg Ala Lys Leu Pro Gly Ser Thr Phe Glu
    50   55   60

Phe Asp Ala Val Pro Val Arg Phe Leu Val Asp Glu Asn Leu Asp Ser
65   70   75   80

Trp Val Gln Met Tyr Lys Trp Met Leu Ser Cys Gln Asn Tyr Ile Asp
                85   90   95

Arg Asp Lys Ser Gly Trp Asn Asn Gly Gly Glu Gly Phe Pro Gly Ala
            100   105   110

Val Leu Met His Val Leu Asp Asn Asp Lys His Asp Ile Val Leu Thr
        115   120   125

Val Arg Tyr Ile Gly Gly Trp Val Ser Asp Leu Ser Glu Ile Glu Tyr
    130   135   140

Ser Leu Thr Glu Glu Ser Asp Pro Ala Met Val Cys Val Ala Thr Leu
145   150   155   160

Gln Tyr Lys Tyr Ile Glu Val Glu Lys Asp Gly Ile Ile Ile Thr Gly
                165   170   175

Arg Pro Ser Val Asn Asp Thr Arg Glu Ser Gln Tyr Gln Gln Lys Val
            180   185   190

Met Gly Met His Pro Ser Met Arg
        195   200

<210> 811
<211> 247
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 811
Leu Lys Leu Leu Phe Leu Ile Gly Lys Lys Arg Ser Gly Lys Asp Thr
1   5   10   15

Thr Ala Asp Tyr Ile Met Asp Asn Tyr Asn Ala Thr Lys His Gln Leu
            20   25   30

Ala Gly Pro Ile Lys Asp Ala Leu Ala Asp Ala Met Leu Thr Glu Trp
        35   40   45

Tyr Arg Asp Thr Ser Arg Glu Phe Pro Arg Ile Thr Arg Ser Met Ile
    50   55   60

Glu Gly Ile Asp Tyr Asp Arg Glu Gln Asp Leu Asn Leu Ser Thr Lys
65   70   75   80

Asp Val Ile Arg Ile Met Ala Asn Ala Ile Glu Tyr Val His His Asp
                85   90   95

Leu Pro Leu Pro Gly Val Val Tyr Asp Asn Lys Arg Lys Ile Leu Asp
            100   105   110

Gly Asp Thr Met Glu Val Ile Arg Lys Val Val Ile Asn Lys Pro Val
        115   120   125

Glu Pro Trp Ser Ile Arg Arg Leu Met Gln Thr Leu Gly Thr Asp Ile
    130   135   140

Val Cys Asp Lys Leu Asp Arg Met Tyr Trp Val Lys Arg Phe Thr Leu
145   150   155   160

Val Met Ala Asp Thr Phe Gly Asp Tyr Asp Tyr Phe Ile Val Pro Asp
                165   170   175

Thr Arg Gln Asp His Glu Leu Asp Val Ala Arg Ala Met Gly Ala Thr
            180   185   190

Val Ile His Val Val Arg Pro Glu Gln Glu Gly Ser Lys Lys Asp Thr
        195   200   205

His Val Thr Glu Arg Gly Leu Pro Ile Arg Glu Gly Asp Ile Val Ile
    210   215   220

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

Leu Gly Ile Gln Asn Asp Tyr
                245

<210> 812
<211> 77
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 812
Met Thr Thr Glu Gln Leu Gln Ala Gln Val Asp Thr Leu Lys Val Arg
1 5 10 15

Val Phe Asp Leu Ser Glu Thr Ile Gln Gly Leu Ser Ala Leu Arg Ala
20 25 30

Gln Tyr Glu Glu Val Leu Gln Lys Leu Ile Ala Val Ser Gly Val Glu
35 40 45

Ile Gly Glu Asp Gly Gln Val Lys Leu Asp Asp Leu Val Ala Lys Ile
50 55 60

Glu Ala Gln Phe Ala Glu Glu Thr Thr Glu Glu Ser Glu
65 70 75

<210> 813
<211> 151
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 813
Met Lys Phe Ser Asp Phe Ser Thr Gly Leu Tyr Val Ala Ala Lys Phe
1 5 10 15

Ser Glu Lys Thr Leu Asp Ala Ile Glu Asp Leu Gln Arg Glu Leu Lys
20 25 30

Val Pro Asn Pro Val Pro Arg His Lys Ile His Thr Thr Ile Cys Tyr
35 40 45

Ser Arg Val His Val Pro Tyr Val Cys Ala Ser Gly Ser Phe Glu Val
50 55 60

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

Leu Val Leu Lys Leu Asp Ser Glu Tyr Leu Lys Phe Arg His Gln Tyr
85 90 95

Ala Arg Ala Leu Gly Ala Thr His Asp Phe Pro Asp Tyr Ser Pro His
100 105 110

Ile Thr Leu Ser Tyr Asn Val Gly Pro Ala His Phe Glu Gly Glu Val
        115   120   125

Gln Val Pro Val Val Leu Asp Arg Glu Tyr Gln Glu Pro Leu Lys Leu
    130   135   140

Asn Trp Ser Glu Asp Leu Lys
145   150

<210> 814
<211> 127
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 814
Met Lys Ser Tyr Gln Glu Phe Leu Met Glu Thr Glu Ala Leu Leu Glu
1   5   10   15

Ser Thr Leu Pro Asp Tyr Met Ile Val Lys Ser Phe Asn Val Lys Asn
            20   25   30

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

Met Ser Asn Asp Ala Gly Ile Ser Val Lys Val Asn Val Gln Phe Ile
    50   55   60

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

Gly Gly Glu Lys Val Val Lys Asn Ile Lys Leu Asp Tyr Asp Glu Ser
                85   90   95

Ala Glu Ser Val Lys Lys Arg Phe Gly Asp Lys Leu Val Lys Ser Ile
            100   105   110

Met Val His Pro Thr Phe Lys Arg Asp Phe Thr Glu Leu Tyr Lys
        115   120   125

<210> 815
<211> 59
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 815
Met Lys Arg Cys Glu Leu Ile Arg Asn Val Ala Ser Ala Ile Cys Leu
1   5   10   15

Thr Ala Val Gly Thr Ser Ile Phe Gly Ala Ile Phe Met Gly Ala Lys
            20   25   30

Glu Ile Met Val Val Leu Val Ala Ala Phe Leu Met Gly Ser Ile Ser
35 40 45

Phe Ile Met Asp Lys Ile Ser His Glu Lys Asp
50 55

<210> 816
<211> 59
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 816
Met Lys Lys Ile Lys Gln Trp Phe Val Lys Thr Tyr Asp Leu Gly Arg
1 5 10 15

Glu Glu Val Thr Lys Tyr Asp Tyr Val Thr Leu Gly Val Gly Leu Gly
20 25 30

Ala Leu Leu Ala Ala Leu His Ser Ser Leu Leu Ala Ile Ala Val Leu
35 40 45

Leu Ile Leu Ala His Tyr Ser Trp Lys Arg Lys
50 55

<210> 817
<211> 61
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 817
Met Tyr Ala Leu Leu Thr Trp Ser Asn Tyr Tyr Pro Ala Pro Gly Ser
1 5 10 15

Asp Gln Ile Arg Gly Val Tyr Ser Thr Val Glu Glu Cys Tyr Glu Ala
20 25 30

Leu Gln Gly Thr Tyr Gln Asp Tyr Phe Glu Ile Leu Asn Ser Arg Phe
35 40 45

Glu Thr Val Ala Lys Gly Ser Thr Glu Ala Tyr Lys Asp
50 55 60

<210> 818
<211> 116
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 818
Met Asn Ile Arg Ala Ala Phe Asn Thr Phe Tyr Gln Glu Asn Tyr Lys
1 5 10 15

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

Asp Leu Val Thr Pro Lys His Val Lys Thr Asp Ser Leu Asp Asn Glu
35 40 45

Ile Gln Pro Gly Asp Leu Val Ser Tyr Tyr Cys Gly Gly Ser Leu Ser
50 55 60

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

Val Val Pro Phe His Thr Ser Pro Ile Pro Glu His Arg Val Leu Leu
85 90 95

Ser His Met Asp Ser Pro His Arg Val Phe Leu Val Lys Ser Lys Ser
100 105 110

Ser Pro Ile Val
115

<210> 819
<211> 84
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 819
ggggaguuag accguagggg uagcgggaca gacuguaaau cuguugcuca aaaggcucga 60

gugguucgac uccauuacuc ccca 84

<210> 820
<211> 74
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 820
gggauacuag cucaguuggu uagagcaccg gacuuuuaau ccggguguac gaaguucgaa 60

ucuucggugu ccca 74

<210> 821
<211> 82
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 821
gggucguugg cugagagggu aagcgacgga cuguuaaucc gugucagaaa ugacuaggca 60

gguucgauac cugcacggcc cg 82

<210> 822
<211> 74
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 822
agugcuguag ucgagauggu uaagacacuc cccugucacg ggagagaucg cggguucgac 60

acccgucagc acug 74

<210> 823
<211> 132
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 823
Leu Thr Phe Asp Glu Trp Leu Ser Trp Trp Lys Ala Thr Gly Lys Tyr
1 5 10 15

His Leu Arg Gly Arg Ala Ser Asp Asn Tyr Cys Met Cys Arg Lys Gly
20 25 30

Asp Val Gly Pro Tyr Ser Leu Asp Asn Ile Tyr Cys Ala Thr Asn Ala
35 40 45

Gln Asn Ala Lys Asp Ala Gly Ala Asn Gly Arg Ile Ile Ser Thr Gly
50 55 60

Phe Thr Gly His Asn His Ser Asp Glu Thr Lys Ile Lys Ile Ser Glu
65 70 75 80

Asn His Ala His Lys Leu Asn Ala Asp Glu Ile Ser Leu Arg Ile Asp
85 90 95

Leu Tyr Asn Ser Ile Asp Phe Thr Gln Arg Gly Ala Leu Val Lys Phe
100 105 110

Ala Asn Lys Leu Gly Ile Ser His Thr Gln Ala Arg Lys Phe Ile Asn
115 120 125

Lys Phe Ile Lys
130

<210> 824
<211> 74

<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 824
ugcggaguaa cuucaguugg uagaauguug ggcucauauc ccgacacgcg cagguucgag 60

uccugccucc gccu 74

<210> 825
<211> 72
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 825
ugaaucauag ccaaguuggu aaggcaguag guuuugaucc uacgaucccu gguucgaguc 60

caggugguuc ag 72

<210> 826
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 826
Met Met Asp Gly Val Asn Ile Asp Val Val Val Val Gln Leu Val Glu
1 5 10 15

Pro Glu Val Val Ile Leu Asp Val Thr Asp Ser Asn Ser Val Gly His
20 25 30

Pro Asn Asn Glu Gly Met Val Glu Lys Tyr Thr Ala Arg Lys Thr Leu
35 40 45

Trp Leu Ser Leu Ser Glu Leu Cys Leu
50 55

<210> 827
<211> 73
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 827
guggucguag uucaguuggu agaacccgag guugugaucc ucgaugucac ggauucgaau 60

uccgucggcc acc 73

<210> 828
<211> 82
<212> RNA

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 828
ggagaguagc gcuaguggua gcaaaccgga cuugaaaucc gggccaccgg aaacggugag 60

gguucaacuc cuuuacucuc cg 82

<210> 829
<211> 73
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 829
gggaguauag cucauuuggu agagcucucg accgauaauc gagcggugac ugguucgagu 60

ccaguuacuc cca 73

<210> 830
<211> 72
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 830
agguucuuag uauaauggcu auuaugcugg gcuccaaacc cagugaugag gguucgauuc 60

cuucagggcc ug 72

<210> 831
<211> 72
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 831
gcauccaucg uauagcggau auuaugucug gcuuccaccc agaagauggg aguucgauuc 60

ucccuggaug cu 72

<210> 832
<211> 74
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 832
cuccguauag cucagccugg uagagcgcuc cauuugggau ggagaggucg aauguucgag 60

ucauucuaug gaga 74

<210> 833

<211> 50
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 833
Met Lys Tyr Tyr Gly Phe Lys Thr Ser His Phe Gly Lys Ala Tyr Arg
1   5   10   15

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

Ala Gly Arg Ser Arg Ala Arg Gln Glu Gly Gln Lys Gln Ala Lys Glu
        35   40   45

Ile Glu
    50

<210> 834
<211> 121
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 834
Met Asn Ile Phe Ile Gly Val Ala Asn Asn Val Asn Ala Ile Thr Val
1   5   10   15

Lys Leu Gln Trp Asn Arg Pro Thr Asn Phe Ala Leu Gly Leu Cys Lys
            20   25   30

Ser Glu Arg Asp Leu Met Leu His Ala Asp Phe Ala Tyr Thr Phe Asp
        35   40   45

Glu Arg Lys Gly Met Trp Val Trp Ile Lys Cys Arg Tyr Glu Ala Leu
    50   55   60

Ile Lys Tyr Glu Tyr Phe Ser Glu Arg Asp Ile Gln Glu Val Ile Ala
65   70   75   80

Tyr His Ser Gly Cys Lys Val Ser Lys Leu Arg Gln Val Ile Pro Phe
                85   90   95

Thr Asn Ala Ser Asn Val Glu Glu Leu Ile Thr Asp Phe Lys Arg Ile
            100   105   110

Tyr Gln Ala Lys Tyr Asp Glu Arg Phe
        115   120

<210> 835
<211> 77
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 835
Met Met Lys Asp Ser Lys Gly Arg Asp Val Gln Val Gly Asp Ile Val
1   5   10   15

Phe Tyr Gly Glu Arg Thr Tyr Asn Lys Gly Gly Arg Gly Ser Met Arg
            20   25   30

Cys Gly Arg Ile Thr Asp Ile Ala Ser Gly Leu Ala Lys Val Asp Asn
        35   40   45

Asp Tyr Val Ala Met Arg Ser Lys Ser Phe Val Lys Val Ser Pro Met
    50   55   60

Phe Ala Thr Met Trp Glu Asn Gly Thr Ile Phe Glu Ile
65   70   75

<210> 836
<211> 74
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 836
Met Lys Arg Ile Ala Leu Ile Val Asp Gln Glu Ala Met Phe Ala Ala
1   5   10   15

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

Ile Val Gly Leu Val Glu Thr Val Ala Gly Asp Val Ile Val Ser Ile
        35   40   45

Lys Thr Ser Glu Ile Ser Pro Val Val Lys Val Ala Val Glu Asn Asp
    50   55   60

Phe Trp Glu Val Ala Asp Phe Met Cys Glu
65   70

<210> 837
<211> 74
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 837
ggcccuguag cucaauuggu agagcguucc ccucauaagg gauugguugc auguucgagu 60

cuuugccagg guca 74

<210> 838
<211> 66
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 838
Met Met Arg Leu Val Lys Val Val Val Glu Glu Ser Glu Tyr Met Gly
1   5   10   15

Asp Ser Arg Met Ile Glu Glu Phe Val Thr Val Glu Ala Asp Ser Glu
            20   25   30

Ser Glu Ile Val Asp Lys Val Tyr Arg His Phe Asp Asn Met Ser Asp
        35   40   45

Ser Tyr Gly Thr Met Tyr Ser Ile Tyr Arg Leu Asp Val Ile Val His
    50   55   60

Ile Asn
65

<210> 839
<211> 185
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 839
Met His Ile Arg Phe Gly Gln Val Ile Pro Lys Gly Leu Ala Met Ala
1   5   10   15

Ile Thr Thr Trp Glu Asn Asp Ala Asp Arg Tyr Ser Thr Gln Met Val
            20   25   30

Tyr Gly Leu Glu Lys Glu Glu Ile Asn Gln Val Ile His Val Leu Glu
        35   40   45

Trp Phe Ser Ser Asn Gly Arg Arg Gly Glu Tyr Leu Gly Asn Asn Asp
    50   55   60

Tyr Asn His Glu Ala Ile Leu Glu Lys Leu His Thr Glu Gln Lys Tyr
65   70   75   80

Val Thr Pro Glu Phe Ser Lys Lys Phe Phe Gly Val Asp Val Pro Ala
                85   90   95

Tyr Asp Cys Thr Asp Glu Glu Phe Asp Ala Tyr Leu Asp Asn His Tyr
            100   105   110

Ser Cys Ser Asn Glu Val Met Tyr Ala Ile Gln Ala Trp Leu Gly Asn

115 120 125

Pro Ile Glu Tyr Asp Tyr Asp Phe Met Arg Val Phe Glu Lys Val Glu
130 135 140

Ile Phe Asp Ile Lys Glu Glu Ile Arg Ile Pro Asp Ala Pro Val Ala
145 150 155 160

Phe His Val Gly Ile Thr Tyr Lys Gln Lys Glu Ser Pro Leu Lys Val
165 170 175

Asp Trp Leu Lys Tyr Val Lys Glu Lys
180 185

<210> 840
<211> 149
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 840
Met Asp Ile Gly Ser Gly Ser Ser Tyr Pro Ser Cys Ala Leu Ser Asn
1 5 10 15

Phe Ala Pro His Lys Phe Ile Tyr Asp Gly Val Glu Cys Ala Ser Met
20 25 30

Glu Gly Phe Leu Gln Ser Leu Lys Phe Ser Ser Pro Glu Met Gln Ala
35 40 45

His Val Cys Thr Leu Val Gly Lys Ser Ala Lys Phe Lys Gly Lys Lys
50 55 60

Lys Arg Trp Trp Pro Thr Gln Thr Leu Tyr Trp Lys Gly Val Pro Ile
65 70 75 80

His Arg Ala Ser Glu Ala Tyr Gln Asn Leu Leu Thr Gly Ala Tyr Asp
85 90 95

Ala Leu Ser Lys Asn Glu Gly Phe Arg Lys Ala Leu Ala Ala Thr Arg
100 105 110

Asn Ala Thr Leu Thr His Ser Met Gly Lys Asn Lys Ile Ser Glu Thr
115 120 125

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

Ala Ile Asn Asn Gln
145

<210> 841
<211> 84
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 841
gcgucgaugu uggaauuggu agacaaagga gacuuaaaau cucccgggau uaaacccgua 60

cgaguucgag ucucguucga cgca 84

<210> 842
<211> 73
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<220>
<223> Description of Unknown:
sequence

<400> 842
gcccuuauag uguaauggau agcacacgau cguuctaagg ucgguagucc ggguucgagu 60

ccuggugggg gua 73

<210> 843
<211> 73
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<220>
<223> Description of Unknown:
sequence

<400> 843
gccgauuuag cucaguuggu agagcgcuuc acuuguaaug aagaugccgc ggguucgacu 60

ccugcaaucg gca 73

<210> 844
<211> 194
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 844
Met Lys Phe Lys Asp Phe Leu Thr Glu Glu Glu Leu Phe Glu Ala Ala
1 5 10 15

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

Pro Arg Gly Glu Arg His Asp Phe Ser Lys Phe Ala Ala Ser Val Glu

35 40 45

Lys Ile Tyr Gly Ile Gly Ile Ser Asp Pro Lys Asp Tyr Ala Lys Val
50 55 60

Ala Ala Ala Phe Glu Ser Leu Gly Gly Lys Val Thr Thr Pro Ala Arg
65 70 75 80

Gly Ala Ser Pro Ala Gln Ala Pro Ala Ala Lys Pro Ala Pro Val Lys
85 90 95

Ala Lys Pro Lys Asn Ile Pro Gly Leu Lys Ile Ser Gly Asp His Gly
100 105 110

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

Pro Leu Val Arg Asp Asn Gly Pro Leu Tyr Lys Ala Val Gln Phe Tyr
130 135 140

Phe Asp Asn Leu Trp Lys Tyr Arg Glu Ser Gln Gly Ala Lys Pro Ser
145 150 155 160

Ala Arg Glu Thr Gln His Ile Gly Glu Val Lys Thr Leu Leu Ala Lys
165 170 175

Leu Asn His His Leu Val Glu Leu Ser Arg Gln Thr Glu Leu Ser Tyr
180 185 190

Asn Val

<210> 845
<211> 96
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 845
Met Ser Lys Phe Asn Phe Ile Gln Ile Glu Arg Gly Tyr Asn Asn Tyr
1 5 10 15

Gly Thr Pro Asp Arg Tyr Arg Ala Ile Trp Ile Lys Gly Glu His Glu
20 25 30

His Ala Val Phe Asn Val Ala Glu Thr Arg Glu Leu Lys Asp Leu Ile
35 40 45

Lys His Val Arg Lys Asp Trp Pro Ala Val Glu Glu Tyr Tyr Val Arg
50 55 60

Val Tyr His Glu Glu Ala Pro Thr Glu Thr Val Gln Ile Lys Phe Ala
65 70 75 80

Lys Thr Ala Ser Ala Leu Thr Lys Arg Ile Glu Ala Val Ile Asn Cys
85 90 95

<210> 846
<211> 197
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 846
Met Ser Ile Leu Lys Lys Leu Val Glu Phe Ile Arg Ser Lys Phe Gly
1 5 10 15

Thr Phe Val Ala Gln Asn Thr Ser Val Glu Asp Gln Tyr Thr Met Ala
20 25 30

Ala Asn Arg Ile Ile Asp Glu Ile Thr Lys Leu Arg Thr Thr His Val
35 40 45

Lys Ser Val Asn Glu Glu Lys Arg Leu Leu Lys Leu Ala Asp Glu Lys
50 55 60

Asp Gln Ala Gly Ala Ser Lys Glu Arg Glu Ile Arg Arg Leu Met Ala
65 70 75 80

Glu Gly Met Asn Val Glu Thr His Ala Lys Leu Gly Leu Leu Tyr Arg
85 90 95

Arg Thr Ala Lys Ala Leu Arg Asp Lys Ala Ala Glu Tyr Lys Glu Met
100 105 110

Arg Ala Gln Ile Glu Glu Thr Val Val Lys Leu Asp Asp Gln Arg Leu
115 120 125

Asp Leu Ala Val Lys Leu Glu Tyr Ile Arg Glu Thr Arg Asn Ala Ser
130 135 140

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

Ala Lys Val Asp Val Gln Asp Ile Met Met Lys Val Glu Thr Phe Ser
165 170 175

Gly Thr Gln Pro Gly Ile Glu Thr Thr Thr Ala Asp Val Gln Glu Tyr
180 185 190

Leu Glu Ser Leu Lys
195

<210> 847
<211> 186
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 847
Met Ala Thr Pro Gln Ile Lys Glu Leu Ile Ala Ala Gly Phe Pro Thr
1 5 10 15

Glu Ile Thr Asp Ile Leu Gly Lys Phe Ala Tyr Pro Asp Thr Arg Pro
20 25 30

Glu Asn Trp Lys Thr Arg Tyr Asn Gly Tyr Asn Thr Thr Val Leu Pro
35 40 45

Arg Ala Ile Val Leu Lys Asp Tyr Ser Lys Leu Lys Asn Leu Ile Ser
50 55 60

Asn Ile Ser Ser Ile Ser Asp Gly Val Lys Leu Val Asp Ile Phe Ala
65 70 75 80

Leu Arg Tyr Gly Ile Tyr Ser Phe Asn Asp Ser Pro Ser Asn Leu Lys
85 90 95

Ser Ala Arg Thr Asn Ala Gly Glu Tyr Ser Thr Ser Gly Ser Thr Thr
100 105 110

Tyr Thr Ile Val Ile Glu Ile Ile His Asn Lys Asn Ser Tyr Arg Leu
115 120 125

Gly Ile Asn Leu Val Lys Tyr Val Thr Ser Gln Asp Asp Tyr Ser Asn
130 135 140

Tyr Leu Asn Tyr Cys Val Asn Glu Leu Pro Ser Lys Val Met Ser Met
145 150 155 160

Phe Asp Ser Asn Asn Met Val Gly Lys Gln Leu Ile Ile Asp Glu Phe
165 170 175

Ile Lys Tyr Cys Arg Glu Arg Val Gln Lys
180 185

<210> 848
<211> 119
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 848
Met Ser Asn Leu Tyr Leu Pro Ser Glu Pro Pro Val Tyr Asn Tyr Val

1 5 10 15

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

Thr Val Gly Ala Met Cys Thr Phe Ala Ala Ile Asp Ile Met His Leu
35 40 45

Thr Asp Ile Thr Pro Ala Val Leu Phe Gly Ile Leu Leu Ala Trp Trp
50 55 60

Gly Thr Ser Leu Leu Ile Met Gly Leu Ile Glu Cys Ser Arg Trp Val
65 70 75 80

Lys Trp Ser Arg Asn Asn Tyr Lys Arg Lys Ala Glu Trp Lys Glu Gln
85 90 95

Cys Lys Asn Leu Thr Leu Glu Trp Asn Arg Lys Lys Ser Phe Glu Phe
100 105 110

Ile Lys Glu Val Arg Arg Lys
115

<210> 849
<211> 98
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 849
Met Asn Glu Tyr Lys Pro Asp Gly Phe Trp Asn Gln Asp Gly Leu Ala
1 5 10 15

Pro Gly Phe Gly Ile Val Thr Trp Leu Leu Tyr Cys Ala Phe Val Ile
20 25 30

Val Gly Gly Thr Phe Phe Gly Leu Asn Val Ser Glu Phe Met Ile Met
35 40 45

Leu Leu Phe Leu Gly Val Phe Ala Phe Ser Leu Met Trp Met Leu Ile
50 55 60

Ile Ala Leu Ile Asn Cys Cys Thr Phe Leu Ala Tyr Arg Met Lys Tyr
65 70 75 80

Lys Lys Trp Lys Glu Lys Glu Asp Phe Asn Thr Trp Ile Arg Ser Cys
85 90 95

Arg Lys

<210> 850
<211> 108
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 850
Met Ile Lys Thr Cys Tyr Arg Gly Met Ile Lys Ser Asp Glu Pro Gly
1   5   10   15

Tyr Phe Phe Leu Phe Leu Leu Ile Trp Phe Ser Leu Ser Ala Phe Val
            20   25   30

Gly Phe Gly Thr Phe Trp Gly Phe Tyr Phe Phe Ser Pro Val Phe Gly
        35   40   45

Asp Ala Leu Tyr Tyr Ile Gly Trp Met Ser Gly Val Gly Thr Trp Phe
    50   55   60

Ala Ile Leu Ala Arg Trp Leu Gln Phe Val Ser Gln Arg Gln Arg Gly
65   70   75   80

Val Phe Asp Lys Pro Lys Val Lys Lys Glu Lys Ser Lys Asp Asp Ser
                85   90   95

Arg Ser Glu Thr Leu Ser Trp Ile Lys Glu Met Lys
            100   105

<210> 851
<211> 78
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 851
Met Ala Val Ala Val His Val Lys Phe Glu Asn Gly Asp Thr Arg Leu
1   5   10   15

Leu Cys Tyr Ser Asp Asn Glu Ser Leu Ser Gly Ile Glu Ile Ser Leu
            20   25   30

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

Glu Gly Ser Asp Asn Cys Asn Asp Asp Leu Glu Ser Met Val Tyr Thr
    50   55   60

Ala Met Glu Asp Ile Leu Glu Glu Ser Trp Asn Glu Cys Gln
65   70   75

<210> 852
<211> 150

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 852
Met Pro Met Lys Glu Leu Ser Ala Gly Ile Leu Phe Phe Thr Asp Asp
1   5   10   15

Lys Arg Leu Leu Met Gly Arg Met Thr Asn Thr Tyr Val Gln Gly Arg
            20   25   30

Gly Ser Arg Trp Asp Ile Pro Lys Gly His Val Glu Pro Gly Glu Thr
        35   40   45

Pro Lys Glu Ala Ala Ile Arg Glu Cys Lys Glu Glu Thr Gly Phe Thr
    50   55   60

Glu Phe Asp Gln Asp Leu Leu Tyr Asp Leu Gly Arg His Asp Tyr Ala
65   70   75   80

Ser Asn Lys Asp Ile His Leu Phe Gly Tyr Met Leu Pro Val Ser Pro
                85   90   95

Glu Met Phe Arg Asn Cys Arg Cys Thr Ala Tyr His Lys Asp Glu Asn
            100   105   110

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

Gln Trp Lys Tyr Val Met Gly Pro Ser Leu Tyr Lys Ile Met Thr Gln
    130   135   140

Met Tyr Ser Thr Ala Gln
145   150

<210> 853
<211> 102
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 853
Met Glu Glu Ala Val Glu Leu Gly Ile Pro His Ile Tyr Lys His Glu
1   5   10   15

Leu Arg Phe Ile His Asp Gly Lys Trp Ile Ser Ile Phe His Pro Arg
            20   25   30

Asp Lys Met Ser Arg Ile Leu Met Lys Ser Arg Tyr Val Phe Ser Asp
        35   40   45

Ser Glu Tyr Ile Lys Ser Ala Tyr Tyr Ile Ala Glu Gln Leu Tyr Pro
50 55 60

Gly Phe Ser Glu Leu Pro Glu Asp Asp Lys Arg Asp Tyr Val Trp Trp
65 70 75 80

Lys Asp Lys Trp Thr Pro Tyr Glu Lys Cys Ser Leu Glu Leu Phe Ile
85 90 95

Ala Lys Cys Arg Ala Lys
100

<210> 854
<211> 164
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 854
Met Asp Ile Phe Gly Met Leu Arg Ile Asp Glu Gly Tyr Asp Ser Lys
1 5 10 15

Ile Tyr Lys Asp Ser Glu Gly Tyr Trp Thr Ile Gly Ile Gly His Leu
20 25 30

Leu Thr Lys Asp Pro Ser Lys Ser Leu Ala Ile Ser Asn Leu Asp Lys
35 40 45

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

Val Ile Phe Ala Lys Asp Val Glu Lys Ala Ile Lys Gly Ile Val Ala
65 70 75 80

Asn Ala Thr Leu Ser Pro Val Tyr Asn Ile Leu Asp Asp Val Arg Arg
85 90 95

Ala Ala Leu Ile Asn Met Val Phe Gln Met Gly Val Ser Gly Val Ala
100 105 110

Gly Phe Pro Ala Ser Met Lys Leu Leu Leu Ala Lys Lys Trp Asp Ala
115 120 125

Ala Ala Lys Glu Leu Ala Asn Ser Arg Trp Tyr Arg Gln Thr Pro Asn
130 135 140

Arg Ala Arg Arg Val Ile Glu Thr Met Arg Thr Gly Thr Trp Ala Ala
145 150 155 160

Tyr Gln Gly Lys

<210> 855
<211> 159
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 855
Met Lys Thr Tyr Gln Glu Phe Leu Asn Glu Ser Arg Leu Ala Thr Val
1 5 10 15

Gly Val Met Thr Glu Ser Val Gly Ser Asn Leu Leu Lys Phe Lys Lys
20 25 30

Gly Gln Lys Met Thr Ala Thr Leu Glu Asp Gly Thr Glu Ile Glu Met
35 40 45

Asp Val Val Gly Tyr Asn Tyr Val Val Asp Gly Lys Leu Tyr Asn Lys
50 55 60

Ser His Ala Lys Phe Asp Ser Phe Asp Asp Phe Val Ser Ser Val Glu
65 70 75 80

Asp Glu Ser Ser Arg Lys Ala Val Ala Ser Gly Asp Ala Arg Ser Leu
85 90 95

Met Ala His Gly His Met Arg Ile Lys Ser Lys Gln Asn Lys Pro Gly
100 105 110

Glu Asp Asn Phe Ala Leu Val Gly Tyr Gln Ser Gly Lys Thr Ser Asn
115 120 125

Gly Tyr Gln Arg Thr Val Thr Met Tyr Met Arg Asn Gly Lys Ile Ala
130 135 140

Phe Val Asn Asp Arg Gly Ala Ile Arg Tyr Ala Lys Ser Ile Lys
145 150 155

<210> 856
<211> 100
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 856
Met Lys Thr Tyr Lys Glu Phe Ile Thr Glu Ala Arg Val Ser Ala Gly
1 5 10 15

Lys Leu Glu Ala Ala Ile Asn Lys Lys Ala His Ser Phe His Asp Leu
20 25 30

Ser Asp Lys Asp Arg Lys Lys Leu Val Ser Leu Tyr Ile Asp Lys Glu

35 40 45

Arg Ile Leu Ala Leu Pro Gly Ala Asn Glu Gly Lys Gln Ala Lys Pro
50 55 60

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

Met Ser Met Asp Asp Leu Gln Gln Ala Ala Ile Glu Ala Ala Lys Val
85 90 95

Ile Lys Gly Lys
100

<210> 857
<211> 177
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 857
Met Lys Tyr Leu Thr Pro Ile Tyr Leu Thr Leu Met His Ala Phe Lys
1 5 10 15

Asp Ala Ala Asp Arg Arg Leu Asn Asn Pro Asn Tyr Ser Phe Tyr Glu
20 25 30

Pro Ser Cys Leu Met Arg Glu Tyr Gly Thr Leu Arg Leu Asp Gly Gly
35 40 45

Arg Gln Thr Gly Lys Thr Ala Ala Leu Cys Gln Phe Ala Thr Asp Trp
50 55 60

Leu Leu Glu Asp Gly Ser Val Ile Ile Leu Ser Thr Arg Tyr Thr Gln
65 70 75 80

Ser Ser Glu Leu Met Glu Gly Ile Leu Arg Glu Tyr Asn Ser Ser His
85 90 95

Leu Ile Asn Lys Leu Pro Ala Asn Glu Ile Ala Lys Ser Ile Val Pro
100 105 110

Met Thr Ile Arg Glu Phe Leu Ser Asn Asp Ser Ser Tyr Lys Phe Arg
115 120 125

Gly Arg Lys Leu Gly Arg Ala Leu Ile Ile Ile Glu Glu Pro Met Lys
130 135 140

Val Pro Asp Met Met Lys Phe Tyr Asp Met Tyr Gln Glu Ala Ile Arg
145 150 155 160

Trp Ser Met Pro Asn Asp Thr Leu Pro Leu Phe Phe Val Ile Gly Met
165 170 175

Gln

<210> 858
<211> 103
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 858
Met Met Thr Gln Thr Glu Ile Val Asp Met Ile Thr Val Met Glu Asn
1 5 10 15

Thr Gly Phe Ala Asp Met Lys Gln Leu Ile Thr Met Val Thr Ala Gly
20 25 30

Asn Leu Leu Glu Tyr Lys Arg Tyr Lys Phe Leu Ser Gly Pro Phe Lys
35 40 45

Gly Ala Glu Phe Ile Ser Asn Ala Pro Asn Thr Lys Trp Met Asn Arg
50 55 60

Tyr Pro Asn Phe Arg Ile Glu Phe Ile Ser Gly Lys Leu Lys Gly Val
65 70 75 80

Ile Ser Ser Ser Leu Ile Thr Tyr Asp Gln Arg Ile Gln Glu Lys Thr
85 90 95

Met Gln Trp Leu Lys Leu Leu
100

<210> 859
<211> 114
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 859
Met Ala Glu Ile Val Ile Arg Cys Pro Pro His Leu Val Glu Ser Phe
1 5 10 15

Cys Glu Trp Phe Ser Asn Ser Gly Glu Gln Asp Phe Tyr Glu Ala His
20 25 30

Gln Asn Gly Thr Trp Asn Glu Thr Thr Lys Gln Trp Glu Glu Ala Thr
35 40 45

Thr Tyr Ile Gly Thr Arg Gly Tyr Gly Val Asn Glu Pro Ile Glu Ile
50 55 60

Val Glu Tyr Asp Lys Glu Thr Asp Glu Glu Val Thr Tyr His Glu Asp
65 70 75 80

Lys Ile Thr Tyr Leu Glu Ala Ala Ala Lys Phe His Ser Asp Glu Trp
85 90 95

Asn Lys Met Ser Val Ile Thr Ala Tyr Met Arg Gly Trp Asn Lys Glu
100 105 110

Ser Asn

<210> 860
<211> 120
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 860
Met Lys Ala Tyr Gln Ile Leu Glu Gly Glu Leu Lys Gly Thr Ile Tyr
1 5 10 15

Ile Glu Asp Gly Asp Asp Ala Arg Val Ile Val Ser Lys Val Leu Lys
20 25 30

Glu Asp Thr Ile Thr Asp Ala Glu Thr Phe Tyr Gly Tyr Lys Ala Arg
35 40 45

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

His Leu Asn Val Asn Val Leu Arg Arg Glu Thr Leu Leu Asp Ala Val
65 70 75 80

Glu His Pro Glu Lys Tyr Pro Gln Leu Thr Ile Arg Val Ser Gly Tyr
85 90 95

Ala Val Arg Phe Asn Ser Leu Thr Pro Glu Gln Gln Arg Asp Val Ile
100 105 110

Ala Arg Thr Phe Thr Glu Ala Leu
115 120

<210> 861
<211> 93
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 861

```
Met Ala Ile Glu Asp Ile Lys Gly Tyr Lys Pro His Thr Asp Glu Lys
1               5                   10                  15

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

Ile Phe Lys Ala Leu Glu Glu Glu His Val Glu Lys Tyr Met Asn Leu
        35                  40                  45

Asp Val Ser Thr Met Ser Asp Lys Glu Phe Asp Leu Ala His Glu Arg
    50                  55                  60

Ile Thr Gln Ile Arg Asn Ala Ile Gln His Leu Lys Glu Ala Ser Met
65                  70                  75                  80

Trp Ala Cys Arg Ser Val Phe Gln Pro Glu Glu Lys Tyr
                85                  90

<210> 862
<211> 152
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 862
Met Ser Thr Asn Pro Glu Val Phe Ile Arg Arg Thr Lys Leu Arg Arg
1               5                   10                  15

Lys Phe Glu Glu Ala Phe Arg Ser Leu Asn Leu Ser Val Arg Ala Arg
            20                  25                  30

Ala Lys Ala Glu Gly Lys Glu Pro Phe Phe Thr Lys Tyr Ser Asp His
        35                  40                  45

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

Ser Val Leu Ser Lys Ile Pro Asn His Leu Lys Glu Ile Asn Glu Phe
65                  70                  75                  80

Leu Ala Met Pro Trp Leu Pro Ile Asp Pro Lys Asp Ile Asp Glu Asn
                85                  90                  95

Ile Glu Tyr Lys Pro Met Arg Leu Glu Ile Thr Asp Gly Asn Leu Trp
            100                 105                 110

Leu Gly Phe Thr Met Asp Ile Pro Arg Pro Gly Lys Gly Pro Ser Ile
        115                 120                 125

Lys Cys Arg Met Ala Phe Val Asn Asp Lys Arg Leu Lys Gly Lys Ile
    130                 135                 140
```

Ser Thr Lys Val Ile His Ile Asn
145 150

<210> 863
<211> 181
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 863
Met Lys Lys Ala Leu Ile Gly Leu Met Ala Leu Cys Ser Thr Ala Phe
1 5 10 15

Gly Ser Glu Pro Thr Phe Ser Asn Val Gln Leu Asp Asn Leu His Tyr
20 25 30

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

Pro His Asn Arg Tyr Asp Asn Asn Gly Leu Gly Tyr Ile Met Ala Ala
50 55 60

Ile Ser Trp Lys Glu Ser Ser Ala Gly Ala Asn Leu Lys Ala Gly Lys
65 70 75 80

Gly His His Ser Tyr Gly Val Phe Gln Asn Tyr Leu Pro Thr Val Lys
85 90 95

Ala Arg Ala Lys Leu Glu Gly Lys Asn Leu Ser Asp Ser Glu Ile Arg
100 105 110

Lys Met Leu Lys Ser Arg Gln Asn Ser Ala Glu Trp Ala Tyr Ile Glu
115 120 125

Leu Ser Tyr Trp Leu Asn Ile His Asn Gly Asn Met Arg Lys Ala Leu
130 135 140

Ala Ser Tyr Asn Ala Gly Trp Asn Val Lys Arg Gly Asn Ser Tyr Ala
145 150 155 160

Ser Asp Val Leu Glu Lys Ala Asn Phe Leu Lys Lys His Lys Met Leu
165 170 175

His Thr Lys Val Glu
180

<210> 864
<211> 106
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F387/08

<400> 864
Met Val Lys Tyr Ala Ala Leu Leu Gly Leu Val Leu Ala Phe Ser Ala
1   5   10   15

Asn Ala Glu Asn Ser Met Thr Asp Ser Leu Arg Ile Ala Lys Thr Phe
            20   25   30

Cys Asn Thr Asn Ser Glu Cys Val Asp Ile Leu Ala Leu Glu Leu Asp
        35   40   45

Ser Ala Phe Ser Asp Gly Val Lys Asp Ser Arg Ser Pro Ala Gln Trp
    50   55   60

Thr Thr Leu Ile Asn Arg Lys Ala Lys Ser Met Lys Asp Leu Cys Val
65   70   75   80

Asn Ala Pro Asn Glu Asn Ile Cys Leu Met Tyr Arg Asp Gln Leu Met
                85   90   95

Ala Arg Tyr Met Ser Gly Leu Ser Ser Lys
            100   105

<210> 865
<211> 130
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 865
Met Lys Lys Ala Ala Ile Leu Leu Cys Cys Ala Phe Ser Val Asn Ala
1   5   10   15

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

Thr Lys Ile Glu Ser Asn Gly Pro Phe Lys Asn Asn Ile Glu Ile Ala
        35   40   45

Phe Val Pro Ser Ser Arg Lys Leu Leu Met Ser Phe Tyr Asn Tyr Gln
    50   55   60

Asp Lys Asp Asp Gln Val Ile Val Pro Leu Val Glu Tyr Asn Ala Arg
65   70   75   80

Gly Cys Gly Met Gln Ser Asp Gly Val Ser Val Asp Gly Val Met His
                85   90   95

Pro Lys Glu Gln Gly Val Leu Asn Pro Ile Leu Asn Cys Asn Asn Ala
            100   105   110

Ile Phe Leu Arg Val Tyr Asn Asn Leu Asn Glu Tyr Ala Thr Tyr Lys
        115   120   125

Ile Pro
    130

<210> 866
<211> 155
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 866
Met Ile Thr Gly Tyr Ile Lys Gly Asn Ile Val Glu Leu Phe Met Lys
1   5   10   15

His Glu Cys Asp Ile Ala His Gly Cys Asn Cys Phe Thr Thr Met Gly
            20   25   30

Ala Gly Val Ala Gly Gln Leu Ala Lys Ala Tyr Pro Pro Ile Leu Asp
        35   40   45

Ile Asp Ile Asp Glu Asp Arg Tyr Tyr Asp Asn Asn Leu Ala Lys Leu
    50   55   60

Gly Thr His Thr Arg Ala Ile His Lys Lys Gly Thr Ala Tyr Cys Tyr
65   70   75   80

Asn Leu Tyr Thr Gln Tyr Ala Pro Gly Pro Asn Val Asp Tyr Gly Ala
                85   90   95

Ile Phe Asn Ala Phe His Glu Leu Asn Ser Gly Arg Ile Val Tyr Asn
            100   105   110

Arg Pro Leu Tyr Ile Pro Lys Ile Gly Ala Gly Ile Ala Gly Gly Asp
        115   120   125

Trp Glu Leu Ile Glu Lys Leu Ile Asn Leu Ala Thr Pro Asp Ile Asp
    130   135   140

Ile Met Val Val Glu Tyr Glu Glu Ala Lys Ser
145   150   155

<210> 867
<211> 55
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 867
Met Ile Thr Glu Glu Gln Lys Thr Lys Leu Trp Gln Leu Ile Asp Asp
1   5   10   15

Tyr Ala Gly Ala Glu Gln Val Val Ala Ile Ser Ala Ile Tyr Gly Asn
            20   25   30

Gly Leu Pro Glu Glu Tyr Asp Glu Leu Ile Arg Ser Lys Asn Ala Ile
        35   40   45

Ser Asp Phe Met Glu Thr Leu
    50   55

<210> 868
<211> 199
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 868
Met Ala Gln Leu Tyr Phe Asn Tyr Ala Ser Met Asn Ala Gly Lys Ser
1   5   10   15

Ala Asn Leu Leu Thr Ala Ala His Asn Tyr Lys Glu Arg Gly Met Gly
            20   25   30

Thr Leu Ile Leu Lys Pro Ala Ile Asp Thr Arg Asp Ser Ala Thr Glu
        35   40   45

Val Thr Ser Arg Ile Gly Leu Arg His Glu Ala Asn Thr Val Asp Glu
    50   55   60

Ser Ile Asp Ile Leu Glu Phe Phe Lys Trp Ala Gln Thr Gln Arg Asp
65   70   75   80

Ile His Cys Val Phe Val Asp Glu Ala Gln Phe Leu Thr Ala Glu His
                85   90   95

Val Leu Gln Leu Cys Lys Ile Val Asp Leu Tyr Asp Val Pro Val Met
            100   105   110

Ala Tyr Gly Leu Arg Thr Asp Phe Arg Gly Glu Leu Phe Glu Gly Ser
        115   120   125

Lys Ala Leu Leu Ser Val Ala Asp Lys Leu Val Glu Leu Lys Gly Val
    130   135   140

Cys His Cys Gly Arg Lys Ala Thr Met Val Ala Arg Ile Asp Glu Asn
145   150   155   160

Gly Asn Ala Ile Thr Asp Gly Glu Val Val Glu Leu Gly Gly Glu Asp
                165   170   175

Lys Tyr Val Ser Leu Cys Arg Lys His Trp Cys Glu Leu Val Gly Val

180 185 190

Tyr Asn Glu Ala Lys Asn Val
195

<210> 869
<211> 64
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 869
Met Lys Pro Arg Thr Tyr Asn Thr Ile Leu Met Leu Val Leu Ser Met
1 5 10 15

Leu Phe Ile Trp Met Gly Val Ala Ala Ser Ile Gln Ser Asp Arg Arg
20 25 30

Glu Glu Leu Gln Asn Arg Leu Asp Ser Gly Cys Lys Val Leu Ala Gln
35 40 45

Gly Lys Asp Phe Ile Ala Asn Thr Asn Gly Cys Tyr Ile Lys Tyr Glu
50 55 60

<210> 870
<211> 127
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 870
Met Ser Arg Thr Ile Arg Arg Lys Gly Trp His Val Val Lys Ser Ser
1 5 10 15

Lys Trp Asn Asp Gln Asn Asn Asn Glu Phe Ala Tyr Ile Lys Ser Tyr
20 25 30

Asn Glu Tyr Val Lys Thr Gln Lys Asp Lys Glu Asn Gln Gln Lys Tyr
35 40 45

Val Glu Leu Arg Ile Ser Glu Asn Ser Glu Arg Pro Leu Glu Ala Lys
50 55 60

Lys Leu Ile Ala Lys Ser Lys Arg Asp Gly Phe Trp Lys Thr Leu Arg
65 70 75 80

Trp Thr Arg Tyr Ala Met Pro Val Pro Arg Leu Phe His Lys Ala Glu
85 90 95

Ile Lys Arg Ala Leu Lys Tyr Asp Glu Glu Tyr Asn Trp Asp Glu Ala
100 105 110

Gly Ala Arg Thr Ile Glu Gln Gly Ile Cys Glu Trp Leu Trp Asp
        115   120   125

<210> 871
<211> 70
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 871
Met Gln His Leu Ser Glu Lys Gln Leu Arg Asn Leu Thr Val Glu Gln
1   5   10   15

Leu Asp Glu Leu Arg Arg Glu Ile Gly His Gly Ile Ser His Leu Gln
            20   25   30

Glu Glu Ile Arg Gln His Ser Ser Lys Ala Asp Tyr Thr Arg Lys Arg
        35   40   45

Thr Leu Glu Lys Tyr Leu Lys Glu Val Lys Ala Val Leu Gln His Lys
    50   55   60

Arg Asn Thr Gly Gln Lys
65   70

<210> 872
<211> 95
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 872
Met Ala Phe Asn His Ile Cys Leu Ala Leu Val Leu Gly Cys Gly Ile
1   5   10   15

Ser Phe Pro Ala Ala Ser His Asp Asp Ile Ser Asp Tyr Asn Ser Tyr
            20   25   30

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

Gln Glu Ser Glu Gln Phe Tyr Ala Phe Val Gln Ser Lys Trp Lys Ser
    50   55   60

Glu Ser Cys Ser Lys Asp Cys Asp Ser Leu Gly Arg Ser Ala Gly Glu
65   70   75   80

Glu Tyr Ala Asn Arg Met Arg Ile Gln Phe Asp Asn Glu Val Gln
                85   90   95

<210> 873

<211> 128
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 873
Met Lys Phe Asn Asp Phe Val Lys Asp Gly Lys Leu Thr Pro Gln Asp
1   5   10   15

Glu Phe Ile Gly Leu Leu Met Val Ser Gln Ala Tyr Phe His Ser Ala
            20   25   30

His Phe Asp Thr Lys Ser Tyr Ala Arg His Lys Ala Tyr Glu Val Phe
        35   40   45

Phe Asn Glu Ile Pro Asp Leu Ile Asp Ala Phe Gly Glu Gln Trp Leu
    50   55   60

Gly Phe Ser Gly Lys Ser Tyr Thr Pro Ala Leu Pro Ser Gln Lys Glu
65   70   75   80

Leu Pro Lys Asp Thr Ile Glu Met Leu Asp Phe Ile Leu Ala Lys Ala
                85   90   95

Asp Gly Ile Tyr Lys Ser Val Pro Ala Ala Leu Gln Ser Val Leu Asp
            100   105   110

Asp Ile Thr Gly Leu Cys Tyr Lys Thr Lys Tyr Leu Leu Ser Leu Gln
        115   120   125

<210> 874
<211> 162
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 874
Met Ile Lys Leu Thr Thr Glu Leu Gln Pro Gly Lys Ile Phe Tyr His
1   5   10   15

Val Cys Gly Val Asn Arg Thr Glu Thr Lys Pro Gly Glu Ile Thr Arg
            20   25   30

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

Val Tyr Ser Arg Lys Ser Pro Phe Phe Gln Val Ile Cys Glu Tyr Glu
    50   55   60

Asn Tyr Ala Gly Gln Thr Glu Ser Tyr Ser Thr Glu Arg Ser Ala His
65   70   75   80

Asp Met Gly Ile Phe Lys Pro Gly Glu Lys Arg Ser Val His Asn Leu
85 90 95

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

Leu Gln Glu Asn Lys Phe Ser Asp Pro Asp Asp Gln Ala Tyr Ala Asp
115 120 125

Arg Leu Thr Pro Ser Glu Asp Phe Arg Arg Gln Gln Glu Phe Met Asp
130 135 140

Ser Tyr Leu Asp Ser Cys Asp Tyr Asp Tyr Tyr Asp Phe Asp Asp Gly
145 150 155 160

Glu Glu

<210> 875
<211> 88
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 875
Met Asn Gly Trp Gly Pro Ser Asp Asp Gly Phe Ala Thr Arg Glu Ala
1 5 10 15

Thr Ile Ala Asp Gly Ile Glu Trp Ala Arg Leu Gln Lys Gln Leu Gln
20 25 30

Glu Gln Arg Glu Ser Glu Glu Phe Cys Val Asp Cys Asp Glu Glu Ile
35 40 45

Pro Val Ala Arg Arg Leu Leu Val Lys Gly Cys Gln Arg Cys Val Glu
50 55 60

Cys Gln Gly Lys Trp Asp Thr Val Met Thr Ser Ala Tyr Asn Arg Arg
65 70 75 80

Gly Ser Lys Asp Ser Gln Leu Arg
85

<210> 876
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 876
Met Glu Ser Ile Leu Asp Ser Thr Asn Leu Asp Asn Pro Tyr Ser Asp

1 5 10 15

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

Val Val Leu Lys Gln Gly Asn Asp Ile Ile His Leu Asp Thr Lys Gln
35 40 45

Ile Asp Ser Leu Ile Gln Phe Leu Ile Glu Ala Lys Asp Gly Glu
50 55 60

<210> 877
<211> 77
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 877
Met Ala Ser Lys Leu Val Trp Asp Gly Lys Pro Arg Lys Gly Asp Ala
1 5 10 15

Val Ile Glu Asp Glu Ser Pro His Val Ile Asp Leu Tyr Leu Thr Val
20 25 30

Phe His Thr Tyr Glu His Asn Thr Ile Ile Glu Ile Glu Arg Asp Gly
35 40 45

Asp Cys Val Ala Ile Asp Lys Ser Asp Ala Ile Glu Leu Val Lys Tyr
50 55 60

Leu Thr Ala Met Ile Pro Thr Met Lys Gln Asp Asn Leu
65 70 75

<210> 878
<211> 166
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 878
Met Asn Ile Asn Lys Asn Ser Trp His Phe Lys Met Asn Leu Trp Phe
1 5 10 15

Lys Ser Gly Asn Ile Trp Lys Met Pro Lys Thr Leu Cys Gly Tyr Phe
20 25 30

Trp Thr Thr Val Leu His Ile Leu Phe Ser Ser Ala Ile Ala Ile Phe
35 40 45

Ile Gly Ser Val Ala Trp Met Phe Gly Trp Pro Leu Ile Ala Gln Thr
50 55 60

Gly Ile Leu Ala Trp Ile Gly Val Ser Leu Ser Ala Phe Trp Leu Asn
65 70 75 80

Val Val Ala Val Pro Val Gly Ala Val Phe Ile Ala Thr Phe Val Leu
85 90 95

Ala Phe Val Ala Ile Val Phe Gly Phe Ile Phe Gly Leu Glu Lys Phe
100 105 110

Lys Glu Tyr Arg Lys Asn Lys Gln Phe Thr Lys Lys Leu Ala Arg Val
115 120 125

Lys Ala Gly Leu Pro Ala Glu Ser Glu Pro Leu Val Phe Ile Gln Tyr
130 135 140

Leu Lys Ala Arg Lys Arg Lys Val Cys Pro Met Ile Asp Tyr Val Glu
145 150 155 160

Gly Lys Thr Ser Glu Glu
165

<210> 879
<211> 74
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 879
Val Lys Asn Asp Gln Val Tyr Ile Val Asn Gly Arg Lys Ala Val Phe
1 5 10 15

Arg Ala Lys Thr Glu Arg Gly Ile Ile Ser Thr Tyr Pro Ile Ala Glu
20 25 30

Phe Thr Phe Glu Asp Gly Glu Gln Ile Lys Ile Lys Tyr Val Pro Leu
35 40 45

Ser Gln Thr Tyr Arg Phe Ile Gly Gly Glu Ile Asp Leu Asp Ile Tyr
50 55 60

Tyr Glu Gly Gly Val Trp Lys Leu Lys Ser
65 70

<210> 880
<211> 140
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 880
Met Glu Ile Glu Ile Val Thr Thr Lys Lys Lys Leu Ser Met Ser Leu

1 5 10 15

Leu Lys Gln Met Lys Met Ala Ser Ser Ser Glu Ile Lys Phe Ala Met
20 25 30

Phe Asp Arg Val His Arg Val Leu Gly Tyr Val Asn Ala Phe Lys Trp
35 40 45

Asn Lys Met Asp Ile Gln Val Ala Ile Ile Asn Thr Gly Asn Asp Trp
50 55 60

Ala Leu Val Pro Met Tyr Asp Thr His Val Ile Lys Thr Ala Arg Arg
65 70 75 80

Glu Pro His Pro Asp Gly Gln Glu Tyr His Phe His Asp Val Val Tyr
85 90 95

Tyr His Thr Met Gln Lys Ile Gly Asn Val His Arg Asn Ser Lys Lys
100 105 110

Ser Thr Asp Lys Glu His Val Glu Ala Cys Ala Lys Ala Ser Asn Asp
115 120 125

Leu Ile Lys Phe Ala Lys Gly Asn His Ile Tyr Leu
130 135 140

<210> 881
<211> 336
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 881
Met Lys Thr Ile Val Lys Ser Tyr Phe Gly Ser His Leu Tyr Gly Thr
1 5 10 15

Ser Thr Pro Glu Ser Asp Val Asp Phe Lys Glu Ile Phe Val Pro His
20 25 30

Pro Arg Asp Ile Leu Met Cys Gln Ala Met Asn His Thr Asn Cys Asn
35 40 45

Thr Asn Asn Ser Ala Thr Lys Asn Thr Lys Asp Asp Val Asp His Glu
50 55 60

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

Val Ala Leu Asp Met Leu His Thr Pro Pro Glu Leu Val Val Ala Ser
85 90 95

```
Asp Leu Pro Glu Val Trp Lys Phe Ile Gln Asp Asn Arg Ala Arg Phe
            100                 105                 110

Tyr Thr Thr Asp Met Lys Ala Tyr Leu Gly Tyr Val Arg Lys Gln Ala
        115                 120                 125

Gly Lys Tyr Gly Val Lys Gly Ser Arg Leu Ala Asp Leu His Lys Val
    130                 135                 140

Leu Asp Val Ile Arg Asp Val Pro Glu Trp Lys Tyr Asp Asp Arg Pro
145                 150                 155                 160

Gln Gln Lys Gly Ile Asn Glu Arg Trp Lys Val Gln Asp Ile Ala Glu
                165                 170                 175

Lys Leu Pro Leu Gly Glu Phe Leu Glu Trp Thr Thr Phe Val Asp His
            180                 185                 190

Lys Ser Gly Glu Gln Lys Phe Tyr Asn Val Leu Gly Arg Lys Phe Gln
        195                 200                 205

Thr Thr Ile Thr Ile Lys Glu Met Lys Tyr Ser Leu Glu Lys Leu Asp
    210                 215                 220

Ala Glu Tyr Gly Glu Arg Ala Arg Lys Ala Glu Ala Asn Glu Gly Val
225                 230                 235                 240

Asp Trp Lys Ala Leu Ser His Ala Leu Arg Ala Gly Leu Gln Leu Gln
                245                 250                 255

Glu Ile Tyr Met Thr Gly Asp Leu Gln Phe Pro Leu Thr His Ala Lys
            260                 265                 270

Met Val Lys Met Val Lys Ala Gly Glu Leu Pro Phe Lys Glu Val Gln
        275                 280                 285

Glu Leu Leu Glu Ser Val Val Asp Glu Val Glu Ile Leu Ala His Thr
    290                 295                 300

Ala Glu Lys Asn Gly Met Pro Lys Lys Val Asp Met Lys Phe Trp Asp
305                 310                 315                 320

Asp Phe Val Glu Lys Val Tyr Leu Glu Asn His Asn Ser Tyr Tyr Lys
                325                 330                 335

<210> 882
<211> 62
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08
```

<400> 882
Met Lys Val Phe Leu Asn Tyr Gly Arg Pro His Lys Gly Arg Arg Trp
1 5 10 15

Tyr Leu Glu Ala Val Cys Arg Glu Thr Gly Arg Arg Glu Asn Ala Lys
20 25 30

Phe Ser Ala Arg Pro Thr Arg Lys Gln Ile His Gln Phe Met Ser Trp
35 40 45

Ala Gly Glu Thr Leu Arg Phe Ser Leu Tyr Trp Ala Glu Ile
50 55 60

<210> 883
<211> 79
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 883
Met Ile Leu Leu Trp Ser Val Val Val Pro Ile Val Val Ala Ile Ile
1 5 10 15

Tyr Phe Ile Val Gly Trp Ser Val Cys Lys His Leu Ile Lys Asn Gly
20 25 30

Thr Ile Glu Lys Val Gly Glu Tyr Trp Phe Tyr Leu Ile Phe Trp Phe
35 40 45

Pro Ala Phe Ile Val Gly Ala Ile Ile Met Phe Phe Arg Trp Ala Gly
50 55 60

Lys Leu Pro Lys Arg Ile Ala Glu Asn Ala Ile Asn Lys His Ala
65 70 75

<210> 884
<211> 71
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 884
Met Lys Thr Leu Glu Ile Val Val Asn Asn Ile Asp Lys Ala Phe Lys
1 5 10 15

Ala Ala Glu Ala His Gly Val Glu Phe Glu Pro Met Met Val Gly Glu
20 25 30

Ala Phe Ser Lys Leu Ala Ile Ile Arg Gly Glu Thr Asp Asn Leu Ile
35 40 45

Asp Phe Val Asp Asp Phe Tyr Leu Gly Ser Lys Val Arg Pro Tyr Tyr

50 55 60

Ile Asn Glu Ile Leu Glu Lys
65 70

<210> 885
<211> 325
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 885
Met Ser Thr Ile Thr Ile Lys Lys Gly Ile Tyr Phe Gly Lys Glu Ile
1 5 10 15

Ser Gly Thr Tyr Glu Leu Leu Gly Glu Trp Phe Pro Asp Ser Leu Ser
20 25 30

Ala Glu Asp Ser Arg Gln Gly Asp Gly Lys Val Phe Val Glu Leu Asn
35 40 45

Gly Lys Lys Arg Gly Val Trp Val Phe Lys Asp Asp Ile Thr Ile Asp
50 55 60

Gly Val Ala Ala Lys Ile Glu Val Val Glu Ser Val Asp Glu Met Lys
65 70 75 80

Glu Arg Ile Lys Lys Arg Phe Asn Val Met Gly Leu Met Thr Asn Gly
85 90 95

Leu Ile His Gly Asn Ile Arg Ser Leu Ile Ile Ser Gly Ala Ala Gly
100 105 110

Ile Gly Lys Thr Tyr Ser Leu Asp Lys Ala Leu Gln His Ala His Asp
115 120 125

Thr Asn Ala Ile Asp Tyr Lys Ser Val Asn Gly Lys Ile Ser Gly Ile
130 135 140

Gly Leu Tyr Cys Arg Leu Trp Glu Ser Arg Glu Ala Asn Ser Val Leu
145 150 155 160

Leu Ile Asp Asp Val Asp Val Phe Ser Asp Met Asp Ile Leu Asn Leu
165 170 175

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

Thr Ala Ser Ser Phe Leu Glu Asp Lys Gly Ile Pro Asn Glu Phe Glu
195 200 205

Phe Glu Gly Thr Val Val Phe Ile Thr Asn Val Asp Ile Asp Arg Glu
    210   215   220

Leu Glu Arg Gly Ser Lys Leu Ala Pro His Leu Gln Ala Leu Val Ser
225   230   235   240

Arg Ser Val Tyr Leu Asp Leu Gly Val His Thr Asn Glu Glu Ile Met
                245   250   255

Val Arg Val Gln Asp Val Ile Met Thr Thr Ser Met Leu Gln Asn Arg
            260   265   270

Gly Leu Arg Asn Ser Glu Val Ile Glu Val Leu Glu Phe Met Lys Asp
        275   280   285

Asn Val Asn Arg Leu Arg Asn Val Ser Leu Arg Thr Ala Leu Tyr Ile
    290   295   300

Gly Asp Phe Val Ala Thr Asp Arg Lys Asn Trp Arg Thr Ile Ala Glu
305   310   315   320

Val Thr Met Leu Lys
                325

<210> 886
<211> 48
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 886
Met Ala Thr Leu Ile Ser Asn Asp Val Lys Arg Val Leu Phe Lys Gly
1   5   10   15

Gly Met Tyr Ile Val Asp Thr Pro Lys Gly Asp Thr Ser Ser Trp Thr
            20   25   30

Ile Asn Glu Trp Ile Asn Tyr Ile Asp Glu Asn Gly Ala Trp Val Gln
        35   40   45

<210> 887
<211> 141
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 887
Met Ser Leu Ala Ala Ile Lys Asp Ile Glu Cys Trp Leu Asn Asp Ile
1   5   10   15

Lys Val Tyr Pro Pro Gly His Ile Phe Ala Gly Lys Pro Lys Gly Lys
            20   25   30

Ala Glu Lys Ala Cys Glu Ala Ile Cys Glu Lys Leu Tyr Lys Phe Asn
        35   40   45

Phe Gly Asp Lys Lys Asn Val Leu Ala Glu Val His Ser Ser Tyr His
    50   55   60

Glu Leu Arg Val Met Val Asn Val Phe Arg Ala Pro Pro Phe Ile Glu
65   70   75   80

Leu Arg Lys Glu Tyr Ala Asn Lys Val Phe Asp Thr Phe Leu Ala Asn
                85   90   95

Val Gln Asp Ala Val Lys His Leu Asp Glu Met His Lys Gln His Gln
            100   105   110

Asp Leu Asn Ala Tyr Tyr Lys Pro Trp Arg Lys Ser Tyr Gln Glu Leu
        115   120   125

Lys Asn Arg Ile Glu Leu Ile Arg Tyr Glu Val Leu Lys
    130   135   140

<210> 888
<211> 112
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 888
Met Lys Asn Trp Val Met Thr Glu Ser Glu Ala Tyr Ala Ala Tyr Val
1   5   10   15

Ser Pro Asp Asp Arg Arg Ser Glu Leu Phe Gly Tyr Tyr Gly Ser Tyr
            20   25   30

Cys Val Ala Glu Glu Ala Val Lys Gly Gln Ser Trp Trp Gly Ser Asp
        35   40   45

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

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

Glu Glu Thr Pro Glu Ala Lys Arg Lys Arg Leu Glu Lys Ile Lys Glu
                85   90   95

Ser Ala Leu Ala Lys Leu Asn Pro Asp Glu Arg Glu Ala Leu Gly Leu
            100   105   110

<210> 889

<211> 106
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 889
Met Ser Lys Glu Phe Ser Thr Thr Arg Met Val Asp Ala Phe Gly Tyr
1   5   10   15

Pro Cys Asn Gly Tyr Arg Glu Phe Ile His Pro Glu Val Glu Asn Gln
            20   25   30

Phe Lys Glu Val Val Arg Asn Ile Leu Leu Asn Ala Phe Lys Thr Gln
        35   40   45

Gly Thr Asn Pro Arg Asp Leu Gly Ile Tyr Leu Glu Glu Ala Ile Arg
    50   55   60

Asp Val Gln Lys Ser Val Ser Ala Lys Leu His Trp Ala Glu Glu Asn
65   70   75   80

Ile Ala Trp Ser Asn Lys Lys Arg Ser Asp Leu Asn Trp Pro Ala Asp
                85   90   95

Arg Glu Gln Ile Val Asn Tyr Ala Lys Gly
            100   105

<210> 890
<211> 96
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 890
Met Phe Asn Thr Ile Val Ser Ile His Ala Tyr Tyr Glu Gly Gln Leu
1   5   10   15

Asn Ala Ala Arg Thr Lys Tyr Lys Arg Gly Met Glu Glu Ser Val Glu
            20   25   30

Cys Leu Lys Asp Ile Gln Thr Phe Ala Gln Lys Thr Gln Asn Leu Ile
        35   40   45

Leu Met Asp Arg Lys Gln Val Ser Leu Ala Glu Glu Leu Lys Ala Ser
    50   55   60

Lys Met Ile Ile Glu Asp Asn Arg Lys His Gln Leu Lys Leu Leu Lys
65   70   75   80

Arg Arg Gln His Gln Ser Pro Trp Phe Asn Ser Asp Phe Arg Ser Phe
                85   90   95

<210> 891
<211> 54
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 891
Met Lys Ala Pro Thr Trp Asn Glu Leu Gln Glu Met Phe Asn Thr Glu
1 5 10 15

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

Pro Ser Glu Asp Asn Leu Leu Cys Leu Ala Gln Phe Ile Ile Glu Thr
        35 40 45

Tyr Ile Glu Asn Gln Lys
    50

<210> 892
<211> 88
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 892
Met Thr Val Tyr Val Asp Val Leu Met Asn His Gly Trp Lys Met Arg
1 5 10 15

Gly His Gln Val Lys Asn Cys His Met Phe Ser Asp Asn Leu Asp Glu
            20 25 30

Leu His Ala Met Ala Glu Ala Ile Gly Met Lys Arg Ser Trp Phe Gln
        35 40 45

Asp Lys Arg Val Pro His Tyr Asp Leu Arg Asp Val Arg Arg Lys Gln
    50 55 60

Ala Val Ala Leu Gly Ala Val Glu Val Ser Arg Arg Asp Ala Val Leu
65 70 75 80

Leu Trp Arg Lys Phe Phe Thr Lys
                85

<210> 893
<211> 262
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 893

```
Met Lys Thr Leu Thr Glu Ile Ile Ser Ala Leu Val Glu Glu Asn Arg
1               5                  10                  15

Val Ala Arg Gln Ala His Arg Ala Lys Val Glu Lys Arg Ala Glu Glu
            20                  25                  30

Leu Asn Ala Gly Trp Ala Lys Thr Arg Phe Gly Arg Glu Tyr Phe Asp
        35                  40                  45

Lys Val Val Ala Pro Thr Trp Gly Lys Asp Asp Arg Pro His Ala Pro
    50                  55                  60

Phe Asp Gly Tyr Leu Trp Glu Asn Glu Leu Gly Glu Val Glu Ala Tyr
65                  70                  75                  80

His Ala Gly Ser Tyr Leu Pro Tyr Val Thr Glu Leu Asp Ser Leu Asp
                85                  90                  95

Lys Pro Glu Tyr Thr Gly Asp His Gly Trp Trp Lys Ile Arg Leu Thr
            100                 105                 110

Gln Glu Glu Tyr Lys Glu Leu Arg Glu Tyr Gly Tyr Pro Leu Glu Val
        115                 120                 125

Arg Ile Pro Tyr Lys Glu Trp Lys Leu Gln Asp Gly Thr Asn Val Val
    130                 135                 140

Met Ala Glu Val Arg Ala His Lys Ser Ile Leu Glu Ala Ile Gln Glu
145                 150                 155                 160

His Ser Lys Glu Val Phe Asp Asn Ile Phe Asn Glu Leu Asn Lys Asn
                165                 170                 175

Lys Gly Asp Ala Pro Glu Gly Arg Val Thr Val Ser Gly Thr Val Thr
            180                 185                 190

Ser Val Lys Val Tyr Glu Asp Tyr Tyr Gly Val Gln Cys Lys Met Met
        195                 200                 205

Val Val Leu Glu Asn Gly Ala Thr Val Tyr Gly Ser Leu Pro Lys Ser
    210                 215                 220

Ile Pro Phe Glu Tyr Arg Gly Lys Val Gln Phe Thr Ala Thr Phe Glu
225                 230                 235                 240

Leu Ala Lys Asp Asp Lys Thr His Ala Phe Tyr Lys Arg Pro Ser Lys
                245                 250                 255

Val Ile Met Leu Asp Glu
            260
```

<210> 894
<211> 324
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 894
Met Asn Lys Asn Glu Leu Lys Met Phe Val Glu Ala Glu Phe Asn Lys
1   5   10   15

Leu Lys Asp Lys Thr Leu Thr Lys Arg Glu Lys His Val Lys Val Leu
            20   25   30

Ser Ala Leu His Asp Leu Asn Pro Arg Ala Tyr Asp Val Ala Ile Ala
        35   40   45

Gly Asn Val Ala Arg Arg Val Leu Asn Ser Met Ala Ser His Glu Ala
    50   55   60

Asn Tyr Ala Gly Phe Val Val Glu Asn Ile Arg Arg Ser Arg Trp Leu
65   70   75   80

Gly Ala Met Ser Ala Glu Lys Gln Leu Lys Lys Phe Ala Ile Gly Asn
                85   90   95

Ala Lys Ile Tyr Gly Gln Arg Tyr Ser Phe Ala Ala Gly Ala Phe Lys
            100   105   110

Thr Glu Glu Arg His Asp Arg Ser Ala Ala Gln Ile Phe Cys Ser Glu
        115   120   125

Phe Asn Ala Asn Leu Arg Arg Ile Leu Asn Arg Ser Ile Cys Leu Leu
    130   135   140

Lys Gly Asp Asp Arg Val Lys Tyr Gln Ala Ser Ser Thr Ser Ser Arg
145   150   155   160

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

Thr Val Arg Ile His Ile Asn Ser His Leu Ser Ser Gly Lys Tyr Pro
            180   185   190

Ala Arg Ala Leu Leu Ala Gln Val Arg Thr Ala Leu Asp His Met Asp
        195   200   205

Val Val Lys Lys Ser Cys Cys Lys Gln Gln Gly Glu Asn Ser Ser Val
    210   215   220

Leu Glu Val His Leu Asp Pro Phe Lys Ile Phe Pro Lys Thr Leu Ser
225   230   235   240

```
Thr Thr Pro Val Ile Asp Glu Asp Val Ala His Met Tyr Leu Asn Val
                245                 250                 255


Val Lys Pro Leu Pro Leu Thr Pro Val Asn His Ile Glu Ile Ala Lys
            260                 265                 270


Asn Ser Ile Thr Ala Glu Met Glu Ser Val Lys Arg Phe Ile Asp Thr
        275                 280                 285


Lys Glu Ala Glu Leu Ala Lys His Glu Leu Thr Met Ala Asp Leu Val
    290                 295                 300


Lys Ser Leu Asn Glu Tyr Lys Glu Arg Tyr Glu Ser Leu Glu Tyr Ala
305                 310                 315                 320


Arg Ser Leu Leu
```

<210> 895
<211> 86
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 895

```
Val Lys Asn Gln Leu Lys Glu Asp Met Val Val Asp Asp Asn Asp Leu
1               5                   10                  15


Glu Ile Glu Phe Glu Tyr Pro Pro Val Pro Glu Phe Lys Ile Asp Trp
            20                  25                  30


Asp Ala Cys Leu Glu Met Val Asp Arg Arg Glu Ala Ala Ala Lys Gln
        35                  40                  45


Val Val Pro Cys Glu Lys Cys Gly Ser Ile Gln Val Gln Leu Val Asp
    50                  55                  60


Trp Thr Thr Asp Ile Leu Lys Met Lys Cys Arg Thr Cys Lys His Arg
65                  70                  75                  80


Phe Glu Arg Lys Leu Lys
                85
```

<210> 896
<211> 104
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 896

```
Met Ile Thr Lys Thr Ile Thr Gly Ala Asn Thr Lys Phe Phe Val Glu
```

1 5 10 15

Tyr Ala Asn Asn Leu Ile Lys Asp Lys Asn Phe Asp Asn Ile Ile Ala
20 25 30

Asp Met Ile Leu Asp Ala Tyr Glu Ser Gly Ile Asp Pro Met Gln Leu
35 40 45

Lys Glu Tyr Leu Arg Ala Thr Met Asp Phe Thr Val Leu Asn Met Met
50 55 60

Leu Arg Thr Asp Thr Glu Phe Asn Glu Met Ile Ala Arg Arg Asn Glu
65 70 75 80

Gly Lys Phe Asn Leu Thr Asp Asp Glu Val Leu Ala Cys Ala Ala His
85 90 95

Glu Ala Trp Lys Lys Val Ile Lys
100

<210> 897
<211> 111
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 897
Met Lys Thr Thr Gly Ala Leu Trp Lys Glu Phe Tyr Asn Asp Glu Ala
1 5 10 15

Phe Trp Glu Gly Tyr Tyr His Asp Asp Thr Leu Ile Leu Phe Asp Asp
20 25 30

Val Glu Val Glu Glu Tyr Glu Asp Pro Ser Pro Asp Ala Val Val Lys
35 40 45

Ile Glu Ser Gly Tyr Val Tyr Lys Thr Asp Asp Asp Ser Phe Thr Ser
50 55 60

His Asp Leu Ser Leu Glu Thr Phe Phe Lys Arg Trp Lys Lys Lys Gln
65 70 75 80

Thr Thr Arg Thr Met Val Val Thr Val Asp Lys Asp Asp Phe Ala Lys
85 90 95

Val Phe Glu Thr Ile Ser Asn Ile Pro Gly Val Lys Lys Val Lys
100 105 110

<210> 898
<211> 170
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 898
Met Ile Asp Ile Lys Leu Asp Thr Tyr Ala Val Arg Gln Leu Phe Pro
1   5   10   15

Glu Gly Thr Ala Ala Arg Ala Gln Leu Gln Gln Ser Val Ile Asn Asn
            20   25   30

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

Ala Val Gln Ser Glu Val Asn Ile Ala Ala Val Thr Ile Pro Asp Val
    50   55   60

Arg Ala Glu Val Lys Lys Gln Val Gln Gln Met Phe His Thr Arg Gly
65   70   75   80

Trp Asn Asp Met Ser Ala Lys Glu Glu Met Ser Gln Met Met Arg Asn
                85   90   95

Ala Ala Gln Ser Cys Ala Lys Asn Ala Ile Asp Asp Met Val Arg Gln
            100   105   110

Thr Ile Asp Asp Ala Val Lys Gln Ala Glu Gly Arg Ile Lys Met Ser
        115   120   125

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

Asn Lys Asn Phe Ala Asp Gln Ile Asn Ala Ala Ile Ala Ala Lys Leu
145   150   155   160

Ala Glu His Phe Pro Val Thr Ala Asn Gly
                165   170

<210> 899
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 899
Met Asp Lys Ile Asp Phe Ser Lys Leu Asn Ile Pro Arg Met Gly Ile
1   5   10   15

Pro Asp Asp Ile Ala Lys Gln Leu Ala Ser Val Gln Pro Met Pro Asp
            20   25   30

Asn Cys Ile Lys Asp Ile Phe Asp Ala Leu Asp Gly Lys Thr Leu Val
        35   40   45

Ile Thr Thr Lys Ala Glu Asn Gly Ser
50 55

<210> 900
<211> 96
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 900
Met Ala Arg Lys Arg Tyr Met Glu Glu Ala Glu Arg Val Met Leu Leu
1 5 10 15

Met Tyr Ser Val Tyr Tyr Asn Glu Thr Gly Gln Ile Val Asp Ser Ser
20 25 30

Lys Leu Lys Gly Ala Met Thr Arg Gly Arg Gly Phe Ala Gln Ala Ala
35 40 45

Ile Asp Lys Glu Ile Ile Ser Arg Leu Gly Ile Lys Tyr Ser Ser Lys
50 55 60

Met Tyr Leu His Pro Gly Trp Asn Gln Val Gln Ala Gln Val Phe Lys
65 70 75 80

Glu Ile Glu Glu Asp Val His Ser Phe Trp Leu Arg Gln Gln His Pro
85 90 95

<210> 901
<211> 89
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 901
Met Phe Thr Val Phe Gly Tyr Asp Ser Asn Ile His Lys Cys Val Phe
1 5 10 15

Cys Asp Asn Ala Lys Arg Leu Leu Asp Val Lys Lys Gln Glu Tyr Ala
20 25 30

Phe Ile Asn Val Met Pro Glu Lys Gly Val Phe Asp Glu Val Val Ile
35 40 45

Ser Asp Leu Leu Arg Arg Leu Gly Arg Glu Ser Gln Val Gly Leu Thr
50 55 60

Met Pro Gln Ile Phe Ala Pro Asp Gly Thr His Ile Gly Gly Phe Asp
65 70 75 80

Glu Leu Arg Lys Phe Lys Phe Asn Ala
85

<210> 902
<211> 62
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 902
Met His Asp Tyr Arg Gly Thr Leu Leu Arg Glu Gly Asp Ile Val Ala
1 5 10 15

Leu Tyr Tyr Gly Tyr Gly Gly Leu Glu Thr Gly Glu Ile Lys Gln Ile
20 25 30

Lys Asn His Arg Ala Lys Val Glu Val Thr Tyr Ser Asn Gly Val Lys
35 40 45

Val Met Ser Lys Trp Lys Tyr Gly Glu Cys Met Val Lys Leu
50 55 60

<210> 903
<211> 56
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 903
Met Ser Tyr Asp Ile Gly Asp Leu Lys Ala Pro Cys Thr Val Thr Ile
1 5 10 15

Ser Ala Glu Glu Phe Ile Arg Leu Gln Ala Ile Glu Glu Leu Leu Trp
20 25 30

Glu Ile Glu Cys Ala Leu Pro Ser Gly Leu Glu Ser Trp Ile Asp Asp
35 40 45

Glu Asp Leu Gln Lys Leu Arg Gly
50 55

<210> 904
<211> 129
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 904
Met Thr Asn Ala Glu Leu Val Lys Glu Ile Lys His Ile Ala Gly Val
1 5 10 15

Thr Gly Glu Trp Asp Asp Asn Tyr Asp Phe Glu Tyr Pro Pro Asn Ala

20 25 30

Pro Asp Asp Asp Ala Glu Glu Ile Phe Val Leu Val Glu Asp Asp Glu
35 40 45

Trp Thr Gln Asp His Lys Tyr Gln Ser Arg Ser Gln Ile Trp Tyr Tyr
50 55 60

Pro Ala Arg Gly Val His Phe Met Val Ser Glu Ser Arg Ser Gly Ser
65 70 75 80

Tyr His Thr Asp Trp Tyr Tyr Asn Pro Pro Glu Val Asp Ile Val Thr
85 90 95

Arg His Glu Lys Val Val Thr Arg Thr Glu Val Glu Trp Arg Ile Glu
100 105 110

Tyr Asp Ser Val Asn Asp Ser Ala Pro Ala Pro Cys Lys Ala Ala Lys
115 120 125

Ala

<210> 905
<211> 52
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 905
Met Gln Ser Ser Lys Gly Ile Lys Pro Trp Tyr Thr Ala Arg Trp Glu
1 5 10 15

Thr Val Glu Pro Glu Glu Asp Ala Ile Pro Glu Glu Asp Tyr Asn Thr
20 25 30

Ser Glu Pro Thr Ile Asn Glu Leu Leu Asp Tyr Glu Asp Lys Val Asn
35 40 45

Gly Thr Tyr Trp
50

<210> 906
<211> 150
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 906
Met Glu Leu Ile Gly Lys Gln Phe Glu Val Ile Glu Asn Asp Asp Glu
1 5 10 15

```
Leu Thr Glu Gln Phe Pro Gln Phe Val Pro Gly Phe Lys Phe Gln Val
            20                  25                  30

Ile Asn Ala Val Asn Glu Asp Asp Leu Glu Thr Cys Gly Ile Thr Ala
        35                  40                  45

Val Ile Asp Leu Leu Thr Asn Lys Ile Ile Thr Ile Asn Asp Pro Thr
    50                  55                  60

Pro Phe Gly Glu Ser Trp Phe Trp Cys Phe Tyr Ser Glu Asp Thr Met
65                  70                  75                  80

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

Glu Ile Lys Leu Asp His Phe His Gly Lys Ile Val Pro Ile Thr Lys
            100                 105                 110

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

Asp Leu Met Gln Lys Ala Ala Asp Tyr Ile Val Ala Leu Glu Thr Arg
    130                 135                 140

Leu Gly Val Gln Tyr Val
145                 150
```

<210> 907
<211> 102
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 907

```
Met Ser Lys Ser Cys Val Thr Lys Thr Ile Thr Val Lys Ile Leu Asp
1               5                   10                  15

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

Tyr Lys Ile Gly Asp Ile Ile Lys Phe Ser Asn Gly Tyr Tyr Asp Asp
        35                  40                  45

Asp Ile Gly Gly Met Ala Trp Pro Lys Met Ser Ile Ile His Lys Glu
    50                  55                  60

Thr Asn Ser Tyr Ile Glu Phe Asn Ala Asp Asp Tyr Glu Gly Ile Tyr
65                  70                  75                  80

Ala Phe Cys Thr Ser Phe Cys Ile Lys Glu Ser Asn His Asn Ile Tyr
                85                  90                  95
```

Ser Ser Tyr Ser Leu Ile
100

<210> 908
<211> 157
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 908
Met Leu Leu Thr Gly Lys Leu Tyr Lys Glu Glu Lys Glu Lys Leu Tyr
1 5 10 15

Gln Ala Gln Asn Gly Leu Cys Pro Cys Cys Lys Arg Pro Leu Asp Glu
20 25 30

Asp Ile Gln Lys Asn His Leu Asp His Asp His Ala Leu Glu Gly Asp
35 40 45

Asn Ala Gly Lys Val Arg Gly Leu Leu Cys Asn Leu Cys Asn Ala Ala
50 55 60

Glu Gly Gln Met Lys His Lys Phe Asn Arg Ser Gly Leu Lys Gly Gln
65 70 75 80

Asp Ile Asp Tyr Leu Glu Trp Leu Glu Asn Leu Leu Val Tyr Leu Arg
85 90 95

Gln Asn Arg Lys Asp Ser Asn Ile His Pro Gln Tyr Val Ala Asp Met
100 105 110

Ala Lys Arg Phe Ser Arg Leu Gly Lys Pro Glu Met Ile Ala Glu Met
115 120 125

Glu Leu His Gly Phe Thr Tyr Glu Glu Ser Asp Gly Lys Ser Gln Leu
130 135 140

Ala Ser Lys Tyr Lys Lys Gln Leu Arg Lys Ser Leu Lys
145 150 155

<210> 909
<211> 612
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 909
Met Asn Ile Glu Leu Glu Ile Gln Gly Leu Ile Asn Lys Thr Asn Lys
1 5 10 15

```
Asp Leu Leu Asn Glu Asn Ala Asn Lys Asp Ser Arg Val Phe Pro Thr
            20                  25                  30

Gln Arg Asp Leu Met Ala Gly Ile Val Ser Lys His Ile Ala Asn Gln
        35                  40                  45

Val Ile Pro Phe Ser Val Met Glu Ala His Lys Glu Gly Val Ile His
    50                  55                  60

Phe His Asp Met Asp Tyr Ser Pro Ala Leu Pro Phe Thr Asn Cys Cys
65                  70                  75                  80

Leu Val Asp Leu Lys Gly Met Leu Gln Asn Gly Phe Lys Leu Gly Asn
                85                  90                  95

Ala Gln Ile Glu Thr Pro Lys Ser Ile Gly Val Ala Thr Ala Ile Met
            100                 105                 110

Ala Gln Ile Thr Ala Gln Val Ala Ser His Gln Tyr Gly Gly Thr Thr
        115                 120                 125

Phe Ala Asn Val Asp Leu Val Leu Ala Pro Tyr Val Glu Lys Thr Phe
    130                 135                 140

Ala Lys His Val Arg Asp Ala Arg Lys Tyr Gln Val Ala Leu Val Lys
145                 150                 155                 160

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

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

Pro Phe Val Thr Ile Thr Phe Gly Met Gly Thr Ser Trp Glu Glu Lys
        195                 200                 205

Leu Ile Gln Arg Ala Ile Leu Asp Asn Arg Ile Arg Gly Leu Gly Arg
    210                 215                 220

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

Gly Ile Asn Leu Arg Lys Glu Asp Pro Asn Tyr Asp Ile Lys Gln Leu
                245                 250                 255

Ala Leu Glu Cys Ala Ala Lys Arg Met Tyr Pro Asp Ile Ile Ser Ala
            260                 265                 270

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

```
Gly Cys Arg Ser Phe Leu Gly Ala Trp Arg Asp Ser Ser Gly Lys Pro
    290                 295                 300

Val Leu Asp Gly Arg Asn Asn Leu Gly Val Val Thr Leu Asn Leu Pro
305                 310                 315                 320

Arg Ile Ala Leu Asp Ala Asn Tyr Lys Ser Ser Asp Asp Ser Asn Lys
                325                 330                 335

Leu Phe Lys Leu Leu Asp Glu Arg Leu Asp Ile Cys Lys Glu Ala Leu
            340                 345                 350

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

Ile Leu Tyr Gln Glu Gly Ala Phe Gly Val Arg Met Lys Pro Asp Asp
    370                 375                 380

Glu Ile Leu Glu Leu Phe Lys Asn Gly Arg Ser Ser Ile Ser Leu Gly
385                 390                 395                 400

Tyr Ile Gly Ile His Glu Phe Asp Met Leu Thr Phe Lys Gly Ser Gly
                405                 410                 415

Lys Leu Val Leu Lys Tyr Ile Asn Thr Lys Leu Asn Lys Trp Thr Glu
            420                 425                 430

Glu Thr Gly Tyr Ala Phe Ser Leu Tyr Ser Thr Pro Ala Glu Ser Leu
        435                 440                 445

Cys Tyr Arg Phe Cys Lys Ile Asp Gln Ala Lys Phe Gly Asp Val Lys
    450                 455                 460

Gly Val Thr Asp Lys Gly Trp Tyr Thr Asn Ser Phe His Val Ser Val
465                 470                 475                 480

Glu Glu Asn Leu Ser Pro Phe Glu Lys Ile Asp Arg Glu Ala Pro Tyr
                485                 490                 495

His Ser Ile Ala Lys Gly Gly His Ile Ser Tyr Val Glu Leu Pro Asp
            500                 505                 510

Met Lys Arg Asn Leu Glu Gly Leu Glu Val Val Trp Asp Tyr Ala Ile
        515                 520                 525

Glu Lys Leu Asp Tyr Phe Gly Val Asn Met Pro Val Asp Lys Cys Leu
    530                 535                 540

Ser Cys Gly Ser Thr His Glu Met Thr Pro Thr Glu Asn Gly Phe Thr
545                 550                 555                 560
```

Cys Ser Ile Cys Gly Glu Thr Asp Pro Lys Lys Met Asn Thr Ile Arg
565 570 575

Arg Thr Cys Gly Tyr Leu Gly Asn Pro Ser Glu Arg Gly Phe Asn Leu
580 585 590

Gly Lys Asn Lys Glu Ile Met His Arg Val Lys His Val Arg Glu Thr
595 600 605

Asn Glu Ala Ser
610

<210> 910
<211> 77
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 910
Met Leu Glu Lys Pro Met Lys Gln Val Asp Trp Asn Gln Leu Ser Glu
1 5 10 15

Trp Gly Leu Ile Trp Lys Ile Asn Lys Glu Val Leu His Pro Leu Gly
20 25 30

Ile Ala Ile Thr Arg Asp Pro Glu Ser Gly Leu Ser Ala Gly Ala Ile
35 40 45

Gln Thr Asp Glu Pro Trp Lys Tyr Asp Ala Glu Val Glu Ala Arg Asn
50 55 60

Glu Val Arg Phe Asn Glu Phe Arg Gln Asn Leu Pro Phe
65 70 75

<210> 911
<211> 156
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 911
Met Asn Phe Asp Arg Ile Tyr Pro Ser Asp Phe Val Asn Gly Pro Gly
1 5 10 15

Cys Arg Val Val Leu Phe Val Thr Gly Cys Leu His Lys Cys Glu Gly
20 25 30

Cys Tyr Asn Lys Ser Thr Trp Asn Ala Arg Asn Gly Gln Leu Phe Thr
35 40 45

Met Asn Thr Val Lys Glu Ile Ala Ser His Leu Ser Lys Ser Tyr Ile
50 55 60

Gln Gly Leu Thr Leu Thr Gly Gly Asp Pro Leu Tyr Pro Gln Asn Arg
65 70 75 80

Glu Glu Ile Ser Asn Leu Val Ser Trp Val Lys Ala Arg Phe Pro Glu
85 90 95

Lys Asp Ile Trp Met Trp Thr Gly Tyr Lys Phe Glu Asp Ile Lys Asp
100 105 110

Leu Asp Leu Leu Gln His Ile Asp Val Ile Ile Asp Gly Lys Tyr Glu
115 120 125

Lys Ser Leu Pro Thr Thr Lys Asn Trp Arg Gly Ser Asp Asn Gln Arg
130 135 140

Leu Trp Val Arg Asn Gly Ser Thr Trp Thr His Asp
145 150 155

<210> 912
<211> 44
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 912
Met Val Leu Pro Gly His Met Ile Glu Glu Ile Tyr Met Leu Thr Tyr
1 5 10 15

Lys Ile Met Phe Thr Leu Asn His Met Ala Thr Glu Leu Phe Gly Pro
20 25 30

Glu Phe Leu Ala Met Thr Ala Phe Ile Leu Thr Ile
35 40

<210> 913
<211> 70
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 913
Met Lys Phe Ile Asn Ala Ile Arg Lys Phe Ile Ser Asn Val Ile Ala
1 5 10 15

Leu Val Ala Leu Thr Ala Gly Ala Phe Val Ala Ile Pro Phe Ile Val
20 25 30

Leu Ile Ile Ile Ala Asp Trp Ile Asn Pro Thr Lys Lys Asp Glu Lys
35 40 45

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

Leu Gln Gln Val Met Lys
65   70

<210> 914
<211> 100
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 914
Met Ile Glu Ile Tyr Gly Ile Pro Glu Glu Val Trp Arg Cys Pro Gly
1   5   10   15

Cys Lys Ala Val Arg Asp Leu Leu Asp Lys Leu Gln Leu Pro Tyr Glu
            20   25   30

Phe Tyr Asn Val Ile Asn Glu Val Asp Gly Gln Pro Val Tyr Asp Arg
        35   40   45

Pro Leu Ile Glu Ser Leu Ala Lys Arg Ile Gly Cys Tyr Pro Ser Leu
    50   55   60

Ala Ile Arg Tyr Pro Val Ile Phe Met Asp Asn Val Lys Gln Tyr Asp
65   70   75   80

Ile Pro Thr Phe Lys Thr Asn Leu Ile Ala Ala Gly His Asp Pro Asp
                85   90   95

Ile Ile Glu Asp
            100

<210> 915
<211> 62
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 915
Met Asn Trp Leu Asn Trp Gln Glu Ala Leu Glu Ala Met Ser Lys Gly
1   5   10   15

Cys Lys Val Lys His Val His Phe Thr Asp Asp Glu Tyr Phe Leu Met
            20   25   30

Lys Asn Lys Val Ile Cys Asp Glu Asn Gly Tyr Asp Met Thr Arg Trp
        35   40   45

Tyr Lys Gly Glu Ser Trp Gln Asn Glu His Trp Tyr Ile Ala
    50   55   60

<210> 916
<211> 80
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 916
Met Lys Thr Phe Ala Val Gly Asp Ile Val Arg Thr Arg Ile Trp Asp
1   5   10   15

Gly Leu Gln Phe Glu Val Val Val Tyr Val Gly Ser Asp Gly Val Leu
            20   25   30

Leu His Arg Ile Asn Asn Leu Ile Lys Trp His Leu Glu Arg Phe Val
        35   40   45

Lys Tyr His Glu Phe Asn Ser Tyr His Cys Thr Val Ala Pro Val Ala
    50   55   60

Ser Lys Glu Tyr Tyr Asp Met Leu Glu Glu Leu Lys Ser Leu Lys Asp
65   70   75   80

<210> 917
<211> 110
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 917
Met Ser Gln Ala Ile Lys Asn Ala Leu Asn Ala Phe Ala Tyr Tyr Lys
1   5   10   15

Val Ser Ala Met Leu Glu Glu Gly Arg Cys Val Thr Pro Ser Leu Leu
            20   25   30

Asp Gln Trp Glu Val Glu Leu His Gly Thr Met Lys Glu Glu Gly Gln
        35   40   45

Lys Ile Gly Lys Ala Arg Ile Arg Glu Leu Val Val Ala Tyr Leu Leu
    50   55   60

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

Val Gly Glu Ile Ser Glu Ser Ala Ile Arg Lys Met Lys Asn Gln Arg
                85   90   95

Lys Lys Gly Phe Arg Asp Val Lys Ala Val Lys Ala Ala Lys
            100   105   110

<210> 918
<211> 91
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 918
Met Lys Leu Asn Gln Asn Gly Cys Pro Ser Arg Val Arg Phe Cys Ile
1   5   10   15

Leu Glu Leu Arg Ser Asn Ile Val Val Ile Asp Glu Tyr Thr Thr Ile
            20   25   30

Val Gly Val Gln Gln Tyr Leu Asp Arg Arg Phe Asp Thr Arg Thr His
        35   40   45

Met Lys Tyr Gly Phe Pro Gly Lys Cys Lys Phe Tyr Pro Met Ser Ala
    50   55   60

Asp His Gln Ser Val Val Asn Asp Glu Tyr Lys Trp Ala Glu Gly Leu
65   70   75   80

Thr Leu Lys Glu Leu Glu Glu Tyr Leu Asp Ala
                85   90

<210> 919
<211> 93
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 919
Met Arg Lys Val Ile Leu Tyr Thr Glu Ile Phe Thr Ser Arg Trp Val
1   5   10   15

Phe Asp Ser Val Arg Ile Ser Asn Ala Ser Lys Glu Asp Val Arg Asn
            20   25   30

Ala Gln Arg Leu Ala Tyr Asp Glu Ala Gly Lys Ser Pro Ala Phe Val
        35   40   45

Lys Ile Glu Tyr Ile Ile Thr Asp Ser Ala Leu Ile His Asn Val Ser
    50   55   60

Glu Ser Val Leu Lys Lys Phe Cys Val Asp Arg Ile Asn Lys Gly Thr
65   70   75   80

Ser Met Glu Tyr Phe Leu Leu Ala Arg Glu Leu Lys Trp
                85   90

<210> 920
<211> 74

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 920
Met Val Glu Glu Gln Ile Ala Glu Ile Gly Leu Leu Gly Trp Phe Val
1   5   10   15

Ser Lys Thr Lys Asp Gly Arg Asn Leu Ile Glu Thr Pro Glu Gly Glu
            20   25   30

Phe Ile Ile Glu Glu Asp Phe Asp Ala Phe Trp Ile Tyr Glu Arg Ser
        35   40   45

Gly Glu Asn Glu Tyr Thr Ser Val Asp Ala Phe Ser Lys Phe Glu Asp
    50   55   60

Ala Ile Asp Ser Val Lys Ala Trp Leu Lys
65   70

<210> 921
<211> 92
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 921
Met Ala Lys Val Asn Gln Ile Met Ile Val Val Glu Gly Ile Gly Gly
1   5   10   15

Phe Thr Ile Asp Ser Tyr Met Gly Val Trp Phe Asp Asn Glu Glu Gly
            20   25   30

Met Tyr Trp Glu Thr His Ala Ser Met Leu Asn Glu Thr His Tyr Glu
        35   40   45

Ser Leu Tyr Ser Ser Phe Met Glu Met Met His Glu Val Asp Glu Ser
    50   55   60

Asp Trp Phe Glu Leu Ser Leu Val Glu Phe Lys Arg Ile Met Glu Gln
65   70   75   80

Leu Phe Gln Cys Tyr Arg Ile Met Lys Gly Glu Leu
                85   90

<210> 922
<211> 81
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 922
Met Lys Ile Gln Leu Thr Leu Thr His Glu Asn Ile Lys Gly Val Phe
1 5 10 15

Cys Leu Glu Asn Ser Gln Ile Thr Phe Ala Gln Asp Gly Thr Tyr Trp
20 25 30

Tyr Ala Glu Ser Asp Asp Ile Ala Gly Tyr Gly Met Glu Arg Val Phe
35 40 45

Glu Asp Phe Glu Ala Val Ile Asp Val Pro Leu Asp Phe Thr Tyr Asn
50 55 60

Asp Phe Tyr Arg Ile Met Met Lys Leu Ile Ala Cys Ala Glu Leu Ile
65 70 75 80

Lys

<210> 923
<211> 182
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 923
Met Ser Asn Tyr Val Asn Asn Lys Glu Leu Tyr Lys Ser Ile Cys Ser
1 5 10 15

Trp Lys Glu Lys Cys Arg Glu Ser Glu Ala Ala Gly Gly Pro Arg Val
20 25 30

Val Lys Gln Asn Asp Thr Ile Gly Leu Ala Ile Met Leu Ile Ala Glu
35 40 45

Gly Leu Ser Lys Arg Phe Asn Phe Ser Gly Tyr Thr Gln Ser Trp Lys
50 55 60

Gln Glu Met Ile Ser Asp Gly Ile Glu Ala Ala Ile Lys Gly Leu Ile
65 70 75 80

Asn Phe Asp Glu Thr Lys Tyr Asp Asn Pro His Ala Tyr Ile Thr Gln
85 90 95

Ala Cys Phe Asn Ala Phe Val Gln Arg Ile Lys Lys Glu Arg Lys Glu
100 105 110

Met Ala Lys Lys Tyr Ser Tyr Phe Val His Asn Val Tyr Asp Ser Arg
115 120 125

Asp Asp Asp Met Val Ala Leu Ala Asp Glu Thr Phe Ile Gln Asp Ile
130 135 140

```
Tyr Asp Lys Met Thr Gln Tyr Glu Ser Thr Ala Tyr Lys Ala Pro Gly
145                 150                 155                 160


Ser Ala Lys Lys Ser Glu Pro Thr Ser Asp Gly Pro Asn Leu Glu Phe
                165                 170                 175


Leu Tyr Glu Ala Glu Asp
            180


<210> 924
<211> 76
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 924
Met Arg Leu Lys Ile Asn Leu Asp Gly Phe Leu Glu Asp Val Gln Asp
1               5                   10                  15


Leu Asp Ala Ile Pro Tyr Leu Leu Lys Met Tyr Leu Arg Glu Val Leu
            20                  25                  30


Asp Leu Asp Ile His Ile Asp Pro Lys Asn Pro His Asp Ala Asp Phe
        35                  40                  45


Arg Ser Asp Ser Ala Ile Ile Glu His Ser Tyr Asn Trp Thr Asp Thr
    50                  55                  60


Glu Phe Thr Phe Glu Ile Asn Tyr His Pro Lys Glu
65                  70                  75


<210> 925
<211> 100
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 925
Met Asn Asn Ile Thr Gln Glu Glu Arg Asp Glu Leu Gln Gln Lys Leu
1               5                   10                  15


Met Glu Ala Ala Glu Glu Gln Ala Ile Ala Arg Ala Asn Lys Ile Val
            20                  25                  30


Arg Lys Asn Arg Arg Glu Ile Glu Arg Leu Lys Ala His Ala Gly Asp
        35                  40                  45


Ala Val Leu Asp Asn Asn Phe Pro Ala Tyr Lys Tyr Ala Ile Glu Lys
    50                  55                  60
```

Leu Arg Thr Ile Leu Lys Gln Pro Phe Thr Asp Glu Ile Ile Leu Thr
65 70 75 80

Cys Trp Asn Thr Ser Arg Lys Ser Val Trp Asp Ile Leu Asn Ala Gly
85 90 95

Thr Ser Lys Ile
100

<210> 926
<211> 65
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 926
Met Leu Val Gln Val Lys Phe Lys Arg Val Arg Lys Asp Ala Gly Phe
1 5 10 15

Thr Leu Asn Thr Ala Thr Gly Thr Met Ala Val Lys Val Ala Asp Asn
20 25 30

Gln Tyr Arg Val Leu Gly Ser Thr Glu Gly Cys Lys Leu Ile Asp Lys
35 40 45

Asn Ser Leu Val Trp Val Asp Thr Phe Gln Val Lys Arg Trp Tyr Glu
50 55 60

Trp
65

<210> 927
<211> 81
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 927
Met Gly Ser Asn Pro Gly His Asp Trp Pro Glu Gly Asn Tyr Ala Cys
1 5 10 15

Arg Cys Ser Asn Cys Ser Glu Arg Tyr Thr Gly Pro Lys Arg Ser Tyr
20 25 30

Phe Cys Tyr Lys Cys Asp Thr Ala Arg Arg Glu Ala Pro Ala Pro Asp
35 40 45

Tyr Glu Ala Ile Arg Asn Ala Lys Ile Asp Met Leu Lys Arg Phe Glu
50 55 60

Glu Ala Lys Arg Ile Cys Glu Ala Ala Gly Tyr Val Val Tyr Lys Lys
65 70 75 80

Ile

<210> 928
<211> 398
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 928
Met Lys Ile Asn Ile Leu Met Ala Arg Gly Leu Glu Gly Cys Gly Val
1 5 10 15

Thr Lys Phe Ser Leu Glu His Arg Glu Trp Leu Val Lys His Gly His
20 25 30

Glu Val Asn Ile Ile Tyr Ala Lys Asp Lys Ala Phe Thr Arg Asn Arg
35 40 45

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

Tyr Asp Lys Thr Leu Ser Leu Leu Asn Ala Cys Asp Ile Leu Ile Ile
65 70 75 80

Asn Ser Val Pro Ala Val Asn Ala Pro Glu Ala Ala Ile Asp Asn Tyr
85 90 95

Lys Lys Leu Ile Glu Asn Ile Lys Pro Glu Val Arg Val Val Val Tyr
100 105 110

Gln His Asp His Arg Ala Leu Ser Leu Arg Arg Asn Ala Gly Leu Glu
115 120 125

Glu Thr Val Lys Arg Ala Asp Val Leu Phe Ser His Ser Ser Asn Gly
130 135 140

Asp Phe Asn Thr Val Leu Met Glu Glu Tyr Phe Pro Ser Gly Gly Leu
145 150 155 160

Ser Phe Phe Asp Asp Ser Asp Ser Ala Pro Pro Val Tyr Asn Phe Gln
165 170 175

Pro Ala Met Asn Ile Lys Ala Ile Arg Asp Lys Tyr Trp Lys Asp Phe
180 185 190

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

Trp Lys Gly Tyr Phe Leu Met Phe Asp Phe His Glu Ser His Leu Arg

210 215 220

Pro Ala Gly Lys Thr Thr Ile Leu Glu Gly Leu Glu Arg Ser Pro Ala
225 230 235 240

Phe Ile Asn Ile Lys Glu Arg Tyr Glu Ile Asp Tyr Cys Arg His Tyr
245 250 255

His Gln Val Lys Thr Gly Pro Gly Leu Asn Pro Gln Val Leu Asp Arg
260 265 270

Tyr Val Asn Ser Glu Met Leu Glu Arg Met Ser Gln Ser Gly Phe Gly
275 280 285

Tyr Gln Leu Ser Arg Leu Pro Asp Lys Phe Leu Glu Arg Ser Leu Glu
290 295 300

Tyr Thr His Leu Glu Leu Gly Ala Cys Gly Thr Ile Pro Val Phe His
305 310 315 320

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

Thr Ser His Asp Ser Gly Ile Leu Trp Leu Asn Asp Glu Asn Lys Asn
340 345 350

Glu Val Phe Glu Arg Met Lys His Leu Ser Ser Asp Gln Lys Leu Tyr
355 360 365

Asp Lys Glu Arg Asn Lys Ala Phe Glu Phe Leu Val Glu His Gln Asp
370 375 380

Ser Glu His Cys Phe Lys Glu Gln Phe Glu Leu Met Thr Lys
385 390 395

<210> 929
<211> 340
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 929
Met Lys Ile Ile His Ser Gly Asp Trp His Leu Gly Val Arg Ala Asp
1 5 10 15

Asp Pro Trp Val Gln Asp Val Gln Arg His Gly Ile Lys Gln His Ile
20 25 30

Asp Tyr Ala Lys Lys His Gly Ile Lys Thr Ile Ile Gln Tyr Gly Asp
35 40 45

```
Ile Phe Asp Val Arg Lys Ala Ile Thr His Lys Thr Met Glu Phe Ala
    50                  55                  60

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

Ile Val Gly Asn His Asp Met His Tyr Lys Asn Thr Leu Thr Pro Asn
                85                  90                  95

Ala Ser Thr Glu Val Leu Gly Lys Tyr Lys His Ile Thr Val Ile Glu
            100                 105                 110

Lys Pro Val Thr Met Asp Phe Asp Gly Thr Leu Ile Asp Leu Cys Pro
        115                 120                 125

Trp Met Cys Glu Glu Asn Thr Ser Glu Ile Met Lys His Ile Lys Glu
    130                 135                 140

Ser Ser Ala Glu Tyr Cys Ile Gly His Trp Glu Leu Asn Gly Phe Tyr
145                 150                 155                 160

Phe Tyr Lys Gly Met Lys Ser His Gly Leu Glu Pro Asp Phe Leu Lys
                165                 170                 175

Lys Tyr Lys Gln Val Trp Ser Gly His Phe His Thr Ile Ser Ser Ala
            180                 185                 190

Ala Asn Val Lys Tyr Ile Gly Thr Pro Trp Thr Leu Thr Ala Gly Asp
        195                 200                 205

Glu Asn Asp Pro Arg Gly Phe Trp Val Gln Asp Thr Glu Leu Ser Thr
    210                 215                 220

Phe Asp Phe Val Pro Asn Glu Ile Thr Trp His Arg Lys Leu Ile Tyr
225                 230                 235                 240

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

Arg Ile Ile Ile Thr Ala Val Asp Glu Asp Leu Pro Lys Phe Glu Ser
            260                 265                 270

Glu Leu Glu Lys Val Val His Glu Leu Arg Thr Val Ser Lys Val Asp
        275                 280                 285

Asn Ser Val Glu Ser Glu Asp Gly Glu Glu Val Glu Val Lys Ser Leu
    290                 295                 300

Leu Asp Leu Met Glu Glu Tyr Ile Gln Ala Leu Glu Asp Leu Ser Ala
305                 310                 315                 320
```

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

Ala Gln Asn Gln
340

<210> 930
<211> 560
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 930
Val Lys Thr Phe Lys Leu Asn Arg Val Lys Tyr Lys Asn Ile Met Ser
1 5 10 15

Val Gly Gln Ala Ala Ile Asp Ile Gln Leu Asp Lys Cys Gln Lys Thr
20 25 30

Leu Ile Thr Gly Lys Asn Gly Gly Gly Lys Ser Thr Met Leu Glu Ala
35 40 45

Ile Thr Phe Ala Leu Phe Gly Lys Pro Phe Arg Asp Ile Lys Lys Gly
50 55 60

Gln Leu Ile Asn Ser Phe Asn Lys Lys Asp Ser Val Val Glu Leu Trp
65 70 75 80

Met Glu Tyr Asp Gly His Ser Phe Tyr Ile Lys Arg Gly Gln Lys Pro
85 90 95

Asn Val Phe Glu Ile Leu Arg Asp Gly Asn Lys Leu Asp Glu Ala Ala
100 105 110

Ser Ser Lys Asp Phe Gln Ser Tyr Phe Glu Ser Leu Ile Gly Met Ser
115 120 125

Tyr Thr Ser Phe Lys Gln Ile Val Val Leu Gly Thr Ala Gly Tyr Thr
130 135 140

Pro Phe Met Gly Leu Ser Thr Ala Asn Arg Arg Lys Leu Val Glu Asp
145 150 155 160

Leu Leu Glu Val Ser Leu Leu Ala Asp Met Asp Lys Leu Asn Lys Thr
165 170 175

Gln Ile Arg Glu Ile Asn Gln Gln Ile Gln Val Asn Asp Val Gln Arg
180 185 190

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

```
Gln Lys Lys Leu Ser Gly Asp Asn Val Ala Arg Leu Gln Ala Met Tyr
    210                 215                 220

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

Leu Gln Arg Glu Leu Leu Glu Leu Val Ile Gly Asp Asp Pro Ala Glu
                245                 250                 255

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

Glu Ser Tyr Ser Lys Val Leu Gly Leu Tyr Asp Lys Gly Gly His Cys
        275                 280                 285

Pro Thr Cys Leu Gln Asp Leu His Ser Asn Asp Thr Leu Ile Thr Lys
    290                 295                 300

Ile Asn His His Val Glu Glu Cys Asn Thr Ile Leu Gly Glu Leu Lys
305                 310                 315                 320

Thr Arg Gln Ser Glu Leu Asp Glu Leu Ala Arg Glu Tyr Asn Thr Val
                325                 330                 335

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

Met Thr Ile Thr Ala Val Glu Lys Ala Arg Arg Ile Lys Ala Ala Ile
        355                 360                 365

Asp Lys Ala Ser Gln Glu Phe Ile Asp Asn Ser Asp Lys Ile Lys Leu
    370                 375                 380

Leu Gln Glu Glu Leu Asp Lys Ile Ile Leu Val Lys Thr Asn Leu Val
385                 390                 395                 400

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

Gly Ile Lys Gly Ala Ile Ile Lys Lys Tyr Ile Pro Met Phe Asn Lys
            420                 425                 430

Gln Ile Asn Ser Tyr Leu Lys Ile Met Glu Ala Asp Tyr Ser Phe Thr
        435                 440                 445

Leu Asn Glu Glu Phe Ser Glu Thr Ile Lys Ser Arg Gly Arg Glu Glu
    450                 455                 460

Phe Ser Tyr Ala Ser Phe Ser Gln Gly Glu Lys Ala Arg Ile Asp Ile
465                 470                 475                 480
```

Ala Leu Leu Phe Thr Trp Arg Asp Ile Ala Glu Lys Val Ser Gly Val
485 490 495

Lys Ile Asn Cys Leu Phe Leu Asp Glu Val Tyr Asp Ser Ala Thr Asp
500 505 510

Ala Glu Gly Val Lys Ala Ile Thr Ala Ile Leu Asn Lys Met Val Asp
515 520 525

Ala Asn Val Phe Ile Ile Ser His Arg Asp His Asp Pro Gln Ala Tyr
530 535 540

Gly Gln His Leu Gln Met Lys Lys Val Gly Arg Phe Thr Val Met Glu
545 550 555 560

<210> 931
<211> 64
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 931
Met Asn Glu Phe Thr Thr Gly Gln His Leu Leu Ala Phe Pro Glu Leu
1 5 10 15

Lys Arg Tyr Val Leu Val Asn Leu Phe Ser Asp Glu Arg His Leu Val
20 25 30

Thr Glu Glu Met Leu Arg Asp Ala Phe Thr Gly Asn Glu Tyr Asn Arg
35 40 45

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

<210> 932
<211> 125
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 932
Met Ile Asn Phe Val Asp Val Lys Asp Ile Gln Val Lys Asn Val Arg
1 5 10 15

Ala Asp Ser Asn Pro Asn Asn Gln Asn Arg Ile Arg Lys Ser Trp Val
20 25 30

Leu Ala Leu Thr Glu Glu Thr Lys Gln Ala Ile Lys Asp Lys Ile Lys
35 40 45

Asp Ser Glu Ala Arg Phe Ala Phe Tyr Lys Ser Ile Asp Asp Glu Val

50 55 60

Ala Glu Lys Trp Ile Glu Leu Met Arg Lys His Tyr Asn Glu Ser Ile
65 70 75 80

Lys Ala Gly Ala Lys Ile Val Thr Asp Arg His Gly Gly Glu Arg Leu
85 90 95

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

Gln Ile Val Ala Glu Glu Leu Thr Ala Thr Phe Ala Ala
115 120 125

<210> 933
<211> 233
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 933
Met Lys Phe Ser Lys Glu Thr Leu Asn Ile Leu Lys Asn Phe Ser Thr
1 5 10 15

Ile Asn Ser Gly Ile Met Leu Lys Pro Gly Asn Phe Ile Met Thr Arg
20 25 30

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

Asp Thr Asp Val Ala Ile Tyr Asp Leu Asn Ser Phe Leu Ser Ile Leu
50 55 60

Ser Leu Val Gly Asp Asp Ala Asp Ile Ile Met Gln Glu Asp Gly Asn
65 70 75 80

Leu Ala Ile Lys Asp Ala Arg Ser Thr Ile Phe Trp Pro Ala Ala Asp
85 90 95

Pro Ser Thr Ile Val Phe Pro Thr Lys Pro Ile Pro Phe Pro Val Ala
100 105 110

Asn Val Ile Ile Asp Phe Lys Gly Glu Asp Leu Gln Gln Leu Met Arg
115 120 125

Val Ser Arg Gly Met Gln Ile Asp Thr Ile Ala Ile Thr Asn Val Asp
130 135 140

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

Thr Arg Pro Lys Tyr Ser Leu Thr Leu Gly Asp Tyr Glu Gly Glu Gly
165 170 175

Asn Phe Asn Phe Ile Ile Asn Met Ser Asn Met Lys Met Thr Ile Gly
180 185 190

Asp Tyr Lys Leu Met Leu Trp Ala Lys Met Asn Gly Ser Lys Lys Gln
195 200 205

Thr Ala Ala Lys Phe Glu Gly Ala Ser Ala Ser Tyr Val Val Ala Met
210 215 220

Glu Ala Asp Ser Thr Phe Asp Phe Glu
225 230

<210> 934
<211> 320
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 934
Met Lys Leu Thr Val Asn Glu Ala Asp Phe Met Trp Glu Gln Lys Tyr
1 5 10 15

Arg Pro Gly Thr Ile Ser Glu Cys Val Leu Pro Ala Glu Asp Lys Glu
20 25 30

Ile Phe Ser Ala Leu Val Ala Lys Gly Lys Ile Pro His Leu Ile Leu
35 40 45

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

Cys Asn Asp Ile Asn Ala Glu Met Met Phe Val Asn Gly Ser Asp Cys
65 70 75 80

Lys Ile Asp Phe Val Arg Gly Pro Leu Thr Ala Phe Ala Ser Ser Ala
85 90 95

Ser Ile Ala Gly Lys Gln Lys Ile Ile Val Ile Asp Glu Phe Asp Arg
100 105 110

Ala Gly Leu Ala Glu Ser Gln Arg His Leu Arg Ser Phe Met Glu Ala
115 120 125

Tyr Ser Thr Asn Cys Thr Ile Ile Ile Thr Ala Asn Asn Leu Asp Gly
130 135 140

Ile Ile Lys Pro Leu Gln Ser Arg Cys Arg Val Ile Asn Phe Gly Lys
145 150 155 160

```
Pro Ser Pro Ser Asp Val Lys Pro Met Gln Ile Glu Met Leu Lys Arg
                165                 170                 175

Cys Leu Ala Ile Cys Glu Asn Glu Gly Val Val Val Glu Asp Lys Lys
            180                 185                 190

Val Val Ala Ala Leu Val Lys Lys Asn Phe Pro Glu Phe Arg Lys Thr
        195                 200                 205

Ile Asn Met Leu Asp His Tyr Ser Ser Lys Gly Val Ile Asp Ala Gly
    210                 215                 220

Ile Leu Ser Ile Val Leu Asn Asp Arg Gly Ser Ile Glu Asp Val Ile
225                 230                 235                 240

Glu Ala Ile Lys Thr Lys Asn Ile Lys Glu Leu Arg Ala Leu Ala Pro
                245                 250                 255

Lys Tyr Ala Ala Asp Tyr Thr Trp Phe Val Asp Lys Leu Ser Ser Glu
            260                 265                 270

Leu Tyr Thr Met Val Thr Gly Pro Ser Ile Ile Arg Met Tyr Glu Ile
        275                 280                 285

Ile Gly Glu Asn Asn Gln Tyr His Gly Ile Ala Ala Ser Ile Glu Leu
    290                 295                 300

His Leu Val Tyr Met Leu Ile Gln Leu Val Val Glu Met Gln Trp Lys
305                 310                 315                 320
```

<210> 935
<211> 188
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 935

```
Met Ser Leu Phe Glu Asp Asp Asp Gln Tyr Asn Glu His Gln Ile Ala
1               5                   10                  15

Trp Leu Gly Lys Asp Trp Thr Lys Val Gln Glu Leu Ser Asp Ser Tyr
            20                  25                  30

Lys Glu Lys Ala Glu Asn Gln Phe Phe Thr Ile Ile Gly Ser Ile Asn
        35                  40                  45

Glu Lys Gln Glu His Leu Asn Ile Ser Thr Met Asp Tyr Ser Lys Phe
    50                  55                  60

Met Val Glu Asn Ala Leu Ser Gln His Pro Asp Cys Met Pro Ser Val
65                  70                  75                  80
```

Tyr Val Met Asn Leu Val Gly Gln Gly Leu Ser Asp Gln Ala His Tyr
85 90 95

Asn Tyr Met Met Ala Ser Val Pro Arg Gly Arg Arg Tyr Gly Lys Trp
100 105 110

Ala Lys Leu Thr Glu Asn Ile Gln Asp Ala Leu Ile Leu Gln Val Ile
115 120 125

Met Thr Tyr Tyr Lys Val Asn Ala Ile Asp Ala Arg Met Tyr Arg Glu
130 135 140

Thr Leu Glu Ala Lys Asn Lys Leu Lys Pro Ala Leu Lys Lys Met Lys
145 150 155 160

Gly Leu Val Thr Asp Glu Leu Val Lys Thr Ile Thr Lys Asn Val Lys
165 170 175

Glu Gln Lys Asn Leu Lys Lys Thr Ala Leu Glu Trp
180 185

<210> 936
<211> 123
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 936
Met Val Lys Met Ile Glu Ile Thr Leu Lys Gln Pro Glu Asp Phe Leu
1 5 10 15

Lys Val Lys Glu Thr Leu Thr Arg Met Gly Ile Ala Asn Asn Lys Asp
20 25 30

Lys Val Leu Tyr Gln Ser Cys His Ile Leu Gln Lys Gln Gly Arg Tyr
35 40 45

Tyr Ile Val His Phe Lys Glu Met Leu Lys Leu Asp Gly Arg Pro Val
50 55 60

Thr Ile Asp Leu Glu Asp Glu Ile Arg Arg Asp Ser Ile Ala Gln Leu
65 70 75 80

Leu Ala Asp Trp Gly Leu Leu Ser Ile Asn Arg Gly Gln Thr Leu Ala
85 90 95

Gln Met Gln Asn Asn Phe Arg Val Ile Thr Phe Lys Gln Lys His Glu
100 105 110

Trp Thr Leu Lys Ser Lys Tyr Thr Ile Gly Ala

115 120

<210> 937
<211> 66
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 937
Met Thr Asp Gln Glu Phe Tyr Asp Lys Leu Lys Asn Ile Arg Ile Thr
1 5 10 15

Ala Pro Glu Trp Phe Ser Leu Pro Ile Asp Glu Gln Ile Gln Tyr Gln
20 25 30

Val Lys Glu Thr Leu Glu Lys Tyr Pro Gly Arg Lys Val Met Met Cys
35 40 45

Phe Thr Tyr Asp Lys Asn Arg Val Pro Arg Ile Gln Lys Gln Val Ile
50 55 60

Glu Val
65

<210> 938
<211> 902
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 938
Met Lys Glu Phe Tyr Ile Ser Val Glu Ser Leu Gly Asn Asp Ile Val
1 5 10 15

Glu Arg Tyr Ile Asp Ser Thr Gly Glu Glu Arg Met Arg Arg Val Pro
20 25 30

Tyr Ser Pro Val Met Phe Ser His Cys Met Glu Glu Thr Lys Tyr Lys
35 40 45

Asp Ile Tyr Gly Lys Tyr Cys Lys Lys Asn Thr Phe Pro Thr Met Lys
50 55 60

Asp Ala Arg Asp Trp Met Arg Arg Met Glu Asp Met Gly Met Glu Ala
65 70 75 80

Met Gly Met Asp Asp Phe Lys Leu Ala Tyr Ile Ser Asp Thr Tyr Gly
85 90 95

Ser Glu Ile Val Tyr Asn Lys Lys Phe Ile Arg Ile Ala Asn Cys Asp
100 105 110

```
Ile Glu Val Thr Ala Ser Gln Phe Pro Asp Pro Met Lys Ala Glu Tyr
        115                 120                 125

Glu Ile Asp Ala Ile Thr His Tyr Asp Ser Val Asp Asp Lys Phe Tyr
    130                 135                 140

Val Phe Asp Leu Leu His Ser Leu Tyr Gly Ser Val Ser Glu Trp Asp
145                 150                 155                 160

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

Gln His Ile Leu Asp Arg Val Val Tyr Met Pro Phe Asn Ser Glu Lys
            180                 185                 190

Glu Met Met Leu Glu Tyr Ile Asn Leu Trp Glu Gln Lys Cys Pro Ala
        195                 200                 205

Ile Phe Thr Gly Trp Asn Ile Glu Gly Phe Asp Ile Pro Tyr Ile Met
    210                 215                 220

Asn Arg Val Lys Gln Ile Leu Gly Glu Arg Ala Met Lys Arg Phe Ser
225                 230                 235                 240

Pro Leu Asn Lys Val Ser Ser Lys Ile Ile Thr Asn Met Tyr Gly Asp
                245                 250                 255

Lys Glu Ile Tyr Ser Ile Met Gly Val Thr Ile Leu Asp Tyr Met Asp
            260                 265                 270

Leu Tyr Lys Lys Phe Ser Phe Thr Asn Gln Pro Thr Tyr Lys Leu Asp
        275                 280                 285

Phe Ile Ala Tyr Tyr Glu Thr Lys Lys Gly Lys Leu Ala Tyr Asp Gly
    290                 295                 300

Pro Ile Asn Lys Leu Arg Glu Thr Asn His Gln Arg Tyr Ile Ser Tyr
305                 310                 315                 320

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

Phe Ile Asp Leu Ala Ile Ser Met Ser Tyr Tyr Ala Lys Met Pro Tyr
            340                 345                 350

Gln Gly Val Met Ser Pro Ile Lys Thr Trp Asp Ala Ile Ile Phe Asn
        355                 360                 365

Ser Leu Lys Glu Gln Asp Lys Val Ile Pro Gln Ser Arg Ser His Val
    370                 375                 380
```

```
Lys Gln Ser Tyr Pro Gly Ala Tyr Val Lys Glu Pro Val Pro Ala Ala
385                 390                 395                 400

Tyr Arg Tyr Ile Met Ser Phe Asp Leu Thr Ser Leu Tyr Pro Ser Ile
                405                 410                 415

Ile Arg Gln Val Asn Ile Ser Pro Glu Thr Ile Val Gly Gln Phe Lys
            420                 425                 430

Leu His Pro Leu Gly Glu Tyr Ile Asn Lys Thr Ala Pro Arg Pro Ser
        435                 440                 445

Asp Glu Tyr Ser Cys Ser Pro Asn Gly Trp Met Tyr Arg Lys Asp Val
    450                 455                 460

Asp Gly Val Ile Pro Val Glu Ile Ala Lys Val Phe Tyr Gln Arg Lys
465                 470                 475                 480

Glu Trp Lys Asn Lys Met Met Gly Ala Lys Arg Asn Gln Glu Leu Ile
                485                 490                 495

Lys Lys Val Leu Asn Asp Lys Lys Phe Gly Thr Ile Asp Lys Phe Ala
            500                 505                 510

Glu Val Asn Val Tyr Glu Asp Phe Ser Asp Asp Met Lys Ala Glu Leu
        515                 520                 525

Leu Thr Tyr Thr Glu Glu Cys Leu Asp Lys Leu Met Phe Glu Cys Lys
    530                 535                 540

His Ala Glu Ile Leu Gly Asn Thr Asn Gln Leu Asn Arg Lys Ile Leu
545                 550                 555                 560

Ile Asn Ser Leu Tyr Gly Ala Leu Gly Asn Ile Tyr Phe Arg Tyr Tyr
                565                 570                 575

Asp Leu Arg Asn Ala Ser Ala Ile Thr Leu Phe Gly Gln Met Ala Ile
            580                 585                 590

Gln Trp Ile Glu Arg Lys Val Asn Glu Tyr Leu Asn Lys Val Cys Gly
        595                 600                 605

Thr Glu Gly His Ser Phe Val Val Ala Gly Asp Thr Asp Ser Ile Tyr
    610                 615                 620

Val Cys Val Asp Lys Val Ile Glu Lys Val Gly Leu Glu Arg Phe Lys
625                 630                 635                 640

Glu Thr Asn Asp Leu Val Glu Phe Leu Asn Gln Phe Gly Lys Lys Lys
                645                 650                 655
```

```
Met Glu Pro Trp Ile Asp Gln Ser Tyr Arg Glu Met Cys Glu Tyr Met
            660                 665                 670

Asn Asn Lys Glu His Leu Met Phe Met Asp Arg Glu Ala Ile Ser Cys
        675                 680                 685

Pro Pro Leu Gly Ser Asn Gly Ile Gly Gly Phe Trp Lys Ala Lys Lys
    690                 695                 700

Arg Tyr Ala Leu Asn Val Tyr Asp Met Glu Gly Thr Arg Tyr Ala Glu
705                 710                 715                 720

Pro His Leu Lys Ile Met Gly Met Glu Thr Gln Gln Ser Ser Thr Pro
                725                 730                 735

Thr Ala Val Gln Asn Ala Leu Glu Glu Ser Ile Arg Arg Met Leu Gln
            740                 745                 750

Glu Gly Glu Glu Ser Leu Gln Gln Tyr Tyr Lys Gln Phe Glu Ser Glu
        755                 760                 765

Tyr Arg Glu Leu Asp Tyr Lys Val Ile Ala Glu Val Lys Thr Ala Asn
    770                 775                 780

Asn Ile Gly Lys Tyr Asp Asp Gly Ala Gly Tyr Pro Asp Lys Gly Thr
785                 790                 795                 800

Pro Tyr His Val Lys Gly Ala Leu Ala Tyr Asn Arg Ala Thr Ala Gly
                805                 810                 815

Phe Glu Gly Ile Thr Pro Ile Met Glu Gly Glu Lys Val Met Val Ile
            820                 825                 830

Pro Leu Arg Glu Gly Asn Pro Tyr Gly Glu Lys Cys Met Ala Trp Pro
        835                 840                 845

Ser Gly Thr Glu Leu Pro Gln Glu Ile Arg Gln Glu Val Leu Val Trp
    850                 855                 860

Leu Asp His Ser Val Leu Phe Gln Lys Ser Phe Val Lys Pro Leu Thr
865                 870                 875                 880

Gly Met Ser Glu Ala Ala Gly Leu Asp Tyr Glu Glu Lys Ser Ser Leu
                885                 890                 895

Leu Asp Met Phe Asp Phe
            900
```

<210> 939
<211> 147
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 939
Met Lys Ser Leu Leu Ala Val Ile Val Ala Leu Thr Leu Thr Gly Cys
1 5 10 15

Gln Met Pro Gln Gly Asp Ile Val Pro Ala Ser Ser Val Gly Gln Val
20 25 30

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

Ser Ala Glu Ser Leu Ala Val Glu Arg Arg Leu Ala Lys Glu Lys Ala
50 55 60

Asn Pro Asn Arg Gln Leu Ser Ala Met Glu Leu Asp Met Ile Glu Gln
65 70 75 80

Asn Lys His Glu Leu Glu Glu Ile Lys Arg Leu Arg Lys Thr Gln Lys
85 90 95

Glu Arg Thr Cys Thr Ala Gln Ala Ala Ala Val Asn Asp Gln Ile Arg
100 105 110

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

Arg Met Glu Gln Leu Lys Ser Leu Gln Asn His Ile Tyr Asn Lys Cys
130 135 140

Met Ser Asn
145

<210> 940
<211> 68
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 940
Met Glu Ala Val Phe Gly Leu Ile Ile Leu Phe Phe Ile Tyr Phe Leu
1 5 10 15

Pro Thr Phe Val Ala Cys Ser Arg Lys His Lys Ser Arg Gly Gly Ile
20 25 30

Phe Ile Thr Asn Leu Val Phe Gly Trp Ser Ile Ile Gly Trp Leu Ile
35 40 45

Ala Leu Ile Trp Ser Ala Ser Asn Ala Gln Gln Asn Thr Ile Ile Ile

50 55 60

Gln Gln Val Lys
65

<210> 941
<211> 244
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 941
Met Ile Val Thr Pro Met Thr Val Gln Asp Ile Arg Gln Glu Phe Ala
1 5 10 15

Asp Ala Leu Leu Asn Lys Glu Phe Val Ile Asp Lys Thr Gly Val Lys
20 25 30

Thr Ile Glu Ile Val Gly Ala Ser Phe Ile Ala Asp Glu Asn Leu Ile
35 40 45

Phe Gly Ala Val Asn Asp Gly Tyr Ile Ala Arg Glu Leu Glu Trp Tyr
50 55 60

Lys Ser Gln Ser Leu Phe Val Lys Asp Ile Pro Gly Glu Thr Pro Ala
65 70 75 80

Ile Trp Lys Ala Ile Ala Ser Lys His Gly Glu Ile Asn Ser Asn Tyr
85 90 95

Gly Trp Ala Val Trp Ser Thr Gln Asn Tyr Ser Gln Phe Ala Asn Cys
100 105 110

Ala Lys Glu Leu Ile Asn Asn Pro Asp Ser Arg Arg Gly Ile Met Ile
115 120 125

Tyr Thr Arg Pro Gln Met Gln Tyr Asp Phe Glu Arg Asp Gly Met Ser
130 135 140

Asp Phe Met Cys Thr Asn Asn Val Gln Tyr Leu Ile Arg Asp Asn Arg
145 150 155 160

Val His Ala Val Val Asn Met Arg Ser Asn Asp Val Val Phe Gly Tyr
165 170 175

Arg Asn Asp Tyr Ala Trp Gln Leu Tyr Val Leu Glu Gln Leu Thr Lys
180 185 190

Leu Leu Asn Ala Ser Gly Lys Asn Tyr Ser Val Gly Asp Ile Ile Trp
195 200 205

Asn Val Gly Ser Leu His Val Tyr Ser Arg His Phe Tyr Leu Val Asp
    210   215   220

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

Gly Glu Trp Lys

<210> 942
<211> 278
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 942
Met Ile Gln Phe Val Ile Pro Ser Tyr Lys Arg Ala Gly Ala Val Thr
1   5   10   15

Ala Leu Thr Met Phe Pro Glu Gly Tyr Val Pro His Leu Val Val Arg
            20   25   30

Glu Ser Glu Lys Glu Ala Tyr Glu Thr Trp His Gly His Ala Ala Lys
        35   40   45

Ile Val Thr Val Pro Asp Asp Val Asp Gly Ile Ala Gly Thr Arg Arg
    50   55   60

Leu Ile Thr Glu Met Tyr Ala Gly Gln Arg Ile Trp Met Leu Asp Asp
65   70   75   80

Asp Thr Thr Ile His Leu Thr Glu Ile Arg Glu Arg Asp Asp Arg Arg
                85   90   95

Val Pro Leu Gly Val Gly Glu Ala Met Ser Gln Glu Val Phe Asp Asp
            100   105   110

Met Val Lys Tyr Val Glu Thr Ala Met Asp Cys Gly Tyr Tyr His Gly
        115   120   125

His Ala Arg Leu Pro Ile Phe Lys Ile Thr Ser Ser Trp Gly His Tyr
    130   135   140

Arg Glu Asn Ser Phe Gly Phe Thr Asn Thr Phe Tyr Asp Leu Thr Lys
145   150   155   160

Leu Thr Ala Glu Asp Ile Gly Tyr Gly Ile Ile Asp Leu Asn Glu Asp
                165   170   175

Ala Tyr Ala Phe Leu Lys Leu Ile Asn Met Gly His Pro His Leu Ala
            180   185   190

Leu Phe Lys Tyr Leu Val Lys Ser Gly Lys Val Gln Ser Pro Gly Gly
195 200 205

Cys Ser Thr Gln Arg Asp Thr Ala Arg Gln Asn Arg Ala Leu Glu Gln
210 215 220

Leu His Ala Ala Phe Pro Asn Gln Ala Arg Trp Lys Ser Lys Asp Gly
225 230 235 240

Glu Arg Arg Gly Leu Phe Gly Asp Asp Glu Pro Leu Lys Ser Ile Arg
245 250 255

Met Cys Ile Asn Thr Arg Val Lys Ser Gln Ala Phe His Glu Phe Gly
260 265 270

Lys Val Glu Pro Tyr Leu
275

<210> 943
<211> 83
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 943
Val Arg Ala Lys Ala Leu Gln Gly Pro Leu Met Asn Ile Tyr Asp Lys
1 5 10 15

Ser Asp Val Ala Gly Asn Ile Phe Lys Ala Glu Glu Phe Arg Cys Phe
20 25 30

Val Cys Lys Ser Asp Glu Phe Val His Glu Gly Thr Thr Gly Ser Asp
35 40 45

Gly Met His Cys Trp Trp His Gly Met Cys Val Gly Cys Lys Ile His
50 55 60

Tyr Glu Ile Asp Met Glu Thr Val Val Tyr Asn Thr Lys Lys Lys Trp
65 70 75 80

Asn Phe Cys

<210> 944
<211> 391
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 944
Met Ser Asp Leu Lys Ser Arg Leu Ile Lys Ala Ser Thr Ser Lys Met

1 5 10 15

Thr Ala Glu Leu Thr Lys Ser Lys Phe Phe Asn Glu Lys Asp Val Val
20 25 30

Arg Thr Lys Ile Pro Met Leu Asn Ile Ala Ile Ser Gly Ala Leu Asp
35 40 45

Gly Gly Met Gln Ser Gly Leu Thr Ile Phe Ala Gly Pro Ser Lys His
50 55 60

Phe Lys Ser Asn Met Ser Leu Thr Met Val Ser Ala Tyr Leu Asn Lys
65 70 75 80

Tyr Pro Asp Ala Val Cys Leu Phe Tyr Asp Ser Glu Phe Gly Ile Thr
85 90 95

Pro Ala Tyr Leu Lys Ser Met Gly Val Asp Pro Asp Arg Val Ile His
100 105 110

Thr Pro Val Gln Ser Val Glu Gln Leu Lys Ile Asp Met Val Asn Gln
115 120 125

Leu Glu Ala Ile Glu Arg Gly Glu Lys Val Ile Val Phe Ile Asp Ser
130 135 140

Ile Gly Asn Met Ala Ser Lys Lys Glu Thr Glu Asp Ala Leu Asn Glu
145 150 155 160

Lys Ser Val Ala Asp Met Thr Arg Ala Lys Ser Leu Lys Ser Leu Phe
165 170 175

Arg Ile Val Thr Pro Tyr Phe Ser Ile Lys Asn Ile Pro Cys Val Ala
180 185 190

Val Asn His Thr Ile Glu Thr Ile Glu Met Phe Ser Lys Thr Val Met
195 200 205

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

Gly Lys Arg Gln Ile Lys Asp Gly Ser Glu Leu Glu Gly Tyr Gln Phe
225 230 235 240

Val Leu Asn Ala Glu Lys Ser Arg Thr Val Lys Glu Lys Ser Lys Phe
245 250 255

Phe Ile Asp Val Lys Phe Asp Gly Gly Ile Asp Pro Tyr Ser Gly Leu
260 265 270

Leu Asp Met Ala Leu Asp Ile Gly Phe Val Val Lys Pro Lys Asn Gly

275 280 285

Trp Tyr Ala Arg Glu Phe Leu Asp Val Glu Thr Gly Glu Met Ile Arg
290 295 300

Glu Glu Lys Ser Trp Arg Ala Lys Asp Thr Ser Ser Thr Glu Phe Trp
305 310 315 320

Gly Pro Leu Phe Lys His Glu Pro Phe Arg Asp Ala Ile Lys Ala Arg
325 330 335

Tyr Gln Leu Gly Ala Ile Asp Ser Asn Ala Ala Val Asp Glu Ala Val
340 345 350

Ala Glu Met Ile Asn Ser Lys Val Ser Thr Lys Val Asp Gly Val Lys
355 360 365

Leu Pro Glu Ser Gly Ser Val Ser Ala Ala Glu Val Glu Asp Glu Leu
370 375 380

Glu Asn Phe Met Asn Glu Asp
385 390

<210> 945
<211> 116
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 945
Met Lys Thr Glu Phe Asp Leu Glu Ser Glu Leu Glu Lys Phe Glu Gln
1 5 10 15

Glu Ser Pro Ser Glu Glu Gly Asp Phe Glu Arg Gln Glu Arg Val Phe
20 25 30

Lys Lys Ser His Glu Ile Ile Gln Glu Ala Met Lys Thr Val Ile Gln
35 40 45

Glu Ile Val Ile Lys Leu Asn Gly Gln Ser His Leu Val Tyr Val His
50 55 60

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

Pro Ser Glu Ala His Lys Asp Glu Leu Tyr Pro His Val Glu Ala Cys
85 90 95

Val Lys Gln Gln Ile Gln Ser Ala Leu Lys Thr Lys Lys Lys Ser Leu
100 105 110

Trp Lys Ile Phe
        115

<210> 946
<211> 479
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 946
Val Val Glu Thr Ile Leu Ala Asn Leu Ile Tyr Asn Gln Ala Phe Phe
1   5   10   15

Thr Lys Val Trp Pro Tyr Met Asp Lys Glu Tyr Phe Glu Gln Gly Pro
            20   25   30

Ala Gln Thr Val Phe Asn Ile Ile Lys Lys His Val Asn Glu Tyr Thr
        35   40   45

Ala Ile Pro Ser Lys Thr Ala Leu Cys Val Ala Leu Asp Asn Ser Ser
    50   55   60

Ile Thr Glu Thr Glu His Glu Gly Ala Lys Lys Leu Ile Asp Lys Leu
65   70   75   80

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

Tyr Val Gln Glu Lys Ala Met Tyr Asn Ala Thr Ser Arg Ile Ile Glu
            100   105   110

Ile Gln Thr Asn Ala Gln Leu Glu Pro Asn Lys Arg Asp Lys Arg Leu
        115   120   125

Pro Asp Ile Gly Ala Ile Pro Asp Ile Met Arg Glu Ala Leu Ser Val
    130   135   140

Ser Phe Asp Ser Tyr Ile Gly His Asp Trp Met Glu Asp Tyr Glu Ala
145   150   155   160

Arg Trp Leu Ser Tyr Gln Asn Lys Ala Arg Lys Val Pro Phe Lys Leu
                165   170   175

Ser Ile Leu Asn Lys Ile Thr Lys Gly Gly Ala Glu Thr Gly Thr Leu
            180   185   190

Asn Val Leu Met Ala Gly Val Asn Val Gly Lys Ser Leu Gly Leu Cys
        195   200   205

Ser Leu Ala Ala Asp Tyr Leu Gln Met Gly His Asn Val Leu Tyr Ile
    210   215   220

```
Ser Met Glu Met Ala Glu Glu Val Cys Ala Lys Arg Ile Asp Ala Asn
225                 230                 235                 240

Leu Leu Asp Val Ser Leu Asp Asp Ile Asp Asp Gly Cys Val Ser Tyr
                245                 250                 255

Ala Glu Tyr Lys Gly Lys Met Glu Lys Trp Arg Ser Ser Ser Thr Leu
            260                 265                 270

Gly Arg Leu Ile Ile Lys Gln Tyr Pro Thr Gly Gly Ala Asn Ala Asn
        275                 280                 285

Thr Phe Arg Ala Leu Leu Asn Glu Leu Lys Leu Lys Lys Asn Phe Lys
    290                 295                 300

Pro Thr Val Ile Ile Ile Asp Tyr Leu Gly Ile Cys Ala Ser Cys Arg
305                 310                 315                 320

Ile Arg Gln Tyr Thr Glu Asn Ser Tyr Thr Leu Val Lys Ala Ile Ala
                325                 330                 335

Glu Glu Leu Arg Ala Leu Ala Val Glu Ser Glu Thr Val Leu Trp Thr
            340                 345                 350

Ala Ala Gln Val Gly Arg Ser Ala Trp Asp Ala Ser Asp Met Asp Met
        355                 360                 365

Ser Asp Ile Ala Glu Ser Ala Gly Leu Pro Ala Thr Ala Asp Phe Met
    370                 375                 380

Leu Ala Val Ile Glu Thr Pro Glu Leu Ala Gln Met Lys Gln Gln Leu
385                 390                 395                 400

Ile Lys Gln Ile Lys Ser Arg Tyr Gly Asp Lys Asn Ile Asn Asn Lys
                405                 410                 415

Phe Ser Met Gly Val His Lys Ala Asn Gln Arg Trp Val Glu Ile Glu
            420                 425                 430

Gln Gln Asn Asp Pro Thr Lys Pro Asn Pro Ser Asn Thr Val Arg Glu
        435                 440                 445

Gly Ala Gly Ala Gln Asn Arg Val Ala Glu Ser Asn Arg Gln Glu Arg
    450                 455                 460

Val Ser Arg Ser Lys Leu Asp Ala Leu Ala Glu Glu Leu Lys Phe
465                 470                 475
```

<210> 947
<211> 77
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 947
Met Ile Phe Val Phe Ser Val Ile Arg Asp Gln Ser Gly Arg Ser Phe
1   5   10   15

Val Val Thr Ala Ser Asp Ser Val His Arg Gly Val Ile Ala Tyr Asn
            20   25   30

Lys Ala Asp Leu Ser Ser Tyr Asp Tyr Gly Glu Val Lys Ala Tyr Asn
        35   40   45

Asp Glu Gly Ile Trp Val Asn Ser Ala Ile Tyr Leu Pro Thr Lys Asn
    50   55   60

Leu Thr Ser Asp Glu Val Leu Glu Lys Leu Phe Lys Arg
65   70   75

<210> 948
<211> 97
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 948
Met Lys Lys Ile Val Leu Ala Leu Ile Phe Ala Val Ser Ser Cys Ser
1   5   10   15

Ala Val Pro Ala Leu Ala Asn Tyr Asp Lys Asp Leu Cys Glu Trp Ser
            20   25   30

Met Thr Ala Asp Glu Lys Asp Val Ala Glu Gln Ile Arg Ala Asp Val
        35   40   45

Gly His Ile Ile Asp Asn Thr Asp Pro Ser Lys Met Lys Glu Val Gln
    50   55   60

Ala Glu Ile Ser Asn Asp Gly Ala Ala Ile Lys Leu Asn Tyr Ala Leu
65   70   75   80

Tyr Cys Asp Ala Asn Phe Asp Asn Phe Thr Ile Ala Ser Trp Ile Leu
                85   90   95

Gly

<210> 949
<211> 72
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 949
Met Ile Thr Tyr Val Leu Val Met Ala Ile Met Thr Gly Ala Gly Gly
1   5   10   15

Val Ser Thr Glu Lys Leu Ser Phe Thr Gly Met Asn Glu Ser Ser Leu
            20   25   30

Ala Gln Lys Cys Glu Asp Ala Gly Lys Gln Phe Thr Gly Ile Lys Ala
        35   40   45

Asp Ser Gly Phe Gly Ser Pro Ser Val Tyr Thr Thr Tyr Lys Cys Ile
    50   55   60

Arg Ile Asp Gly Gly Asn Asn Lys
65   70

<210> 950
<211> 55
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 950
Met Lys Thr Phe Lys Glu Phe Val Lys Leu Asn Glu Glu Met Val Ala
1   5   10   15

Gly Asp Ala Gly Gly Asn Pro Gln Asn Ile Ala Ser Gly Thr Thr Ser
            20   25   30

Gly Ala Val Val Asn Lys Gly Pro Glu Thr Leu Pro Lys Lys Lys Arg
        35   40   45

Asp Lys Ser Lys Pro Glu Thr
    50   55

<210> 951
<211> 340
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 951
Met Ser Trp Val Asp Asn Glu Phe Ala Ile Arg Ala Ile Ser His Leu
1   5   10   15

Pro Lys Phe Arg His Val Thr Thr Ser Ser Thr Phe Lys Leu Asn Cys
            20   25   30

Arg Cys Pro Ile Cys Gly Asp Ser Gln Lys Asp Ile Asn Lys Ala Arg
        35   40   45

```
Phe Trp Ile Phe Asp Ala Gly Gln Gly Leu Arg Cys His Cys Phe Asn
    50                  55                  60

Cys Glu Tyr Asn Lys Trp Leu Ser Gln Tyr Leu Lys Asp Asn Glu Pro
65                  70                  75                  80

Asp Leu Tyr Arg Glu Tyr Leu Leu Glu Lys Arg Lys Glu Gln Val Phe
                85                  90                  95

Asp Lys Pro Lys Thr Val Glu Pro Ser Glu Lys Ile Asn Ala Lys Leu
            100                 105                 110

Pro Val Ile Glu Lys Leu Asn Phe Cys Glu Arg Leu Asp Arg Leu Pro
        115                 120                 125

Lys Glu His Pro Ile Val Lys Tyr Val Thr Ala Arg Cys Ile Pro Ser
    130                 135                 140

Thr Ser Trp Lys Arg Leu Trp Phe Thr Asn Gln Trp Pro Ser Leu Val
145                 150                 155                 160

Asn Ser Val Asn Pro Gly Thr Tyr Lys Asn Glu Thr Asn Glu Pro Arg
                165                 170                 175

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

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

Ala His Glu His Ala Thr Lys Ile Tyr Gly Leu Asp Thr Ile Asp Glu
    210                 215                 220

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

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

Pro Cys His Asp Asn Arg Ala Trp Ile Met Asp His Glu Pro Arg His
            260                 265                 270

Pro Asp Thr Ile Lys Arg Met Lys Arg Leu Val Asp Ala Gly Glu Lys
        275                 280                 285

Val Val Phe Trp Asp Lys Ser Pro Trp Lys Ser Lys Asp Ile Asn Asp
    290                 295                 300

Met Ile Met Lys Glu Gly Ala Thr Ala Ser Glu Ile Thr Asp Tyr Ile
305                 310                 315                 320
```

Asn Gln Asn Ile Ser Gln Gly Leu Met Ala Lys Leu Arg Leu Asp Lys
325 330 335

Tyr Ala Lys Ile
340

<210> 952
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 952
Met Ser Glu Val Lys Arg Glu Cys Lys Asp Lys Gly Gly Phe Gly Arg
1 5 10 15

Tyr Leu Tyr Val Gly Ile Ala Thr Ala Ala Leu Ala Ala Trp Asn Tyr
20 25 30

Val Val Val Pro Leu Ala Ser Thr His Gly Leu Val Leu Pro Pro Met
35 40 45

Pro Leu Glu Lys Val Val Ser Phe Ile Met Thr Gly Gly Leu Leu
50 55 60

<210> 953
<211> 173
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 953
Met Pro His Phe Asn Glu Cys Ser Gln Leu Ile Ala Gly Ala Asp Lys
1 5 10 15

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

Leu Gln Val Met Leu Asp Met Gln Lys Ser Leu Gln Val Arg Leu Ala
35 40 45

Asn Asp Lys Pro Gly Thr Asn Met His Pro Asp Glu Leu Ala Gln Ala
50 55 60

Gly Asp Ile Val Gln Trp Leu Arg Asn Gln Lys Asp Tyr Ile Asp Asp
65 70 75 80

Glu Phe Arg Glu Leu Leu Thr Ser Leu Gly Gly Met Ser Asn Gly Glu
85 90 95

Lys Ala Ala Ser Ala Val Trp Lys Pro Trp Lys Ser Asp His Val Lys
100 105 110

Met Gln Glu Thr Tyr Ile Lys Asp Leu Ser Asp Lys Asp Gln Leu Glu
115 120 125

Ile Lys Phe Glu Met Ile Asp Ile Leu His Phe Val Leu Asn Met Phe
130 135 140

Met Ala Leu Gly Leu Asp Ser Glu Glu Ile Phe Lys Leu Tyr Tyr Leu
145 150 155 160

Lys Asn Ala Glu Asn Phe Ala Arg Gln Asp Ser Gly Tyr
165 170

<210> 954
<211> 45
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 954
Met Ala Lys Arg Ile Ser Lys Arg Arg Leu Lys Ile Ile Arg Lys Gln
1 5 10 15

Lys Glu Arg Ala Leu Val Leu Ala Leu Arg Glu Glu Ile Thr Arg Glu
20 25 30

Ile Asp Lys Glu Ile Leu Lys Ala Leu Thr Ala Ala Ile
35 40 45

<210> 955
<211> 78
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 955
Met Ala Tyr Val Asn Ile Lys Thr Phe Asp His Thr Thr Ala Asp Gly
1 5 10 15

Glu Val Lys Gly Thr Glu Val Ser Val Ala Phe Lys Val Tyr Ser Asp
20 25 30

Ser His Arg Ile Ala Asn Ala Gln Tyr Gln Ile Phe Pro Ser Glu Lys
35 40 45

Ala Ala Tyr Ser Thr Val Val Asp Asp Ala Ala Thr Trp Ala Thr Thr
50 55 60

Asn Ala Lys Met Phe Glu Ala Val Pro Ser Asp Ala Glu Val
65 70 75

<210> 956
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 956
Met Ile Cys Tyr Thr Lys Pro Trp Tyr Gln Ser Ser Leu Lys Lys Ser
1   5   10   15

His Phe Asp Cys Trp Tyr Arg Gly Val Arg Ala Ala Ala Leu Leu Leu
            20   25   30

Lys Ala Ala Pro Ala Leu Ile Lys Ala Asn Asp Lys Trp Phe Glu Asp
        35   40   45

Asn Asn Met Thr Glu Gly Ala Leu Cys Gly Lys Arg Lys Asn Leu
    50   55   60

<210> 957
<211> 174
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 957
Val Ala Asn Ala Lys Ile Tyr Asn Ala Lys Ile Tyr Lys Val Ser Leu
1   5   10   15

Gln Arg Ala Val Gln Ser Arg Ser Asp Ala Asn Gly Val Leu Arg Leu
            20   25   30

Asp Gln Asp Arg Ile Phe Thr Val Ala Leu Tyr Ser Thr Phe Asp Lys
        35   40   45

Asp Phe Lys Asp Leu Val Asn Lys Phe Glu Ala Phe Gly Trp Cys Pro
    50   55   60

Ser Glu Asp Tyr Gly Ile Ile Lys Thr Ala His Val Phe Asp Val Asp
65   70   75   80

Thr Val Pro Gly Ser Pro Val Ala Ile Leu Arg Ala Leu His Leu Lys
                85   90   95

Gly Tyr Thr Asn Val Cys His Glu Thr Ser Leu Tyr Glu Tyr Glu Asn
            100   105   110

Asp Ile Ile Ser Arg Gly Lys Lys Ile Ile Ile Asp Ser Thr Asp Ser
        115   120   125

Leu Ile Glu Phe Thr Lys Leu Val Trp Leu Tyr Met Gly Ala Asp Phe
130 135 140

Ile Lys Leu Thr Pro Ser Pro Leu Leu Gln Lys Ala Ala Asp Gly Tyr
145 150 155 160

Asn Ser Ser Ser Cys Leu Tyr Arg Asn Asn Glu Trp Phe Met
165 170

<210> 958
<211> 62
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 958
Met Asp Leu Phe Glu Met Met Glu Glu Pro Gln Glu Glu Val Gln Val
1 5 10 15

His Pro Val Ile Ser Lys Asp Ile Lys Asp Glu Tyr Arg Ile Ile Ile
20 25 30

Gln Lys Tyr Gly Ile Lys Ala Pro Glu Ala Leu Leu Asp Glu Leu Ala
35 40 45

Ser Ile Trp Ser Asp Pro Pro Pro Trp Ser Pro Trp Ala Lys
50 55 60

<210> 959
<211> 229
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 959
Met Ala Ile Ser Leu Asn Pro Ser Ile Ser Val Lys Leu Ser Lys Val
1 5 10 15

Ile Pro Ile Glu Lys Pro Ile Arg Ser Ile Asp Val Leu Asn Phe Ala
20 25 30

Arg Glu Ser Lys Gly Leu Pro Leu Tyr Asp Leu Ser Val Trp Glu Ala
35 40 45

Leu Ala Asn Arg Phe Asp Cys Lys Glu Gln Ser Ile Leu Trp Gln Cys
50 55 60

Met Asn Asn Lys Ile Gly Glu Glu Phe His Lys Lys Leu Asp Ser Ile
65 70 75 80

Val Arg Arg His Gln Ile Asp Asn Ser Asp Ile Leu Tyr Arg Gly Leu
85 90 95

```
Ser Cys Arg Glu Ser Lys Ala Phe Tyr Asp Ala Leu Ile Lys Gly Glu
            100                 105                 110

Lys Phe Gly Phe Gly Lys Val Ala Ser Phe Thr Thr Asp Glu Thr Ile
        115                 120                 125

Ala Arg Glu Phe Ala Gly Lys Trp His Tyr Ser Thr Phe Val Val Ile
    130                 135                 140

Glu Val Asn Asn Cys His Gln Ser Phe Asp Tyr His Thr Asn Met Lys
145                 150                 155                 160

Ser Leu Leu Ile Thr Ala Pro Asp Ser Glu Phe Met Arg Pro Asn Asp
                165                 170                 175

Val Ile Asp Asn Ile Ala Gln Arg Arg Ser Ala Asp Ile Glu Met Ile
            180                 185                 190

Asp Lys Glu Gln Glu Arg Met Leu Pro Met Gly Thr Lys Phe Lys Val
        195                 200                 205

Val Gly His Asn Lys Val Glu Lys Ser Gly Leu Leu Met Asp Tyr Phe
    210                 215                 220

Ser Val Thr Ile Ala
225


<210> 960
<211> 252
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 960
Met Met Lys Phe Thr Ala Glu Thr Ala Lys Ile Tyr Thr Arg Leu Ile
1               5                   10                  15

Thr Thr Leu Gly Ser Ala Gln Arg Arg Asn Lys Glu Phe Asn Leu Thr
            20                  25                  30

Pro Glu Tyr Leu Phe Asn Ile Met Gln Gln Thr His Cys Ala Tyr Ser
        35                  40                  45

Gly Glu Lys Phe Gly Thr Val Lys Gly Asn His Pro Asp Ser Met Thr
    50                  55                  60

Leu Glu Arg Trp Asn Asn Asp Leu Gly Tyr Val Met Gly Asn Val Ile
65                  70                  75                  80

Pro Val Lys Gln Lys Tyr Asn Thr Leu Arg Gly Asn Asn Thr Ile Glu
```

85 90 95

Gly Leu Glu Arg Lys Ala Asn Glu Ile Ala Ala Arg Ile Val Arg Ser
100 105 110

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

Lys Ile Arg Glu Tyr Glu Lys Thr Ile Thr Ser Ile Lys Thr Asn Leu
130 135 140

His Asn Arg Glu Asn His Leu Ser Gln Phe Val Gln Lys Glu Lys Asn
145 150 155 160

Gly Thr Ala Thr Ser Ala Asp Leu Glu Leu Ile Asn Ala Leu Arg Thr
165 170 175

Arg Ile Ser Gly Gly Lys Ser Glu Leu Ala Lys Val Glu Arg Lys Leu
180 185 190

Ser Ala Ile Leu Ala Ser Val Pro Asn Arg Pro Ser Asp Ala Glu Ile
195 200 205

Arg Val Gln Ser Ile Arg Leu Ile Val Ser Ser Leu Arg Arg Leu Glu
210 215 220

Glu Cys Ser Met Leu Asp Lys Leu Lys Leu Lys Lys Gly Leu Pro Leu
225 230 235 240

Thr Ala Ser Phe Phe Gln Leu Leu Arg Gly Lys Met
245 250

<210> 961
<211> 104
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 961
Met Gln His Tyr Gly Tyr Val Val Ala Tyr Lys Asp Lys Asp Gly Phe
1 5 10 15

Asp His Pro Val Thr Thr Asp Met Tyr Asp Gly Glu Arg Cys Val Val
20 25 30

Phe Thr Asn Glu Glu Ser Ala Asn Lys Ala Arg Ile Arg Thr Met Ser
35 40 45

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

Thr Lys Gly Met Leu Trp Trp Lys Thr Thr Glu Leu Val Tyr Glu Pro
65 70 75 80

Leu Ser Asp Val Glu Arg Glu Lys Leu Lys Ala Lys Ile Lys Asn Leu
85 90 95

His Val Val Arg Val Lys Val Ala
100

<210> 962
<211> 443
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 962
Met Ile Thr Phe Asp Gln Leu Lys Glu Ser Gln Lys Ala Ile Phe Asn
1 5 10 15

Lys Val Ile Glu Met Val Lys Gln Gly Ala Lys Gly Gln His Ile Thr
20 25 30

Ile Asn Gly Pro Ala Gly Thr Gly Lys Thr Thr Leu Thr Lys Phe Ile
35 40 45

Ile Asp Ala Leu Ile Ser Gln Gly Ile Ser Gly Ile Ala Leu Ala Ala
50 55 60

Pro Thr His Gly Ala Lys Lys Val Leu Ser Lys Leu Ser Gly Met Gln
65 70 75 80

Ala Ser Thr Ile His Ser Leu Leu Lys Ile Asn Pro Thr Thr Tyr Glu
85 90 95

Glu Asn Val Leu Phe Glu Gln Lys Lys Val Pro Asp Met Ala Ser Ile
100 105 110

Arg Val Leu Ile Cys Asp Glu Ala Ser Met Tyr Asp Arg Lys Leu Phe
115 120 125

Lys Ile Leu Met Ala Thr Ile Pro Ala Trp Cys Ile Val Ile Ala Ile
130 135 140

Gly Asp Lys Ala Gln Ile Arg Pro Val Glu Pro Gly Ser Asn Glu Pro
145 150 155 160

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

Thr Glu Val Met Arg Ser Asn Ala Pro Ile Ile Glu Val Ala Thr Glu
180 185 190

```
Ile Arg Asn Gly Gly Trp Ile Arg Asp Cys Val Val Asp Gly His Gly
        195                 200                 205

Val Arg Gly Phe Thr Lys Gly Thr Ala Leu Lys Asp Phe Met Leu Asn
    210                 215                 220

Tyr Phe Asn Leu Val Lys Thr Pro Glu Asp Leu Phe Glu Asn Arg Met
225                 230                 235                 240

Leu Ala Phe Thr Asn Lys Ser Val Asp Lys Leu Asn Glu Ile Ile Arg
                245                 250                 255

Arg Arg Ile Tyr Glu Thr Glu Arg Pro Phe Val Val Gly Glu Ile Val
            260                 265                 270

Val Met Gln Glu Pro Leu Thr Lys Glu Leu Lys Phe Glu Gly Lys Lys
        275                 280                 285

Phe Ser Glu Ile Leu Phe Asn Asn Gly Gln Phe Val Arg Ile Leu Asp
    290                 295                 300

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

Tyr Leu Val Arg His Trp Val Leu Asp Ile Glu Thr Tyr Gly Asp Asp
                325                 330                 335

Glu Glu Tyr Ala Arg Glu Lys Ile Cys Val Ile Ser Ser Glu Glu Glu
            340                 345                 350

Met Asn Lys Phe Gln Phe Phe Leu Ala Lys Thr Ala Asp Thr Tyr Lys
        355                 360                 365

Asn Trp Asn Lys Gly Gly Lys Ala Pro Trp Ser Glu Phe Trp Asp Ala
    370                 375                 380

Lys Arg Lys Phe His Lys Val Lys Ala Leu Pro Ala Ser Thr Phe His
385                 390                 395                 400

Lys Ala Gln Gly Ile Ser Ile Asp Arg Ser Phe Ile Tyr Thr Pro Cys
                405                 410                 415

Ile His Met Ala Asp Ala Ser Leu Ala Gln Gln Leu Leu Tyr Val Gly
            420                 425                 430

Thr Thr Arg Gly Arg Tyr Asp Val Phe Tyr Val
        435                 440
```

<210> 963
<211> 84
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 963
Met Phe Glu Leu Lys Leu Glu Asp Leu Gln Thr Met Ile Val Gly Leu
1   5   10   15

Gln Glu Ser Lys Phe Glu Ala Pro Asp Asn Val Lys Arg Ala Ile Asn
            20   25   30

Ile Lys Ile Asp Ile Val Leu Asn Glu Leu Arg Asp Ile Ala Asp Asn
        35   40   45

Ala Asn Ala Ile Thr Trp Phe Thr Gly Tyr Asp Pro Lys Val Tyr Leu
    50   55   60

Ser Glu Tyr Ile Gly Cys Gln Leu Arg Glu Ile Lys Phe Met Leu Glu
65   70   75   80

Ala Gln Asn Gly

<210> 964
<211> 229
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 964
Met Ala Lys Asp Phe Ile Ile Asp Phe Glu Thr Phe Gly Asn Val Ser
1   5   10   15

Ser Ser Ser Val Ile Asp Leu Ala Leu Ile Thr Phe Asp Ser Asp Pro
            20   25   30

Glu Val Leu Glu Ser Phe Asp Glu Leu Val Lys Arg Gly His Arg Ile
        35   40   45

Lys Phe Asp Leu Lys Ser Gln Lys Gly His Arg Leu Phe Gly Lys Ser
    50   55   60

Thr Leu Glu Trp Trp Lys Lys Gln Ser Ala Glu Ala Arg Ala Asn Leu
65   70   75   80

Ala Ser Thr Pro Asp Asp Leu Ser Val Ile Ala Gly Ile Lys Glu Ala
                85   90   95

Gln Gln Tyr Leu Ile Asp Asn Gly Ile His Pro Trp Asp Ser Phe Gly
            100   105   110

Trp Cys Arg Gly Gln Ser Phe Asp Phe Pro Ile Phe Val Asp Cys Leu

115 120 125

Arg Asp Val Gln Arg Ala Gln Gly Ile Ser Glu Glu Glu Ile Asp Thr
130 135 140

Phe Lys Glu Glu Pro Cys Lys Phe Trp Asn Gln Arg Asp Ile Arg Thr
145 150 155 160

Ala Ile Glu Ser Leu Leu Leu Thr Arg Gly Leu Thr Thr Thr Pro Leu
165 170 175

Pro Lys Gly Thr Leu Asn Gly Phe Ile Ala His Asp Ser Ile His Asp
180 185 190

Cys Ala Lys Asp Ile Leu Met Leu Lys Tyr Ala Gln Arg Tyr Ala Leu
195 200 205

Gly Leu Ser Glu Ala Pro Ser Pro Glu Asp Thr Asp Pro Leu Ser Leu
210 215 220

Pro Lys Gly Arg Gly
225

<210> 965
<211> 55
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 965
Met Glu Glu Phe Glu Phe Asp Glu Asn Phe Glu Glu Trp Phe Asn Arg
1 5 10 15

Glu Ile Leu Pro Lys Ile Ser Pro Thr Met Val Leu Val Ala Lys Ala
20 25 30

Leu Met Ala Lys Gly Trp Asp Ala Gly Tyr Met Phe Gly Val Asp Val
35 40 45

Gly Cys Glu Ile Ser His Arg
50 55

<210> 966
<211> 147
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 966
Met Met Lys Asn Leu Val Val Gly Glu Asn Val Lys Val Ile Gly Gly
1 5 10 15

```
Lys His Ile Gly Lys Glu Gly Val Ile Val Gly Ile Phe Asn Arg Ser
            20                  25                  30

Asn Lys Met Ser Ser Tyr Leu Leu Gln Leu Glu Asn Glu Asp Lys Ala
        35                  40                  45

Val Tyr Ser Leu Gln Lys Phe Val Val Ala Leu Glu Ser Arg Asp Leu
    50                  55                  60

Leu Asp Ser Met Phe Asn Glu Ser Tyr Leu Arg Lys Trp Val His Val
65                  70                  75                  80

Asn Ser Leu Asp Asn Val Ile Thr Gln Ser Val Ser Ser Thr Asn Ser
                85                  90                  95

Ala Thr Asn Leu Ser Leu His Lys Asn Val Leu Val Thr Asp Glu Trp
            100                 105                 110

Glu Glu Asp Gly Lys Thr Leu Val Asn Val Val Phe Gln Gly Asn Tyr
        115                 120                 125

Ala Val Leu Pro Lys Ala Asp Val Glu Pro Thr Glu Ser Gln Arg Gln
    130                 135                 140

Gly Leu Val
145


<210> 967
<211> 71
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 967
Met Lys Thr Glu Asn Thr Val Lys Ile Thr Ala Glu Ala Phe Glu Asp
1               5                   10                  15

Ile Leu Phe Asn Pro Asp Leu Ile Val Val Gln Lys Glu Lys Thr Phe
            20                  25                  30

Gly Lys Glu Glu His Trp Thr Trp Leu Tyr Val Phe Ala Asn His Gly
        35                  40                  45

Asp Ile Val Pro Val Arg Thr Phe Ala Arg Val Ile Thr Val Asp Gly
    50                  55                  60

Pro Glu Tyr Met Glu Ile Val
65                  70


<210> 968
<211> 121
```

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 968
Met Asn Phe Lys Glu Gly Val Gln Tyr Lys Phe Val Asn Asp Glu Ala
1   5   10   15

Glu Glu Glu Phe Ser Ser Arg Tyr Glu Val Asn Glu Asp Phe Val Tyr
            20   25   30

Glu Leu Tyr Glu Asn Gly Gly Ser Phe Thr Val Thr Lys Val Asp Arg
        35   40   45

Gln Asn Asn Arg Val Ser Gly Ile Met Trp Ala Asn Gly Thr Glu Cys
    50   55   60

Asp Glu Val Gly Gly Glu Asp Leu Val Ile Phe Asp Ser Glu Phe Lys
65   70   75   80

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

Val Met Asn Leu Ser Ile His Asn Arg Gly Gln Ala Ile Ala Ala Ile
            100   105   110

Ala Ala Leu Gln Ser Ala Tyr Gln Cys
        115   120

<210> 969
<211> 111
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 969
Met Leu Asn Leu Ala Pro Ile Phe Glu Ala Ser Lys Leu Ser Tyr Pro
1   5   10   15

Ile Pro Asn Arg Ser Ile Gly Asn Val Met Leu Gln Leu Ser Ser Glu
            20   25   30

Thr Gly Glu Met Cys Asp Trp Ile Asn Arg Pro Trp Arg Gln Lys Glu
        35   40   45

Glu Phe Glu Gly Glu Cys Ala Asp Val Ile Asn Cys Val Val Asp Ala
    50   55   60

Leu Trp Leu His Phe Arg Asn Arg His Lys Asn Asp Thr His Val Ser
65   70   75   80

Asp Asp Glu Ile Ser Met Met Val Thr Arg Ala Leu Asn Glu Gln Ile
85 90 95

Met Val Lys Thr Gln Lys Trp Lys Asp Ala Val Asn Ala Asn Val
100 105 110

<210> 970
<211> 58
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 970
Met Pro Met Tyr Asp Tyr Lys Cys Glu Val Cys Gly Lys Lys Ile Glu
1 5 10 15

Ile Met Arg Lys Ile Ser His Arg Asp Tyr Thr Val Asn Cys Phe Asn
20 25 30

Pro Lys Cys Glu Gly Gln Met Lys Arg Val Val Ser Ala Pro Ala Val
35 40 45

His Tyr Asp Gly Leu Lys Ser Gly Asp Tyr
50 55

<210> 971
<211> 82
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 971
Met Lys Lys Ile Leu Ile Thr Ala Leu Ala Phe Met Met Ile Gly Cys
1 5 10 15

Thr Asp Ala Asp Asn Ala Thr Arg Val Leu Glu Asn Ala Gly Phe Thr
20 25 30

Glu Val Asp Ile Thr Gly Tyr Lys Phe Phe Ser Cys Ser Glu Asp Asp
35 40 45

Phe Gln His Thr Gly Phe Lys Ala Val Gly Pro Thr Gly Lys Thr Val
50 55 60

Lys Gly Thr Val Cys Ser Gly Ile Phe Leu Lys Asn Ser Thr Ile Arg
65 70 75 80

Phe Glu

<210> 972
<211> 65

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 972
Met Lys Tyr Ile Ile Leu Thr Leu Ile Ala Leu Val Ile Ser Ile Gly
1 5 10 15

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

Lys Ser Ser Ile Gly Ile Gly Val Asn Gly Gln Val Gly Val Lys Ile
35 40 45

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

Phe
65

<210> 973
<211> 612
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 973
Met Ile Lys Asn Glu Ile Lys Ile Leu Ser Asp Arg Glu His Ile Ile
1 5 10 15

Lys Arg Ser Gly Met Tyr Ile Gly Ser Ser Ala Cys Glu Ala His Asp
20 25 30

Arg Phe Leu Phe Gly Lys Phe Gln Ser Val Lys Tyr Val Pro Gly Ile
35 40 45

Ile Lys Leu Ile Asp Glu Ile Ile Asp Asn Ser Val Asp Glu Ala Ile
50 55 60

Arg Thr Asn Phe Lys His Ala Asn Lys Ile Ser Val Asp Ile Lys Gly
65 70 75 80

Asn Lys Ile Ile Val Thr Asp Asn Gly Arg Gly Leu Pro Gln Ala Pro
85 90 95

Val Val Thr Pro Glu Gly Glu Thr Ile Pro Gly Pro Val Ala Ala Trp
100 105 110

Thr Arg Pro Arg Ala Gly Gly Asn Phe Gly Asp Asp Ala Glu Arg Lys
115 120 125

```
Thr Gly Gly Met Asn Gly Val Gly Ser Ala Leu Thr Asn Ile Phe Ser
    130                 135                 140

Val Ser Phe Thr Gly Ala Thr Cys Asp Gly Lys Asn Glu Ile Ile Val
145                 150                 155                 160

Arg Cys Ser Asn Gly Ser Glu Asn Ile Ser Trp Glu Glu His Pro Ala
                165                 170                 175

Lys Asp Lys Glu Phe Ile Lys Asp Lys Thr Gly Thr Val Val Ser Phe
            180                 185                 190

Ile Pro Asp Phe Ser His Phe Glu Ser Thr Gly Leu Thr Asp Val Asp
        195                 200                 205

Gln Ser Ile Ile His Asp Arg Leu Met Thr Leu Ala Val Val Tyr Pro
    210                 215                 220

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

Ala Tyr Ala Gln Met Tyr Asp Glu Asn Ala Val Val Gln Asp Ser Asp
                245                 250                 255

Thr Cys Ala Ile Ala Ile Gly Arg Ser Asp Asp Gly Phe Arg Gln Leu
            260                 265                 270

Ser Tyr Val Asn Asn Ile His Thr Lys Asn Gly Gly Thr His Val Asp
        275                 280                 285

Leu Val Leu Asp Glu Leu Ser Asn Glu Leu Ile Pro Ala Leu Lys Arg
    290                 295                 300

Lys Tyr Lys Leu Glu Val Asn Lys Ala Arg Ile Lys Glu Cys Leu Thr
305                 310                 315                 320

Val Ile Met Phe Ile Arg Asp Met Ser Asn Met Arg Phe Asp Ser Gln
                325                 330                 335

Thr Lys Glu Arg Leu Thr Ser Pro Trp Gly Glu Ile Arg Ser His Ile
            340                 345                 350

Asp Ile Asp Tyr Lys Lys Leu Ala Asn Ala Ile Met Lys Ser Glu Asp
        355                 360                 365

Ile His Met Pro Ile Ile Glu Ala Met Leu Ala Arg Lys Leu Ala Ala
    370                 375                 380

Glu Lys Ala Ala Glu Thr Lys Ala Ala Lys Lys Ala Gln Lys Ala Lys
385                 390                 395                 400
```

```
Val Ala Lys His Ile Lys Ala Asn Lys Tyr Gly Lys Asp Ala Asp Thr
                405                 410                 415

Thr Leu Phe Leu Thr Glu Gly Asp Ser Ala Ile Gly Tyr Leu Leu Thr
            420                 425                 430

Thr Arg Asp Arg Glu Leu His Gly Gly Tyr Pro Leu Arg Gly Lys Phe
        435                 440                 445

Met Asn Thr Trp Gly Met Ser Ala Ala Asp Ala Met Lys Asn Lys Glu
    450                 455                 460

Val Phe Asp Ile Cys Ala Ile Thr Gly Leu Thr Ile Gly Glu Pro Ala
465                 470                 475                 480

Glu Asn Thr Asn Tyr Arg Asn Ile Ala Ile Met Thr Asp Ala Asp Val
                485                 490                 495

Asp Gly Val Gly Ser Ile Phe Pro Ser Leu Leu Ala Phe Phe Ser Asn
            500                 505                 510

Trp Pro Glu Leu Phe Glu Gln Gly Arg Ile Arg Phe Val Lys Thr Pro
        515                 520                 525

Val Ile Ile Leu Thr Lys Gly Lys Glu Gln Arg Trp Phe Tyr Ser Leu
    530                 535                 540

Gly Glu Tyr Glu Asp His Lys Asp Asp Phe Lys Gly Trp Lys Leu Arg
545                 550                 555                 560

Tyr Ile Lys Gly Leu Gly Ser Leu Glu Glu Asp Glu Tyr Glu Arg Val
                565                 570                 575

Ile Gln Asp Pro Val Tyr Asp Val Val Ser Leu Pro Glu Asn Trp Lys
            580                 585                 590

Glu Leu Phe Glu Leu Ile Met Gly Asn Asp Ala Ala Pro Arg Lys Thr
        595                 600                 605

Trp Met Ser Glu
    610


<210> 974
<211> 50
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 974
Met Gln Arg Tyr Trp Ile Thr Leu Val Ser Gly Asp Tyr Gly Tyr Met
1               5                   10                  15
```

Phe Ala Glu Lys Lys Pro Leu Pro Gly Thr Trp Val Thr Ile Trp Val
            20   25   30

Glu Asn Ser Asp Gly Ser Lys His Glu Val Tyr Gly Arg Val Ser Arg
        35   40   45

Val His
    50

<210> 975
<211> 82
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 975
Met Lys Ser Thr Ile Ile Ser Ile Leu Arg Thr Glu Ala Leu Lys Tyr
1   5   10   15

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

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

Asn His Ser Leu Phe Ala Met Lys Val Ile Arg Phe Leu Arg Pro Asp
    50   55   60

Ile Lys Ile Ala Asp Met Val Lys Val Ile Lys Ser Ser Gly Ala Val
65   70   75   80

Lys Cys

<210> 976
<211> 69
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 976
Met Leu Lys Lys Ser Tyr Val Pro Asn Lys Glu Leu Phe Asp Asp Ala
1   5   10   15

Ile Tyr Arg Glu Tyr Arg Ile Ile Gln Arg Phe Phe Asp Ile Gln Ala
            20   25   30

Ala Glu Glu Phe Lys Asp Arg Phe Lys Gln Ile Ser Asp Lys Ile Phe
        35   40   45

Thr Thr Asn Thr Ala Thr Ala Glu Glu Leu Leu Glu Val Ala Glu Ile

50 55 60

Ile Lys Arg His Asn
65

<210> 977
<211> 725
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 977
Met Lys Ile Lys Cys Asp Asp Glu Val Ile Ile Gly Ser Ser Asp Ala
1 5 10 15

Glu Asp Ser Thr Phe Thr Ile Lys Ala Ser Gly Lys Ala Phe Asp Ile
20 25 30

Leu Ser Asn Lys Leu Tyr Lys Tyr Lys Val Arg Ala Val Val Arg Glu
35 40 45

Leu Ser Thr Asn Cys Asp Asp Ala His Lys Leu Asn Gly Asn Glu Asn
50 55 60

Arg Pro Phe Tyr Ile Lys Ala Pro Thr Arg Leu Asp Pro Arg Phe Val
65 70 75 80

Ile Arg Asp Tyr Gly Pro Gly Leu Asn His Asn Asp Met Met Thr Met
85 90 95

Tyr Lys Thr Phe Phe Glu Ser Thr Lys Asn Asn Ser Asn Asp Phe Ile
100 105 110

Gly Ala Leu Gly Leu Gly Ser Lys Ser Pro Leu Ser Tyr Thr Ser Thr
115 120 125

Phe Asn Val Val Ser Tyr His Asn Gly Lys Ala Thr Gly Tyr Thr Val
130 135 140

Met Lys Asn Arg Gly Glu Pro Thr Ile Arg Pro Met Phe Val Asp Asp
145 150 155 160

Met Lys Glu Asp Glu Glu Thr Gly Leu Glu Ile Thr Val Pro Val Lys
165 170 175

Val Glu Asp Ile Asp Thr Trp His Tyr Glu Ile Ala Tyr Ile Leu Arg
180 185 190

Thr Phe Gly Ala Val Pro Pro Lys Val Asp Ser Leu Arg Arg Glu Ile
195 200 205

```
Glu Tyr Phe Pro Val Asp Lys Thr Asp Trp Phe Ser Val Asn Ser Ser
    210                 215                 220

Tyr Glu Ser Tyr Gly Leu Tyr Ala Val Tyr Gly Lys Ile Val Tyr Pro
225                 230                 235                 240

Ile Ser Gly Val Asp Val Lys Ala Asp Trp Leu Leu Asn Arg Tyr Gly
                245                 250                 255

Lys Val Tyr Val His Phe Pro Leu Gly Glu Leu Asp Ile Thr Pro Ser
            260                 265                 270

Arg Glu Glu Leu Ser Leu Asp Glu Glu Thr Ile Ala Asn Ile Gln Lys
        275                 280                 285

Arg Val Asn Ala Leu Glu Glu Glu Val Ile Thr Ala Asp Ile Lys Ala
    290                 295                 300

Phe Glu Ala Tyr Glu Ser Asp Arg Glu Phe Leu Arg Glu Phe Asn Lys
305                 310                 315                 320

Leu Ser Ser Lys Glu Arg Ser Ile Leu Gln Ser Arg Gly Ile Thr Ile
                325                 330                 335

Gly Asn Arg Asp Ile Lys Gln Val Val Ala Lys Tyr Asn Leu Asp Lys
            340                 345                 350

Ile Arg Ser Tyr Tyr Val Asp Asn Glu Val Ser Val Tyr Val Ser Cys
        355                 360                 365

Asp Glu Pro Ala Arg Arg Lys Val Ser Ser Ser Ser Trp His Arg His
    370                 375                 380

Asn Gln Val Asn Ile Ser Asp Ile Cys Gly Val Asp Arg Thr Lys Ala
385                 390                 395                 400

Phe Val Leu Ile Asp Asp Lys Ala Gly Lys Arg Ile Ala Thr Val Arg
                405                 410                 415

Ala Leu Cys Lys Ser Gly Leu Val Pro Ile Trp Ala His Ile Thr Val
            420                 425                 430

Ile Lys Asp Asn Glu Asp Glu Leu His Val Ile Asp Glu Leu Lys Lys
        435                 440                 445

Ile Met Asp Thr Asp Glu Val Val Val Phe Arg Val Ser Glu Leu Glu
    450                 455                 460

Ala Gln Arg Lys Ala Leu Pro Asp Tyr Asp Thr Gly Pro Lys Glu Lys
465                 470                 475                 480
```

```
Arg Pro Lys Ser Pro Asn Val Ser Leu His Trp Ile Asp Lys Asp Gly
                485                 490                 495

Tyr Trp Glu Glu Asp Arg Gln Thr Leu Leu Ser Ser Glu Ile Thr Glu
            500                 505                 510

Leu Glu Gly Tyr Ala Ile Gly Arg Asn Arg Asp Glu Ile His Thr Phe
        515                 520                 525

Pro Asp Asn Val Trp Trp Trp Asn Met Ser Ile Thr Asp Met Arg Ser
    530                 535                 540

Leu Ala Glu Ala Cys Gly Ile Lys Lys Phe Tyr Ala Ile Arg Pro Ser
545                 550                 555                 560

Ala Met Lys Ala Ala Ala Lys Ala Asp Gly Leu Leu Ser Phe Asp Arg
                565                 570                 575

Phe Ile Ile Asp Gln Tyr Ile Lys Cys Ile Asp Lys Val Asp Tyr Asp
            580                 585                 590

Gln Tyr Met Pro Ser Asn Ala Thr Gly Asn Arg Ile Cys Gly Asn Ile
        595                 600                 605

Ala His Tyr Asp Lys Leu Asn Phe Leu Ser Ser Lys Phe Thr Ala Ser
    610                 615                 620

Gly Met Lys Asn Pro Phe Leu Thr Lys Leu Asn Lys Ile Ala Lys Val
625                 630                 635                 640

Cys Arg Thr Ser Lys Ile Lys Asp Glu Asn Asp Glu Asn Asn Asp Leu
                645                 650                 655

Ala Leu Cys Asn Lys Ile Tyr Asn Lys Leu Ser Ser Asp Ala Glu Thr
            660                 665                 670

Ile Phe Tyr Lys Lys Ile Glu Gln Phe Lys Asp Asp Tyr Pro Val Ile
        675                 680                 685

Ala Ser Val Leu Asp Thr Trp Arg Thr Asp Ser Lys Leu Val Asp Asp
    690                 695                 700

Ile Val Lys Ile Met Glu Leu Leu Asp Gly Ala Ser Thr Gln Asn Ser
705                 710                 715                 720

Glu Asn Lys Gly Glu
                725
```

<210> 978
<211> 303
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 978

```
Met Ala Val Thr Cys Leu Ser Glu Ile Gln Lys Asp Ala Ile Val Lys
1               5                  10                  15

Asn Phe Lys Asn Gly Leu Tyr Thr Lys Lys Glu Leu Ala Glu Asn Tyr
            20                  25                  30

Gly Val Ser Arg Asp Thr Ile Arg Arg Val Phe Lys Glu Arg Glu Ala
        35                  40                  45

Arg Ala Ala Ala Ala Ala Val Pro Ala Lys Val Glu Ala Pro Val Glu
    50                  55                  60

Arg Glu Phe Lys Trp Ala Ala Ser Ser Lys Phe Ile Ser Ile Thr Glu
65                  70                  75                  80

Gly Arg Thr Thr Tyr Asn Ala Asp Ser Gln His Pro Gly Phe Lys Ser
                85                  90                  95

Ala Leu Gln Lys Leu Val Asp Gly Asp Ile Ala Gly Ala Ile Asp His
            100                 105                 110

Ile Asn Leu Glu Gln Gly Ile Lys Lys Phe Val Gln Gly Asn Val Arg
        115                 120                 125

Ile Glu Asp Gly Thr Leu Phe Tyr Lys Asp Ile Glu Leu Lys Ser Gly
    130                 135                 140

Leu Thr Glu Arg Ile Val Arg Ala Met Glu Asp Gly Glu Asp Phe Lys
145                 150                 155                 160

Arg Tyr Leu Pro Phe Leu Glu Asn Leu Met Leu Asn Pro Ser Arg Arg
                165                 170                 175

Ala Val Tyr Arg Leu Phe Asp Phe Leu Asn Ala Asn Asp Ile Asp Ile
            180                 185                 190

Thr Asp Asp Gly His Phe Ile Gly Trp Lys Val Val Arg Ser Asn Tyr
        195                 200                 205

Phe Asp Cys Ala Ser Asn Thr Phe Asp Asn Ser Pro Gly Lys Thr Val
    210                 215                 220

Thr Met Pro Arg Asn Gln Val Asp Glu Asp Asp Gln Arg Thr Cys Ser
225                 230                 235                 240

Thr Gly Leu His Val Cys Ser Lys Ser Tyr Ile Gly His Phe Gly Ser
                245                 250                 255
```

Gly Ser Asp Arg Ile Val Ser Val Lys Val His Pro Arg Asp Val Val
260 265 270

Ser Ile Pro Val Asp Tyr Asn Asp Ala Lys Met Arg Thr Cys Gly Tyr
275 280 285

Val Val Leu Glu Asp Val Thr Asp Arg Trp Gly Ser Glu Leu Arg
290 295 300

<210> 979
<211> 98
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 979
Met Ile Asn Pro Phe Asn Val Ser His Ser Lys Val Val Asn Leu Arg
1 5 10 15

Gly Thr His His Ala Ala Thr Val Phe Cys His His Val Val Lys His
20 25 30

Glu Gly Asp Val His Tyr Ala Trp Leu His Cys Asp Glu Leu Val Glu
35 40 45

Leu Gly Asp Asp Phe Val Val Glu Pro Asp Thr Cys Asn His Asp Asp
50 55 60

Arg Val Tyr Phe Gly Glu Leu His Ile Arg Gly Ile Tyr Gly Ile Asp
65 70 75 80

Glu Gln Ser Pro Ala Glu Ile Glu Pro Thr Pro Asp Ile Tyr Pro Arg
85 90 95

Phe Glu

<210> 980
<211> 195
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 980
Met Ala Leu Met Asn Lys Ala Leu Gln Arg Leu Asn Gln Leu Arg Thr
1 5 10 15

Phe Thr Leu Asp Leu Asn Lys Leu Arg Gly Glu Ala Lys Val Lys Ile
20 25 30

Ile Asp Thr Ala Arg Tyr Ser Leu Asp Ile Asp Pro Ser Gln Asp Arg

35 40 45

Ile Asp Val Leu Lys Arg Cys Arg Ile Ala Ile Pro Ala Glu Tyr Val
50 55 60

Val Ala Asp Phe Leu Asp Gly Tyr Val Asn Asp Gln Val Val Asp His
65 70 75 80

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

His Tyr Gln Gly Val Arg Val Glu Val Lys Thr His Phe Val His Asp
100 105 110

Arg Ala Asn His Lys Pro Trp Ile Asn Val Thr Thr Gly Lys Asp Gly
115 120 125

Pro Phe Pro Asp Gly Ser Gly Ile Asn Leu Gly Pro Met Phe Lys His
130 135 140

Lys Val Ala Asp Cys Ile Ile Ile Phe Val Ala Glu Glu Val Ser Gln
145 150 155 160

Asn Val Ile Arg Tyr Thr Pro Met Phe Ala Gly Gly Ile Glu Gln Leu
165 170 175

Met Glu Val Val Lys Pro Ser Arg Val Gly Ala Gly Gly Tyr Ile Met
180 185 190

His Lys Phe
195

<210> 981
<211> 79
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 981
Met Ser Tyr Leu Glu Leu Lys Ser Leu Arg Ala Lys Arg Gly Asn Ala
1 5 10 15

Ser Ile Lys Ala Glu Leu Leu Lys Glu Tyr Arg Ile Leu Glu Ser Met
20 25 30

Asn Trp His Tyr Ala Ile Ile Ala Cys Asp Asn Gly Asp Ser Thr Tyr
35 40 45

Gly Gly Leu Tyr Pro Asn Gly Ala Ala Ala Ala Arg Asp Glu His Lys
50 55 60

Asp Lys Val Lys Ala Leu Glu Glu Lys Ile Arg Asn Leu Cys Ile
65 70 75

<210> 982
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 982
Met Ile Arg Ser Ser Phe Asp Arg Arg Phe Asn Leu Met Arg Thr Val
1 5 10 15

Val Leu Ser Phe Ile Val Ala Val Ala Leu Gly Ile Val Ala Ile Phe
20 25 30

Gly Phe Gly Ile Tyr Phe Ala Ile Gln Ala Val Asp Ile Ile Gln Thr
35 40 45

Asp Gly Leu Lys Ser Leu Val Glu Thr Val Trp Glu Gly Gln Lys
50 55 60

<210> 983
<211> 151
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 983
Met Arg Asn Ile Met Thr Phe Ala Asp Leu Asp Asn Ala Gly Ala Glu
1 5 10 15

Leu Ile Gly Ser Ile Arg Asn Gly Asp Trp Ala Ala Gly Ala Pro Ser
20 25 30

Arg Glu Ile Thr Glu Arg Glu Gly Phe Tyr Phe Leu Met Phe Asn Asp
35 40 45

Gly Lys Ala Gly Tyr Ile Gly Ala Ser Ala Arg Phe Phe Val Ala Lys
50 55 60

Gln Arg Ser Lys Ala Gly Phe Glu Ser Val Leu Ser His Ile Arg Ser
65 70 75 80

Gly Arg Ser Gln Leu Gly Arg Thr Leu Arg Ser Asn Cys Val Thr Tyr
85 90 95

Gly Val Phe Trp Ile Pro Ala Asn Lys Met Lys Pro Leu Thr Thr Gly
100 105 110

Tyr Gly Lys Gly Gln Leu Ala Leu Ala Phe Thr Arg Gln His Ser Ser
115 120 125

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

Ile Phe Thr Leu Gln Lys Tyr
145   150

<210> 984
<211> 47
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 984
Met Ile Lys Gly Ile Ala Gly Gly Ile Trp Ala Ala Leu Cys Val Ser
1   5   10   15

Thr Leu Thr Thr Gly Glu Thr Ser Val Ile Ser Gln Ala Leu Ala Gln
            20   25   30

Gly Thr Leu Ser Ile Ile Leu Ile Ile Ala Ala Phe Ser Asn Asp
        35   40   45

<210> 985
<211> 46
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 985
Met Ile Lys Lys Ile Leu Ile Gly Ala Ala Leu Val Ala Ala Leu Leu
1   5   10   15

Leu Ile Leu Tyr Tyr Gly Met Ile Tyr Gly Met Ile Tyr Ile Val Leu
            20   25   30

Phe Ile Ser Asp Val Ile Val Gln Ile Gly Ser Leu Ile Trp
        35   40   45

<210> 986
<211> 462
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 986
Met Asp Ile Phe Asp Thr Leu Leu Lys Gln Ala Gly Ser Ile Asp Asp
1   5   10   15

Leu Ala Lys Ala Ser Asn Leu Arg His Arg Asp Leu Lys Ser Ile Ile
            20   25   30

```
Asp Asn Glu Ala Lys Glu Tyr Ala Ile Tyr Thr Val Glu Asn Arg Ala
        35                  40                  45

Ile Pro Asn Leu Ile Asp Gly Phe Lys Pro Val Gln Arg Phe Val Ile
    50                  55                  60

Ala Arg Ala Leu Asp Leu Ala Arg Gly Asn Lys Glu Lys Phe His Lys
65                  70                  75                  80

Leu Ala Ser Val Ala Gly Gly Val Ala Asp Leu Gly Tyr His His Gly
                85                  90                  95

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

Asn Asn Tyr Pro Leu Leu Asp Gly Gln Gly Asn Phe Gly Ser Arg Leu
        115                 120                 125

Val Gln Ser Ala Ala Ala Ser Arg Tyr Ile Phe Cys Arg Ile Ser Asp
    130                 135                 140

Asn Phe Arg Lys Ile Tyr Lys Asp Thr Glu Ile Ala Pro Val His Lys
145                 150                 155                 160

Asp Lys Glu His Val Pro Pro Ala Tyr Tyr Leu Pro Val Ile Pro Thr
                165                 170                 175

Val Leu Leu Asn Gly Val Arg Gly Ile Ala Thr Gly Tyr Ser Thr Ser
            180                 185                 190

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

Leu Arg Gly Glu Met Met Glu Pro Glu Val Gln Phe Pro Lys Phe Asn
    210                 215                 220

Gly Lys Ile Val Gln Thr Glu Asp Gly Ser Val Glu Leu His Gly Val
225                 230                 235                 240

Tyr Lys Glu Thr Ser Arg Asn Ser Ile Tyr Ile Ser Glu Ile Pro Tyr
                245                 250                 255

Lys Phe Glu Arg Ala Ser Tyr Val Glu Lys Val Leu Asp Pro Leu Glu
            260                 265                 270

Asp Ala Gly Tyr Ile Thr Tyr Asp Asp Asp Cys Ser Lys Thr Gly Phe
        275                 280                 285

Gly Phe Lys Val Lys Phe Arg Lys Asp Tyr Ala Leu Ser Glu Asp Pro
    290                 295                 300
```

Glu Gln Arg His Ala Lys Ile Met Lys Asp Phe Lys Leu Ile Glu Lys
305 310 315 320

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

Lys Phe Lys Thr Ser Gly Glu Leu Ile Arg His Phe Val Glu Val Arg
340 345 350

Lys Thr Phe Thr Ala Lys Arg Ile Glu His Lys Ile Ala Glu Thr Lys
355 360 365

Gln Ala Phe Asn Leu Ala Gln Ala Lys Ala Gln Phe Ile Lys Glu Val
370 375 380

Ile Ala Gly Asn Ile Val Ile Gln Gly Lys Thr Arg Lys Gln Leu Thr
385 390 395 400

Lys Glu Ile Glu Gln Asn Glu Leu Phe Lys Asp His Ser Glu Lys Leu
405 410 415

Val Ser Met Asn Ile Tyr His Ile Thr Asp Asp Glu Ala Lys Lys Leu
420 425 430

Ala Gln Glu Ala Lys Arg Leu Ala Gln Glu Val Lys Tyr Trp Glu Lys
435 440 445

Thr Thr Pro Glu Ala Glu Tyr Leu Lys Asp Leu Glu Glu Leu
450 455 460

<210> 987
<211> 87
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 987
Met Ile Thr Ser Leu Lys Ser Asp Ile Lys Asn Ile Leu Tyr Ile Ser
1 5 10 15

Thr Gln Ala Asp Gly Thr Arg Leu Ser His Tyr Val Lys Gly Asn Ile
20 25 30

Val Val Leu Asp Glu Phe Glu Val Asn Arg Glu Tyr Pro Met Arg Gln
35 40 45

Val Ile Gln Ala Ser Asn Tyr Glu Asp Gly Glu Glu Tyr Gln Val Val
50 55 60

Leu Cys Val Tyr Asp Asp Phe Trp Val Leu Lys Leu Glu Asn Gly Asp
65 70 75 80

Lys Phe Leu Ile Phe Asn Val
85

<210> 988
<211> 214
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 988
Met Ser Lys Val Thr Tyr Ile Ile Lys Ala Ser Glu Asp Ala Leu Asn
1 5 10 15

Glu Lys Thr Ala Ala Ile Leu Val Gln Val Ala Lys Lys Asp Phe Ile
20 25 30

Thr Ser Ser Glu Leu Arg Glu Ile Leu Glu Glu Thr Met Asn Ala Ser
35 40 45

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

Lys Ser Gly Asp Gly Leu Ile Ile Thr Gly Glu Ala Gln Asp Ile Ile
65 70 75 80

Ser Lys Ala Ala Val Ile Tyr Ala Glu Glu Asn Lys Pro Glu Leu Leu
85 90 95

Lys Lys Arg Asn Thr Arg Lys Ala Arg Pro Leu Thr Glu Asp Met Asn
100 105 110

Glu His Lys Asp Leu Met Met Lys Leu Leu Gly Glu Met Glu Asp Ile
115 120 125

Leu Pro Leu Lys Glu Leu Thr Val Tyr Arg Ser Asn Tyr Ile Ala Val
130 135 140

Leu Glu Lys Arg Thr Phe Gly Ile Arg Ser Leu Glu Val Asn Asn Lys
145 150 155 160

Gly Thr Phe Arg Ile Phe Gly Tyr Lys Ile Ser Glu Glu His Gln Lys
165 170 175

His Phe Thr Asp Leu Gly Met Ser Cys Arg Val Ala Ala Thr Gly Asn
180 185 190

Thr Tyr Leu Asp Ile Ala Arg Thr Ala Glu Asn Ile Glu Thr Ile Ile
195 200 205

Arg Ser Ile Lys Glu Leu

210

<210> 989
<211> 56
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 989
Met Glu Leu Trp Glu Ile Ile Tyr Glu Asp Asp Val Asn Ile Arg Gly
1 5 10 15

Ser Ile Phe Ile Lys Ala Leu Asp Lys Tyr His Ala Ile Glu Leu Phe
20 25 30

Glu Gln Leu Gln Gln Gln Thr Tyr Ile Asn Glu Ser Arg Tyr Leu Ile
35 40 45

Lys Leu Ala Met Phe Leu Val Glu
50 55

<210> 990
<211> 113
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 990
Met Asn Lys Phe Lys Val Leu Asn Glu Leu Gln Arg Cys Val Glu Lys
1 5 10 15

Val Asn Leu Asn Ala Asn Ile Pro Thr Asp Cys Trp Asp Val Trp Phe
20 25 30

Arg Gly His Phe Ile Gly Tyr Ile Asp Lys Lys Phe Thr Lys Cys Tyr
35 40 45

Ala Ile Tyr Asn Ala Asp Gly Lys His Ile Met Asp Val Asp Asn Tyr
50 55 60

Gln Lys Ala Leu Ala Lys Phe Val Pro Leu Ala Glu Ala Val Asn Ser
65 70 75 80

Met Glu Trp Leu Glu Lys Ile Gln Gly Glu Pro Val Ile Arg Gln Ile
85 90 95

Gly Ile Arg Glu Lys Lys Ser Leu Trp Gln Lys Ile Lys Gly Phe Phe
100 105 110

Lys

<210> 991
<211> 141
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 991
Met Ser Lys Phe Ser Glu Gln Met Asn Lys Phe Val Asp Ala Ser Arg
1 5 10 15

His Gly Ala Leu Ile Asn Glu Pro Glu Glu Val Ser Ile Pro Glu Ile
20 25 30

Cys Phe Lys Val Ala Asp Trp Trp Asp Gly Arg Leu Leu Gln Arg Arg
35 40 45

Ile Val Cys Ala Ala Asn Arg Phe Glu Leu Lys Ser Gly Gly Thr Ile
50 55 60

Val Val Pro Gly Thr Arg His Tyr Ser Val Asp Met Ala Asn Val Leu
65 70 75 80

Asp Met Phe Arg Asp Lys Leu Val Ser Asp His Val His Gly Asp Asn
85 90 95

Gln Gly Phe Val Asp Gln Trp Gly Glu Tyr Phe Thr Arg Glu Glu Ala
100 105 110

Leu Ile Ile Ala Thr His Ala Gly Gln Val Asn Thr Val Arg Pro Lys
115 120 125

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

<210> 992
<211> 100
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 992
Met Ile Ser Thr Leu Lys Asn Asn Ile Thr Leu Leu Lys Ile Gln Arg
1 5 10 15

Lys Ser Leu Gln Arg Ser Leu Glu Met Met Asp Asp Asn Trp Gly Thr
20 25 30

Tyr Thr Asn Glu Ala Gly Phe Lys Met Ala Asp Ser Lys Phe Met Lys
35 40 45

Thr Leu Met Asp Lys Glu Tyr Ile Cys Pro Phe Ser His Pro Phe Asn

50 55 60

Gly Gly Ala Lys Pro Phe Leu Ala Glu Met Tyr Lys Ile Met Thr Glu
65 70 75 80

Glu Met Ile Lys Asp Ile Asp Tyr Tyr Ile Lys Glu Leu Glu Cys Lys
85 90 95

Glu Asp Lys Val
100

<210> 993
<211> 70
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 993
Val Arg Ala Ile Ser Ala Lys Ala Asp Tyr Phe Asn Ser Leu Asn Arg
1 5 10 15

Ser Glu Lys Ala Gln Ile Lys Arg Phe Ile Leu Glu Leu Gly Tyr Val
20 25 30

His Ala Gly Asp Leu Lys Ala His Ile Gln Glu Cys Gly Ile Ala Lys
35 40 45

Arg Phe Asp Ile Thr Arg Asn Cys Leu Asn Glu Val Ile Ala His Val
50 55 60

Gln Pro Ser Ser Glu Glu
65 70

<210> 994
<211> 41
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 994
Met Tyr Asn Pro Val Ala Lys Asn Asp Phe Asn Lys Gly Gly Ala His
1 5 10 15

Lys Asp Lys Lys Arg Ala Ala Lys Glu Ser Lys Arg Lys Gln Lys His
20 25 30

Lys Gly Lys Asp Asn Ala His Ser Glu
35 40

<210> 995
<211> 40
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 995
Met Val His Asp Trp Asn Asn Gly Thr Phe Thr Val Ala Ile Ile Ala
1   5   10   15

Asn Val Glu Pro Glu Glu Val Leu Glu Gln Phe Gln Lys Cys Val Asp
            20   25   30

Ala Tyr Asp Ile Gly Asp Tyr Leu
        35   40

<210> 996
<211> 108
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 996
Met Asn Thr Glu Thr Leu Arg Arg Glu Asp Glu Ala Lys Ala Tyr His
1   5   10   15

Lys Arg Val Glu Leu Leu Ser Ala Ile Lys Val Glu Tyr Thr Leu Gln
            20   25   30

Val Arg Leu Lys Val Leu Asn Ser Trp Ala Asn Asp Leu Glu Val Lys
        35   40   45

His Leu Glu Gln Ala Val Met Phe Thr Phe Thr Gln Glu Ala Ser Lys
    50   55   60

Pro Phe Ser Leu Ser Ala Asp Phe His Thr Tyr Gly Ile Ile Thr Ile
65   70   75   80

Lys Ala Lys Asp Arg Gly Asp Ile Ile Ser Gly Val Glu Tyr Ile Glu
                85   90   95

Ser Ile Leu Gly Asn Arg Gly Glu Val Val Leu Ala
            100   105

<210> 997
<211> 88
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 997
Met Ser His Asn Leu Glu Ser Val Ile Glu Ser Gln Arg Tyr Leu Glu
1   5   10   15

Ala Leu Met Asn Lys Ile Ala Leu Gly Ser Leu Ile Asp Leu Ser Phe
            20   25   30

Gln Glu Ala Met Asp Val Cys His Trp Met Asn Arg Arg Val Arg Pro
        35   40   45

Ile Gly Lys Glu Trp Tyr Leu Thr Ala Lys Val Lys Asp Gly Arg Tyr
    50   55   60

Gly Leu Trp Met Ser Ser Gly Ala Glu Tyr Ile Thr Thr Lys Glu Asp
65   70   75   80

Leu Asn Ser Arg Trp Glu Leu Ala
                85

<210> 998
<211> 90
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 998
Met Thr Lys Phe Glu Ile Val Gln Glu Ile Val Thr Val Ala Ser Ile
1   5   10   15

Leu Thr Lys Phe Asn Ala Glu His Ile Met Glu Lys Arg Asp Glu Phe
            20   25   30

Ile Ala Phe Leu Asn Glu Ile Gly Ile Lys Asn Glu Gln Gly Arg Gln
        35   40   45

Leu Asn Gln Ser Asn Phe Arg Lys Met Val Ser Glu Leu Thr Asp Glu
    50   55   60

Glu Lys Arg Ile Leu Val Glu Glu Tyr Asn Glu Gly Phe Glu Ser Ile
65   70   75   80

Tyr Arg Thr Met Ala Met His Ser Asn Lys
                85   90

<210> 999
<211> 218
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 999
Met Ala Ser Lys Gln Ser Ile Pro Phe Phe Asp Met Phe Leu Gly Leu
1   5   10   15

Leu Glu Leu Leu Phe Lys Asp Gly Ala Thr Gly Arg Val Leu Phe Ser
            20   25   30

```
Arg Val Phe Val Val Ile Leu Leu Ala Leu Leu Ala Phe Ala Gly Tyr
        35                  40                  45

Lys Ser Asp Ser Leu Ile Thr Ala Tyr Val Asp Ser Thr Tyr Asp Lys
    50                  55                  60

Tyr Asp Lys Leu Val Gln Lys Asp Arg Asp Thr Arg Phe Asp Asn Thr
65                  70                  75                  80

Ala Leu Glu Gln Leu Gln Ile Val His Ile Ser Ser Gly Ala Asp Phe
                85                  90                  95

Ser Ala Val Phe Thr Phe Arg Pro Lys Asn Leu Asn Tyr Phe Val Asp
            100                 105                 110

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

Leu Gly Gly Tyr Pro Ile Asp Lys Thr Ser Ala Glu Tyr Ser Thr His
    130                 135                 140

Leu Ser Gly Arg Tyr Phe Trp Thr Asp Lys Glu Phe Val Phe Leu Pro
145                 150                 155                 160

Thr Lys Arg Lys Pro Pro Glu Ile Ser Tyr Met Phe Ser Cys Pro Tyr
                165                 170                 175

Phe Asn Leu Asp Asn Val Tyr Ala Gly Thr Val Glu Met Tyr Trp Tyr
            180                 185                 190

Asn Ser Lys Pro Ala Leu Ser Asn Glu Arg Leu Thr Ser Ile Cys Gly
        195                 200                 205

Gln Ala Val Arg Ala Leu Gly Arg Ala Lys
    210                 215


<210> 1000
<211> 179
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1000
Met Ala Val Thr Gly Pro Trp Val Gly Ser Ser Ala Lys Ala Glu Thr
1               5                   10                  15

Gly Glu Pro Trp Met Ala Gln Ala Gly Ala Lys Leu Arg Leu Gly Thr
            20                  25                  30

Pro Phe Trp Met Ser Asn Met Ile Gly Arg Ser Val Phe Asn Phe Ser
```

35 40 45

Leu Thr Val Gln Tyr Arg Asn Trp Asn Asn Ile Tyr Tyr Arg Gly Ser
50 55 60

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

Thr Val Gln Gly Asn Phe Glu Gly Lys Glu Val Thr Leu Phe Val Ser
85 90 95

Val Ser Gly Gln Gly Gly Val Asn Tyr Trp Asn Gly Asp Pro Gln Gly
100 105 110

Thr Thr Leu Gly Ile Arg Asn Gly Asp Ala Ile Asn Leu Arg Val Met
115 120 125

Met Ser Asp Gly Thr Thr Phe Asp Phe Thr Pro Gly Lys Met Asp Gly
130 135 140

Asp Val Arg Asn Tyr Gln Ile Ala Ser Asn Asp Glu Ala Asn Lys Leu
145 150 155 160

Lys Asn Trp Phe Ser Asp Arg Thr Asp Gln Tyr Trp Gln Gly Leu Ile
165 170 175

Thr Arg Arg

<210> 1001
<211> 1525
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1001
Met Ala Asp Gln Asn Leu Lys Gln Ile Gln Phe Lys Arg Thr Ser Thr
1 5 10 15

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

Leu Asn Thr His Gly Arg Thr Leu Ala Ile Tyr Thr Lys Asp Glu Ala
35 40 45

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

Ala Gly Asn Leu Asn Val Asp Gly Ile Thr Thr Leu Lys Asp Asn Val
65 70 75 80

```
Thr Ile Ser Pro Asn Lys Ala Ile Asn Phe Glu Ala Thr Asp Leu Ser
                85                  90                  95

Gly Ala Ile Val Arg His Ile Val Gly Lys Cys Ala Thr Asn Asp Gly
            100                 105                 110

Trp Tyr Ile Gly Ala Gly Gly Thr Ser Asn Ser Gly Ile Leu Glu Ile
        115                 120                 125

Gly Thr Ile Asp Asp Gly Ala Glu Thr Ile Gln Phe Val Gln Arg Gly
    130                 135                 140

Ser Gly Asn Val Glu Ala Arg Lys Leu Val Leu Leu Asp Gly Ser Gly
145                 150                 155                 160

Asn Thr Thr Leu Pro Gly Asp Leu Arg Leu Ser Thr Asn Lys Thr Val
                165                 170                 175

Lys Ile Asn Asn Gly Ser Thr Leu Val Leu Glu Met Gly Val Gly Ser
            180                 185                 190

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

Thr Asn Asp Ser Asn Leu Thr Phe Arg Asn Ser Gln Val Tyr Tyr Ala
    210                 215                 220

Met Asn Gly Arg Gly Pro Gly Lys Ser Gly Thr Leu Leu Thr Asn Val
225                 230                 235                 240

Glu Asn Asn Arg Gln Ala Trp Gln Tyr Val Ile Ser Ala Ala Thr Ala
                245                 250                 255

Gly Thr Pro Arg Trp Val Lys Val Ala Thr Ile Lys His Pro Gly Asp
            260                 265                 270

Ala Ser Ser Gln Leu Asp Leu Met Ile Thr Gly Gly Ile Asp Ser Gly
        275                 280                 285

His Gly Arg His Tyr Val Asp Phe Ile Thr Leu Ser Gly Arg Asn Leu
    290                 295                 300

Thr Ser Trp Ser Thr Ser Asn Leu Asp Asn Trp Val Glu Trp Arg Arg
305                 310                 315                 320

Ile Gly Ser Pro Asn Lys Gly Asn Val Pro Glu Tyr Tyr Val Val Lys
                325                 330                 335

Asn Asp Ala Ala Thr Asp Ser Glu Ala Ser Phe Asp Phe Tyr Ala Lys
            340                 345                 350
```

```
Val Pro Arg Tyr Gly Asn Gly Leu Tyr Val Thr Val Leu Asn Thr Ala
        355                 360                 365

Glu Tyr Asn Gly Gln Asp Ser Gly Lys Val Ile Ile Tyr Glu Thr Gly
    370                 375                 380

Gln Asp Thr Gly Ala Thr Thr Pro Ser Gly Ser Ile Leu Val Ser Met
385                 390                 395                 400

Lys Gln Val Phe Asp Ser Ile Ser Lys Pro Asp Phe Ser Asp Thr Thr
                405                 410                 415

Gly Thr Leu Pro Val Asn Arg Gly Gly Thr Gly Ala Thr Asn Val Gly
            420                 425                 430

Asp Ala Arg Asn Asn Leu Gly Leu Arg Thr Ala Ala Val Arg Asp Val
        435                 440                 445

Gly Glu Ser Ser Gly Asn Val Met Glu Val Gly Ala Phe Gly Ile Gly
    450                 455                 460

Gly Asn Gly Lys Ser Leu Val Asp Ile Thr Ser Asp Val Asp Leu Met
465                 470                 475                 480

Thr Arg Leu Lys Ala Leu Gly Gly Thr Thr Phe Arg Ala Asn Val Ala
                485                 490                 495

Ser Gly Tyr Thr Gly Ala Pro Tyr Tyr Ser His Gly Ala Gly Phe Phe
            500                 505                 510

Ser Arg Thr Gly Asp Thr Met Ser Ala Leu Asn Ile Asp Tyr Ala Thr
        515                 520                 525

Gly Asn Val Arg Val Phe Ala Ile Asn Asp Ser Gly Leu Ala Ser Gly
    530                 535                 540

Arg Val Asn Ser Asn Val Leu Tyr Gly Thr Ala Asn Lys Pro Ser Lys
545                 550                 555                 560

Ala Asp Val Gly Leu Gly Asn Leu Thr Asn Asp Thr Gln Val Lys Lys
                565                 570                 575

Ala Gly Asp Thr Met Thr Gly Asp Leu Thr Val Pro Asn Leu His Ala
            580                 585                 590

Ser Gly Thr Gly Thr Ala Ser Val Tyr Val Asn Ala Gly Ser Gly Asn
        595                 600                 605

Ala His Val Trp Phe Arg Thr Gly Gly Asn Glu Arg Gly Val Ile Trp
    610                 615                 620
```

```
Ala Thr Pro Asn Thr Ala Asp Leu Gly Gln Ile Asn Ile Arg Ala Lys
625                 630                 635                 640

Thr Thr Gly Asp Val Ser Ala Gly Asp Phe Ser Phe Arg Ser Asp Gly
                645                 650                 655

Arg Leu Asp Val Pro Val Ala Val Lys Val Gly Gly Ala Ala Met Leu
            660                 665                 670

Thr Lys Asp Gly Asn Ile Thr Ser Gly Ser Met Phe Gly Gly Asn Leu
        675                 680                 685

Asn Asn Tyr Leu Thr Ser Ile Lys Asn Asp Ile Thr Thr Gly Asp Ser
    690                 695                 700

Lys Gln Val Ser Lys Thr Gly Asp Thr Met Thr Gly Asn Leu Thr Ile
705                 710                 715                 720

Asn Ala Asn Leu Lys Val Glu Asn Pro Asn Gly Ser Met Val Asp Leu
                725                 730                 735

Gly Ser Glu Asn Ser Asp Lys Tyr Ser Arg Leu Thr Leu Ala Arg Lys
            740                 745                 750

Val Gly Ser Gly Ala Ala Val Ala Met Leu Lys Ile Thr Pro Glu Gly
        755                 760                 765

Tyr Val Gln Phe Gly Tyr Gln Asp Ala Val Ala Thr Pro Ala Pro Ser
    770                 775                 780

Lys Tyr Ile Arg Val Lys Pro Asp Gly Leu Asp Val Glu Gly Asp Leu
785                 790                 795                 800

Val Phe Asn Gln Thr Tyr Arg Gly Thr Glu Asp Ala Ile Asn Ile Thr
                805                 810                 815

Asp Lys Thr Asn Asp Leu Asn Asn Met Val Ile Lys Gly Ser Asp Leu
            820                 825                 830

Gly Thr Arg Gln Leu Tyr Lys Cys Val Ser Ser Gly Gly Gly Ser Asn
        835                 840                 845

Ile Ser Asn Lys Pro Thr Ser Asp Gly Asn Phe Val Leu Glu Val Leu
    850                 855                 860

Ser Leu Arg Lys Ile Ser Asp Ser Asp Trp Thr Cys Lys Gln Thr Phe
865                 870                 875                 880

Thr Thr Lys Asn Gly Asn Val Glu Gly Thr Tyr Val Arg Tyr Cys Gln
                885                 890                 895
```

```
Asn Gly Thr Trp Ser Ala Trp Lys Glu Val Val Ala Gly Val Gln Pro
            900                 905                 910

Ile Asn Leu Gly Gly Thr Gly Ala Thr Ser Val Ala Ala Ala Arg Asn
        915                 920                 925

Asn Leu Gly Val Gly Glu Gly Gln Ser Val Lys Phe Gly Trp Leu Val
    930                 935                 940

Val Asn Gly Val Gly Thr Ser Asp Pro Thr Ile Thr Phe Lys Asn Gly
945                 950                 955                 960

Ala Val Val Arg Glu Ala Gln Gly Gly Ser Thr Gly Ala Leu Ile Met
                965                 970                 975

Ser Ala Ser Ala Thr Ala Ala Ala Ser Ala Lys Tyr Ile Ala Phe Arg
            980                 985                 990

Pro Phe Gly Asp Ser Ser Gly Ser  Glu Ile Arg Val Lys  Ala Asn Gly
        995                 1000                1005

Ser Glu  Pro Leu Leu Glu Trp  Ser Tyr Gly Pro Gly  Ile Arg Ser
    1010                1015                1020

Asn Asp  Ser Gly Ala Phe Val  Ile Tyr Ala Lys Thr  Gly Gln Ala
    1025                1030                1035

Leu His  Leu Arg Pro Asn Gly  Asp Asp Ser Asn Gln  Ala Thr Val
    1040                1045                1050

Ile Asp  Gln Lys Gly Lys Met  Thr Val Gly Gly Glu  Phe Glu Ala
    1055                1060                1065

Gln Asn  Ser Lys Ile Thr Gly  Asn Leu Asn Val Ser  Glu Asp Asn
    1070                1075                1080

Arg Met  Ile Val Leu Gly Lys  Asn Ser Asp Ile Gly  Leu Val Lys
    1085                1090                1095

Lys Asn  Gly Met Pro Gly Lys  Met Ala Ile Gly Lys  Ser Asn Ser
    1100                1105                1110

Phe Thr  Val Met Val Ser Ala  Asn Thr Asn Asn Gln  Ile Asn Pro
    1115                1120                1125

Ala Asp  Thr Phe Ser Asp Ile  Phe Lys Val Asp Ala  Ser Gly Asn
    1130                1135                1140

Gln Thr  Val Tyr Gly Asn Ala  Gln Ile Asn Arg Gln  Leu Thr Val
    1145                1150                1155
```

```
Thr Ser  Asn Thr Asn Leu Asn  Ser Asp Leu Ile Val  Lys Gly Asn
    1160                1165                1170

Ser Arg  Phe Ser Gly Val Ile  Asn Ala Asp Gly Asn  Ile Asn Val
    1175                1180                1185

Ala Ser  Gly Lys Phe Val Ile  Ala Gly Gln Ala Pro  Thr Asp Asn
    1190                1195                1200

Ser His  Leu Thr Asn Lys Lys  Tyr Val Asp Asp Lys  Val Ala Ser
    1205                1210                1215

Ala Ile  Ser Asn Ala Gly Asp  Thr Tyr Leu Pro Leu  Ala Gly Gly
    1220                1225                1230

Thr Val  Thr Gly Thr Leu Ile  Val Thr Gly Asn Gln  Leu Lys Thr
    1235                1240                1245

Thr Ser  Leu Trp Thr Thr Gly  Asp Ala Ala Val Asn  Gly Val Leu
    1250                1255                1260

Thr Val  Asp Gly Lys Ala Arg  Phe Asn Gln Glu Phe  Ser Val Ser
    1265                1270                1275

Thr Ser  Val Asn Val Gln Asn  Thr Gly Asn Ser His  Val Phe Phe
    1280                1285                1290

Arg Lys  Ala Asp Gly Thr Glu  Lys Gly Leu Leu Trp  Ala Asp Glu
    1295                1300                1305

Pro Gly  Asn Val Ser Ile Arg  Ala Gly Gly Ala Ser  Gly Pro Val
    1310                1315                1320

Trp Asn  Phe Trp Ala Ser Gly  Ser Cys Gln Phe Pro  Gly Ala Ile
    1325                1330                1335

Ser Asn  Tyr Asn Gly Ile Ser  Ser Thr Thr Asn Tyr  Pro Ala Gly
    1340                1345                1350

Gln Pro  Asn Gly Thr Tyr Asn  Asn Thr Ala Gly Leu  Val Ser Arg
    1355                1360                1365

Phe Ser  Asn Gly Ala Tyr Ala  Ser Leu Tyr Phe Gln  Glu Tyr Val
    1370                1375                1380

Gly Asn  Phe His Gln Ala Ile  Ile Asn Val Asn Gly  Phe Gly Arg
    1385                1390                1395

Asp Asp  Ser Phe Tyr Phe Arg  Ala Gly Gly Asp Phe  Ile Cys Thr
    1400                1405                1410
```

Arg Asn Gly Ser Phe Asp Asn Val Glu Ile Arg Ser Asp Arg Arg
1415 1420 1425

Ala Lys Ser Asp Ile Lys Val Ile Glu Asn Ala Leu Glu Lys Val
1430 1435 1440

Glu Thr Leu Ser Gly Asn Thr Tyr Glu Leu His Asn Thr Ser Gly
1445 1450 1455

Gly Thr Thr Arg Ser Ala Gly Leu Ile Ala Gln Glu Val Gln Glu
1460 1465 1470

Val Leu Pro Glu Ala Val Thr Gln Asp Ile Glu Ala Asp Gly Gly
1475 1480 1485

Leu Leu Arg Leu Asn Tyr Asn Ser Val Ile Ala Leu Leu Val Glu
1490 1495 1500

Ser Val Lys Glu Leu Ser Ala Glu Val Lys Gly Leu Lys Ala Glu
1505 1510 1515

Ile Glu Glu Leu Lys Ser Lys
1520 1525

<210> 1002
<211> 220
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1002
Met Ala Asp Leu Lys Ala Gly Ser Thr Val Gly Gly Asn Pro Ile Trp
1 5 10 15

His Ala Gly Thr Phe Pro Leu Val Pro Ala Gly Asn Ser Leu Thr Tyr
20 25 30

Arg Gly Lys Lys Val Tyr Thr Glu Ile Asp Lys Pro Gln Ala Ala Asp
35 40 45

Asn Asp Phe Val Ser Lys Ala Asn Gly Gly Ser Tyr Ser Arg Thr Val
50 55 60

Thr Phe Glu Thr Gly Leu Arg Val Gln Thr Thr Gly Ser Gly Gly Met
65 70 75 80

Glu Leu Val Asn Gly Gly Val Asp Gly Ala Thr Leu Asn Gly Val Asn
85 90 95

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

Ser Asn Gly Ile Thr Ile Ala Phe Asp Leu Arg Ser Gly Asn Ile Thr
115 120 125

Thr Lys Gly Gly Ile Thr Ser Asn Asn Gln Val Ser Val Ala Ala Ala
130 135 140

Ala Pro Thr Ala Asn Ser His Leu Thr Arg Lys Asp Tyr Val Asp Glu
145 150 155 160

Leu Ile Asn Thr Val Ser Asn Val Ala Asn Ala Ala Val Lys Lys Ala
165 170 175

Gly Asp Thr Met Thr Gly Val Leu Arg Ala Asn Ala Gly Val Val Ile
180 185 190

Val Asn Lys Ala Thr Ser Gly Glu Tyr Ala Pro Arg Leu Asp Gln Val
195 200 205

Ile Ser Arg Gly Val Thr Ile Asp Phe Gly Thr Tyr
210 215 220

<210> 1003
<211> 378
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1003
Met Ala Asp Pro Ile Leu Met Ala Ala Phe Gly Glu Asp Phe Val Glu
1 5 10 15

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

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

Asn Gly Ala Phe Asp Met Thr Ser Ser Leu Arg Arg Gly Ile Asn Val
50 55 60

Val Gln Val Asn Gly Asp Arg Phe Ile Asn Phe Lys Thr Phe Asp Val
65 70 75 80

Thr Thr Asp Asp Asn Asn Ala Asn Asn Lys Ala Phe Val Glu Tyr Ala
85 90 95

Asn Gly Leu Thr Ser Gly Leu Tyr Ile Ile Met Thr His Glu Arg Phe
100 105 110

Gln Ser Ser Pro Leu Ile Asp Arg Trp Phe Lys Asn Lys Trp Ser Ala
115 120 125

```
Ser Trp Pro Gly Ser Asp Phe Ser Lys Ser Phe Pro Asn Ser Ala Tyr
    130                 135                 140

Val Gly Val Leu Gly Ala Ala Lys Gly Arg Ile Leu Ile Glu Ser Phe
145                 150                 155                 160

Tyr Gly Asn Asp Gly Lys Val Lys Glu Asp Ser Arg Ala Lys Val Asp
                165                 170                 175

Thr Val Tyr Asp Asn Val Gly Asp Val Gly Tyr Thr Gly Cys Pro Tyr
            180                 185                 190

Arg Ser Ile Glu Asp Thr Asn Glu Tyr Ser Asp Ser Thr Gly Tyr Glu
        195                 200                 205

Tyr Lys Arg Tyr Pro Val Gln Asn Glu Ser Ile Ser Lys Ile Ala Asp
    210                 215                 220

Tyr Gly Leu Ser Pro Gly Asp Ser Val Phe Leu Val Cys Asp Met Tyr
225                 230                 235                 240

Ala Ser Lys Ser Leu Leu Asp Ala Gly Ser Thr Thr Arg Ala Ser Leu
                245                 250                 255

Arg Trp Phe Lys Gly Thr Ser Leu Leu Ser Ser Asn Val Ser Leu Glu
            260                 265                 270

Val Pro Lys Asn Gly Ala Asp Arg Trp Leu Arg Phe Glu Arg Phe Thr
        275                 280                 285

Ala Val Pro Thr Asp Ala Asp Gly Phe Thr Ile Val Val Ser Arg Tyr
    290                 295                 300

Pro Lys Thr Ser Val Val Gly Asp Ser Lys Ile Lys Asn Leu Val Phe
305                 310                 315                 320

Val Gln Thr Ser His Gly Glu Gln Leu Asn Ser Val Ile Gln Glu Phe
                325                 330                 335

Gly Val Asn Gly Ile Arg Met Asn Lys Gly Val Glu Gly Gly Thr Thr
            340                 345                 350

Met Ile Met Glu Leu Pro Asn Ser Lys Val Asp Pro Ser Gly Val Ile
        355                 360                 365

Pro Val Gln Ser Phe Arg Glu Thr Ser Asp
    370                 375
```

<210> 1004
<211> 1281

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1004
Met Ser Asp Leu Leu Lys Gln His Phe Arg Ala Thr Asn Gly Leu Asp
1 5 10 15

Ala Gly Gly Asn Lys Val Ile Asn Val Ala Leu Ala Asp Arg Asn Val
20 25 30

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

Gln Lys Tyr Asp Pro Thr Arg Gly Tyr Leu Thr Asp Phe Ala Val Thr
50 55 60

Tyr Gly Arg Arg Ile Trp Ile Ala Asn Lys Asp Ile Pro Lys Pro Ala
65 70 75 80

Gly Glu Phe Asn Gln Ala Asn Trp Thr Ser Leu Arg Val Asp Pro Asn
85 90 95

Trp Ile Tyr Thr Val Arg Lys Gly Glu Phe Glu Ile Gln Ser Gly Gln
100 105 110

Phe Ile Asn Val Asp Ser Asn Ala Ala Gly Asn Ala Thr Leu Leu Leu
115 120 125

Pro Leu Ala Pro Asp Glu Gly Asp Thr Ile Val Val Arg Asp Ile Gly
130 135 140

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

Ala Ser Ile Val Phe Gly Glu Ser Arg Leu Arg Glu Val Arg Leu Thr
165 170 175

Arg Pro Tyr Ser Gln Ile Met Leu Thr Phe Ser Asn Gly Ala Trp Arg
180 185 190

Ala Ser Leu Thr Asp Phe Gly Asp Thr Ala Lys Met Val Val Pro Asn
195 200 205

Gly Ile Val Pro Thr Gln Val Gln Ser Gly Asp Asn Val Val Arg Arg
210 215 220

Tyr Thr Ser Asn Ser Glu Ile Phe Ile Thr Leu Pro Leu Phe Ala Asn
225 230 235 240

Ser Asn Asp Ile Ile Asn Phe Thr Asp Leu Asp Gly Thr Ser Pro Ile

245 250 255

Asn His Met Thr Val Arg Thr Phe Asp Pro Thr Ile Ser Ile Gly Thr
260 265 270

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

Val Tyr Asp Ala Ile Asp Lys Ile Trp Arg Ile Phe Glu Asn Asp Leu
290 295 300

Arg Thr Arg Val Arg Ile Ile Thr Ser Asp Val Thr Leu Met Pro Asn
305 310 315 320

Glu His Ile Ser Val Phe Gly Ala Asp Asn Ser Thr Val Lys Thr Ile
325 330 335

Asn Ile Thr Leu Pro Thr Asp Val Ala Val Gly Asp Thr Val Lys Ile
340 345 350

Ala Met Asn Tyr Met Arg Lys Gly Gln Thr Val Val Ile Lys Ala Ser
355 360 365

Asp Gly Asp Thr Ile Ala Ser Asn Leu Asn Leu Leu Gln Phe Pro Lys
370 375 380

Arg Ser Glu Tyr Pro Pro Asp Ala Ala Trp Val Gln Ser Ser Ser Ile
385 390 395 400

Thr Phe Asn Gly Thr Thr Ser Tyr Val Pro Val Leu Glu Leu Ala Tyr
405 410 415

Ile Glu Asp Lys Ala Ser Gly Lys Ser Tyr Trp Ile Val Thr Glu Ser
420 425 430

Asp Pro Thr Val Glu Arg Val Asp Ala Lys Asp Asn Thr Thr Arg Ala
435 440 445

Arg Leu Gly Val Ile Ala Leu Ala Thr Gln Ala Gln Ala Asn Ala Glu
450 455 460

Ser Asn Pro Glu Lys Glu Leu Ala Ile Thr Pro Glu Thr Leu Asn Gly
465 470 475 480

Arg Arg Ser Thr Glu Thr Gln Thr Gly Ile Ala Arg Ile Ala Thr Ser
485 490 495

Gly Glu Val Asn Gln Ala Thr Thr Ala Ser Tyr Leu Asp Asn Val Ile
500 505 510

Val Thr Pro Lys Lys Leu Asn Glu Arg Ser Ala Thr Glu Thr Arg Arg

515 520 525

Gly Leu Ala Glu Ile Ala Ser Asn Ala Lys Met Asp Ala Gly Thr Asp
530 535 540

Asp Phe Thr Ile Val Thr Pro Lys Lys Leu Leu Tyr Arg Thr Thr Ser
545 550 555 560

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

Asn Thr Thr Ala Asp Arg Ser Ser Ala Gly Thr Gly Ile Phe Asp His
580 585 590

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

Ala Thr Val Asn Gln Ser Gly Ile Val Trp Leu Ala Ser Asp Ser Glu
610 615 620

Val Arg Asn Gly Thr Pro Ala Ser Ser Asn Ile Pro Thr Val Val Thr
625 630 635 640

Pro Glu Ser Leu His Lys Lys Val Ala Thr Asp Gly Ala Ile Gly Leu
645 650 655

Ile Gln Ile Ala Thr Gln Thr Glu Val Asn Ala Gly Gly Val Thr Asn
660 665 670

Lys Ala Val Thr Pro Lys Thr Leu Asn Asp Arg Thr Ala Thr Asn Asp
675 680 685

Arg Thr Gly Ile Ala Arg Phe Ala Thr Pro Gly Ala Gln Gly Glu Phe
690 695 700

Glu Ala Gly Thr Ser Ser Thr Val Met Val Asn Pro Lys Leu Leu Phe
705 710 715 720

Asp Lys Phe Ala Asn Thr Ser Arg Ile Gln Val Asn Thr Ser Ser Gly
725 730 735

Leu Thr Ile Thr Gly Asn Leu Trp Asp His Tyr Thr Ile Asn Ile Gln
740 745 750

Glu Ala Ser Thr Ser Gln Arg Gly Thr Thr Thr Leu Ala Thr Ala Ala
755 760 765

Glu Val Arg Thr Gly Thr Asp Ala Lys Lys Ile Val Thr Ala Ala Thr
770 775 780

Leu His Ala Lys Thr Ala Thr Glu Gly Ala Ile Gly Leu Ala Gln Tyr

785 790 795 800

Ala Thr Gln Ala Gln Val Asp Ala Gly Thr Leu Ser Asp Arg Ile Val
805 810 815

Pro Pro Ala Tyr Leu Lys Gln Thr Ile Gln Val Thr Glu Ser Trp Gln
820 825 830

Ala Thr Asp Ser Val Arg Gly Thr Val Arg Leu Ser Thr Gly Asp Gly
835 840 845

Thr Trp Lys Gly Asn Asp Thr Asn Gly Ser Thr Leu Pro Asp Asn Gly
850 855 860

Tyr Ala Ser Lys Gly Val Ala Val Ser Pro Tyr Glu Leu Asn Leu Thr
865 870 875 880

Leu Lys His Tyr Leu Pro Arg Leu Gly Lys Ala Tyr Asp Thr Gly Met
885 890 895

Leu Gly Gly Gln Thr Pro Asp Lys Tyr Ala Arg Arg Asp Ile Ala Gln
900 905 910

Thr Ile Ser Gly Ala Trp Thr Phe Ser Gln Asp Thr Val Phe Asn Asn
915 920 925

Asn Ile Ser Val Gln Asn Ile Leu Tyr Ala Asn Gly Gly Glu Val Lys
930 935 940

Ile Ser Pro Thr Ala Asp Thr Gly Asn Ala His Val Arg Phe Gln Asn
945 950 955 960

Arg Asp Gly Thr Glu Arg Gly Ile Ile Tyr Ala Glu Thr Gln Thr Ala
965 970 975

Ser Ala Gly Asn Leu Lys Val Arg Val Lys Asn Gly Thr Gly Thr Thr
980 985 990

Ala Ala Ser Gln Thr Tyr Thr Phe Gly Gly Asn Gly Thr Leu Asp Val
995 1000 1005

Pro Asn Glu Val Ser Thr Lys Thr Leu Arg Ser Ser Gly Asn Thr
1010 1015 1020

Ile Val Gly Gly Thr Val Met Val Lys Asp Thr Val Leu Leu Thr
1025 1030 1035

Ile Glu Thr Gln Asn Ala Ile Ile Gly Ala Arg Ser His Ser Ala
1040 1045 1050

Phe Ile Asp Thr Arg Asp Ala Asp Thr Gln Ile Phe Ala Arg Asp

1055 1060 1065

Asn Thr Asn Ser Tyr Pro Ile Leu Thr Thr Lys Asn Tyr Ala Arg
1070 1075 1080

Leu Ala Asp Gly Arg Tyr Val Lys Lys Ala Gly Asp Thr Met Thr
1085 1090 1095

Gly Asn Leu Asn Ile Asn Ser Ser Ala Ile Val Ile Thr Gly Ser
1100 1105 1110

Glu Ser Trp Tyr Val Pro Thr Asn Asp Thr Val Leu Arg Gln Gly
1115 1120 1125

Ser Trp Thr Ala Glu Ile Lys Asp Ala Thr Lys Leu Lys Gly Leu
1130 1135 1140

Arg Gly Tyr Met Val Pro Ile Arg Thr Pro Ile Asp Pro Ala Asn
1145 1150 1155

Pro Ser Thr Leu Val Val Thr Gly Tyr Glu Glu Lys Thr Ala Ala
1160 1165 1170

Gly Gly Val Leu Thr Gln Val Gly Val Thr Thr Asn Asn Thr Tyr
1175 1180 1185

Gln Leu Trp Thr Pro Tyr Pro Pro Thr Thr Glu Thr Ala Asp Lys
1190 1195 1200

Arg Phe Ala His Thr Val Trp Met Arg Ile Tyr Asn Pro Asn Leu
1205 1210 1215

Asn Lys Phe Asp Asp Trp Met Arg Val Phe Thr Ser Ala Thr Pro
1220 1225 1230

Pro Thr Ala Ala Asp Ile Gly Ala Pro Ser Ser Val Ser Thr Gln
1235 1240 1245

Val Lys Thr Leu Glu Val Leu Glu Trp Ile Lys Leu Gly Pro Val
1250 1255 1260

Lys Ile Trp Pro Asp Arg Pro Asn Gln Thr Leu Lys Phe Glu Trp
1265 1270 1275

Val Gly Asp
1280

<210> 1005
<211> 308
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1005
Met Ser Asp Leu Asn Cys Leu Phe Ala Glu Glu Asp Gln Val Lys Glu
1   5   10   15

Gly Val Ile Leu Ile Asp Leu Ser Gln Ile Ala Met Ala Thr Ile Leu
            20   25   30

His Thr Tyr Lys Glu Gly Asp Lys Leu Thr Thr Pro Met Val Arg His
        35   40   45

Leu Ile Leu Ser Thr Leu Lys Phe Asn Ala Phe Lys Trp Lys Lys Asp
    50   55   60

Gly Tyr Thr Lys Ile Val Ile Cys Val Asp Asn Ala Val Asn Gly Tyr
65   70   75   80

Trp Arg Arg Asp Val Ala Tyr Tyr Tyr Lys Lys Asn Arg Ala Lys Ala
                85   90   95

Arg Glu Glu Ser Asn Trp Asp Trp Glu Gly Tyr Phe Glu Gly Leu Arg
            100   105   110

Thr Val Ile Asp Glu Phe Lys Gln Tyr Met Pro Tyr Tyr Val Ile Asp
        115   120   125

Ile Asp Lys Ala Glu Ala Asp Asp Ser Ile Ala Val Leu Thr Lys Lys
    130   135   140

Phe Ser Leu Glu Gly His Pro Val Met Ile Val Ser Ser Asp Gly Asp
145   150   155   160

Phe Thr Gln Leu His Lys Tyr Pro Asn Val Lys Gln Trp Ser Pro Met
                165   170   175

Gln Lys Lys Leu Val Lys Ser Lys Thr Gly Ser Pro Ala Leu Asp Cys
            180   185   190

Met Val Lys Ile Ile Lys Gly Asp Lys Lys Asp Asn Val Ala Ser Ile
        195   200   205

Lys Val Arg Ser Asp Phe Trp Tyr Thr His Val Asp Gly Glu Arg Thr
    210   215   220

Pro Ser Thr Lys Met Thr Phe Val Glu Glu Cys Leu Asp Ala Gly Glu
225   230   235   240

Asn Ile Lys Asp Leu Leu Thr Glu Glu Gln Tyr Lys Arg Phe Leu Glu
                245   250   255

Asn Arg Val Leu Ile Asp Phe Asp Tyr Ile Arg Glu Asp Ile Val Ala
260 265 270

Asn Ile Leu Asp Cys Tyr Asn Asn Tyr Gln Leu Pro Gly Arg Gly Lys
275 280 285

Ile Tyr Ser Tyr Phe Val Lys Ser Gly Leu Ser Lys Leu Met Lys Glu
290 295 300

Ile Asn Asn Phe
305

<210> 1006
<211> 90
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1006
Met Ala Lys Lys Glu Lys Glu Gln Val Val Phe Asp Glu Ala Val His
1 5 10 15

Gly Gln Ala Leu Arg Asp Met Ile Lys Glu Ala Ser Gly Asn Lys Leu
20 25 30

Lys Ala Glu Ser Tyr Leu Glu Leu Asn Lys Asp Ile Lys Asp Arg Ala
35 40 45

Lys Lys Glu Leu Gly Val Glu Gly Lys Leu Phe Asn Gln Leu Leu Ala
50 55 60

Leu Phe His Lys Gly Thr Arg Asp Arg Phe Glu Thr Glu Lys Asp Glu
65 70 75 80

Val Val Glu Ala Tyr Asp Ser Ile Phe Ala
85 90

<210> 1007
<211> 99
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1007
Met Thr Leu Phe Ser Leu Lys Asp Glu Gly Asp Thr Ser Pro Ser Glu
1 5 10 15

Ser Ile Asn Gln Leu Leu Asp Lys Gln Ala Asn Gly Phe Ala Ile Glu
20 25 30

Ser Met Val Thr Glu Leu Gly Met Gly Tyr Leu Glu Ala Thr Thr Gln
35 40 45

```
Trp Leu Glu Glu Asn Ser Ile Pro Glu Gly Asn Phe Ser Arg Tyr Ile
    50                  55                  60

Pro Pro Ala Ile Ile Glu Lys Ile Met Ser Glu Ala Leu Glu Glu Asn
65                  70                  75                  80

Met Leu Arg Pro Ser Phe Ser Gln Thr His Lys Thr Asn Ser Leu Asp
                85                  90                  95

Phe Leu Leu
```

<210> 1008
<211> 220
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1008

```
Met Ile Arg Leu Arg Met Pro Gln Asn Asn Asn Arg Tyr Val Asn Gly
1               5                   10                  15

Lys Ser Val Tyr Leu Leu Tyr Leu Met Leu Lys Gln His Phe Ala Gly
            20                  25                  30

Arg Tyr Asp Val Val Lys Tyr Asn Trp Val Met Arg Val Ser Asp Lys
        35                  40                  45

Ala Tyr Gln Lys Arg Arg Asp Lys Tyr Phe Phe Glu Lys Leu Ala Glu
    50                  55                  60

Lys Tyr Thr Leu Lys Glu Leu Thr Leu Ile Phe Met Ser Asn Leu Val
65                  70                  75                  80

Ala Asn Gln Asp Ala Trp Ile Gly Asp Ile Ser Asp Ala Asp Ala Leu
                85                  90                  95

Ile Phe Tyr Arg Glu Tyr Ile Gly Lys Leu Lys Gln Ile Lys Thr Thr
            100                 105                 110

Phe Ser Glu Asp Val Lys Asn Ile Tyr Tyr Phe Ala Lys Lys Val Asn
        115                 120                 125

Val Asp Lys Leu His Asp Ile Phe Glu Tyr Asn Glu Lys Val Gly Thr
    130                 135                 140

Ser Tyr Val Phe Lys Leu Leu Gln Ser Asn Val Ile Ser Phe Glu Thr
145                 150                 155                 160

Phe Ile Met Leu Asp Ser Phe Leu Asp Ile Ile Asn Thr His Asp Thr
```

165 170 175

Ala Thr Asp Asn Leu Val Trp Ser Asn Tyr Ser Thr Lys Leu Lys Ala
180 185 190

Tyr Lys Lys Leu Leu Asn Val Asp Gly Ala Glu Ala Lys Lys Leu Phe
195 200 205

Ile Ser Ile Ile Lys Ser Cys Lys Glu Ile Ser Ile
210 215 220

<210> 1009
<211> 305
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1009
Met Phe Lys Arg Lys Asn Pro Ala Gln Leu Gln Gln Gln Leu Ala Gly
1 5 10 15

Leu Lys Gly Gly Ser Ser Phe Ser Asn Glu Asp Lys Asn Glu Trp Lys
20 25 30

Leu Lys Thr Asp Asn Ala Gly Asn Gly Gln Ala Val Ile Arg Phe Leu
35 40 45

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

Gly Phe Lys His Ala Gly Lys Trp Tyr Ile Glu Asn Cys Thr Ser Thr
65 70 75 80

His Gly Asp Phe Asp Ser Cys Pro Val Cys Ala His Leu Ser Lys Asn
85 90 95

Asp Ser Tyr Asn Ser Asn Pro Ala Glu Tyr Lys Leu Leu Lys Arg Lys
100 105 110

Thr Ser Phe Trp Ser Asn Ile Leu Val Ile Lys Asp Pro Ala Asn Pro
115 120 125

Glu Asn Glu Gly Lys Val Phe Lys Phe Arg Phe Gly Gln Lys Ile Met
130 135 140

Asp Lys Ile Asn Ala Met Val Glu Val Asp Val Asp Met Gly Glu Thr
145 150 155 160

Pro Val Asp Val Thr Cys Val Tyr Glu Gly Ala Asn Phe Val Met Lys
165 170 175

Val Lys Lys Val Gly Gly Phe Gln Asn Tyr Asp Glu Cys Lys Phe Leu
180 185 190

Gly Gln Ser Glu Ile Ala Asn Ile Asn Asp Glu Glu Thr Gln Lys Phe
195 200 205

Leu Thr Glu Asn Met Ala Asp Leu Ser Glu Ile Val Ala Pro Ser Gln
210 215 220

Phe Lys Ser Phe Glu Val Asn Glu Ala Lys Phe Lys Gln Ile Met Gly
225 230 235 240

Thr Ala Ala Leu Gly Gly Ala Ala Ala Lys Ala Ala Ala Gln Ala Asp
245 250 255

Lys Ile Gly Asp Asp Leu Asp Ser Phe Asp Lys Asp Leu Ser Asp Phe
260 265 270

Glu Ser Lys Pro Thr Ser Ser Arg Ser Ala Asp Asp Ile Met Gly Asp
275 280 285

Ala Gly Asp Ser Val Gly Asp Asp Asp Leu Asn Asp Ile Leu Asn Asp
290 295 300

Leu
305

<210> 1010
<211> 85
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1010
Met Gly Lys Leu Asn Ile Asp Ile Val Ala Glu Pro Tyr Ile Asn Lys
1 5 10 15

Ser Gly Phe Cys Thr Asp Leu Ile Phe Glu Asp Gly Ser Arg Phe Tyr
20 25 30

Asp Thr Asp His Gly Ile Asp Phe Asp Leu Val Ile Lys Glu Gly Pro
35 40 45

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

Arg Ala Trp Leu Glu Ala Asn Glu Trp Glu Asp Ile Asp Leu Met Met
65 70 75 80

Glu Asp Trp Lys Glu
85

<210> 1011
<211> 73
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1011
Met Ala Gln Val Thr Val Glu Ile Tyr Asp Tyr Glu His Phe Ile Glu
1 5 10 15

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

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

Leu Trp Leu Glu Gln Glu Tyr Phe Pro Gly Met Asp Asp Glu Cys Arg
50 55 60

Glu Asp Thr Leu Thr Thr Phe Ser Gly
65 70

<210> 1012
<211> 121
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1012
Met Lys Leu Asn Thr Glu Tyr Arg Ile Ile Pro Ser Leu Ala Ala Glu
1 5 10 15

Trp Asp Leu Ser Ser Ser Gly Asn Arg Arg Met Arg Leu Met Ile Glu
20 25 30

Glu His Gly Gly Ser Phe Phe Pro Thr Lys Met Leu Asp Glu Asp Asn
35 40 45

Ser Phe Ile Thr Glu Val Lys Phe Lys Asp Gly Thr Thr Ala Asp Ala
50 55 60

Glu Gly Phe Gly Asp Ala Tyr Phe Glu Ile Ser Asp Tyr Glu Phe Lys
65 70 75 80

Tyr Phe Glu Pro Val Tyr Glu Ile Gly Ser Ala Ile Gln Pro Gly Pro
85 90 95

Thr Arg Leu Asp Leu Ile Val Thr Pro Glu Asn Ala Glu Glu Met Ile
100 105 110

Asp Leu Ile Lys Lys Val Phe Lys Lys

115 120

<210> 1013
<211> 92
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1013
Met Lys Leu Gln Arg Gln Ser Ile Lys Leu Gly Ser Glu Tyr Arg Gly
1 5 10 15

Lys Trp Asn Phe Cys Ile Cys Asp Lys Asn Pro Glu Glu Leu Glu Arg
20 25 30

Val Glu Glu Val Leu Cys Gln Met Glu Ala Pro Phe Thr Met Gly Gly
35 40 45

Glu Thr Val Tyr Trp Asn Asp Tyr Cys Asp Asn Cys Pro Cys Tyr Glu
50 55 60

Asp Gly Tyr Gly Ser Gly Phe Trp Ile Pro Val Glu Asp Val Glu Glu
65 70 75 80

Phe Lys Lys Ala Phe Lys Leu Ala Lys Ala Lys Lys
85 90

<210> 1014
<211> 106
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1014
Met Ser Lys Phe Ser Val Thr Gly Tyr Pro Arg Val Asn Ile Arg Cys
1 5 10 15

Gln Phe Asp Glu Ile Pro Gly Val Thr His Ile Glu Leu Val Phe Asp
20 25 30

Pro His Ser Arg Cys Asn Gln Val Ser Gly Lys Ile Asp Ser Ala Tyr
35 40 45

Gly Glu Phe Leu Ile Asn Asp Gln Val Val Val Ser Ala Ile Ser Gly
50 55 60

Glu Gln Ala Gly Ser Leu Tyr Ile Leu Lys Arg Glu Val Phe Glu Glu
65 70 75 80

Ile Ser Glu Ala Ile Lys Glu Gly Phe Lys Thr Leu Gln Ser Met Ile
85 90 95

Lys Ala Ser Glu Tyr Lys Ser Cys Gly Phe
100 105

<210> 1015
<211> 54
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1015
Met Glu Asn Phe Ala Val Asp Asp Tyr Asp Asp Leu Ile Trp Trp Asp
1 5 10 15

Gly Arg Glu Trp Val Thr Ile Cys Ala Met Ser Asn Ile Asp Ser Ala
20 25 30

Ile Lys Arg Leu Gln Glu Leu Gln Gln Lys Trp Glu Asp Gly Asn Val
35 40 45

Glu Arg Val Glu Phe Tyr
50

<210> 1016
<211> 199
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1016
Met Ile Gln Ile Val Tyr Ala Phe Ala Pro Thr Lys Thr Val Asp Gly
1 5 10 15

Lys Asn Glu Asn Ala Phe Gly Leu Gly Asp Gly Leu Pro Trp Lys His
20 25 30

Ile Ser Gln Asp Met Lys Asn Phe Ala Asn Arg Thr Arg Asp Thr Ile
35 40 45

Leu Ile Cys Gly Ala Lys Thr Phe Met Ser Phe Pro Glu Pro Leu Pro
50 55 60

Gly Arg Lys Thr Ile Val Val Gln Asp Met Ser Arg Ala Leu Ala Thr
65 70 75 80

Ala Lys Asn Gly Phe Phe Ala Asp Ala Tyr Val Ser Glu Leu Glu Phe
85 90 95

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

Ser Thr Ile Thr Phe Asn Arg Asp Leu Asn Tyr Ser Ile Ile Gly Gly

115 120 125

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

Thr Ile Ile Arg Lys Ser His Arg Val Asn Ser Asp Val Thr Leu Pro
145 150 155 160

Ala Glu Phe Val Thr Ala Pro Thr Trp Pro Glu Ser Gly Phe Ile Thr
165 170 175

Lys Glu Asn His Trp Tyr His Ile Asp Glu Val Thr Asn Ile Ser Glu
180 185 190

Val Val Tyr Glu Arg Lys Leu
195

<210> 1017
<211> 105
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1017
Met Ser Ala Asn Tyr Asp Ile Thr Gln Leu Ser Glu Asp Lys Val Gln
1 5 10 15

Lys Arg Trp Lys Arg Phe Pro Phe Lys His Gly Ile His Leu Leu Val
20 25 30

Phe Ser Tyr Asn Gly Leu Ser Thr Tyr Asn Gly Ser Thr Thr Val Tyr
35 40 45

Asn Arg Asn Gly Asn Ile Pro Ile Glu Ile Glu Arg Asp Tyr Lys Lys
50 55 60

Met Phe Ile Gly Met Ser His Gly Asn Val Thr Val Asn Asp Asp Val
65 70 75 80

Val Ser Ile Ile Gly Arg Phe Glu Lys Arg Gly Asp Gln Leu Phe Phe
85 90 95

Thr Pro Leu Gln Glu Lys Phe Asn Ala
100 105

<210> 1018
<211> 286
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1018
Met Arg Glu Tyr Gln Glu Leu Ile Lys Asp Ile Phe Glu Asn Gly Tyr
1   5   10   15

Glu Thr Asp Asp Arg Thr Gly Thr Gly Thr Ile Ala Lys Phe Gly Thr
            20   25   30

Gln His Arg Phe Asp Leu Gln Glu Gly Phe Pro Ala Val Thr Thr Lys
        35   40   45

Arg Leu Ala Trp Lys Ala Cys Ile Ala Glu Leu Ile Trp Phe Met Cys
    50   55   60

Gly Ser Thr Asn Val His Glu Leu Arg Leu Ile Gln His Asp Ser Leu
65   70   75   80

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

Asp Met Gly Tyr Ser Gly Gly Glu Leu Gly Pro Val Tyr Gly Lys Gln
            100   105   110

Trp Arg Asp Phe Met Gly Val Asp Gln Leu Lys Leu Ile Ile Asp Arg
        115   120   125

Ile Lys Gln Leu Pro Tyr Asp Arg Arg Gln Ile Val Thr Ala Trp Asn
    130   135   140

Pro Val Asp Leu Asp Lys Met Ala Leu Pro Pro Cys His Leu Leu Tyr
145   150   155   160

Gln Phe Asn Val Arg Gln Gly His Leu Asp Leu Gln Trp Tyr Gln Arg
                165   170   175

Ser Val Asp Val Phe Leu Gly Leu Pro Phe Asn Ile Ala Ser Tyr Ala
            180   185   190

Ala Leu Val His Ile Ile Ala Lys Met Thr Asn Leu Lys Pro Gly His
        195   200   205

Leu Val Phe Thr Gly Gly Asn Thr His Ile Tyr Leu Asn His Ile Glu
    210   215   220

Gln Cys Lys Glu Ile Leu Arg Arg Glu Pro Lys Glu Leu Cys Glu Leu
225   230   235   240

Glu Ile Ala Phe Pro Asp Thr Tyr Glu Thr Trp Gln Thr Ser Ser Gln
                245   250   255

Ile Arg Trp Leu Glu Gln Phe Ala Arg Pro His His Phe Glu Leu Val
            260   265   270

Gly Tyr Lys Ser His Pro Thr Ile Lys Gly Lys Met Ala Ile
        275   280   285

<210> 1019
<211> 68
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1019
Met Asn Ile Arg Phe Val Arg Lys Gly His Gln Ser Lys Thr Val Leu
1   5   10   15

Gly Glu Met Gln Asp Ala Phe Ser Ser Asp Leu Pro Glu Val Asn Asp
            20   25   30

Thr Ile Val Phe Asp Gly Thr Glu Gln Arg Val Leu Ser Val Ile Lys
        35   40   45

Ser Tyr Glu Trp Ser Ile Gly Lys Thr Gln Leu Ile Cys Trp Phe Glu
    50   55   60

Val Asp Ile Thr
65

<210> 1020
<211> 101
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1020
Met Lys Ile Cys Arg Val Val Asn Lys Tyr His Ser Asp Phe Asp Val
1   5   10   15

Asn Ile Gln Arg Gly Thr Met Trp Gly Asn Tyr Val Gly Lys Asp Cys
            20   25   30

Asp Asn Arg Pro Asp Ala Ile Ala Ala Phe Lys Asp Asp Phe Ile Ala
        35   40   45

Lys Ile Arg Asn Gly Glu Ile Lys Arg Glu His Leu Glu Thr Leu Arg
    50   55   60

Gly Met Arg Leu Gly Cys Thr Cys Lys Pro Leu Pro Cys His Gly Asp
65   70   75   80

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

Glu Asp Leu Cys Lys

100

<210> 1021
<211> 748
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1021
Met Gln Val Ile Lys Ser Ser Gly Val Ser Gln Glu Phe Asp Met Gln
1 5 10 15

Lys Ile Ile Lys Val Leu Glu Trp Ala Cys Glu Gly Thr Lys Val Asp
20 25 30

Pro Tyr Glu Leu Tyr Glu Ile Ile Lys Ser His Leu Arg Asp Gly Met
35 40 45

Ser Thr Ala Asp Ile Gln Lys Thr Ile Val Lys Val Ala Ala Asn Ser
50 55 60

Ile Ser Ile Asp Glu Pro Asp Tyr Gln Tyr Val Ala Ser Asn Ala Ala
65 70 75 80

Met Phe Glu Ile Arg Lys Arg Val Tyr Gly Gln Phe Glu Pro Pro Ala
85 90 95

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

Glu Ile Leu Ser Lys Trp Ser Ala Glu Glu Ile Thr Leu Leu Asp Ser
115 120 125

Tyr Ile Lys His Glu Arg Asp Phe Thr Met Thr Tyr Ala Gly Thr Met
130 135 140

Gln Leu Ile Glu Lys Tyr Leu Val Lys Asp Arg His Thr Gly Glu Leu
145 150 155 160

Tyr Glu Thr Pro Gln Phe Ala Phe Met Leu Ile Gly Met Cys Leu His
165 170 175

Gln Asp Asp Gly Glu Asn Arg Leu Ala Asn Val Ile Arg Phe Tyr Asp
180 185 190

Ala Val Ser Thr Lys Lys Ile Ser Leu Pro Thr Pro Ile Met Ser Gly
195 200 205

Val Arg Thr Pro Thr Arg Gln Phe Ser Ser Cys Val Val Ile Glu Gly
210 215 220

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

Tyr Ile Ser Lys Arg Ala Gly Ile Gly Ile Asn Ala Gly Met Ile Arg
                245                 250                 255

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

Ile Pro Phe Trp Lys His Phe Gln Thr Ala Val Lys Ser Cys Ser Gln
        275                 280                 285

Gly Gly Val Arg Gly Gly Ala Ala Thr Leu Tyr Tyr Pro Ile Trp His
    290                 295                 300

Leu Glu Val Glu Asn Leu Leu Val Leu Lys Asn Asn Lys Gly Val Asp
305                 310                 315                 320

Glu Asn Arg Ile Arg His Leu Asp Tyr Gly Val Gln Ile Asn Asn Leu
                325                 330                 335

Met Ile Glu Arg Leu Ile Lys Asn Asp Tyr Ile Thr Leu Phe Ser Pro
            340                 345                 350

Asp Val Cys Leu Gly Ala Leu Tyr Thr Glu Tyr Phe Arg Asp Ala Gln
        355                 360                 365

Ala Phe Arg Thr Leu Tyr Glu Glu Leu Glu Lys Asn Pro Asp Ile Arg
    370                 375                 380

Lys Lys Arg Ile Lys Ala Arg Glu Leu Phe Glu Leu Phe Leu Thr Glu
385                 390                 395                 400

Arg Ala Gly Thr Ala Arg Ile Tyr Pro Tyr Met Val Asp Asn Val Gly
                405                 410                 415

Glu Tyr Gly Pro Phe Ile Arg Asp Val Ala Thr Val Lys Gln Ser Asn
            420                 425                 430

Leu Cys Leu Glu Ile Ala Leu Pro Thr Ser Asp Val Gly Gln Glu Asp
        435                 440                 445

Gly Glu Ile Ala Leu Cys Thr Leu Ala Ala Phe Val Leu Asp Asn Phe
    450                 455                 460

Asn Trp Gln Asp Gln Glu Glu Val Asn Glu Ile Ala Glu Val Met Val
465                 470                 475                 480

Arg Ala Leu Asp Asn Leu Leu Asp Tyr Gln Asp Tyr Pro Val Asp Lys
                485                 490                 495
```

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

Tyr Ala Ala Trp Leu Ala Ser Asn Phe Ala Ser Tyr Ala Asp Ala Asn
        515                 520                 525

Asp Ile Thr His Glu Met Met Glu Arg Ile Gln Tyr Ala Leu Ile Lys
    530                 535                 540

Ala Ser Val Lys Leu Ala Ser Glu Lys Gly Pro Cys Ala Leu Tyr Lys
545                 550                 555                 560

Glu Thr Arg Tyr Gly Arg Gly Glu Leu Pro Ile Asp Trp Tyr Asn Lys
                565                 570                 575

Arg Ile Asp Gln Leu Ala Ala Pro Asn Tyr Val Cys Asp Trp Glu Leu
            580                 585                 590

Leu Arg Glu Asp Leu Lys Arg Tyr Gly Ile Arg Asn Ser Thr Leu Ser
        595                 600                 605

Ala Leu Met Pro Cys Glu Ser Ser Ser Gln Val Ser Asn Ser Thr Asn
    610                 615                 620

Gly Ile Glu Pro Pro Arg Gly Pro Val Ser Val Lys Glu Ser Lys Glu
625                 630                 635                 640

Gly Ser Phe Asn Gln Val Val Pro Asn Val Glu His Asn Ala Ser Leu
                645                 650                 655

Tyr Asp Tyr Ala Trp Gln Leu Ala Lys Gln Gly Asn Lys Pro Tyr Leu
            660                 665                 670

Asn Gln Val Leu Ile Met Gln Lys Phe Val Asp Gln Ser Ile Ser Ala
        675                 680                 685

Asn Thr Tyr Tyr Asp Pro Ala Asn Phe Pro Lys Gly Lys Val Glu Met
    690                 695                 700

Ser Val Met Met Asp Asp Leu Leu Tyr Phe Trp Tyr Phe Gly Gly Lys
705                 710                 715                 720

Thr Leu Tyr Tyr His Asn Thr Arg Asp Gly Ser Gly Asn Asp Asp Met
                725                 730                 735

Ile Gln Asp Ser Ala Asp Cys Ala Ala Cys Lys Leu
            740                 745

<210> 1022
<211> 213
<212> PRT
<213> Unknown
```

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1022
Met Asn Tyr Gln Asn Val Tyr Asn Ser Leu Ile Ser Arg Ala Arg Ala
1 5 10 15

Arg Glu Ser Leu Leu Gly Tyr Lys Glu Thr His His Ile Ile Pro Arg
20 25 30

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

Arg Glu His Phe Ile Ala His Trp Leu Leu Cys Lys Ile Tyr Glu Ala
50 55 60

Pro Gly Leu Lys Lys Ala Phe Gly Leu Met Cys Leu Thr Gly Lys Asn
65 70 75 80

Arg Ser Tyr Lys Val Ser Ser Gln Leu Tyr Glu Leu Gly Lys Arg Arg
85 90 95

Leu Ser Glu Ala Ala Thr Gly Arg Lys Ala Ser Ile Glu Thr Arg Glu
100 105 110

Lys Ile Ser Lys Ser Leu Lys Gly Arg Glu Phe Thr Glu Glu His Leu
115 120 125

Ala Asn Met Arg Lys Pro Lys Thr Glu Glu Thr Lys Lys Asn Ile Ala
130 135 140

Ala Ala Lys Val Gly Val Leu Asn Pro Met Tyr Gly Lys Ile Ser Pro
145 150 155 160

Thr Arg Asp Val Pro His Thr Lys Glu Thr Arg Asp Val Ile Ser Leu
165 170 175

Arg Thr Lys Gln Gly Thr Glu Tyr Pro Pro Cys Pro His Cys Gly Lys
180 185 190

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

Phe Lys Asp Pro Lys
210

<210> 1023
<211> 380
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1023
Met Ser Thr Val Phe Asn Lys Glu Pro Val Asp Ile Met Asn Glu Pro
1   5   10   15

Met Phe Leu Gly Ser Gly Leu Gly Ile Ala Arg Tyr Asp Val Gln Arg
            20   25   30

His Lys Val Phe Glu Glu Leu Ile Glu Lys Ser Leu Ser Phe Phe Trp
        35   40   45

Arg Pro Glu Glu Val Asn Val Met Met Asp Arg Gly Gln Phe Glu Lys
    50   55   60

Leu Pro Glu His Gln Arg Asn Ile Phe Thr Asp Asn Leu Lys Tyr Gln
65   70   75   80

Ser Leu Leu Asp Ser Ile Gln Gly Arg Ala Pro Ala Ala Val Leu Ser
                85   90   95

Ala Leu Ile Ser Asp Pro Ser Leu Asp Thr Trp Asn Gln Thr Trp Thr
            100   105   110

Phe Ser Glu Thr Ile His Ser Arg Ser Tyr Thr His Ile Met Arg Asn
        115   120   125

Leu Tyr Val Asp Pro Ala Lys Ile Phe Asp Glu Ile Val Leu Asp Glu
    130   135   140

Ala Ile Met Lys Arg Ala Glu Ser Ile Gly Val Tyr Tyr Asp Asp Val
145   150   155   160

Ile Ala Lys Thr Arg Ala Trp Glu Asn Ala Lys Asn Arg Cys Phe Asn
                165   170   175

Gln Asp Asn Ile Glu Ile Lys Glu Ala Lys Arg Asp Leu Met Lys Ser
            180   185   190

Leu Tyr Leu Cys Leu His Val Ile Asn Ala Leu Glu Ala Ile Arg Phe
        195   200   205

Tyr Val Ser Phe Ala Cys Thr Phe Asn Phe His Lys Asn Met Glu Ile
    210   215   220

Met Glu Gly Asn Ala Lys Ile Met Lys Phe Ile Ala Arg Asp Glu Gln
225   230   235   240

Leu His Leu Lys Gly Thr Gln Tyr Ile Leu Arg Gln Leu Gln Thr Gly
                245   250   255

Thr Asp Gly Glu Glu Trp Val Glu Ile Ala Lys Glu Cys Glu Gln Glu
            260   265   270

Ala Ile Glu Ile Phe Met Glu Val Asn Arg Gln Glu Lys Asp Trp Ala
275 280 285

Ile His Leu Phe Arg Asn Gly Gly Leu Pro Gly Leu Asn Val Lys Ile
290 295 300

Leu His Asp Phe Ile Asp Tyr Leu Thr Val Ser Arg Met Arg Ser Cys
305 310 315 320

Gly Leu Pro Cys Pro Ile Thr Asp Ala Pro Thr Arg His Pro Ile Pro
325 330 335

Trp Ile Arg Glu Tyr Leu Asn Ser Asp Ala Val Gln Ser Ala Pro Gln
340 345 350

Glu Val Glu Ile Ser Ser Tyr Leu Val Ala Gln Ile Asp Asn Asp Val
355 360 365

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

<210> 1024
<211> 138
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1024
Met Asn Asp Ile Ala Asn Glu Phe Ser Phe Ile Lys Tyr Val Gln Leu
1 5 10 15

Glu Leu Glu Pro Asp Phe Ser Ile Lys Pro Val Leu Val Ala Asn Lys
20 25 30

Leu Asn Val Val Tyr Ala Ile Ala Val Asp Asp Glu Leu Val Tyr Ile
35 40 45

Gly Lys Thr Lys Asn Leu Arg Lys Arg Ile Asn Tyr Tyr Arg Thr Ala
50 55 60

Ile Asn Arg Lys Asp Gln Thr Ser Asp Ser Ala Lys Ser Ala Lys Ile
65 70 75 80

Phe Glu Ala Leu Met Ala Gly Lys Lys Val Glu Phe Tyr Ala Arg Gln
85 90 95

Cys Phe Asn Leu Leu Ile Asn Asn Glu Leu Gly Glu Met Ser Ile Ser
100 105 110

Thr Met Asp Leu Glu Glu Pro Met Phe Ile Lys Lys Phe Asn Pro Pro

115 120 125

Trp Asn Thr Gln His Lys Val Lys Lys Cys
130 135

<210> 1025
<211> 383
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1025
Met Leu Glu Leu Tyr Lys Asn Leu Met Asn Leu Cys Glu Ser Ser Glu
1 5 10 15

Val Ala Lys Phe Phe Tyr Lys Asp Phe Thr Gly Pro Met Asp Gly Lys
20 25 30

Phe Arg Val Phe Ser Tyr His Tyr Ala Ser Tyr Ser Glu Trp Leu Lys
35 40 45

Pro Asp Ala Leu Glu Cys Arg Gly Ile Met Phe Glu Met Asp Gly Asp
50 55 60

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

Asn Glu Asn Pro Leu Thr Met Gly Ile Asp Ile Ser Asp Val Glu Tyr
85 90 95

Ile Met Asp Lys Ala Asp Gly Ser Leu Val Ser Ser Tyr Val Asp Asp
100 105 110

Gly Tyr Leu Tyr Leu Lys Ser Lys Thr Ser Leu Tyr Ser Asp Gln Ala
115 120 125

Arg Gln Ala Ser Ala Leu Leu Asn Ser Glu Glu Tyr Ser Ser Leu His
130 135 140

Gln Val Ile Leu Glu Leu Ala Leu Asp Gly Tyr Thr Val Asn Met Glu
145 150 155 160

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

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

Tyr Asp Asp Leu Tyr Ala Asn Ala Lys Ile Arg Pro Tyr Leu Ile Asn
195 200 205

```
Ala Tyr Gly Ile Ser Asp Pro Thr Thr Trp Val Glu Gly Val Arg Glu
    210                 215                 220

Leu Glu Gly Val Glu Gly Tyr Ile Ala Val Leu Asn Thr Gly Gln Arg
225                 230                 235                 240

Phe Lys Val Lys Thr Glu Trp Tyr Ser Ala Leu His His Thr Lys Asp
                245                 250                 255

Ser Ile Thr Ser Asn Glu Arg Leu Phe Ala Ser Val Val Ser Ala Asn
            260                 265                 270

Ser Asp Asp Leu Arg Ser Leu Phe Ala Gly Asp Glu Tyr Thr Ile Lys
        275                 280                 285

Lys Ile Ser Ala Phe Glu Gln Ala Tyr Leu Asp Tyr Leu Gly Lys Ser
    290                 295                 300

Leu Glu Leu Cys Gln Ser Phe Tyr Asp Glu Tyr Arg Gly Arg Ala Arg
305                 310                 315                 320

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

Leu Phe Gly Val Ile Met Asn Met Tyr Glu Gly Thr Val Asp Val Asp
            340                 345                 350

Lys Leu Leu Lys Asp Leu Glu Arg Val Phe Leu Lys Tyr Trp Ala Gly
        355                 360                 365

Tyr Val Pro Lys Glu Tyr Glu Lys Glu Ile Glu Ile Ser Glu Glu
    370                 375                 380
```

<210> 1026
<211> 169
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1026

```
Met Asp Met Gln Ala Ile Thr Leu Asp Met Val Val Asn Lys Tyr Gly
1               5                   10                  15

Thr His Ser Asp Gly Ile Phe Val Trp Asn Gly Thr Lys Lys Val Gly
            20                  25                  30

Phe Val Thr Asp Leu Arg Thr His Met Ala Arg Lys Glu Ala Ala Arg
        35                  40                  45

Lys Lys Gln Lys Glu Tyr Thr Asn Arg Val Asn Glu Gln Arg Ala Glu
    50                  55                  60
```

```
Ala Leu Pro Glu Ala Val Asp Glu Met Ile Asp Phe Leu Asp Asn His
65                  70                  75                  80

Leu Ala Lys Tyr Gly Ala Glu Val Phe Lys Asn Ile Thr Gln Pro Asn
                85                  90                  95

Val His Ala Asn Gly Cys Lys Cys Tyr Val Ile Val Asp Pro Ile Tyr
            100                 105                 110

Gly Lys His Arg Leu Gly Ile Met His Arg Glu Leu Asn Tyr Ser Glu
        115                 120                 125

Met Ala Glu Tyr Val Glu Ala Cys Phe Lys Cys Ser Pro Ser Glu Ser
    130                 135                 140

Ser Asp Arg His Ile Leu Ile Ser Gly Leu Ser Arg Asp Asp Ile Val
145                 150                 155                 160

Glu Val Ile Leu Lys Leu Cys Ser Lys
                165
```

<210> 1027
<211> 117
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1027

```
Met Leu Lys Ile Asn Thr Thr Trp Leu Leu Ile Gly Val Leu Ala Leu
1               5                   10                  15

Ser Ala Gly Gly Leu Lys Tyr Leu Ser Trp Arg Val Glu Asn Leu Lys
            20                  25                  30

Ala Asp Leu Lys Val Val Gln Asp Glu Ser Asp Arg Gln Ala Lys Glu
        35                  40                  45

Ile Glu Asn Ile Gly Val Ser Ile Lys Asn Leu Gln Thr Thr Tyr Lys
    50                  55                  60

Gly Tyr Gln Glu Asn Arg Ala Ala Arg Asp Thr Ser Asn Ala Lys Met
65                  70                  75                  80

Asn Lys Asp Ser Lys Arg Gly Asn Val Val Ala Ala Lys Pro Gly Leu
                85                  90                  95

Val Glu Lys Gln Ile Asn Ala Ser Phe Asn Lys Phe Ala Glu Asp Ile
            100                 105                 110

Gln Glu Ala Thr Arg
        115
```

<210> 1028
<211> 95
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1028
Met Lys Arg Ser Leu Leu Ala Met Cys Ile Ile Ser Leu Leu Ala Gly
1   5   10   15

Cys Ser Ser Ser Ala Pro Asp Val Pro Val Leu His Pro Glu Trp Pro
            20   25   30

Asp Pro Ile Gln Lys Trp Glu Gly His Trp Glu Val Lys Val Ile Asp
        35   40   45

Gly Lys Ala Trp Val Gly Met Pro Phe Glu Glu Ser Gln Glu Tyr Arg
    50   55   60

Ile Trp Met Asn Asp Ile Leu Arg Tyr Thr Lys Asp Ala Asn Gly Met
65   70   75   80

Ile Cys Tyr Tyr Arg Ser Glu Leu Lys Glu Pro Arg Cys Val Lys
                85   90   95

<210> 1029
<211> 161
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1029
Met Glu Pro Ser His Phe Tyr Ser Tyr Phe Val Lys Asp Ala Ser His
1   5   10   15

Leu Leu Ser Ile Lys Asn Thr Gln Leu Arg Asn Met Leu Ala Val Gly
            20   25   30

Ser Cys Gln Leu Thr Pro Leu Ala Lys Lys Ala Thr Val Ile Pro Glu
        35   40   45

Asn Ile Ser Asn Gly Tyr Val Tyr Thr Val Arg Val Ser Val Pro Gly
    50   55   60

Ala Leu Lys Glu Arg Leu Phe Glu Leu Asn Asp Gln Thr Arg Ile Ser
65   70   75   80

Phe Asp Val Trp Phe Lys Leu Phe Met Val Glu Phe Met Tyr Pro Asp
                85   90   95

Phe Leu Lys Phe Val Gln Arg Lys Glu Ala Leu Lys Glu Ala Ile Ser
100 105 110

Glu Leu Glu Asp Ala Ser Ile Glu Phe Gly Lys Ala Leu Gln Phe Val
115 120 125

Glu Ser Gly Gly Val Glu Gln Asp Ala Val Asn Gly Phe Leu Lys Lys
130 135 140

Tyr Gly Lys Arg Arg Ser Leu Ala His Arg Asn Leu Ser Lys Met Val
145 150 155 160

Met

<210> 1030
<211> 70
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1030
Val Asn Gln Glu Gln Tyr Glu Thr Leu Lys Gly Leu Ile Ala Glu Asn
1 5 10 15

Glu Leu Ala Cys Ile Val Phe Gly Arg Ala Ala Glu Asn Tyr Asp Lys
20 25 30

Asn Asp Ile Leu Ser Met Asn Lys Pro Leu Arg Ala Ile Lys Glu Lys
35 40 45

Tyr Arg Ala Asn Trp Gly Glu Lys Ser Lys Ala Leu His Asp Phe Ile
50 55 60

Asp Thr Leu Lys Asp Val
65 70

<210> 1031
<211> 297
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1031
Met Lys Lys Leu Val Leu Thr Gln Gly Ala Pro Gly Ser Gly Lys Thr
1 5 10 15

Thr Trp Ala Asn Glu Tyr Val Ala Ala Asn Pro Gly Trp Tyr Val Leu
20 25 30

Ser Arg Asp Asp Leu Arg Glu Gly Ile Phe Gly Leu Asp Lys Arg Asn
35 40 45

```
Asp Tyr Lys Tyr Ser Lys Leu Arg Glu Lys Ser Val Ser Val Cys Gln
    50                  55                  60

Phe Ser Met Ala Lys Thr Leu Leu Glu Met Glu Thr Thr Lys Gly Val
65                  70                  75                  80

Ile Ile Ala Asp Thr Asn Leu Asn Pro Thr Thr Ile Lys Lys Trp Gln
                85                  90                  95

Glu Leu Ala Tyr Glu Ile Asp Gly Val Lys Trp Glu Ile Lys Arg Phe
            100                 105                 110

Asp Val Pro Trp Thr Glu Leu Val Lys Arg Asn Leu Tyr Arg Gly Ala
        115                 120                 125

Asn Ala Val Pro Ile Glu Val Leu Arg Ser Phe Tyr Ser Lys Met His
    130                 135                 140

Pro Tyr Asp Leu Tyr Ile Pro Asp Glu Ser Leu Pro Lys Ala Val Ile
145                 150                 155                 160

Phe Asp Leu Asp Gly Thr Leu Ala Asp Asn Asn His Arg Ser Pro Tyr
                165                 170                 175

Asp Leu Ala Lys Cys Gly Lys Asp His Pro Lys Glu Met Val Ile Glu
            180                 185                 190

Phe Leu Lys Met Leu Arg Asn Lys Gly Tyr Lys Ile Leu Thr Val Ser
        195                 200                 205

Gly Arg Glu Ser Gly Thr Lys Glu Asp Pro Thr Val Tyr Gln Arg Ile
    210                 215                 220

Thr Lys Lys Trp Leu Leu Asp His Val Gly Glu Thr Gly Glu His Phe
225                 230                 235                 240

Gln Arg Lys Gln Gly Asp Ser Arg Lys Asp Asp Val Val Lys Glu Glu
                245                 250                 255

Ile Phe Trp Asp Arg Ile Ala Asp Arg Tyr Asn Val Lys Leu Ala Val
            260                 265                 270

Asp Asp Arg Ala Gln Val Val Glu Met Trp Arg Arg Ile Gly Val Glu
        275                 280                 285

Cys Trp Gln Val Ala His Gly Asp Phe
    290                 295

<210> 1032
<211> 94
```

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1032
Met Phe Pro Lys Tyr Ser Glu Val Val Lys Val Ser Phe Thr Gln Val
1   5   10   15

Val Ala Asn His Leu Thr Asp Glu Phe Thr Pro Ala Glu Val Ala Lys
            20   25   30

Met His Ala Glu Phe Leu Ser Ala Met Asn Ala Leu Ile Pro Asn Gly
        35   40   45

Glu Val Val Lys Phe Ser Ile Asp Arg Leu Gly Gly Ser Ser Glu Ile
    50   55   60

Lys Ile Ser Cys Gly Glu Gly Glu His Asp Trp Phe Ile Val Gly Ile
65   70   75   80

Ile Ala Asn Phe Glu Thr Gln Gln Val Glu Thr Tyr Val Val
                85   90

<210> 1033
<211> 78
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1033
Met Leu Ser Asp Ala Lys Phe Ser His Asp Glu Phe Ile Ser Lys Val
1   5   10   15

Lys Ile Phe Ala Gln Glu Val Ala Asn Arg Val Pro Gly Ser Lys Val
            20   25   30

Thr Leu Arg Arg Glu Ser Ser Phe Asn Tyr Val Asp Ala Tyr Ile Ile
        35   40   45

Thr Val Asn Asn Gly Lys Ser Asn Gln His Thr Gln Leu Ala Leu Thr
    50   55   60

Gly Thr Gly Gln Val Glu Met Thr Asn Ile Leu Gly His Ile
65   70   75

<210> 1034
<211> 114
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1034
Met Thr Leu Arg Glu Ala Val Glu Ala Leu Leu Ile Glu His Ala Arg
1 5 10 15

Gly Ile Lys Ala Glu Ile Ser Pro Asn Gly Ile Arg Leu Ile Ser Ala
20 25 30

Val Ile Gly Ser Asp Gln Gly Val Trp Ser Ile Pro Arg Glu Glu Tyr
35 40 45

Asp Ala Ile Leu Tyr Ser Asn Val Asn Val Lys Glu Gly Gln Pro Met
50 55 60

Tyr Gly Tyr Val Phe Ser Asp Ser Leu Glu Arg Gly Asn His Pro Phe
65 70 75 80

Pro Asp Gly Thr Gly Ile Arg Thr Ser Arg Val Glu Ser Phe Ala Ser
85 90 95

Pro Thr Asp Glu Leu Lys Leu Val Lys Thr Asn Asn Thr Thr Tyr Leu
100 105 110

Val Ile

<210> 1035
<211> 189
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1035
Met Lys Ala Ser Thr Val Leu Gln Ile Ala Tyr Leu Val Ser Gln Glu
1 5 10 15

Ser Lys Cys Cys Ser Trp Lys Val Gly Ala Val Ile Glu Lys Asn Gly
20 25 30

Arg Ile Ile Ser Thr Gly Tyr Asn Gly Ser Pro Ser Gly Gly Val Asn
35 40 45

Cys Cys Asp His Ala Ala Glu Gln Gly Trp Ile Gly Glu Ile Pro Tyr
50 55 60

Lys Ser Thr Gly Leu Arg Gln Asp Gly Phe Gln Val Lys Lys Val Gly
65 70 75 80

Leu Leu Lys Glu His Arg Ala Ala His Ser Ala Trp Ser Lys Val Asn
85 90 95

Glu Ile His Ala Glu Leu Asn Ala Ile Leu Phe Ala Ala Arg Asn Gly
100 105 110

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

Asp Cys Ala Lys Ala Ile Ala Gln Ser Gly Ile Lys Lys Leu Val Tyr
130 135 140

Cys Glu Thr Tyr Asp Lys Asn Glu Pro Gly Trp Asp Asp Ile Leu Arg
145 150 155 160

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

Leu Asn Trp Tyr Asn Ile Lys Glu Phe Cys Gly Ile Glu
180 185

<210> 1036
<211> 66
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1036
Met Lys Leu Arg Ile Val Glu Ile Asn Lys Leu Asn Leu Ser Gly Asp
1 5 10 15

Val Val Ile Ser Tyr Ser Val Glu Arg Arg Tyr Trp Phe Lys Trp Lys
20 25 30

Pro Leu Ala Thr Phe Lys Phe Glu Asp Gln Ala Val Arg Leu Leu Lys
35 40 45

Glu Leu Ser Lys Arg Lys Ser Val Ile Ile Lys Thr Ile Lys Glu Thr
50 55 60

Ser Lys
65

<210> 1037
<211> 102
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1037
Met Lys Leu Thr Thr Glu Gln Asn Ile His Ile Arg Glu Thr Leu Lys
1 5 10 15

Ala Val Leu Ser Met Gly Glu Ser Gln Ile Val Phe Glu Lys Ala Asp
20 25 30

Gly Thr Ile Arg Thr Leu Arg Cys Thr Arg Asp Lys Asp Ile Ile Pro
        35   40   45

Ser Asp Leu Val Glu Ser Thr Thr Lys Ser Ala Arg Ala Glu Ser Thr
    50   55   60

Thr Ser Leu Pro Val Tyr Asp Thr Glu Lys Glu Gly Trp Arg Ser Phe
65   70   75   80

Ala Phe Asp Lys Leu Ile Ser Val Asn Gly Met Lys Val Glu His Leu
                85   90   95

Leu Gln Met Ile Gly Lys
            100

<210> 1038
<211> 107
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1038
Met Glu Leu Pro Ile Lys Ala Leu Gly Glu Tyr Val Ile Leu Val Ser
1   5   10   15

Glu Pro Ala Gln Gln Gly Asp Glu Ile Val Ser Pro Ser Gly Ile Ile
            20   25   30

Leu Gly Lys Glu Glu Gln Gly Gln Leu Pro Asp Met Cys Glu Ile Tyr
        35   40   45

Ser Ile Gly Asp Asp Val Pro Lys Gly Phe Val Glu Val Gly Asp Leu
    50   55   60

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

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

Cys His Tyr Lys Ser Leu Ala Cys Val Tyr Lys
            100   105

<210> 1039
<211> 82
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1039
Met Asn Lys Gln Leu Thr Lys Ala Leu Glu Leu Gln Arg Asn Ala Trp
1   5   10   15

Asn Ser Gly His Glu Asn Tyr Gly Ala Ser Ile Asp Ile Tyr Ala Glu
            20   25   30

Ala Leu Glu Val Leu Lys Gly Phe Lys His Leu Asn Pro Ala Gln Ala
        35   40   45

Glu Phe Arg Asp Thr Leu Glu Ala Met Asp Glu Leu Lys Tyr Ala Lys
    50   55   60

His Leu Gly Ser Ala Ala Arg Lys Ala Val Arg His Phe Val Val Thr
65   70   75   80

Leu Lys

<210> 1040
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1040
Met Glu Asp Asp Lys Met Ala Lys Gln Ala Lys Ala Lys Thr Ala Val
1   5   10   15

Lys Glu Val Val Gly Thr Ser Lys Arg Ala Gly Tyr Lys Arg Gly Ser
            20   25   30

Asn Lys Arg Ile Asn Gln Thr Val Glu Lys Ile Met Arg Arg Ala Arg
        35   40   45

Ala Val Leu Arg Asp Asp Ala Ser Arg Phe Gly Lys Pro Lys Ala
    50   55   60

<210> 1041
<211> 119
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1041
Met Asn Phe Thr Asn Phe Asn Arg Lys Tyr Val Gln Asn Asn Ala Trp
1   5   10   15

Asp Val Ser Thr Thr Leu Leu Trp Glu His Asn Asn Gly Thr Val Ala
            20   25   30

Gln Ile Asp Met Tyr Trp Glu Asp Asn Tyr Val Phe Phe Ser Phe Glu
        35   40   45

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

Gly Phe His Asp Glu Val Arg Lys Arg Asp Leu Ser Ser His Pro Ser
65   70   75   80

Trp Asn Thr Asn Arg Gln Leu Leu Val Lys Ile Tyr Leu Arg His Ile
                85   90   95

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

Val Ser Asn Glu Ile Lys Phe
        115

<210> 1042
<211> 160
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1042
Met Glu Lys Gly Lys Phe Tyr Lys Leu Lys Lys Thr Pro Ser Leu Ser
1   5   10   15

Pro Gly Ala Leu Ile Lys Gly Val Phe Glu Gln Ile Gly Asn Asn Pro
            20   25   30

Ile Lys Ile Thr Arg Thr Phe Lys Tyr Ala Glu Asn Thr Gly Leu Val
        35   40   45

Glu Phe Glu Ile Ile Lys Pro Asp Gly Glu Tyr Lys Arg Val Ser Ile
    50   55   60

Asp Glu Val Arg Phe Ser Arg Met Trp Cys Ile Ile Thr Asn Gln Glu
65   70   75   80

Phe Gln His Tyr Phe Glu Glu Thr Thr His Lys Glu Pro Glu Pro Lys
                85   90   95

Thr Asp Asp Gly Ser Asn Asp Trp Gly Val Trp Thr Ser Asn Lys Gly
            100   105   110

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

Ala Lys Val Gln Arg Leu Asn Ala Thr Lys Asp Thr Lys Val Val Ile
    130   135   140

Met Gln Pro Phe Ala Val Pro Val Val His Val Asn Ile Arg Pro Phe
145   150   155   160

<210> 1043
<211> 92
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1043
Met Ile Val Ser Ala Phe Tyr Asp Ser Arg Lys Lys Lys Val Glu Thr
1   5   10   15

Ile Ile Ser Asp Thr Arg Asp Gly Thr Pro Ala Asn Lys Asn Gly Val
            20   25   30

Lys Ala Tyr Ile Asp Lys Tyr Cys Pro Pro Glu Phe Arg Met Ile Asp
        35   40   45

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

Ile Asn Glu Thr Val Pro Ile Gly Tyr Ser Asp Gly Asp Gly Ser Asn
65   70   75   80

Ala Lys Met Pro Lys Glu Lys Phe Ile Thr Lys Phe
                85   90

<210> 1044
<211> 56
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1044
Met Ile Val Ser Val Pro Lys Ser Lys Asp Gly Ile Phe Ser Cys Gly
1   5   10   15

Leu Lys Asn His Pro Met Val Asp Ile Met Ser Ala Asn Val Lys Gln
            20   25   30

His Thr Val Glu Tyr Glu Ile Asp Ala Pro Asp Phe Phe Glu Leu Pro
        35   40   45

Glu Trp Ala Val Arg Leu Asp Ala
    50   55

<210> 1045
<211> 66
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1045

Met Lys Tyr His Ile Phe Asn Thr Val Arg Leu Ala Asn Gly Ile Pro
1   5   10   15

Gly Val Val Cys Asp Thr Ala Pro Ala Ile Lys Ala Tyr Ser Val Glu
            20   25   30

Pro Trp Tyr Glu Val Asn Trp Val Asp Gly Asn Arg Ser Ile His Ala
        35   40   45

Glu Ser Glu Leu Tyr Pro Ile Thr Gln Leu Arg Ala Ala Asn Asp Asp
    50   55   60

Val Tyr
65

<210> 1046
<211> 69
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1046
Met Ser Ile Asn Pro His Phe Gly His Met Val Ala Arg Arg Ile Thr
1   5   10   15

Arg Glu Met Leu Lys Thr Ala Glu Tyr Tyr Asn Ile Glu Leu Ile Asp
            20   25   30

Ile Glu Pro Ser Asp Ala Pro Gly Leu Ile Trp Phe Asn Phe Thr Gly
        35   40   45

Ala Ala Asn Ser Val Ala Lys Phe Lys Gln Ala Leu Arg Asn Phe Pro
    50   55   60

Glu Cys Gln Asn Gln
65

<210> 1047
<211> 280
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1047
Met Ser Lys Pro Val Ile Ala Thr Asp Val Asp Gly Ile Ile Val Lys
1   5   10   15

Trp Gln Ser Gly Leu Pro Tyr Phe Ala Gln Lys Tyr Asn Leu Pro Val
            20   25   30

Glu His Ile Leu Asp Met Met Thr Thr Glu Lys Phe Ile Lys Pro Ala
        35   40   45

```
Glu Leu Phe Asp Cys Glu Glu Asp Leu Ala Val Lys Leu Leu Leu Lys
    50                  55                  60

Tyr Asn Asn Ser Asp Phe Ile Arg Tyr Leu Ala Pro Tyr Ala Asp Ala
65                  70                  75                  80

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

Thr Ala Leu Gly Asn Ser Val Asp Ala Asn Leu Asn Arg Arg Phe Asn
            100                 105                 110

Leu Asn Ala Leu Phe Pro Asp Ala Phe Thr Glu Ile Met Val Cys Asp
        115                 120                 125

Tyr Asp Glu Ser Lys Asp Ala Leu Leu Glu Lys Ala Lys Val Lys Tyr
    130                 135                 140

Gly Asp Arg Ile Val Cys Tyr Val Asp Asp Leu Pro Lys His Ile Ala
145                 150                 155                 160

Ala Ala Ser Lys Val Phe Glu Asp Thr Glu Thr Arg Val Phe Tyr Met
                165                 170                 175

Pro Arg Gly Glu Arg Glu Gly Ser Val Thr Ala Pro Gly Ile Met Val
            180                 185                 190

Glu Asp Trp His Gln Ile Val Thr Cys Leu Glu Ser Leu Glu Ser Val
        195                 200                 205

Lys Lys Pro Gln Lys Ser Leu Ser Arg Leu Trp Glu Glu Ala Ile Lys
    210                 215                 220

Asp Gln Ile Arg Lys Glu Gln His Pro Phe Asn Trp Pro Pro Arg Gln
225                 230                 235                 240

Val Pro Gly Asp Trp Trp Lys Gln Pro Ile Ile Pro Phe Ser Pro Ser
                245                 250                 255

Pro His Val Pro Pro Gly Asn Asp Trp Trp Asn Asn Gly Arg Ile Thr
            260                 265                 270

Cys Asp Asn His Gln Ile Asn Cys
        275                 280
```

<210> 1048
<211> 68
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F387/08

<400> 1048
Met Phe Val Val His Thr Lys Val Gly Lys Arg Trp Leu Ser Cys Asp
1   5   10   15

Tyr Gly His Val Asn Gln Phe Tyr Arg Trp Asn Pro Ile Trp Arg Glu
            20   25   30

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

Tyr Ile Asp Gly Leu Thr Tyr His Arg Ser Val Ser Glu Leu Ser Lys
    50   55   60

Glu Leu Gly Glu
65

<210> 1049
<211> 490
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1049
Met Ile Phe Asp Ile Ile Lys Ala Ile Glu Asp Ala Lys Gly Ser Lys
1   5   10   15

Ala Lys Thr Gln Ile Leu Ile Asp Asn Lys Asp Asn Val Asp Leu Lys
            20   25   30

Arg Ala Tyr Leu Leu Ala Tyr Ser Gly Arg Phe Lys Phe Phe Ile Lys
        35   40   45

Lys Val Pro Glu Tyr Thr Pro Val Lys Tyr Pro Asn Val Pro Ser Lys
    50   55   60

Thr Phe Ser Asp Gly Leu Asp Tyr Leu Gln Asp Ile Leu Ala Ala Arg
65   70   75   80

Val Leu Thr Gly Asn Met Ala Ile Gln Gly Leu Val Asp Leu Leu Ser
                85   90   95

Lys Met Asn Glu Gly Asp Ala Ser Val Leu Val Arg Val Leu Leu Lys
            100   105   110

Asp Met Arg Cys Gly Ala Ser Gly Ser Ile Ala Asn Lys Val Trp Lys
        115   120   125

Lys Leu Ile Pro Glu Met Pro Gln Met Leu Ala Ser Ala Tyr Ser Glu
    130   135   140

```
Lys Ala Leu Ser Tyr Ile Lys Phe Pro Ala Phe Ala Gln Leu Lys Ala
145                 150                 155                 160

Asp Gly Ala Arg Cys Phe Ala Glu Ile Arg Gly Asp Asp Leu Asp Asp
                165                 170                 175

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

Leu Lys Arg Gln Leu Ile Glu Met Thr Lys Glu Ala Arg Glu Arg His
        195                 200                 205

Pro Asn Gly Val Met Ile Asp Gly Glu Leu Val Tyr His Val Glu Val
    210                 215                 220

Lys Glu Glu Glu Asn Asp Leu Phe Asp Met Phe Lys Glu Pro Glu Leu
225                 230                 235                 240

Pro Glu Leu Ser Lys Ala Lys Glu Phe Gln Gln Thr Ala Arg Thr Glu
                245                 250                 255

Ser Asn Gly Leu Ala Asn Lys Ala Ile Lys Gly Thr Ile Ser Ala Glu
            260                 265                 270

Glu Ala Glu Gly Met Arg Phe Gln Val Trp Asp Tyr Val Pro Leu Asp
        275                 280                 285

Val Val Tyr Ser Glu Gly Lys Val Pro Gly Phe Ala Tyr Asp Val Arg
    290                 295                 300

Phe Arg Ala Leu Glu Met Met Ser Lys Gly Tyr Asp Lys Ile Ile Leu
305                 310                 315                 320

Ile Glu Asn His Val Val His Asn Ile His Glu Ala Arg Ala Ile Tyr
                325                 330                 335

Lys Thr Tyr Val Asp Gln Gly Leu Glu Gly Ile Ile Leu Lys Asn Ile
            340                 345                 350

Gly Ala Tyr Trp Glu Asp Lys Arg Ser Lys Asn Leu Val Lys Phe Lys
        355                 360                 365

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

Lys Gln Pro Gly Lys Met Gly Gly Leu Met Phe Val Ser Glu Cys Gly
385                 390                 395                 400

Arg Ile Arg Val Asn Ala Gly Ser Gly Leu Lys Asp Lys Pro Glu Glu
                405                 410                 415
```

Leu His Glu Leu Asp Arg Thr His Leu Trp Lys Ile Arg Asp Ser Leu
420 425 430

Pro Gly Thr Ile Trp Glu Leu Glu Cys Asn Gly Trp Val Thr Ala Glu
435 440 445

Gly Arg Asp Asp Gly Thr Val Gly Leu Phe Leu Pro Ile Ile Lys Gln
450 455 460

Arg Arg Tyr Asp Lys Glu Val Ala Asn Thr Phe Glu Ala Ala Phe Gly
465 470 475 480

Val Asn Phe Thr Glu Ala Thr Gly Ile Lys
485 490

<210> 1050
<211> 59
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1050
Met Lys Val Leu Tyr Glu Val Ile Ala Lys Thr Asp Asp Gly Arg Gly
1 5 10 15

Gly Ile Ser Val His Thr Glu Val Leu Asp Phe Asp Asn Ile Asp Val
20 25 30

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

Leu Gln Val Trp Arg Thr Ala Thr Ile Ile Asn
50 55

<210> 1051
<211> 708
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1051
Met Glu Leu Leu Asn Glu Val Phe Asp Glu Glu Asn Ser Lys Ile Tyr
1 5 10 15

Pro Val Glu Asn Val Lys Pro Lys Leu Lys Val Pro Gln Val Phe Leu
20 25 30

Ile Lys Val Pro Gly Asn Asn Asn Leu Met Ile Arg Leu Val His Gly
35 40 45

Ser Gly Gln Gly Asp Ala Val Lys Asn Ile Lys Met Gly Asp Lys Phe
50 55 60

```
Ile Gln Val Tyr Val Phe Ser Val Ser Glu Lys Gly Asn Ile Gly Ala
65                  70                  75                  80

Leu Lys Gly Gly Leu Gly Gln Asp Pro Ile Gly Ala Ile Asn Thr Ile
                85                  90                  95

Phe Glu Thr Val Asn Lys Val Val Lys Gln Ile Lys Ala Asp Ala Val
            100                 105                 110

Met Phe Arg Phe Asn Pro Lys Lys Met Gln Gly Gln Asp Lys Ala Ile
        115                 120                 125

Gln Arg Ile Leu Ala Arg Leu Ile Thr Thr Arg Thr Gly Gly Arg Phe
    130                 135                 140

Asn Leu Met Lys Asp Met Ala Tyr Tyr Lys Gly Lys Tyr Ala Tyr Ser
145                 150                 155                 160

Ile Met Val His Lys Gly Lys Lys Leu Glu Glu Ile Glu Gly Ile Pro
                165                 170                 175

Glu Ile Ser Asp Glu Leu Tyr Thr Lys Val Glu Ser Lys Val Gly Glu
            180                 185                 190

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

Leu Ala Asn Ser Ile Gly Glu Lys Glu Asp Lys Lys Ser Glu Leu Ala
    210                 215                 220

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

Tyr Gly Lys Phe Val Ser Tyr Val Asp Glu Asp Trp Pro Glu Asn Lys
                245                 250                 255

Arg Glu Arg Trp Tyr Glu Leu Thr Thr Asn Thr Pro Val Leu Asn Ala
            260                 265                 270

Glu Gly Asp Thr Val Asp Leu Gln Lys Asp Ile Lys Ala Gly Leu Glu
        275                 280                 285

Lys Ser Ile Pro Phe Tyr Val Asp Asp Ile Lys His Tyr Arg Val Arg
    290                 295                 300

Gly Gly Tyr Gly Ser Asn Phe Gly Asp Ala Val Glu Arg Leu Phe Val
305                 310                 315                 320

Gly Gln Met Ser Arg Met His Asp Asp Trp Lys Val Phe Ile Pro Ser
                325                 330                 335
```

```
Gly Ser Asp Lys Met Lys Ile Ala Glu Gln Arg Ile Ser Asp Val Ala
            340                 345                 350

Asp Val Ile Ala Gln Ala Lys Asn Pro Ala Ser Met Glu Thr Met Arg
        355                 360                 365

Lys Ile Val Glu Val Ala Thr Arg Gly Phe Asp Met Pro Pro Ala Asp
    370                 375                 380

Asp Phe Gly Ala Leu Arg Gln Tyr Gln Asn Leu Val Asn Tyr Met Ile
385                 390                 395                 400

Ser Ala Tyr Val Ser Ile Val Gly Asp Ser Ile Ser Lys Ala Ile Glu
                405                 410                 415

Tyr Asn Arg Glu Met Gln Ser Arg Leu Ser Glu Glu Glu Arg Asp Ala
            420                 425                 430

Ile His His Tyr Cys Gly Ser Gly Tyr Ser Phe Val Asn Asn Tyr Leu
        435                 440                 445

Ile Gly Met Glu Ser Leu Gly Asp Pro Ile Ile Asp Lys Lys Ile Arg
    450                 455                 460

Pro Leu Asp Ser Ala Phe Glu Lys Gly Leu Arg Leu Glu Pro Gly Thr
465                 470                 475                 480

Leu Leu Tyr Arg Gly Gln Arg Gly Lys Tyr Glu Asp Phe Lys Asp Asn
                485                 490                 495

Ile Glu Ser Lys Met Phe Tyr Phe Gln Asn Tyr Val Ser Thr Ser Leu
            500                 505                 510

Ser Pro Ile Ile Phe Gly Ala Tyr Ser Asn Ala Gly Asp Ser Leu Met
        515                 520                 525

Pro Asp Ala Pro Ser Ser Asp Leu Glu Asn Lys Glu Thr Thr Ala Asn
    530                 535                 540

Ala Val Ser Ser Val Ile Gly Thr Asp Asn Leu Glu Arg Val Asp Arg
545                 550                 555                 560

Gly Glu Glu Val Ala Tyr Gly Asp Glu Phe Lys Phe Gly Phe Val Ile
                565                 570                 575

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

Phe Ser Asp Glu Ala Glu Val Ile Leu Pro Arg Gly Leu Ala Met Lys
        595                 600                 605
```

Val Asn Lys Val Trp Gly Thr Pro Phe Arg Asn Gly Val Gly Val Ala
610 615 620

Asn Asn Lys Thr Phe Met Val Glu Met Thr Val Val Pro Pro Glu Gln
625 630 635 640

Ile Asp Glu Ser Val His Leu Tyr Asp Gly Asp Ile Leu Met Glu Gln
645 650 655

Gly Lys Val Glu Pro Leu Glu Glu Ser Lys Phe Lys Gly Phe Leu Asn
660 665 670

Glu Ile Tyr Phe Ser Pro Asp Arg Ser Thr Asp Lys Val Ser Tyr Thr
675 680 685

Arg Thr Met Glu Leu Leu Ala Gly Ala Ile Asn Leu Asp Gly Ile Pro
690 695 700

Glu Lys Leu Ala
705

<210> 1052
<211> 92
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1052
Met Lys His Val Phe Arg Phe Asn Gly Ile Glu Trp Ser Ala Asp Val
1 5 10 15

Lys Asp Ala Glu Lys Phe Asn Glu Glu Val Leu Ile Met Leu Glu Gly
20 25 30

Phe Asn Glu Gly Thr Pro Thr Val Leu Ile Gln Asp Ile Phe Arg Lys
35 40 45

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

Gly Ile Ile Pro Val Lys Val Val Trp Thr Thr Lys Glu Met Lys Leu
65 70 75 80

Leu Arg Thr Glu Pro Gly Phe Ile Gly Cys Ile Ala
85 90

<210> 1053
<211> 308
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1053
Met Phe Thr Leu Glu Glu Phe Lys Ser Gln Ala Ala Asp Ile Asp Phe
1   5   10   15

Gln Arg Thr Asn Met Phe Ser Val Val Phe Ala Thr Val Pro Ser Ser
            20   25   30

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

Met Gly Leu Asp Gly Asn Trp Leu Gly Leu Thr Pro Gly Glu Phe Asn
    50   55   60

Gln Gly Ile Thr Thr Ile Val Thr Gln Gly Thr Arg Gln Val Val Arg
65   70   75   80

Lys Ser Gly Val Asn Thr Phe Met Ile Gly Ala Met Thr Gln Arg Val
                85   90   95

Val Gln Ser Leu Leu Gly Glu Phe Thr Val Gly Thr Tyr Leu Leu Asp
            100   105   110

Phe Phe Asn Met Ala Phe Pro Thr Ala Gly Leu Met Val Tyr Ser Ala
        115   120   125

Lys Ile Pro Glu Asn Arg Leu Ser Tyr Glu Met Asp Lys Phe His Asn
    130   135   140

Ala Pro Asn Ile Lys Ile Thr Gly Arg Asp Met Glu Pro Leu Val Leu
145   150   155   160

Ser Phe Arg Met Asp Pro Glu Ala Ser Asn Tyr Arg Ala Met Gln Asp
                165   170   175

Trp Val Asn Ala Val Glu Asp Pro Val Thr Gly Leu Arg Gly Leu Pro
            180   185   190

Gln Asp Val Glu Cys Asp Ile Gln Val Asn Leu His Ala Arg Asn Gly
        195   200   205

Leu Pro His Thr Val Cys Leu Phe Ser Gly Ala Met Pro Val Ala Cys
    210   215   220

Gly Ala Pro Glu Phe Thr Tyr Asp Gly Glu Asn Thr Ile Ala Val Phe
225   230   235   240

Asp Val Thr Phe Ala Tyr Arg Ser Met Gln Thr Gly Ser Val Gly Lys
                245   250   255

```
Gln Ala Ala Met Asp Trp Leu Glu Asp Lys Thr Ile Gln Lys Ile Glu
            260                 265                 270

Thr Ile Asn Pro Asn Gln Gly Leu Ser Thr Ser Ala Ser Arg Leu Ser
        275                 280                 285

Arg Leu Gly Gly Ala Gly Gly Gly Ile Ser Asn Ile Thr Thr Ser Thr
    290                 295                 300

Ser Arg Ile Ile
305
```

<210> 1054
<211> 350
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1054

```
Met Ile Phe Glu Glu Leu Ala Asp Gly Leu Glu Asn Ile Lys Lys Ser
1               5                   10                  15

Gly Thr Arg Ile Ser Gln Gly Lys Ser Lys Leu Thr Asn Ala Pro Thr
            20                  25                  30

Thr Lys Val Ala Gln Phe Pro Ala Glu Arg Ser Ala Gly Asn Asp Ser
        35                  40                  45

Ala Gln Asp Met Arg Val His Asp Leu Tyr Arg Asn Gly Leu Leu Phe
    50                  55                  60

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

Arg Arg Asp Val Met Leu Ser Ser Val Phe Asp Ser Pro Met Ser Ala
                85                  90                  95

Leu Ala Asn Ser Ser Ser Ser Thr Thr Ser Thr Ala Pro Val Ala Asn
            100                 105                 110

Ile Leu Leu Pro Arg Ser Lys Ser Asp Val Asp Ser Val Ser His Lys
        115                 120                 125

Phe Asn Asp Val Gly Asp Ser Leu Val Thr Arg Gly Ser Gly Thr Ala
    130                 135                 140

Thr Gly Val Leu Ser Asn Val Ala Ser Thr Ala Val Phe Gly Ser Ile
145                 150                 155                 160

Glu Ser Leu Thr Gln Gly Leu Met Ala Asp Asn Gly Glu Gln Ile Tyr
                165                 170                 175
```

```
Asn Thr Ala Arg Ser Met Tyr Ala Gly Pro Asp Asn Arg Thr Lys Val
            180                 185                 190

Phe Thr Trp Asp Leu Thr Pro Arg Ser Ala Asp Asp Leu Ile Gln Ile
        195                 200                 205

Ile Arg Ile Tyr Glu Ile Phe Asn Tyr Tyr Ser Tyr Gly Val Thr Gly
    210                 215                 220

Asn Ser Ser Tyr Ala Lys Glu Val Lys Ala Ala Ile Asp Glu Trp Tyr
225                 230                 235                 240

Lys Gly Thr Leu Lys Ser Ala Ala Pro Asp Gly Ala Lys Val Glu Asn
                245                 250                 255

Thr Val Phe Glu Gln Ile Thr Ser Phe Leu Ser Asn Val Ile Val Val
            260                 265                 270

Ser Asn Pro Thr Ile Trp Thr Val Arg Asn Phe Gly Tyr Ser Thr Ser
        275                 280                 285

Met Asp Gly Arg Glu Asp Ile Phe Gly Pro Cys Gln Ile Gln Ser Ile
    290                 295                 300

Arg Phe Asp Lys Thr Pro Asn Gly His Phe Asn Gly Leu Ala Ile Ala
305                 310                 315                 320

Pro Asn Leu Pro Ser Thr Phe Thr Leu Glu Ile Thr Met Arg Glu Ile
                325                 330                 335

Leu Thr Leu Asn Arg Gly Asn Val Tyr Ile Gly Gly Ile Glu
            340                 345                 350


<210> 1055
<211> 577
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1055
Met Thr Lys Lys Ser Glu Met Asn Ser Met Arg Arg Arg Val Ile Ala
1               5                   10                  15

Asp Ser Ala Pro Gln Lys Lys Ala Glu Ser Gln Ala Asp Ala Gln Ile
            20                  25                  30

Asn Thr Leu Glu Asp Ile Gly Arg Arg Leu Asp Asp Gln Gln Ala Ser
        35                  40                  45

Thr Asp Leu Ile Ser Asp Val Ile Glu Thr Lys Ser Asn Glu Ile Ile
    50                  55                  60
```

```
Lys Ser Val Glu Asp Val Ser Ala Gly Val Glu Leu Thr Ala Glu Ala
65                  70                  75                  80

Ser Glu Arg Thr Thr Asp Ala Val Ser Lys Leu Asn Asp Thr Ala Ser
                85                  90                  95

Leu Ile Asn Asp Lys Leu Thr Lys Leu Ala Asp Leu Leu Ser Lys Lys
            100                 105                 110

His Asp Val Gln Gln Asp Val Gln Lys Thr Gly Thr Gly Thr Ser Leu
        115                 120                 125

Glu Thr Ile Thr Glu Gln Val Pro Asp Ala Pro Val Gln Gln Pro Leu
    130                 135                 140

Glu Glu Leu Leu Glu Arg Leu Ile Pro Pro Gln Asp Asp Arg Arg Pro
145                 150                 155                 160

Asp Ala Asp Phe Phe Pro Asn Thr Glu Glu Gln Glu Glu Arg Lys Glu
                165                 170                 175

Pro Asn Lys Glu Thr Glu Asp Lys Asn Lys Lys Phe Leu Gly Leu Lys
            180                 185                 190

Phe Gly Glu Leu Ile Lys Ser Val Lys Ser Gly Phe Gly Lys Thr Ile
        195                 200                 205

Ser Leu Thr Asp Lys Ile Ser Ser Met Leu Phe Ser Tyr Thr Val Ser
    210                 215                 220

Ala Leu Ala Gln Met Ala Lys Thr Ala Ala Met Val Leu Gly Val Ile
225                 230                 235                 240

Met Leu Ile Asp Leu Ile Lys Val His Phe Asn Tyr Trp Thr Lys Leu
                245                 250                 255

Phe Glu Lys Asn Phe Val Glu Phe Asn Lys Gln Ala Lys Glu Trp Gly
            260                 265                 270

Pro Leu Leu Thr Ala Ile Ser Glu Met Ser Asn Glu Ile Val Lys Ser
        275                 280                 285

Phe Val Lys Gly Asp Trp Gly Gly Leu Ala Lys Ala Ile Gly Ser Gly
    290                 295                 300

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

Ser Lys Leu Leu Ala Gly Met Leu Arg Ala Leu Gly Phe Asn Asp Ser
                325                 330                 335
```

```
Ala Asp Asn Ile Glu Gly Ala Ala Leu Asp Arg Phe Gln Thr Val Thr
            340                 345                 350

Gly Ala Glu Leu Asp Glu Glu Asp Ala Lys Met Arg Ala Lys Tyr Val
        355                 360                 365

Asp Arg Gln Glu Arg Glu Tyr Asp Glu Gln Pro Glu Trp Lys Arg Lys
    370                 375                 380

Leu Ser Ala Lys Phe Gln Lys Phe Thr Gly Gln Ile Asp Asp Asp Glu
385                 390                 395                 400

Tyr Asn Lys Leu Leu Ser Gly Glu Lys Lys Gln Ser Ala Tyr Ala Asp
                405                 410                 415

Leu Pro Glu Asp Glu Arg Leu Lys Ile Ile Thr Ala Arg Asn Asn Ala
            420                 425                 430

Glu Ala Glu Leu Lys Arg Thr Lys Ala Tyr Val Glu Lys Thr Asp Ala
        435                 440                 445

Ser Asp Ser Thr Arg Leu Asp Ser Ala Lys Asp Ala Val Gln Ser Thr
    450                 455                 460

Thr Thr Arg Tyr Lys Glu Leu Glu Lys Leu Ser Pro Glu Val Ala Lys
465                 470                 475                 480

Asp Leu Lys Val Glu Leu Asp Gln Leu Gln Lys Leu Leu Asp Ser Lys
                485                 490                 495

Ile Ser Glu Pro Ala Pro Thr Ala Glu Ala Ile Pro Ala Thr Glu Gln
            500                 505                 510

Pro Glu Val Lys Gln Ser Ala Ser Ile Lys Ala Ala Ala Asp Ser Arg
        515                 520                 525

Glu Ala Ala Arg Thr Arg Glu Ser Asn Thr Gln Ser Gln Pro Ile Gln
    530                 535                 540

Val Asn Thr Ala Val Asn Lys Asn Ser Thr Tyr Val Tyr Arg Thr Pro
545                 550                 555                 560

Pro Gln Thr Ser Thr Ala Ala Pro Gly Met Gln Gly Ala Met Lys Thr
                565                 570                 575

Ser
```

<210> 1056
<211> 175

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1056
Met Asn Leu Asn Val Ile Leu Pro Ile Lys Lys Ile Val Ile Asn Glu
1   5   10   15

Lys Thr Ile Ser Ile Pro Lys Leu Gly Leu Lys His His Asn Leu Met
            20   25   30

Lys Asp Val Lys Gly Pro Asp Glu Asn Met Asn Leu Leu Leu Asp Ser
        35   40   45

Ile Cys Pro Gly Leu Thr Ala Ala Glu Ser Asp Ile Val Val Leu His
    50   55   60

Leu Leu Ala Phe Asn Asn Arg Ile Lys Glu Thr Val Val Lys Asp Asp
65   70   75   80

Phe Thr Tyr Asp Leu Asn Lys Val Tyr Ile Cys Gln Arg Leu Thr Gln
                85   90   95

Arg Leu Asp Gly Lys Glu Phe Lys Phe Arg Ala Pro Pro Arg Tyr Ser
            100   105   110

Lys Leu Gly Ser Val Asp Ser Ile Leu Ser Glu Phe Leu Glu Ser Val
        115   120   125

Asp Gly Lys Pro Met Asp Ile Asn Phe Met Lys Leu Pro Ala Phe Val
    130   135   140

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

Glu Gly Pro Ile Lys Gly Met Leu Asn Val Met Glu Ile Phe Glu
                165   170   175

<210> 1057
<211> 380
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1057
Met Thr Ala Gln Arg Leu Gly Tyr Pro Asn Ile Ser Ile Lys Leu Tyr
1   5   10   15

Ser Gly Tyr Asp Ala Trp Leu Ala Asn Arg Phe Val Glu Leu Ala Ala
            20   25   30

```
Thr Phe Ile Thr Leu Thr Met Arg Asp Ser Leu Arg Gly Thr Asn Glu
        35                  40                  45

Gly Leu Leu Gln Phe Tyr Asp Ser Lys Asn Met His Thr Arg Met Asn
    50                  55                  60

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

Thr Gln Thr Arg Ile Tyr Gly Ile Lys His Phe Thr Val Gly Val Asp
                85                  90                  95

Asp Lys Gly Asp Ser Ile Ile Thr Leu Gln Leu Gly Thr Leu His Asp
            100                 105                 110

Ile Met Asn Leu Lys Phe Ser Arg Ala Phe Phe Ser Ser Ala Tyr Glu
        115                 120                 125

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

Ala Pro Pro Ile Asn Gly Ile Asn Ala Tyr Val Pro Arg Val Pro Trp
145                 150                 155                 160

Thr Ser Thr Leu Lys Asp Tyr Leu Arg Tyr Val Arg Asn Val Gly Ile
                165                 170                 175

Ser Thr Asp Asn Asp Gln Phe Ile Phe Ala Trp Glu Asp Ile Thr Gly
            180                 185                 190

Ile Asn Met Met Asp Tyr Glu Ser Met Ile Ser Gln Asn Pro Asn Val
        195                 200                 205

Phe Met Phe Gly Ala Pro Gln Thr Ile Gly Gln Phe Ala Ala Gly Leu
    210                 215                 220

Lys Tyr Pro Leu Ala Trp Asp Phe Glu Trp Leu Val Lys Ser Asn Arg
225                 230                 235                 240

Tyr Asn Arg Asn Pro Met Lys Asn Ala Thr Phe Tyr Ala His Ser Phe
                245                 250                 255

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

Val Phe Ile Asn Arg Ser Gly Gly Tyr Ser Asp Met Ile Phe Arg Asn
        275                 280                 285

Gly Tyr Glu Glu Ala Leu Arg Ile Ser Thr Met Ala Gln Tyr Asp Gly
    290                 295                 300
```

```
Tyr Ala Gln Thr Lys Cys Tyr Gly Asn Phe Glu Leu Thr Pro Gly Met
305                 310                 315                 320

Lys Ile Asn Phe Val Asp Leu Lys Asp Gln Phe Arg Thr Asp Phe Tyr
                325                 330                 335

Val Asp Glu Val Ile His Glu Ile Ser Asn Asn Thr Ser Ile Thr Asn
            340                 345                 350

Leu Tyr Met Phe Thr Asn Gly Ser Ala Leu Glu Pro Val Asp Leu Ile
        355                 360                 365

Lys Val Lys Asn Glu Leu Lys Arg Asp Ser Ser Tyr
    370                 375                 380


<210> 1058
<211> 252
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1058
Met Ala Asn Ile Val Arg Cys Glu Leu Pro Asp Gly Val Gln Arg Phe
1               5                   10                  15

Lys Pro Phe Thr Val Glu Asp Tyr Arg Asp Leu Leu Leu Val Arg Asn
            20                  25                  30

Asp Met Asn Thr Lys Ser Glu Glu Glu Gln Lys Gln Leu Ile Ala Glu
        35                  40                  45

Leu Met Asp Asp Tyr Phe His Asp His Pro Ala Glu Tyr Arg Pro Tyr
    50                  55                  60

Ile Phe Leu Lys Val Phe Leu Ser Ser Ile Gly Lys Thr Lys Ile Pro
65                  70                  75                  80

Val Arg Met Lys Cys Pro Lys Cys Gly Lys Tyr Lys Gln Tyr Leu Phe
                85                  90                  95

Asn Leu Asn Gln Pro Pro Leu Val Asn Pro Lys Val Glu Val Ala Gly
            100                 105                 110

Leu Thr Leu Lys Phe Lys Lys Pro Ile Glu Ile Ile Asp Asp Thr Gly
        115                 120                 125

Lys Met Ile Leu Asp Asn Ile Ile Ser Val Lys Asp Ser Ser Gly Glu
    130                 135                 140

Tyr Ala Trp Asn Glu Leu Ser Asp Ser Asn Lys Leu Thr Val Ile Asp
145                 150                 155                 160
```

Ala Ile Asp Val Glu Thr Leu Glu Lys Ile Leu Ser Gln Met Lys Pro
165 170 175

Phe Asn Phe Glu Leu Lys Thr Ser Cys Cys Asp Thr Thr Thr Ile Leu
180 185 190

Lys Tyr Asp Asn Ile Val Asp Ile Phe Lys Leu Leu Leu His Pro Asp
195 200 205

Glu Ile Phe Thr Phe Tyr Gln Ile Asn His Arg Leu Val Ser Gln Gly
210 215 220

Lys Tyr Asp Leu Asn Ser Ile Met Lys Met Leu Pro Ile Glu Arg Gly
225 230 235 240

Ile Thr Leu Ser Leu Ile Glu Lys Asp Leu Lys Ser
245 250

<210> 1059
<211> 209
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1059
Met Asn Ile Thr Tyr Lys Phe Glu Thr Arg Ile Asn Gly Lys Asn Ile
1 5 10 15

Gln Cys Arg Ala Phe Thr Leu Glu Glu Tyr Ala Asn Leu Ile Ala Ala
20 25 30

Lys Lys Asn Gly Thr Ile Asp Glu Cys Ile Lys Ala Leu Leu Arg Glu
35 40 45

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

Val Ile Leu Trp Ala His Ser Ile Gly Glu Val Asn His Glu Val Thr
65 70 75 80

Trp Asn Cys Thr Cys Gly Arg Lys Ile Pro Val Pro Leu Asn Tyr Thr
85 90 95

His Ala Gln Ile Asp Pro Pro Glu Asp Leu Trp Tyr Asp Leu Lys Gly
100 105 110

Phe Lys Ile Lys Phe Lys Tyr Pro Ser Leu Phe Asp Asp Ser Asp Ile
115 120 125

Pro Met Met Ile Ser Lys Cys Ile Asp Tyr Ile Val Val Gly Asn Glu
130 135 140

Gln Ile Tyr Phe Asn Asp Leu Asn Asp Ala Glu Ile Asp Asp Leu Tyr
145 150 155 160

Ser Ala Ile Thr Thr Glu Asp Val Val Asn Ile Lys Asn Met Leu Leu
165 170 175

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

Ser His Ile His Val Ile Lys Gly Leu Lys Glu Phe Phe Lys Ile Met
195 200 205

Ser

<210> 1060
<211> 136
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1060
Met Ser Asn Ile Asp Lys Leu Tyr Ser Asp Leu Asp Pro Glu Met Arg
1 5 10 15

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

Lys Asn Ser Leu Leu Gly Ile Ile Thr Thr Arg Lys Gly Ser Arg Pro
35 40 45

Phe Asp Pro Ala Phe Gly Cys Asp Ile Thr Asn Glu Leu Phe Glu Asn
50 55 60

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

Val Arg Asn Tyr Glu Pro Arg Ile Asn Arg Leu Ser Val Asp Val Leu
85 90 95

Pro Leu Tyr Asp Asp Asn Ala Ile Ile Val Thr Val Gln Phe Ser Ile
100 105 110

Val Asp Asp Pro Asp Thr Leu Glu Arg Ile Arg Ile Gln Met Arg Ser
115 120 125

Asn Ala Asn Ser Ser Ser Arg Val
130 135

<210> 1061

<211> 138
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1061
Met Arg Leu Glu Glu Leu Gln Asp Glu Leu Asp Asn Asp Leu Ile Ile
1   5   10   15

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

Gly Lys Trp Val Arg Lys His Ser Thr Cys Arg Lys Glu Met Leu Arg
        35   40   45

Leu Asp Ala Leu Lys Lys Gln Asn Leu Lys Ala Arg Leu Asp Tyr Tyr
    50   55   60

Thr Gly Arg Gly Glu Val Gly Gly Glu Val Cys Met Asp Val Tyr Glu
65   70   75   80

Lys Ser Glu Met Lys Thr Val Leu Ser Ala Asp Lys Glu Ile Leu Gly
                85   90   95

Val Asp Thr Lys Leu Gln Tyr Trp Gly Ile Leu Leu Glu Phe Cys Ser
            100   105   110

Asp Ala Met Asp Ala Ile Lys Ser Arg Gly Phe Ser Ile Lys His Ile
        115   120   125

Ile Asp Leu Arg Gln Phe Glu Ala Gly Ala
    130   135

<210> 1062
<211> 55
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1062
Met Ser Asn Thr Val Cys Val Val Cys Lys Gly Pro Ile Asp Glu Ala
1   5   10   15

Leu Val Val Gln Thr Asp Lys Gly Pro Val His Pro Gly Ala Cys Tyr
            20   25   30

Asn Tyr Ala Ile Glu Leu Pro Val Thr Glu Asp Thr Glu Glu Gln Leu
        35   40   45

Gln Glu Thr Gln Leu Leu Ile
    50   55

<210> 1063
<211> 80
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1063
Met Ile Lys Phe Glu Asp Ile Tyr Glu Ala Thr Ile Arg Glu Ala Thr
1 5 10 15

Ile Asp Asn Phe Met Ser Lys Ile Asn Ala Cys Gln Thr Leu Asp Gly
20 25 30

Leu Lys Glu Leu Glu Lys Tyr Tyr Asp Lys Arg Ser Lys Glu Thr Thr
35 40 45

Leu Ala Asp Ser Asp Asp Ile Ile Val Arg Asp Ala Leu Ala Gly Arg
50 55 60

Arg Gln Ala Leu Glu Ala Asp Ser Glu Asp Asp Glu Asp Glu Asp Phe
65 70 75 80

<210> 1064
<211> 500
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1064
Val His Asp Ile Gln Val Lys Phe Lys Asp Phe Ser His Val His Ile
1 5 10 15

Glu Cys Asp Asp Ser Ile Phe Tyr Glu Leu Arg Asp Tyr Phe Ser Phe
20 25 30

Glu Ala Asp Gly Tyr Arg Phe Asn Pro Lys Tyr Arg Tyr Gly His Trp
35 40 45

Asp Gly Arg Ile Arg Leu Leu Asp Tyr Asn Arg Leu Leu Pro Phe Gly
50 55 60

Leu Val Gly Gln Ile Arg Lys Phe Ala Asp Gln Phe Gly Tyr Lys Val
65 70 75 80

Tyr Phe Asp Pro Ala Ile Phe Glu Gln Glu Thr Leu Ser Arg Glu Asp
85 90 95

Phe Asp Asn Trp Leu Ser Thr Lys Glu Ile Tyr Ser Gly Leu Thr Lys
100 105 110

Ile Glu Pro His Trp Tyr Gln Lys Asp Ala Val Tyr Glu Gly Leu Val

115 120 125

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

Ile Gln Ala Leu Leu Ala Arg Tyr Tyr Val Glu Asn Tyr Glu Gly Lys
145 150 155 160

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

Asp Phe Cys Asp Tyr Arg Leu Phe Pro Arg Asn Ala Met Leu Gly Ile
180 185 190

Arg Gly Gly Thr Ala Arg Asp Ser Asn Ala Leu Val Tyr Val Ser Thr
195 200 205

Trp Gln Thr Ala Val Lys Gln Pro Lys Glu Trp Phe Ser Gln Phe Gly
210 215 220

Met Met Met Asn Asp Glu Cys His Leu Ala Thr Gly Lys Ser Ile Ser
225 230 235 240

Thr Ile Ile Ala Gly Leu Thr Asn Cys Met Phe Lys Tyr Gly Leu Ser
245 250 255

Gly Ser Leu Lys Asp Gly Lys Ala Asn Ile Met Gln Tyr Val Gly Met
260 265 270

Phe Gly Glu Ile Phe Arg Pro Val Ser Thr Ser Lys Leu Met Glu Asp
275 280 285

Gly Gln Val Thr Glu Leu Lys Ile Asn Thr Ile Phe Leu Arg Tyr Pro
290 295 300

Asp Ala Ala Ala Asn Ala Leu Lys Gly Lys Thr Tyr Gln Glu Glu Ile
305 310 315 320

Lys Phe Ile Thr Asn Val Lys Lys Arg Asn Arg Trp Ile Ala Asn Leu
325 330 335

Ala Thr Lys Leu Ala Ala Arg Asp Glu Asn Ala Phe Val Met Phe Lys
340 345 350

His Val Ala His Gly Lys Glu Leu Phe Glu Met Ile Lys Ala Ala Gly
355 360 365

His Glu His Val Tyr Tyr Val Ser Gly Glu Val Asn Thr Glu Thr Arg
370 375 380

Asn Ala Leu Lys Ala Met Ala Glu Asn Gly Lys Gly Ile Ile Ile Val

385 390 395 400

Ala Ser Tyr Gly Val Phe Ser Thr Gly Ile Ser Val Lys Asn Leu His
405 410 415

His Val Ile Leu Ala His Pro Val Lys Ser Lys Ile Ile Val Leu Gln
420 425 430

Thr Ile Gly Arg Val Leu Arg Lys His Lys Asp Lys Ser Leu Ala Thr
435 440 445

Val Trp Asp Ile Ile Asp Asp Leu Gly Val Lys Pro Lys Ser Ala Asn
450 455 460

Ala Lys Lys Lys Tyr Thr His Leu Asn Tyr Cys Leu Lys His Ala Leu
465 470 475 480

Glu Arg Ile Gln Arg Tyr Ala Asp Glu Lys Phe Asn Tyr Val Met Lys
485 490 495

Thr Val Asn Leu
500

<210> 1065
<211> 264
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1065
Met Leu Asp Lys Asp Tyr Ile Lys Glu Ile Gln Ala Leu Asp Lys Lys
1 5 10 15

Glu Ala Lys Asp Lys Leu Asp Glu Tyr Ala Gln Thr Phe Gly Ile Lys
20 25 30

Leu Lys Lys Thr Arg Ser Phe Asp Asn Met Val Ala Asp Leu Glu Lys
35 40 45

Glu Leu Ala Lys Leu Ala Asn Glu Pro Met Pro Glu Asp Asn Asp Gly
50 55 60

Leu Ser Ile Ala Asp Leu Ile Gln Ala Asp Asp Glu Ile Glu Gly Lys
65 70 75 80

Ala Val Phe Lys Asp Glu Ala Ser Asp Glu Ala Lys Leu Leu Phe Asp
85 90 95

Ala Pro Val Asn Val Gly Ile Lys Ile His Asp Ile Asp Pro Gly Phe
100 105 110

Tyr Lys Glu Thr Pro Lys Val Asn Asp Pro Gly Phe Glu Val Lys Thr
115 120 125

Pro Ser Ile Asn Asp Lys Gly Phe Tyr Ala Glu Ala Pro Ile Gly Asp
130 135 140

Ser Val Ile His Ile Asp Asp Glu Gly Gln Val Thr Asn Ile Pro Val
145 150 155 160

Ser Ile Thr Asp Pro Glu Glu Phe Ser Lys Ala Met Asp Lys Val Val
165 170 175

Lys Ile Ile Lys Thr Asp Glu Ile Ile Glu Leu Pro Glu Asn Phe Ser
180 185 190

Pro Asn Met Gln Leu Leu Gly Lys Asn Pro Gly Tyr Ile Thr Leu Pro
195 200 205

Trp Trp Ile Tyr Gln Trp Ile Lys Asp Asn Pro Asp Trp Lys Ser Arg
210 215 220

Pro Thr Ser Phe Glu His Pro Ser Ala His Gln Thr Leu Phe Ser Leu
225 230 235 240

Ile Tyr Tyr Ile Lys Arg Asn Gly Ser Val Met Ile Arg Glu Thr Arg
245 250 255

Asn Ser Ser Phe Val Thr Leu Lys
260

<210> 1066
<211> 469
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1066
Met Ala Tyr Ser Val Ser Ile Ala Pro Leu Ala Ala Ser Ala Val Ile
1 5 10 15

Gly Ala Thr Thr Asn Phe Thr Ala Thr Thr Ser Gly Ala Ala Ala Glu
20 25 30

Gly Thr Glu Thr Phe Val Trp Thr Val Asn Gly Val Lys Gln Ser Ser
35 40 45

Val Thr Ala Ala Met Asn Tyr Val Thr Ala Gly Pro Ala Gly Ser Lys
50 55 60

Thr Val Lys Val Val Ala Thr Val Thr Pro Ala Glu Gly Glu Val Glu
65 70 75 80

```
Thr Ala Glu Ala Glu Thr Thr Leu Thr Val Lys Asn Lys Thr Met Pro
                85                  90                  95

Ala Ile Thr Leu Thr Leu Ser Pro Thr Ser Val Ser Lys Glu Ile Gly
            100                 105                 110

Gln Ser Gln Val Val Thr Ala Asp Val Thr Gly Ala Pro Ser Gly Ala
        115                 120                 125

Ser Ile Ala Tyr Val Trp Lys Arg Gly Ser Ser Val Ile Ser Gly Gln
    130                 135                 140

Thr Gly Lys Thr Ile Thr Leu Thr Glu Ser Thr Glu Thr Ser Tyr Thr
145                 150                 155                 160

Leu Asn Cys Glu Val Thr Val Ser Ala Pro Asp Tyr Asn Asn Gly Thr
                165                 170                 175

Ala Thr Lys Gly Ile Ala Val Ala Phe Thr Lys Lys Thr Met Ser Gly
            180                 185                 190

Val Ser Val Thr Leu Ser Pro Thr Ser Val Ser Lys Glu Ile Gly Gln
        195                 200                 205

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

Ile Ala Tyr Val Trp Lys Arg Gly Thr Val Val Ile Glu Gly Gln Thr
225                 230                 235                 240

Ala Lys Thr Ile Thr Ile Thr Glu Ser Ala Glu Ala Asn Tyr Thr Leu
                245                 250                 255

Asn Cys Glu Ala Thr Val Ser Ala Pro Asp Tyr Asn Pro Val Thr Val
            260                 265                 270

Ser Lys Gly Ala Ser Val Thr Ile Thr Lys Lys Thr Met Ser Gly Val
        275                 280                 285

Ser Val Thr Leu Thr Pro Glu Ser Ile Thr Val Glu Gln Gly Ser Asp
    290                 295                 300

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

Thr Tyr Ser Trp Thr Lys Asp Gly Ser Pro Val Glu Gly Ser Thr Ser
                325                 330                 335

Thr Leu Val Ile Asp Thr Ser Asp Ile Gly Ser Gln Val Ile Gly Val
            340                 345                 350
```

Ser Val Glu Val Ser Ala Glu Asp Tyr Asn Ser Val Thr Val Thr Thr
355 360 365

Thr Gly Asn Val Thr Ile Thr Lys Arg Val Ala Pro Thr Pro Asn Gly
370 375 380

Glu Leu Pro Tyr Ile His Pro Leu Pro Phe Arg Glu Thr Ala Tyr Ile
385 390 395 400

Trp Cys Gly Trp Trp Val Met Asp Glu Ile Gln Arg Met Thr Val Glu
405 410 415

Gly Lys Asp Trp Lys Leu Asp Asp Pro Asp Ser Asp Tyr Tyr Leu His
420 425 430

Arg Tyr Thr Leu Ala Lys Met Leu Asp Asp Tyr Pro Glu Val Asp Val
435 440 445

Gln Glu Ser Arg Asn Gly Tyr Ile Val His Arg Thr Ala Leu Glu Ala
450 455 460

Gly Ile Ile Tyr Pro
465

<210> 1067
<211> 75
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1067
Met Lys Ala Ile Gln Ala His Leu Met His Glu Ser Gly Lys Asp Phe
1 5 10 15

Gln Glu Ile Ala Arg Ala Leu Asp Ile Thr Pro Ala Glu Ala Ala Lys
20 25 30

Leu Trp Val Ser Val Glu Lys Ala His Glu Arg Phe Lys Gln Lys Glu
35 40 45

Lys Val Val Tyr Arg Lys Arg Leu Thr Asn Val Gly Ile Lys Ser Arg
50 55 60

His Lys Lys Leu Val Lys His Met Arg Thr Leu
65 70 75

<210> 1068
<211> 108
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F387/08

<400> 1068
Met Met Ser Lys Val Asp Pro Ile Val Val Glu Arg Phe Glu Glu Met
1   5   10   15

Leu Ser Lys Lys Phe Thr Pro Ala Ala Asn Gly Val Asn Val Trp Leu
            20   25   30

Phe Ala Ser Lys Phe Val Ser Lys Met Met Ala Val Gln Ser Ser Tyr
        35   40   45

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

Tyr Gly Lys Ile Asp Trp Met Leu Met Asp Lys Asp Ile Pro Leu Val
65   70   75   80

Leu Glu Val Gly Ser Lys Ser Gln Phe Glu Ile Met Leu Thr Lys Ser
                85   90   95

Gly Tyr Ile Met Tyr Arg Phe Val Pro Ser Gly Tyr
            100   105

<210> 1069
<211> 85
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1069
Met Asn Leu Ala Asp Arg Met Ala Asn Thr Ala Ile Asn Val Ala Thr
1   5   10   15

Glu Glu Leu Ser Ala Ala Lys Glu Glu Val Leu Thr Gln Ile Glu Lys
            20   25   30

Thr Ala Leu Ala Gly Lys Arg Glu Leu Ile Met Tyr Pro Ser Ser Leu
        35   40   45

Val Lys Lys His Ile Thr Asn Val Leu Asn Tyr Leu His Asp Glu Gly
    50   55   60

Phe Val Thr Asn Tyr Thr Ser Ala Gln Arg Asn Gly Asp Thr Asp Phe
65   70   75   80

Met Lys Ile Thr Phe
                85

<210> 1070
<211> 335
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1070

```
Met Phe Ala Lys Tyr Ser Ser Leu Glu Asn His Tyr Asn Asn Lys Phe
1               5                  10                  15

Ile Glu Lys Ile Arg Gly Ala Gly Phe Asp Met His Thr Val Glu Trp
            20                  25                  30

Val Ala Arg Glu Lys Ile His Gly Thr Asn Phe Ser Val Ile Ile Thr
        35                  40                  45

Pro Thr Glu Ile Val Pro Ala Lys Arg Thr Gly Pro Ile Leu Glu Gly
    50                  55                  60

Glu Ser Phe Phe Gly His Glu Ile Ile Met Lys Lys Tyr Lys Asp Ser
65                  70                  75                  80

Phe Val Lys Met Gln Asn Met Leu Asn Thr Met Asp Leu Val Ser Val
                85                  90                  95

Gln Ile Phe Gly Glu Phe Ala Gly Gly Gly Ile Gln Lys Gly Val Asp
            100                 105                 110

Tyr Gly Asp Lys Asp Phe Tyr Val Phe Asp Ile Leu Ser Asp Ser Gly
        115                 120                 125

Asn Glu Lys Val Tyr Trp Asp Asp Tyr Val Val Glu Ser Phe Ala Thr
    130                 135                 140

Gly Leu Gly Leu Lys Leu Ala Pro Leu Leu Gly Arg Gly Ser Phe Ala
145                 150                 155                 160

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

Asn Glu Leu Val Asp Thr Thr Asp Leu Glu His Ala Asn Lys His Val
            180                 185                 190

Phe Gly Pro Gln Ala Ser Ser Glu Thr Gly Val Ala Glu Gly Tyr Val
        195                 200                 205

Leu Lys Pro Val Asn Pro Lys Phe Phe Asn Asn Gly Thr Arg Val Ala
    210                 215                 220

Ile Lys Cys Lys Asn Ser Lys Phe Ser Glu Lys Ala Lys Ser Asp Lys
225                 230                 235                 240

Pro Ile Lys Ala Lys Val Glu Leu Thr Asp Thr Asp Lys Arg Val Leu
                245                 250                 255
```

Glu Ile Phe Ser Glu Tyr Val Thr Trp Asn Arg Val Ser Asn Val Leu
260 265 270

Ser His Ile Gly Thr Val Thr Ala Lys Asp Phe Gly Arg Val Met Gly
275 280 285

Leu Thr Met Lys Asp Ile Ile Asn Glu Ala Ala Arg Glu Gly His Asp
290 295 300

Met Leu Phe Ala Asp Asn Pro Ser Ala Val Lys Lys Glu Leu Thr Thr
305 310 315 320

Leu Ile Gln Asn Thr Ile Arg Ser Lys Trp His Glu Val Leu Glu
325 330 335

<210> 1071
<211> 182
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1071
Met Arg Leu Ala Leu Ile Gly Ser Arg Glu Ala Pro Arg Arg Val Leu
1 5 10 15

Ser Leu Met Thr Ile Ile Gly Gln Arg Leu Ser Glu Glu Gly His Phe
20 25 30

Ser Tyr Ser Gly Gly Ala Pro Gly Ser Asp Glu Ala Trp Leu Ala Lys
35 40 45

Tyr Asp Arg Ser Asn Ser Cys Arg Ile Ile Pro Tyr Ser Gly Phe Cys
50 55 60

Gly His Val Pro Asp Thr Gly Val Val Val Trp Ser Glu Leu Ser Asn
65 70 75 80

Glu Ala Lys Ile Lys Ser Ile Ile Lys Ala Arg Glu Val Thr Ser Tyr
85 90 95

Trp Asp Glu Cys Ser Lys Ile Val Gln Thr Leu Phe Ala Arg Asn Ser
100 105 110

Met Gln Val Leu Gly Leu Glu Cys Thr Glu Pro Val Asp Lys Val Leu
115 120 125

Tyr Trp Ala Pro Glu Lys Arg Cys Gly Ser Val Ser Gly Gly Thr Arg
130 135 140

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

Tyr Asp Lys Asn Val Phe Lys Ser Leu Glu Glu Glu Tyr Ser Pro Arg
165 170 175

Phe Asp Ile Phe Ser Leu
180

<210> 1072
<211> 426
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1072
Met Ala Lys Ile Asn Glu Leu Leu Arg Glu Ser Thr Thr Thr Ser Ser
1 5 10 15

Asn Leu Ile Gly Arg Pro Asn Leu Val Ala Leu Thr Arg Ala Thr Thr
20 25 30

Lys Leu Ile Tyr Thr Asp Leu Val Ala Thr Gln Arg Thr Lys Gln Pro
35 40 45

Val Ala Ala Leu Tyr Gly Ile Lys Tyr Leu Asn Pro Asn Gly Asp Leu
50 55 60

Thr Phe Asn Thr Gly Ala Thr Tyr Ala Gly Gln Ile Gly Ala Pro Glu
65 70 75 80

Arg Glu Ser Ile Glu Glu Leu Thr Met Ala Asn Lys Asp Ser Phe Asn
85 90 95

Lys Asp Asp Met Phe Lys Tyr Gln Asn Val Val Phe Lys Val Leu Lys
100 105 110

Asp Ser Pro Phe Thr Asp Thr Ala Glu Thr Asp Glu Phe Gly Ile Val
115 120 125

Ser Glu Ala Val Ala Ala Asn Asn Ile Arg Met Leu Ser Asp Ala Ala
130 135 140

Val Thr Glu Lys Phe Glu Gly Pro Asp Ser Asp Pro Ile Thr Glu Ala
145 150 155 160

Ser Phe Lys Ile Asp Lys Trp Gln Thr Gln Val Lys Ser Arg Lys Leu
165 170 175

Lys Thr Asp Leu Thr Val Glu Leu Ala Gln Asp Leu Glu Ala Asn Gly
180 185 190

Phe Asp Ala Pro Glu Leu Ile Asp Asp Leu Leu Ala Thr Glu Met Ala

195 200 205

Glu Asp Ile Asn Lys Asp Ile Leu Gln Ser Leu Ile Thr Val Ser Ser
210 215 220

Arg Phe Lys Val Ala Gly Val Ser Asp Lys Gly Val Leu Asp Leu Thr
225 230 235 240

Lys Gln Asp Ser Ala Pro Glu Gln Gly Arg Thr Leu Tyr Arg Phe Ile
245 250 255

Cys Glu Met Asn Ser Ala Val Gln Arg Asn Thr Ser Tyr Ser Gly Thr
260 265 270

Tyr Ala Val Ala Ser Thr Arg Cys Ala Ala Val Leu Ala Ala Ser Gly
275 280 285

Trp Leu Thr Gln Lys Asn Asp Gly Ser Ile Pro Glu Asn Ala Tyr Gly
290 295 300

Met Leu Asn Asn Gly Leu Pro Leu Tyr Cys Asp Thr Asn Ser Pro Val
305 310 315 320

Asp Tyr Val Ile Val Gly Val Lys Ala Glu Phe Gly Gly Lys Glu Thr
325 330 335

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

Asp Pro Glu His Val Gly Ala Phe Lys Val Ile Val Asp Pro Ala Ser
355 360 365

Leu Gln Pro Ser Val Ala Leu Leu Val Arg Tyr Ala Leu Ser Val Asn
370 375 380

Pro Tyr Thr Val Gly Leu Asp Glu Asp Glu Ala Arg Val Ile Asn Ala
385 390 395 400

Ala Asp Met Asp Lys Met Ala Gly Arg Ser Lys Met Ser Val Leu Leu
405 410 415

Gly Val Lys Leu Pro Lys Leu Ile Ala Asp
420 425

<210> 1073
<211> 78
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F387/08

<400> 1073

Met Asp Ala Gly Ile Tyr Tyr Ala Pro Tyr Val Ala Leu Thr Pro Leu
1 5 10 15

Arg Gly Ser Asp Pro Lys Asn Phe Gln Pro Val Met Gly Phe Lys Thr
20 25 30

Arg Tyr Gly Ile Gly Ile Asn Pro Phe Ala Asp Ser Ala Ala Gln Gln
35 40 45

Pro Lys Gly Arg Ile Thr Ser Gly Met Pro Ser Ile Val Asn Ser Val
50 55 60

Gly Lys Asn Ala Tyr Phe Arg Arg Val Trp Val Lys Gly Ile
65 70 75

<210> 1074
<211> 144994
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1074
ctttgttcaa attcctatat ttagtttaat accaatacta aggtataaat tagaagaaca 60

aggtatagga ttaatagaaa cagaagaatc ctacacaagt aaaacgtctt ttattgataa 120

tgaaaaacca atcaaacata atgtttataa aggtaaaaga gtaaaaagag gtctctttaa 180

aacagaagag ggtagaatat taaatgctga tgtaaatggt gcatttcaaa taatgaaaaa 240

agtattccct gatgtagaaa taccaaggga taatgggttt gtgtataacc cattcttaat 300

aaattgttaa aaaaacaaca aaataagaaa aaatttctca aaaagtagca ttatgtgaag 360

agaagtgtta cattattatc gagaattcaa taataaagca tagggaaggc tttttctatg 420

tcttatagaa tgctttaaaa tagattacta aaataaagat tggagattaa gcttatggct 480

aaaaagaatg ttaatgatgt attacaacaa gaatctgtta cagtagcaga taagtattta 540

caagttaaag ttaaccgtga cggttatact cgtacacatg aaggacaata tgcgtacaaa 600

gtagtttcag agggagaaga actattctta taccctgtac aaacagatgg taaaggtaca 660

ttaaatgtaa tgaagaaatc acctattgct tacactgatg gggacaatat ccatttcgta 720

gtaaacacag tagtagaccc ttataatcac tcatttatcc gtactgaaga tatcaaagga 780

ttagataaag gtaaacaact tattcaagct ttcttagctt tcgttgaaga ccgtttcaaa 840

tttggtgttt ataacgtatt tgttgcaaac agcaaagagg atgtattatc tattgtagac 900

cctacagata atgatgcaga tgaagttaaa gatagtttag agcacgcaca tgaagatgta 960

attgcggatt tccctgctag ccctgctcgt aaggacgtta aaggcgtaga ttcaggagaa 1020

ggtcaaggag acacttcaga accatcagca cctaagaacg ttcaagttac tcctaaggaa 1080

gacggagcag acgtatcagc agaataatat atagataagg atggtaaatt tggctaagtt 1140

aaatttatac aaaggtaatg agttactaaa cagcgtagag aaaacagaag gaaaatcaac 1200

aatcacgatt gagaatttag atgctaatac ggattatcct aaaggtactt ttaaagtatc 1260

attctcaaat gattcaggag agtcagagaa ggtcgatgtc cctcagttta agacaaaagc 1320

aattaaagtt atttcagtta cccttgacgt tgatagttta gaccttacag ttggagatac 1380

tcaccaacta tcaacaacta tcacgcctag tgaagcatct aacaaaaatg tgtcatttga 1440

atcagacaaa tcaggtgttg ctagcgtaac atcagaaggc ttaattgaag cagttagtgc 1500

aggaacagct aatgttactg taactactga agatggtagt cacactgata ttgttgctgt 1560

aacagttaag gaacctattc ctgaagcacc tgcagacgta acagttgaac ctggtgaaaa 1620

tagcgcagat attactgcat aggaggacaa taaagaatgg aaaagacatt aaaagtttat 1680

agtaatggtg aagttgtagg ctctcaagta gctaataacg atggagctac tacagtatct 1740

attacgggct tagaagccgg aaaaacttat gctaagggag cttttaaagt agcatttgct 1800

aatgattcag gtgaatcaga aaaagtagat gttcctgaat ttacaactaa aactcctact 1860

gaagaacctt caggagaagc atagtaatta agaccaacta aaaagttggt ctttttttat 1920

tgacaattta taatatctat gatacactat ataagaatta agaaaaggag ggaaagtaat 1980

ggatattcca acaatattat ttagaaatcc atatgattat acgaaagtaa aaaaactaat 2040

ggaaaacaaa gagcagtaca ttgtagtaaa gtttgattct gtttctgttc ataatttaaa 2100

tgttcaaggt atgatgaatg tcatccaaga ttacctacac atctatggtt atagggttaa 2160

agagtacggg caagaaaatg cttctaaaga tgatgaaaga gacgttaaag gttacttata 2220

tgaaagagta ggtgagtagg atatgggaat tatagtaaac tccaaccata ttcaatcaga 2280

cactttatat gagtatgata gctttttga tattgagaaa gtagatacat ttgaagaagg 2340

attgctttca atacaagatg aaccaactgt tttagcagga ttcatctatg atgacatcac 2400

atttaataag gttattaatt ctaattcaga tattgatgat tatattaaga ataatgatat 2460

ttattatgtc tctgatatag ggttactccc tgatactttt atcactgttg attctgataa 2520

aaaatattat tcattattac aacaggtagt tgagttaagt aaagaccctt ttcctaaatg 2580

ggtagaggat gatgcaaaag gcttaactaa gtattataac tttcaagact ttgaagatgt 2640

atttgattta aatagttttt acaaaaaaga agttgacatg gtaagagaaa agtgctataa 2700

taatggtaat gtatatttat tatatgaggt tctgcctgat tataaattac ctctagctta 2760

tagtttactt tcaaacaaag agcatggtat tgttattatc ggttcacaga cacgttctaa 2820

taatgatata ctgacttttt atgttaaagg tatggatgct aaagcaatag ctagtatgtt 2880

caatgtagaa catgattatg attctaatat tttccataca tttgtaaaca gtcacattaa 2940

tattttagga aatcaaataa ctaagtttat aagagagaaa ggaagcagtt atgagtaact 3000

ataaaacaat agaagaagta caagcagtta ttattggggt attatttaaa gatgaaggta 3060

aaattgtaac atctaagttt aataaaatta ctaaagagtt tggtttagat agaatcggta 3120

aagatgacct taaagaaatt gtagaggata ttagacaaga cgcttatcta aatgaactta 3180

aaaacaaagc aattaaaggt aaagtaacgt taggtgattt aaaagatgtt gcagataacc 3240

aagtattcga aggtaataac taccatgaag aagtatctac ttacgtagta gctaaagaaa 3300

aagaattgtc tcacttaaga gaacagcgta agcacaatag gcatactgca taccctcaaa 3360

ttatgtttga tgaacttaaa gaacatatgg ttaaagaatt acaaggggaa acattagtag 3420

aacatcatgg aagtaaagct aatattaatg atacagagct aattgtgtta ttatcagatt 3480

tccatattgg aagtattgta tctgatatga ctaatggtaa atatgatttt gaagttctta 3540

aagcaagatt aaatcatttt attaatacaa cagttaaaga aattgaagat agagaaattt 3600

ctaatgtaac tgtttacttt gttggggact tagtagaaca tattaatatg agagatgtta 3660

accaagcatt tgaaacagag tttactttag cagaacaaat ttctaaaggt actcgattac 3720

ttattgatat tctgaatgta ctatctaatg tagtttcagg agaattaaga tttggtatta 3780

ttggtggtaa ccacgaccgt atgcaaggta acaagaatca gaagatttat aatgataata 3840

ttgcttatgt agtgttagat tctttattat tattccaaga acaaggatta ctaaatggtg 3900

tagatattat tgataaccgt gaagatattt atactattag agataccttt ggcggtaaat 3960

ctattatcat taatcacgga gatgggttaa aaggtaaagg taatcatatc aataaattta 4020

tcctagatag tcatatcgac ttattaatta caggtcatgt acatcatttc tcagtaaaac 4080

aagaagattt taatagaatg catatcgtag cttcatctcc aatgggatat aataactatg 4140

ctaaagagtt acatttatca aaaactaaac cttcacagca gttattattt gtaaataagg 4200

aaaataaaga tattgatatt aaaacagtat ttttagatta aggatggtta ataaatggat 4260

acaattttta ttataggtgt agcgtttata acttttgcaa catttaacat agtctttaga 4320

ctatttgatt tatggactac cgagaaaaaa atggtaagtc aaggacaacc cccgctaagt 4380

aattttgagt actatcatgt gatagtacct tacttagtag gtgttattgt tattacacta 4440

agtattattt ttagagattc cttgtattcc gcacaatcag ggttcggtat tattattaca 4500

agctttattt acatgctagt ttatgttata attggtcttg tagggtcatt tatacttaca 4560

atattccaag ctagaaaagc tagacagtat caaacacagg aggataataa tgaagttcaa 4620

tgatatttat gagcaattaa ttaaaaatga tacagtacaa aacattcatg agtctcaaga 4680

tgacaaagga aatatttata caatccaatt tgataaaggt aatgataagt atttatttaa 4740

tgttattaat gatggattct tgaaagaaat gacaaacggt atggtagacc atcctgaagg 4800

tcagccatac tcagtaagtt taatcaataa agaaacacct agtatgtcag tgaaacaata 4860

tttaacagat gtagaagata ttgtacctac tattagaaaa atggaaaagg atttcttata 4920

gagtcaagtc tttacttgac tctttttact atatatggta tattaatata gaggtgactt 4980

aaaaatggat tttaatttta gtgcttttga taatagctca ttagcaatga gaattagtga 5040

gggtgtatac tatttcaatg atactcctta ttactttatt gagcatgtag aagaagaaat 5100

gtctgagtat gttattgtgt atgacataca tgacagagag gaaaaagaaa atcctcagaa 5160

gaaatataga atagaacctt accaacgtac aatacctggg ggaacacctc ttagtaactt 5220

aattaagagt atgatgcctc aacgtaagta tcctaagaag gttacagaag accctatatt 5280

tgtagctaat gttattcctt taggaacaga tacagtaaca ggtaaaaccg gtaaaggatt 5340

ttttgaaaga gataaggata gaactatcta ttctcaaaag gaaccaacta aagtcgttca 5400

tggtcaatat acaggtgttt ttataggtct aacaagtgtt aagtggaata gaacatatac 5460

ccctctagaa agtgttgttg agtactacaa aagggttaaa ggggataggt taaatgtcta 5520

atgatgtagt taagttttat gaaaaagata ttaaagacct tatcagaact aaaaaacaca 5580

tgttcaaaga cgatgaaata actagtgata taaacgatat acgaatcttt aatgagaaag 5640

tcatttgtca aggtaagtgc agaacagatt gtttagtact agaccgtaat ggtacagtaa 5700

tgggtataga gataaaaaca gaacgagact ctacacagag actaaataac caattaaagt 5760

attatagtct agtatgtaag tatgtatatg taatgtgtca tgataaacat gtacctaaag 5820

tagaacaaat acttaaaagg tataaacata atcatgtagg tataatgagc tacattagtt 5880

ttaaaggcaa acctgttgta ggtaaataca aagatgctac accatcacca catagaagcc 5940

cttatcatac aatgaatata ttatggaaga caaacttaat gacaatactt agattgatta 6000

gagaccctca tacgtataga acagggtata gctataatgc tagtggtaga tatagtggcg 6060

gagaaggtaa tttctcccaa acaactcaaa gtaaaagaat gaaaaaacct gctattatta 6120

atcaaataat tcattatgta ggggtagata atacttataa actctttaca agaggtgtta 6180

tctatggtta taataatagg tgggaagtta tagaagaaga tttctttaat actatgaaga 6240

atggggtaag agtaatcaat gagcaaagac aaaccaaata gacgtaaaga gatacaacat 6300

cagcctgtta actttgcccc tatgaatact ctaacagggg ctaataatag tttctttgct 6360

aaaaagcctt cagagcctaa ggatgcaaca tctgttattg aatatcgtat actatttatt 6420

aaaagatttg ataacgtaac aagtacagat gtgaaattac agaaaaagta tgcactaaat 6480

cttattagtg aagcacttga tgttaaagaa acttacttgt ctcttaagca aaaaggaaaa 6540

aaaacagaat ctattttgca tacagataga gtttattatg ttcatagagg taaaaaactt 6600

attggaaagt gtagtatcag agaacaaaga acatttaaag gtaaacattt gatatttata 6660

ttcaaaacaa gacatagagt taaagcagaa aggaaagata aataatgtta aaaggatttt 6720

cagaacatgt agacaaacct acaactacta agaccttata caagacctta acaagtggta 6780

aagtagaatt actaggtgta tcctacgata gtgattactt cccttcaggt gttacagtac 6840

aatcttacat tgaggatata ggtaatgaag atgagggtct acagtttgtt aataagataa 6900

atgtagtaga atcaatgaaa caggctgtag taggtatgaa taatcagtta ggttcttcag 6960

gtcttggcta tgtgagaact gaacaactta aaaaagagtt agaagagact ggactaatga 7020

cagatttact tgctagaggt actaacttaa cctctactaa gaaagtagat attgtaagta 7080

cttttattga gcctgaggta acataccagg atattactat agctaaagat attaaactac 7140

gtttgtataa attagaagaa gaatcaccat taaatggtta cactcatatt gtatacttac 7200

ttactacaga aaagctatat gatggtcaaa cactattcgg tatgctctct aaaaaagata 7260

agttatctaa aggagatact gataaattat tagcattctt cagaaacaat agcttaataa 7320

gtaaaagtgt attttgtgtt aagttattaa gtaaagacta ctactttaat ttatataaca 7380

cacatgagac agggatattc tttttagaag acacagatgt tattactatt gcttgtggtc 7440

agtcatatgt taaagttaat actaaagata ttaaatctag ttatgttaaa attgaagaca 7500

agactcataa attaactgag ctagtaatta acttaaaagg tgacgacaca ttaactattt 7560

tattctaaga gaatgttata aatatgtgat aattaagtat aaatatacgt tatatgagaa 7620

gttttcataa tgtttttaat acagaaacta gttaagtttt ttctacttgc tctagtttct 7680

gtgaaattat atttatgaaa agttaaaata tcttttaggt aaaggctttg taaatagtta 7740

aaaaatatat taaaatttta tacaaagtag ttaataaaat tatattacat ttatatatta 7800

tgaaataata acagaaattg tgatatatta tatagtgtaa ccttgaaaca gttgatgttg 7860

tagggtttgt ttatgttcgt taaactggtt tcagaacacc agttaccata aataaatgac 7920

agttaaggag agctatataa tggctagaaa aaagaattta cgaaataaaa acagtgatat 7980

aaaagttgtt cctgataaag aaaaagaaag catattatct aagctatatc ataataaatt 8040

actacgctca aaggtagata atgcattaga tgaagatatg agttatgatg atattataga 8100

attatgtaaa gaatatgatt tagaattgtc taagtcagct attacaagat ataaaagtaa 8160

aagaaaagaa gctattgaaa acggttggga tttagaagaa ttaattgata aacgtaaaaa 8220

aacaagtgta aaagatatta aggaaaaaga aactcctata ttagaagagg agcaactttc 8280

tccatttgaa caatcaaaac atcacacaca aacaatttac gatgatattc aagtactaga 8340

tatgattatt tctaaaggtg caaaaggact agaatttgta gaaactttag accctgcgtt 8400

gatgatacgt gcaatggaaa caaaagataa gattaccgga aaccaattaa aaggtatgtc 8460

atttattgga cttagagagt tacaattaaa acaaacagct caagatacag ctatgagtga 8520

agtattatta gaatttatac ctgaagagaa acatgaagag gtattacaac gattagaaga 8580

actacaaaat gaattctaca aaaacctaga tttagatgag gaaagtagaa aattaaaaga 8640

agctcttgat agagtaggct acacaattta gatagtgagg ttagagtaat ggcagatgag 8700

attagtttaa atccaataca agatgctaag ccaattgatg atatagtaga gattatgaca 8760

tatttaaaag acggaagagt actgagagtt aagcaagaca accaagggga tatccttgtt 8820

agaatgagcc cagggaaaca caaatttact gaagtatcta gagacttaga taaagaatca 8880

ttctactata aaagacattg ggttctctat aatgtatctg ttaactctct tataacattt 8940

gatgtttatc tagatgaaga atattcagaa acaactaagg ttaagtatcc taaagatact 9000

attgtagaat atacaagaga agaccaagaa aaagatgttg ctatgattaa agaaatactt 9060

acagataata atggtaatta tttctatgca cttacaggag aaacaatgct ctttgatgaa 9120

aataaattaa ataaagttaa agattagggt tgacagcttc tatagtttat gatatagtat 9180

atgtatacta aaaataaagg agctaacaat tatgtttatt tcattaaatc aagaagagaa 9240

agaattatta actaaagagg aaagtaaata cacaccacta gaaacatcaa gagagtttaa 9300

cacacctaaa gaagaattca ttgtaacaag ttataacgaa ggtaaacctt tagattacat 9360

tgcaaaagaa gctaaggtaa gtatgggatt aatttacaca gttctaaact actataaagt 9420

aggtaagcgt aataagaaat cacctgtaga agaaagaatt gcacatatct taaaagataa 9480

aaacttagtc aaagagatta ttaaggatta ccaatatatg aatttacagg acatttatag 9540

taaatataat cttcataaga atggtttata ttacatctta gatttatacc atgtagaaag 9600

aaaatctgaa cttaaggaca aagcattaga agaggataat attgtcgttg agtaagtaaa 9660

gaggttataa tatgagaaat aaaaaatcat ttcaagagca gttaaatgac atgcgtaata 9720

aagagaaatg ggtatctgaa gaggagttca ctgaagaagt ggctccttct gaagaacctg 9780

aagtagaaga agaaaaacta tatactttaa atgagttaaa agagaactta ctagatgctc 9840

aaggattaaa agatgttgta gctgattttc ctgcatctaa agatttatat gaacctaata 9900

aactatatat ctgtacaata cctaaaggat atcagtctac tgaagtacaa ccaggacaat 9960

atattggtat tagtactgga ttattatcag agtcagaaga cttcagtcat ttaagaggtc 10020

aaatgcctag aaatctttat gaaacttctc atgttttaaa acctttagtc cgtattaata 10080

atacaagtat cgaatatcaa cagcatgagt tacttgaaga tattaaagaa gacaagaatg 10140

tatatgatgt tgaattagaa gacttgagat tagcaacagg agaagaaatt tcttatttag 10200

agattgttga tagtaagttt tttgaaagtc gtattaatga agttcttgat ttttaccatg 10260

aactaacgga ttccgatgat ttgcttgagt attataacaa attacgagag ttagtcggaa 10320

atgatagaat gatttattgt ccgcttttaa ataaatgtgt taaaattata gattaatagt 10380

agtctcctct tatattataa ctgtaagagg agacattttt gtatagaggt gttaattatg 10440

tcaagaaaag caagtatatt ttatatacta gtggttattg ttttggcttt ctctatctca 10500

tcttattata tatcttcttt catgtatcac gacaaagcaa aaaatgaagt ctctactgag 10560

ttatcgaaca caggaaagat taaagaagaa aagaacgtag aatttgttgg tgactacaca 10620

ttgaaaaaag tggaagataa taaagcttat tttatggaaa cattacctac ttacctacca 10680

ggtagaacag gagataacag catagatatg aggtactaca aaacaagtag atttaaggaa 10740

ggggtaaatt tcaagcttat tagggtatat actgaagatg gagaagataa tccaattcat 10800

aagtataggt ttgaagcagt accaaccaaa aagtaataag gaggtgactt aaatgacaac 10860

attaattgtc gtcatcttta ttgctatcat ttattactta tggaacagtg attgagtcaa 10920

gttaattctt gactctcttt ttgttttatg gtatattaat atatagaaag gagagattaa 10980

ttatggaaat ggcagattta gaaagatttg atgcatttgt aagactaatt tcagatgatg 11040

agctttcgga ggaaagaata ctggagttaa gcgtagactt actaaacccg atactagaag 11100

gaggtacagc ttacagagct aaaaaacgta ttaaaagtaa atttggtaag ttagaagcaa 11160

aaaactttaa acgaaactat aaattcttac ttaagtcgat agctcaaata gaccaaagga 11220

gataggacaa tgacagaaag ggaaaaatta attaaagaga ttgaagaggc taacagagac 11280

atacagttac agttaaaaga agtagataat tataaggata gtatacgctc taaaggaaca 11340

agaaattata tctctacaaa ggtattagat tctattacgg ttggtttcat agttagtttt 11400

ttaatactca ttataatgcg tgtacttgaa tactttgtaa caggtaatgc tgtttattca 11460

cctttagcgc ctgcagttat cattatgttt gttttagcac tcggtacatg gaaagtaagt 11520

aagatgaaca aaatagtatc ttatagagga actattaaga tgtactggga gctaagtaat 11580

gctgagcaaa aacaagctaa ggtatttaag tatcctaatg atgaagtaga tattgtatca 11640

aaacataact taaggcaaat aacttttagt gagattaata tacttcatct taaatatatg 11700

agatataata aagcagtaga acagcatact aaattatcta aagaactttt taaaaaagat 11760

aaagaaacgg ttgacaagaa taaataagtg tagtatagta ttactaaagg aggagagata 11820

ttatggttat acctagtatt aaagcacaaa acaaattcaa gaatgaatta gagtattata 11880

aacaaggtca cattagtgaa agtaaaatgt tagaattagc ttttgattac atccaagaat 11940

tagaacaaaa taacgaatac gttactaatt tgctagaaga ggagagatat ggtgagtaaa 12000

tttatcggag tgtacttatt taatttacta gtggtagctc tagtttacac agtaggattt 12060

ttattctttt atggtgtagc tagcttagtt attattttaa ctcatgctac tattgacccg 12120

ttcgtattag ctactttctt aggaatagga ttcttagtta ttagaactgc acacagaatt 12180

atggcacgag taatcaatga cgcagtagcc caagccatta aggataaaga aaatgaataa 12240

aggggaattt attatggata aaacattacc aaagtttagt gtatatgaag ttattgtaaa 12300

gactgtaatt atgacaccaa cagaaggaag ttctgaccta gaatcatttt acttttcaac 12360

tagagagtta gcagaaagat ttgttgaaga gaacacagtg gaaacaaaaa acggtaaacg 12420

tgtatctttt gctgttaaag aacgtaaagt aaatcaacca ggctaacatt aatttgttag 12480

ctttttttta ttgacaaatc attttatata gtgtatagta atattataca gaaaaggagg 12540

aattattatg aaagtttcag aagaagtaaa acagagttac ctagagaata aagctaatac 12600

taaaatggat aagataagtt ggtctgagtt aaaagctagt cctttaggta ttaccttagg 12660

tgatattata ttttatagtg tagttattat agataacatt atagctatta ttttaacttt 12720

aaccttgata ggtactatta ctgactcaat tgagagtact ttagcccaaa taatcgtagg 12780

ggtgttcata atcattacta tatatggaat cctatcagcg ttaataccta ttctaattca 12840

taaagctgta tcaccgggat ggagttatac tgaatggaat gaatcctatt acatcagatt 12900

acctggggaa gagaactaca aatactatag taaatggtat ttagatttat taggagttaa 12960

agaattttac tataaaagag atagtggaga agaagtaaaa gaaaaaaata tatcatgggc 13020

ttttcaagct gaagtgaaaa gacctgaaga tgttaaccac tggaaaaacc agttgcttac 13080

taatagacct ttaacaattt tagaatataa aaaattaaag aaattagata aggaaagtga 13140

aattaggaaa caagaagatt tagaagaata caaacaatac aatagtaatt aaagaggtgg 13200

aaagcaatga taagctcatt tgatagtata ctacttgtca tatacattat tatagctttt 13260

gcagtagcta tggcaattat ctacttagta tttaaaggta tgactatttt actagataaa 13320

ctaatgatgt tattattaag taaaactaca ttagatgtag aagcttgttc tatgataatg 13380

gcagtcatca gtacaattgt gtttggaatt attgtacttt taatatggct agcagtaaac 13440

aatattttac tataaggagt tttattatgg attttaatga ttttataaac agtgaatcgg 13500

atagagtagg taatcctaaa caaaagaaga aggtagagaa taagctacct tcttctattc 13560

ctattgaaga tagagaaaag aaattaaaag agataagaaa gaaatcatta tatattgatt 13620

taaggagaaa aagaaatgac taaagaaaca aatgtacttt acaaagataa gtatagagat 13680

tatactatag ttgtaagact agcaggtaat attattgtta ctgaggtaga taagaaacat 13740

aaaacagcat ttacacctat tatatttgac aatggtgtag aaggcgtaga gcttgtaatg 13800

cgtataggtt ctgtagagct tagcatgaca gatttacgtg agttcacaaa ggaagtatct 13860

acagctcaga aagctttaga atattttaat aaaaaacttt acattaaagg cttgacagat 13920

gaagcatttt aatatatact aaaagtataa ataaaataaa gaaaagagga atgattatta 13980

tgttattagg aattttatgg tttatatggg gatttgtatc gtactttgta ttgatgtttg 14040

gaattgagtt ttgtaaagat agatggatgc caggtgttat cggagcagga gccttactac 14100

tattcttatt ttggattatg aaatctatcc ataatgctat gacagtagta tacttgtatt 14160

aggaggttgt atagatggat atactaatta ttcattataa agaaacaaat aaacgagttt 14220

taaaagaaac aatacaaaca atacaaaatc atttaaatga tgaacatggt ttggttaaga 14280

tgacagcaac aaaacttagc agagagaata tagagaaaag atttaataac tataatatag 14340

tcattgcaga agatgaccct gataattcgt atcattacag tgaagctgta gaagaagcag 14400

attttattat agacatacca atttcatatt tagatataca tgcaggagta gaatgggatg 14460

ttgataatcc tgtagatatg ctagatagga atccggattt tatagaagct gtaaataaat 14520

taaatgaaga cttaatgtta taaggaggaa atagaatgct aaatgaaaaa ctaaaaaacc 14580

tggaagatac aaaagtatac atgattaata gtattgcaag tttactaagc gcaagtacag 14640

gaaaatcaag taaagtattt tttgatgaag gaactattaa aattgtaagt ggtgaaacaa 14700

aagcagtaga agttattgat aacttagttc acccacactc aggacgttta cctattaaaa 14760

caacagaacg tattgcgcta ggtagattaa cagattcttt acagtttgtt atttcagaaa 14820

tagaagtagt taaagaccaa attatagatg aagaaaatga agcttacatt gattttgtga 14880

tggaagactg ggactgggat taatacctat ggacttatta actattgctt ctgttgcttt 14940

tatagctgta gtcattattg atttgattaa tgatgatatg agctatatgc ttactggtac 15000

tgcaatctta ataaatattt gggcaggatt ttatggatgg tttttcttac tacaagcagg 15060

tatgttactt ttcttactat tagctaggaa agttaaagat gataaggagt caatactata 15120

ctctagtgct tcattaatat gtgcactagg aatgataata aatcttcttt cattttctta 15180

aaaataagta ttgacacctt tgtacttttg tattatactt agtatataac aagtacagga 15240

gatgattaat atgagtaaag aaacaatcag aagacaattt tcaaacgcaa ttgagattat 15300

ggcaacaact aaggaatggt ggaattttcc taaaagtttt aatacaagta aagagtttaa 15360

aattaaaact tttaaaaatg acacacttgt atttgaagtt agggaaggta gtagaaattt 15420

aggaagcttt gtaattttta caaacattga ttttgattac gataaactag aaggaacttc 15480

aacacaatat atgattaatt actttgctaa gaaattaact aaagatatgt ttaactatca 15540

taagttacaa ttatagtagg aggtggaaag atgagagaag agttaaaacc ttttaatagg 15600

aaacaagtta atgttaaggg ttacttagat gatgttaagt attcaaagcg tagaagacat 15660

aaaggtaatc aacatgggtg tgttaaaatc acagttactg atgtaaagat taatggtata 15720

cctattgacc acgttaacat tgaagttggt atctctttct acgaaaaact aaaggagctt 15780

caaggaaaga gaattcaatt tgtaggtact gtttataagt atgttaaaca tgctagaggg 15840

cgcaaaggta gaattaaagg attttataaa gaggattata gcgtaacttt agataagaag 15900

ttacaaaagg aggaaaaata atgattaaaa gaagaaaaca tttagaccac tcattacagc 15960

ctgagaaagg atggagaaca gtacctttta atgggtatta tgaagcgcat cctacgggtt 16020

taattagaaa taaagtaacg aaaaagttaa ttaaaggtac acagacaaga aagaaccatc 16080

ctaagtggac tgctcatgag attgtatact taattaaccc taagaaaaca agttattcta 16140

ggggagtagt tattgcacat acattccctg aaatgattag ccaatcaaga ggagacctta 16200

agaacggtca tgtgtgtttt aaagatggtg accgaagtaa ttgtcatgta gacaacatgt 16260

ttattggtaa aggtaatgtt aacaaaaata tctataaatt aaatgattct tatttaacta 16320

gaaaagatat tgaagaggat gttaataatt tagttaatga aagattattc tctcaattag 16380

aattattgat taagaaaaat gaaccggaaa gaattacacc tagtaatcac tttattaaaa 16440

gagataataa tgtgttcagt atcacagatt tatctaaaaa ctcactagta gagtttgagt 16500

tagaaatcaa gaatattaag taaggtggtt atataaatga atgagtggta tgctttatgt 16560

tattacgaca aagtaggtaa aaagaaaata cctaggcaaa ttaaagctca cagggatgta 16620

tctgtattag aggatttaaa agatagatta gaagaacaaa atcctaaaga agaatacaag 16680

attaaaacaa caaaagaatt tgataaggag agataattaa tgttaacacc tcaacaaaag 16740

gattcattaa aagagcaaca aaaaaaatta agtaaaaaga agaaataagt cttgacaatt 16800

gagtatacat aggttatact taagttaaca aataaagagg aggtatgacc tatgttattc 16860

gtaattttta tattggcagt actgtttgta cttggattta tgaatggatg gaactcagaa 16920

gactagataa ggagtggttg taatgaagtt agaagataaa gtgttagaga gaattgattc 16980

tcttggaaat aaagcaggta acttaagtaa tcaagcaatg gagtcattag taaagtatca 17040

aattacgtac ggtattatag atattgttgt aagtatttta gttattgcac taacaatatt 17100

tttaggtaag gtttacctta aagaatataa gaaggttaaa atggatttaa aagaaagctt 17160

attgtatgat gactacgata ttctctcttt acgcaatagt tgcaggtata ccaactgata 17220

ttatgagatt aattaatccg gaagtttatg cagtaaaaga tttaattgag caagttaaag 17280

gaggaaattg atatgaagca gagagatttt gaatttgaag aggattttgt attaacttac 17340

gagtgtgagg attgtaagca ttttgaagac tggggtcatg atgaagagcc tgaagaatgt 17400

agtgaatgtg gaagtagtga cttaatcaat aatacaagtc atgaagatac tgagtgtgat 17460

atgtgtcgag gatatattga tatgtggcaa gatggatata gatatatggg agataataaa 17520

gagtatattg aaaaagagga atcaggttta atttgtgaag attgttatga gaaattagat 17580

atttaataag gaggaaatta atatgaataa agcagtagaa caagcaagta atgcattagg 17640

tcaaggattt tcagctatgg tatggcatca agtattagca gggttagggt ttattttatt 17700

aggattggta ttatctttac tggtttgggt attagtaaaa aaattccatg tacctttaa 17760

tcacccgaca gcttttgtag tgtactcaat tatgttagtt agtattgttg ctagttttat 17820

ttggggcggt ttacatgtaa ttaaccctga gtattatgct attttagaac ttaaaggttt 17880

tataaagtag gaggaattct atgactaaag aagagttaga gcaaaaagta aaagaacttg 17940

aagcagagaa taaagagctt aaaaaacaaa tagaacgttt tgaagacgaa ggaggaaaaa 18000

caaaagatga acagtagaca aaagaaaatt ttaacattaa cagtaagtaa ctttttaatt 18060

ctagccttag atactgtagc actaattaga tataaaaaag gtaaaattaa acaagagaat 18120

tataacacag ggcaaattac aagaatgata gctacaacag ctaactcatt aggtattctt 18180

tacttagaag agcaagagcg taaagaagtt aaagatatta aagtaggtac ttttgaaatt 18240

ggagccttaa aaagatttac aaataataaa taaaaaaagt ttaagaaacc tattgacatt 18300

aggtttcttt tattatatac taatattata agaaataagg aggttaactt atgaaaggta 18360

ttatcatatt ttacaaggaa gagaccaaag aggatttagg atattttctt gggtttataa 18420

actttaagct agaaggatta tcttacacaa ctgaaggtac tttagtagat aatgatgtag 18480

tagttttaaa ggataaccaa attaatgagg ataatttaga gcagtttagt atgtcaaaca 18540

ataatttagt tattggaata ctaggtcatt catctctttc agtacgcatc tatgaaaaag 18600

gtattagaca agagtttgat agagtagaag aatatttaga ggagttgaga caataatgat 18660

atttatatta atttttggtt tactatttat tttatcttta ctaggtattt ttatttattt 18720

tatagtttta cgaaagaaaa aacaattaat agaagaaaga gaatcatttg gtatttataa 18780

tagaacaaaa gaaaaactgg gtgatgtaac acgtttaggg tatgaggaag atgtatataa 18840

gttaatccat aaccaatcta ataaaacaat catagaggat aaaaagagta aagttgtaga 18900

tacaattaaa aagatgtatg agctagaatt aacgtcagta gatgtttcta aggtagaagg 18960

attatctcca cttgatacag aacctatgac aaatatgaaa ttactttcat ataagctaga 19020

tagagaagga ttatatagtt taagtaaatt tatttaggag tgatacaatg gaatttatag 19080

ataaaaataa tgtaattaaa gcttatgata taccaaatgt ttatttaaaa ggttatgtat 19140

tacaggcatg tgataaaaat ggagatacaa cagcttatga tggttatgac caaatacact 19200

ataaagaagg tagagtatta acattccctt ttgataaacc attaagaaag ataaatgtac 19260

tatcaggata ttacaaacta tttaaaaagg aggacataat atgatttatt ttgttagtga 19320

tttacatttc ggtcatgata atattagaga attcgaagca cctacaagaa gtcactggaa 19380

ctcagtagaa gaaatgaatg aaggtttaat tgagttgtgg aataatacaa ttacaaataa 19440

cgatattgtt tataacattg gagacttctt tttcaatatg aaaccttcta aagtagaaga 19500

tatacttaat agactaaatt ataaagagat gatactgatt gcaggtaacc atgaccataa 19560

gaaacttata aaactatatg aacgtaatgg tattacagta aagtacgcag acatgattaa 19620

aaaggatggt aagagatttt atctaagcca ttatcctaca ctaataggta gaaaaaacat 19680

gtttaatatt catggtcata tacactcaca attaatgggt actgaatatc acatcaatgt 19740

aggttatgat gtagagggta aaattgccta tagttttgat gatattataa gtagagcagg 19800

tgaatataat ggagaaattc aaaggtaaag atttatataa aactagaatt agaaaacaaa 19860

caattaaaaa tttagttata aaaacagaga agctacataa taaacacgga aagtatagac 19920

ctattggtca tgtttattac tatccgaaaa caaaagagtt tactttatct aagcctgaac 19980

aaaagatatt tatagagtat atgaaagaat taggttttaa tgtaaaacac aggagacgta 20040

agaaaacact tattatttat aagaatgcat tcactgaata cattagtatg tatcatgaag 20100

caatagagca gattgaagga gggacataat ggaatattta tttttattta taggtattgg 20160

catgataatt tggggtttca tagcacctta tcttgcattt gtagtttact ataaacatgt 20220

aagagaaaat cataatggat tcagtgatga ggaatctcta gaagaggcta cagtacttgg 20280

tatgggattc atgtttatag catttattcc tataggtata ctagttgtaa ttgaagaaat 20340

taagatttta ttcttttaag tgttgacaac tacaatatag tgtgttacag tataaaaaag 20400

gaggttaact aatgaagcat tttattttaa ttttagggat tgtaatccta gttattgcat 20460

tagggattgt aatcctagtt attgcattag gtattgtttt accggcatgg attttacagc 20520

tagtattatc tgcattcgga gttaaagtaa gtatttgggt atgtatcgga atatttattt 20580

taatcagtgc aataggaagt atgtttagta gaaattaaag gaggaattac aaatggcaaa 20640

atatgaatca aatattaatg gagagaatta tattgcaaca ccgtcacaag ctttaagaga 20700

agcactagca aaattaataa ctgaggaaaa gagctttgca gagtaccaaa ctaaaggtgg 20760

ggaacagtat gaatcacagt tacaactaag acactttgat gcaatgatat ctcagtatga 20820

ggaagctatt agagtactag aagataaata tagacctcag atttttattc cgaaagataa 20880

taaggaggaa aattaattat gaaagcagaa tcaatagcaa gatttttaa tgacaaagta 20940

ttacaaatag aaggttataa agtaagattt ccgcaggcta gttcatctta tattttagat 21000

atagatactg tagatgaatc agtattgttt ttagacgctc aagtatctac actttcaggt 21060

aagcatttat tagatacagc tattacaatt gagagacctg aaacattaag tgctaaagag 21120

ttatatacag aaattagtaa taaactgcaa gctattgtag gagaccaaac taaaacaact 21180

atagaactat caagatattt taaggaggaa aaataagtgt ctaataaaac tattacaaat 21240

catttattaa atttaaaagg aataaacatt gaaacgtata gtattattgc tcgtatcaag 21300

aaacaaacta gttggggtga taaaggagat tcttttgaaa taagcataag ttataaagct 21360

gataaagacc ctagaacagt gagatatatt acaactgaaa ttactattga ttatagtagt 21420

aataatccaa aagaaatttt attacaatta aaagataaga ttttttctat tgttgaggaa 21480

caggtagaga ctgacaatga ttttattgaa tctattaaag aaattaattc aactaaagca 21540

ttagaaaaac taaagcctta tatcaataat gaatattatt caatgtttaa atcttctatt 21600

gaaaaggaaa tacctgtagc tttatcttct gaagtactca atagatgtac aggtaaaaca 21660

agcacattag cttatttagc actagaaaag gatttaccct tagtagtgtc aaatgaacct 21720

atgagaaaaa tgcttaaaaa taaattccct caccttagag tatcttctgc tgaagattat 21780

tcaaattatg atattaaagg tgaaattgta ttaatagatg aagtagatat tgaccagtta 21840

tatagtgctg ataaagtatc tgttgatgca ctattagtag gtatcattaa aaattaaata 21900

aatttataaa tacctgttga caacaggtat tttttatagt atactttaga tataaagaaa 21960

aaggaggtaa tataatgata cctataatag ttatacttat tggactcata ttatttttat 22020

ctagtggtta taagttggta ttaggtaagt actatgatga tgtagattta aaaatactat 22080

ttaccatatt tggtgttggg attgcattac tacttggagg atttatatta taaaggagga 22140

aacaataaat gaattatgaa gaggtactaa gaactattaa ggaaaataaa ccctgtaaag 22200

ttagattcac aggaaatatt ttagcaattg ttaatgagga atttaatgca gatactgata 22260

aaggagtttt acagcttgat gtatcgaata tcaacaaaga gggctatata agattacagc 22320

aatattgttt agaaagagat gactatacgg tagtaggagc tattttattt taaggagagg 22380

taaatatgaa ttatagagat tttattacag attgtattag cggtggttac aacgtacaca 22440

tcagtgttac agaaaaaaga gtgcacatca tttctgagat gacatcagca tcttatccta 22500

aaaaggaaat taacttagat gaactacaag cttatgtgta ctatatgaat aactttggaa 22560

gtcaaattac aacggagggg ttataaatgg aattggttat taatattgta gcagtattgg 22620

tcggtatgta tgctatttat ttctatgtta caaaatttag tactggctta tcaggtattt 22680

taattgtttt agggatggct attggtcttt acttctactt agactattta aatgtcagag 22740

aaaatgttat tcgattagtt tcagtaatgt ttggagcttt cctatttagt attgaaatga 22800

tttataataa aattatgttc gaaattaaaa aaagcaatgt tcagaagact gttagagtgt 22860

atgataaaga gcagtaatga tttttaccat aaagagtatc taaattactt taagtgctct 22920

ctatggtacc ttaaaatagc ttagaattga aattaaggag atgaatattt atgtatcctg 22980

aaatagatgt agaaaaatta gcgtacaagc taaaaagtac gagagaatat ttagaaagca 23040

ttaaaataaa agaagtagaa atttatgaaa tctatcatct taaaacaggt aagttagttt 23100

ttaaaggtga atatattgaa gtaaaagaat tactgaggaa aatgtataaa gagaatttaa 23160

cacttgtaga tgtagataca atgttaagta ttggtaaagg atttattgat gtaattaaga 23220

atatatcagc agaaaatgta ttccaaataa catataaaaa ggagctctca acaaaatgat 23280

taaaatattt tcagaagtag ataaagaata caaacccatt attactgaaa agtttcctaa 23340

tggtgagatt aattttaaat acgatgattt aaagtattta gtagaagaga acttaagatt 23400

tgatgttttc tttaaatggg aaaatgacgc agatttaatg catttgtata tgtttactaa 23460

gtatttagag caactaggta ttaaagataa agctgaattt ttagagattg catatctacc 23520

ttatagcaga atggatagag tagaagaagg gcataataat atgttcagtc ttaaatacat 23580

tacagaattt attaataacc ttaattataa atcggtatgg gtagtagaac ctcatagtcc 23640

tgtaacagaa gaattactta ctaattctgt tgctattgat gttacactta aattattaaa 23700

tcagtatatt gaaatgtccg aagagcctgt aacaatagta ctacctgata aaggggcata 23760

cgatagatat ctatttgatg tagaacgtat cttaatggaa tctaatattg aatcatattc 23820

aattgtatat ggtgagaaga aacgagattt tgaaacaggt aagattaaag gtattaaaat 23880

aattaaagat aaaaatactt tatatgataa ttgtattata ctagatgact taacaagtta 23940

cggcgggaca tttgtaggtt gtaaaaaagc ccttgacaaa cttaaggtaa gtagtgtatc 24000

attaatattg actcatgcag aacgagcttt tgcagaagga gcattactta gctcaggatt 24060

taaagatatt attgtaacag actctatgtt ccctaaaaat aattgggaaa aagctattgc 24120

taaacataga gctagaatca acggaactga attacaaata aaagatatcg aaagatattt 24180

ataaaaggag aaaaacaaat tatgctaaac ccaactttaa tgtgtgactt ctataaacta 24240

agtcacagag aacaatatcc tgaaggtaca gaaattgtat atagtacatt agtacctaga 24300

agtaataaat attatgaaca cagtgataat attgtagtat tcggtattca atcacttgtt 24360

aaaaaatatt ttattgatat gtttaataaa gagttcttta acagacctaa agaggaagtt 24420

attaatgaat acaaacgtac agttaaattt acactaggac aagaaaatcc tgatgctaaa 24480

cacttagaac aattacatga cttaggttat ttacctattg atgtaagagc tttaaaagaa 24540

ggtactgttg ttcatcctaa cacacctgtt atgacaattg aaaatactca ctcagatttc 24600

ttttggttaa ctaattactt agaaacgatt attagtactc aaacatggca agcaatgact 24660

agtgctacac tagcatatga tatgcgtaaa atgctagata aatatgcaat ggaaacagta 24720

ggtaatattg aagcagtgga tttccagggt catgacttca gtatgcgtgg tatgagttct 24780

ttagaaacag ctcaattaag ttcagcaggt catgcaatta gttttaaagg cagtgataca 24840

gtacctgtag tggatttctt agaatcatat tacaatgcag acgtagagaa ggaaatggtt 24900

gttgcttcta tccctgctac tgagcactca gtaatgtgcg caaatggtaa ttatgaaacc 24960

atggatgagt atgaaacata taaacgtatg ttaacagaaa tatatccaac aggaatttc 25020

tctattgtat ctgatacttg ggacttttgg ggtaatatga ctaaaacttt acctagatta 25080

aaggatatta ttatggaacg tgatggtaaa gtagtaatca gacctgatag tggagaccct 25140

gttaaaatta tttgcggaga ccctgatgca gatactgaat atgaacgtaa aggtgcagta 25200

gaagtacttt gggatacctt tggaggtact gaaactgaaa aagggtacaa agtattagat 25260

gaacatgtag gattaattta cggagactct attaactatg aacgtgctca acaaatttgt 25320

gaaggattaa aagaaaaagg ttttgcaagt attaatgttg tattaggtgt aggtagtttc 25380

tcttaccaat ttaatactcg tgatactcac gggtttgcaa tcaaagcaac gtatgctaag 25440

attaaaaatg aagaaaaact tatctataaa aatcctaaaa cagatagtgg taaacgttca 25500

cataaaggtc gagtagctgt atataaagac ggttcatggg aagataactt aaccttacat 25560

caatggctaa acaaacaaaa tgttaatcaa ttagaaagag tatttgaaga tggtaagctt 25620

tatagagacc agtcgttaag tgaaattaga gaaataatta aaaataatta ataaatattt 25680

aaactcccta ttgacaaagg gagtttttta ttatatagta gggttatagt aaataaagga 25740

gtgaaagaaa tgatttataa aatatcaaaa cataattact atagtaggtt tgaatattca 25800

tcttatttac ctgatgaagg atttgcatac atagattatg tagatgtcat tcttataggt 25860

gtagataatc cgaggaagag aaaagttatt actttaaaag cagatgagtt taatcctagt 25920

gattttaagg ttggtcataa atataatatt ataaaaatac tatggtttga gaaatgggaa 25980

tggttacagc catagggagg agaggtatac aatgattata gataaattaa atggagttaa 26040

attagagatt ggcggtcatg ttgtatcatt tagtgtaagc aaatttaaaa cgattaatgg 26100

tgagagacaa ttacttgatt accaccatat caaaagacgt aaacagaaat attttagaac 26160

tactgaagaa ttctataatg agtacaaaga aataaaaccc gataagaatg aaatagatga 26220

aatgtttgaa tctttaggtt atgtagatac taaactagaa gatgtagtaa gaaaccaaga 26280

gaaagtgaca gagatattag gagttagtga acaatactta aaccaattgt cttataaggc 26340

tatagaggaa tatgtagaca aaatagttac cttagaaatt aaagaattaa aaggagaaaa 26400

atagtatgag taatagttgg gaaaaagaag gagttaacta ctgggaaaat gaagattgcc 26460

ctagagaata cttagagaaa gcatttatag aattagttga atacgtagaa ggtgttacag 26520

taccatctag agatgttcag cagttgagag aggataagct tagagaagat attggatttt 26580

atgagtatgt agcagataaa taaatacaca tctacctatt gacttaggta gatacttatt 26640

atataatagt atacaaggag atgaagtatg atgaatggaa aacaaattta tgtattttta 26700

agtgaccagt atagtaaaga tatactcagt ttacaattag gacttattaa ggaatggtct 26760

agaagagaac taacttattc agatgatgtc gggtcagatg cagatgttgt tatttgtact 26820

gatatagtaa gagatgattt cgtaaaaaaa ctaagtaaaa ataatagcaa tgcattattt 26880

gtgtttatta gttctttta ttggataggt tataaaggcg gagaattttt tgttgcagtt 26940

caagactatg tgaaaggtat gtaagatatg aaaaaattat taatattatt tacattagct 27000

agtactttac tattagcagg atgtacaccg gataatcatg aaggaaaagt tttaggaaca 27060

ggagaatata gagagccaac tacttatatc aagtcaggaa gtgttactgt accagttatt 27120

ggtgaaatga aatactatgt agatttagaa acagataaag gtgaagaccg tgtttatctt 27180

aatagagaag tttatcataa atttgataaa ggtgatgatt tctctaatgt aggtaaaaaa 27240

gtatataaaa atgatgaatt aatatataaa ggggactaat tagtatgaaa caatttatac 27300

atgataaaaa agatagttat aatagtacaa atcgtaattt tgatattcaa tattataaag 27360

gtataccttt acaacaaatt gataggggat atggtcaagc aagagctagg agatttacaa 27420

taaataatac gaaccaaaat atatggatac ctatgacata tttaaaacct aatggtactc 27480

ttaaaaataa cattgatata gattggatac ttgttaaaga aaaatgtagt ttaaagaaag 27540

caggattagt aataaaaata aaaattacag gagatgtatt ataatgtata tattagaaag 27600

aacaattaga ggttttgccg gtcaaacaga agatatttta ccttattact ttaaaagtaa 27660

gaaagaaatt gttaattttt taaaactaat ggagttcctt aaagaagaaa caaattattg 27720

ggttaaaaag aacggtaatt atactattat aatcagggct aaaaggatat tatacattga 27780

agaacatata cagaagttaa aggagtggga gaatgactta tgatgtttat gtattatata 27840

aaagaggaga acctattgca caaggtagta tggaacattg cttagatgtc tattattggg 27900

aaagggtaca cggttatagt aataaaggtt atgaactatt acctatggga tatgaacagg 27960

aggaataact aatgataaat atagaacatg attatacaat aagaactgta gataatagaa 28020

agtatactta ctatagtaaa catgaatctc cagttacttt atataaaaat attataggta 28080

aagattgtat tgaagtaact aaatacggga aagataaaaa agttattata gctactaaat 28140

atattgtatc tattgaacga tggtaaataa ggaggtataa ctaatgaatg ctaggaaagc 28200

acgtaagaac actaaaaact ataaggactc taatgtagta actaaagagc aacacctaac 28260

ttatatttat aataagttaa actacttgat tgcaaataat agtagtcagg gtaaaacata 28320

tgtggtaatg aacctaagaa cagattatcc tgatgagttt tctttatcta aattaaaata 28380

tctaaaagaa attaaacagc actataaaga cctagtattt aatgtgaaaa cgcaagtaag 28440

gaaggcacag tggtcagaga aaagtataat caggtactac tttaacctag gctatataga 28500

cagcgtgtta gtacctatta tacacattag ttggtaatta caaggagagg tagttatgtt 28560

ttttaaaaaa aagaagttaa gcaatgtaga gaaacaaata agacaaaacc gtaataaaga 28620

agacaaagaa agaaaagaac atcaagataa gttagataca gatatgtata aaacatatga 28680

attagataaa attgtagaag aacatttaag aaagttaaac actatatccc ttgaagaatt 28740

ataattaact tcagtgtgtt tagggacaag acttgtttat tattactcaa taggtaagga 28800

ttggaataaa caagtatata gtttaaacga attagaatat atgaagaaga aatttaagaa 28860

attaggattt gaaactcaga taacaaacga agatataggg tttcaacctt atatttattt 28920

aagattatta tgggatgcat aagtaattat tattaaagga gggatagttg gtgctgtacc 28980

tctaatgact attattattg cacagttaat tacagattat catgatagac attaagtatt 29040

gaatactgtt gactaataag gaggatatat taagaagtta aagttacctg gtaatattgt 29100

tgactagcaa gaagaagaaa atattattac tattaagtac ctgggaaaac ttttacctct 29160

ctcactcagc ctattactta ctaccgactt ccctaactac ttattctata gttataatat 29220

tcatttatta tacaatggta aactatagta ttccacctgt aaactatgct gaagcggtag 29280

taatctattg ttattatata ataatcttat ataatggtac gttaatctag tatattacat 29340

tagaatgatt ctaatctagg attttaatct ttagacccta ggaaaagtgg tactaaaata 29400

taaaacccta taggtatggg attcttattt ttaaaattac taaaaagtat taggttttcc 29460

ctagggcaaa gttttaatgt acctaaaata gtaagtagct ccttatcatt tagggttcta 29520

taattgagaa tattgaaagc taatccgctt caattgtaat taattgttga caactatgaa 29580

gtgggtatgt tatacttagt atataaaata ataggaggaa ttaataatga atctgacatt 29640

tgaagataag ttagaagact tactaaaaaa ggtacgtagt ggtgagatag aacctatcga 29700

gtactctcaa gttaatgatg agcaccctaa tggtaaaact acttgtggcg ttacttttaa 29760

gtttgatatc gacacaccaa ctaaatagga atatgaagcg gttaattccg cttctcttac 29820

ttagagtata taagtaactg tatattgtaa gtaggagtaa tcaaatttag gagatgagat 29880

agatgataat attatttacg caggattatg ataaaaccct aatgaaagtg atattagggg 29940

atattaatac tatgagacct aattggaagt acagtgttaa ccatcctgag aaagaagagg 30000

atgttcatat acaagcttat gaaggggaag atatatttga tgatatagag gagttatcag 30060

atagtacaca ggatatagtt ataggtgtta ctgaagatga ttgtatatca gagtctcctt 30120

atgactttaa tggtgggctt agattagtca ctaaacatat taaggaacat atagagaaat 30180

tcttataggg agtgataata tgattgatat atacttagga gaaggttata ataaagaata 30240

cttgtctaag gcactcagat taatcaatga ccatgctcct agggagttaa gttatgattt 30300

taataatgta gaagcggatg ttaatattca cacgatgtta tatgttaaac ctgaagatag 30360

gtatgtctat aaggatatat cttatgactt cccgggtgat ttaattattt gtatagttga 30420

agatgatgct attgtgtatc accaaggtaa acaggtttca ggtattagta ttttaagaat 30480

aatagaagag ctcatttaag aagcagttaa gtaaaaaagg ataaattgta ctagaaaatg 30540

tataccgctt ctgtatggaa ggctgagagg gcttagaatt gaaaggggag atataatgat 30600

agagatatac cttagtgaaa attatgataa ggatttatta aaagcggaat taaaatggat 30660

taaggagacc gcttcaagag aactaactta tgatgttaat aggaatccta acttagatgt 30720

acatgttagc ccatttagat atactaaaga tgaagtaaaa gaaataagtt tacatcctca 30780

atttgaagac gatgtatgtg tatttatagc ggagacgtgg atacatgaat accatagagg 30840

taaatcaata ggcgtagata gtatggaaga atatgtaaag gagatgtaag tatgtttaaa 30900

gtatattaca cagtctacca taaaggtagt atgaaaacaa ttaaagataa gctagataga 30960

agtagtttaa tatacttctt gtatgatact tggtataaag atattagtaa tgtattccct 31020

aatcactata ataaagagtt tggaagtaat agtgatgata tagacataga taaacttatt 31080

gaagcggtta atgaggaggg tatattactt atcaatagag gtaattatgt tacaataaga 31140

gaatggtagg ataggataaa cttaggatag aaaataattt aggatgagtt acgataggat 31200

aggatacgat aggataggat acgataggat aggatacgat aggataggat agggggttaa 31260

gttaggatgg ttactttaac atacactatt attcataaag aatctgatag ggtaatagct 31320

agtggtttag atgagttaga ggttataaac ttagttcaaa ggatggtaaa tactaatcta 31380

gttactgata tatcattaga tgattatata cgcagaccaa gtggagatat agatgtactc 31440

aatttactag tagatattag aagacaaggc gtatttgatt tcaatcacac ttggcacgta 31500

ggataggagg gataggatga tagttatata tacagatgtt tctaaggatt atttaaaaga 31560

cgagttctta ccttggctta atgaaaggga tagatactta gaagactata aagatgaatt 31620

acctgaggat atagattcct cttatattgt atcagttgta tactgtaagg atatggaagg 31680

tctattagaa agaaaagaca ttgttattgg taatagctat aatgaacctg tagctttatt 31740

aggtgttcct gagtttttg gtaattatag taattatttc tactatagag gagaaagtat 31800

tagtaaacat gacctaggag aaattgttag gttaaaagct tggcaacgta tgggcggaga 31860

ttgactaagt agctctccct aatttcacta agtagctccc taggaattgc ctaagtagct 31920

cggtatgatt ttaccctaag tagctccctc tgttttctac tagtttattt taaccgcttc 31980

aggtgtctat atatagacgg ttggaataat agcagaccgc aaaaataaat acactaggat 32040

attattccca gtgtattata taatttttt atttaaatct ttttatattt ctatttattg 32100

ttattctact tacattatac atatttgata attcttcttg tgtaaaacct ttttcagtat 32160

ataatttata aatatttttt ctttcattat ctgttaatga tttaccacgt ttaaaattgt 32220

ttattgtttc atctttatga tgtaaattat tatgttctgt agggctaata cattgtaaat 32280

tatttatatg gttattttgt ttattgccat ctatatggtg tatatgataa tcttgattaa 32340

aatcattgcc aaaatattca tatactaaac gatgtataga atgatgttta taattaattt 32400

taactatttt atagccttgc ttatgattat gaggttttac taacttttca atcatataat 32460

aattaccgtg tcttttttatt ctaccatagt tagatactga ataattaaat atattattaa 32520

tattattttc tatgcgtttc catttctcat taggtaaatt attaatacta ttataatctt 32580

ttaaattgta ttgtaataaa gtatcaattt taacttttct tgccttgttt atatcatctg 32640

tcatacgata aaagttattt ttatcttttt ttaattcctt atttgttttc tttgaatata 32700

ctttgttttc ttttatatag tattttgaaa acatttcaat gttatttata ttatgtttca 32760

tcttctcaac tccttaacta tattctacta tataataggt aatttgtcaa gttaaaaaag 32820

tttttaaaaa cctattgact tattactttt tagggtgtaa tatagatact gtaataaata 32880

acacgaaggg aattgatgaa aatggaaatc aaagaaattg ccgatacaat tatgtattta 32940

tttaatatgg atggttacag atgtgcagaa cctccattat atgaaagcac actaaaccac 33000

acacgcacac acacggcgtt aattgtttct attaagggaa actatgacac agtgcagatg 33060

ttccgcaaaa cgcctataat gagcatgaga gggcaaagcc aaccggctag tatgttagta 33120

aatgtaattg atgatgtaat tataatagta tatgaaaatg tagtgtacgg agttcaaaac 33180

aaagaaataa aattcattga agaaatttaa aaataggggt tgcaatcctc aagcatctat 33240

agtaatataa taggtgtagg ggatagcaac acacctcaaa aaaacttttt aaaaaagtta 33300

aagaaaagtg ttgacacctt ataagataca tgttattatt aagataacaa ataagacaag 33360

ccacttagca aataacgaaa ttaaataaaa aaattataga ataggatttg attattatga 33420

caaacaaaaa ttacttatac gaagaaactc acacagtaca agggcaagac attacggctt 33480

tcagaattcc aaacgacaca aacggcaacc cacgttatgt agtgcatttc atggatttaa 33540

atattaaact agcagactat gacaacatca ataaactata cggatttaat aaatatcgtg 33600

ctaaatggtt tggcggtggt gtagtattcc aaagctataa tatagaagat acattaaatt 33660

ttgcactaga taaagttaaa gaaatagaag cggttaagaa ttaaaaccgc ttctgaatta 33720

aataaaaaaa ttatataaaa aggatatgat aatatgatat tagaaataga aactaaacca 33780

gttaaaacat tgaaagcaat taaagacgat acaaaaaata ttaaaaatag tatagcagaa 33840

catttaggat taaatagaga acaatttaaa ttatcaaatg gtttaataac tttaaaaggt 33900

tattcagaag aatttaaatg ttggtataat ttaactagca caattggtaa ttttcctaaa 33960

tatttaaaat cagaattata taatgaatat aaattatatt gtaatgtaga attaaaaact 34020

aaataaatta aataaaaaaa ttatacaatt ccctaggatt agatttctag ggatttttat 34080

ttattttaat ttatataaaa aatttattta ttaaataaat tagtgtaaaa ttgactattg 34140

acaaggttgt atttttatg gtataatgaa gtgaagacct tttttagtat aaaaaaatta 34200

ttatataaaa aatttatatt aaatgatttt agaaccgctc tttctcgtta cctcgtcatt 34260

tatatagcgc aagggatagg caacttagcg ctttgtttta ctttctatat atagtatact 34320

atgaataatg gtaattgtca acacctttca gaaacttttt ttactttctt ttattattat 34380

ataaaaaaat tatacatatt ttatggctcc acttccatta tataataatt cagtcttaat 34440

gtcaatagat aaatgtaaaa aagtttttta aattaatttc attaaatcta ttgacttgtg 34500

tttctttcta tagtaatata taggtatacc aacaagggag gcaatacaaa tgctaaaatt 34560

caaatggaaa aacaaaacaa ttaaatcaac tcaaaaaacg gataacattc tattacttat 34620

tataggtggt ttagttgcaa caatcacacc taaacttgta aactggtttt tactactaca 34680

agataatata aatatttttt taagataact attgacaacc tagaaacaac atgttaatat 34740

taagatacaa ggtaagggaa gcggttgacc gcttccaacc taaataaaaa aagtttaaaa 34800

aaactattga cagtcacttg aaaccatgat attattaaga taacaaaaaa caaacagaaa 34860

aggaattgat gaaaatgttc aaattacaaa ataaagtgga aattatcgta cctaaggaag 34920

ataacaacgg cgttgagatt gcagacaaac gtattaaaga atatgtaaac agtatcacaa 34980

tggaagcggg cggttgcact attacagaaa ttaaggggca atggtattca gaagatgaaa 35040

agcgtatcat ggaagataac aacttaaatc ttgaatggta ctacattcca gaccgtgcaa 35100

aattcatgac agttgaatta aaaggcattg taagacgttt aattgaagtt tacggacaag 35160

aggcaatcag tattaaagtt aatggcacat tgtacattgt agaccaatca gacattgaag 35220

aattacacac aacattatta aatatcatga aataaaaaat ttatataaac cgcttcggat 35280

taaattcttg aagcggtttt tttatgtaaa atttatgctt gacaaatgta ttaaaaaatg 35340

agataataga gtgacgactt tttttagtat aaaaataata ttatataaaa aagttataga 35400

gtttttaagg ctccaagtcc attatatcaa ttttgctact ggttgtcaat actttctttt 35460

tttatataat aatttaatta tcttaaagat accgtccact tccattatct caaattttcc 35520

cccaaagtca agaactttct ttcaaataat ttatttaaaa aagtttacaa aaagggttga 35580

cttattttgt actatagtgt aatatataaa gtgtagtaag gaagcggagg aaataaccta 35640

aaaaaagaat ttaaaaaaac ttttaaaaag gtgttgacaa acttccaaat acatgataat 35700

attaagatag ttaaaaaaac aaaaaaacga aaaggaattg ataattatga acagattaga 35760

aatagtaaaa gatacggcaa tggaatatat ccttatgatg gataacagtg ttatggacgg 35820

agttatgaca caagaggaat acaacgaagc ggttagcttt gaaaaggtgt atgactacac 35880

tctatcagaa gcaaataaag aatgtaaatt cttaggcggt aaagttttaa ctttcctagt 35940

acatgaagca atcgaagaat acgcataaaa aaacttaata aaaggggttg acattcaacc 36000

cctaccatgt taatattaat atataccaaa tgagaggaat tgataattat gagatacgaa 36060

attgtaacgc tagttaatca agaattgttt atgtatgcaa cattcaacaa gcaggaagca 36120

gaagcaaaat atagtgaatg gtgtgaactg tacggtcaag aaaatgtaag catggaaaaa 36180

aattaaaata agctgttgac aaactaaccg cttcatgata atattaaact atactaaaga 36240

aaaggaaatg atacaaatga aattattaaa ccaagaaaac caaatcgtaa ttagcatagc 36300

aacattagag agtgtcaaac aagccctaat ttgggaatac atcgaccaca tagattataa 36360

catctggaac aatgaacttg atgacacaga agcggttgta aaaatttctg gtattcttca 36420

atcaatcaaa tttgcagaca ctatggaaga cctgcaggaa tatattgggg atattggttg 36480

gaaattaatt taaaagaatt tcaaataact gttgacacct tagcagatag atggtaacat 36540

tagggtagtt aaaaaatact aaatgaaaag gatttgattt attatgaaaa aaaatgttaa 36600

agcaagcact attgaatggt tagaattgac tcaagggcat ggggagtttg atggtttcga 36660

tgaagaagat atggacttca gaaaactaga tgatgaagat attaaatggt attttgaaaa 36720

ttggtacttt acagaggaaa aacaagaaca gattatagac gaaataggtc aagaggaatt 36780

tgaagaagcc tattcagatg atattaaaga atacaacaat taatacagga agcacacaga 36840

gacacacaga gaagcttaac cgcttctcta atattaaact attaggagat gtttataatg 36900

acaaaattta aattgattga taaaaatagc ttttacgtaa atgacaatta caataacgaa 36960

acttatttaa cttctcaaat tgttctatca ggtgaagcgg gtagattgtt agatgatatg 37020

atagaagatt gtgaagacga acacgacaaa gacaattaca agaaactaga cactaacaat 37080

attgatgata ttgattatat attggaatgt gctaacgttt atatttaccc ttacaataaa 37140

acggaattta aatattaaaa taggagatgt tgaatatgaa cacaagacgg gcaaataaag 37200

cgttaaacga agcggttaga ttattagata agcaaataga agacacacag aagaccatgc 37260

aggagctaaa caaacaacta gaacaacaaa taaaagctaa acaggaacta atgacactag 37320

ttgacgttat gactggtgat gatgagtaat gaacattaaa gaagctcaca aggtcgttag 37380

gagtgcaaag agcaaactcc tgcaggagca ggagcacata acaaaccata tcatagagga 37440

ctacatcata gaggagcttc acagacgcac acagggaagc ggaacaatac agatgaacaa 37500

taacaccgct tcatatagca atggctcata tggtagctta gaagagctta gagaagctta 37560

tgacctatcg tcattatcta ctggtgagat taaagaattg cttgaaacat ttgtttaaat 37620

ttatttaaaa aagtttagtc aaaactattg caatatcttc agaatactgt ataatagtac 37680

ttgtaagata aataaaacaa agaaaaggaa tgattaatta tgaaagaaca aatcaaacaa 37740

tttgagaaag aattagaaat ggcggtaaat aacttattcg tattacatga ttgtggcgta 37800

tcacaagcaa agattgaaga acaaaaccaa aaagttgtgt accttaaagc tatcgttgag 37860

aacatgaaag cctacgaaga aatcagagtt gagccaaaga gtgaagagca atttttcaaa 37920

gaacttgaag aagaacttga agaagaagaa aaaattttaa aaggaattta agaggagggc 37980
aaacgccctt ctttattttt atcctattat ataatttttt tatattatac gggggcaggg 38040
gtaaaatgcc actcaatggg ggtgggtcta tataccccta cggtctaccc aggtacttat 38100
tttttggagg aaattatgaa aataaatatt taaaagtcaa caccctatat gataagtcaa 38160
cattataacc ctaccctgta agtcaacaat ttatagtata aataagaagc ccttaaatat 38220
aaagtcaaca tatctaaaat aaaaaaagag aaagaatatt attcttcctc tgaggtatta 38280
ttaataactt ctaattcatg aatagtaatc atatcttctc taaataatgg tacatcttct 38340
atattatctt tataatagta agtatacccg tcttgaaggt atccgcttat tttttcttca 38400
tagccttctg ctttaatacg tttaattaag ttctccttat ttgtgtaaac tttatcttct 38460
ctgtaagaat agttatcttc atagggttca caattatcgt gttctacttg atatagtttc 38520
atattagtta tcctcccttt cataagacca ttcaccgtat tctgcactaa agtgggctgt 38580
gtctgtaccc tcatcttcat attctacact ataccatgca tcttcttctg tttctgcatc 38640
tatatatctt acttcttctg tagtaataat acgttttacc ttaaatctct ccatttgttt 38700
ttcctccttt atattttcct ctagtatttg ttttaatgtt tggcagtctt tttggtctag 38760
agtatcccaa ctctctagat tttgtaattg ataaagtaac tcatttacaa tttcatcgaa 38820
ggcttctgct tttctatata cttcttctag ttctgtttct gctaattttc tatccccttt 38880
aatttgttct gctttagtta ctaagatatg ggctttattc atttcctcta taataaagtt 38940
tttatagttt tccattatta tttatccctt ctattttcta tccgttgttt tatctcttcc 39000
ctattgcggt ggtgctcctt actcatttct ttacgttcct tatttgttaa ccttattcta 39060
taaacaaggt aattaatgta tagggtgccg gctgaccata gtagcaagaa tgttattaga 39120
taagtccatg agatactaat ttctatcatt gtgattcctc cttatctatt gtaaaggatt 39180
tacctgttct agagaatagt ttaaacattt cttcttcaaa atgcccatca ctcatatctt 39240
tatctttcag catttcacag agtttgtccc atgcttctgc tttattataa attgtttcta 39300
cttctctatc tgtttcatca ctataatttt catatataat ttgtaataca aaatccttct 39360
catcgtaaca tttttcatta atatcatatc tcattataat tcctccttat attctttata 39420
gctcttgatg gctattttac aaatacctct atttacagca acaaatacta taaatgataa 39480
tagtgttata actgctctta catctcctgt aaaaggtaat aattggaaga gcaaatagct 39540
ttctaaaaca ctaatagctg taatggtagt tagatataat atagatagta agtaatcctt 39600
taattttagt ttaacaaatg gtttttgtg ctcatctgtt cttacaatac cataaagtat 39660
tataaaccac ataacaggta ctaactgtat aataaaatca ttatctatat tcaatgcatg 39720
tagagcgtaa ataataactg caggaatacc tataatgaat gctaggaata cagaaaatat 39780
aattaacatt atagggaggg ctacaagaaa acctagcccc tgttttgaat actctaatgt 39840
gtttttacct aggaacttaa aaaatgtttt attcatcttc ttcctccctg gaattacttt 39900
ctgtaattgt aatttctaac atattattgt aataatcatt cttttgattg atattatagt 39960

tatcattgta ttcattaaag tctacataaa tatattcatt tgcgtcattt tcataaataa 40020

tatctatagc tgtaatatct gaatatgctg taatcatttc ataagcgttc gtattatcag 40080

gataagcaaa accaacttga ggtatttcca taggcttatc aataagaata ccaaaataag 40140

tacagtgacg tgttcggctt atatttgaag tctctttata tgtaccgtag taatctatac 40200

cttctgtaat acctgatata tggaacctgc ttacgtcttt agattctaat cttacaacat 40260

cgcaattttc taatactaaa tcaatatatt tgatattcat tttaactctc cttttatatt 40320

aataattctt tccattcttt atcaaccttt ttaagttctt ttttattata gtctccatct 40380

ttagttacta cagtgttcca ttgaaacttc tgtaataagc taaaattatt tataatccat 40440

atattacttt tactataata catattatct tcaaatctta tatcttttc tataaaatat 40500

ttatatattt tatatcttct ttcatctgca cctgatattt taataatttc attagtattt 40560

aattgagtgg ataactggaa gataacatct tttactttca ataggtcttt aacattacct 40620

ctacctacat ggtcattata ataatcgtac ttaacttttt tcttttgttt tctatcatta 40680

actacaatga atatattata tacgatataa gctttaaaat gggtataggt agtaggtgct 40740

tctgaatcat cacattcttt tcttaggtct gtacattgta tttttaacat aatattattt 40800

gatatgttga ctacggtaga accatcatgt tttttattga gatttatctt atccatttta 40860

taattaccta cttattgtag atacaatgta ctcgaacatc ttccattact ttgcctaata 40920

gattctgacc tttccagtta ctttgctcta atattttagg gtcatttgct ttaagaccta 40980

ctccccatat tttatcataa ggtgaagctt ctacgaaatc tttacgtaca tctgtgtcta 41040

atattctttg ctttaggtgt gtagtcataa atttatcttt aactacttct accataatat 41100

catatcttac tttattccat tgctcttcat taaaattacg aactttacga cctaaacttt 41160

tagcatggtt tggattctta gcatttagta tttcacctgc tatttgaaag tcattaaagt 41220

atcttgcttt acgccacata aaggcttgct ctgagttatt aaatgttctt ccttgatgtt 41280

taaactttat agggtagaag ttagaataaa tatcctcttt accccaaaac ataatatatt 41340

cacttgtttc tctcataata tttctccttt aattccatag tgatggtaat acaattttaa 41400

aattatctaa tattttactt tgtacctgtt caagctcatc atatttatcc atatcaaaat 41460

catccatttc tttatgataa tattttatta agcttaaaat atgttttatc atatctattt 41520

gtgttctttc tttgccgtct acatctacaa aagtatggta ttccatatcc acatggttac 41580

tactctctac aaatgcgttt aagtcagcgt ataactggat aaagaaggac atgtcataat 41640

tccaatactt aggctcattt ctacctagtt ttttcttcat tttcttatat tttttattct 41700

tttttagtcc aaaaacttct ttttcaaagt catttaattt aagaccttta aaatattttt 41760

tcttcatttc ttaacctcca atttaataaa tggaaaatca atgtttctaa atactgcgcc 41820

gacatcacac attaatatgt ctccattaat ttctacttct ccactgtcag ttggtgtatg 41880

accacataca taggtaaaac catcttttct aggttgaaaa tctcttgacc atattaattg 41940

gtcaattgtt tgttcttcta caggcttcca actaacccca cctgaatgag agaatatata 42000

cttgtcttct ttatagtact ttctacaatt aaccataagt attttaaatt ttctatagtc 42060

gtctgattct ttaagtttct ttagttcact tttaataaaa tcataattat ttcttagatt 42120

ttcctctaca ctactatatt ttaaagttac cgtactcaca ccgtaagagt taagtgtttc 42180

tatacaatat cttgagagcc attcaatatc atagatactt aatcggtcta cgttttccat 42240

aatattataa aactcatcat catggttccc taacagagtt actacattat catcattaga 42300

cattaaatca aatatatagt taacaacatc ttttgacctt ttacctctat ctacataatc 42360

tcctaaaaat actattgttt cttcaggttt tctttcatta tttattttat ccataattgt 42420

taataatttt tggtattctc cgtgaatatc gggaacaacg tatatagcca tctaatctcc 42480

tccttattgt atataactat cttaccatac ttagtaaaaa aagtcaataa aaaaacctac 42540

cttagtaggt aggtaattaa aattatttat atgttaattt aatttcaaca tttttatact 42600

ttttacgacc atctgttcct gttgactcta gtgtaagaac agatacaaaa tctttaacct 42660

ccggtgttct gttattagtt gtaccttccg ttgcagtagg tactgttaac cagtaagggg 42720

agttagatgc taagcttgta ttattaacta gtgttttgcc attatattct aacttagtaa 42780

cagacttacc tgttaaatct aacttagttt tatctatatt aatcatgaaa ctttggtctt 42840

ctttccagta tatagctgtt ggtgtgaatg ttgctgtata cgtaccatca ccattactta 42900

caggtgttat agttcctgat gtatctcctg ttggtggtgt actggctgta gtatctttgt 42960

aacctacttg agtatattcc cctacaatat tagtttttgt tttatctaca tagataactt 43020

taatgtaatc tctcataaac tctagtcctt gagcattatc atctatagtt atgaaagcat 43080

ttaagaagtt ttgaacttcg gaaattctat tatatttgtt accatcttca taagcaggta 43140

aagtatacca gtaaggtgaa ttagatgtgt agccttcggg gtttatcaag ctcttaccat 43200

tataagaaac atttaatatc ttattagcag ttaagtctat atcatctgta ctcatgttca 43260

taacaaagct tgtatctttc ttccatctca ttccagttgg tctgattaat ttagaataaa 43320

caccattacc taaatcctta acagaagtgt caatagatgg tgggcttgct atagcaccta 43380

cagtaccttt actttctaag aatgattgta tagtgtatga tataaattca tgacctttag 43440

cattaggatg taagccatcc tccatgcctt ctttccaagc aaagaatgtt ttatttacat 43500

tgttatccca tactctaata ttactctccc tatataagtc taatacagga aatgaaaatt 43560

gttttgctat ttcttttata acatctacca attgtcctaa agtatatcct tgtccgtttt 43620

caacttcttt aaaaggatta ctttcaatcc taggtgttgg tgttagaaca acaataggta 43680

ctgtaggaaa aaccttagat agttgataat aagtataata gattgaacct gctactgtag 43740

tgtaagagtg ttctttagct gttcctaggg gttttgtttt acccccaact aaaccatagt 43800

catttgtacc taacataacg caaattaaat caggtttatc tgtaatagtg taggctacgt 43860

ttttacggtc ttggtagcct gttccacttg tacctttatt aacatttatt aatcctgttc 43920

tgtcagcaat aaattggtgg tagtttttg ttgttcttgc atttacttcc gtaatactat 43980

ctcctatgaa tataactttc ttatctttca aaggtgagat agttgttgta cttggttgtt 44040

gtgttggttt attatcagct ataagcttat ttatttctgc cataaattct tcttttatat 44100

ggtcgttaaa ttgggtatct ataacatcct gtaaacctat aatattttct gcttttatat 44160

tcataggttc tacttcatta taagtaacaa taataagttt gtcctgggat gatgttaagg 44220

taacaaattt tggtatatct acttttattg attcttcacc attaatatcc caacaaattt 44280

taaagtgccc tgcttcgtat gttgtatcag gatttaaatt ctctataact atttgaccta 44340

ttgaatcttc tatgttttca cttgatttta aaagattatt ttcatagtca taaagcttca 44400

atttcttagt catatttact tctcctttta ttgaattttg tacaactata atatatcaaa 44460

aaaaatttaa aaaaacacct atttaactta aataggtgtc cgacagagct cccgtactta 44520

gattacggtt aataatattt tacgacaatt atatgagacc ctctgtcgtt gaaacgctcg 44580

tcactgcgtt atacctcaca agatattttg acagttagct tgtgagaaga agattgtttt 44640

ttattgtact tagtttatac actctcaaaa gtacatgtgt actatatatt tatacaccaa 44700

gcgtttggtg ttagatacgg aatggaggga cactaccatc cggagtctac ggtcagatac 44760

aaagcctctg ccgggcaaca tacggtatct ctcgtacatc aggttgacta aacctttaga 44820

gcttttcact ccttctctta taaccagtaa cttaagagaa ataggtttta cttagtagat 44880

atgaaacaat aaatccacat acaatattaa atcatagtca agtgattgca catatgtcta 44940

atacctataa gttttctgct agcctggtat atggactctg caggactcga acctacagtc 45000

aaaccgttat gagcggttgg ctttaccttt aagctaagag tcctagaaat atcctgagag 45060

aggactcgaa cctcaacgac taggtagcta catctagcca atgccattac tcaggattgc 45120

tagtaacgct aaatagaatt ataacgttac cgtagacctt ttctacgctt ggtagatagg 45180

taaaatataa tgatttcaaa gtacccatat agttaggctc ttactctcat tatcaggtta 45240

aaaaggctaa ctgtatttag cattatataa gaggctttag ttaactacta tactaataat 45300

ataccataaa ttatacttaa tgtcaagtta atttatcaat tgaatctata atttttgatg 45360

tgctacgtat atccgcttct ctactatgtt taaggagata ttttaatttc attaaaaaag 45420

aatttttttc tttttctata atatcttctt tatcattgta ttctgaaaac ataatgaatt 45480

ctatacctat actatttcta ttatgtgaaa acatatttat agaaaaaggt gaatcaaaat 45540

ttttatcatc tttattaata ctaaagtctt cagtaacatg taattcattt atttcagata 45600

tttcaaagta cccattaact cttttaagtt caagataact attatatcta aaataacgct 45660

gttcttctat taacttctct tttgttagat aaggatactc atttataaat ataggattac 45720

ttgttccata gttatctcta atatattctg cgtcctctaa agaatcagta taacctaaaa 45780

cttcataact tgttgtatac actgtatctt cttcccacaa gtcatagtcc atttcctcta 45840

tttcttcttc taatatataa atttttttcca tatattactc ccaaatacca ataagatttt 45900

taagcttagc tataacctct tcttctgttt gataagaaaa taccctgta atatgttcat 45960

agttacctac aatttcataa tcttgtgtac catgtttatc tactaagtat gagttattca 46020

taacatttaa actatcttct gagtaactaa aatttatgtt atagtctact aaaaaattaa 46080

taatattttt catttacata acctctccta tcggatattg tcctagcatt cttgttccat 46140

tttcattata aaaagtatat tctactacaa taatattcat catatctaca tatatagctt 46200

ctatatatgg tgtaatattt tcctcttctt gtatgtgctt acctatgata tcatataata 46260

attctgagtg tattctttta tctctcatta tagacctccg taaggaatgc tacagttttg 46320

tctttcaaag atttttctac taattccata gcatctttat agtgtttgat attagattca 46380

ttatacttaa gtttatcttt tacttcttga attagaggct ctactttatt aaccaaatct 46440

tttttctttt caatacttac attgcttctc ttattgtcta atacttcttt tggcatatat 46500

ttaacttttg caaagtcttt atagctaaca tttaagttat ctaaatcatc taataaatca 46560

ttatagtatt ctaaatgatt atagaatgta taaaacttaa caaggtcttt accagttaat 46620

tctccttttt ttagtatgtt attaatatta ccgataaccg aatatgctat aggcttaaaa 46680

ttagctctaa cataagttaa aaatataaaa tcatcataaa ataaatctaa aacagtttta 46740

ttaaatctag tatttttagc ttgctctaat tgagcacata aattaagaac attatcaaac 46800

ccacttttta gcactaaaga gataaatctt tctactgcat agtatcttga tacttctgta 46860

tgcttacttg ctttttcatt attcctaaat atagtatctg ataaaggttg aacaactaaa 46920

ctcatgtaat ctttatctga atgctcatct gatgttcctt gataagtact tccaaattct 46980

attgttgata ataagaaact tttttctagg ttcattataa catcctcctt ttatttgtta 47040

tttaaataat aacatatatt gataataatg tcaatactta tatatcttct tctgtatcaa 47100

cttcatcttg tttatactta aagtgttcat agactttaaa tagtataatc cctagtgtta 47160

ttaatcctaa aatatatttc atagtaatcc tccttaataa ccatgtttag ttacccatcc 47220

tgctaaagca tccatagcca tatcatattc ttcttcattt ttaattctta taattttctc 47280

tatttcttcc tttgctttct tagaactaat aaaatcaata tcagtatcct ctaggttagt 47340

taattctaaa ttttctctaa taaaattctt ttgacttggt gttatagaat taactcttac 47400

attttcgtga tttagaaatt ggtaaaagtc catattactc atccttttta acgtattctg 47460

ccatatcttt taaaatactt agtacatact ctaaatctct atattggtca tctaatgacc 47520

ctataatagc atatggtgtc atatcccagg catgtgcaca gtcaaaccct aatactctct 47580

taccctcata gtcataatca tcgtaagtga tacctctatg agcacgtctt tctaaggagt 47640

catattcttt ttcattgata tctgaaggta aagttatata tccatttaga tgaccagttt 47700

cagggtgtct cttaacagtt agtttaactc ctttataata aatatcaaga cttaaatctt 47760

ctcctagaat attgttttct ttttctactt tttccataat gtattgaggt gctttttaa 47820

acataatcag tcatctcctt tttatttata tctttactat acactatttt ttctattttg 47880

tcaacaaaaa aaggctacta attaaagtag cctaaatact aattatttag cattgtattt 47940

ccattgccaa taaccatttt tctgtgagaa ctcaaagtga aaaccatcat agtcaaattc 48000

aatattatag tctccatctt gaagtggttt tgaatttagt acaggactat tactctttgc 48060

caattctgct agaaactcat gatttacttt ttccataggg tttactcctc ctaattattc 48120

ttacagtact aatatatcat aggtcttttt ctaagtcatt tttaaaagtt tcctcgtagg 48180

aactagcgta agtaacctca taacccacta cgttagtata tcctacatat aatgacttat 48240

aattagattt tatcttaata tcttctgatt gttctagctt atttaagact tcatttaaat 48300

catctgagga atagtgttca ttatctattg ttattgtttt tccttgggta tagatatcaa 48360

tttcttgtat catcatttca tccttttgat tattcattat ttgattataa gtttctaaat 48420

catcaatgtt atctgtatct gaacctttta ctaaccattc tcctctcttc ttaaggaggt 48480

catcaaactt ctcatgctct ttaattatct tttctacctc acttggtatt aacacagccc 48540

tagcatagtt tatatgccac atagacatat tatcaataag ataattaacc attcttataa 48600

tctctttttc atttgccata taccaacctc cttatatcta ttattaatat aagagaaaag 48660

cagacttatt aaaagtctgc ttctttacct aattctaatc ttctattttt catatgagga 48720

atcgtttttt tatttcctgt taataatgat aattctctag ctttttcttt agataatgtt 48780

agtagtccat tataattatc tactttacta ttatattgtc tgactaagta ctctagttca 48840

tcttctatac ctgctagttc tcctgattta actccaagta actttctata catgtcataa 48900

tcttcagaaa gactttctac tttgttttta gatacagaat cataaactgc ttgtaaatta 48960

ccttcttcaa taagtttaaa attatattca ccaatgatta attctttttc agaagagtca 49020

agggtaacta aaccacttgt attacctgta aagtcacctt tataatctac aacaattcct 49080

tcagttattt tatctcctaa ttcaatagtc ccatcttcat tttctttaaa tttatgagca 49140

tcataaactt ctactttgtc acctaatctc aaatcttgag ttaagttatg tttaccgata 49200

attctatcca ttacttaacc tctcctttat taatagggtc ttgtgttaag aacatttcta 49260

agttctcttt tgtaataggt aaccaaaaat atttactttc cggaattgta actgtataga 49320

agtcttcatc attattaact ttgatgttaa catctgtaaa ctcatcttgc attaaccaat 49380

gagttacagt taagttatat gacccatcac taacataccc taaatcaata tcatgtctaa 49440

aagccaaatc ttctaaatgt tctaataaat cattcttttc attatgtttt tcttcttctg 49500

tattattttt aattgggtta attaactctg tacaaacgat atcgtacaat tcaccatctg 49560

taacctcata gttcttttca attaatacat cttgtatttt attgattgaa tttgtaacta 49620

ctttcccata ttcttcttct gtaaatttac atttatctaa atcaacatct gtaattaatt 49680

ctgcaatcca tttatttaaa attgatactg ccattgttct agaaataata ctatcgtata 49740

ccatatttat ttaatctcct tatttaggtg aatgtggtct tctaatgaaa aatcaaaagg 49800

cgctacacca tttcttttat tatttgtttc ttttttaagt ataacataag ttagtgaaaa 49860

agtcaagata gttactacag ctattgataa aagtttaatc gggtttttca tagttactct 49920

aactccttaa gtttattttt tactttctct ttatcgtact tataatcttt actagagttt 49980

tcatttttt ctttctcttc ttcattaagt tctctatact gagcttcttc tacctcttgt 50040

tctttattat cgttattttc ttctgctttt tgaatttcta cattttact attaccacca 50100

tttacctttt ttctaaaaag aaaccaaagt attaataaaa tgatgagtaa aataataatg 50160

cttaatacaa cagcccaaat attattagcc attacaacct acctccgaat agtttttta 50220

cagctcttaa attttcagat gaatcgttat ttatatcaat ccctacgcta gaatcaaaaa 50280

ttacagcatt atcaagtata tgctctgtta atttattacc ataactactt ttacttacca 50340

cactaccata accatgatta gttaggtcaa ccatatcagg ttcaacttct agtactctaa 50400

aagatattct acgtaagaat gaaggattta ctaagtaaaa ggaagattta aaaacattta 50460

atctttgata agaatgtttt atattaacaa caaaccctgt taacttatct tcataccctg 50520

aatttgataa tttacctaag taaaggttta tactatatcc ttttgtttct aatgtttgaa 50580

tagcacttaa cattatagca cctctataag caagattttc agggtcttcc ctccaactaa 50640

tactagaatt ataaaataca tcaataactt tcttctctgc tttaactctt tgctgagaca 50700

tcatagaatt aggtaatcct tttatagcat taggtacgtg aggttgatat ccttccggag 50760

ctacgacagg ttttcttttt actgacttat ccattctaaa taatgcatct gtcatttttt 50820

taagtttaac taccatatca tatgactctc tatcaccctt aaccattaag ttataggctt 50880

cttgaaaact atgagtccct gtaaaatcat agctacctgt atcggatgaa ttatctctac 50940

ctgaaactct attctttttt aaagcagaaa agaaatcagg tagaccatca tatttaatta 51000

catttaattc tgagttatct attaatcgtc tacccattga tttgcctcct attctaatcc 51060

taatttatcc ataattgtat caaaatccat tgaatctttt gatgtactat cagattttct 51120

aggttcctgc ttaggctctt gttgcatacc taaaagcttt cttgttgctt ctgtgtatct 51180

gttaccttca ggtaaagagc taataaattg attaatctca tctttcggta cagatttaaa 51240

gataatactt tctacaacaa actcatcttc cattactcca tctaatttac taccattaat 51300

aattgcacgc attgagaata cataaggtaa tccttttca tcattctcat gtcttaattg 51360

ttgtacaaag tttactaggt cttcattgct tgatagttga tgttccacct tagtatcata 51420

gtcaaattca acttgagcaa agcggtctaa tgtagctccg tctaattgtt gtctacctac 51480

ataaatatgg tctgctcctg ttcccatagt attacctgct gacacaactc tgaaatcttc 51540

atgagctgtt acacgtccaa tagggaagtc aaagtattta tttgcaatag ctgaattaag 51600

aattaatagt acttcaggaa tagatgcatc catttcatct aagaagaata acccaccttt 51660

tgtaaatgct ttatagaatt gagtttcatg aaacttacca tttgcatcaa taaatcctgt 51720

taatttaaat tcttgcgtaa ttgcattact aaaatagaaa tctaaatcta gggcttctgc 51780

tacttgttcc aatacatggt tcttacctga acctgctcca ccttttaaaa atactggaat 51840

attttggtta actagcttta gtatatcttg gtatctataa tgaaagattc ctgagatatc 51900

tttaattgtt tttccttctt gttgtaattc aattttaact ggtaaattac taagttgttc 51960

ttctacatat tcttcaattt gtttttttaac gtcagtaata ataatttctc tactctcagt 52020

tcctgctttc tcaacaattg catctacaat tgcttgttcg tacggattag agtttttctc 52080

tcctagtttt tttgctaaat ctgctgttgt ttccatttgt tgctctacca atctctctaa 52140

tctttcaata gtatcttgct ttgccatatt tatcattctc ctttgatttg ttatacattt 52200

attatattac aagtatttga atttgtcaac aactttctaa aacttttttt agttgctaat 52260

aaaaaaatac cttacaccta taacttaaca tagggtaagg taattgtcaa cacttttgtt 52320

aaaaatacat taatttaaaa aaatcatcaa tatctttagt ttcatgtgta tccatatcat 52380

acataaacat acaattatat gtatgattat tcattatttc taacatgtta tgcatagaag 52440

ttgcattatt gaattcctct aaatcaatag ttaccgtaag ttcttgacct tcataaagta 52500

tgtttgctat ataatatttc ttaacacctt ccattgttcc atgagaagtt tcattatgat 52560

taagtacttc tacacctagt gaaggtaaat attctgaaaa gtaatattta cagaaatata 52620

taaaattgtc tgttctttta gacacgagta ctatctccgt actttatatt tctttctaat 52680

cgtacataat atgttttaat tttttgtact tctttatcta ctgcatcctt tcttcctaac 52740

cttgtagtat attttacaat attaaatatc atagaatcaa caaagccatc ataagaaaaa 52800

tgttcttcta gaaaagaaat aacatccttg ctacctttat agtgctcagg taaatgtgca 52860

tctacttgta tattataata attttctaaa agacctatac tctcaccaag actagacaaa 52920

gcgtaaccta aatcatttga atcattagac cattccttag atactgatag tgcatcttct 52980

ataattgtta cttttaattt atctaaataa tcttctactt gagcttgtgt tttcataaat 53040

tcttttgcgt tcatgtaata ccctcctaaa ttatataaaa aaacaccctg cttggctaca 53100

agcaaggtga aaaaggaaag atattatgga agtgtactat ctaagtacac ctcataatat 53160

aacagttttc cttgctagtt attacttatt ttttaaggtc ttcttctttt acaaacactc 53220

cattaataag cttacctttt ctgtctttta tctcatcata agccatatca atacactctt 53280

caatatctat atctaactgt aagcatagta ctgttaatac tacaaaaata tccccaacac 53340

tatctcttgt tacatggtca ttacttttag caatacctga agctaattct cctgcttctt 53400

ctaataattt tagcatttga ccctcgggtt tacctgtttg taagtttcta tcttttgccc 53460

attgtttaat aagttctact ttttccatta ttctatatct cctttaattt ctgtatcttt 53520

gataattagg ctatcagagt cacttgttac atttaaatta tcttcaacta attcatgtaa 53580

attattagta atatcttctt catacctata acctacacga acataagctt taactctgat 53640

atctatatta acataatctt cttggaattt ttccatttct aacttccttt attgtatcat 53700

attattatac tattgtcaat taatctgagt agtttccttt agcaagttga tacttttgt 53760

gtaattcttc atataattct ctcatacctt cgtagtttct catatcatct tccaagaaac 53820

taagataatc taataatact tttacatcct caggttctaa agttataact ggttttacca 53880

ttaggcaacc tccttaaatt cttctttatt tattttctta atatcttttt ctaatgcttc 53940

ttttaattca ttaggtaatt tataggcatc aattgattgt tgttgcccta gtacatatcc 54000

attatctgta atacgtattt caactgtaaa ccatgaatta tctaaatctt cttctagtct 54060

tgctaacaat attaagcaac tgttctttat aattcgatta gcatacccgc caacacaatg 54120

agatagcatt ttaccttcat ttttcagttt acttacggta tctgcaggaa ggaattttac 54180

ttttctacca tcttttaatt tataagtttt atcaattatt ttttctaatt tattttcata 54240

tttagattta agctctgcat catctaattg ttgttgaata gattgtttct cgtctgtaac 54300

tatatcatgt tctaatttta gagagaatgg tgttaagtta acactttcta atgttctata 54360

accttctcgt attaatattg ataaatcatg aagataatct aaatagtagc tatccagtgc 54420

atatcctgtt atacgttgtc tatcttgagc atctacatct aaataatgag tcatttttt 54480

gtaattagca aaagatatag ataatatttc atttacaata ggttttactt ttaaagcatc 54540

tgtaacattt cttacatcct gaaccattaa aaatgtatca tcaaatagtt gatgtagatt 54600

aacttcattg tgtaaatgat tatagtaatt atacaatgta tctgaaaatc ttaaataatt 54660

actctgttca aaattattta atgttagtaa ttttttatac gtttgctttg taagattaaa 54720

tgcttcatgt attttccact taggattttt aggtatatga aatagtaatg aatttctttc 54780

aaataattca aattcctcta agttatttat tttgtcaata tttttaacaa tatctgttaa 54840

gattgttaag taattagaag ttgaattttc tcctttgagt ggtttatatt tgtttcctcc 54900

ataatttaca cgcccatata catcaacctc atcaaggcac caactagaaa gtccaaaacc 54960

atcatttctt aatgtttctt caattatttt aataataaca ttcttactta aattaggtgt 55020

tgaataattt tttaaaataa catttaataa aacagccaaa tttaattcat ttttatattc 55080

acttttacta atatcgtctt tgtatagatt taaagttatt tctttattaa caagactgtc 55140

tgttaagaaa accttaactt ctcctgtttt aacatcaaat gaacttttat tttctaaaac 55200

ccatctattt cccatattat atttatctct aatgtgtcta actttaagac caaaagatga 55260

actattctca gtacttggat gcatgtacca agtactactg tacaatgaat ctgatatttc 55320

cttataatac ttactagagc ctttttctgt atcttcatta agtctggaag taatagatga 55380

ctttattaaa ccgtacttac cttggtataa gatatccata atatcattat tcaaactatc 55440

tactacttcc ttatactcat ctaattgtct agattcatac caccttaaac gggtttcatt 55500

ttctaattct ttaatttttt cttctacata acctttagat tttatttgtg ttatacgttt 55560

actaccatat aaaggaaatt cttttctttc ttctctactg gatgcaatat attctttgta 55620

acttcttcct ttattttctt caattacacc ttcaactaat ttttcaattg tttcataagg 55680

attacctgta aagtttgtta cttctttatt accacatagt gctaagaata aatgtatttc 55740

tgtagcagta tcaaaactaa atatattatg aatatctcta aatagttcct tagagcctaa 55800

gttaattata ttatttttct tcttcttaag gaatacatct tcttctccta tatagataca 55860

tcctttatta actttaggta aattaataat ttcttgttct gttaatcctt tttgtttata 55920

tgttattgcc atttaaaatc actccttatt tgttatgtac taatcatacc atagtaaata 55980

atatttgtca acaaaaaaag aagaactttt taaagttctt ctaagtgagt ttcgtagata 56040

acctttgaa ttttatttaa tggtttcaaa tctaaattac gaataagttt ttcgtacttt 56100

ctagaatttt taaaattgat agtatttggc atagcaagag cctcatcaat gtctttagta 56160

tagcttataa catctgaata aatatctact tcttttacat atagaccttg agttaaactt 56220

ttaaatacta cctcattatg tgctacaact tcttctttct tttctatgct cattttgta 56280

aacctcctgg tctattctac acaaacaagt acgtactcta aactagttaa tgttactgat 56340

ttaatattat ttaattcttg taatttctta atatctacac catagttttt acttatagtc 56400

cataatgtct ctcctgctct tactttatgg taatacttat tcccttcttt aataaggtca 56460

ttcaatatta cctacctcct tgagtaatag ttagcttgta gataacatat aagtataaga 56520

acaaagttta caaattcagt agctataatg tgaacataag tatgtgataa aaccatactt 56580

aatattaatg aagctaatcc taatccaata ataaggaata gaaatctgtt tgttccttct 56640

gcacttttag ttttatagaa tgttgttatc tgagttacat acgcaaggat aatagtaata 56700

gttgcaatag tttgtgttaa ggctgtaaag tcacttaata aaaatagtaa cactgagaac 56760

acaataataa aaggtataga gaaataatcc ttttttctat acgaagctac taataagcaa 56820

acaataccaa gagttaaatt aacaccaact gatactactt gaaacattgt agcgtcagtt 56880

ataagtaaat tgtaaaagct aatacctact gtagctacaa ttaaatacca aaaataacta 56940

ctaactcctt taacactatc tgatttaact aaagctatta gacctggtat ataacctact 57000

gtaactaata tagcatataa tatacttaag taatgtgata agttatccat cttgtcctcc 57060

taatttctct agtcttttta aaacttcttc ccaagaaata aacccttctc cattagttag 57120

gcttagcaca catccgtaaa taaattggtt cgtactaaat tcagccctat cagggtcatc 57180

ataacctttt ccatgtcctt gacgaatatc agagcaatag attaaaacag gtttatttac 57240

aatattataa gcttctaaaa tatcatattg tgttaagggc tctaagtctc taaagtctat 57300

atcttcatat ttatcaataa ttttttgagc ttggtgtttc attcctaata aaataccaag 57360

ttctgcaatc gttcctagcc cctcattaag aatgtcaaat acaaaaatat ctgattcttg 57420

catagcttta aaatcattgt ttaagatacg ttcagctaat ccagtttgtt ctgcattagc 57480

tttatcgttg attgatttgt cctgatgagg gctataagga gttactccta caataccctc 57540

tacttgttcg tgttgtttag ttctatattc taccatagct tggttaagta gatgacctcc 57600

catgtaacaa accttatctt tagtataatt aaccatctat agtatctcct ttttcttcta 57660

gaatacctct taaaatgtgt ggcatctttt tcttaatttg tttttctata attttcatca 57720

tattttcttt ttcttcttcc atgatatcat caacaaaatt ttgacctact tgtttcataa 57780

ttaaaccaaa attttccaat tctaaatcat ctttagacaa tctgttttct tctatagctc 57840

taaaaatcat tttttccatt cttgattttg tgatagcata atctgctaca gaatcattac 57900

ttctaacttc tgatttcatt ttcttacgac taaactcttt aaattcctta gatactaatt 57960

taaaataatc atcatgttct gatttaccat ctaaatattt aataacaata ccttctcctg 58020

tattaggttt aacagtcata tctgattttc ctactaaatc ttgaatttct tgagggttta 58080

atttattaag ataaaaagat ggttctataa tcattaaagt ttttacagtt ttcaaaccta 58140

atgtttctga taaagaaatg acttctgaat aaggtaaata ggtttcacta tccttatcgt 58200

atacatcgaa tacataaaaa ttattataac actcttcttt ataatttacc ttatgtttaa 58260

ctaaccattc tccaaatata ataatacctt ctaatataga taaatctaat ttatctgtca 58320

tgttttcatg tacccaatta taaaaaccgt ttaatgtttc gttttcattt aatttttttc 58380
tacgagagaa acatactaac tcaccattct ctgtagtaaa acttgcgttg cttccatcta 58440
atttttcttg aactacaaaa cctctatctt taaatttgtc taaagataat cctttatttt 58500
ttactttagt ataagatttc attaattagt tatcctcctt tgaattatgt actattgaaa 58560
ataaaataag acttacactt gccaaaaatg ctaatactac taaaccaggt aaatttagaa 58620
ctgttgataa gaataatgct actgcactta taacataaac tagaccgcct aataataaag 58680
ttaataatac aattgttata agttttacca accagttatt attaataaat actttagcta 58740
aataattcat aaaaaagcct ccttagttat tataatataa gtataccata tctaaggagg 58800
tttgtcaaca tattatttta ccatttgaaa ttatctgcgt attgggctaa cttagaacgg 58860
aaattaactg taaaattatg gaatactgca ccatcatatt ttttaaaata ctccatgtaa 58920
tccccaaaac ctgatttact ttcatttttt aaatctattt gtttaaagtt accttctact 58980
attacagtag aatttttgt atgaaccctt gtaagaactt ttttaagttc actacgttta 59040
aagttctgtg cttcatttat aattatagta gaatctctta gatttccacc tcttaggaat 59100
agatgtgata tttgagatac ccaacaatct cctagtttat cttctttaac attatcttcc 59160
atcattaaca tttcagttat ttgttgttca ggattcatat taagttcaat aagggcatcg 59220
tgtaatccca tgaaataagc catttctttt tctgtctgat tacctggtct gcttcctaaa 59280
tcctctgata ctggtgaaat tataaatact agctttctat ctttattaag atagtctgcg 59340
taagcacagg ctactgagca cattgtttta cctgtaccgg cttgactctc attccaaagt 59400
atttcaacat tatcattaaa gaaatcctca cagaaatcta actgctcggt tgtagctttt 59460
tcaaggaatt cattaaagac tagatgttct cccatgttgt atcttacatt aggataatct 59520
tttaacttaa agtctaactc ttttagttgt attgccatat tttaaagttc ccctatctat 59580
aaatagtttt actctctttt aatatagtac taatttccga tatattctcc tgttgaagag 59640
caataattac tacattcaca ttcagggtag ttatcacaaa cttcttcgtc ttctacatca 59700
tcataaccaa tatcataatt attataatta aaatctacaa tacaattttc actattacct 59760
ttagataatc ctgtataaat aatatcatcc acagaatccc aatcgttatc tgccaaataa 59820
tttacgctat ctaatactga ttcattatca ggtaaataaa tactaccgtc tgaaaattta 59880
attagaatat caccttgagg taaagtatca ttaattaaat caatctttgt ttcttcttca 59940
atagtgaata cagttccttc taatctttcc ggtgtagtat gcgttaaatg ttttacagta 60000
tctcctgatt cttcatagaa tcctactgca ttcatatctt tattatattt tgcaataaat 60060
ttaccattgt cacttaccaa atattgacta gttgaattat agtcgtttgc gtcatctact 60120
gtcatgcaag ggttataatc tttaacataa taactaattt tcctaacatc tgttgtttgt 60180
actttcttac cttcaccttt aattactgaa ttaatttttt tcataatatt ttctcctttt 60240
tatatatcaa ttgatttttt tgcaagatta tcggcatagt cattccattt atcatttgaa 60300
tggctcttta cttttacaaa atttatatct attacttttt ggtattctct tatcatattg 60360

atatatgttt tacttagaat atttcttgca gaccaagtac cttcatacca atgtattaaa 60420
ccaatataat ctatataaac tattgcctga ttgtatccta gttttatagc ctcttcaata 60480
ccataacaac aagccaatat ttcacctgca acattattat actttattaa tcctggtttg 60540
tcaacacttt tactaatttc cgctattata tttccttctt tacttaccaa gacagcacct 60600
gagcctactt tacctttatt atatgaggag ctaccatctg tgtatatatt tacactatcc 60660
tgcatattta taatcctcca taaattgagg gaattcacaa tctgagtata cttctctaca 60720
aaaagatact gagatataat taaaatcaaa acatttgaaa cagtgttctt gaacttcttt 60780
tttatcttta gcaatcacat taaatttaaa accatcagct attactgtaa atactccttt 60840
tttcataaaa caaatacctc caccaatttt attttaaatt aataactaat tcaataaatg 60900
atttaatagt tttattttta ccttcatcaa tatctgaaaa gaagttaatt aaactatcat 60960
cctcatcaaa taaatcttca acatcatcaa atttatttaa tatgtctgta acactataac 61020
cttcttctga tatatactca tgcaagtctt ctccatcttc tgacagtgtt gcttctattt 61080
taccattttt actttcaatt aaatataaag tatttaacac tttaacagaa tctacaacta 61140
cactgtagtt actaatagta ggatattctg tataaagtat ttctacatta gtattcatat 61200
aactatcaat tacagagtta actgtatctc tttttagctc agatacatta tgttttcgta 61260
tagtagggaa ttcttcatca tattctacta attcttttct atctgtgttc aataacttgt 61320
ctaaagaaga caacaatact attttatact ggttatcagg gagactatct gtaatttcca 61380
ttattgttaa aaacgtatct tcacctagaa ctttgtttat atcttgtaac tcaaatgaat 61440
ctaccatttc aatagtatca tctatatcat ctgtagtcat taaaaaatta actaaattat 61500
tattctccat catcttcctc caattctttg aataactctt ttcctggagt atttaacgct 61560
ttctctaacc gcattaaatt agcgcttctt ggtttctttt ttccatactc ccaataagat 61620
ataagagagt aatgaacacc tatctcagaa gctaggctcc ttaatgtatg tccttttttct 61680
actctaattt tttgaaggtt tagaggttta ctttcctttt tttcatccat aattatttct 61740
cctctacttt taaaaattta aaatcctcag atgcttttgc atttttagt atatactcgt 61800
gtgacttatc tcttgcctct gccttgcttt tagcatataa ctctatatga aatacatgag 61860
gtttttttaa agacggtgat tcatatctcc aataaacttt aaaaagtagt gtttcttttt 61920
ttaaaacatt aattcgaaac catcttttaa atttattcat tcattatcct cctttattta 61980
tttgttaaac taattatagc atagttaact tatgaagtca actataatat acaaaaaaga 62040
ctaagaaatt aatcttagtc taaatcgtta ctaatagttt ccgttggcat tatggaagtt 62100
taaagctcct gatgttgaac cgtaacggtc aatcatatat tgttttgcac ctttagtttg 62160
ttctgctata gaaccaccac tccatgattt acctaatcct tggaataacc cttgggctcc 62220
tgatgttgga ttaacagcat tcgggttcaa tgtagattca cgcatagcaa tttcaatcat 62280
tgcttcatct ccgcctgctt gtctaatctg ttctgctaca gaaccacctg tacttttagt 62340
agctgtagtc ttagtttcta ctttaggagc ttctactgac ttaggagctt cttgagtagt 62400

tgtttcttgt ttaggttgtt ctactgcttt attttgtgta tcaaattgtg cttgttgttg 62460

gtctactttt tgttcaggtg tttgctcttc tcctgctaat ctagatactg tattatctac 62520

ttgagttgaa cctgaatgat attcataacc aaagttacca ttataattat agaaatgata 62580

agtaaattca ccatcactaa atgagaaatc ataattacct tcttgaattg gttttgtatt 62640

aacttctact gaatttgatt tagcttgttc tgctaactta ttatagtcaa tttcgtctgc 62700

actagcttcg tttgtagcca tacctccaaa agtaatagct gtacctaatg ctaatgttgc 62760

aaaaattgtt ttcttcataa atttaaaact ccttaaataa ttttttagaa ttgtttattt 62820

gtaaaccgac ataagtaatc ataacatata tctttaaata acgcaagtat aatatagcac 62880

taattagtgt aatattatta aggttttatt acaaacatta cagttatcag ataattaaat 62940

acaaaaaaga gaggtattaa cctatctaat ttattatttt cctgttacat ctacaatagt 63000

tccgtctccg ccaatttgaa taggttgttt tccatcccat ttttcaatta gctgttgttg 63060

taaaacttca tctgttaatg attcacttct gatatcatta gctttcttct caccttttgc 63120

ttctacttct tttttcttag cattttcttc agctatctgt ttatcgactt ttgtacgttc 63180

taattcttga tttgctttta ctctttcgtc aattgctttt tgagtattct tatctgcttt 63240

aggactagat aatgcaatat cttcaattac aaatccttgt ttttctaaat tatcatttaa 63300

gctatctaaa gtatcttttt taatttgtcc tgttttaaca ccaaatgcat caattactga 63360

gtacttagat actgattgac gtacattatc ttgtacacga gaacgtaagt aacctttttc 63420

taattcttca atgtcagcac taccaaaacg attaaataag tctacagctt tagttgcatc 63480

tactttatat gaaacatcaa tatccatttg taaattctta ccgtctgaag ttgccacgtt 63540

taaatcttta tatttatgtg tttgtgtttt agttggatat ttgtttacct tatcaaaagg 63600

tgctgttaag tgccaacctg gtgatttagt atcttcctta acaccattta ctgagtacac 63660

aactccaaca tgaccttgtg gaatctttgt aatacacatt aataaaataa taaatcctat 63720

aattgctaaa aaccctatta ctcctgaaat aactactgac ttcctcattt acatttctcc 63780

tttttctatc tcttttatta aactatttaa agcttttcc tctttgtcta tttcctgttt 63840

gtctgctttg gtaacaagag attgcctacg gtcatttaag aattgttttt tatattttac 63900

atattgttct aaaccgtatt cttctaatgt accttgccta actaattccc tgtattgttt 63960

tcttatgtta cttttcttct ctctcattga aagaaaatca aatacgtaac tcataccaaa 64020

acctacaagg actagaaaaa caataaaaat agcaaagtat gttaaaaata atgccatgta 64080

attcctcctt tatttgatta catatataac tatacactat gtattacgtt ttgtcaacac 64140

ttttttgcaa aaaaaataga cggatttaaa atccgtctaa atttatactt tatttaaata 64200

ttgttatact tttagtttct tcatactctt tcaacattct atctctaaga tttattgctt 64260

cttttatact atctacttga tatgattggt accttatatt atttcttgtt atagaaactc 64320

tatatttacc attagttctt tcttgtatgt tttttaatcc ttctagttta gagggtctat 64380

taactatatt ttcacttcta gtagtccatc tacaattttc cggagaatag ttaccatcat 64440

tatcttttct atctaattgg tatttatcag aaggtctttt acccatatca tataaaaaag 64500

attcgaaaga gtttttccat ctatcacaaa cttcaatacc tcttcctcca taatatggat 64560

aactgtcttg atttttgtta tagcatcttt ctttcatttt tctccatact gtatactcag 64620

gatgtttttt agaaccatta cgtgatttca tacaaccaca acttttataa tagtataatt 64680

gacttttaga taaaactcta tccataccgc aatcacataa gcataaatat aatttacctt 64740

taatcttatc tgaacctaca tattcttcaa caaataattt ttctattttt ttacctataa 64800

tattttccat aaaatctctc ctttgaaaat attataacat atatataagg ggtattgcaa 64860

ccccttttatt tattaacctt tgaatacacc ccaggcaact ccaggtacat gtgaaggtgg 64920

aacaccttga caagttctaa cagggcaata tactctgtta ccattgtaag cattataacc 64980

tatccaaata tgacctgctt ggatacaaac ttcgtcatat acaattgtag cccctgccgg 65040

taagttaccg cctactggag catttaagaa tggagaacct attctagtta ctataggttg 65100

gttaccatta acaaatgttg cattttccgg tttataccaa gttccgtact ggttcttttt 65160

ccaagagcct gtaactggtc tagttgccgg tgtacttgcg ctacttgttt ttccatcttt 65220

aactactgta gaacttgaag tccctttatc catgtagttt ttaatttgtt taatgaaata 65280

atcttttaat ttattcatta ttgcttgtga tggtcttcct tgtgttactg gattaaatcc 65340

tgtatgaaga accatagaac ggtgagggca ggcagttggt acaaattcca tatgcaatct 65400

tacagtttta cggttaggag taagacccca ttctttaaat ttctccgctg taaattggaa 65460

tactgcttgt tcatttttaa ggaattgagc atcactagca ctcattgatt gacagacttc 65520

aatacctgca aatctaaagt tacctgagtt tgctcctgtt ccatctcctg tgtgccaagc 65580

aatttgattc ttagcatcta ttgcttccca tacataacct tcagagccgt agtaatgagc 65640

aataccatta gcgtatctag cataacctgc attagctaat gaattctcgt attgttgtcc 65700

tgaagaacga cctgcatcgt tgtgtattac cattccttca ggtttttac cacgtttatc 65760

cattgtatag ttaatgtgat tcttagaaac ttttagtgtt gctttctttt taggtgcagg 65820

agttttactt gcgcttttct tagctgtttc ttttttaaca gtagttcctg cttttacagg 65880

tatttcaatg aagtgagtta atccgtaata attatctaca cgttttgtag gttttttatt 65940

agcataacca ttccagtttt gctctaaaat agtaaacgta gaagtattac ctccatcata 66000

tacaatacct atgtgacccc actgttcata actaccggat gtaaataccg caatccaacc 66060

ttttttaggt acagtagaag gtttattttc atgtatttta aatccagtac cataactctg 66120

tttaatttgg tctttagcat taccccaagt tctaacttta ttatctgtta accataaaac 66180

atagtctgta ataaggtctt gacactgagc gtgatagtaa ccatctgcgt caatggctcc 66240

tgcttccatt acaccaaatg atgggtcata acttgtagct tttttaactc tgtaagggct 66300

atctactgtt ccttttgcat aagcgtctaa acgtttattt atttctgctt gagtcttagc 66360

cattacttaa cttcctcctc tgcaaatact ttaccatgtt cctcggtatc ttcttcatct 66420

tgagaaggtg ctgaaccacc atcaatttca tcttcaatag caggtacttc atcactatca 66480

tctgtgtcag gttctgcatt gttttcgtag ctgtctatct caaaagtact agcgttattt 66540

gcatttgctt gccattgaac gaattcatta gggtctttac tatcacgagg tttaagatag 66600

tctgtttgaa caatatcact atctttaaga cctttagtat tattatcaac aataatacct 66660

aaacctgcta atagtgttag tatagaacct acaatattta caccttgctc aatttgagct 66720

gagtagtcta aaccgaaagc acctgtaatt tggttagcaa ataatgctac tgctgatata 66780

attgctaccc aaaatgtttt gctcttagtt cttgtgctaa ggtttattcc tccaacaact 66840

ttaggttgtt tagtttcatt agccattaaa aaaccgacct ttctattata tttatttcta 66900

acaataatat aacagtaggt cggtcatgtt tatctatatt aatttaacac ttactcatta 66960

atttggttta gttttttgat aacttcagac atttgtttgt tatctaaatc ttctaattta 67020

gtttcaggaa gtagctctaa cttatcccaa acttcttctt tattagatac tttattatta 67080

ataattgcct taccaactaa actttccgta taatataatt gttttgctga tgccatttgt 67140

atctctcctt ttaaatatgt aaagtatata gctagtatcg tatcctagga acaaacactt 67200

gcgctatata ctcaatgaaa tcctaccctc attcgaggac acagcaaacc ggttcgtcaa 67260

ccgcacatat gaattctcag atttcattta tgtaaaacac accctctttg atttgcacaa 67320

agactaaggg ttttggagac ccttgtacta ctaattatac taagggtgtt tattatggtt 67380

tctattggat ttgaaccaat gacacctaga gcttcaatct agtgctctac catctgagct 67440

aagaaacctt aaaacgaccc atacgagact cgaactcgta ctctctgccg tgacagggca 67500

gtgtgttaac cagttacacc aatgagccaa aattataatg ctatacccta accttacctt 67560

aatgtatagc aggtttttat ataagctcga agcaacgatt attaccactc ataacaacta 67620

tatattaagt gaaaggaggt gaaatgaaca aaacgtggta attggtactt atataggaaa 67680

tatgtataat ctacaaggag taagttattg gttcataaag gagtgtgaac aataaataca 67740

tgaaagagtg aaagtttact ccctgtagat tctttttaa ttatcaatca aaggaggaaa 67800

ctgataattg ttaataataa actataaaga ggaaaatatt tatagtcaca ttctgatata 67860

atgcaactaa atatccaagc ataacccgtc tcacgaggaa cctacctata agacctgtta 67920

ttaagtgaat cactacgatt gactctatta aggagctacc ttaagtccat ctcacgcaat 67980

ttaaaaggga cttacaaacc gtaaaacggt aataagttta ttaaataatg tgatattaac 68040

atattagtta ataactttca catggtcgaa gaaaagtaaa tttatttgat taccaaatta 68100

tttttatcaa atatagctct tttgaacctg tagatttatg ctactcatac tgataacctc 68160

tattatctaa cacatttctg tgctccaact acagttagtc gttacagcgt atctttctag 68220

gattccgcta agaccctaga aagaaattaa accctagccg ttatcatact ctacagacct 68280

tataagtaag taccaagtat accaatcgta tttaacaata ctaatgacga cccatcctac 68340

cgatatatct ccgataggtt ttgattcgtt tgattatctt gtaccttatg actaccaaat 68400

cattattcag tcactatgct cagatattta gttgtattat ttatatatta attataacat 68460

aatttttatt acttgtcaag ttaattttaa aaaaaattat agaagtaggg acgtttacct 68520

acttccattt aatttacaca aggatgataa cattgttatt gttttatact ggaaaacaat 68580

gtaataaaaa cagtgatgtg taaggtattt gttttattgt taattacatt atagcatata 68640

ctgatacctt tgtcaagtta atttaatact ttttttaaaa tattagttat cttttgttaa 68700

ttcttcctga atagcatccc atcttctttc tgcttcacta cgattatctt ctatatgctt 68760

tgtagtttta caacatttaa tacaatatat atctttgata tgaccttctt ctcttttatt 68820

tgctcttttt cttggtactt tgaatacatt tccacattct ttacatatta aacttgagta 68880

aaacattttt tgtcttttca taattaatca attccttttc tcttttattt gataatttaa 68940

ctatatacta tactgataaa taagtcaaca gttttctaaa aaataattta aattattttg 69000

aagaatcctt taatatcagt acttacaaga gaaaaagtac gtatttagaa aataaggagt 69060

actcctatta tatataatta tattctgata tacagtaatt aataatatta aatatataat 69120

tataattaat agggttggga aaattgatat aaacataact gatactgttt ataaatactc 69180

agtataaaag taaaatccct tagtatcagt acttacaggc aaaaaagtac gtatttagaa 69240

aataaggagc tctcctatta tagttatata tatatattta ttactattat taattactat 69300

ttaaatatat aattataatt aacaatgtta gaaagtcaac aatagcataa ataaaaaagt 69360

gactacttaa agtcactcaa taattagaat actattttaa aagattctat tctgtttgga 69420

ttaatatata cttgaggtga agttatagca ctttcagtat atacttttat agaggtttca 69480

tccattcctc ttaacatata atctatatct tgcctattgt aactcttttc atcagtagat 69540

actaaaaagt atttagctcc acttgacatt gttatttcaa tatgttttga catctacaat 69600

ctctcctatg caaatttgtt aaagacaaag gataatatag ctcctagaac aagtaaaaga 69660

accttctcag ttgtatcctt tttcttagta tccttagttt ttgtactttc agcaagttct 69720

gaaatctttt catcaagtct ttctaattgg acgtaaattg ctgattgttt ttcactattg 69780

acagctacat ctttatctat actaactatc atttttctta gttcagctac ctcaacttct 69840

aaatctttga aagttcctct atctatataa ttaccttctt gtatcttaga cttaatagtt 69900

tctacttgag aaacaaggtt gtttatctcc ttatccaact agaatcacct ctaaggtcta 69960

accgtttcag attcagaatg gatatcataa ttttctaaga aatcattgat aatctccata 70020

taattatccg taacgacttt tccgtaagat gtttttgtat caatttcgaa tctaagttta 70080

ccgaagtctt ggaggtctaa ctcttttatt acaatattcg ggtcatcaga aggaaggtaa 70140

taatagtcga agtatataat tgagccattt attagtagac ggtctattct atacatatga 70200

aagaatcttc tgtctcgttt gaaatgagct agtgaatctt taaactctaa cttaagtata 70260

tccttatatt tagtcaaagt ggtaacctcc ttactattaa tttttaaatt tacttatttt 70320

gtgttataat agttatgata aaggcagtta ttataattat attaagaata aagataataa 70380

ttatttttc tgagaaaata agccaaatac tacaaacaga taaaacatag atagctgata 70440

gatatactat attaatagtt accttacttt tatcttttct atagatagaa taacctaaag 70500

aagttgtaac accactaagt ataaaataat agaaacaaaa aagaggtata gacagaaaaa 70560

aagatacgat aatcattgtt aaacacctat ttctttttga cctattattt ctagaacttt 70620

tagattatac cactaatata acattaaaag ccagtcataa aagtcaattg ttagattaat 70680

aatataataa aaaaagacaa taggaggtta aagtggttga ataataacat agctatattc 70740

atattcaaaa cattggttat cattatattc ttactgctat ttttgtctgt tgttaattcc 70800

ttatccctta tttactcaat aagaccgagt gtagttatgg catactttac ctttggaggt 70860

attgtttctg atgtcgcact tactatgaca gataagttct tacttaagaa agaagaccct 70920

ctacctgagt atgttcttaa aaaagtagag ataaatgata aagaaataag cataattaag 70980

aaaatcatag aaagtaatta tgatataaca tcagaagaga taaaagttag agctaaagca 71040

caacagagat tagaggaaga tagcaaagag gaagataacg atgaaaacga agaaagaaat 71100

taaagaacaa aggaaagaac ttaaagacgg tgctacaact gtttctttag taaaaaaagg 71160

ggataagaga atagctagcc ctagtagaat ttgtagttta tgtggtcagc agttatcagg 71220

tatgagttac actaaaggaa aagcattatc aaaagttaat cattttcatt tacagtactc 71280

taagtacatt tattttgata tttgtgcaga tattaacaat tgttataaaa atttaagaaa 71340

acgaggtgaa atggattgag tgcagaaaat attagagata taattaataa gaaaaagtta 71400

gaagaagagg atacaagaaa atatatagct gatggattta tgaatggtat cggtaaatta 71460

atgtatgaat tcaataaaaa agtagataat aaagaaatag aagttaaaga ccctaacgat 71520

ttatataaac tatttgtgat attctctcaa atgcagaata tggttaatga aacttctgaa 71580

ggtggagcaa tacctcaact atctagacct caacaagaat tatttgaaga gattacaact 71640

gaagatagta atggggagtc tactgtagac ttacaaaaaa tatcagaaat gtcagcagaa 71700

gatattacag aaatgatttc tgaaaaagag aaagtaatga atgaggaaaa ttcaaaaaca 71760

ttctaagggg aaagatataa catggatgga aaagaactaa ttaaaatagc acaagaaaca 71820

tttcaaacag aaaaaataac aagagagcag atagaccata taatcaatat gttaaaccct 71880

tctacctata tgcttaagta tcacacgcta agaggtcacc ctataacttt cagtattcct 71940

aatagggata gaagtaaagc acaagcacac cgaccttggc aagtccgtaa acatactatg 72000

cggactataa acctttttcta aaattggaaa ctcctaacaa gtgaagttga ggacaatcaa 72060

ttgctaaatc gtaactaaga taaatatttt aattacgtaa atgcctaacg actaaatttc 72120

caagtaagca ataaaatggt attgtgtaga attggaagag agggaaaccg taacgaaaag 72180

gacttttacg cctaactgta aaagtatgat atagtctaat cccctaataa atatcgggaa 72240

accgagggta gtaaatgata gtaaatgaca ctcatccaaa caaagcagtt attaaaagca 72300

gacaattggg gcttagtgag atgggtgtaa tggaaatggt tcattttgca gatatgcata 72360

gctatgccaa tgcaaaatgt ttatatacct ttaattagag aggcttcacg tagcaatgcg 72420

tgttgaaaaa ccttgttaaa cggggaaacc cctaacgtaa agacgagggc aatcccgtgc 72480

taaatgttga ctaacctaat attatatgat atattagtta tagtcagcta aatgccgaac 72540

gactaaattt ctaggtaggt atctaaatgg aggtactgag aactagataa aaaaactact 72600

taaaataatt agacttaaaa aaatactgtt ggaaggagga tatttaatgg gaaaaaaatt 72660

aactaatact gagtttttaa atagagtatt tcagttagtt agtgatgaat actcattttt 72720

agaagagtat aaagggagac ataccaaatt aagatgtaaa cataatttat gtagttacga 72780

gtgggatgta gaacctggag ctttttttagg taataagaac aaagcaggaa gtagatgtcc 72840

tagttgttat ggtaatgtta ctaaaacaac agataaattt aaaaaagaaa tatacaattt 72900

aactaaagat gaatataggt tactttctga gtatattaat gctaaaacaa aagtaaaaat 72960

taaacattct aaatgtggta atacttttttc tatgacacct aatactttta taaatggaag 73020

tagatgtcct gaatgtaacc ctcaaaaacc gtataataca gattctgcta aagataggat 73080

aaataaagaa acgaatggta cttttgaact agttagtgaa tacaaaggtt gttatgagct 73140

tatgaagtta aagcatcatg aatgtggaaa tattgtagaa ataaatatgc agagtattga 73200

tagcaataga ctaaattgtc cttattgtta taataggtct agaggtgaat tactagtatc 73260

ctcatttctt ctttcaaaaa acataccatt cgaagtccaa aaaagatttg atgggtttaa 73320

gaaatatcct tatgattttt atatagctga ttataatacg gttatagaat atcatggaga 73380

acaacattat aaacctatta agttttatgg tggagaagat agattggtaa ggcagaaaaa 73440

tatagattta aagaagaaaa attttgttga gggtaaaggt ataaattact tagaaatacc 73500

ttacacatta aacaatcaaa ataaagtaaa tgagttttta attaattatt ttaagtagaa 73560

gtaaagcaag gaacccttaa ccaaacttaa gggttatgat atagtctaaa ccgtatataa 73620

atactaggaa actagcggta taattgtcct acaaatgaac aaatgaagaa atttgttcag 73680

tctcgtttaa atcctgtatt agaaaaagaa tattttaggg atattgttga ttgggataaa 73740

gactctttag gttttaaaaa gataagaaat tctagtttat tctttagaac aagttctaaa 73800

gcaagtactg tagagggtgt ggatattgac tatttatctt tagatgagta tgacagggta 73860

aacttattag cagaatcgtc tgcactagaa tcaatgtctt catcaccttt taagattgtg 73920

agaagatgga gcacaccttc tgtaccgggg atgggtatac acaaattata ccaacaatca 73980

gaccaatggt attacggtca tagatgtcaa cattgtgatt acttaaatga aatgagttat 74040

aatgattaca accctgataa tcttgaagaa agtggaaata tgttatgtgt taatcctgaa 74100

ggggtagatg agcaagctaa aacagtacaa aatggtagtt accaatttgt ttgccaaaaa 74160

tgtggtaaac cactagatag atggtataat ggtgagtggc attgtaagta ccctgagcgt 74220

acaaaaggta ataaaggggt acgaggatac ctaataacac aaatgaacgc tgtatggatt 74280

tctgctgatg aattaaaaga gaaagaaatg aatacagaat ctaaacaagc attctacaac 74340

tatattttag gttatccttt tgaagatgtt aaacttagag ttaatgaaga agatgtttat 74400

ggtaacaaat cacctattgc agaaacacaa ttaatgaaac gagatagata ttctcatata 74460

gctattggta tagattgggg aaatactcac tggataactg ttcatggtat gttacctaat 74520

ggcaaggtag acttaatacg attattctct gttaaaaaaa tgacaagacc tgatttagtt 74580

gaagcagatt tagaaaaaat aatttgggaa atatctaagt acgaccctga tattataatt 74640

gcagataatg gagactcagg taataacgtt ttaaaactca ttaatcattt tggaaaagat 74700

aaagtatttg gatgtactta taaatcttct cctaaatcta caggacaatt aagacctgaa 74760

tttaatgaga acaataatag ggttacagtg gataaattaa tgcagaataa aagatatgta 74820

caagcactta agacaaagga tataagtgtt tatagtacag tagatgatga tttaaaaact 74880

ttcttaaaac attggcaaaa tgttgttatt atggatgaag aagatgaaaa aactggagaa 74940

atgtaccaag ttatcaaacg taaaggtgac gaccactatg cacaagcaag tgtttacgcc 75000

tatataggat taacaagaat aaaagaactt cttaaagaag gaaacggtac aagctttggt 75060

tctacatttg tttctactga ttacaatcaa gaaggaaata aacaattcta ctttgatgaa 75120

tagaggtgaa atagacttga cagataaatt attttatggt acaattagta atgaagaaat 75180

taataaaagt gtattgaatt tgttattggg tgaggaatta tccttagatt atgtttctaa 75240

aaatagtgat actttagatg ttaaatatga acatgtctat aaatctctag gattcgataa 75300

tttctttgat tgtttttat atgctaatag agagcctgaa atagtccaca aaggtggaga 75360

taaaaatctt ggtggactaa ataaggttaa acgtactgtt attcgtaatg gtaaagaaat 75420

ggaaatgaca gtttacgaag acggtaataa agagaacgat agtaaagaaa aacaagaagg 75480

aaaagaagaa gttagtagaa gtgcagtagg agcaagagct atttctaatg gtgaagaagg 75540

aaaggtaaac cctaaaaaag tagcaaattc attatctagt ttaagtaaaa agggtgtaga 75600

tgtatcccat attaatacaa acttatcatt gtataaagag tttgttgatg ataacggtga 75660

tacattagga attacatctt ttaaacgaac tgaaaatgat ataatattag aatcttatgc 75720

aagttcacct gattcagatg gtgtaggagc aagagctatt atggaattat tacgtttaag 75780

tattaaggaa aataaaaatg cagttgtgta tgacatagaa ttacctgaag cagtagagta 75840

tttaaaaact ttaggattta aacctaataa agatgggtac atcttaagaa aaaaagatgt 75900

aaaacaattc ttaggtgatt atagtgattt tatttagcac tatagtcatc tattctattg 75960

tatttattct atatattgta ttaaaaacaa tttatataaa gtctaatatg agtagaatag 76020

ataacacaac tgaattatta aaaatattac aggaagatat tgaaggtaag ataaaaaagg 76080

aaggaagaaa taaatgactt tagaagaaaa taaattaaca ttagaagaat caataactcc 76140

acttagtaaa gaggagaaag aagatagtat taaagaattt agtagtttat tatgtgaaat 76200

ggtaaatagg ctatacaagt cttataatgt atttagacaa gaccctatgg atgaaactca 76260

acgtctagat ggctctttaa tggtctttca aagtagatta aatgaccctt taacaggaga 76320

tttacatgat aagatgtata aacttgcttt ttcaaaacgt attgatattt tcgaagctaa 76380

taagcaattt agaaaagatg tagaagcagg taaagcaatt gagttaggtg atgtagctat 76440

tatagataca gcattaagta acatcctttc aggcaatgag ttccaaggaa gtatttcatt 76500

tatgcttaga aaagactttg aagaaaaaga acgaattaga aaagaagaag aagagaaact 76560

taataactta taaaagggaa gaattatgag actatataaa atgaggtatc ataattgaaa 76620

aagaaaccac aaggcaatga ggtaatcata accataataa cggttatgat agcagtattt 76680

gtagtcatta tgaccatatt ttttaataaa tatcaagatg ctaaagaaga taaagataga 76740

tatcaaagat tagtagagat ttataaaaaa gcagatgata atgatggtga gactaaaaag 76800

aaatatgtta aaagattaaa taaggctgaa gaagaactta aaaaagtaaa aaaagaaaca 76860

aattataaag attataataa gaagtcaagt aaagaaagac aaaaagaaga taaagaaact 76920

agagagaaaa tatatgatgt aactggtgat gatgacttaa tattagtaaa aaataatatt 76980

gattttagtg ataaagtaga caagcccgaa atacttatta gtgaagatgg aattggtacg 77040

ataactgttc ctgtagatag tgggtatgaa aaacaaacag taggttctat tattactagt 77100

gtattaggtt ctcctttcct atcacctggt tcaaatagta tagatggttt aagtgttatt 77160

aacgataatg tttatccaaa tacagtagat agcatagtag aagatacaaa accttctatt 77220

aacttaccaa tggataatcc tattataaca aatccggttg aaccaactat accttcagat 77280

actatacctc ctattgataa tccttcagtt ccggtatttc ctgagaatcc agtagataat 77340

aatcaaggaa atacagataa tccaaaccca ccgcctccag gatatacaga tgaagatggt 77400

ggaaggggct ccggtggtgg aggaaattct gaaccaccat caacggaaga accttcggat 77460

aatggtaaca ctggaggagg agattgggaa gaaaaacctg acccaggaga agaaccttca 77520

gataatggta atacaggagg caatggtgga gaagttacgc ctgaacctga ccctacccct 77580

tctgaacctg aacaaccgaa tgaaaattct gatgaaggta atgaagaaaa accatctgaa 77640

ccgtctgaca atcctgatga aaatggagga tgggaaactg aaccaactga acctgagtca 77700

ccttcagagc cggacgataa agtggacgaa gaggataaaa atgaagatac tacagatgat 77760

aaacagccca ctgaacaacc ggacgataac aacatagata atgaagataa aactgaagag 77820

gagtaattac tcctcttttt tgtttgctat attaaataag agttaaatat aaaaaaaatt 77880

gaacattacg gtggtgaaaa ctttgttagg aatgaatatt ataacgtcac tatcagtagt 77940

atttacctgt ttaagtcttt taactttaat gatttttgtt catagtaagt tctctagtaa 78000

aaacgttttt gttttgtatg taatttatgc tataatagga ataggtacat acatagtttt 78060

aactatgttt caaacaacat ctgtacttat taagaatgat gtaatagatt ccatagaaaa 78120

tactgaacat tatattggat tcaatgaccc tataattata tttactataa gttttatagg 78180

tgcaatactt ggaggaattt ggtacaagat gatgaaaatt attaaaaaga gtaactttaa 78240

agataaaaaa taaaaaagac ggtgaatagg ttgatattct ctaaagataa aaaatgggat 78300

gaagcaaaag atttcatcaa aggtcaaggt atgcaagata attggataga gattgtagat 78360

tattatagac agataggtgg aaaacacgta gctgttttta ttgctttaaa caaagtaaaa 78420

tacatgattc tagaagcaac aaaagacaat aaagtaatat tagtagataa agataataat 78480

atactattag aagattatga tattgttatg gaaagtaaga agatgtttta ttacattgaa 78540

gaaccgttcg aggttaaaat aaatatccct caacatatta gagatgtaac ttataataat 78600

actgttgtat taactacagt aagagggagt agaggtgact agtaattggc agatttattt 78660

aagcaattca gattaggtaa agactatggt aataatagta ccattgctca agttcctatt 78720

gatgaaggat tacaagctaa cattaaaaaa atagaacaag acaataaaga gtatcaagat 78780

ttaactaagt ctttatacgg acagcaacag gcttatgcag agccatttat agaaatgatg 78840

gatactaatc ctgaatttag agataagaga agttacatga agaacgaaca taacttacat 78900

gatgttttga aaaagtttgg taataaccct atccttaatg ctatcatact tacacgttca 78960

aatcaagtag ctatgtattg tcaacctgca agatattcag agaaaggttt aggttttgag 79020

gtaagattaa gagacctaga tgcggaacct ggtagaaaag aaaaagaaga aatgaaacgt 79080

atagaagatt ttattgttaa tactggtaaa gataaagatg tagatagaga ttcatttcaa 79140

actttctgta agaaaattgt tagagatact tatatctatg accaagttaa ctttgaaaaa 79200

gtatttaata agaataataa gactagacta gaaaaattca tagcagtaga cccttctact 79260

atttttatg caacagataa aaaaggtaaa attattaagg gtggtaagag atttgttcaa 79320

gtagtagata aaagagtagt agctagtttt acttctagag aattagctat gggtataaga 79380

aaccctagaa ctgaattatc ttcctcagga tatggattat cagaagtaga gatagctatg 79440

aaagagttta ttgcctataa taacactgaa tctttcaatg atagattttt ctcacatggt 79500

ggtactacta gaggtatttt acagatacgt tcagaccaac aacaatcaca acatgcatta 79560

gagaacttta agcgtgaatg gaaatctagt ttatcaggta ttaatggttc atggcaaatt 79620

ccagtagtaa tggcagatga tattaaattt gtcaatatga caccgactgc taatgatatg 79680

caatttgaga aatggttaaa ttaccttatc aatattatat ctgctttata tggtattgac 79740

cctgcagaaa ttggtttccc taatagagga ggagctacag gttctaaagg tggctctact 79800

ttaaatgagg ctgacccagg taaaaaacaa caacaatctc aaaataaagg tttacaacct 79860

ttacttagat ttattgaaga tttagttaat agacatatta tatcagaata tggagataag 79920

tatacattcc aattcgtagg tggagatact aagagtgcta ctgataaact taatattctt 79980

aaactagaga ctcaaatatt taaaacagtt aatgaggcta gagaagagca aggtaagaaa 80040

cctattgaag gtggagacat tattctagat gcttcattct tacaaggaac agcccaatta 80100

caacaagata aacaatataa tgatggtaaa caaaaagaac gtttacaaat gatgatgagt 80160

ttactagaag gagacaatga tgattctgaa gaaggacaat cagcagattc tagtaatgat 80220

gataaaagta accctgaagt aggaactgac tctcaaataa aaggggattc aaacgtttat 80280

agaacagaaa cttctaacaa gggtcaaggt aaaaaagggg aaaagtcttc tgattttaaa 80340

cactaataag gaggtaaaat taaatgtcag ttatatataa agataataat tggattgatt 80400

taactaatgt tccttattta caaaaaggtg atagtggata tcgtaaagat ataccaagga 80460

aaaattggaa aaagtgttta aatacagaag taagtttttc ttataaaggt aaaaagggtc 80520

tattttatgt aacttatcgt aaggaagata aaggaaaagt taaagttgaa tatgataagt 80580

atgttaagat aatagaccct catgatttaa agacactaaa tataaataaa atagttaatc 80640

ctcctaataa agctaagtat cgtgagcagg aagtaattaa tggtgatact gtaagaaata 80700

ttagaaaagt taagaataca ggaattgttt atactatgtt atgttcagag tatgaagaag 80760

aatatgatat aagagaaagt gatttattaa gagggagagg tagcccttat aaatcaggta 80820

gaaaagtatg ttataacaat tcattatatt ctgttgaaaa tttgagagaa tatatctgtg 80880

atttagaata tgctaaaact gtaactaagt tttcacataa agatataaaa tgcaagtgcc 80940

ctatatgtag tgaagagaaa gttatgaagg ttaataaatt agttaataac ggtttttctt 81000

gtcatagatg tagctcaact ataacatatc ctgaacgatt aatgatagga ttactagaat 81060

taaataattt aaactatgaa tatcaaaaag tatttaaaga cctacctaat agaaaatttg 81120

atttttattt acctaaatta aatatggtta ttgaaactca tggattacaa cattataggg 81180

aattaaatgg ttacatgaat catgaaaaaa caaaggaatc ggatttagag aagtataact 81240

attgcaagaa taataatata gattatattg aaatagattg tagttacagt gatttatcct 81300

ttatattaag taatgttgag aatagtaagt taaatagcat acttaaaaat aagaattacg 81360

ataatcttag caattatatt ataagaagta aaaatgatga tgttaagtat aatatatatt 81420

tggattactg caaaggatta agcaagaaag aattgaaaga taaatataat aaaacgagtt 81480

attatataaa caggtctatt gagatattta aacattaatt aataagccta gaataaatct 81540

aggctttgtt tatttttttt gtaatttaat tttgataaat gtaataacta tggtatacta 81600

tatgtaattg atattaatac ataaaaaata ttaatatttc acttacaagt tattattgtt 81660

atattattaa cgtaaaagta aataaaataa caagtggagg tgtagacacc tttggaagaa 81720

ataaaattta atgcttttgt acctatggat ttgaagaaat ctgtatcaac agcttctgat 81780

actaatgagt attctatcgt ttcaggatgg gctagtactc caagtatgga tttacagaat 81840

gatatagtta atcctaaagg aatagatata gagtatttta agtcacaagg gtacattaat 81900

tatgagcatc aaagtgataa ggttgtaggg atacctacag agaattgcta tgtggatata 81960

gaaaaaggtt tatttattga agcaaagcta tggaagaatg acgaaaatgt tgttaagatg 82020

cttgatttag ctgagaaatt agaaaaatca ggtagtggaa gacgtttagg tttttctatt 82080

gaaggtgcag ttaaaaaacg taatataaat gacaatagag ttattgatga agttatgata 82140

accggagttg cattagttaa aaaccctgct aatcctgaag caacatggga aagctttatg 82200

aaatcatttt taactggtca tggtacatca cctgacactc aagttgatgc aggagcttta 82260

agaaaagaag aaatagcatc tagcattaca aatttagctt acgtcactaa gattaaagat 82320

ttaaaagagt ttaatgatgt atggaatggc gttgttgaag atttgagtaa atctaatagt 82380

atgggatatg aggaatcagt ccttacgtta caactagcta aaggtttatc tcgtaaagat 82440

gcagaactag cagtaatgga tataaacaaa caaaaactag aataggtaag gagaatacat 82500

tctatgagta aagaaatgca aaatatttta gaagagtatg ataagttaaa tgctcaagag 82560

gcagtttcga aatctgtaga agatgatgaa aagaatacag tagaatctac cgaagagcaa 82620

gtagcagaaa caactgaaga acctgctaaa gaacctgaaa aagtatctga ggaagatgct 82680

aaagaagcac aagagcaagg tgaaaaagtt gaatctgaag aggtagcaga ggacaatgaa 82740

gatgaggaag ttgaaaaatc agctaaagaa tcaaaagacc ctgtagacca aaaagatact 82800

aagacagaaa ataaagacaa cgagaaacgt aaaaataaaa aagataaaaa agaagattct 82860

gattctgacg atgaagataa agatactgac gatgataaag ataagaaaga agataagaag 82920

gaaaaaactt ctaaatcaat ttctgatgaa gatatcacaa cagtatttaa atctatctta 82980

acatcttttg aaaacttaaa taaagagaaa gaaaactttg ctactaaaga agatttaagt 83040

gaagttagta aatctattaa tgagttatca gcaaaaattt ctgaaatcca agctgaagat 83100

gtttctaaat cagtagacac tgatgaagaa gctgtagaaa aatcagtaac atctacaaat 83160

ggagagcaag aaaaagtaga aggttatgtt tctaaatcag tagacactga agaacaagct 83220

gaaactggtg aagcaaaatc agaagaagct gaagaagtac aagaagataa cacatttaaa 83280

ggattaagtc aagaagaacg aactaagttc atggattctt acaaagcaca agctaaagac 83340

cctagagctt ctaaacatga cttacaatca gcttaccaat cttacttgaa cattaacact 83400

gaccctacta acgcatcaga gaaagatatt aaaactgtaa aagactttgc acaaatttaa 83460

ttaatgcaca aagttgtgtt atattatacg gtgtaactaa agaatataaa tagggtacat 83520

tttactgtac cctacataaa ataaaaagaa cacaaatgaa aggtgataaa tttatatgac 83580

tatcgaaaag aacctgtcag acgttcaaca aaagtacgct gaccaattcc aagaagacgt 83640

agtaaagtca ttccaaactg gttatggaat cactcctgat acacaaattg acgcaggagc 83700

tttacgtaga gaaattttag atgaccaaat cacaatgtta acatggacta atgaagattt 83760

aatcttctat cgtgatatct cacgccgtcc tgctcaatct acagtagtaa aatacgacca 83820

atatttacgt catggtaacg taggtcactc tcgtttcgtt aaagaaatcg gagtagcacc 83880

agtatctgac ccaaatatcc gtcaaaaaac tgtatcaatg aaatacgttt ctgatactaa 83940

aaacatgtca attgcatcag gtttagtaaa taacattgct gacccatcac aaatccttac 84000

agaagatgct atcgcagttg ttgcaaaaac aattgagtgg gcttcattct acggtgacgc 84060

ttcattaact tctgaagttg aaggtgaagg tttagagttt gatggtttag ctaaattgat 84120

tgacaaaaat aacgtaatta acgctaaagg taaccaatta actgagaaac acttaaatga 84180

ggcggcggta cgtatcggta aaggtttcgg tacagctaca gatgcttaca tgcctatcgg 84240

tgtacacgca gacttcgtta actcaatctt aggtcgtcaa atgcaattaa tgcaagacaa 84300

cagcggtaac gttaacactg gttacagcgt aaatggtttc tactcatctc gtggattcat 84360

taaattacat ggttctacag taatggaaaa tgaattaatc ttagatgaat cattacaacc 84420

attaccaaat gctccacaac ctgctaaagt tacagctact gttgaaacta agcaaaaagg 84480

tgcttttgaa aatgaagaag accgtgcagg attatcatat aaagtagtag ttaactcaga 84540

tgacgctcaa tcagctcctt ctgaagaagt aacagctaca gtatctaacg tagacgatgg 84600

tgttaaactt tcaattagtg ttaacgctat gtaccaacaa caaccacaat tcgtttctat 84660

ctaccgtcaa ggtaaagaaa caggtatgta cttcctaata aaacgtgtac cagttaaaga 84720

tgcacaagaa gatggaacaa tcgtattcgt agataagaac gaaacattgc ctgaaacagc 84780

agacgtattt gttggtgaaa tgtcaccaca agtagttcac ttattcgaat tacttccaat 84840

gatgaaatta ccattagctc aaattaatgc ttctattaca tttgcagtat tatggtatgg 84900

tgcattagca ttacgtgctc ctaaaaaatg ggctcgtatt aaaaacgttc gttatatcgc 84960

agtttaatag aataagaaaa actgaataca agagaatagg gataaactta gggtttatcc 85020

ctttttatt aaaataaact tgaagggatt taataaatat gttatactat aagaaactat 85080

tagataaaaa aatggctact gtttatggta cagtggagat tgacaaagat ggagtagtta 85140

aaggattaac taaagagcaa gaaaaagaat ttgcaaatgt tccaggtttt gaatttgaag 85200

aagaaaagaa aactactaga aaacaatcag cttctactag taaagaagaa gagcctaagg 85260

aagaggaaaa gaaagcctct actagaaaaa ctacaagtac tactagaaaa tctacagcac 85320

gtaaaacaac agccaaaaaa gatgaaaata agtaaagggt gaattaaatg gttaactcaa 85380

tgtttggagg ggacttagac ccttatgaaa aatcattaaa ctatgaatat ccttatcatc 85440

ctagtggtaa tcctaaacat atagacgtaa gtgagataga taatttaaca ttagctgatt 85500

atggatggtc accggatgca gttaaagcat atatgttcgg tatcatagtt caaaatcctg 85560

atacaggaca acctatgggt gatgagtttt ataaccatat attagaaaga gcggtaggta 85620

aagctgaaag agcattagat atatctatac tacctgacac tcaacatgag atgagagatt 85680

atcatgagac agagtttaat agttatatgt ttgtacatgc ttatagaaaa cctatattac 85740

aggtagagaa cttacagcta cagtttaatg gtagaccgat atataaatac cctgctaact 85800

ggtggaaagt agagcatcta gcaggacatg ttcaattatt ccctacagca cttatgcaaa 85860

caggacaatc aatgtcatat gatgcggtat tcaatggata ccctcaatta gcaggtgtat 85920

acccaccatc aggagcaaca tttgcacctc aaatgatacg attagaatat gtatcaggta 85980

tgcttccacg taaaaaagca ggaagaaata aaccttggga aatgcctcct gagttagaac 86040

aattagttat aaaatatgca ttgaaagaaa tataccaagt atggggtaac ttaatcattg 86100

gtgccggtat tgctaataaa acattagaag tagacggtat tacagagaca ataggtacca 86160

ctcaatcagc tatgtatggt ggagctagtg ctcagatact tcaaataaat gaagatataa 86220

aagaactatt agatggttta agagcttact ttggatataa tatgatagga ttataaggag 86280

ggttagaaaa tggaaaaacc gtatatgata ggagccaact ctaaccctaa tgttattaat 86340

aagtcaacaa catatactac tacaacacaa gcagatgaac aagataaacc taagtatact 86400

actagactag agtttgatac gattgacatg attaggttta ttaatgaccg aggtataaaa 86460

gtattatggg aagaagcata tttctgccct tgtcttaatc ctgatacagg acatcctaga 86520

gtcgattgtc ctagatgtca tggtaaaggg attgcatatc tacctcctaa agagactata 86580

atggcaatac agtctcaaga gaaaggaact aaccagttag atataggtat attagacaca 86640

ggtactgcaa taggtaccac tcaattagaa aagaggattt cctatagaga caggtttact 86700

gttcctgagg tattgatgcc tcaacaaatg atttattttg tgaataaaga tagaattaaa 86760

aaaggtatac ctctatacta cgatgtaaaa gaagtaactt atatagccac tcaagatggt 86820

acagtctatg aagaagatta tgaaattaag aataatagat tgtatttaaa tgaaaaatat 86880

gagaatcata cagtaacttt aaagatactt atgactttaa gatatgtagt atcagatata 86940

ctaaaagaaa gtcgttacca atatactaag tttaatcaac ctaaatcaaa atttgaaaac 87000

ttacctcaaa aattacttct taaaagggaa gatgttattg tactacaaga cccttataaa 87060

gttaatgatg gtatagaaga agacctagaa attcaagtag atgaccctaa ggcttcggca 87120

tctaatccta gtaatttagg tggattcttc ggaggtgcat ttaaataatg ccagttcacg 87180

gaaagagacc taatttattt aaaaataaaa actataagca ggtaggtaag agaacaattg 87240

atggtatgcg ttcagaagtt cttgataaat tacaagcaac agcacagcaa gtagagaata 87300

ctagtattaa acgtatgcct acttacctac aaataacaga gaaaaagctt gaaaaagaag 87360

gagtagtaga ccttaaaaaa gcttttgctc actcatctaa aaagaaaact agtaaagatg 87420

gcggatggta tttaactgta ccaatccgca tcaaaactag tagaatgaat aacagtactt 87480

accaagatat gagaacttta aaagtagata aaggtacagg ttcagtctct aagataactg 87540

attacctaga aggacgtaga aagaatgtaa gccacccttc aatgaagcct gagcctatga 87600

ctcataatat gactaaagtt aaaagaggaa agcaatcttc ttactttata tttagaactg 87660

tttctagtaa gtcacctgct agttcttgga tacttaacag agataaagtt aatgaagata 87720

acttctctaa aacaactcta aaaactgtta agcaattaat gaactggaag atgaaaaatt 87780

taaattaaga ggagggatag tattaaatgg caataacatc agttgattca tatttattat 87840

cagaaataaa gcctagactt aacactgtgc tagagaattg ttatattata gatgaagttt 87900

taaaagactt tgattatcaa actagagaga gctttaaaga agctttctgt ggtaagaatg 87960

cacaacatga agtaacggta ggatttaact tcccaaaatt taaaaataac tatgaagctc 88020

attacttgat acaattaggt caaggacaag agacaaaaaa ctctttaggg agtattcagt 88080

catcttactt tgaggcaaca ggagatacct tagtcgaatc ttctacagca ataagagaag 88140

atgataagtt agtttttact gtttctaaac caataggaga gttaataaag gtagaagata 88200

tagagtttgc taaatacgat aatcttcaag ttgaaggtaa taaggtatca tttaagtatc 88260

aaacaaatga agattatgag aactacaatg ctaacattat atttaccgaa aagaaaaatg 88320

attctaaagg tttagtaaaa ggattcacag ttgaagaaca agtaacagtt gtaggtcttt 88380

catttaatgt agacgttgca agatgtttgg atgctgtact gaaaatgatt ttaatatcta 88440

tgagagatag tatagaagag caacaaacat tccaattaca gaatttgtct tttggtgata 88500

ttgcaccaat aatagaagat ggtgactcaa tgatttttgg tagaccaaca attattaagt 88560

acacaagttc tctagatttg gattatacta ttacacaaga tattaataaa ctaactttta 88620

aagaaagaaa ggattggaag taggatggct agaaaaaaga cacctgaaaa taacactcct 88680

aaatttaatg gttatgttca tatagataca ttccttgata ctgcaaaaac ccttttaat 88740

atgaaggatt cacaagtagc aggatttaaa gcttatatgg aaggtagtca ttatttgttt 88800

agtgagcaag aattcttacc atcattagag aagtatctag gtaggaaatt agatatataa 88860

taacattcag ataaggagaa ttaaatatgg cagtagaacc attcccaaga agacctatta 88920

cccgtcctca tgcatctatt gaagtagata cttcaggtat cggtggctca gcaggttcaa 88980
gtgaaaaagt attttgctta atcggtcagg ctgaaggcgg agaaccaaat acagtttatg 89040
aattacgtaa ctatgcacaa gctaaacgtt tattccgttc aggagaatta cttgatgcaa 89100
tagaattagc atggggttct aaccctaact atacagcagg taagatttta gctatgcgta 89160
tagaagatgc taaacctgct tcagcggaaa tcggtggatt aaaagtaaca tctaaaatct 89220
atggtaatgt tgctaacaac attcaagtag gattagaaaa gaatacatta agtgattcat 89280
tacgtttaag agtaatcttc caagatgacc gtttcaatga ggtttatgat aatatcggta 89340
atatcttcac aatcaagtac aaaggagaag aagctaacgc aactttctct gtagaacatg 89400
atgaagaaac tcaaaaagca agtcgtttag tattaaaagt tggagaccaa gaagttaagt 89460
catatgattt aactggtgga gcttatgact acactaatgc tattattaca gacattaatc 89520
aattacctga tttcgaagct aaattatcac ctttcggaga taagaactta gaatctagta 89580
aattagataa aattgaaaat gcaaatatca aagataaagc tgtatatgta aaagcagttt 89640
ttggtgactt agaaaaacaa acagcttaca acggtatcgt atctttcgag caacttaatg 89700
cagaaggaga agtaccaagt aatgtagagg ttgaagcagg agaagaatca gctacagtaa 89760
ctgctacttc acctattaaa actattgagc cgtttgagtt aactaagtta acgggcggta 89820
ctaatggaga accacctgct acatgggcag acaagttaga taaatttgca catgaaggcg 89880
gatactacat tgtcccatta tcatctaaac aatcagttca tgcagaggta gcttcttttg 89940
ttaaagaacg ttctgatgca ggggaaccaa tgagagctat tgttggtgga ggattcaatg 90000
aatctaaaga acaattgttc ggtagacaag catcattatc taatccacga gtatcattag 90060
tagctaactc aggtactttt gttatggatg atggacgtaa aaaccacgta cctgcttaca 90120
tggtagccgt agctctaggt ggtcttgcaa gtggtttaga aatcggtgaa tcaatcacat 90180
tcaaaccact acgtgtaagt tcattagacc aaatctatga gtcaatagat ttagatgaat 90240
taaatgaaaa tggtattatt agtatcgagt ttgttcgtaa ccgtactaat acattcttca 90300
gaatcgttga tgacgtaact acattcaatg ataaatcaga cccagttaag gctgaaatgg 90360
ctgttgggga agctaatgac ttcttagtaa gtgagcttaa agttcaactt gaagaccaat 90420
ttattggtac tcgtactatc aatacaagtg cttcaatcat taaagacttt atccaatctt 90480
acttgggtcg taagaaacgt gataatgaaa ttcaagactt ccctgctgaa gacgtacaag 90540
ttattgttga aggtaacgaa gcaagaattt caatgacagt ttacccaatc agaagcttca 90600
agaaaatctc tgttagcttg gtttacaagc aacagacatt acaagcctag tctaggtgac 90660
ggagtacctg gattaggtac tcctattaat ataatttgaa tactttagga gagtgaatac 90720
agatggcatc agaagctaaa caaaccgtcc atactggtaa taccgtccta cttatgatta 90780
aaggtaaacc ggtaggaaga gcacaatcag catcaggtca acgtgaatac ggtacaactg 90840
gtgtatacga aatcggttct atcatgcctc aagaacacgt atacttacgt tatgaaggta 90900
caattacagt agaacgttta cgtatgaaaa aagaaaactt tgcagattta ggatatgctt 90960

cacttggtga agaaattctt aagaaagata tcattgatat tttagtggta gataacttaa 91020
cgaaacaagt tattatctca tatcatggtt gctctgcaaa taactacaat gaaacttggc 91080
agacaaatga aattgtaaca gaagaaatcg agttcagtta cctttaacta atagaggcta 91140
tgtttggtga caagcataga aaacacttta aattgcgtga aagtcttaaa gactagataa 91200
ctacaacgta actcgaaagg gtaagcgtga atgttgagaa atcagaaaaa atatctagta 91260
tagtataagg ttaaatccta agtacagtaa aatagatgat acgcaggcaa gcctacaaat 91320
gtgggaagct tcaacgacta taataggtga gtcttagtta cacattaaga ttatggtata 91380
gtctactccc tttaaaatat atcgaaagat agggtacaaa ggacagcatc agataaagct 91440
agaacttaaa tttcttatta agaccaacaa taaaagttgg tcttatattt tatacttgct 91500
ttgtctgagg cagtgtgcta taattaaaat acaaggaggt aataatatgg gaaaaaatca 91560
atatacattt aatattaaag aaaataaaaa taaatggtat gaatggtgta aactacaaaa 91620
cgtaaaacct ttagtagaat atgaaaatgc acaacaaata ttttattttg aatttcttga 91680
aggtaaattt aaaggactaa taggaaaaac atattgggct agtataaata gaggttctaa 91740
tatgcgtatg agttgtttaa catcagaaag taaagataaa tatttaaaaa atttaggaaa 91800
aagaaaaggt atagaggtag tagaagacta taagggtggc agaaaattaa aacataaatt 91860
tatagtttta gaaggtaagt accaaggatg tgaaggatat ataactttaa atgatttaga 91920
gaatttaggt agagtagata atagaagttt atctgaaaaa ggaaggaaac aatactttga 91980
taaacaggca agacttagag attgtattat tctagagtac cctaaagact atagaataaa 92040
aactaaagat aagatagtag taaaagataa agaagggcat gttcataata ttattgttca 92100
ggacttttt gagaaatcat ctttattgga gttatcttgt gctagtgaag gagagaaaat 92160
agttaaagaa atacttacta aaaattctat aaaatttgaa aaagaaaaat catttagaaa 92220
caaagaaggt aaagtacaaa gatttgattt ttatattaat gaaaataata aagaatatgc 92280
aatagagtac aatggtgcac agcactacat agattctaca ggatatctta aagatacttt 92340
ggaaacaacc cagaaaagag ataaactaaa aaaagaatac agtaaagata aaggtataaa 92400
tttattaatt attccttaca caataacaga taagaaagaa atggaaaaaa ttattttaaa 92460
ttttttaaac aaataaccct tgacactccc tcaagggata tgttattata ataacaggtt 92520
aggagtaata agtatgaata ataggcaagc taaaataaaa ggatataacc aatttcatta 92580
ttatgatttt ccaacaacta aaggtaagtt taaagatata atgaaaagaa aatctagaac 92640
agaacttaaa aaagatttac aaaaagaaag gaagtattat cttgacaaat aagagaaaaa 92700
cgataggtaa gatgagtaac acaagagcaa catggaatat taatccggta actaaagtta 92760
aaaaagataa aacaaaatat tctagaaaaa ataaacataa aggtcttgac aattataatt 92820
aactaaggta tattattagt ataacaaaaa aggagatggg tatatgagta cattttggtc 92880
agaaagaaga acaactaata aagataggca agttaaaaaa cattatactc aaatgagtat 92940
gtatgaaaga aagaaatgtg tagagttatt acaagagaca attactgaaa atagaattat 93000

taattttaca cgacatagtg caaagaaagt taaaggtaaa ccaacaacaa atatacctaa 93060

attaataggt tttattttta aaaataagtt tgcctacgaa aatatcatag aatacaataa 93120

cacagattat aatggtaata ttgagaggag aattgttgtt aaacatccta aagttataac 93180

tgtagaagga aaacctagct atcagttttt gacaattagt cttgaagatg ctagagttat 93240

tacagtatgg tacaacagtg tagatgatac acatagaaca ctagatttaa attattatag 93300

taaagacttg acaattcaat aaggaggtat tataatgggt atcacaatag taaatagtta 93360

ttttattctg tctaacatct tcctcatcat attaaccata ttaaatggta agggtactgt 93420

tacaagggaa tcactaacta tgagtaaaat attagtagta ataacatcaa ttcaattttt 93480

agcatgttta attattaatg gtatttattg gtcactaaaa ttttagaata aaagtattga 93540

caaattaaaa ctaataaatt ataataaagg tataacaaat taaaggagaa gatataaaat 93600

gtcacaagat aaattaagag caatttacac agaaatgaaa gtagaattac acaaatttcc 93660

taaagaggta gatataacaa gtaaatcaac tgcaattgca atcaatcaga ttttagataa 93720

attcaaaaca ttaacagaac aagcaggaaa gattactaga aaatatttag aaggtcaaga 93780

aatattaact attgattatg agtattatga ttcattacaa gaatactata tttacctact 93840

tagaaatagt gaaaagattg aacaaagttt acaagaaatt actaagcgca caggtgaata 93900

tgtaaagtaa ttttgattta aaaacaaaat atgatatact atgtttaaag tagtaagcct 93960

acactagtcc gtgttatatt aatattgaat cggataagcg taggctttat taatatttaa 94020

aaaaggaagg tatatcatat tatggcagaa gaaattaaaa aggaacaaga tgtacaagaa 94080

acaactaaag aagaaaaaaa agatgttagt aaaatgacac cggaagaaat agataaatta 94140

aaatatcaag acaaacaaga aaaagaacaa gttattaaca aagttattaa aggtgttaat 94200

gatacttggg aaaaagaata taactttgaa gaattagact taagatttaa agttaaaatt 94260

aaattaccta atgcacgaga acaaggtaat atatttgcgt tacgttctgc ttacttaggt 94320

ggtatggata tgtaccaaac agaccaagta attagagcat atcaaatgtt agctacatta 94380

caggaagtag gtattgaagt tcctaaggaa ttccaagacc ctgacgatat ttataactta 94440

tatcctttaa ctgttatgta tgaagattgg ttaggattct taaactcctt tcgttactaa 94500

tagtatagaa acattagata aagatataga acgattgggc ggtatggaat caattgttaa 94560

acaaccttta tctagaaatc tatgggctat tatgaaagag tttaatgttt tacctactga 94620

gcaaagattt aaggacttag atgattatca gatagagttt attattggga atatgaacag 94680

agatgtttat gaacataaca aacaacttaa acaagctcaa aaaggtggaa aattcgatag 94740

tcaattcgaa gatgatgata gtagttggtg gaatgaatct catgaagact ttgacccagt 94800

acctgatttc ttagatgctg atgatttagc acaacaggtg gaagctaaat tatccgatag 94860

agataaggaa gaaagagcta agagaaacga tgcggagtta aatgatgaaa cagaaggact 94920

tactacacaa catctagcta tgatggaata catcagacag aaacaacaag aattagatga 94980

tgaagtagga aatggtaaga ctagtgaaga ggatgctact atatcacaag atagcgttaa 95040

taaagcacta gaagacctag atgatgactg gtatatgtaa agggtggtag gtgatactac 95100

catccttatt tttttaaaat ggatggtgaa taatgatggc aatgaatgac gattatagat 95160

tggtcttgtc cggtgatagt tcggatttag agaatagtct gaaggcaata gaactttata 95220

tggattcttt agagtctaag aatattgatg ctcctttaga taatttctta aaaaaattaa 95280

aagtaattgc taaagaagtt aaaaatgtac agaacgcaat ggataaacaa gatggtaaat 95340

ctgttatatc ttctaaagac atggatgaat ctattaaatc cactcaatct gctacaaaga 95400

atataaatga attaaagaaa gctttagatg accttcaaaa agagaatata tctaaaggta 95460

ttgcacctga ccctgaagtt gaaaaagcat atgctaagat gggtaaagtt gtagatgaaa 95520

ctcaagaaaa acttgagaaa atgtcttcac aaaaaatagg ttctgatgct agtattcaaa 95580

atagaattaa ggaaatgaaa accttaaatc aagtaactga agaatacaat aaaataagta 95640

aagattctag cgcaactaaa gattatacaa aacgattaag agctaatcgt aatatgacta 95700

gaggttacat ggagcgttca gaaggaacag gacgtttgac atatgaccaa ggtgcacgag 95760

ttagaagtga actaggtaaa ataagttctt atgagagcca aagaaaacaa aaccaacgta 95820

atttaggaca agcaagagag caatatagca actatagaaa ccaacaacaa gacttgacta 95880

aacgtagagc tagcggtcaa attaataagg cacaatatga acaagaatta gcttctatta 95940

aacaggaaat gaaagctaga gaagaactta tatctaacta cgagaaacta ggagcagaac 96000

ttgataaaac agtccagtat tataagggtt cagttcaaaa ggatttccaa tctagagatg 96060

tagaccaaca acgaggaaca tttggtagaa tggttcaaga acgtttgcca tctattggtt 96120

ctcatgctat gatgggtact acagctatgg ctacaggttt atacatgaag ggtgcctcat 96180

taagtgaaac taatagaccg atggttacat cattaggtca aaattccgat aatatggata 96240

tagattctgt aagaaatgca tatggagact tgtcaattga caacaaatta ggttataata 96300

gtactgacat gttaaaaatg gctacttcat atgaagcatc agtagggcat aaaagtgacg 96360

aggacacaat ggcaggaact aaacaacttg ctattggagg acgttcttta ggtattagag 96420

accaagaagc ttatcaagag tctatgggtc aaatcatgca tactggtgga gtaaattctg 96480

ataacatgaa ggaaatgcaa gatgcattcc taggtggtat taaacaatca ggcatggttg 96540

gtcgtcaaga tgaacaactt aaagcactag gttctatagc ggaacaatca ggagaaggaa 96600

gaactctaac taaagaccaa atgagtaatc ttactgccat gcaatctact tttgcagagt 96660

caggaagtaa aggattacaa ggtgaacaag gtgccaatgc tattaacagt atagaccaag 96720

gacttaaaaa tggtatgaat agttcttatg ctcgtatagc aatgggatgg ggaacacaat 96780

accaaggtct tgaaggtgga tatgatttac aaaaacgtat ggatgaaggt atatctaatc 96840

ctgaaaactt gacagatatg gctgatatgg ctactcaaat gggtggcagt gaaaaagaac 96900

aaaaatacct atttaataga agtatgaaag aaataggcgc taacctaact atggagcaat 96960

ctgatgaaat atttaaagat gctcaatccg gaaaactatc taaagaagag ttagctaaga 97020

aagctaagaa aatggaaaaa gaaggtaaaa aagaaggaga agataacgcc actgattata 97080

aagaatctaa atcaggaaaa aatgaccaaa ataaatctaa gactgatgat aaagcagaag 97140

atacttatga tatggctcaa ccattaagag atgctcatag tgctttagca ggtcttcctg 97200

cccctatata tttagctata ggagctatag gagcatttac agcttcacta attgcatctg 97260

caagtcaatt tggagcaggt cacttaattg gtaaaggagc caaaggactt agaaataaat 97320

ttggtagaaa taagggtggt agctccggcg gtaatcctat ggcaggtgga atgcctagtg 97380

gtggtggttc acctaagggc ggaggctcac ctaaaggtgg aggcactcgt tctactggag 97440

gaaaaatact tgatagcgct aaaggtcttg gaggattcct agtaggtggc gcaggatgga 97500

aaggtatgtt tggtggggag tctaaaggta aaggctttaa acaaacatct aaagaagcct 97560

ggtcaggtac tagaaaagta tttaatagag ataatggtag aaaagccatg gataaatcta 97620

aagacatagc taaaggtact ggtagtggtc ttaaagatat ctataatgat agtatatttg 97680

gtaaagaaag aagacaaaac ctaggagaaa aagctaaagg ttttggtggc aaagctaaag 97740

gtctttatgg taaatttgct gataagtttg gtgacggagg taaaaatggt atcctttcac 97800

aatcaccaaa agcaggtgga agtggcatag ggaaacttgg aaaacttgca ggtggacttg 97860

gaaaaggagc cggagtttta ggtgttgcta cgtctgcctt atcattaata cctgctttag 97920

cttccggaga tagtaaagct atcggcggtg gaataggctc tatgggtgga ggaatggcag 97980

gtgcatcagc aggagcttct ataggagctt tatttggtgg tgtaggtgca atacctggag 98040

ctttaatagg tggagctata ggttccttcg gaggaggagc tgttggtgaa aaagtcggag 98100

acatggctaa aaaagctaac actaaagaag gatggaacct aggatggact aatggagata 98160

aagatggtaa gaataaattc caagattctt tattaggaaa acctatatct aaagcatgga 98220

gcggtataac aggtctcttt gataatgacg ctgaagcatc cgaagaagat agtaaagata 98280

agaaaaaagg tgttaaaggc gttaaaggag atactaagaa gaaagaaaaa atgacagcag 98340

aacaacttag agaaaagaat aaccaatctg aaactaagaa tcttaaaatc tatagtgatt 98400

tacttgacag agctcagaaa attattgaga gtgctaaagg tattaatata gatggaggaa 98460

cttctgatag tggttctgat agtggaggct ctgcatctga tgtaggtgga gaaggtgcag 98520

agaagatgta caagttcctt aaaggaaaag gactatctga taatcaggta ggagctgtta 98580

tggggaactt acaacaagaa tctaatcttg accctaatgc taagaatgct tctagtggag 98640

catttggtat tgctcagtgg ttaggagcta gaaaaacagg attagaaaac tttgctaaat 98700

ctaaaggtaa aaaatctagt gacatggatg ttcaattaga ttacctatgg aaagaaatgc 98760

agtctgatta tgaaagcaat aatcttaaaa atgcaggttg gagcaaaggt ggaagcttag 98820

aacagaatac aaaagcattt gctactggat ttgaacgtat gggagcaaac gaggctatga 98880

tgggtactcg tgttaacaat gctaaggaat tcaagaagaa atatggaggc tccggtggcg 98940

gaggtggtgg aggagcttta tcctctactt atcaagaagc tatgagtaat cctgtattaa 99000

ctactggttc taattataga ggctctaatg atgcttctaa tgcttctaca actaacagaa 99060

taacagtcaa tgttaatgtt caaggtggaa ataatcctga agaaactgga gacattatcg 99120

gaggaagaat tagagaagtt ctagatagta atatggatat ctttgcaaat gaacataaga 99180
gaagttatta gtaattttgt attgacacaa gagtagtatc atagtatact actcttatac 99240
atataaaaaa taaaaggaag tatgtgtata tgcgtagaat aagaagacct aaggtaagaa 99300
tagaaatcgt tacagatgat aatacattta cattgagatt tgaagataca cgtgactata 99360
atggtgatga gtttggagct aaacttttag gattccaaac taaaaactct atggaagatg 99420
atagttcagt tttccaaata aatatggcag gagatactta ttgggataag ctagttatgg 99480
ctaatgatat cataagaata tttattacac ctaatgatga ccccaacgat aaagaaggaa 99540
gacaagaacg acttatccag gtaggtatgg tttctcaagt atcaaaagta ggtagttacg 99600
gtaatgacca aactcaattt agaataacag gtcaatcttt tgtaaaacct tttatgaaat 99660
ttggattagg cgttattcag gaagttcaag ctgtattgcc tgaagtaggt tggcttattg 99720
atggtgatgg agataatgaa gtaaaattta ctggtagctc agctcatgaa gtaatgactg 99780
gcattatacg tagatttata ccttatatga aatataacta tactgaaaaa acatataata 99840
caattgataa ctatcttgat tatgatgatt taagtagttg ggatgagttt gaaaaactta 99900
cagaagtttc agcctttact aattttgacg ggtcattaaa acagttaatg gatatggtaa 99960
cagctagacc ttttaatgag ttattcttca aaaattcaga aaaaacacct ggaaaggctc 100020
aacttgtatt aagaaagacc ccttttaatc ctactgagtg gagagcttta gatatgatta 100080
aagtacctac tgaggatttt atagaagagg atgtaggtaa aagtgatgta gagacatatt 100140
ctatatttac agcaacacct gcaggtatgt tgaaagagct taacggtgat gtattttcca 100200
aaccacaatt ccatcctgaa ttaactgata gatacggtta taccaaattt gaagtagaaa 100260
atatttatct tagtacaaaa tcaggttcag ccactgagga ttcagattct tcaggtgatg 100320
ataatggtac agaacgagga acttactcta aaattatgaa agatttaagt aactatggaa 100380
gagataatat atctaaaggt atagataagt atacaagtaa attatcttca aaatataaaa 100440
acttaaaaaa agcccaagct aaaaaaatta tagagaagtt tgtcaaagaa ggaaaagtaa 100500
cagaaaaaga atatgaaaaa ataacaggta ataaggtaga tgatgaatta acatcagata 100560
acagaccgaa gttgacaaaa gataaattaa agagtatact aaaagagaag tttaaaacac 100620
aagatgattt taataattct aagaaaaaga aaaaagctaa gacagatgca cttaaagaat 100680
tgacaactaa atatcgtttt ggtaataaaa cacatgctac aactttgtta gatgaatata 100740
ttaaatacaa aggagaaccg cctaatgatg aggcttttga taaatatctt aaagctattg 100800
aaggtgttag taacgtagct acagacacag gttcagatgc aagtgatagc cctctagtta 100860
tgttttctag aatgttattt aattggtatc atggtaaccc taacttctat gcaggagata 100920
ttattgtttt aggagaccct aagtatgacc taggtaaaag attatttatt gaggataagc 100980
aacgaggaga cacatgggag ttctatattg aatctgtaga acataaattc gattataaac 101040
aagggtatta tacaactgta ggagtaacta gaggtttaaa agacgctatt ctagaagatg 101100
gtaaaggtag tcctcataga tttgcaggat tatggaatca atcatcagac ttcatgggag 101160

gtcttatggg tgaagatact tctaaagaac ttaaagaaaa aggtgtagca gagaaacaaa 101220

gtagtggagg taaagatggt ggttctgata gtggcggagc tcaagatggt ggctctttag 101280

attcacttaa aaaatataac ggcaaacttc ctaaacatga cccaagtttt gttcaacctg 101340

gtaaccgaca ttataagtat cagtgtacat ggtatgctta taatagaaga ggtcaattag 101400

gcattcctgt gcctttatgg ggggacgccg ccgactggat aggcggtgct aaaggagcag 101460

gttatggtgt aggtagaaca cctaaacaag gtgcttgtgt tatatggcaa agaggagttc 101520

aaggaggtag cccacaatat ggtcacgtag cttttgtaga gaaagtatta gatggaggta 101580

aaaaaatatt tatctctgaa cataactatg ctacccctaa tggatatggt actagaacaa 101640

tagatatgag ttcagccata ggtaagaatg ctcaattcat ttacgataag aaataaagga 101700

ggatagtcta tggcaacaga taaagaagct aaagatgtta ttgataaatt tatagacaat 101760

gtatttaatt ttgatgtact tacaaaagaa agaataaaag aaaaagatga agaaattaaa 101820

aaaataacta cagatgatat gtatgaaaag gttgtgtata tacgacccta cgttggagta 101880

atacaaagtc ttaaccctca acatgtgcag tatgaatcat tttctaataa tggttatgat 101940

atagaggcag aattaagttt caggaaagta agttatttag ttgataaagg gtctatacct 102000

acagattctt tatctacttt aacagttcac ttagtagaac gaaatcaaga actattaata 102060

gattactttg atgagataca agatgtgttg tatggagaat atatggaaga agaatatgta 102120

tttgatgaag atgtaccatt aagtacgata ctagcattag acttaaatga taatcttaaa 102180

tccttatcaa atataaagta tatgttcaaa ggtgctccta aagagaatcc atttggaaca 102240

gataaagatg tttatataga tacttataac ttattatact ggttatattt aggtgaagat 102300

gaagagttag cataccctat gaatattaat tacttcttta cagagggaag attctttact 102360

atattcggta aaggacataa gtataaggta gatgttagta aatttatagt tggagatata 102420

ttattctttg gtagaagtga tactaatata ggtatttatg taggagatgg ggagtttata 102480

tctatgatgg gtaaattccc taaagatgaa acacctatag gaaaatataa acttgatgat 102540

tactggaatg aatttaacgg aagagttatg agattcgatg aagaggtgta tatttaatgg 102600

tagtaagatt ccaatcttcc atggggagaa gtttaaaaag agtagattca gatgatttaa 102660

atgtaaaagg attagtttta gctacagtta gtaaaattaa ttataaatat caatcagtag 102720

aagttaaagt taacaactta actctaggaa gccgtatagg tgacgatggt agcttagctg 102780

taccttatcc taaatctttc ataggaagaa cacctgaagg aagcgtattc ggtacaaaac 102840

ctcttattac tgaaggttct gtagtattaa taggatttct aaatgatgat ataaatagtc 102900

ctattatttt aagtgtttat ggtgataatg aacaaaataa aatgattaat accaatcctt 102960

tagatggggg taagtttgat acagaaagtg tctataaata tagtagttca ctatatgaaa 103020

ttttaccatc tttaaattat aaatatgatg atggagaagg aacaagtatt aggacttata 103080

atggtaaatc atttttctct atgacatcag gtgaagaaga gaaacctcag gcaacagatt 103140

tttatactgg aactgagtat caagatttat ttacttctta ttatggtaat aagacattaa 103200

ttgagcctag aatacaaaag gctcctaata tgttatttaa acatcaaggc gtttttatg 103260

atgatggcac gccggataat catataacta ctttatttat atctgaaaga ggggatataa 103320

gagcctcagt tttaaataca gaaacacaga aaagaaccac acaggaaatg tcaagtgatg 103380

ggtcttatag ggttataaaa caagatgacg atttaatgtt ggatgaagct caagtttgga 103440

ttgagtatgg tattagtgaa gataataaat tctatattaa aaatgacaag cataaatttg 103500

aatttactga tgagggaatt tatatagatg ataagcctat gttagaaaac ttagatgaga 103560

gtatagcaga ggctatgaag aatttgaatg aaatacaaaa agaactcgat gatataaatt 103620

accttctcga gggtgtaggt aaggataact tagaagaatt aatagagtct acaaaagagt 103680

ctatagaagc ttctaaaaaa gcaacttcag atgtcaatag acttacaact cagatagcag 103740

aagttagtgg tagaactgaa ggtattataa cacagttcca aaaatttaga gatgagactt 103800

ttaaagattt ttatgaagat gcttctactg ttattaatga agtaaatcag aatttcccta 103860

ctatgaaaac agatgttaag accttaaaga ctaaagttga taacctagag aaaactgaaa 103920

taccaaatat taaaactaga ttaacagaac tagagaacaa taataacaat gctgataaaa 103980

taatatcaga tagaggagaa catataggtg ctatgataca gttagaggaa aatgtcactg 104040

tacctatgag aaaatatatg ccaataccat ggagcaaagt tacttataat aatgcagagt 104100

tttgggattc taataatcct actcgattag tagtacctaa aggaataaca aaagtaagag 104160

ttgcaggtaa tgttttgtgg gactctaacg ccacaggaca acgtatgttg agaatattga 104220

aaaatggtac ttatagtata ggattacctt atacaagaga tgtagctata tctacagcac 104280

ctcagaatgg tactagtgga gttattcctg ttaaagaagg agattacttt gagtttgaag 104340

ctttccaaga ctcagaaggt gacagacaat tcagagcaga cccttataca tggtttagta 104400

ttgaagctat agaattagaa actgaaacta tggagaaaga ctttatgctt ataggacata 104460

gaggagcaac cggatacaca gatgagcaca cgataaaagg atatcaaatg gctttagata 104520

aaggtgcaga ttatatagaa ttagatttac aattaacaaa agataataag ttattgtgta 104580

tgcatgattc tactatagac agaacaacaa caggaacagg taaggtagga gatatgacct 104640

tatcttatat acaaactaac tttacatccc tcaatggtga gccgatacca tctcttgatg 104700

atgtactaaa tcattttgga acaaaagtta aatattatat agaaactaaa cgtccgtttg 104760

atgctaatat ggataaagaa ttattaactc aattaaaagc aaaaggatta ataggaatag 104820

gttcagagag attccaagta attattcaat catttgctag agaatcgtta attaatattc 104880

ataatcaatt ctctaatata cctttagctt acttaacaag tacattctct gaaagtgaaa 104940

tggatgattg tttaagttat ggttcttatg ctattgcgcc taaatataca actataacta 105000

aagaattagt agatttagct catagtaaag ggcttaaagt ccacgcatgg acggtaaata 105060

caaaagaaga aatgcaaagc ttaatacaaa tgggtgtaga tggattcttt acaaactacc 105120

tagatgaata taaaaagatt taatattaaa gacctattaa tttaggtctt tttttagttg 105180

taatttaaac tagttcgtga tatattagta gtatgagatt tatatacata ctgaaaagga 105240

gaggataaaa tgccacaatc agatggaata agtaatcttc atagaatagc tttacgtttc 105300
cctaaagaag gcggtggtta tgatatgtat agatttaaag ttaaccctga gaactacaca 105360
atagattcac cacaacgtac gacagcaatt aaaacaaaat cagatatcgt aatagaagat 105420
tatggtaaag atatagaagt tattaacttc acaggtacaa ctggttttag acctgttaga 105480
gaagcagatg ggttaaaaac aggtaagcag aaaatggaag agttacaaag tagagttagt 105540
gaatatgcta tgcaaggtgg cagtggtaat gtaagtggtt cttacttaca atttttaac 105600
tttacagatg atagttatta taaagttcat ttagctcctc aggggttaaa gataactagg 105660
tctaaagatg aaccattact ttttagatat gaaataacat tagtagttat tggttcatta 105720
acagaagcag atagaagtgc tgtaactact gaagagtttg gtaatgttaa acctaatgct 105780
tctcaaagag tagatgaagg tataaaagaa ttagataaaa atgctcgtaa aacgagagat 105840
agaaacaatc aagaaatatc tagaagagaa aatacaatac ctaaatccac aggagataat 105900
acgaacgagg gtaatagact taagcaaagc ttccctagta gttctatata taatcctaga 105960
caatctacta atggattaaa aggtaatatt gacaatatgg ctctgataat aggttacggt 106020
gatggaggtg tatctagcta atgaataatt ttataccaca acctcaaggt ctacttagat 106080
ttttaaatgc cctagataca gatttaactt cttctcatat gaatttactg gatgaagagg 106140
tatcatttgt atctaaattt tatacaccac agttacaatt aagtgaatta gcaaaaaaag 106200
tattgacaaa tataaagaca gatgatatac ctgtattaga aagggaattt aatgataata 106260
caattatcca taaagctaac gatacattac taaaagtaca ggctccaaga atgtatatga 106320
ttctacagtc tattgtactt gaagcatatg ctattgttaa ttgctttgta gaaaatccaa 106380
gttctttaaa atacttaact gaagaagatg ttagtataac acgagaaaac ttaaattatg 106440
tagctgacta cttaggtaac tatgatgact acaatagtgt tgtattagac ttaagagatt 106500
tagacttatg ttttagtgct atagaattac aattacctct aattaaaaag gaggctaacg 106560
tataatgaga tttaagaagc acgtagttca acatgaagaa acgatgcaag caatagcaca 106620
gagatactat ggtgatgtta gttattggat agacctagta gagcataata atttaaagta 106680
tccctattta gtagaaactg atgaagaaaa aatgaaagac ccggaacgat tagcttctac 106740
cggtgataca ctgattatac ctatagaatc tgatttaaca gatgtatcag caaaagaaat 106800
taattctaga gataaagatg tactagttga attagcttta ggaagagatt taaatattac 106860
tgcagatgaa aagtatttta atgaacatgg tactagtgat aatatactag cattcagcac 106920
aaatggtaat ggagatttag atactgtaaa aggcatagat aatatgaaac agcaattaca 106980
ggcacgttta ttaactccta gaggttcctt aatgttacat cctaattacg gttcagattt 107040
gcataattta tttggtctta atatacctga acaagctacg cttatagaaa tggaagtatt 107100
gagaacatta acatcagata atagagtaaa atctgctaat ttaattgatt ggaaaataca 107160
aggtaatgtt tattcaggtc aattttcagt ggaaataaaa tctgttgaag aatcaataaa 107220
ttttgtctta ggacaagatg aggaaggaat ttttgcttta tttgaatagg aaaggattaa 107280

attatgaaaa ctagaaaatt aactaacata ctatcaaaat taatagataa gacaatggca 107340

ggtacaagca agataacaga ctttactcct ggttcagctt cccgttcatt attagaagct 107400

gtatcattag agatagagca attctatatt ctaacaaaag aaaatattga ttggggtata 107460

caagaaggta tcattgaagc ttttgatttt caaaaaagac aatctaaaag agcttatggt 107520

gatgttacta ttcaattcta ccaaccctta gatatgagaa tgtatatacc tgcaggaaca 107580

acttttactt caacacgaca agaataccct cagcaatttg aaacattagt tgattattat 107640

gcagagcctg attctactga gattgttgtt gaagtttatt gtaaagaaac aggggttgca 107700

ggtaatgttc ctgaaggaac gattaatact atagcatcag gttctagttt gattagaagt 107760

gttaataatg agtattcttt taatacagga actaaagaag aaagtcagga agactttaaa 107820

cgtagattcc actcttttgt agaatctaga ggtagagcaa ctaataaatc agtaagatat 107880

ggtgcactgc agatacctga tgtagaaggt gtttatgttt atgaagaaac agggcatatt 107940

acagtatttg ctcatgatag aaacggtaat ttatcagata ccttaaaaga agatataatt 108000

gatgctttac aagactatag accaagtggt ataatgttag atgttacagg tgtagaaaaa 108060

gaagaagtta atgtttctgc tacagtaact atatctaata aatctagaat tggtgataca 108120

ttacaaaaac atatcgaaag tgttattaga agctatttaa ataatttaaa aacttctgat 108180

gacctaataa ttacagacct tattcaagct ataatgaata ttgatgacgt attaatatat 108240

gatgtgtcat ttgataactt agatgagaac attatagtac caccacaagg gattattaga 108300

gcgggagaaa taaaagtaga attaaagtaa agagaggtga aacttaagtc gtggctaatt 108360

ttttaaagaa tcttcatcca ttattaagaa gagatagaaa taaaaaagat aatcaagacc 108420

ctaactttgc tctgatagat gcactcaatg aagagatgaa tcaagtggag aaagatgcta 108480

tagaaagtaa attacaatcc tctctaaaga catctacaag tgaatattta gataagtttg 108540

gggattggtt tggagtttat cgtaagaccg atgagaacga tgatgtttat agagcaagaa 108600

ttataaaata tttactcttg aaaagaggaa ctaataatgc tataatagat gctataaaag 108660

attatttagg tagagatgat attgatgtaa gtgtatatga gccctttaca aatatttttt 108720

atacgaacaa atcacattta aatggtgaag accatttaat gggatactat tatagatttg 108780

ctgttattaa tgtatctata ggtgattatt ttcctgtaga gattatagat gtaattaatg 108840

aattcaaacc tgcaggtgta actctatatg tcacttatga tggagcttct actattagag 108900

gtggagcaat tattaagtgg ttagatgggt tacctaaaat agaaacatac caagagtttg 108960

atagatttac aggttatgat gatacattct atggtcatat taatatgaat caaagtaaag 109020

atactgataa cagttcatca gatattttta aaacaaatca tagcttaatt aatagtttag 109080

atgttttaac aggttcatct agtgtaggta gacagtatat taactatgga tatgtaacat 109140

catatgttta taatccaggt atgacatcct ctgtaaacca aataagtgct agtacagaag 109200

gtagaggtca agaagtacct actgattact atatgtatac tagtactaag aataacaata 109260

cagtagaact tagtatgcaa actacttccg gtgtgtctta tttatataat aactttaatt 109320

ttagagatta tatgagtaaa tatagacctc aagtagattt acaatctgat gaggctagaa 109380

gaattgtatc tgattatata aaagaattaa gtattgatta ctatcttagt gctgtgatac 109440

ctcctgatga aagtatagaa attaaactac aagtttatga tttttctatt aatagatggc 109500

ttacagtatc aattaataac ttatctttct atgaaaaaaa tattgggagt aatatagggt 109560

atataaaaga ctatctaaac agtgaattaa atatgtttac taggttagag ataaatgcag 109620

gtaaaagaga ttcagtagat attaaagtta attacttaga tttaatgttt tattactatg 109680

aacgaggtat ttatacaata aaaccttata aagcattaat agaaaattat ttagatatat 109740

ctagagagac ttatgtagaa gcatttaaaa tagcatcatt atctaatgga gatattataa 109800

ctaaaacagg ttttcagcct atagggtatt taaaactagt tggtaattat gaaaatacaa 109860

gacctagcac aataaatata gtagctaaag atacagataa taaccctata gaatctaatg 109920

aattagatgt atataataca gtagagaata gaaatctatt acaatcttat aaaggtgcaa 109980

atacgatagc tagagaaata acttctacaa aagagtttac tgtatcagga tgggctaaag 110040

agatatactc aactaattat ctttctaaag tattaaaacc aggtaaagtg tatacgttat 110100

cttttgatat agaaataaca ggtaatgacc taactcttaa atcttattct gataatcatg 110160

gtatatattt atacagtaat actaagggaa ttgttgttaa tggtgttaaa tctatggaac 110220

gtactatagg taacaaagta tccgtaactc aaacttttac agcccctact attactgacc 110280

atagattatt aatatatact ggaagatata catctgatgg taaagcatca actcctccag 110340

tgttctttaa tacagttaaa attacggaat taaaattgtc tgagggtacc tctaatctag 110400

agtactcacc tgctccggaa gataaaccta acgtaataga aaaaggaatt aaatttaata 110460

atatcctaac taatatacag actttaagta ttaattcgga tactatctta aaaaatgtaa 110520

ctttatatta ttcttactat ggtgataatt gggtagaact aaagactcta ggaaatatta 110580

gtactggaga aacaacagaa accaataact taatagattt atatggatta cagacagtag 110640

attattctaa tataaatcca atgtctaaag tatcattacg ttccatttgg aatgttaaac 110700

taggtgaatt gaacaatcaa gaaggttctt tatctaatat gcctaatgat tactttaatg 110760

ctgtatggca ggatatagat aaattatcag atattgagat aggttctatg agaatggtta 110820

aagacactga gggtggagta ttcgatggag ctacaggtga aattattaag gctactctat 110880

ttaatgtcgg ttcttatact gatttagaca tgttagctta tactttgact aactatactg 110940

aaccgttaac tttaggctct agtcgattaa taagtgagtt aaaagaagaa cttctaacat 111000

cagaatcatt taatgttgat aatagaatta aagtaattga ctcaatatat gaggagttac 111060

caaatacaag cattattaaa aatggatttg ttgaaagaga ggttacaggc tctaaatatt 111120

tagattatgg tttatatgag cctatagaag atggtactag atataaactt attgtcgaag 111180

gagaatttaa agataatata gaatttatat atttatacaa ttctaaccct aactttaatg 111240

aaacatttat atatccatca gagataatta atggagttgc tgaaaaagaa tttattgcaa 111300

aaccatccac cgaagacaaa ccaaggttaa atacagatgt tagaatatat atacgacctt 111360

atgattcaac tatctctaaa gtaagaagag tagaattaag gaaagtttaa taaataagtt 111420
gacagaaagt taataatatg gtatacttat aaagtaatat ttagtgggta taccatgtta 111480
tattaataaa gaaaacaaca gatgaaagga attaaaaaat atggcaattg caacgtataa 111540
ttctcatgtt gagttagcaa aatatctagt tagtaaagct gattcagttt acttaacaat 111600
tggaaagagc acaccgtggt ctaatgaaac aaacccaccg caacctgatg aaaatgcaac 111660
agtattacag gaggttattg gatacaaaaa agctactaaa gttactttag ttagaccttc 111720
taaatcacct gaagatgata ataagaattt aatttcttat ggtaataaat catgggtaga 111780
agtaacacct gaaaatgcta aagctgaagg agctaaatgg gtttacttag aaagtagtat 111840
tgttggtgac gaactgcctc ttggaacata tagacaggta ggatttgtta tggacttagt 111900
agcaaaaagt ggtattagta aatttaactt agtacctagt gaagtagaat caactggaac 111960
attattattc tttgataata aacaattcca aaatagaagt gagcagacaa ctgctaaaga 112020
aagatttatt gtagaagttt aaagaaaggg agataattct aaatggcaat taattttaaa 112080
ggttcacctt atttagatag atttgacccg tctaaagata gaacaaaagt attatttaat 112140
cctgatagac ctctacaaca ggcagaatta aatgaaatgc agtctataga ccaatattat 112200
ttaaaaaatc taggagacgc tatttttaaa gacggagata aacagtcagg acttggattc 112260
acattgtctg aagataatgt attgacagta aatcctggtt atgtatatat caacggtaaa 112320
ataagatatt acgataatga cgattcagtt aaaataactg gcgtaggtaa agaaactatc 112380
ggtattaagt taacagaacg tattgttaca cctgatgaag atgctagtct attagaccaa 112440
actagtggag taccaagtta cttctctaaa ggtgcagata gattagaaga aaagatgtca 112500
ttaacagtta atgaccctac atcagcaact atttatactt tcatggatgg agatttatat 112560
attcaatcaa ctaatgctga aatggataaa atcaataaag tattagctga acgtacttat 112620
gatgagtcag gttcatataa agtaaatggt tttgagttat tctcagaagg taatgctgaa 112680
gatgatgacc acgtttctgt agttgtagat gcaggtaaag cttatgtaaa aggttttaaa 112740
gtagataaac ctgtatcaac aagaattagt gtacctaaat cttatgactt aggaacagca 112800
gaaaatgaaa gtactatctt taataagtct aataattcta ttagtttagc taatagccct 112860
gtaaaagaaa ttagacgtgt tacaggtcaa gtacttattg aaaaagaacg agttacaaga 112920
ggagcccaag gtgatgggca agattttctt tcaaataata cagcatttga aattgtaaaa 112980
gtttggactg aaacaagccc tggtgttact acaaaagagt ataaacaagg agaagacttc 113040
agattaacag acggtcaaac gattgattgg tcacctcaag gtcaagaacc ttcaggaggt 113100
acttcatact acgtttctta taaatataac aaacgtatgg aagccggtaa agattatgaa 113160
gtaacaactc aaggtgaagg tttgagtaag aaatggtaca ttaacttcac accttcaaat 113220
ggtgctaaac ctattgacca aacagtagta ttagtagact atacttacta cttggctcgt 113280
aaagattcag tgtttattaa taaatatggt gatattgcaa tattacctgg tgaacctaat 113340
attatgagat tagttacacc accattaaac acagaccctg agaatttaca attaggtaca 113400

gttacagtat tacctgattc agatgaagca gtatgtattt catttgcaat cactagattg 113460

tctatggaag acttacagaa agttaaaaca agagtagata acttagagta taaccaagca 113520

gtaaatgctc tagatgatgg tgctatggaa ggacagaacc cactaacatt acgttcagta 113580

tttagtgaag ggttcattag tcttgacaaa gcagatatta cacatcctga cttcggaatt 113640

gtatttagtt ttgaagatgc agaagctact ttggcttata cagaagcagt taaccaacct 113700

aagattattc caggagatac aacagctcat atttggggta gattaatttc agcaccattt 113760

actgaggaac gtacaatcta tcaaggtcaa gcatcagaaa cattaaatgt taacccttat 113820

aatattccta acaaacaagg tgtgttaaag ttaacaccta gtgaggataa ctggattgat 113880

actgaaaatg ttacaatcac tgaacaaaaa actaaaaaag taactatgaa acgattttgg 113940

agacataatg agagttacta tggtgagact gagcattact tgtattctaa cttacagtta 114000

gatgcaggac aaaagtggaa aggtgaaact tacgcttatg atagagagca tggacgtact 114060

ggtactttat tagaatcagg aggacaacgt actctagaag aaatgattga attcattaga 114120

atcagagatg tatccttcga agttaaagga ctaaacccta atgataataa cttatattta 114180

ttatttgatg gggtaagatg cgctataaca cctgcaactg gttatagaaa aggctctgaa 114240

gatggtacga taatgacaga tgctaaagga acagctaaag gtaaatttac tattcctgca 114300

ggtattcgtt gtggtaaccg agaagttaca cttaagaatg ctaactctac aagtgctaca 114360

acttacacag cccaaggacg taaaaaaacc gttcaagata ttattatcag aactcgtgta 114420

acagtaaact tagtagaccc attagcacaa tcattccaat atgatgagaa cagaactata 114480

tcatcattag gattatactt tgcttctaaa ggtgataaac aatctaatgt tgttatccaa 114540

attagaggta tgggtgacca aggttatcct aataaaacaa tctatgcaga aacagttatg 114600

aatgctgatg atattaaagt atctaataat gctagtgctg aaactagagt atactttgat 114660

gaccctatga tggctgaagg cggtaaggaa tacgctattg ttattattac tgagaacagt 114720

gattatacaa tgtgggtagg tactagaact aagcctaaga ttgataaacc taatgaggtt 114780

atctcaggta acccatacct tcaaggtgta ttattcagtt catcaaatgc atcaacatgg 114840

actcctcatc aaaactctga ccttaaattt ggtatttata cttctaaatt taatgagaca 114900

gcaacaattg aattcgaacc aattaaagat gtatcggcag atagaatagt tcttatgtct 114960

acgtacttaa ctcctgagag aacaggatgt acatgggaaa tgaaattaat tctagatgat 115020

atggcatctt ctacaacatt cgaccaatta aaatgggagc ctatcggtaa ctaccaagat 115080

ttagatgttt taggtctagc aagacaagtt aagttaagag caactttcga atctaataga 115140

tatatctcac cattaatgag ctctagtgat ttaacattca ctacattctt aacagagtta 115200

acaggttcat atgttggtag agctattgat atgacagagg ctccttacaa tacagtaaga 115260

tttagttatg aagctttctt acctaaaggt actaaagttg ttcctaagta ttctgcggat 115320

gatggaaaaa cttggaaaac atttactaaa tcccctacaa ctactagagc caataatgag 115380

tttacacgct atgtcattga cgagaaagta aaatcatcag gaacaaatac taaactacaa 115440

gttagattag atttatcaac tgaaaatagc tttttacgtc ctcgtgttcg tagacttatg 115500

gttactacta gggatgaata aactagaggg gttgattgac ccctctttat ttaataagga 115560

gagatttata tgcctagaga agttagagac ccttattctc aagctaaatt atttatacct 115620

acagttgaag aaaaatcaat taaggaatta gaaaaaacat acaaagaaaa aattgatgaa 115680

gctactaagt taatcaatga attaaagaaa gagagaggag aaaaatagat ggcatttaac 115740

tacacgcctc ttactgaaac acagaagtta aaagatatgt atcctaaagt taatgatata 115800

ggtaactttt taaaaacaga agttaacctt agtgatgtaa aacaaatatc acaacccgac 115860

tttaataata ttttagcatc tatacctgat agtggtaact actatgtaac taattcaaaa 115920

ggtgctccta gtggagaagc tacggcagga tttgtaagat tggataaacg aaatgtaaat 115980

tattataaaa tttactattc accatatagt agtaataaaa tgtatatcaa gacttatgct 116040

aatggtactg tatatgattg gattagtttt aaattagatg aaggtaactt atacaatgaa 116100

ggtaatactt taaatgtaaa ggaacttact gaatctacaa ctcaatatgc aacactagtt 116160

aatcctccaa aagagaactt aaatacaggt tgggttaatt acaaagaaag taaaaatggt 116220

gtttcttctt tagtagaatt taacccggtt aactccactt caacttttaa gatgataaga 116280

aagttaccag tacaagaaca aaagcctaac ttattgaaag atagtttatt tgtttatcct 116340

gaaactagct attctaatat taaaacagat aactgggata cgcctccatt ttggggatat 116400

tcttctaata gtggtcgttc aggagttaga tttagaggag agaatacagt acagatagat 116460

gatgggtcta atacgtaccc tttagtagtt tctaataggt ttaaaatggg taaagaactt 116520

tctgtaggtg atactgtaac ggtatcagta tatgctaaaa ttaatgaccc tgctttactt 116580

aaagataact tagtttactt tgaattagca ggatacgata ctgtagatga tactagtaaa 116640

aatccttata caggaggacg tagagaaata acagcaagtg agataacaac tgagtggaaa 116700

aaatactctt tcacatttac gatacctgaa aatacaatcg gagcatcagg cgttaaagtt 116760

aattacgtat ctttactact aagaatgaat tgttcatcta gtaaaggtaa tggtgctgta 116820

gtatactatg ccttacctaa attagaaaaa tcacctaaag ttacaccatt tattacacat 116880

gaaaatgatg ttcgtaaata tgatgagatt tggtctaatt ggcaagaagt tattagtaaa 116940

gatgaattaa aaggtcactc tcctgtagat attgaatata atgattattt taaatatcag 117000

tggtggaaat ctgaagttaa tgaaaagagt ttaaaagatt tagctatgac agtacctcaa 117060

ggatatcata cattttattg tcaaggctct attgccggga cgcctaaggg acgttctatt 117120

agaggaacca ttcaggtaga ttatgacaaa ggtgacccct acagagctaa taagtttgtt 117180

aaattattgt ttactgacac agaaggtata ccttatacat tatactacgg agggtataat 117240

caaggttgga aactcttaaa gcaatcagaa acttctactt tactatggga aggtacttta 117300

gattttgggt ctacggaagc tgttaactta aatgactcat tagataatta tgatttaatt 117360

gaggtaactt attggactcg ttcagcagga cattttttcta caaaaagatt agatataaaa 117420

aatacatcaa atttactgta tattagagac tttaatattt caaatgatag tacaggttct 117480

agtgtagact tttttgaagg gtattgcact ttccctacta gagcatcagt acaacctggt 117540

atggtaaaat ctataacttt agacgggtct acaaatacaa caaaagtagc atcatggaat 117600

gaaaaggaac gtataaaggt atacaatatt atgggaatta atagaggata aagaaaggtg 117660

gaataaaaaa ctatggctgt taaatatgat ataggtaata atgagatagt attacactta 117720

agagaaggta aatatataac agggtttaca acagtaggag ggtatgacaa ggagttaggg 117780

caagtaaaag ttaatagaga aatcttacct gcttacttct ttgataattt tgcctatgaa 117840

agatatttgt attatagtaa acctgaagag gttatagaaa ataaaaacta tgtaccacca 117900

caaatcaatg atgatgagga atcccaacaa attactgtac ctaaagaaca atatgatagt 117960

ttaaaagaag agctagagct tatgagaaaa caacaagaag ctatgatgga aatgcttcaa 118020

aagctcttag gtcaaaaggg gtaattataa atggcattaa attttactac aataacggaa 118080

aacaatgtta ttagagacct gactactcag gtcaataaca ttggagaaga attaacaaaa 118140

gaaagaaata tatttgacat taccgatgat ttagtttata attttaataa atcacagaaa 118200

attaaactaa ctgatgataa aggattaact aaatcttatg gaaacataac agcccttaga 118260

gatataaaag aacctggtta ttactatata ggtgctagaa cattagcaac attattagat 118320

agacctgata tggaatctct tgatgttgtt ttacatgtag tacctcttga tacttctagt 118380

aaggtagttc aacatttata tacactatct actaacaata accaaattaa aatgttatat 118440

agatttgtct cagggaactc tagttcagaa tggcaattta ttcaaggatt acctagtaat 118500

aaaaatgctg ttatatcggg cactaatatt ctagatatag cttcaccagg tgtttacttt 118560

gttatgggaa tgacaggagg aatgcctagt ggagtaagct ccggattttt agacttaagt 118620

gtagatgcta atgataatag attagctaga ctaactgatg ctgaaactgg taaagaatat 118680

actagcatta agaaacctac aggaacatac acatcttgga aaaaagaatt tgagccaaaa 118740

gatatggaga aatatttact aagtagtatc agagacgatg gtagtgcatc attcccactc 118800

ctagtttata ctagtgataa taaaacgttt caacaagcta ttatagacca tatagataga 118860

acaggtcaaa caacctttac tttctacgtt caaggtggtg tatcaggttc ccctatgtct 118920

aatagttgtc gaggtctatt catgtcagat acacctaaca cttctagttt acatggtgtc 118980

tataatgcta taggtacaga tggtagaaat gtaacaggtt cagtggtagg aggtaattgg 119040

acttcaccaa agacatcacc ttcccataaa gaattatgga cgggagcaca atcattccta 119100

tctgtaggta ctactaagaa tctagcagat gatattagta attactctta tgtagaggtt 119160

tatactaaac ataagacagt agagaagact aaaggtaatg atgactcggg tacaatttgc 119220

cacaagttct acttagatgg tagcggtact tacgtttgct caggaacttt tgtttcagga 119280

gatagaacag atacaaaacc acctgttaca gagttctata gagtaggtgt atctttcaaa 119340

ggttcaacat ggacgcttgt agatagtgca gtacaaaata gtaaaactca atacgttaca 119400

agaattatag gtattaatat gccatagact aggataagtt tcctagtctt tttttcttga 119460

cttgaaaagg attctatggt atactataac tcgtgtaagg atataaggag attaaaatga 119520

gattaagaat taagaactta tatacctatg tagaatttga ggaggatgat aaatacttaa 119580

aagatatatt tttaaagaga gtccatacta ctataggagc aaggcaagaa ggttttcaat 119640

atagccctgc gtacaaaaga ggtagttggg atggttatgt agacttttat gtttatgagg 119700

aagataaatt ccctactgga cttttattta aaattgagtt attattaggt gagttacaat 119760

caaggtataa cttccagttt gaaacaattg atgagcgtga tgaaagtttc ttatctgaag 119820

aagatattga tgatgagata acattgcttg ataataatgt cggtcaaatt accttaagag 119880

attaccaata tgaagcagtg tacaatagct taacatttta caatggtatt gctcacttag 119940

ctactaatgg tggtaaaact gaggttgcta gtggtattat agaccaacta ttacctcaat 120000

tagaaaaagg tgaaagagta gcgttcttca caggctctac ggagatattt catcagtctg 120060

cggatagact acaagaacgt ttaaatattc ctattggtaa agtaggtgca ggtaaatttg 120120

atgttaaaca ggttacagtt gtaatgatac ctactttaaa tgcaaacctt aaagacccaa 120180

cacaaggggt aaaggttaca cctaaacaaa atattagtaa aaagattgct caagagatat 120240

tacctaaatt tgaaggtgga acaaatcaaa agaaattact aaaagtatta cttgataaca 120300

caacacctaa aacaaaagta gaacaaaacg tattaagtgc cttagagata atttaccaaa 120360

atagtaagac agatgcagaa gttttattaa acttaagaaa tcataatgca cattttcaaa 120420

aaattgttag agaaaagaac gaaaagaaat atgataaata tcaagatatg agagattttt 120480

tagactcagt tacagttatg atagttgatg aggcacacca ttctaaatct gattcttggt 120540

acaataatct aatgacatgt gaaaaagctt tatatcgaat tgcattaaca gggtctatag 120600

ataaaaaaga tgaattactt tggatgagat tacaggctct atttggtaat gttattgcac 120660

gaactactaa taagttttta attgatgaag gtcattctgc tagaccaaca ataaatatta 120720

tacctatagc taatcctaat gacatagata gaattgatga ttatagggaa gcttacgata 120780

gaggtataac aaataatgat tttagaaata aacttattgc aaaactaaca gaaaagtggt 120840

ataatcaaga taaaggtaca ttgattattg taaacttcat tgaacatgga gacacgatat 120900

cagaaatgtt aaatgattta gatgtagagc actacttctt acatggagaa atagactctg 120960

aaactaggag agaaaaatta aatgatatga gaagtggtaa gcttaaagta atgatagcta 121020

catcacttat tgatgagggt gtagatatat ccggtattaa tgcactaata ttaggtgcag 121080

gaggtaagtc attaagacaa acattacaac gtattggtcg tgctttacgt aagaaaaaag 121140

acgataatac aacacaaata tttgatttta atgatatgac aaatagattt ttatatactc 121200

atgctaatga gcgtaggaaa atttatgaag aggaagattt tgaaataaaa gacttaggaa 121260

aataggaggg taagagatgg caacaaaaac acaaagaaag ctataccaat atctagagga 121320

aaatgctaca gaaaataaat ttcatatttc tactaagaaa gagctagcag attctctagg 121380

tgtttccatc tctgctttat ccaataacct taaaaagtta gaagaagaaa ataaagtcgt 121440

tactgtttct aaaagaggaa aaaacggcgg agtaataata actttagtta gagagtatga 121500

tacagaagaa ttgaaagaat ttaataattc tacagataat attattactt ccgatttaca 121560

gtatgctaag gcattaagag aaaagcactt cccttcttat agatatgaga gaaaagaaca 121620

acgtagacgt actaaaatag aaatggcaca atacaatgcc attaaggatg agaagagaag 121680

aattatagca gatatgaact tctattcaga aggtcttcct tatccttcta aagatatttt 121740

taatatgtct tatgacccgg aagggtttta taaagcatac atcttatgta agttatacga 121800

ccaatatgct atttctcata tggatgctaa acatacaagt catcttaaag caatgagtaa 121860

ggcaacaact aaagatgaat atgactatca tcaacatatg tctgaatact atagaaataa 121920

aatgattcaa aatttaccta gaaatagcgt tagtgataat ttctttggta gtaaaatgtt 121980

taataccttt tataattttt atttaaaaat aaaagataaa aatattaatg tatttaaata 122040

tatgcaaaac gtatttaaaa atgtaacatt ttattatgag aatggtatgc aacctaatcc 122100

aataccttct cctaacttct ttagttcaga taagtatttt aaaaactata ataattatat 122160

taaaggaata aaaaaaggtg ttaacagtac gaatagacac ctaggtgata cagacagcat 122220

cattaattca tcagactacg tgaaaaaccc tgctgtatta catctacacc aactatatac 122280

tacaggatta aattctactt tacatgatat tgatactatg tttgaacaag ccttagacct 122340

tgaaaatgcc tcctatggac tatttggaga tatgaaacat attattttac tacagtataa 122400

ttctatgatt gaagaagaaa ttaagaattt acctagagaa gaaaaggata ttattaataa 122460

atatgtaaaa caatgcataa ttaatgatta ttcaccaaca agtatttcac catctgcaag 122520

gttatcaatg tttactatgc agaaagagca tatagtttac aataagcagt taaataaggg 122580

aatcaagaga gaggatttat taccattaag tctaggaggt atagtgaata aagattcatt 122640

gagtggtatg gatatacaaa acttagaaca gaatggtaat gaatacctgt atatgagaca 122700

acatacttca acttattata tattaagaat gtttggtgac tatttaggat atgaggtaaa 122760

cttaagagaa gtaaaatata ttgtagagaa atataattta attgataaaa taccattgac 122820

aaaagagggt atgttggatt ataataaact tatacattta gtagaggaag aggttaataa 122880

ctatgagtaa gaagataaag gagcttatcc ttcataaatc aatgaaggat atacattttg 122940

caagagaagt attagataac ttacctaaga atctattttc agcagagtct gaggacatgg 123000

gttacttatt tacagctata aagagaacag cacatatttc cgataagatg tcaaatgaag 123060

cattagcaat taaagtagaa cagcttatgg gtaataataa ggaagatgaa gagaaagtaa 123120

ccaagacatt aacttactta gaagatttat ataaagtaga cgttaatgaa aaagatgaat 123180

ctgttaatta tgaaatagag aagtatatta aaacagaaat gtcaaaagaa gttttagtta 123240

aatttattgc agaaaataaa caagaagact ctgataatct acatgaactt gtagacaaac 123300

taaagcaaat agaagtaagt gacatctcag gaggtaatgg agagtttatt gacttctttg 123360

aagatacaga aaagaaacaa gaactattga gtaatttagc tacaaataaa ttctctactg 123420

gatttacttc tattgacaac catattgaag gtggtatagc aagaggagaa gttggattaa 123480

ttatagctcc tactggtaga ggtaaatcat taatggcttc aaacttagct aagaattatg 123540

ttaaaagtgg attaagtgtt ttatatattg ccttagagga aaaaatggat agaatggttt 123600

tgcgtgctga gcaacaaatg gcaggagcag aaaagagtca aattgtaaat caggatatgt 123660

ctttaaataa taaagtttat gatgcaatac aaaatcatta tcagaagaat agaaagttat 123720

taggtgactt ttatatttct aaacatatgc caggtgaagt tacaccaaac caattagagc 123780

aaattattgt taatacaaca attaagaagg ataaaaatat tgatgttgtt attattgact 123840

atcctcactt aatgagaaat ccttatgcta aatatcattc agaatcagat gcaggaggaa 123900

aattgtttga agatattcgt agattatcac agcaatatgg atttgtttgt tggacgttag 123960

ctcaaactaa ccgtggtgct tatggttcag atgttattac aagtgagcat gtagaaggtt 124020

ctcgtaagat tgtcaatgct gttgaggtgt ctttagcagt aaaccaaaaa gatgaagaat 124080

tcaagagtgg tttcttaaga ttatatttag ataaaattcg taatagctcc aacacaggag 124140

aacgatttgt taatcttaaa gtagaaccaa ctaagatgat tgtaagagat gaaacacctg 124200

aagaaaaaca agagcatata caattgctat cagataatgg aaaagaagac acaagtaaat 124260

ttcaaaataa agataataaa atagaagcta taaataacac attcggagga ttaccgggag 124320

tttaattttt taaaatatac cacttgacat tttatatgtt aggtggtata attattttat 124380

aaagaataaa ggagagatta ataatgaaat ttgtattctt tacagatagt cattttcacc 124440

tatttactaa ctacgctaaa cctgataatg aatttgtgaa tgatagattt aaagaacaga 124500

tagaagcatt acagaaagtt tttgatattg ctaaaaaaga agaagcaaca gttatatttg 124560

gtggagattt atttcataaa cgtaactcgg tagatactag agtatacaac aaagtattta 124620

gtacatttgc caaaaatgat gaggttcctg tattattact tagaggtaat catgatgcta 124680

caactaattc attatatact gattcaagta tagatacatt tgagtatcta cctaatgtaa 124740

gtgtaataaa atcattaaat acaattttaa aagataatgt taatattgtg tttactgctt 124800

atggggatga gacgaaggaa ataaagacat acattaatag taattacgat aaagatatgg 124860

tcaatatact agtaggtcac ttaggtgtag aaggttcatt aactggaaaa ggctctcata 124920

gattagaagg ggcatttgga taccaggatt tattacctga taaatatgat ttcattttac 124980

taggtcatta tcaccgtaga cagtatttcc aaaatccgaa tcatttttat ggtggctcat 125040

taatgcaaca atcattttct gatgaacaag aagctaatgg tgttcattta atagatacag 125100

aaaaaatgac tacagaattc atcccaattc atacacgtag atttattact attcaaggag 125160

aagatattcc tgagaacttt gaacagttaa tcgaggaagg taattttatt agggttatcg 125220

gtacagcaaa tcatgctaag gttttagaaa tggatgacag tatgaaagat aagaatgttg 125280

aagttcaaat taaaaaagaa tatactgtag agaaacgtat tgatagtgat gtatctgatg 125340

acccttttaac aattgctagt acctatgcta aacaatactc acctgaatca gaacaagaaa 125400

tacttgagtg tttgaaggag gttttataat gaaaaaatat agagaatacc taaataagac 125460

agatgcagaa aatttagcag aggattggga gaaagtaacc gaagatttat ggaaagtgtt 125520

taaagatatg aaacctaaaa ttaatacatt agatattagt aatgtagaaa gtaaaaactt 125580

agataaaagt aaacctatac tacaattcca agattcagat ggagtaatag agaatatttg 125640

taatgttgag ggtttagaag atggtttaag taaaatgaaa aaggtttttg atgatagtaa 125700

ctttgaaaag cattattata gtagagtcgt agaccatgat gagtattact ggattgatta 125760

tggttctcat cattgtttct ttagagttac gaaaggggat aagtaatggt tgtatttaaa 125820

caagtagaag ttaataattt tttagcaatt aaagaagcta cgctagagtt agacaataga 125880

ggattaattc taattgaagg tgagaataaa tccaatgagt catttcattc aaacggttca 125940

ggaaaatcaa ctttaatatc tgccattact tacgctttat atggtaaaac tgaaaaagga 126000

ctaaaagcag acgatgtagt aaataatatt gagaagaaaa atacatctgt taaacttaag 126060

tttgatattg gggaagatag ctatttaatt gaacgttatc gtaaggacaa agagaataag 126120

aataaagtaa aattatttgt taatgaaaaa gagattacag gttcaacaaa tgacgttact 126180

gataaacaaa tacaagactt atttggtatt gagtttaata cttacgttaa tgctatcatg 126240

tatggtcaag gagatatccc tatgttctcc caagcaacag ataaaggtaa gaaagaaatt 126300

cttgaatcta ttactaagac agatgtatat aaacaagcgc aagatgtagc aaaagagaaa 126360

gttaaagaag tagaagaaca acaaaataac ataagacagg aaatctataa actaggttat 126420

cagttatcta caaaagatga gtacttccaa agagaaatag aacagtacaa ccagtataaa 126480

gaacaattgg ttcagataga aaacagtaat aaggaaaaag atagattaag agaacaagag 126540

gagaagcaaa tagaagctca aatagagcaa ttagcttcac agataccaac aatacctgaa 126600

gatgaattta agcactcaga ggagtataat aaagcttctc aaagcctaga tttactttct 126660

aataaattaa cggagctaaa tcaagtatac tcagaatata ataccaaaga acaagtacta 126720

aaatctgaaa tagctacatt aagcaatagt ctaaataagt tagatacaaa tgaccattgt 126780

cctgtttgtg gctcccctat agataattct cataaattaa aagaacagga aaatattaat 126840

aatcagattg agaataagaa acaagagatt actagtgtat tagaaatgaa agatacgtat 126900

aaagaagcta ttgataaagt aaaagataaa tcacaagaaa ttaaagataa aatgtcacag 126960

gaagaccaac aagaacggga gcacaataat aagattaaca gtataattca agaggcttct 127020

aggattaaat cagacattag ctcattagag aataataaaa cttatttaaa agtgaaatac 127080

caacatcaat ctgttcaagg attagagaga gaagaaccaa gtaaagaaaa acatgaggaa 127140

gataaaaaag aattacaaga atctattgac aaacatgaag agaatatagt acaattagaa 127200

actaagaaag gtaaatatca acaagctgta gatgctttta gtaataaagg tatacgttca 127260

gtagtgttag actttattac accattctta aatgagaaag caaatgagta ccttcaaact 127320

ttatcaggtt cagatattga aatagagttc caaactcaag tgaagaatgc taaaggagaa 127380

ctaaaagata agtttgatgt tattgttaag aatagcaagg gtggaggctc atacaaatct 127440

aattcagcag gagaacaaaa acgtattgat ttagcaatta gttttgcaat tcaggattta 127500

attatgagta aagatgagat atctacgaac attgcacttt acgatgagtg ttttgatggg 127560

ttagatacta tcggttgtga aaacgtgatt aaattattaa aagatagact taatacagta 127620

ggaacgatat ttgtaattac tcataatacc gaacttaaac cactatttga acaaacaatt 127680

aaaatagtaa aagaaaatgg agtatcaaaa ctggaggaaa aataatgaaa ttaaagattt 127740

tagataaaga taatgcaaca cttaatgtgt ttcatcgtaa taaggagcac aaaacgatag 127800

ataatgtacc aactgctaac ttagttgatt ggtaccctct aagtaatgct tatgaataca 127860

agttaagtag aaatggagaa tatttagaat taaaaagatt acgttctact ttaccttcat 127920

cttatggttt agatgataat aaccaagata ttattagaga taataaccat agatgtaaaa 127980

taggttattg gtacaaccct gcagtacgca aagataattt aaagattata gagaaagcta 128040

aacaatatgg attacctgtt ataacagaag aatatgatgc taatactgta gagcaaggat 128100

ttagagatat tggagttata ttccaaagtc ttaaaactat tgttgttact agatatctag 128160

aaggtaaaac agaggaagaa ttaagaatat ttaacatgaa atcagaggaa tcacaattga 128220

atgaagcact taaagagagt gatttttctg tagacttaac ttatagtgat ttaggacaaa 128280

tttataatat gttgttatta atgaaaaaaa ttagtaaata gtaaggaagg atattatgag 128340

gtttgaagac tttttaaccc aagaattagg agaaccaaaa gaaaatacta taggtgagct 128400

aagatactgt tgtccgtttt gtggagaaaa aagttataag ttctatgtta agcaagccct 128460

agactctagt aatggtcagt atcattgtaa aaaatgtgat gaatcaggta atcctattac 128520

atttatgaag acttattata acattacagg taagcaagct tttgatttat tagagtctaa 128580

gaatatagat atagagagag ccccttttact tacaaccaat aataaggatt taacagaatc 128640

agagaaactt atattaatgc ttagaggtgt gcatcaagat aagggaacta ctagtattaa 128700

acctcctcga ttacctgaag gatataaatt attaaaagat aacttaaata ataaagagat 128760

tatacctttt ttaaaatact taaaaggtag aggtataact ttagaacaaa tcattaataa 128820

caatataggt tatgttatta atgggagctt ttataaagtt gacggggaat ccaaagtatc 128880

attaaggaat agtattatat tttttactta tgataatgat ggaaactacc agtactggaa 128940

tacaagaagt atagagaaga acccttatat taaatctatt aatgctcctg ctaaacaaga 129000

tgaagtaggt agaaaagatg tcatatttaa tttgaatata gcaagaaaga aaaagttctt 129060

agttataact gagggtgtat ttgatgcttt aacctttcat gagtatggag tagcaacatt 129120

aggtaaacaa gtaactgaga atcaaataaa aaaaataatt gattatgtta gtatagatac 129180

atcaatatat attatgttag acactgatgc attagataat aatatagact tagcttataa 129240

gttaaaaaca cattttaaca aagtttactt tgtaccacat ggtgatgaag atgcaaatga 129300

tatgggaaca aggaaagctt ttgagttatt aaaacagaac cgggtgttag taacacctga 129360

aagtatacag agttacaaaa tacaacaaaa acttaaactt taggcttgac cttagagaag 129420

ttttatgtta tactagtaat taagtaatta ataaaggaga aaaaaataat gtcaaataat 129480

aaaaaagata ttttagaatt tgtagatgaa tacattacag ctttaagagt tggtaatgag 129540

caacgacaac atcaattaga agaaatgggt aaagaagaaa cagcaacatt aacagatgta 129600

gctaaagcta ttactaacct tatgttaggt gttaatgagc agatgacaga cttagaatat 129660

aataacgagt taaacttaaa tattttaatt gatgctttat ataaagcaga gcttattaat 129720

gaagatgtat tagactacat tcaagaatca attgataaat cacaagaaga acctaaaaat 129780

gaagaagaaa aaggagaaca agaataatgg aaaaaaatat tagcacacac acaaaaggta 129840

ttagtcaagc agacatggag aaatggattg aagctgtagt acaaggaact gttgatggta 129900

aacaagttga tgagaaaaca gctaaacaat tagatagaat tggttcacga agtgtttctt 129960

tagaagaagc aactcgtatt gctaaagtcc ttaatgctgt aacagctcaa gaggttacag 130020

gagactttaa tgatgcattt aatgcaattg acttaatgat gattatcatg gaagatgagt 130080

taggagtaac tcaagaaaaa gtaggtaaag ctaaagataa actaaatgaa aaacgagaag 130140

cttacctaaa agagaaacaa gaagaattac gtcaaaaaca acaagaagag gcacaaaaag 130200

aaactgaatc tgacagcaat gaaaaagtaa ttcagttgaa gaaaaatgac gaacagtaag 130260

aaaaaagggg atacattcga acgtaaaata gctaaagaat taactgcttg gtggggatac 130320

caattcaata ggtctcctca atcaggtggt gcttcatggg gtaaagataa taatgctgtc 130380

ggagatatag tagtacccca ggaagctaat tttcctttag tagtagaatg taaacataga 130440

gaagaatgga ctatagataa cgttctttta aacaacagag agccacacac atggtgggag 130500

caagtcatta atgatagtag taaggtgaat aagacacctt gcttaatatt tactagaaat 130560

agagctcaga gttatgttgc tttaccttat aatgaaaaag tatatgaaga tttaagaaat 130620

aatgaatacc ctgtcatgag aacagatttt attattgata atattagaaa agataaattt 130680

ttttatgatg tccttataac taccatgaat gggttgacct catttacacc ttcttatatt 130740

atatcttgct acgacaaaaa agatataaaa ccatacaaga aggtcgagtc taatttatct 130800

gaggtaagta agcatgaaga tgaattgatt aatgaccttc ttagtgatat ataaggaagg 130860

taagataagt atgacaagca aagaaagacc attaatcgta tatttttcag gtacaggaca 130920

aacagaaaga ttagtaaaca aaattaatat taataattca tttgaaacat ttagggttaa 130980

gagtggaaaa gaaaaagtaa ataaaccttt tatactaata acacctactt ataagaaagg 131040

tgcaatacct aaacaaatag aaagattcct agaaattaat gggagcccta aagaagttat 131100

tggcacagga aataaacaat ggggctctaa tttctgtgga gcaagtaaaa agatttcaga 131160

gatgtttaag attcctttaa ttgctaaagt agagcaatca ggacacttta acgagataca 131220

accaatatta gaacacttta gtaataaata taaagtagcg taaaggatga gagatatatg 131280

gcaacatatg gaaaatggat tgagttaaat aatgaaataa ctcaattaga tgacaatgga 131340

aaaaataaac tctataaaga ccaagaagct ttagatgagt atttaaaata tattgaagac 131400

aatacaagaa agtttaatag tgaagtagaa agaattagag tattgacaaa agaaggaaca 131460

tatgataaaa tatttgacaa ggttcctgac actattattg atgagatgac taagttagct 131520

tacagtttta attttaaatt ccctagtttc atggcaggac aaaagtttta tgaatcttac 131580

gcatcaaaac agtatgatga aaacaaaaaa cctatttttg ttgaagacta tgaacaacat 131640

aatgttcgag tagctttata tttatttcaa aatgactatg taaaggctag agaattacta 131700

gtacaactta tggagcaaac attccaacca tctacaccta cgtataataa ctcaggtcaa 131760

gctaatagag gtgaactaag ctcatgttat ctatttgtag tagatgattc aattgagtct 131820

ttaaactttg ttgaggatag cgtagctaat gctagttcta atggtggcgg agttgcaatt 131880

gatttaacta gaattagacc taaaggagct ccagtacgta atagacctaa ttcaagtaaa 131940

ggtgttattg cttttgctaa agctattgaa cataaagtta gtatttatga ccagggcggt 132000

gtaagacaag gtagtggtgc tgtttaccta aatatattcc acaatgatat cttggattta 132060

ttaagctcta agaaaatcaa tgccagtgaa tctgttagac tagataaatt atctattggt 132120

gttacaatcc ctaacaaatt tatggagtta gttaaagaag gtagaccttt ctatactttt 132180

gatacttacg acattaataa agtgtatggt aagtatttag atgagctaaa cattgatgaa 132240

tggtatgata agttactaga taatgatagt atcggtaaag taaaacatga tgctagagaa 132300

gttatgacag atattgctaa aacgcaatta gaatcaggat acccttatgt attctatatt 132360

gataatgcta atgataatca tccattgaaa aacctaggta aagttaaaat gagtaactta 132420

tgtacagaaa tttcacaatt acaagaggta tcagaaattt atccgtactc ttacagtaat 132480

aagaatgtta ttaatagaga tgttgtttgt acattaggtt ctcttaactt ggttaatgtg 132540

gttgaaaaag gtttattgaa tgaatctgta gatattggta caagagcatt aacaaaagtt 132600

actgatatta tggatttacc ttacttacct agtgttcaaa aagcaaatga tgatattaga 132660

gctatcggtt taggttcaat gaatttacat ggacttttag ctaagaatat gattagttat 132720

ggttctagag aagcattaga cctagtaaac agtttatata gtgctattaa cttccagtct 132780

attaagacat ctatgttaat ggctaaagaa acaggaaaac catttaaagg atttgagaag 132840

tccgattacg ctacaggtga atactttgta agatatatta gagaatccaa tcaacctaag 132900

acagataaag ctaagaaagt cctagataag gtttatattc caacacaaga tgattgggat 132960

gaattagcta aagcagtaaa agtacatggc ttgtataatg gttatagaaa agcagaagca 133020

cctactcaat ctatatctta tgtacagaat gctacaagtt ctattatgcc agttcctagt 133080

gctatagaga atagacaata tggagatatg gagacatatt acccaatgcc ttacctaagt 133140

cctataactc agttcttcta tgaaggagaa acagcttata agattgacaa taaacgtatt 133200

attaatacaa gcgcagttgt tcagaaacat acagaccaag cagtatctac aatcctttat 133260

gtagagtcag aaatacctac taataaacta gtatcattat actattatgc ttgggaacaa 133320

ggattaaaat cattatacta tacacgttca cgtaaacttt ctgttattga atgtgaaaca 133380

tgttcggttt agaaaggaaa tagatatgga tattacacaa aaagtaaaac aacataataa 133440

aaatgctgta ttaaaagcaa caaactggaa tattgaagat gacgggatgt ctgatattta 133500

ttgggagcaa ggaatttccc aattttggac tcctgaagag tttgatgtat caagagattt 133560

aagttcttgg aatagtttaa ctgaaagtga aaagaacact tataagaaag tccttgcagg 133620

gctcacaggg ctcgatacca agcaaggagg agaaggtatg aacttagtat cctaccacga 133680

accaagacct aaataccaag ctgtatttgc gtttatgggt ggtatggaag agatacatgc 133740

taaatcctat agtcatatct ttacaacatt actaagtaat aaagaaacaa gctatctatt 133800

agatacttgg gtcgaagaaa acgacttttt aaaagtaaaa gctcagttta tcggatatta 133860

ctatgaccaa ctattaaaac ctaaccctac tgtatttgat agatacatgg ctaaagtagc 133920

tagtgccttt ttagaaagtg cactattcta ctcaggattt tattatcctt tacttcttgc 133980

agggagagga cagatgacac aatcaggagc tattatttat aaaattactc aagatgaagc 134040

ttaccatggt tcagcagtag gattaacagc tcaatatgat tataatcttc taacagaaga 134100

agagaaaaaa caagcagata aagaaactta tgaattatta gatattcttt acactaatga 134160

agtagcgtat acacatagtc tatatgaccc attagaatta agtgaagacg taattaacta 134220

cgttcagtat aattttaata gagctcttca aaaccttgga agagaggact attttaatcc 134280

tgaaccttat aaccctattg tagaaaatca aactaatgta gacagattac gaaatgttga 134340

tttctttagt ggtaaagcag actatgaaaa atctacaaat attaaagata ttaaagatga 134400

agatttttca ttcttagata gtaaagaata cagtactgcc aaggaattcc tataaaaagg 134460

agaaaagata ttatggatag aaaagaagca atggatttac taagtaaagc agaaatatta 134520

tttaaaaaac atgatgagtt ttcatgtgta agtgatatca atgaccctat gaagttattc 134580

agtaactcta aggatgctaa agctgatgat acgtctaagt cttttcagtt agagtttatg 134640

catgatatga ccatgtatac tttatcttat ggctcaggac agttaaaact tattgattta 134700

gcagaaggtt atgaagcaca aaaagctaca gtagttaact catttcccga aattattaaa 134760

acattagaaa aggatgattc agaagatgga aaaaatgaat agtttagtag atttaaatac 134820

agcaattaga caaaagaaag atgttattgt catgattaca caagataatt gtggtaagtg 134880

tgagatttta aaaagtgtaa tccctatgtt tcaagagtca ggtgacatta aaaaacctat 134940

cttaacatta aatctagatg ctgaagatgt agatagagaa aaagctgtta agttattcga 135000

tatcatgagt acaccagtat taattggata taaagatggt cagttagtta aaaagtatga 135060

agaccaagtt acacctatgc aattacaaga attagagtca ctttaatttg gaatttccta 135120

ctatctgtgc tatactataa tagtacaagg tagtaggatt ttttaatgga aggaagatga 135180

catatcgcaa agaataaaac attaacgata tataatagtg atagatattt taatatacac 135240

acaaaagata aagataaaat taatgaggct attaaagtca cacatggtaa tgaagaagaa 135300

attgaaaaga atatggatga attaatatct aagtctagac gatatatcat gagagatgaa 135360

aatcattaca tgttatttaa tgaaaagtac aataatgata gacttataga aaaagtatgt 135420

aaacacggtg gcaaagttac atactatact gattcagtat taccctatta tgttttaaaa 135480

gacttatcta gtcaccctga ctcagaagtc gtttatcgta tgcgcaatgg ttttactgca 135540

aaagaagtag ataatatagc tttgtcattt atgggtacaa aagttattat tgatatttct 135600

gtagtatttc cttatgtaaa cccttatgat attattagaa gtttacatga tattaaaaca 135660

aatgtagatg aagttcattt atcatttcca cgaatattag aagtagatga aaaacaagaa 135720

aaattttatt tctttgatgg tgaagcttat gatttaaaac ctgagtataa agtagatttt 135780

gcggataaaa ttagagtatc tttatcagta tggaaaatgt atatctatat cttaacaagt 135840

agtcgtgatt ttgaggatgt agacaatgta attacgaaac taaaacaaca acgaaagatt 135900

aagatataag gtgattatat gagtacagca aatagaagag atatagcaag aaagatatca 135960

gagaatacag gttactatat ccaggatgta gaggaaatac taagtgcaga gacagatgct 136020

atttctgact tactagaaga aggatatact aaagtaaaga atcataaatt tatgcaaata 136080

gaagttattg aaagaaaagg taaaaaagcg tgggatggtc tgaataaaga atacttccat 136140

ttacctaata gaaaagctat aaaattcaaa ccactaaaag aactagaaga ggttattgat 136200

agacttaatg aagaagagaa ataattctct tctttttta ttgacaaggt ttaaaatata 136260

tggtatagta ttattaagtt aaaaaaggag aggaattaaa tgaaagtatt aatcttattt 136320

gaccacatta gagaagagca tttttctgta agtaaagatg ggagtgtgaa atctaatgta 136380

ctaaatacac ctaatggaaa aacacttaag aaattacttg agaagtgttc taatttaaag 136440

agagataaaa caaacagaga ttatgatatt gattttctct acaatgcagt acctacacct 136500

atcagaaatg actatggtaa aattattaaa tatcaagatg ttaaacaagc agaagtaaag 136560

ccatactatg agagaatgaa taatattatt attgataatt cttatgatat gataattcct 136620

gtaggtaaac taggcgttaa atacttatta aatgttacag ctattggtaa agtaagaggt 136680

gtaccaagta aagtaactat tgaaaatgga acatcttctc atgacgtgtg ggtattacct 136740

acttacagta ttgaatatac taatgtaaat aaaaatagtg aacgtcatgt agtatcagat 136800

ttacaaacag ttggtaagtt tgtagagcaa ggagaagagg catttaaacc taaggaagta 136860

tcttacgagt tggtagataa cattgaaaga gtaagagaaa tattcaataa ggaagtaaag 136920

aatgataatt atgatggcgt agatattacc gcatgggact tagagactaa ctcattaaaa 136980

cctgataaag aaggaagtaa acctttagta ctatctctat catggagaaa tggtcaaggt 137040

gtaactatac ctttatacaa atcagacttt aactgggaaa acggtcaaga tgatattgat 137100

gaagtcttag aattacttaa gaactggtta gctagtaaag aagatattaa agtagcacat 137160

aatggtaagt acgatattaa attcttgatg agtactgaga actttaaaga ttttgagagt 137220

attcaagata ctaaagtagg ttggtaccta gctgttaccc aagaagttaa agaatcttta 137280

agattatctg atttagctta tgaggttaca gatgtcggag gttatgataa accattagaa 137340

gattttaaat tatggtttgt tactaagtta ttaagattct tctcagataa aattaaagag 137400

atacagaaag aaaataaaaa gattgctaag aaggagtatg atgttaaagc tcccgaatat 137460

aaagaatggc tagagaataa actaaatgaa acagtagtag aactagatga tactgagaag 137520

aaatttagag ttagtgaatt agagaaaaag tatattcaac taggtctttc acctgaaatt 137580

gtaaatatga atttagttat gaataacgat gagttcataa gtattgcaga acaatcacct 137640

gagtacatgg ggttatctga ctatgctaag tcttacacat taaatactgc aattaattta 137700

attaatgagt atagagatgt aaaagatgta gttaatgata ttgatggagg taactttaat 137760

tatgattggt tccctattga attaatgcat ccatacgcat caggagatac tgatgtatgt 137820

agaagaattc attgtgatgt agttaagaaa cttaaagaac aagatagacc taaatcaatg 137880

catttattag aagttaatta cccaagactt actaagtctt tagctagaat tgaatcaaat 137940
ggtttatatt gtgacttaga ttatatgaaa gaaaatgatg agtcatacga gtctgagatg 138000
gctaaaaatc atgctacaat gagagagcac tgggctgtta aagaatttga agaataccaa 138060
tacaatcttt accaaatggc gttagaagaa catgagaaaa agccaaaaga tagagataaa 138120
gatatccatc agtatagaga taaatttaaa gatggtaaat ggatgttttc cccaagttcc 138180
ggagaccata aaggtagagt aatttatgat attttaggaa ttcaattacc ttatgataaa 138240
gaatatgtta aggaaaaacc atttaatgct aatgttaaag aagcagacct tacttggcag 138300
gactataaaa cagacaagaa agctattggt tatgcgttag ataatttaga attaaaagat 138360
gatgttagag aacttcttga gttacttaaa tatcatgcta gtatgcagac aaaacgtaat 138420
tcatttacta agaaattacc taatatgatt aataaacaaa aacgaacatt acatggttct 138480
ttttctgaga caggtacaga gacatcaaga ctaagtagta gtaaccctaa cttgcaaaac 138540
ttaccggcac acacatcaga tgtaaacaag tttgattaca aacatccaat taaacgttca 138600
tttgtttcta gatttgaaaa tggagtacta ctgggagccg actatagcgc cctagagatg 138660
cgtattattg gattatttac taaagaccct gatatgctac aatcattctt aaatggggaa 138720
gatattcata aggctactgc aagtattgtt tataataaac cagtagaaga ggtaactaag 138780
gaagaacgac aagcaactaa agcagttaac ttcgggttag ccttcggtga atcacccttc 138840
tcatttgcag gtaaaaataa tatggaagta agtgaagcag aagaaatatt tgaaaagtac 138900
ttccaaacaa aaccaagtgt aaaaacttct attgacaatg tacatgagtt tgtgcaacaa 138960
tatggttatg ttgatacaat gcacggacat agaagattta tccgttcagc ccaatcaaca 139020
gataaaaaga taaaaaatga aggtctaaga cagtcattta acactattat ccaaggttca 139080
ggcagtttct taacaaacat gtctttaact tacttagatg attttatcca atctcgtaac 139140
ttaaaatcaa aagttattgc cacagtacat gatagtatct taattgattg tcctcctgaa 139200
gaagctaaaa ttatggctaa agtgacaatt catattatgg aaaacttacc atttgatttc 139260
ttaaaagcag aaattgatgg aaaagaagta caatatccta ttgaagctga tatggaaatt 139320
gggttaaact ataatgatat ggttgaatat gatgaggaag aaatagatac atttaattct 139380
taccaaggtt atattaagta tatgatgaat ttacagacct tagaagatta taaagagtca 139440
ggtaaactaa cagatgaaca atttgaaaag gctactaatg ttgttaaaag tgaaaaacat 139500
atttaccaag aaatttaata aaagtattga caatacattt aacttatgtt atactatata 139560
ggtaataaat ataaggagga aaacagagtg aatacaggag agattagatt taatcgttct 139620
atggatgaat ggattataac aagtatgtac caggatgagc taggtgagat gaatattgtt 139680
gttacattct ataatagaga agaaaataaa catggttcta cagttttacc aacagagtca 139740
tctactggag aagtagcaga ggaattggca agtcttgaag aagaatatcc tctagcttta 139800
cctttaagta gtatctcagt taatatttaa aaggaggaac tgataaatgg aaatacacat 139860
tgattcccta gattttacaa actttactat taaagataga aatgggaact cacaagagtt 139920

tgatattaca gatgagttaa gaattacaga gtatacaata caagaggact ttatgcaaca 139980
atcagctaaa tatgcttttt gggcttctat attagagaag gtaagagcat attctgaaat 140040
ggaacaaaga aatctagaaa caattggtag taagctaaac cttacaatta gacaagagta 140100
cgaacaacaa ggtaaaaagc ctactaaaga tatgattgaa tctagtgttt atattcatga 140160
ttcttaccaa caacaactta aagttgttga ggcttggaat tataaagtta aacaacttca 140220
atatgttgta aaagcttttg agacaagaag agatatgatg attcaattag gtgcagaatt 140280
acgacaaaca aataaaaatg gtggaattac taatccattt tcacattaaa aaataaagta 140340
aagaatataa ttgacaaata taaaaaacta tgttataata aataagtaaa ttaattaaaa 140400
ggagaaaaga taattatgga tttcaatcaa tttattaaca atgaggcaag caaattagaa 140460
agcaataaca gttcttttaa caataatgta gagagctaca aacctaaaaa ccctgtacta 140520
cgtttaggta atattaaaga tgcaaacgga aataaggttg ttaaagaaaa tgcttttgta 140580
cgagtattac ctcctgcaca aggaacaaat gttttcttta aagaatttag aacaacaggt 140640
attaactatt ctaagaaaga tggttctcaa ggattcacag gattaacatt acctgcagaa 140700
gaaggttcat ctgtccttga cccgtacatt caggactgga taacaaatgg tgttcaattt 140760
agtagattcc ctaataaacc aggagtacgc tattacattc atgtgattga atactttaat 140820
aacaatggtc aaattcaacc aaaaacggat gctcaaggaa atgtaatgat tcaacctatg 140880
gaattatcta acacaggata taaagaatta ttagctaact taaaagatac tatgttaaaa 140940
ccatcaccta atgcacctca tagctttatc tcagcaaatg aagcattctt agttaatatt 141000
gttaaagcta agaaaggtga aatgtcatgg aaagtaagtg tttatcctaa tgctccttta 141060
ggtgcgttac cgcaaggttg ggaacaacaa ttatctgacc tagaccaatt agcaaaacca 141120
acagaagaac aaaatcctaa ttttgttaac ttcttaatca ataatgttaa taacacagag 141180
ttaagtcatg ataactttaa atttaaccgt gaaacaaatg tcttaggtga agaaccttca 141240
gagcctaaac aagcacctac gcaacaagat gtagatagtc aaatgccaag taatatggga 141300
ggacaaccta atcagcctca gcaaggtcaa gtaggtcagt atgcacaaca aggtcaaagt 141360
aatggtcaag gacagcagtt acaaggtaca caacaaccta tcaataacac gcaatttggt 141420
caaggaactc cttcaggaca acaaccaagt aacacaggtt ctgttgattg ggataactta 141480
gcgcaacaac aatcacaacc tgattcaaac ccattcaatg attttgatgt tagcagtgtt 141540
gatgattcac aggtaccttt tgagacacaa cctcaaaata cacaacaagc acctgaacca 141600
caccaaacta cacaagagcc tccaaaacaa aaacaaacac aaagtattga cgatgtatta 141660
ggtggtctag acttagataa cctataagat atagagtgcc ttagagcact cttttattta 141720
agatatataa ttactaggag gatattaaat ggcaagagca aaaaaaggta aagaagtaga 141780
tttaacagat ttaaatacaa ttgatttagg taaagaatta ggattaacat tattatcgga 141840
tagcaataga gcagacatta aaaatattgt acctactatg gttcctcagt atgatagaat 141900
tctaggagga ggcatcccat taggtagatt gacagaggtt tacggattaa caggttcagg 141960

taaatcaagt tttgcagtcc atctctctag aatttcaaca cagttaggtg ttataactat 142020

ttggattgat attgaaggta ctgcggacaa taatcgtatg gaacagcttg gcgtagatgt 142080

ttcaaaacta ttctctattc aggcaggtga aggtagactt aaaaatacag tagagttatc 142140

tgtagagact gtaggtaagg aattagatta ctggatagat actttcaacg agaaagcccc 142200

tggagtacct attttattta tttgggattc attaggagca acaagaactc aagcggagat 142260

tgaagaagga gtagaccata ggaaattagg gacaaaagcc acagctactc aaaaagttat 142320

caacgcagta tctcctaaat taaatgatac aaatacagga ttaattgtta ttaatcaagc 142380

tagagataac ttgaatatgt ctaaccctta tgatgaccct attaagtcca caggagggcg 142440

tgcgttcgag catggagcca gtctaagact taaaattact aaaggtaaag agtccgacct 142500

taaacaatct gattcaatga caggtaaacc tacctataaa ggtcatgtga tgagagtaga 142560

gactaaaaaa tctaaactat ctagaccagg acaaaaagca gaagcagact tactatcagg 142620

atatgaggta ggttctggtt cggatattac ccaactaaat ggaattgacc cttaccatac 142680

tatctataag gaagcagttg aaagaggtct aattacgaaa gggacttgga gaaattatat 142740

cacacttaat ggggaggaaa ttaaacttta tgataaagat tgggttcctc gtttaataga 142800

tgaccatgag ttatacttgg aattatttag tagagtctat ggagaacatt tccctaatgg 142860

ttattcacca ttacttaata ctaaagtaat tgtaactcag ttagaagaat atcaagcatt 142920

agagaattac tatgaagagt gggctaaaga taataaacaa gaagaacaag aggaagaatc 142980

aaaaggagaa tctcaagaaa aggattctga ataatagatg tataatttaa tagataaaaa 143040

catgagacag gtaaaagaat ctttggggaa tgcaaattcc tcagatgttc ttcctttacc 143100

ttataaagac atagcaaaga aatttgaaga agtaaaagaa aaaggtgaat caattatcat 143160

tgaagagggt ggattccctt acacagattc tacagtgatg tatatagaac atgtaacaga 143220

tagatgggca ggaggatact ccctaattag gcatgaaggt gaagaggtta aagtacctaa 143280

aactatccat ttctctgata tatatgttaa ggataaatca cataaagtaa gaataatctt 143340

cgagggggct aatccttatg aagaaggcta aaaatggtaa tagatatgta atagatatag 143400

atggtattcc tgttgatttt gaaagagact tggatagttt acttaacagg tataaaaacc 143460

ttaggtggtc attatatcat aagtacgcag ggattttatc taatgatttt gaaagacaag 143520

aactaagaga atatattgat gagcaattta ttaaattagt taaagaatat aatattagaa 143580

gtaaagtgga ttttcctgga tatattaaag ctaaactaac tttaagagtt caaaatagtt 143640

atgttaagaa gaatgaaaaa tataaacgta ctgaaattat tggtaaaaaa gattatacag 143700

tagagtcctt aacagaagat ttaaatgaag acttcgagga taatcaaatt atgagttacg 143760

tatttgatga tatagaattt acagaagttc aaagtgagtt acttaaagaa ttacttatta 143820

atcctgaaag agaagatgat gcctttatcg tttctcaagt agcggaaaag tttgatatga 143880

aaagaaaaga agtagcaagt gagttgacag aactcagaga ctatgttaga tttaaaataa 143940

atgcatacca tgagtactat gctaagaaag aattaaataa ccatagagtt aatactgaaa 144000

atcatatttg ggaaaactag ttacagtgcc ttccttgtgt tatataagta ctactaataa 144060

tattattagt agtacttttg atatattatt tatgtagaag agaagtgaaa atagtgagaa 144120

tagaaaagca taaaataaag aataataaag taattaatga aatgtctata acagcaaata 144180

acctctataa tcatgctaat tttattttaa gacaaaattt ctttaataat aagactaata 144240

aaggatacag aaagttttta aattataata ctattcatag aatattaaaa aatatgaatg 144300

aagagaatta tattaaactc ccaagacaaa catctcaaca agtattaagg gatttaatta 144360

ataactggtc tagttttaga aaatcagaaa aagattattt taaaaaccct aataaataca 144420

gaaatagacc aaaaccacct aaatataaag ctaaaggcgg taaaggaaca attaagttta 144480

ctaatcaaca atgtagaatt cataaaaaag atggtttaat acatttacct acacctttac 144540

aagatataac tataaaacct tataaagcta agaatataag agaacttgtt tgtattccta 144600

aaagtgatta ttttgaagtt ttagtatgtt ataaagaaga aaatagtaat aaaacactaa 144660

atgataacga aaacatagca agtattgatt taggtttaga taacttgata accatggttt 144720

ctattgtaga taaaccaata attataaatg gtaaaggtct aaaatctaaa aataaatatt 144780

ttaataaaaa aataaggtat tatcaaagtc tattacaaaa caatagttac tcttcgaaaa 144840

gaatattaaa atattgggaa aaaagacaca atattatact agattacttt cataaagcaa 144900

caaacgaagt tgttaaatac tgcgtaaaaa atgatattag taaagtagtt atagggtata 144960

ataaacagca aaagtataaa tctaaattaa aaaa 144994

<210> 1075
<211> 102
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1075

```
Phe Val Gln Ile Pro Ile Phe Ser Leu Ile Pro Ile Leu Arg Tyr Lys
1               5                   10                  15

Leu Glu Glu Gln Gly Ile Gly Leu Ile Glu Thr Glu Glu Ser Tyr Thr
            20                  25                  30

Ser Lys Thr Ser Phe Ile Asp Asn Glu Lys Pro Ile Lys His Asn Val
        35                  40                  45

Tyr Lys Gly Lys Arg Val Lys Arg Gly Leu Phe Lys Thr Glu Glu Gly
    50                  55                  60

Arg Ile Leu Asn Ala Asp Val Asn Gly Ala Phe Gln Ile Met Lys Lys
65                  70                  75                  80

Val Phe Pro Asp Val Glu Ile Pro Arg Asp Asn Gly Phe Val Tyr Asn
                85                  90                  95
```

```
Pro Phe Leu Ile Asn Cys
            100


<210> 1076
<211> 210
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1076
Met Ala Lys Lys Asn Val Asn Asp Val Leu Gln Gln Glu Ser Val Thr
1               5                   10                  15


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


Arg Thr His Glu Gly Gln Tyr Ala Tyr Lys Val Val Ser Glu Gly Glu
        35                  40                  45


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


Val Met Lys Lys Ser Pro Ile Ala Tyr Thr Asp Gly Asp Asn Ile His
65                  70                  75                  80


Phe Val Val Asn Thr Val Val Asp Pro Tyr Asn His Ser Phe Ile Arg
                85                  90                  95


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


Phe Leu Ala Phe Val Glu Asp Arg Phe Lys Phe Gly Val Tyr Asn Val
        115                 120                 125


Phe Val Ala Asn Ser Lys Glu Asp Val Leu Ser Ile Val Asp Pro Thr
    130                 135                 140


Asp Asn Asp Ala Asp Glu Val Lys Asp Ser Leu Glu His Ala His Glu
145                 150                 155                 160


Asp Val Ile Ala Asp Phe Pro Ala Ser Pro Ala Arg Lys Asp Val Lys
                165                 170                 175


Gly Val Asp Ser Gly Glu Gly Gln Gly Asp Thr Ser Glu Pro Ser Ala
            180                 185                 190


Pro Lys Asn Val Gln Val Thr Pro Lys Glu Asp Gly Ala Asp Val Ser
        195                 200                 205


Ala Glu
    210
```

<210> 1077
<211> 173
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1077
Met Val Asn Leu Ala Lys Leu Asn Leu Tyr Lys Gly Asn Glu Leu Leu
1   5   10   15

Asn Ser Val Glu Lys Thr Glu Gly Lys Ser Thr Ile Thr Ile Glu Asn
            20   25   30

Leu Asp Ala Asn Thr Asp Tyr Pro Lys Gly Thr Phe Lys Val Ser Phe
        35   40   45

Ser Asn Asp Ser Gly Glu Ser Glu Lys Val Asp Val Pro Gln Phe Lys
    50   55   60

Thr Lys Ala Ile Lys Val Ile Ser Val Thr Leu Asp Val Asp Ser Leu
65   70   75   80

Asp Leu Thr Val Gly Asp Thr His Gln Leu Ser Thr Thr Ile Thr Pro
                85   90   95

Ser Glu Ala Ser Asn Lys Asn Val Ser Phe Glu Ser Asp Lys Ser Gly
            100   105   110

Val Ala Ser Val Thr Ser Glu Gly Leu Ile Glu Ala Val Ser Ala Gly
        115   120   125

Thr Ala Asn Val Thr Val Thr Thr Glu Asp Gly Ser His Thr Asp Ile
    130   135   140

Val Ala Val Thr Val Lys Glu Pro Ile Pro Glu Ala Pro Ala Asp Val
145   150   155   160

Thr Val Glu Pro Gly Glu Asn Ser Ala Asp Ile Thr Ala
                165   170

<210> 1078
<211> 75
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1078
Met Glu Lys Thr Leu Lys Val Tyr Ser Asn Gly Glu Val Val Gly Ser
1   5   10   15

Gln Val Ala Asn Asn Asp Gly Ala Thr Thr Val Ser Ile Thr Gly Leu
            20   25   30

Glu Ala Gly Lys Thr Tyr Ala Lys Gly Ala Phe Lys Val Ala Phe Ala
        35   40   45

Asn Asp Ser Gly Glu Ser Glu Lys Val Asp Val Pro Glu Phe Thr Thr
    50   55   60

Lys Thr Pro Thr Glu Glu Pro Ser Gly Glu Ala
65   70   75

<210> 1079
<211> 86
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1079
Met Asp Ile Pro Thr Ile Leu Phe Arg Asn Pro Tyr Asp Tyr Thr Lys
1   5   10   15

Val Lys Lys Leu Met Glu Asn Lys Glu Gln Tyr Ile Val Val Lys Phe
            20   25   30

Asp Ser Val Ser Val His Asn Leu Asn Val Gln Gly Met Met Asn Val
        35   40   45

Ile Gln Asp Tyr Leu His Ile Tyr Gly Tyr Arg Val Lys Glu Tyr Gly
    50   55   60

Gln Glu Asn Ala Ser Lys Asp Asp Glu Arg Asp Val Lys Gly Tyr Leu
65   70   75   80

Tyr Glu Arg Val Gly Glu
                85

<210> 1080
<211> 251
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1080
Met Gly Ile Ile Val Asn Ser Asn His Ile Gln Ser Asp Thr Leu Tyr
1   5   10   15

Glu Tyr Asp Ser Phe Phe Asp Ile Glu Lys Val Asp Thr Phe Glu Glu
            20   25   30

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

Tyr Asp Asp Ile Thr Phe Asn Lys Val Ile Asn Ser Asn Ser Asp Ile
50 55 60

Asp Asp Tyr Ile Lys Asn Asn Asp Ile Tyr Tyr Val Ser Asp Ile Gly
65 70 75 80

Leu Leu Pro Asp Thr Phe Ile Thr Val Asp Ser Asp Lys Lys Tyr Tyr
85 90 95

Ser Leu Leu Gln Gln Val Val Glu Leu Ser Lys Asp Pro Phe Pro Lys
100 105 110

Trp Val Glu Asp Asp Ala Lys Gly Leu Thr Lys Tyr Tyr Asn Phe Gln
115 120 125

Asp Phe Glu Asp Val Phe Asp Leu Asn Ser Phe Tyr Lys Lys Glu Val
130 135 140

Asp Met Val Arg Glu Lys Cys Tyr Asn Asn Gly Asn Val Tyr Leu Leu
145 150 155 160

Tyr Glu Val Leu Pro Asp Tyr Lys Leu Pro Leu Ala Tyr Ser Leu Leu
165 170 175

Ser Asn Lys Glu His Gly Ile Val Ile Ile Gly Ser Gln Thr Arg Ser
180 185 190

Asn Asn Asp Ile Leu Thr Phe Tyr Val Lys Gly Met Asp Ala Lys Ala
195 200 205

Ile Ala Ser Met Phe Asn Val Glu His Asp Tyr Asp Ser Asn Ile Phe
210 215 220

His Thr Phe Val Asn Ser His Ile Asn Ile Leu Gly Asn Gln Ile Thr
225 230 235 240

Lys Phe Ile Arg Glu Lys Gly Ser Ser Tyr Glu
245 250

<210> 1081
<211> 416
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1081
Met Ser Asn Tyr Lys Thr Ile Glu Glu Val Gln Ala Val Ile Ile Gly
1 5 10 15

Val Leu Phe Lys Asp Glu Gly Lys Ile Val Thr Ser Lys Phe Asn Lys

20 25 30

Ile Thr Lys Glu Phe Gly Leu Asp Arg Ile Gly Lys Asp Asp Leu Lys
35 40 45

Glu Ile Val Glu Asp Ile Arg Gln Asp Ala Tyr Leu Asn Glu Leu Lys
50 55 60

Asn Lys Ala Ile Lys Gly Lys Val Thr Leu Gly Asp Leu Lys Asp Val
65 70 75 80

Ala Asp Asn Gln Val Phe Glu Gly Asn Asn Tyr His Glu Glu Val Ser
85 90 95

Thr Tyr Val Val Ala Lys Glu Lys Glu Leu Ser His Leu Arg Glu Gln
100 105 110

Arg Lys His Asn Arg His Thr Ala Tyr Pro Gln Ile Met Phe Asp Glu
115 120 125

Leu Lys Glu His Met Val Lys Glu Leu Gln Gly Glu Thr Leu Val Glu
130 135 140

His His Gly Ser Lys Ala Asn Ile Asn Asp Thr Glu Leu Ile Val Leu
145 150 155 160

Leu Ser Asp Phe His Ile Gly Ser Ile Val Ser Asp Met Thr Asn Gly
165 170 175

Lys Tyr Asp Phe Glu Val Leu Lys Ala Arg Leu Asn His Phe Ile Asn
180 185 190

Thr Thr Val Lys Glu Ile Glu Asp Arg Glu Ile Ser Asn Val Thr Val
195 200 205

Tyr Phe Val Gly Asp Leu Val Glu His Ile Asn Met Arg Asp Val Asn
210 215 220

Gln Ala Phe Glu Thr Glu Phe Thr Leu Ala Glu Gln Ile Ser Lys Gly
225 230 235 240

Thr Arg Leu Leu Ile Asp Ile Leu Asn Val Leu Ser Asn Val Val Ser
245 250 255

Gly Glu Leu Arg Phe Gly Ile Ile Gly Gly Asn His Asp Arg Met Gln
260 265 270

Gly Asn Lys Asn Gln Lys Ile Tyr Asn Asp Asn Ile Ala Tyr Val Val
275 280 285

Leu Asp Ser Leu Leu Leu Phe Gln Glu Gln Gly Leu Leu Asn Gly Val

290 295 300

Asp Ile Ile Asp Asn Arg Glu Asp Ile Tyr Thr Ile Arg Asp Thr Phe
305 310 315 320

Gly Gly Lys Ser Ile Ile Ile Asn His Gly Asp Gly Leu Lys Gly Lys
325 330 335

Gly Asn His Ile Asn Lys Phe Ile Leu Asp Ser His Ile Asp Leu Leu
340 345 350

Ile Thr Gly His Val His His Phe Ser Val Lys Gln Glu Asp Phe Asn
355 360 365

Arg Met His Ile Val Ala Ser Ser Pro Met Gly Tyr Asn Asn Tyr Ala
370 375 380

Lys Glu Leu His Leu Ser Lys Thr Lys Pro Ser Gln Gln Leu Leu Phe
385 390 395 400

Val Asn Lys Glu Asn Lys Asp Ile Asp Ile Lys Thr Val Phe Leu Asp
405 410 415

<210> 1082
<211> 122
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1082
Met Asp Thr Ile Phe Ile Ile Gly Val Ala Phe Ile Thr Phe Ala Thr
1 5 10 15

Phe Asn Ile Val Phe Arg Leu Phe Asp Leu Trp Thr Thr Glu Lys Lys
20 25 30

Met Val Ser Gln Gly Gln Pro Pro Leu Ser Asn Phe Glu Tyr Tyr His
35 40 45

Val Ile Val Pro Tyr Leu Val Gly Val Ile Val Ile Thr Leu Ser Ile
50 55 60

Ile Phe Arg Asp Ser Leu Tyr Ser Ala Gln Ser Gly Phe Gly Ile Ile
65 70 75 80

Ile Thr Ser Phe Ile Tyr Met Leu Val Tyr Val Ile Ile Gly Leu Val
85 90 95

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

Gln Thr Gln Glu Asp Asn Asn Glu Val Gln
        115   120

<210> 1083
<211> 103
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1083
Met Lys Phe Asn Asp Ile Tyr Glu Gln Leu Ile Lys Asn Asp Thr Val
1   5   10   15

Gln Asn Ile His Glu Ser Gln Asp Asp Lys Gly Asn Ile Tyr Thr Ile
            20   25   30

Gln Phe Asp Lys Gly Asn Asp Lys Tyr Leu Phe Asn Val Ile Asn Asp
        35   40   45

Gly Phe Leu Lys Glu Met Thr Asn Gly Met Val Asp His Pro Glu Gly
    50   55   60

Gln Pro Tyr Ser Val Ser Leu Ile Asn Lys Glu Thr Pro Ser Met Ser
65   70   75   80

Val Lys Gln Tyr Leu Thr Asp Val Glu Asp Ile Val Pro Thr Ile Arg
                85   90   95

Lys Met Glu Lys Asp Phe Leu
            100

<210> 1084
<211> 178
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1084
Met Asp Phe Asn Phe Ser Ala Phe Asp Asn Ser Ser Leu Ala Met Arg
1   5   10   15

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

Glu His Val Glu Glu Glu Met Ser Glu Tyr Val Ile Val Tyr Asp Ile
        35   40   45

His Asp Arg Glu Glu Lys Glu Asn Pro Gln Lys Lys Tyr Arg Ile Glu
    50   55   60

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

```
Lys Ser Met Met Pro Gln Arg Lys Tyr Pro Lys Lys Val Thr Glu Asp
                85                  90                  95

Pro Ile Phe Val Ala Asn Val Ile Pro Leu Gly Thr Asp Thr Val Thr
            100                 105                 110

Gly Lys Thr Gly Lys Gly Phe Phe Glu Arg Asp Lys Asp Arg Thr Ile
        115                 120                 125

Tyr Ser Gln Lys Glu Pro Thr Lys Val Val His Gly Gln Tyr Thr Gly
    130                 135                 140

Val Phe Ile Gly Leu Thr Ser Val Lys Trp Asn Arg Thr Tyr Thr Pro
145                 150                 155                 160

Leu Glu Ser Val Val Glu Tyr Tyr Lys Arg Val Lys Gly Asp Arg Leu
                165                 170                 175

Asn Val



<210> 1085
<211> 255
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1085
Met Ser Asn Asp Val Val Lys Phe Tyr Glu Lys Asp Ile Lys Asp Leu
1               5                   10                  15

Ile Arg Thr Lys Lys His Met Phe Lys Asp Asp Glu Ile Thr Ser Asp
            20                  25                  30

Ile Asn Asp Ile Arg Ile Phe Asn Glu Lys Val Ile Cys Gln Gly Lys
        35                  40                  45

Cys Arg Thr Asp Cys Leu Val Leu Asp Arg Asn Gly Thr Val Met Gly
    50                  55                  60

Ile Glu Ile Lys Thr Glu Arg Asp Ser Thr Gln Arg Leu Asn Asn Gln
65                  70                  75                  80

Leu Lys Tyr Tyr Ser Leu Val Cys Lys Tyr Val Tyr Val Met Cys His
                85                  90                  95

Asp Lys His Val Pro Lys Val Glu Gln Ile Leu Lys Arg Tyr Lys His
            100                 105                 110

Asn His Val Gly Ile Met Ser Tyr Ile Ser Phe Lys Gly Lys Pro Val
```

115 120 125

Val Gly Lys Tyr Lys Asp Ala Thr Pro Ser Pro His Arg Ser Pro Tyr
130 135 140

His Thr Met Asn Ile Leu Trp Lys Thr Asn Leu Met Thr Ile Leu Arg
145 150 155 160

Leu Ile Arg Asp Pro His Thr Tyr Arg Thr Gly Tyr Ser Tyr Asn Ala
165 170 175

Ser Gly Arg Tyr Ser Gly Gly Glu Gly Asn Phe Ser Gln Thr Thr Gln
180 185 190

Ser Lys Arg Met Lys Lys Pro Ala Ile Ile Asn Gln Ile Ile His Tyr
195 200 205

Val Gly Val Asp Asn Thr Tyr Lys Leu Phe Thr Arg Gly Val Ile Tyr
210 215 220

Gly Tyr Asn Asn Arg Trp Glu Val Ile Glu Glu Asp Phe Phe Asn Thr
225 230 235 240

Met Lys Asn Gly Val Arg Val Ile Asn Glu Gln Arg Gln Thr Lys
245 250 255

<210> 1086
<211> 148
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1086
Met Ser Lys Asp Lys Pro Asn Arg Arg Lys Glu Ile Gln His Gln Pro
1 5 10 15

Val Asn Phe Ala Pro Met Asn Thr Leu Thr Gly Ala Asn Asn Ser Phe
20 25 30

Phe Ala Lys Lys Pro Ser Glu Pro Lys Asp Ala Thr Ser Val Ile Glu
35 40 45

Tyr Arg Ile Leu Phe Ile Lys Arg Phe Asp Asn Val Thr Ser Thr Asp
50 55 60

Val Lys Leu Gln Lys Lys Tyr Ala Leu Asn Leu Ile Ser Glu Ala Leu
65 70 75 80

Asp Val Lys Glu Thr Tyr Leu Ser Leu Lys Gln Lys Gly Lys Lys Thr
85 90 95

Glu Ser Ile Leu His Thr Asp Arg Val Tyr Tyr Val His Arg Gly Lys
100 105 110

Lys Leu Ile Gly Lys Cys Ser Ile Arg Glu Gln Arg Thr Phe Lys Gly
115 120 125

Lys His Leu Ile Phe Ile Phe Lys Thr Arg His Arg Val Lys Ala Glu
130 135 140

Arg Lys Asp Lys
145

<210> 1087
<211> 287
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1087
Met Leu Lys Gly Phe Ser Glu His Val Asp Lys Pro Thr Thr Thr Lys
1 5 10 15

Thr Leu Tyr Lys Thr Leu Thr Ser Gly Lys Val Glu Leu Leu Gly Val
20 25 30

Ser Tyr Asp Ser Asp Tyr Phe Pro Ser Gly Val Thr Val Gln Ser Tyr
35 40 45

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

Ile Asn Val Val Glu Ser Met Lys Gln Ala Val Val Gly Met Asn Asn
65 70 75 80

Gln Leu Gly Ser Ser Gly Leu Gly Tyr Val Arg Thr Glu Gln Leu Lys
85 90 95

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

Thr Asn Leu Thr Ser Thr Lys Lys Val Asp Ile Val Ser Thr Phe Ile
115 120 125

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

Leu Arg Leu Tyr Lys Leu Glu Glu Glu Ser Pro Leu Asn Gly Tyr Thr
145 150 155 160

His Ile Val Tyr Leu Leu Thr Thr Glu Lys Leu Tyr Asp Gly Gln Thr
165 170 175

```
Leu Phe Gly Met Leu Ser Lys Lys Asp Lys Leu Ser Lys Gly Asp Thr
            180                 185                 190

Asp Lys Leu Leu Ala Phe Phe Arg Asn Asn Ser Leu Ile Ser Lys Ser
        195                 200                 205

Val Phe Cys Val Lys Leu Leu Ser Lys Asp Tyr Tyr Phe Asn Leu Tyr
    210                 215                 220

Asn Thr His Glu Thr Gly Ile Phe Phe Leu Glu Asp Thr Asp Val Ile
225                 230                 235                 240

Thr Ile Ala Cys Gly Gln Ser Tyr Val Lys Val Asn Thr Lys Asp Ile
                245                 250                 255

Lys Ser Ser Tyr Val Lys Ile Glu Asp Lys Thr His Lys Leu Thr Glu
            260                 265                 270

Leu Val Ile Asn Leu Lys Gly Asp Asp Thr Leu Thr Ile Leu Phe
        275                 280                 285


<210> 1088
<211> 243
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1088
Met Ala Arg Lys Lys Asn Leu Arg Asn Lys Asn Ser Asp Ile Lys Val
1               5                   10                  15

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

Lys Leu Leu Arg Ser Lys Val Asp Asn Ala Leu Asp Glu Asp Met Ser
        35                  40                  45

Tyr Asp Asp Ile Ile Glu Leu Cys Lys Glu Tyr Asp Leu Glu Leu Ser
    50                  55                  60

Lys Ser Ala Ile Thr Arg Tyr Lys Ser Lys Arg Lys Glu Ala Ile Glu
65                  70                  75                  80

Asn Gly Trp Asp Leu Glu Glu Leu Ile Asp Lys Arg Lys Lys Thr Ser
                85                  90                  95

Val Lys Asp Ile Lys Glu Lys Glu Thr Pro Ile Leu Glu Glu Glu Gln
            100                 105                 110

Leu Ser Pro Phe Glu Gln Ser Lys His His Thr Gln Thr Ile Tyr Asp
        115                 120                 125
```

Asp Ile Gln Val Leu Asp Met Ile Ile Ser Lys Gly Ala Lys Gly Leu
130 135 140

Glu Phe Val Glu Thr Leu Asp Pro Ala Leu Met Ile Arg Ala Met Glu
145 150 155 160

Thr Lys Asp Lys Ile Thr Gly Asn Gln Leu Lys Gly Met Ser Phe Ile
165 170 175

Gly Leu Arg Glu Leu Gln Leu Lys Gln Thr Ala Gln Asp Thr Ala Met
180 185 190

Ser Glu Val Leu Leu Glu Phe Ile Pro Glu Glu Lys His Glu Glu Val
195 200 205

Leu Gln Arg Leu Glu Glu Leu Gln Asn Glu Phe Tyr Lys Asn Leu Asp
210 215 220

Leu Asp Glu Glu Ser Arg Lys Leu Lys Glu Ala Leu Asp Arg Val Gly
225 230 235 240

Tyr Thr Ile

<210> 1089
<211> 152
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1089
Met Ala Asp Glu Ile Ser Leu Asn Pro Ile Gln Asp Ala Lys Pro Ile
1 5 10 15

Asp Asp Ile Val Glu Ile Met Thr Tyr Leu Lys Asp Gly Arg Val Leu
20 25 30

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

Gly Lys His Lys Phe Thr Glu Val Ser Arg Asp Leu Asp Lys Glu Ser
50 55 60

Phe Tyr Tyr Lys Arg His Trp Val Leu Tyr Asn Val Ser Val Asn Ser
65 70 75 80

Leu Ile Thr Phe Asp Val Tyr Leu Asp Glu Glu Tyr Ser Glu Thr Thr
85 90 95

Lys Val Lys Tyr Pro Lys Asp Thr Ile Val Glu Tyr Thr Arg Glu Asp

100 105 110

Gln Glu Lys Asp Val Ala Met Ile Lys Glu Ile Leu Thr Asp Asn Asn
115 120 125

Gly Asn Tyr Phe Tyr Ala Leu Thr Gly Glu Thr Met Leu Phe Asp Glu
130 135 140

Asn Lys Leu Asn Lys Val Lys Asp
145 150

<210> 1090
<211> 147
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1090
Met Phe Ile Ser Leu Asn Gln Glu Glu Lys Glu Leu Leu Thr Lys Glu
1 5 10 15

Glu Ser Lys Tyr Thr Pro Leu Glu Thr Ser Arg Glu Phe Asn Thr Pro
20 25 30

Lys Glu Glu Phe Ile Val Thr Ser Tyr Asn Glu Gly Lys Pro Leu Asp
35 40 45

Tyr Ile Ala Lys Glu Ala Lys Val Ser Met Gly Leu Ile Tyr Thr Val
50 55 60

Leu Asn Tyr Tyr Lys Val Gly Lys Arg Asn Lys Lys Ser Pro Val Glu
65 70 75 80

Glu Arg Ile Ala His Ile Leu Lys Asp Lys Asn Leu Val Lys Glu Ile
85 90 95

Ile Lys Asp Tyr Gln Tyr Met Asn Leu Gln Asp Ile Tyr Ser Lys Tyr
100 105 110

Asn Leu His Lys Asn Gly Leu Tyr Tyr Ile Leu Asp Leu Tyr His Val
115 120 125

Glu Arg Lys Ser Glu Leu Lys Asp Lys Ala Leu Glu Glu Asp Asn Ile
130 135 140

Val Val Glu
145

<210> 1091
<211> 234
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1091
Met Arg Asn Lys Lys Ser Phe Gln Glu Gln Leu Asn Asp Met Arg Asn
1 5 10 15

Lys Glu Lys Trp Val Ser Glu Glu Glu Phe Thr Glu Glu Val Ala Pro
20 25 30

Ser Glu Glu Pro Glu Val Glu Glu Glu Lys Leu Tyr Thr Leu Asn Glu
35 40 45

Leu Lys Glu Asn Leu Leu Asp Ala Gln Gly Leu Lys Asp Val Val Ala
50 55 60

Asp Phe Pro Ala Ser Lys Asp Leu Tyr Glu Pro Asn Lys Leu Tyr Ile
65 70 75 80

Cys Thr Ile Pro Lys Gly Tyr Gln Ser Thr Glu Val Gln Pro Gly Gln
85 90 95

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

His Leu Arg Gly Gln Met Pro Arg Asn Leu Tyr Glu Thr Ser His Val
115 120 125

Leu Lys Pro Leu Val Arg Ile Asn Asn Thr Ser Ile Glu Tyr Gln Gln
130 135 140

His Glu Leu Leu Glu Asp Ile Lys Glu Asp Lys Asn Val Tyr Asp Val
145 150 155 160

Glu Leu Glu Asp Leu Arg Leu Ala Thr Gly Glu Glu Ile Ser Tyr Leu
165 170 175

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

Asp Phe Tyr His Glu Leu Thr Asp Ser Asp Asp Leu Leu Glu Tyr Tyr
195 200 205

Asn Lys Leu Arg Glu Leu Val Gly Asn Asp Arg Met Ile Tyr Cys Pro
210 215 220

Leu Leu Asn Lys Cys Val Lys Ile Ile Asp
225 230

<210> 1092
<211> 104
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1092
Met Tyr His Asp Lys Ala Lys Asn Glu Val Ser Thr Glu Leu Ser Asn
1   5   10   15

Thr Gly Lys Ile Lys Glu Glu Lys Asn Val Glu Phe Val Gly Asp Tyr
            20   25   30

Thr Leu Lys Lys Val Glu Asp Asn Lys Ala Tyr Phe Met Glu Thr Leu
        35   40   45

Pro Thr Tyr Leu Pro Gly Arg Thr Gly Asp Asn Ser Ile Asp Met Arg
    50   55   60

Tyr Tyr Lys Thr Ser Arg Phe Lys Glu Gly Val Asn Phe Lys Leu Ile
65   70   75   80

Arg Val Tyr Thr Glu Asp Gly Glu Asp Asn Pro Ile His Lys Tyr Arg
                85   90   95

Phe Glu Ala Val Pro Thr Lys Lys
            100

<210> 1093
<211> 80
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1093
Met Glu Met Ala Asp Leu Glu Arg Phe Asp Ala Phe Val Arg Leu Ile
1   5   10   15

Ser Asp Asp Glu Leu Ser Glu Glu Arg Ile Leu Glu Leu Ser Val Asp
            20   25   30

Leu Leu Asn Pro Ile Leu Glu Gly Gly Thr Ala Tyr Arg Ala Lys Lys
        35   40   45

Arg Ile Lys Ser Lys Phe Gly Lys Leu Glu Ala Lys Asn Phe Lys Arg
    50   55   60

Asn Tyr Lys Phe Leu Leu Lys Ser Ile Ala Gln Ile Asp Gln Arg Arg
65   70   75   80

<210> 1094
<211> 185
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1094
Met Thr Glu Arg Glu Lys Leu Ile Lys Glu Ile Glu Glu Ala Asn Arg
1   5   10   15

Asp Ile Gln Leu Gln Leu Lys Glu Val Asp Asn Tyr Lys Asp Ser Ile
            20   25   30

Arg Ser Lys Gly Thr Arg Asn Tyr Ile Ser Thr Lys Val Leu Asp Ser
        35   40   45

Ile Thr Val Gly Phe Ile Val Ser Phe Leu Ile Leu Ile Ile Met Arg
    50   55   60

Val Leu Glu Tyr Phe Val Thr Gly Asn Ala Val Tyr Ser Pro Leu Ala
65   70   75   80

Pro Ala Val Ile Ile Met Phe Val Leu Ala Leu Gly Thr Trp Lys Val
                85   90   95

Ser Lys Met Asn Lys Ile Val Ser Tyr Arg Gly Thr Ile Lys Met Tyr
            100   105   110

Trp Glu Leu Ser Asn Ala Glu Gln Lys Gln Ala Lys Val Phe Lys Tyr
        115   120   125

Pro Asn Asp Glu Val Asp Ile Val Ser Lys His Asn Leu Arg Gln Ile
    130   135   140

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

Lys Ala Val Glu Gln His Thr Lys Leu Ser Lys Glu Leu Phe Lys Lys
                165   170   175

Asp Lys Glu Thr Val Asp Lys Asn Lys
            180   185

<210> 1095
<211> 58
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1095
Met Val Ile Pro Ser Ile Lys Ala Gln Asn Lys Phe Lys Asn Glu Leu
1   5   10   15

Glu Tyr Tyr Lys Gln Gly His Ile Ser Glu Ser Lys Met Leu Glu Leu
            20   25   30

Ala Phe Asp Tyr Ile Gln Glu Leu Glu Gln Asn Asn Glu Tyr Val Thr
35 40 45

Asn Leu Leu Glu Glu Glu Arg Tyr Gly Glu
50 55

<210> 1096
<211> 83
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1096
Met Val Ser Lys Phe Ile Gly Val Tyr Leu Phe Asn Leu Leu Val Val
1 5 10 15

Ala Leu Val Tyr Thr Val Gly Phe Leu Phe Phe Tyr Gly Val Ala Ser
20 25 30

Leu Val Ile Ile Leu Thr His Ala Thr Ile Asp Pro Phe Val Leu Ala
35 40 45

Thr Phe Leu Gly Ile Gly Phe Leu Val Ile Arg Thr Ala His Arg Ile
50 55 60

Met Ala Arg Val Ile Asn Asp Ala Val Ala Gln Ala Ile Lys Asp Lys
65 70 75 80

Glu Asn Glu

<210> 1097
<211> 77
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1097
Met Asn Lys Gly Glu Phe Ile Met Asp Lys Thr Leu Pro Lys Phe Ser
1 5 10 15

Val Tyr Glu Val Ile Val Lys Thr Val Ile Met Thr Pro Thr Glu Gly
20 25 30

Ser Ser Asp Leu Glu Ser Phe Tyr Phe Ser Thr Arg Glu Leu Ala Glu
35 40 45

Arg Phe Val Glu Glu Asn Thr Val Glu Thr Lys Asn Gly Lys Arg Val
50 55 60

Ser Phe Ala Val Lys Glu Arg Lys Val Asn Gln Pro Gly

65 70 75

<210> 1098
<211> 214
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1098
Met Lys Val Ser Glu Glu Val Lys Gln Ser Tyr Leu Glu Asn Lys Ala
1 5 10 15

Asn Thr Lys Met Asp Lys Ile Ser Trp Ser Glu Leu Lys Ala Ser Pro
20 25 30

Leu Gly Ile Thr Leu Gly Asp Ile Ile Phe Tyr Ser Val Val Ile Ile
35 40 45

Asp Asn Ile Ile Ala Ile Ile Leu Thr Leu Thr Leu Ile Gly Thr Ile
50 55 60

Thr Asp Ser Ile Glu Ser Thr Leu Ala Gln Ile Ile Val Gly Val Phe
65 70 75 80

Ile Ile Ile Thr Ile Tyr Gly Ile Leu Ser Ala Leu Ile Pro Ile Leu
85 90 95

Ile His Lys Ala Val Ser Pro Gly Trp Ser Tyr Thr Glu Trp Asn Glu
100 105 110

Ser Tyr Tyr Ile Arg Leu Pro Gly Glu Glu Asn Tyr Lys Tyr Tyr Ser
115 120 125

Lys Trp Tyr Leu Asp Leu Leu Gly Val Lys Glu Phe Tyr Tyr Lys Arg
130 135 140

Asp Ser Gly Glu Glu Val Lys Glu Lys Asn Ile Ser Trp Ala Phe Gln
145 150 155 160

Ala Glu Val Lys Arg Pro Glu Asp Val Asn His Trp Lys Asn Gln Leu
165 170 175

Leu Thr Asn Arg Pro Leu Thr Ile Leu Glu Tyr Lys Lys Leu Lys Lys
180 185 190

Leu Asp Lys Glu Ser Glu Ile Arg Lys Gln Glu Asp Leu Glu Glu Tyr
195 200 205

Lys Gln Tyr Asn Ser Asn
210

<210> 1099
<211> 82
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1099
Met Ile Ser Ser Phe Asp Ser Ile Leu Leu Val Ile Tyr Ile Ile Ile
1   5   10   15

Ala Phe Ala Val Ala Met Ala Ile Ile Tyr Leu Val Phe Lys Gly Met
            20   25   30

Thr Ile Leu Leu Asp Lys Leu Met Met Leu Leu Leu Ser Lys Thr Thr
        35   40   45

Leu Asp Val Glu Ala Cys Ser Met Ile Met Ala Val Ile Ser Thr Ile
    50   55   60

Val Phe Gly Ile Ile Val Leu Leu Ile Trp Leu Ala Val Asn Asn Ile
65   70   75   80

Leu Leu

<210> 1100
<211> 58
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1100
Met Asp Phe Asn Asp Phe Ile Asn Ser Glu Ser Asp Arg Val Gly Asn
1   5   10   15

Pro Lys Gln Lys Lys Lys Val Glu Asn Lys Leu Pro Ser Ser Ile Pro
            20   25   30

Ile Glu Asp Arg Glu Lys Lys Leu Lys Glu Ile Arg Lys Lys Ser Leu
        35   40   45

Tyr Ile Asp Leu Arg Arg Lys Arg Asn Asp
    50   55

<210> 1101
<211> 98
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1101
Met Thr Lys Glu Thr Asn Val Leu Tyr Lys Asp Lys Tyr Arg Asp Tyr

1 5 10 15

Thr Ile Val Val Arg Leu Ala Gly Asn Ile Ile Val Thr Glu Val Asp
20 25 30

Lys Lys His Lys Thr Ala Phe Thr Pro Ile Ile Phe Asp Asn Gly Val
35 40 45

Glu Gly Val Glu Leu Val Met Arg Ile Gly Ser Val Glu Leu Ser Met
50 55 60

Thr Asp Leu Arg Glu Phe Thr Lys Glu Val Ser Thr Ala Gln Lys Ala
65 70 75 80

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

Ala Phe

<210> 1102
<211> 60
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1102
Met Leu Leu Gly Ile Leu Trp Phe Ile Trp Gly Phe Val Ser Tyr Phe
1 5 10 15

Val Leu Met Phe Gly Ile Glu Phe Cys Lys Asp Arg Trp Met Pro Gly
20 25 30

Val Ile Gly Ala Gly Ala Leu Leu Leu Phe Leu Phe Trp Ile Met Lys
35 40 45

Ser Ile His Asn Ala Met Thr Val Val Tyr Leu Tyr
50 55 60

<210> 1103
<211> 122
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1103
Met Asp Ile Leu Ile Ile His Tyr Lys Glu Thr Asn Lys Arg Val Leu
1 5 10 15

Lys Glu Thr Ile Gln Thr Ile Gln Asn His Leu Asn Asp Glu His Gly
20 25 30

Leu Val Lys Met Thr Ala Thr Lys Leu Ser Arg Glu Asn Ile Glu Lys
35 40 45

Arg Phe Asn Asn Tyr Asn Ile Val Ile Ala Glu Asp Asp Pro Asp Asn
50 55 60

Ser Tyr His Tyr Ser Glu Ala Val Glu Glu Ala Asp Phe Ile Ile Asp
65 70 75 80

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

Asp Asn Pro Val Asp Met Leu Asp Arg Asn Pro Asp Phe Ile Glu Ala
100 105 110

Val Asn Lys Leu Asn Glu Asp Leu Met Leu
115 120

<210> 1104
<211> 115
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1104
Met Leu Asn Glu Lys Leu Lys Asn Leu Glu Asp Thr Lys Val Tyr Met
1 5 10 15

Ile Asn Ser Ile Ala Ser Leu Leu Ser Ala Ser Thr Gly Lys Ser Ser
20 25 30

Lys Val Phe Phe Asp Glu Gly Thr Ile Lys Ile Val Ser Gly Glu Thr
35 40 45

Lys Ala Val Glu Val Ile Asp Asn Leu Val His Pro His Ser Gly Arg
50 55 60

Leu Pro Ile Lys Thr Thr Glu Arg Ile Ala Leu Gly Arg Leu Thr Asp
65 70 75 80

Ser Leu Gln Phe Val Ile Ser Glu Ile Glu Val Val Lys Asp Gln Ile
85 90 95

Ile Asp Glu Glu Asn Glu Ala Tyr Ile Asp Phe Val Met Glu Asp Trp
100 105 110

Asp Trp Asp
115

<210> 1105
<211> 90

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1105
Met Asp Leu Leu Thr Ile Ala Ser Val Ala Phe Ile Ala Val Val Ile
1   5   10   15

Ile Asp Leu Ile Asn Asp Asp Met Ser Tyr Met Leu Thr Gly Thr Ala
            20   25   30

Ile Leu Ile Asn Ile Trp Ala Gly Phe Tyr Gly Trp Phe Phe Leu Leu
        35   40   45

Gln Ala Gly Met Leu Leu Phe Leu Leu Leu Ala Arg Lys Val Lys Asp
    50   55   60

Asp Lys Glu Ser Ile Leu Tyr Ser Ser Ala Ser Leu Ile Cys Ala Leu
65   70   75   80

Gly Met Ile Ile Asn Leu Leu Ser Phe Ser
                85   90

<210> 1106
<211> 101
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1106
Met Ser Lys Glu Thr Ile Arg Arg Gln Phe Ser Asn Ala Ile Glu Ile
1   5   10   15

Met Ala Thr Thr Lys Glu Trp Trp Asn Phe Pro Lys Ser Phe Asn Thr
            20   25   30

Ser Lys Glu Phe Lys Ile Lys Thr Phe Lys Asn Asp Thr Leu Val Phe
        35   40   45

Glu Val Arg Glu Gly Ser Arg Asn Leu Gly Ser Phe Val Ile Phe Thr
    50   55   60

Asn Ile Asp Phe Asp Tyr Asp Lys Leu Glu Gly Thr Ser Thr Gln Tyr
65   70   75   80

Met Ile Asn Tyr Phe Ala Lys Lys Leu Thr Lys Asp Met Phe Asn Tyr
                85   90   95

His Lys Leu Gln Leu
            100

<210> 1107
<211> 116
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1107
Met Arg Glu Glu Leu Lys Pro Phe Asn Arg Lys Gln Val Asn Val Lys
1 5 10 15

Gly Tyr Leu Asp Asp Val Lys Tyr Ser Lys Arg Arg Arg His Lys Gly
            20 25 30

Asn Gln His Gly Cys Val Lys Ile Thr Val Thr Asp Val Lys Ile Asn
        35 40 45

Gly Ile Pro Ile Asp His Val Asn Ile Glu Val Gly Ile Ser Phe Tyr
    50 55 60

Glu Lys Leu Lys Glu Leu Gln Gly Lys Arg Ile Gln Phe Val Gly Thr
65 70 75 80

Val Tyr Lys Tyr Val Lys His Ala Arg Gly Arg Lys Gly Arg Ile Lys
                85 90 95

Gly Phe Tyr Lys Glu Asp Tyr Ser Val Thr Leu Asp Lys Lys Leu Gln
            100 105 110

Lys Glu Glu Lys
        115

<210> 1108
<211> 200
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1108
Met Ile Lys Arg Arg Lys His Leu Asp His Ser Leu Gln Pro Glu Lys
1 5 10 15

Gly Trp Arg Thr Val Pro Phe Asn Gly Tyr Tyr Glu Ala His Pro Thr
            20 25 30

Gly Leu Ile Arg Asn Lys Val Thr Lys Lys Leu Ile Lys Gly Thr Gln
        35 40 45

Thr Arg Lys Asn His Pro Lys Trp Thr Ala His Glu Ile Val Tyr Leu
    50 55 60

Ile Asn Pro Lys Lys Thr Ser Tyr Ser Arg Gly Val Val Ile Ala His
65 70 75 80

```
Thr Phe Pro Glu Met Ile Ser Gln Ser Arg Gly Asp Leu Lys Asn Gly
                85                  90                  95

His Val Cys Phe Lys Asp Gly Asp Arg Ser Asn Cys His Val Asp Asn
            100                 105                 110

Met Phe Ile Gly Lys Gly Asn Val Asn Lys Asn Ile Tyr Lys Leu Asn
        115                 120                 125

Asp Ser Tyr Leu Thr Arg Lys Asp Ile Glu Glu Asp Val Asn Asn Leu
    130                 135                 140

Val Asn Glu Arg Leu Phe Ser Gln Leu Glu Leu Leu Ile Lys Lys Asn
145                 150                 155                 160

Glu Pro Glu Arg Ile Thr Pro Ser Asn His Phe Ile Lys Arg Asp Asn
                165                 170                 175

Asn Val Phe Ser Ile Thr Asp Leu Ser Lys Asn Ser Leu Val Glu Phe
            180                 185                 190

Glu Leu Glu Ile Lys Asn Ile Lys
        195                 200


<210> 1109
<211> 59
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1109
Met Asn Glu Trp Tyr Ala Leu Cys Tyr Tyr Asp Lys Val Gly Lys Lys
1               5                   10                  15

Lys Ile Pro Arg Gln Ile Lys Ala His Arg Asp Val Ser Val Leu Glu
            20                  25                  30

Asp Leu Lys Asp Arg Leu Glu Glu Gln Asn Pro Lys Glu Glu Tyr Lys
        35                  40                  45

Ile Lys Thr Thr Lys Glu Phe Asp Lys Glu Arg
    50                  55


<210> 1110
<211> 91
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1110
```

Met Lys Leu Glu Asp Lys Val Leu Glu Arg Ile Asp Ser Leu Gly Asn
1   5   10   15

Lys Ala Gly Asn Leu Ser Asn Gln Ala Met Glu Ser Leu Val Lys Tyr
            20   25   30

Gln Ile Thr Tyr Gly Ile Ile Asp Ile Val Val Ser Ile Leu Val Ile
        35   40   45

Ala Leu Thr Ile Phe Leu Gly Lys Val Tyr Leu Lys Glu Tyr Lys Lys
    50   55   60

Val Lys Met Asp Leu Lys Glu Ser Leu Leu Tyr Asp Asp Tyr Asp Ile
65   70   75   80

Leu Ser Leu Arg Asn Ser Cys Arg Tyr Thr Asn
                85   90

<210> 1111
<211> 22
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1111
Met Arg Leu Ile Asn Pro Glu Val Tyr Ala Val Lys Asp Leu Ile Glu
1   5   10   15

Gln Val Lys Gly Gly Asn
            20

<210> 1112
<211> 97
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1112
Met Lys Gln Arg Asp Phe Glu Phe Glu Glu Asp Phe Val Leu Thr Tyr
1   5   10   15

Glu Cys Glu Asp Cys Lys His Phe Glu Asp Trp Gly His Asp Glu Glu
            20   25   30

Pro Glu Glu Cys Ser Glu Cys Gly Ser Ser Asp Leu Ile Asn Asn Thr
        35   40   45

Ser His Glu Asp Thr Glu Cys Asp Met Cys Arg Gly Tyr Ile Asp Met
    50   55   60

Trp Gln Asp Gly Tyr Arg Tyr Met Gly Asp Asn Lys Glu Tyr Ile Glu
65   70   75   80

Lys Glu Glu Ser Gly Leu Ile Cys Glu Asp Cys Tyr Glu Lys Leu Asp
85 90 95

Ile

<210> 1113
<211> 95
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1113
Met Asn Lys Ala Val Glu Gln Ala Ser Asn Ala Leu Gly Gln Gly Phe
1 5 10 15

Ser Ala Met Val Trp His Gln Val Leu Ala Gly Leu Gly Phe Ile Leu
20 25 30

Leu Gly Leu Val Leu Ser Leu Leu Val Trp Val Leu Val Lys Lys Phe
35 40 45

His Val Pro Phe Asn His Pro Thr Ala Phe Val Val Tyr Ser Ile Met
50 55 60

Leu Val Ser Ile Val Ala Ser Phe Ile Trp Gly Gly Leu His Val Ile
65 70 75 80

Asn Pro Glu Tyr Tyr Ala Ile Leu Glu Leu Lys Gly Phe Ile Lys
85 90 95

<210> 1114
<211> 38
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1114
Met Thr Lys Glu Glu Leu Glu Gln Lys Val Lys Glu Leu Glu Ala Glu
1 5 10 15

Asn Lys Glu Leu Lys Lys Gln Ile Glu Arg Phe Glu Asp Glu Gly Gly
20 25 30

Lys Thr Lys Asp Glu Gln
35

<210> 1115
<211> 88
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1115
Met Asn Ser Arg Gln Lys Lys Ile Leu Thr Leu Thr Val Ser Asn Phe
1   5   10   15

Leu Ile Leu Ala Leu Asp Thr Val Ala Leu Ile Arg Tyr Lys Lys Gly
            20   25   30

Lys Ile Lys Gln Glu Asn Tyr Asn Thr Gly Gln Ile Thr Arg Met Ile
        35   40   45

Ala Thr Thr Ala Asn Ser Leu Gly Ile Leu Tyr Leu Glu Glu Gln Glu
    50   55   60

Arg Lys Glu Val Lys Asp Ile Lys Val Gly Thr Phe Glu Ile Gly Ala
65   70   75   80

Leu Lys Arg Phe Thr Asn Asn Lys
                85

<210> 1116
<211> 101
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1116
Met Lys Gly Ile Ile Ile Phe Tyr Lys Glu Glu Thr Lys Glu Asp Leu
1   5   10   15

Gly Tyr Phe Leu Gly Phe Ile Asn Phe Lys Leu Glu Gly Leu Ser Tyr
            20   25   30

Thr Thr Glu Gly Thr Leu Val Asp Asn Asp Val Val Val Leu Lys Asp
        35   40   45

Asn Gln Ile Asn Glu Asp Asn Leu Glu Gln Phe Ser Met Ser Asn Asn
    50   55   60

Asn Leu Val Ile Gly Ile Leu Gly His Ser Ser Leu Ser Val Arg Ile
65   70   75   80

Tyr Glu Lys Gly Ile Arg Gln Glu Phe Asp Arg Val Glu Glu Tyr Leu
                85   90   95

Glu Glu Leu Arg Gln
            100

<210> 1117
<211> 133

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1117
Met Ile Phe Ile Leu Ile Phe Gly Leu Leu Phe Ile Leu Ser Leu Leu
1 5 10 15

Gly Ile Phe Ile Tyr Phe Ile Val Leu Arg Lys Lys Lys Gln Leu Ile
20 25 30

Glu Glu Arg Glu Ser Phe Gly Ile Tyr Asn Arg Thr Lys Glu Lys Leu
35 40 45

Gly Asp Val Thr Arg Leu Gly Tyr Glu Glu Asp Val Tyr Lys Leu Ile
50 55 60

His Asn Gln Ser Asn Lys Thr Ile Ile Glu Asp Lys Lys Ser Lys Val
65 70 75 80

Val Asp Thr Ile Lys Lys Met Tyr Glu Leu Glu Leu Thr Ser Val Asp
85 90 95

Val Ser Lys Val Glu Gly Leu Ser Pro Leu Asp Thr Glu Pro Met Thr
100 105 110

Asn Met Lys Leu Leu Ser Tyr Lys Leu Asp Arg Glu Gly Leu Tyr Ser
115 120 125

Leu Ser Lys Phe Ile
130

<210> 1118
<211> 78
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1118
Met Glu Phe Ile Asp Lys Asn Asn Val Ile Lys Ala Tyr Asp Ile Pro
1 5 10 15

Asn Val Tyr Leu Lys Gly Tyr Val Leu Gln Ala Cys Asp Lys Asn Gly
20 25 30

Asp Thr Thr Ala Tyr Asp Gly Tyr Asp Gln Ile His Tyr Lys Glu Gly
35 40 45

Arg Val Leu Thr Phe Pro Phe Asp Lys Pro Leu Arg Lys Ile Asn Val
50 55 60

Leu Ser Gly Tyr Tyr Lys Leu Phe Lys Lys Glu Asp Ile Ile
65 70 75

<210> 1119
<211> 175
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1119
Met Ile Tyr Phe Val Ser Asp Leu His Phe Gly His Asp Asn Ile Arg
1 5 10 15

Glu Phe Glu Ala Pro Thr Arg Ser His Trp Asn Ser Val Glu Glu Met
20 25 30

Asn Glu Gly Leu Ile Glu Leu Trp Asn Asn Thr Ile Thr Asn Asn Asp
35 40 45

Ile Val Tyr Asn Ile Gly Asp Phe Phe Phe Asn Met Lys Pro Ser Lys
50 55 60

Val Glu Asp Ile Leu Asn Arg Leu Asn Tyr Lys Glu Met Ile Leu Ile
65 70 75 80

Ala Gly Asn His Asp His Lys Lys Leu Ile Lys Leu Tyr Glu Arg Asn
85 90 95

Gly Ile Thr Val Lys Tyr Ala Asp Met Ile Lys Lys Asp Gly Lys Arg
100 105 110

Phe Tyr Leu Ser His Tyr Pro Thr Leu Ile Gly Arg Lys Asn Met Phe
115 120 125

Asn Ile His Gly His Ile His Ser Gln Leu Met Gly Thr Glu Tyr His
130 135 140

Ile Asn Val Gly Tyr Asp Val Glu Gly Lys Ile Ala Tyr Ser Phe Asp
145 150 155 160

Asp Ile Ile Ser Arg Ala Gly Glu Tyr Asn Gly Glu Ile Gln Arg
165 170 175

<210> 1120
<211> 106
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1120
Met Glu Lys Phe Lys Gly Lys Asp Leu Tyr Lys Thr Arg Ile Arg Lys
1 5 10 15

```
Gln Thr Ile Lys Asn Leu Val Ile Lys Thr Glu Lys Leu His Asn Lys
            20                  25                  30

His Gly Lys Tyr Arg Pro Ile Gly His Val Tyr Tyr Tyr Pro Lys Thr
        35                  40                  45

Lys Glu Phe Thr Leu Ser Lys Pro Glu Gln Lys Ile Phe Ile Glu Tyr
    50                  55                  60

Met Lys Glu Leu Gly Phe Asn Val Lys His Arg Arg Arg Lys Lys Thr
65                  70                  75                  80

Leu Ile Ile Tyr Lys Asn Ala Phe Thr Glu Tyr Ile Ser Met Tyr His
                85                  90                  95

Glu Ala Ile Glu Gln Ile Glu Gly Gly Thr
            100                 105
```

<210> 1121
<211> 76
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1121

```
Met Glu Tyr Leu Phe Leu Phe Ile Gly Ile Gly Met Ile Ile Trp Gly
1               5                   10                  15

Phe Ile Ala Pro Tyr Leu Ala Phe Val Val Tyr Tyr Lys His Val Arg
            20                  25                  30

Glu Asn His Asn Gly Phe Ser Asp Glu Glu Ser Leu Glu Glu Ala Thr
        35                  40                  45

Val Leu Gly Met Gly Phe Met Phe Ile Ala Phe Ile Pro Ile Gly Ile
    50                  55                  60

Leu Val Val Ile Glu Glu Ile Lys Ile Leu Phe Phe
65                  70                  75
```

<210> 1122
<211> 68
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1122

```
Met Lys His Phe Ile Leu Ile Leu Gly Ile Val Ile Leu Val Ile Ala
1               5                   10                  15
```

Leu Gly Ile Val Ile Leu Val Ile Ala Leu Gly Ile Val Leu Pro Ala
            20   25   30

Trp Ile Leu Gln Leu Val Leu Ser Ala Phe Gly Val Lys Val Ser Ile
        35   40   45

Trp Val Cys Ile Gly Ile Phe Ile Leu Ile Ser Ala Ile Gly Ser Met
    50   55   60

Phe Ser Arg Asn
65

<210> 1123
<211> 87
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1123
Met Ala Lys Tyr Glu Ser Asn Ile Asn Gly Glu Asn Tyr Ile Ala Thr
1   5   10   15

Pro Ser Gln Ala Leu Arg Glu Ala Leu Ala Lys Leu Ile Thr Glu Glu
            20   25   30

Lys Ser Phe Ala Glu Tyr Gln Thr Lys Gly Gly Glu Gln Tyr Glu Ser
        35   40   45

Gln Leu Gln Leu Arg His Phe Asp Ala Met Ile Ser Gln Tyr Glu Glu
    50   55   60

Ala Ile Arg Val Leu Glu Asp Lys Tyr Arg Pro Gln Ile Phe Ile Pro
65   70   75   80

Lys Asp Asn Lys Glu Glu Asn
                85

<210> 1124
<211> 105
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1124
Met Lys Ala Glu Ser Ile Ala Arg Phe Phe Asn Asp Lys Val Leu Gln
1   5   10   15

Ile Glu Gly Tyr Lys Val Arg Phe Pro Gln Ala Ser Ser Ser Tyr Ile
            20   25   30

Leu Asp Ile Asp Thr Val Asp Glu Ser Val Leu Phe Leu Asp Ala Gln
        35   40   45

Val Ser Thr Leu Ser Gly Lys His Leu Leu Asp Thr Ala Ile Thr Ile
50 55 60

Glu Arg Pro Glu Thr Leu Ser Ala Lys Glu Leu Tyr Thr Glu Ile Ser
65 70 75 80

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

Leu Ser Arg Tyr Phe Lys Glu Glu Lys
100 105

<210> 1125
<211> 226
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1125
Val Ser Asn Lys Thr Ile Thr Asn His Leu Leu Asn Leu Lys Gly Ile
1 5 10 15

Asn Ile Glu Thr Tyr Ser Ile Ile Ala Arg Ile Lys Lys Gln Thr Ser
20 25 30

Trp Gly Asp Lys Gly Asp Ser Phe Glu Ile Ser Ile Ser Tyr Lys Ala
35 40 45

Asp Lys Asp Pro Arg Thr Val Arg Tyr Ile Thr Thr Glu Ile Thr Ile
50 55 60

Asp Tyr Ser Ser Asn Asn Pro Lys Glu Ile Leu Leu Gln Leu Lys Asp
65 70 75 80

Lys Ile Phe Ser Ile Val Glu Glu Gln Val Glu Thr Asp Asn Asp Phe
85 90 95

Ile Glu Ser Ile Lys Glu Ile Asn Ser Thr Lys Ala Leu Glu Lys Leu
100 105 110

Lys Pro Tyr Ile Asn Asn Glu Tyr Tyr Ser Met Phe Lys Ser Ser Ile
115 120 125

Glu Lys Glu Ile Pro Val Ala Leu Ser Ser Glu Val Leu Asn Arg Cys
130 135 140

Thr Gly Lys Thr Ser Thr Leu Ala Tyr Leu Ala Leu Glu Lys Asp Leu
145 150 155 160

Pro Leu Val Val Ser Asn Glu Pro Met Arg Lys Met Leu Lys Asn Lys

165 170 175

Phe Pro His Leu Arg Val Ser Ser Ala Glu Asp Tyr Ser Asn Tyr Asp
180 185 190

Ile Lys Gly Glu Ile Val Leu Ile Asp Glu Val Asp Ile Asp Gln Leu
195 200 205

Tyr Ser Ala Asp Lys Val Ser Val Asp Ala Leu Leu Val Gly Ile Ile
210 215 220

Lys Asn
225

<210> 1126
<211> 52
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1126
Met Ile Pro Ile Ile Val Ile Leu Ile Gly Leu Ile Leu Phe Leu Ser
1 5 10 15

Ser Gly Tyr Lys Leu Val Leu Gly Lys Tyr Tyr Asp Asp Val Asp Leu
20 25 30

Lys Ile Leu Phe Thr Ile Phe Gly Val Gly Ile Ala Leu Leu Leu Gly
35 40 45

Gly Phe Ile Leu
50

<210> 1127
<211> 74
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1127
Met Asn Tyr Glu Glu Val Leu Arg Thr Ile Lys Glu Asn Lys Pro Cys
1 5 10 15

Lys Val Arg Phe Thr Gly Asn Ile Leu Ala Ile Val Asn Glu Glu Phe
20 25 30

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

Asn Lys Glu Gly Tyr Ile Arg Leu Gln Gln Tyr Cys Leu Glu Arg Asp
50 55 60

Asp Tyr Thr Val Val Gly Ala Ile Leu Phe
65 70

<210> 1128
<211> 66
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1128
Met Asn Tyr Arg Asp Phe Ile Thr Asp Cys Ile Ser Gly Gly Tyr Asn
1 5 10 15

Val His Ile Ser Val Thr Glu Lys Arg Val His Ile Ile Ser Glu Met
20 25 30

Thr Ser Ala Ser Tyr Pro Lys Lys Glu Ile Asn Leu Asp Glu Leu Gln
35 40 45

Ala Tyr Val Tyr Tyr Met Asn Asn Phe Gly Ser Gln Ile Thr Thr Glu
50 55 60

Gly Leu
65

<210> 1129
<211> 96
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1129
Met Glu Leu Val Ile Asn Ile Val Ala Val Leu Val Gly Met Tyr Ala
1 5 10 15

Ile Tyr Phe Tyr Val Thr Lys Phe Ser Thr Gly Leu Ser Gly Ile Leu
20 25 30

Ile Val Leu Gly Met Ala Ile Gly Leu Tyr Phe Tyr Leu Asp Tyr Leu
35 40 45

Asn Val Arg Glu Asn Val Ile Arg Leu Val Ser Val Met Phe Gly Ala
50 55 60

Phe Leu Phe Ser Ile Glu Met Ile Tyr Asn Lys Ile Met Phe Glu Ile
65 70 75 80

Lys Lys Ser Asn Val Gln Lys Thr Val Arg Val Tyr Asp Lys Glu Gln
85 90 95

<210> 1130

<211> 102
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1130
Met Tyr Pro Glu Ile Asp Val Glu Lys Leu Ala Tyr Lys Leu Lys Ser
1   5   10   15

Thr Arg Glu Tyr Leu Glu Ser Ile Lys Ile Lys Glu Val Glu Ile Tyr
            20   25   30

Glu Ile Tyr His Leu Lys Thr Gly Lys Leu Val Phe Lys Gly Glu Tyr
        35   40   45

Ile Glu Val Lys Glu Leu Leu Arg Lys Met Tyr Lys Glu Asn Leu Thr
    50   55   60

Leu Val Asp Val Asp Thr Met Leu Ser Ile Gly Lys Gly Phe Ile Asp
65   70   75   80

Val Ile Lys Asn Ile Ser Ala Glu Asn Val Phe Gln Ile Thr Tyr Lys
                85   90   95

Lys Glu Leu Ser Thr Lys
            100

<210> 1131
<211> 302
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1131
Met Ile Lys Ile Phe Ser Glu Val Asp Lys Glu Tyr Lys Pro Ile Ile
1   5   10   15

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

Lys Tyr Leu Val Glu Glu Asn Leu Arg Phe Asp Val Phe Phe Lys Trp
        35   40   45

Glu Asn Asp Ala Asp Leu Met His Leu Tyr Met Phe Thr Lys Tyr Leu
    50   55   60

Glu Gln Leu Gly Ile Lys Asp Lys Ala Glu Phe Leu Glu Ile Ala Tyr
65   70   75   80

Leu Pro Tyr Ser Arg Met Asp Arg Val Glu Glu Gly His Asn Asn Met
                85   90   95

```
Phe Ser Leu Lys Tyr Ile Thr Glu Phe Ile Asn Asn Leu Asn Tyr Lys
            100                 105                 110

Ser Val Trp Val Val Glu Pro His Ser Pro Val Thr Glu Glu Leu Leu
        115                 120                 125

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

Ile Glu Met Ser Glu Glu Pro Val Thr Ile Val Leu Pro Asp Lys Gly
145                 150                 155                 160

Ala Tyr Asp Arg Tyr Leu Phe Asp Val Glu Arg Ile Leu Met Glu Ser
                165                 170                 175

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

Glu Thr Gly Lys Ile Lys Gly Ile Lys Ile Ile Lys Asp Lys Asn Thr
        195                 200                 205

Leu Tyr Asp Asn Cys Ile Ile Leu Asp Asp Leu Thr Ser Tyr Gly Gly
    210                 215                 220

Thr Phe Val Gly Cys Lys Lys Ala Leu Asp Lys Leu Lys Val Ser Ser
225                 230                 235                 240

Val Ser Leu Ile Leu Thr His Ala Glu Arg Ala Phe Ala Glu Gly Ala
                245                 250                 255

Leu Leu Ser Ser Gly Phe Lys Asp Ile Ile Val Thr Asp Ser Met Phe
            260                 265                 270

Pro Lys Asn Asn Trp Glu Lys Ala Ile Ala Lys His Arg Ala Arg Ile
        275                 280                 285

Asn Gly Thr Glu Leu Gln Ile Lys Asp Ile Glu Arg Tyr Leu
    290                 295                 300


<210> 1132
<211> 489
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1132
Met Leu Asn Pro Thr Leu Met Cys Asp Phe Tyr Lys Leu Ser His Arg
1               5                   10                  15

Glu Gln Tyr Pro Glu Gly Thr Glu Ile Val Tyr Ser Thr Leu Val Pro
            20                  25                  30
```

```
Arg Ser Asn Lys Tyr Tyr Glu His Ser Asp Asn Ile Val Val Phe Gly
        35                  40                  45

Ile Gln Ser Leu Val Lys Lys Tyr Phe Ile Asp Met Phe Asn Lys Glu
    50                  55                  60

Phe Phe Asn Arg Pro Lys Glu Glu Val Ile Asn Glu Tyr Lys Arg Thr
65                  70                  75                  80

Val Lys Phe Thr Leu Gly Gln Glu Asn Pro Asp Ala Lys His Leu Glu
                85                  90                  95

Gln Leu His Asp Leu Gly Tyr Leu Pro Ile Asp Val Arg Ala Leu Lys
            100                 105                 110

Glu Gly Thr Val Val His Pro Asn Thr Pro Val Met Thr Ile Glu Asn
        115                 120                 125

Thr His Ser Asp Phe Phe Trp Leu Thr Asn Tyr Leu Glu Thr Ile Ile
    130                 135                 140

Ser Thr Gln Thr Trp Gln Ala Met Thr Ser Ala Thr Leu Ala Tyr Asp
145                 150                 155                 160

Met Arg Lys Met Leu Asp Lys Tyr Ala Met Glu Thr Val Gly Asn Ile
                165                 170                 175

Glu Ala Val Asp Phe Gln Gly His Asp Phe Ser Met Arg Gly Met Ser
            180                 185                 190

Ser Leu Glu Thr Ala Gln Leu Ser Ser Ala Gly His Ala Ile Ser Phe
        195                 200                 205

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

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

Glu His Ser Val Met Cys Ala Asn Gly Asn Tyr Glu Thr Met Asp Glu
                245                 250                 255

Tyr Glu Thr Tyr Lys Arg Met Leu Thr Glu Ile Tyr Pro Thr Gly Ile
            260                 265                 270

Phe Ser Ile Val Ser Asp Thr Trp Asp Phe Trp Gly Asn Met Thr Lys
        275                 280                 285

Thr Leu Pro Arg Leu Lys Asp Ile Ile Met Glu Arg Asp Gly Lys Val
    290                 295                 300
```

```
Val Ile Arg Pro Asp Ser Gly Asp Pro Val Lys Ile Ile Cys Gly Asp
305                 310                 315                 320

Pro Asp Ala Asp Thr Glu Tyr Glu Arg Lys Gly Ala Val Glu Val Leu
                325                 330                 335

Trp Asp Thr Phe Gly Gly Thr Glu Thr Glu Lys Gly Tyr Lys Val Leu
            340                 345                 350

Asp Glu His Val Gly Leu Ile Tyr Gly Asp Ser Ile Asn Tyr Glu Arg
        355                 360                 365

Ala Gln Gln Ile Cys Glu Gly Leu Lys Glu Lys Gly Phe Ala Ser Ile
    370                 375                 380

Asn Val Val Leu Gly Val Gly Ser Phe Ser Tyr Gln Phe Asn Thr Arg
385                 390                 395                 400

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

Glu Glu Lys Leu Ile Tyr Lys Asn Pro Lys Thr Asp Ser Gly Lys Arg
            420                 425                 430

Ser His Lys Gly Arg Val Ala Val Tyr Lys Asp Gly Ser Trp Glu Asp
        435                 440                 445

Asn Leu Thr Leu His Gln Trp Leu Asn Lys Gln Asn Val Asn Gln Leu
    450                 455                 460

Glu Arg Val Phe Glu Asp Gly Lys Leu Tyr Arg Asp Gln Ser Leu Ser
465                 470                 475                 480

Glu Ile Arg Glu Ile Ile Lys Asn Asn
                485


<210> 1133
<211> 81
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1133
Met Ile Tyr Lys Ile Ser Lys His Asn Tyr Tyr Ser Arg Phe Glu Tyr
1               5                   10                  15

Ser Ser Tyr Leu Pro Asp Glu Gly Phe Ala Tyr Ile Asp Tyr Val Asp
            20                  25                  30

Val Ile Leu Ile Gly Val Asp Asn Pro Arg Lys Arg Lys Val Ile Thr
```

35 40 45

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

Tyr Asn Ile Ile Lys Ile Leu Trp Phe Glu Lys Trp Glu Trp Leu Gln
65 70 75 80

Pro

<210> 1134
<211> 130
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1134
Met Ile Ile Asp Lys Leu Asn Gly Val Lys Leu Glu Ile Gly Gly His
1 5 10 15

Val Val Ser Phe Ser Val Ser Lys Phe Lys Thr Ile Asn Gly Glu Arg
20 25 30

Gln Leu Leu Asp Tyr His His Ile Lys Arg Arg Lys Gln Lys Tyr Phe
35 40 45

Arg Thr Thr Glu Glu Phe Tyr Asn Glu Tyr Lys Glu Ile Lys Pro Asp
50 55 60

Lys Asn Glu Ile Asp Glu Met Phe Glu Ser Leu Gly Tyr Val Asp Thr
65 70 75 80

Lys Leu Glu Asp Val Val Arg Asn Gln Glu Lys Val Thr Glu Ile Leu
85 90 95

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

Glu Tyr Val Asp Lys Ile Val Thr Leu Glu Ile Lys Glu Leu Lys Gly
115 120 125

Glu Lys
130

<210> 1135
<211> 65
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1135
Met Ser Asn Ser Trp Glu Lys Glu Gly Val Asn Tyr Trp Glu Asn Glu
1   5   10   15

Asp Cys Pro Arg Glu Tyr Leu Glu Lys Ala Phe Ile Glu Leu Val Glu
            20   25   30

Tyr Val Glu Gly Val Thr Val Pro Ser Arg Asp Val Gln Gln Leu Arg
        35   40   45

Glu Asp Lys Leu Arg Glu Asp Ile Gly Phe Tyr Glu Tyr Val Ala Asp
    50   55   60

Lys
65

<210> 1136
<211> 98
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1136
Met Met Asn Gly Lys Gln Ile Tyr Val Phe Leu Ser Asp Gln Tyr Ser
1   5   10   15

Lys Asp Ile Leu Ser Leu Gln Leu Gly Leu Ile Lys Glu Trp Ser Arg
            20   25   30

Arg Glu Leu Thr Tyr Ser Asp Asp Val Gly Ser Asp Ala Asp Val Val
        35   40   45

Ile Cys Thr Asp Ile Val Arg Asp Asp Phe Val Lys Lys Leu Ser Lys
    50   55   60

Asn Asn Ser Asn Ala Leu Phe Val Phe Ile Ser Ser Phe Tyr Trp Ile
65   70   75   80

Gly Tyr Lys Gly Gly Glu Phe Phe Val Ala Val Gln Asp Tyr Val Lys
                85   90   95

Gly Met

<210> 1137
<211> 103
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1137
Met Lys Lys Leu Leu Ile Leu Phe Thr Leu Ala Ser Thr Leu Leu Leu

1 5 10 15

Ala Gly Cys Thr Pro Asp Asn His Glu Gly Lys Val Leu Gly Thr Gly
20 25 30

Glu Tyr Arg Glu Pro Thr Thr Tyr Ile Lys Ser Gly Ser Val Thr Val
35 40 45

Pro Val Ile Gly Glu Met Lys Tyr Tyr Val Asp Leu Glu Thr Asp Lys
50 55 60

Gly Glu Asp Arg Val Tyr Leu Asn Arg Glu Val Tyr His Lys Phe Asp
65 70 75 80

Lys Gly Asp Asp Phe Ser Asn Val Gly Lys Lys Val Tyr Lys Asn Asp
85 90 95

Glu Leu Ile Tyr Lys Gly Asp
100

<210> 1138
<211> 99
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1138
Met Lys Gln Phe Ile His Asp Lys Lys Asp Ser Tyr Asn Ser Thr Asn
1 5 10 15

Arg Asn Phe Asp Ile Gln Tyr Tyr Lys Gly Ile Pro Leu Gln Gln Ile
20 25 30

Asp Arg Gly Tyr Gly Gln Ala Arg Ala Arg Arg Phe Thr Ile Asn Asn
35 40 45

Thr Asn Gln Asn Ile Trp Ile Pro Met Thr Tyr Leu Lys Pro Asn Gly
50 55 60

Thr Leu Lys Asn Asn Ile Asp Ile Asp Trp Ile Leu Val Lys Glu Lys
65 70 75 80

Cys Ser Leu Lys Lys Ala Gly Leu Val Ile Lys Ile Lys Ile Thr Gly
85 90 95

Asp Val Leu

<210> 1139
<211> 79
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1139
Met Tyr Ile Leu Glu Arg Thr Ile Arg Gly Phe Ala Gly Gln Thr Glu
1 5 10 15

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

Leu Lys Leu Met Glu Phe Leu Lys Glu Glu Thr Asn Tyr Trp Val Lys
        35 40 45

Lys Asn Gly Asn Tyr Thr Ile Ile Ile Arg Ala Lys Arg Ile Leu Tyr
    50 55 60

Ile Glu Glu His Ile Gln Lys Leu Lys Glu Trp Glu Asn Asp Leu
65 70 75

<210> 1140
<211> 51
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1140
Met Thr Tyr Asp Val Tyr Val Leu Tyr Lys Arg Gly Glu Pro Ile Ala
1 5 10 15

Gln Gly Ser Met Glu His Cys Leu Asp Val Tyr Tyr Trp Glu Arg Val
            20 25 30

His Gly Tyr Ser Asn Lys Gly Tyr Glu Leu Leu Pro Met Gly Tyr Glu
        35 40 45

Gln Glu Glu
    50

<210> 1141
<211> 64
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1141
Met Ile Asn Ile Glu His Asp Tyr Thr Ile Arg Thr Val Asp Asn Arg
1 5 10 15

Lys Tyr Thr Tyr Tyr Ser Lys His Glu Ser Pro Val Thr Leu Tyr Lys
            20 25 30

Asn Ile Ile Gly Lys Asp Cys Ile Glu Val Thr Lys Tyr Gly Lys Asp

35 40 45

Lys Lys Val Ile Ile Ala Thr Lys Tyr Ile Val Ser Ile Glu Arg Trp
50 55 60

<210> 1142
<211> 117
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1142
Met Asn Ala Arg Lys Ala Arg Lys Asn Thr Lys Asn Tyr Lys Asp Ser
1 5 10 15

Asn Val Val Thr Lys Glu Gln His Leu Thr Tyr Ile Tyr Asn Lys Leu
20 25 30

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

Met Asn Leu Arg Thr Asp Tyr Pro Asp Glu Phe Ser Leu Ser Lys Leu
50 55 60

Lys Tyr Leu Lys Glu Ile Lys Gln His Tyr Lys Asp Leu Val Phe Asn
65 70 75 80

Val Lys Thr Gln Val Arg Lys Ala Gln Trp Ser Glu Lys Ser Ile Ile
85 90 95

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

Ile His Ile Ser Trp
115

<210> 1143
<211> 62
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1143
Met Phe Phe Lys Lys Lys Lys Leu Ser Asn Val Glu Lys Gln Ile Arg
1 5 10 15

Gln Asn Arg Asn Lys Glu Asp Lys Glu Arg Lys Glu His Gln Asp Lys
20 25 30

Leu Asp Thr Asp Met Tyr Lys Thr Tyr Glu Leu Asp Lys Ile Val Glu
35 40 45

Glu His Leu Arg Lys Leu Asn Thr Ile Ser Leu Glu Glu Leu
50 55 60

<210> 1144
<211> 62
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1144
Val Cys Leu Gly Thr Arg Leu Val Tyr Tyr Tyr Ser Ile Gly Lys Asp
1 5 10 15

Trp Asn Lys Gln Val Tyr Ser Leu Asn Glu Leu Glu Tyr Met Lys Lys
20 25 30

Lys Phe Lys Lys Leu Gly Phe Glu Thr Gln Ile Thr Asn Glu Asp Ile
35 40 45

Gly Phe Gln Pro Tyr Ile Tyr Leu Arg Leu Leu Trp Asp Ala
50 55 60

<210> 1145
<211> 53
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1145
Met Asn Leu Thr Phe Glu Asp Lys Leu Glu Asp Leu Leu Lys Lys Val
1 5 10 15

Arg Ser Gly Glu Ile Glu Pro Ile Glu Tyr Ser Gln Val Asn Asp Glu
20 25 30

His Pro Asn Gly Lys Thr Thr Cys Gly Val Thr Phe Lys Phe Asp Ile
35 40 45

Asp Thr Pro Thr Lys
50

<210> 1146
<211> 101
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1146
Met Ile Ile Leu Phe Thr Gln Asp Tyr Asp Lys Thr Leu Met Lys Val
1 5 10 15

Ile Leu Gly Asp Ile Asn Thr Met Arg Pro Asn Trp Lys Tyr Ser Val
            20   25   30

Asn His Pro Glu Lys Glu Glu Asp Val His Ile Gln Ala Tyr Glu Gly
        35   40   45

Glu Asp Ile Phe Asp Asp Ile Glu Glu Leu Ser Asp Ser Thr Gln Asp
    50   55   60

Ile Val Ile Gly Val Thr Glu Asp Asp Cys Ile Ser Glu Ser Pro Tyr
65   70   75   80

Asp Phe Asn Gly Gly Leu Arg Leu Val Thr Lys His Ile Lys Glu His
                85   90   95

Ile Glu Lys Phe Leu
            100

<210> 1147
<211> 99
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1147
Met Ile Asp Ile Tyr Leu Gly Glu Gly Tyr Asn Lys Glu Tyr Leu Ser
1   5   10   15

Lys Ala Leu Arg Leu Ile Asn Asp His Ala Pro Arg Glu Leu Ser Tyr
            20   25   30

Asp Phe Asn Asn Val Glu Ala Asp Val Asn Ile His Thr Met Leu Tyr
        35   40   45

Val Lys Pro Glu Asp Arg Tyr Val Tyr Lys Asp Ile Ser Tyr Asp Phe
    50   55   60

Pro Gly Asp Leu Ile Ile Cys Ile Val Glu Asp Asp Ala Ile Val Tyr
65   70   75   80

His Gln Gly Lys Gln Val Ser Gly Ile Ser Ile Leu Arg Ile Ile Glu
                85   90   95

Glu Leu Ile

<210> 1148
<211> 97
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1148
Met Ile Glu Ile Tyr Leu Ser Glu Asn Tyr Asp Lys Asp Leu Leu Lys
1   5   10   15

Ala Glu Leu Lys Trp Ile Lys Glu Thr Ala Ser Arg Glu Leu Thr Tyr
            20   25   30

Asp Val Asn Arg Asn Pro Asn Leu Asp Val His Val Ser Pro Phe Arg
        35   40   45

Tyr Thr Lys Asp Glu Val Lys Glu Ile Ser Leu His Pro Gln Phe Glu
    50   55   60

Asp Asp Val Cys Val Phe Ile Ala Glu Thr Trp Ile His Glu Tyr His
65   70   75   80

Arg Gly Lys Ser Ile Gly Val Asp Ser Met Glu Glu Tyr Val Lys Glu
                85   90   95

Met

<210> 1149
<211> 85
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1149
Met Phe Lys Val Tyr Tyr Thr Val Tyr His Lys Gly Ser Met Lys Thr
1   5   10   15

Ile Lys Asp Lys Leu Asp Arg Ser Ser Leu Ile Tyr Phe Leu Tyr Asp
            20   25   30

Thr Trp Tyr Lys Asp Ile Ser Asn Val Phe Pro Asn His Tyr Asn Lys
        35   40   45

Glu Phe Gly Ser Asn Ser Asp Asp Ile Asp Ile Asp Lys Leu Ile Glu
    50   55   60

Ala Val Asn Glu Glu Gly Ile Leu Leu Ile Asn Arg Gly Asn Tyr Val
65   70   75   80

Thr Ile Arg Glu Trp
                85

<210> 1150
<211> 79
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1150
Met Val Thr Leu Thr Tyr Thr Ile Ile His Lys Glu Ser Asp Arg Val
1   5   10   15

Ile Ala Ser Gly Leu Asp Glu Leu Glu Val Ile Asn Leu Val Gln Arg
            20   25   30

Met Val Asn Thr Asn Leu Val Thr Asp Ile Ser Leu Asp Asp Tyr Ile
        35   40   45

Arg Arg Pro Ser Gly Asp Ile Asp Val Leu Asn Leu Leu Val Asp Ile
    50   55   60

Arg Arg Gln Gly Val Phe Asp Phe Asn His Thr Trp His Val Gly
65   70   75

<210> 1151
<211> 115
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1151
Met Ile Val Ile Tyr Thr Asp Val Ser Lys Asp Tyr Leu Lys Asp Glu
1   5   10   15

Phe Leu Pro Trp Leu Asn Glu Arg Asp Arg Tyr Leu Glu Asp Tyr Lys
            20   25   30

Asp Glu Leu Pro Glu Asp Ile Asp Ser Ser Tyr Ile Val Ser Val Val
        35   40   45

Tyr Cys Lys Asp Met Glu Gly Leu Leu Glu Arg Lys Asp Ile Val Ile
    50   55   60

Gly Asn Ser Tyr Asn Glu Pro Val Ala Leu Leu Gly Val Pro Glu Phe
65   70   75   80

Phe Gly Asn Tyr Ser Asn Tyr Phe Tyr Tyr Arg Gly Glu Ser Ile Ser
                85   90   95

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

Gly Gly Asp
        115

<210> 1152
<211> 230
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1152
Met Lys His Asn Ile Asn Asn Ile Glu Met Phe Ser Lys Tyr Tyr Ile
1   5   10   15

Lys Glu Asn Lys Val Tyr Ser Lys Lys Thr Asn Lys Glu Leu Lys Lys
            20   25   30

Asp Lys Asn Asn Phe Tyr Arg Met Thr Asp Asp Ile Asn Lys Ala Arg
        35   40   45

Lys Val Lys Ile Asp Thr Leu Leu Gln Tyr Asn Leu Lys Asp Tyr Asn
    50   55   60

Ser Ile Asn Asn Leu Pro Asn Glu Lys Trp Lys Arg Ile Glu Asn Asn
65   70   75   80

Ile Asn Asn Ile Phe Asn Tyr Ser Val Ser Asn Tyr Gly Arg Ile Lys
                85   90   95

Arg His Gly Asn Tyr Tyr Met Ile Glu Lys Leu Val Lys Pro His Asn
            100   105   110

His Lys Gln Gly Tyr Lys Ile Val Lys Ile Asn Tyr Lys His His Ser
        115   120   125

Ile His Arg Leu Val Tyr Glu Tyr Phe Gly Asn Asp Phe Asn Gln Asp
    130   135   140

Tyr His Ile His His Ile Asp Gly Asn Lys Gln Asn Asn His Ile Asn
145   150   155   160

Asn Leu Gln Cys Ile Ser Pro Thr Glu His Asn Asn Leu His His Lys
                165   170   175

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

Glu Arg Lys Asn Ile Tyr Lys Leu Tyr Thr Glu Lys Gly Phe Thr Gln
        195   200   205

Glu Glu Leu Ser Asn Met Tyr Asn Val Ser Arg Ile Thr Ile Asn Arg
    210   215   220

Asn Ile Lys Arg Phe Lys
225   230

<210> 1153
<211> 102

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1153
Met Glu Ile Lys Glu Ile Ala Asp Thr Ile Met Tyr Leu Phe Asn Met
1   5   10   15

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

His Thr Arg Thr His Thr Ala Leu Ile Val Ser Ile Lys Gly Asn Tyr
        35   40   45

Asp Thr Val Gln Met Phe Arg Lys Thr Pro Ile Met Ser Met Arg Gly
    50   55   60

Gln Ser Gln Pro Ala Ser Met Leu Val Asn Val Ile Asp Asp Val Ile
65   70   75   80

Ile Ile Val Tyr Glu Asn Val Val Tyr Gly Val Gln Asn Lys Glu Ile
                85   90   95

Lys Phe Ile Glu Glu Ile
            100

<210> 1154
<211> 95
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1154
Met Thr Asn Lys Asn Tyr Leu Tyr Glu Glu Thr His Thr Val Gln Gly
1   5   10   15

Gln Asp Ile Thr Ala Phe Arg Ile Pro Asn Asp Thr Asn Gly Asn Pro
            20   25   30

Arg Tyr Val Val His Phe Met Asp Leu Asn Ile Lys Leu Ala Asp Tyr
        35   40   45

Asp Asn Ile Asn Lys Leu Tyr Gly Phe Asn Lys Tyr Arg Ala Lys Trp
    50   55   60

Phe Gly Gly Gly Val Val Phe Gln Ser Tyr Asn Ile Glu Asp Thr Leu
65   70   75   80

Asn Phe Ala Leu Asp Lys Val Lys Glu Ile Glu Ala Val Lys Asn
                85   90   95

<210> 1155
<211> 90
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1155
Met Ile Leu Glu Ile Glu Thr Lys Pro Val Lys Thr Leu Lys Ala Ile
1   5   10   15

Lys Asp Asp Thr Lys Asn Ile Lys Asn Ser Ile Ala Glu His Leu Gly
            20   25   30

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

Gly Tyr Ser Glu Glu Phe Lys Cys Trp Tyr Asn Leu Thr Ser Thr Ile
    50   55   60

Gly Asn Phe Pro Lys Tyr Leu Lys Ser Glu Leu Tyr Asn Glu Tyr Lys
65   70   75   80

Leu Tyr Cys Asn Val Glu Leu Lys Thr Lys
                85   90

<210> 1156
<211> 52
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1156
Met Leu Lys Phe Lys Trp Lys Asn Lys Thr Ile Lys Ser Thr Gln Lys
1   5   10   15

Thr Asp Asn Ile Leu Leu Leu Ile Ile Gly Gly Leu Val Ala Thr Ile
            20   25   30

Thr Pro Lys Leu Val Asn Trp Phe Leu Leu Leu Gln Asp Asn Ile Asn
        35   40   45

Ile Phe Leu Arg
    50

<210> 1157
<211> 126
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1157
Met Phe Lys Leu Gln Asn Lys Val Glu Ile Ile Val Pro Lys Glu Asp

1 5 10 15

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

Ser Ile Thr Met Glu Ala Gly Gly Cys Thr Ile Thr Glu Ile Lys Gly
35 40 45

Gln Trp Tyr Ser Glu Asp Glu Lys Arg Ile Met Glu Asp Asn Asn Leu
50 55 60

Asn Leu Glu Trp Tyr Tyr Ile Pro Asp Arg Ala Lys Phe Met Thr Val
65 70 75 80

Glu Leu Lys Gly Ile Val Arg Arg Leu Ile Glu Val Tyr Gly Gln Glu
85 90 95

Ala Ile Ser Ile Lys Val Asn Gly Thr Leu Tyr Ile Val Asp Gln Ser
100 105 110

Asp Ile Glu Glu Leu His Thr Thr Leu Leu Asn Ile Met Lys
115 120 125

<210> 1158
<211> 73
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1158
Met Asn Arg Leu Glu Ile Val Lys Asp Thr Ala Met Glu Tyr Ile Leu
1 5 10 15

Met Met Asp Asn Ser Val Met Asp Gly Val Met Thr Gln Glu Glu Tyr
20 25 30

Asn Glu Ala Val Ser Phe Glu Lys Val Tyr Asp Tyr Thr Leu Ser Glu
35 40 45

Ala Asn Lys Glu Cys Lys Phe Leu Gly Gly Lys Val Leu Thr Phe Leu
50 55 60

Val His Glu Ala Ile Glu Glu Tyr Ala
65 70

<210> 1159
<211> 45
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Bacteriophage F125/10

<400> 1159
Met Arg Tyr Glu Ile Val Thr Leu Val Asn Gln Glu Leu Phe Met Tyr
1   5   10   15

Ala Thr Phe Asn Lys Gln Glu Ala Glu Ala Lys Tyr Ser Glu Trp Cys
            20   25   30

Glu Leu Tyr Gly Gln Glu Asn Val Ser Met Glu Lys Asn
        35   40   45

<210> 1160
<211> 92
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1160
Met Ile Ile Leu Asn Tyr Thr Lys Glu Lys Glu Met Ile Gln Met Lys
1   5   10   15

Leu Leu Asn Gln Glu Asn Gln Ile Val Ile Ser Ile Ala Thr Leu Glu
            20   25   30

Ser Val Lys Gln Ala Leu Ile Trp Glu Tyr Ile Asp His Ile Asp Tyr
        35   40   45

Asn Ile Trp Asn Asn Glu Leu Asp Asp Thr Glu Ala Val Val Lys Ile
    50   55   60

Ser Gly Ile Leu Gln Ser Ile Lys Phe Ala Asp Thr Met Glu Asp Leu
65   70   75   80

Gln Glu Tyr Ile Gly Asp Ile Gly Trp Lys Leu Ile
                85   90

<210> 1161
<211> 79
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1161
Met Lys Lys Asn Val Lys Ala Ser Thr Ile Glu Trp Leu Glu Leu Thr
1   5   10   15

Gln Gly His Gly Glu Phe Asp Gly Phe Asp Glu Glu Asp Met Asp Phe
            20   25   30

Arg Lys Leu Asp Asp Glu Asp Ile Lys Trp Tyr Phe Glu Asn Trp Tyr
        35   40   45

Phe Thr Glu Glu Lys Gln Glu Gln Ile Ile Asp Glu Ile Gly Gln Glu
    50   55   60

Glu Phe Glu Glu Ala Tyr Ser Asp Asp Ile Lys Glu Tyr Asn Asn
65   70   75

<210> 1162
<211> 86
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1162
Met Thr Lys Phe Lys Leu Ile Asp Lys Asn Ser Phe Tyr Val Asn Asp
1   5   10   15

Asn Tyr Asn Asn Glu Thr Tyr Leu Thr Ser Gln Ile Val Leu Ser Gly
            20   25   30

Glu Ala Gly Arg Leu Leu Asp Asp Met Ile Glu Asp Cys Glu Asp Glu
        35   40   45

His Asp Lys Asp Asn Tyr Lys Lys Leu Asp Thr Asn Asn Ile Asp Asp
    50   55   60

Ile Asp Tyr Ile Leu Glu Cys Ala Asn Val Tyr Ile Tyr Pro Tyr Asn
65   70   75   80

Lys Thr Glu Phe Lys Tyr
                85

<210> 1163
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1163
Met Asn Thr Arg Arg Ala Asn Lys Ala Leu Asn Glu Ala Val Arg Leu
1   5   10   15

Leu Asp Lys Gln Ile Glu Asp Thr Gln Lys Thr Met Gln Glu Leu Asn
            20   25   30

Lys Gln Leu Glu Gln Gln Ile Lys Ala Lys Gln Glu Leu Met Thr Leu
        35   40   45

Val Asp Val Met Thr Gly Asp Asp Glu
    50   55

<210> 1164
<211> 89

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1164
Met Asn Ile Lys Glu Ala His Lys Val Val Arg Ser Ala Lys Ser Lys
1   5   10   15

Leu Leu Gln Glu Gln Glu His Ile Thr Asn His Ile Ile Glu Asp Tyr
            20   25   30

Ile Ile Glu Glu Leu His Arg Arg Thr Gln Gly Ser Gly Thr Ile Gln
        35   40   45

Met Asn Asn Asn Thr Ala Ser Tyr Ser Asn Gly Ser Tyr Gly Ser Leu
    50   55   60

Glu Glu Leu Arg Glu Ala Tyr Asp Leu Ser Ser Leu Ser Thr Gly Glu
65   70   75   80

Ile Lys Glu Leu Leu Glu Thr Phe Val
                85

<210> 1165
<211> 83
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1165
Met Lys Glu Gln Ile Lys Gln Phe Glu Lys Glu Leu Glu Met Ala Val
1   5   10   15

Asn Asn Leu Phe Val Leu His Asp Cys Gly Val Ser Gln Ala Lys Ile
            20   25   30

Glu Glu Gln Asn Gln Lys Val Val Tyr Leu Lys Ala Ile Val Glu Asn
        35   40   45

Met Lys Ala Tyr Glu Glu Ile Arg Val Glu Pro Lys Ser Glu Glu Gln
    50   55   60

Phe Phe Lys Glu Leu Glu Glu Glu Leu Glu Glu Glu Glu Lys Ile Leu
65   70   75   80

Lys Gly Ile

<210> 1166
<211> 87
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1166
Met Lys Leu Tyr Gln Val Glu His Asp Asn Cys Glu Pro Tyr Glu Asp
1   5   10   15

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

Ile Lys Arg Ile Lys Ala Glu Gly Tyr Glu Glu Lys Ile Ser Gly Tyr
        35   40   45

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

Pro Leu Phe Arg Glu Asp Met Ile Thr Ile His Glu Leu Glu Val Ile
65   70   75   80

Asn Asn Thr Ser Glu Glu Glu
                85

<210> 1167
<211> 143
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1167
Met Glu Asn Tyr Lys Asn Phe Ile Ile Glu Glu Met Asn Lys Ala His
1   5   10   15

Ile Leu Val Thr Lys Ala Glu Gln Ile Lys Gly Asp Arg Lys Leu Ala
            20   25   30

Glu Thr Glu Leu Glu Glu Val Tyr Arg Lys Ala Glu Ala Phe Asp Glu
        35   40   45

Ile Val Asn Glu Leu Leu Tyr Gln Leu Gln Asn Leu Glu Ser Trp Asp
    50   55   60

Thr Leu Asp Gln Lys Asp Cys Gln Thr Leu Lys Gln Ile Leu Glu Glu
65   70   75   80

Asn Ile Lys Glu Glu Lys Gln Met Glu Arg Phe Lys Val Lys Arg Ile
                85   90   95

Ile Thr Thr Glu Glu Val Arg Tyr Ile Asp Ala Glu Thr Glu Glu Asp
            100   105   110

Ala Trp Tyr Ser Val Glu Tyr Glu Asp Glu Gly Thr Asp Thr Ala His
        115   120   125

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

<210> 1168
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1168
Met Ile Glu Ile Ser Ile Ser Trp Thr Tyr Leu Ile Thr Phe Leu Leu
1 5 10 15

Leu Trp Ser Ala Gly Thr Leu Tyr Ile Asn Tyr Leu Val Tyr Arg Ile
20 25 30

Arg Leu Thr Asn Lys Glu Arg Lys Glu Met Ser Lys Glu His His Arg
35 40 45

Asn Arg Glu Glu Ile Lys Gln Arg Ile Glu Asn Arg Arg Asp Lys
50 55 60

<210> 1169
<211> 82
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1169
Met Arg Tyr Asp Ile Asn Glu Lys Cys Tyr Asp Glu Lys Asp Phe Val
1 5 10 15

Leu Gln Ile Ile Tyr Glu Asn Tyr Ser Asp Glu Thr Asp Arg Glu Val
20 25 30

Glu Thr Ile Tyr Asn Lys Ala Glu Ala Trp Asp Lys Leu Cys Glu Met
35 40 45

Leu Lys Asp Lys Asp Met Ser Asp Gly His Phe Glu Glu Glu Met Phe
50 55 60

Lys Leu Phe Ser Arg Thr Gly Lys Ser Phe Thr Ile Asp Lys Glu Glu
65 70 75 80

Ser Gln

<210> 1170
<211> 160
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1170
Met Asn Lys Thr Phe Phe Lys Phe Leu Gly Lys Asn Thr Leu Glu Tyr
1 5 10 15

Ser Lys Gln Gly Leu Gly Phe Leu Val Ala Leu Pro Ile Met Leu Ile
            20 25 30

Ile Phe Ser Val Phe Leu Ala Phe Ile Ile Gly Ile Pro Ala Val Ile
        35 40 45

Ile Tyr Ala Leu His Ala Leu Asn Ile Asp Asn Asp Phe Ile Ile Gln
    50 55 60

Leu Val Pro Val Met Trp Phe Ile Ile Leu Tyr Gly Ile Val Arg Thr
65 70 75 80

Asp Glu His Lys Lys Pro Phe Val Lys Leu Lys Leu Lys Asp Tyr Leu
                85 90 95

Leu Ser Ile Leu Tyr Leu Thr Thr Ile Thr Ala Ile Ser Val Leu Glu
            100 105 110

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

Val Ile Thr Leu Leu Ser Phe Ile Val Phe Val Ala Val Asn Arg Gly
    130 135 140

Ile Cys Lys Ile Ala Ile Lys Ser Tyr Lys Glu Tyr Lys Glu Glu Leu
145 150 155 160

<210> 1171
<211> 143
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1171
Met Asn Ile Lys Tyr Ile Asp Leu Val Leu Glu Asn Cys Asp Val Val
1 5 10 15

Arg Leu Glu Ser Lys Asp Val Ser Arg Phe His Ile Ser Gly Ile Thr
            20 25 30

Glu Gly Ile Asp Tyr Tyr Gly Thr Tyr Lys Glu Thr Ser Asn Ile Ser
        35 40 45

Arg Thr Arg His Cys Thr Tyr Phe Gly Ile Leu Ile Asp Lys Pro Met
    50 55 60

Glu Ile Pro Gln Val Gly Phe Ala Tyr Pro Asp Asn Thr Asn Ala Tyr
65 70 75 80

Glu Met Ile Thr Ala Tyr Ser Asp Ile Thr Ala Ile Asp Ile Ile Tyr
85 90 95

Glu Asn Asp Ala Asn Glu Tyr Ile Tyr Val Asp Phe Asn Glu Tyr Asn
100 105 110

Asp Asn Tyr Asn Ile Asn Gln Lys Asn Asp Tyr Tyr Asn Asn Met Leu
115 120 125

Glu Ile Thr Ile Thr Glu Ser Asn Ser Arg Glu Glu Glu Asp Glu
130 135 140

<210> 1172
<211> 180
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1172
Met Asp Lys Ile Asn Leu Asn Lys Lys His Asp Gly Ser Thr Val Val
1 5 10 15

Asn Ile Ser Asn Asn Ile Met Leu Lys Ile Gln Cys Thr Asp Leu Arg
20 25 30

Lys Glu Cys Asp Asp Ser Glu Ala Pro Thr Thr Tyr Thr His Phe Lys
35 40 45

Ala Tyr Ile Val Tyr Asn Ile Phe Ile Val Val Asn Asp Arg Lys Gln
50 55 60

Lys Lys Lys Val Lys Tyr Asp Tyr Tyr Asn Asp His Val Gly Arg Gly
65 70 75 80

Asn Val Lys Asp Leu Leu Lys Val Lys Asp Val Ile Phe Gln Leu Ser
85 90 95

Thr Gln Leu Asn Thr Asn Glu Ile Ile Lys Ile Ser Gly Ala Asp Glu
100 105 110

Arg Arg Tyr Lys Ile Tyr Lys Tyr Phe Ile Glu Lys Asp Ile Arg Phe
115 120 125

Glu Asp Asn Met Tyr Tyr Ser Lys Ser Asn Ile Trp Ile Ile Asn Asn
130 135 140

Phe Ser Leu Leu Gln Lys Phe Gln Trp Asn Thr Val Val Thr Lys Asp

145 150 155 160

Gly Asp Tyr Asn Lys Lys Glu Leu Lys Lys Val Asp Lys Glu Trp Lys
165 170 175

Glu Leu Leu Ile
180

<210> 1173
<211> 162
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1173
Met Arg Glu Thr Ser Glu Tyr Ile Met Phe Trp Gly Lys Glu Asp Ile
1 5 10 15

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

Asn Asn Ser Glu Gln Ala Phe Met Trp Arg Lys Ala Arg Tyr Phe Asn
35 40 45

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

Ala Lys Ser Leu Gly Arg Lys Val Arg Asn Phe Asn Glu Glu Gln Trp
65 70 75 80

Asn Lys Val Arg Tyr Asp Ile Met Val Glu Val Val Lys Asp Lys Phe
85 90 95

Met Thr Thr His Leu Lys Gln Arg Ile Leu Asp Thr Asp Val Arg Lys
100 105 110

Asp Phe Val Glu Ala Ser Pro Tyr Asp Lys Ile Trp Gly Val Gly Leu
115 120 125

Lys Ala Asn Asp Pro Lys Ile Leu Glu Gln Ser Asn Trp Lys Gly Gln
130 135 140

Asn Leu Leu Gly Lys Val Met Glu Asp Val Arg Val His Cys Ile Tyr
145 150 155 160

Asn Lys

<210> 1174
<211> 132
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1174
Met Lys Lys Lys Tyr Phe Lys Gly Leu Lys Leu Asn Asp Phe Glu Lys
1   5   10   15

Glu Val Phe Gly Leu Lys Lys Asn Lys Lys Tyr Lys Lys Met Lys Lys
            20   25   30

Lys Leu Gly Arg Asn Glu Pro Lys Tyr Trp Asn Tyr Asp Met Ser Phe
        35   40   45

Phe Ile Gln Leu Tyr Ala Asp Leu Asn Ala Phe Val Glu Ser Ser Asn
    50   55   60

His Val Asp Met Glu Tyr His Thr Phe Val Asp Val Asp Gly Lys Glu
65   70   75   80

Arg Thr Gln Ile Asp Met Ile Lys His Ile Leu Ser Leu Ile Lys Tyr
                85   90   95

Tyr His Lys Glu Met Asp Asp Phe Asp Met Asp Lys Tyr Asp Glu Leu
            100   105   110

Glu Gln Val Gln Ser Lys Ile Leu Asp Asn Phe Lys Ile Val Leu Pro
        115   120   125

Ser Leu Trp Asn
    130

<210> 1175
<211> 235
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1175
Met Ala Ile Tyr Val Val Pro Asp Ile His Gly Glu Tyr Gln Lys Leu
1   5   10   15

Leu Thr Ile Met Asp Lys Ile Asn Asn Glu Arg Lys Pro Glu Glu Thr
            20   25   30

Ile Val Phe Leu Gly Asp Tyr Val Asp Arg Gly Lys Arg Ser Lys Asp
        35   40   45

Val Val Asn Tyr Ile Phe Asp Leu Met Ser Asn Asp Asp Asn Val Val
    50   55   60

Thr Leu Leu Gly Asn His Asp Asp Glu Phe Tyr Asn Ile Met Glu Asn
65   70   75   80

```
Val Asp Arg Leu Ser Ile Tyr Asp Ile Glu Trp Leu Ser Arg Tyr Cys
                85                  90                  95

Ile Glu Thr Leu Asn Ser Tyr Gly Val Ser Thr Val Thr Leu Lys Tyr
            100                 105                 110

Ser Ser Val Glu Glu Asn Leu Arg Asn Asn Tyr Asp Phe Ile Lys Ser
        115                 120                 125

Glu Leu Lys Lys Leu Lys Glu Ser Asp Asp Tyr Arg Lys Phe Lys Ile
    130                 135                 140

Leu Met Val Asn Cys Arg Lys Tyr Tyr Lys Glu Asp Lys Tyr Ile Phe
145                 150                 155                 160

Ser His Ser Gly Gly Val Ser Trp Lys Pro Val Glu Glu Gln Thr Ile
                165                 170                 175

Asp Gln Leu Ile Trp Ser Arg Asp Phe Gln Pro Arg Lys Asp Gly Phe
            180                 185                 190

Thr Tyr Val Cys Gly His Thr Pro Thr Asp Ser Gly Glu Val Glu Ile
        195                 200                 205

Asn Gly Asp Ile Leu Met Cys Asp Val Gly Ala Val Phe Arg Asn Ile
    210                 215                 220

Asp Phe Pro Phe Ile Lys Leu Glu Val Lys Lys
225                 230                 235


<210> 1176
<211> 616
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1176
Met Thr Lys Lys Leu Lys Leu Tyr Asp Tyr Glu Asn Asn Leu Leu Lys
1               5                   10                  15

Ser Ser Glu Asn Ile Glu Asp Ser Ile Gly Gln Ile Val Ile Glu Asn
            20                  25                  30

Leu Asn Pro Asp Thr Thr Tyr Glu Ala Gly His Phe Lys Ile Cys Trp
        35                  40                  45

Asp Ile Asn Gly Glu Glu Ser Ile Lys Val Asp Ile Pro Lys Phe Val
    50                  55                  60

Thr Leu Thr Ser Ser Gln Asp Lys Leu Ile Ile Val Thr Tyr Asn Glu
```

65 70 75 80

Val Glu Pro Met Asn Ile Lys Ala Glu Asn Ile Ile Gly Leu Gln Asp
85 90 95

Val Ile Asp Thr Gln Phe Asn Asp His Ile Lys Glu Glu Phe Met Ala
100 105 110

Glu Ile Asn Lys Leu Ile Ala Asp Asn Lys Pro Thr Gln Gln Pro Ser
115 120 125

Thr Thr Thr Ile Ser Pro Leu Lys Asp Lys Lys Val Ile Phe Ile Gly
130 135 140

Asp Ser Ile Thr Glu Val Asn Ala Arg Thr Thr Lys Asn Tyr His Gln
145 150 155 160

Phe Ile Ala Asp Arg Thr Gly Leu Ile Asn Val Asn Lys Gly Thr Ser
165 170 175

Gly Thr Gly Tyr Gln Asp Arg Lys Asn Val Ala Tyr Thr Ile Thr Asp
180 185 190

Lys Pro Asp Leu Ile Cys Val Met Leu Gly Thr Asn Asp Tyr Gly Leu
195 200 205

Val Gly Gly Lys Thr Lys Pro Leu Gly Thr Ala Lys Glu His Ser Tyr
210 215 220

Thr Thr Val Ala Gly Ser Ile Tyr Tyr Thr Tyr Tyr Gln Leu Ser Lys
225 230 235 240

Val Phe Pro Thr Val Pro Ile Val Val Leu Thr Pro Thr Pro Arg Ile
245 250 255

Glu Ser Asn Pro Phe Lys Glu Val Glu Asn Gly Gln Gly Tyr Thr Leu
260 265 270

Gly Gln Leu Val Asp Val Ile Lys Glu Ile Ala Lys Gln Phe Ser Phe
275 280 285

Pro Val Leu Asp Leu Tyr Arg Glu Ser Asn Ile Arg Val Trp Asp Asn
290 295 300

Asn Val Asn Lys Thr Phe Phe Ala Trp Lys Glu Gly Met Glu Asp Gly
305 310 315 320

Leu His Pro Asn Ala Lys Gly His Glu Phe Ile Ser Tyr Thr Ile Gln
325 330 335

Ser Phe Leu Glu Ser Lys Gly Thr Val Gly Ala Ile Ala Ser Pro Pro

340 345 350

Ser Ile Asp Thr Ser Val Lys Asp Leu Gly Asn Gly Val Tyr Ser Lys
355 360 365

Leu Ile Arg Pro Thr Gly Met Arg Trp Lys Lys Asp Thr Ser Phe Val
370 375 380

Met Asn Met Ser Thr Asp Asp Ile Asp Leu Thr Ala Asn Lys Ile Leu
385 390 395 400

Asn Val Ser Tyr Asn Gly Lys Ser Leu Ile Asn Pro Glu Gly Tyr Thr
405 410 415

Ser Asn Ser Pro Tyr Trp Tyr Thr Leu Pro Ala Tyr Glu Asp Gly Asn
420 425 430

Lys Tyr Asn Arg Ile Ser Glu Val Gln Asn Phe Leu Asn Ala Phe Ile
435 440 445

Thr Ile Asp Asp Asn Ala Gln Gly Leu Glu Phe Met Arg Asp Tyr Ile
450 455 460

Lys Val Ile Tyr Val Asp Lys Thr Lys Thr Asn Ile Val Gly Glu Tyr
465 470 475 480

Thr Gln Val Gly Tyr Lys Asp Thr Thr Ala Ser Thr Pro Pro Thr Gly
485 490 495

Asp Thr Ser Gly Thr Ile Thr Pro Val Ser Asn Gly Asp Gly Thr Tyr
500 505 510

Thr Ala Thr Phe Thr Pro Thr Ala Ile Tyr Trp Lys Glu Asp Gln Ser
515 520 525

Phe Met Ile Asn Ile Asp Lys Thr Lys Leu Asp Leu Thr Gly Lys Ser
530 535 540

Val Thr Lys Leu Glu Tyr Asn Gly Lys Thr Leu Val Asn Asn Thr Ser
545 550 555 560

Leu Ala Ser Asn Ser Pro Tyr Trp Leu Thr Val Pro Thr Ala Thr Glu
565 570 575

Gly Thr Thr Asn Asn Arg Thr Pro Glu Val Lys Asp Phe Val Ser Val
580 585 590

Leu Thr Leu Glu Ser Thr Gly Thr Asp Gly Arg Lys Lys Tyr Lys Asn
595 600 605

Val Glu Ile Lys Leu Thr Tyr Lys

610 615

<210> 1177
<211> 72
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1177
ggacucuuag cuuaaaggua aagccaaccg cucauaacgg uuugacugua gguucgaguc 60

cugcagaguc ca 72

<210> 1178
<211> 182
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1178
Met Glu Lys Ile Tyr Ile Leu Glu Glu Glu Ile Glu Glu Met Asp Tyr
1 5 10 15

Asp Leu Trp Glu Glu Asp Thr Val Tyr Thr Thr Ser Tyr Glu Val Leu
20 25 30

Gly Tyr Thr Asp Ser Leu Glu Asp Ala Glu Tyr Ile Arg Asp Asn Tyr
35 40 45

Gly Thr Ser Asn Pro Ile Phe Ile Asn Glu Tyr Pro Tyr Leu Thr Lys
50 55 60

Glu Lys Leu Ile Glu Glu Gln Arg Tyr Phe Arg Tyr Asn Ser Tyr Leu
65 70 75 80

Glu Leu Lys Arg Val Asn Gly Tyr Phe Glu Ile Ser Glu Ile Asn Glu
85 90 95

Leu His Val Thr Glu Asp Phe Ser Ile Asn Lys Asp Asp Lys Asn Phe
100 105 110

Asp Ser Pro Phe Ser Ile Asn Met Phe Ser His Asn Arg Asn Ser Ile
115 120 125

Gly Ile Glu Phe Ile Met Phe Ser Glu Tyr Asn Asp Lys Glu Asp Ile
130 135 140

Ile Glu Lys Glu Lys Asn Ser Phe Leu Met Lys Leu Lys Tyr Leu Leu
145 150 155 160

Lys His Ser Arg Glu Ala Asp Ile Arg Ser Thr Ser Lys Ile Ile Asp
165 170 175

Ser Ile Asp Lys Leu Thr
            180

<210> 1179
<211> 72
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1179
Met Lys Asn Ile Ile Asn Phe Leu Val Asp Tyr Asn Ile Asn Phe Ser
1   5   10   15

Tyr Ser Glu Asp Ser Leu Asn Val Met Asn Asn Ser Tyr Leu Val Asp
            20   25   30

Lys His Gly Thr Gln Asp Tyr Glu Ile Val Gly Asn Tyr Glu His Ile
        35   40   45

Thr Gly Val Phe Ser Tyr Gln Thr Glu Glu Glu Val Ile Ala Lys Leu
    50   55   60

Lys Asn Leu Ile Gly Ile Trp Glu
65   70

<210> 1180
<211> 64
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1180
Met Arg Asp Lys Arg Ile His Ser Glu Leu Leu Tyr Asp Ile Ile Gly
1   5   10   15

Lys His Ile Gln Glu Glu Glu Asn Ile Thr Pro Tyr Ile Glu Ala Ile
            20   25   30

Tyr Val Asp Met Met Asn Ile Ile Val Val Glu Tyr Thr Phe Tyr Asn
        35   40   45

Glu Asn Gly Thr Arg Met Leu Gly Gln Tyr Pro Ile Gly Glu Val Met
    50   55   60

<210> 1181
<211> 245
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1181

```
Met Asn Leu Glu Lys Ser Phe Leu Leu Ser Thr Ile Glu Phe Gly Ser
1               5                  10                  15

Thr Tyr Gln Gly Thr Ser Asp Glu His Ser Asp Lys Asp Tyr Met Ser
            20                  25                  30

Leu Val Val Gln Pro Leu Ser Asp Thr Ile Phe Arg Asn Asn Glu Lys
        35                  40                  45

Ala Ser Lys His Thr Glu Val Ser Arg Tyr Tyr Ala Val Glu Arg Phe
    50                  55                  60

Ile Ser Leu Val Leu Lys Ser Gly Phe Asp Asn Val Leu Asn Leu Cys
65                  70                  75                  80

Ala Gln Leu Glu Gln Ala Lys Asn Thr Arg Phe Asn Lys Thr Val Leu
                85                  90                  95

Asp Leu Phe Tyr Asp Asp Phe Ile Phe Leu Thr Tyr Val Arg Ala Asn
            100                 105                 110

Phe Lys Pro Ile Ala Tyr Ser Val Ile Gly Asn Ile Asn Asn Ile Leu
        115                 120                 125

Lys Lys Gly Glu Leu Thr Gly Lys Asp Leu Val Lys Phe Tyr Thr Phe
    130                 135                 140

Tyr Asn His Leu Glu Tyr Tyr Asn Asp Leu Leu Asp Asp Leu Asp Asn
145                 150                 155                 160

Leu Asn Val Ser Tyr Lys Asp Phe Ala Lys Val Lys Tyr Met Pro Lys
                165                 170                 175

Glu Val Leu Asp Asn Lys Arg Ser Asn Val Ser Ile Glu Lys Lys Lys
            180                 185                 190

Asp Leu Val Asn Lys Val Glu Pro Leu Ile Gln Glu Val Lys Asp Lys
        195                 200                 205

Leu Lys Tyr Asn Glu Ser Asn Ile Lys His Tyr Lys Asp Ala Met Glu
    210                 215                 220

Leu Val Glu Lys Ser Leu Lys Asp Lys Thr Val Ala Phe Leu Thr Glu
225                 230                 235                 240

Val Tyr Asn Glu Arg
                245
```

<210> 1182
<211> 34
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1182
Met Lys Tyr Ile Leu Gly Leu Ile Thr Leu Gly Ile Ile Leu Phe Lys
1   5   10   15

Val Tyr Glu His Phe Lys Tyr Lys Gln Asp Glu Val Asp Thr Glu Glu
            20   25   30

Asp Ile

<210> 1183
<211> 82
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1183
Met Ser Asn Met Asp Phe Tyr Gln Phe Leu Asn His Glu Asn Val Arg
1   5   10   15

Val Asn Ser Ile Thr Pro Ser Gln Lys Asn Phe Ile Arg Glu Asn Leu
            20   25   30

Glu Leu Thr Asn Leu Glu Asp Thr Asp Ile Asp Phe Ile Ser Ser Lys
        35   40   45

Lys Ala Lys Glu Glu Ile Glu Lys Ile Ile Arg Ile Lys Asn Glu Glu
    50   55   60

Glu Tyr Asp Met Ala Met Asp Ala Leu Ala Gly Trp Val Thr Lys His
65   70   75   80

Gly Tyr

<210> 1184
<211> 129
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1184
Met Phe Lys Lys Ala Pro Gln Tyr Ile Met Glu Lys Val Glu Lys Glu
1   5   10   15

Asn Asn Ile Leu Gly Glu Asp Leu Ser Leu Asp Ile Tyr Tyr Lys Gly
            20   25   30

Val Lys Leu Thr Val Lys Arg His Pro Glu Thr Gly His Leu Asn Gly
35 40 45

Tyr Ile Thr Leu Pro Ser Asp Ile Asn Glu Lys Glu Tyr Asp Ser Leu
50 55 60

Glu Arg Arg Ala His Arg Gly Ile Thr Tyr Asp Asp Tyr Asp Tyr Glu
65 70 75 80

Gly Lys Arg Val Leu Gly Phe Asp Cys Ala His Ala Trp Asp Met Thr
85 90 95

Pro Tyr Ala Ile Ile Gly Ser Leu Asp Asp Gln Tyr Arg Asp Leu Glu
100 105 110

Tyr Val Leu Ser Ile Leu Lys Asp Met Ala Glu Tyr Val Lys Lys Asp
115 120 125

Glu

<210> 1185
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1185
Met Glu Lys Val Asn His Glu Phe Leu Ala Glu Leu Ala Lys Ser Asn
1 5 10 15

Ser Pro Val Leu Asn Ser Lys Pro Leu Gln Asp Gly Asp Tyr Asn Ile
20 25 30

Glu Phe Asp Tyr Asp Gly Phe His Phe Glu Phe Ser Gln Lys Asn Gly
35 40 45

Tyr Trp Gln Trp Lys Tyr Asn Ala Lys
50 55

<210> 1186
<211> 160
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1186
Met Ala Asn Glu Lys Glu Ile Ile Arg Met Val Asn Tyr Leu Ile Asp
1 5 10 15

Asn Met Ser Met Trp His Ile Asn Tyr Ala Arg Ala Val Leu Ile Pro
20 25 30

Ser Glu Val Glu Lys Ile Ile Lys Glu His Glu Lys Phe Asp Asp Leu
35 40 45

Leu Lys Lys Arg Gly Glu Trp Leu Val Lys Gly Ser Asp Thr Asp Asn
50 55 60

Ile Asp Asp Leu Glu Thr Tyr Asn Gln Ile Met Asn Asn Gln Lys Asp
65 70 75 80

Glu Met Met Ile Gln Glu Ile Asp Ile Tyr Thr Gln Gly Lys Thr Ile
85 90 95

Thr Ile Asp Asn Glu His Tyr Ser Ser Asp Asp Leu Asn Glu Val Leu
100 105 110

Asn Lys Leu Glu Gln Ser Glu Asp Ile Lys Ile Lys Ser Asn Tyr Lys
115 120 125

Ser Leu Tyr Val Gly Tyr Thr Asn Val Val Gly Tyr Glu Val Thr Tyr
130 135 140

Ala Ser Ser Tyr Glu Glu Thr Phe Lys Asn Asp Leu Glu Lys Asp Leu
145 150 155 160

<210> 1187
<211> 180
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1187
Met Asp Arg Ile Ile Gly Lys His Asn Leu Thr Gln Asp Leu Arg Leu
1 5 10 15

Gly Asp Lys Val Glu Val Tyr Asp Ala His Lys Phe Lys Glu Asn Glu
20 25 30

Asp Gly Thr Ile Glu Leu Gly Asp Lys Ile Thr Glu Gly Ile Val Val
35 40 45

Asp Tyr Lys Gly Asp Phe Thr Gly Asn Thr Ser Gly Leu Val Thr Leu
50 55 60

Asp Ser Ser Glu Lys Glu Leu Ile Ile Gly Glu Tyr Asn Phe Lys Leu
65 70 75 80

Ile Glu Glu Gly Asn Leu Gln Ala Val Tyr Asp Ser Val Ser Lys Asn
85 90 95

Lys Val Glu Ser Leu Ser Glu Asp Tyr Asp Met Tyr Arg Lys Leu Leu

100 105 110

Gly Val Lys Ser Gly Glu Leu Ala Gly Ile Glu Asp Glu Leu Glu Tyr
115 120 125

Leu Val Arg Gln Tyr Asn Ser Lys Val Asp Asn Tyr Asn Gly Leu Leu
130 135 140

Thr Leu Ser Lys Glu Lys Ala Arg Glu Leu Ser Leu Leu Thr Gly Asn
145 150 155 160

Lys Lys Thr Ile Pro His Met Lys Asn Arg Arg Leu Glu Leu Gly Lys
165 170 175

Glu Ala Asp Phe
180

<210> 1188
<211> 177
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1188
Met Val Tyr Asp Ser Ile Ile Ser Arg Thr Met Ala Val Ser Ile Leu
1 5 10 15

Asn Lys Trp Ile Ala Glu Leu Ile Thr Asp Val Asp Leu Asp Lys Cys
20 25 30

Lys Phe Thr Glu Glu Glu Tyr Gly Lys Val Val Thr Asn Ser Ile Asn
35 40 45

Lys Ile Gln Asp Val Leu Ile Glu Lys Asn Tyr Glu Val Thr Asp Gly
50 55 60

Glu Leu Tyr Asp Ile Val Cys Thr Glu Leu Ile Asn Pro Ile Lys Asn
65 70 75 80

Asn Thr Glu Glu Glu Lys His Asn Glu Lys Asn Asp Leu Leu Glu His
85 90 95

Leu Glu Asp Leu Ala Phe Arg His Asp Ile Asp Leu Gly Tyr Val Ser
100 105 110

Asp Gly Ser Tyr Asn Leu Thr Val Thr His Trp Leu Met Gln Asp Glu
115 120 125

Phe Thr Asp Val Asn Ile Lys Val Asn Asn Asp Glu Asp Phe Tyr Thr
130 135 140

Val Thr Ile Pro Glu Ser Lys Tyr Phe Trp Leu Pro Ile Thr Lys Glu
145 150 155 160

Asn Leu Glu Met Phe Leu Thr Gln Asp Pro Ile Asn Lys Gly Glu Val
165 170 175

Lys

<210> 1189
<211> 54
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1189
Met Lys Asn Pro Ile Lys Leu Leu Ser Ile Ala Val Val Thr Ile Leu
1 5 10 15

Thr Phe Ser Leu Thr Tyr Val Ile Leu Lys Lys Glu Thr Asn Asn Lys
20 25 30

Arg Asn Gly Val Ala Pro Phe Asp Phe Ser Leu Glu Asp His Ile His
35 40 45

Leu Asn Lys Glu Ile Lys
50

<210> 1190
<211> 92
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1190
Met Ala Asn Asn Ile Trp Ala Val Val Leu Ser Ile Ile Ile Leu Leu
1 5 10 15

Ile Ile Leu Leu Ile Leu Trp Phe Leu Phe Arg Lys Lys Val Asn Gly
20 25 30

Gly Asn Ser Lys Asn Val Glu Ile Gln Lys Ala Glu Glu Asn Asn Asp
35 40 45

Asn Lys Glu Gln Glu Val Glu Glu Ala Gln Tyr Arg Glu Leu Asn Glu
50 55 60

Glu Glu Lys Glu Lys Asn Glu Asn Ser Ser Lys Asp Tyr Lys Tyr Asp
65 70 75 80

Lys Glu Lys Val Lys Asn Lys Leu Lys Glu Leu Glu
85 90

<210> 1191
<211> 281
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1191
Met Gly Arg Arg Leu Ile Asp Asn Ser Glu Leu Asn Val Ile Lys Tyr
1 5 10 15

Asp Gly Leu Pro Asp Phe Phe Ser Ala Leu Lys Lys Asn Arg Val Ser
20 25 30

Gly Arg Asp Asn Ser Ser Asp Thr Gly Ser Tyr Asp Phe Thr Gly Thr
35 40 45

His Ser Phe Gln Glu Ala Tyr Asn Leu Met Val Lys Gly Asp Arg Glu
50 55 60

Ser Tyr Asp Met Val Val Lys Leu Lys Lys Met Thr Asp Ala Leu Phe
65 70 75 80

Arg Met Asp Lys Ser Val Lys Arg Lys Pro Val Val Ala Pro Glu Gly
85 90 95

Tyr Gln Pro His Val Pro Asn Ala Ile Lys Gly Leu Pro Asn Ser Met
100 105 110

Met Ser Gln Gln Arg Val Lys Ala Glu Lys Lys Val Ile Asp Val Phe
115 120 125

Tyr Asn Ser Ser Ile Ser Trp Arg Glu Asp Pro Glu Asn Leu Ala Tyr
130 135 140

Arg Gly Ala Ile Met Leu Ser Ala Ile Gln Thr Leu Glu Thr Lys Gly
145 150 155 160

Tyr Ser Ile Asn Leu Tyr Leu Gly Lys Leu Ser Asn Ser Gly Tyr Glu
165 170 175

Asp Lys Leu Thr Gly Phe Val Val Asn Ile Lys His Ser Tyr Gln Arg
180 185 190

Leu Asn Val Phe Lys Ser Ser Phe Tyr Leu Val Asn Pro Ser Phe Leu
195 200 205

Arg Arg Ile Ser Phe Arg Val Leu Glu Val Glu Pro Asp Met Val Asp
210 215 220

Leu Thr Asn His Gly Tyr Gly Ser Val Val Ser Lys Ser Ser Tyr Gly

225 230 235 240

Asn Lys Leu Thr Glu His Ile Leu Asp Asn Ala Val Ile Phe Asp Ser
245 250 255

Ser Val Gly Ile Asp Ile Asn Asn Asp Ser Ser Glu Asn Leu Arg Ala
260 265 270

Val Lys Lys Leu Phe Gly Gly Arg Leu
275 280

<210> 1192
<211> 372
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1192
Met Ala Lys Gln Asp Thr Ile Glu Arg Leu Glu Arg Leu Val Glu Gln
1 5 10 15

Gln Met Glu Thr Thr Ala Asp Leu Ala Lys Lys Leu Gly Glu Lys Asn
20 25 30

Ser Asn Pro Tyr Glu Gln Ala Ile Val Asp Ala Ile Val Glu Lys Ala
35 40 45

Gly Thr Glu Ser Arg Glu Ile Ile Ile Thr Asp Val Lys Lys Gln Ile
50 55 60

Glu Glu Tyr Val Glu Glu Gln Leu Ser Asn Leu Pro Val Lys Ile Glu
65 70 75 80

Leu Gln Gln Glu Gly Lys Thr Ile Lys Asp Ile Ser Gly Ile Phe His
85 90 95

Tyr Arg Tyr Gln Asp Ile Leu Lys Leu Val Asn Gln Asn Ile Pro Val
100 105 110

Phe Leu Lys Gly Gly Ala Gly Ser Gly Lys Asn His Val Leu Glu Gln
115 120 125

Val Ala Glu Ala Leu Asp Leu Asp Phe Tyr Phe Ser Asn Ala Ile Thr
130 135 140

Gln Glu Phe Lys Leu Thr Gly Phe Ile Asp Ala Asn Gly Lys Phe His
145 150 155 160

Glu Thr Gln Phe Tyr Lys Ala Phe Thr Lys Gly Gly Leu Phe Phe Leu
165 170 175

```
Asp Glu Met Asp Ala Ser Ile Pro Glu Val Leu Leu Ile Leu Asn Ser
            180                 185                 190

Ala Ile Ala Asn Lys Tyr Phe Asp Phe Pro Ile Gly Arg Val Thr Ala
        195                 200                 205

His Glu Asp Phe Arg Val Val Ser Ala Gly Asn Thr Met Gly Thr Gly
    210                 215                 220

Ala Asp His Ile Tyr Val Gly Arg Gln Gln Leu Asp Gly Ala Thr Leu
225                 230                 235                 240

Asp Arg Phe Ala Gln Val Glu Phe Asp Tyr Asp Thr Lys Val Glu His
                245                 250                 255

Gln Leu Ser Ser Asn Glu Asp Leu Val Asn Phe Val Gln Gln Leu Arg
            260                 265                 270

His Glu Asn Asp Glu Lys Gly Leu Pro Tyr Val Phe Ser Met Arg Ala
        275                 280                 285

Ile Ile Asn Gly Ser Lys Leu Asp Gly Val Met Glu Asp Glu Phe Val
    290                 295                 300

Val Glu Ser Ile Ile Phe Lys Ser Val Pro Lys Asp Glu Ile Asn Gln
305                 310                 315                 320

Phe Ile Ser Ser Leu Pro Glu Gly Asn Arg Tyr Thr Glu Ala Thr Arg
                325                 330                 335

Lys Leu Leu Gly Met Gln Gln Glu Pro Lys Gln Glu Pro Arg Lys Ser
            340                 345                 350

Asp Ser Thr Ser Lys Asp Ser Met Asp Phe Asp Thr Ile Met Asp Lys
        355                 360                 365

Leu Gly Leu Glu
    370


<210> 1193
<211> 108
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1193
Val Ser Lys Arg Thr Asp Asn Phe Ile Tyr Phe Cys Lys Tyr Tyr Phe
1               5                   10                  15

Ser Glu Tyr Leu Pro Ser Leu Gly Val Glu Val Leu Asn His Asn Glu
            20                  25                  30
```

Thr Ser His Gly Thr Met Glu Gly Val Lys Lys Tyr Tyr Ile Ala Asn
35 40 45

Ile Leu Tyr Glu Gly Gln Glu Leu Thr Val Thr Ile Asp Leu Glu Glu
50 55 60

Phe Asn Asn Ala Thr Ser Met His Asn Met Leu Glu Ile Met Asn Asn
65 70 75 80

His Thr Tyr Asn Cys Met Phe Met Tyr Asp Met Asp Thr His Glu Thr
85 90 95

Lys Asp Ile Asp Asp Phe Phe Lys Leu Met Tyr Phe
100 105

<210> 1194
<211> 138
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1194
Met Asn Ala Lys Glu Phe Met Lys Thr Gln Ala Gln Val Glu Asp Tyr
1 5 10 15

Leu Asp Lys Leu Lys Val Thr Ile Ile Glu Asp Ala Leu Ser Val Ser
20 25 30

Lys Glu Trp Ser Asn Asp Ser Asn Asp Leu Gly Tyr Ala Leu Ser Ser
35 40 45

Leu Gly Glu Ser Ile Gly Leu Leu Glu Asn Tyr Tyr Asn Ile Gln Val
50 55 60

Asp Ala His Leu Pro Glu His Tyr Lys Gly Ser Lys Asp Val Ile Ser
65 70 75 80

Phe Leu Glu Glu His Phe Ser Tyr Asp Gly Phe Val Asp Ser Met Ile
85 90 95

Phe Asn Ile Val Lys Tyr Thr Thr Arg Leu Gly Arg Lys Asp Ala Val
100 105 110

Asp Lys Glu Val Gln Lys Ile Lys Thr Tyr Tyr Val Arg Leu Glu Arg
115 120 125

Asn Ile Lys Tyr Gly Asp Ser Thr Arg Val
130 135

<210> 1195
<211> 100

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1195
Met Glu Lys Val Glu Leu Ile Lys Gln Trp Ala Lys Asp Arg Asn Leu
1   5   10   15

Gln Thr Gly Lys Pro Glu Gly Gln Met Leu Lys Leu Leu Glu Glu Ala
            20   25   30

Gly Glu Leu Ala Ser Gly Ile Ala Lys Ser Asn Asp His Val Thr Arg
        35   40   45

Asp Ser Val Gly Asp Ile Phe Val Val Leu Thr Val Leu Cys Leu Gln
    50   55   60

Leu Asp Ile Asp Ile Glu Glu Cys Ile Asp Met Ala Tyr Asp Glu Ile
65   70   75   80

Lys Asp Arg Lys Gly Lys Leu Ile Asn Gly Val Phe Val Lys Glu Glu
                85   90   95

Asp Leu Lys Lys
            100

<210> 1196
<211> 62
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1196
Met Glu Lys Phe Gln Glu Asp Tyr Val Asn Ile Asp Ile Arg Val Lys
1   5   10   15

Ala Tyr Val Arg Val Gly Tyr Arg Tyr Glu Glu Asp Ile Thr Asn Asn
            20   25   30

Leu His Glu Leu Val Glu Asp Asn Leu Asn Val Thr Ser Asp Ser Asp
        35   40   45

Ser Leu Ile Ile Lys Asp Thr Glu Ile Lys Gly Asp Ile Glu
    50   55   60

<210> 1197
<211> 53
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1197
Met Val Lys Pro Val Ile Thr Leu Glu Pro Glu Asp Val Lys Val Leu
1 5 10 15

Leu Asp Tyr Leu Ser Phe Leu Glu Asp Asp Met Arg Asn Tyr Glu Gly
20 25 30

Met Arg Glu Leu Tyr Glu Glu Leu His Lys Lys Tyr Gln Leu Ala Lys
35 40 45

Gly Asn Tyr Ser Asp
50

<210> 1198
<211> 683
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1198
Met Ala Ile Thr Tyr Lys Gln Lys Gly Leu Thr Glu Gln Glu Ile Ile
1 5 10 15

Asn Leu Pro Lys Val Asn Lys Gly Cys Ile Tyr Ile Gly Glu Glu Asp
20 25 30

Val Phe Leu Lys Lys Lys Lys Asn Asn Ile Ile Asn Leu Gly Ser Lys
35 40 45

Glu Leu Phe Arg Asp Ile His Asn Ile Phe Ser Phe Asp Thr Ala Thr
50 55 60

Glu Ile His Leu Phe Leu Ala Leu Cys Gly Asn Lys Glu Val Thr Asn
65 70 75 80

Phe Thr Gly Asn Pro Tyr Glu Thr Ile Glu Lys Leu Val Glu Gly Val
85 90 95

Ile Glu Glu Asn Lys Gly Arg Ser Tyr Lys Glu Tyr Ile Ala Ser Ser
100 105 110

Arg Glu Glu Arg Lys Glu Phe Pro Leu Tyr Gly Ser Lys Arg Ile Thr
115 120 125

Gln Ile Lys Ser Lys Gly Tyr Val Glu Glu Lys Ile Lys Glu Leu Glu
130 135 140

Asn Glu Thr Arg Leu Arg Trp Tyr Glu Ser Arg Gln Leu Asp Glu Tyr
145 150 155 160

Lys Glu Val Val Asp Ser Leu Asn Asn Asp Ile Met Asp Ile Leu Tyr
165 170 175

```
Gln Gly Lys Tyr Gly Leu Ile Lys Ser Ser Ile Thr Ser Arg Leu Asn
            180                 185                 190

Glu Asp Thr Glu Lys Gly Ser Ser Lys Tyr Tyr Lys Glu Ile Ser Asp
        195                 200                 205

Ser Leu Tyr Ser Ser Thr Trp Tyr Met His Pro Ser Thr Glu Asn Ser
    210                 215                 220

Ser Ser Phe Gly Leu Lys Val Arg His Ile Arg Asp Lys Tyr Asn Met
225                 230                 235                 240

Gly Asn Arg Trp Val Leu Glu Asn Lys Ser Ser Phe Asp Val Lys Thr
                245                 250                 255

Gly Glu Val Lys Val Phe Leu Thr Asp Ser Leu Val Asn Lys Glu Ile
            260                 265                 270

Thr Leu Asn Leu Tyr Lys Asp Asp Ile Ser Lys Ser Glu Tyr Lys Asn
        275                 280                 285

Glu Leu Asn Leu Ala Val Leu Leu Asn Val Ile Leu Lys Asn Tyr Ser
    290                 295                 300

Thr Pro Asn Leu Ser Lys Asn Val Ile Ile Lys Ile Ile Glu Glu Thr
305                 310                 315                 320

Leu Arg Asn Asp Gly Phe Gly Leu Ser Ser Trp Cys Leu Asp Glu Val
                325                 330                 335

Asp Val Tyr Gly Arg Val Asn Tyr Gly Gly Asn Lys Tyr Lys Pro Leu
            340                 345                 350

Lys Gly Glu Asn Ser Thr Ser Asn Tyr Leu Thr Ile Leu Thr Asp Ile
        355                 360                 365

Val Lys Asn Ile Asp Lys Ile Asn Asn Leu Glu Glu Phe Glu Leu Phe
    370                 375                 380

Glu Arg Asn Ser Leu Leu Phe His Ile Pro Lys Asn Pro Lys Trp Lys
385                 390                 395                 400

Ile His Glu Ala Phe Asn Leu Thr Lys Gln Thr Tyr Lys Lys Leu Leu
                405                 410                 415

Thr Leu Asn Asn Phe Glu Gln Ser Asn Tyr Leu Arg Phe Ser Asp Thr
            420                 425                 430

Leu Tyr Asn Tyr Tyr Asn His Leu His Asn Glu Val Asn Leu His Gln
        435                 440                 445
```

```
Leu Phe Asp Asp Thr Phe Leu Met Val Gln Asp Val Arg Asn Val Thr
    450                 455                 460

Asp Ala Leu Lys Val Lys Pro Ile Val Asn Glu Ile Leu Ser Ile Ser
465                 470                 475                 480

Phe Ala Asn Tyr Lys Lys Met Thr His Tyr Leu Asp Val Asp Ala Gln
                485                 490                 495

Asp Arg Gln Arg Ile Thr Gly Tyr Ala Leu Asp Ser Tyr Tyr Leu Asp
            500                 505                 510

Tyr Leu His Asp Leu Ser Ile Leu Ile Arg Glu Gly Tyr Arg Thr Leu
        515                 520                 525

Glu Ser Val Asn Leu Thr Pro Phe Ser Leu Lys Leu Glu His Asp Ile
    530                 535                 540

Val Thr Asp Glu Lys Gln Ser Ile Gln Gln Gln Leu Asp Asp Ala Glu
545                 550                 555                 560

Leu Lys Ser Lys Tyr Glu Asn Lys Leu Glu Lys Ile Ile Asp Lys Thr
                565                 570                 575

Tyr Lys Leu Lys Asp Gly Arg Lys Val Lys Phe Leu Pro Ala Asp Thr
            580                 585                 590

Val Ser Lys Leu Lys Asn Glu Gly Lys Met Leu Ser His Cys Val Gly
        595                 600                 605

Gly Tyr Ala Asn Arg Ile Ile Lys Asn Ser Cys Leu Ile Leu Leu Ala
    610                 615                 620

Arg Leu Glu Glu Asp Leu Asp Asn Ser Trp Phe Thr Val Glu Ile Arg
625                 630                 635                 640

Ile Thr Asp Asn Gly Tyr Val Leu Gly Gln Gln Gln Ser Ile Asp Ala
                645                 650                 655

Tyr Lys Leu Pro Asn Glu Leu Lys Glu Ala Leu Glu Lys Asp Ile Lys
            660                 665                 670

Lys Ile Asn Lys Glu Glu Phe Lys Glu Val Ala
        675                 680
```

<210> 1199
<211> 87
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F125/10

<400> 1199
Met Ser Ile Glu Lys Lys Glu Glu Val Val Ala His Asn Glu Val Val
1   5   10   15

Phe Lys Ser Leu Thr Gln Gly Leu Tyr Val Lys Glu Val Asp Ile Tyr
            20   25   30

Ser Asp Val Ile Ser Tyr Thr Lys Asp Ile Asp Glu Ala Leu Ala Met
        35   40   45

Pro Asn Thr Ile Asn Phe Lys Asn Ser Arg Lys Tyr Glu Lys Leu Ile
    50   55   60

Arg Asn Leu Asp Leu Lys Pro Leu Asn Lys Ile Gln Lys Val Ile Tyr
65   70   75   80

Glu Thr His Leu Glu Glu Leu
                85

<210> 1200
<211> 57
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1200
Leu Asn Asp Leu Ile Lys Glu Gly Asn Lys Tyr Tyr His Lys Val Arg
1   5   10   15

Ala Gly Glu Thr Leu Trp Thr Ile Ser Lys Asn Tyr Gly Val Asp Ile
            20   25   30

Lys Lys Leu Gln Glu Leu Asn Asn Ile Lys Ser Val Thr Leu Thr Ser
        35   40   45

Leu Glu Tyr Val Leu Val Cys Val Glu
    50   55

<210> 1201
<211> 192
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1201
Met Asp Asn Leu Ser His Tyr Leu Ser Ile Leu Tyr Ala Ile Leu Val
1   5   10   15

Thr Val Gly Tyr Ile Pro Gly Leu Ile Ala Leu Val Lys Ser Asp Ser
            20   25   30

Val Lys Gly Val Ser Ser Tyr Phe Trp Tyr Leu Ile Val Ala Thr Val
35 40 45

Gly Ile Ser Phe Tyr Asn Leu Leu Ile Thr Asp Ala Thr Met Phe Gln
50 55 60

Val Val Ser Val Gly Val Asn Leu Thr Leu Gly Ile Val Cys Leu Leu
65 70 75 80

Val Ala Ser Tyr Arg Lys Lys Asp Tyr Phe Ser Ile Pro Phe Ile Ile
85 90 95

Val Phe Ser Val Leu Leu Phe Leu Leu Ser Asp Phe Thr Ala Leu Thr
100 105 110

Gln Thr Ile Ala Thr Ile Thr Ile Ile Leu Ala Tyr Val Thr Gln Ile
115 120 125

Thr Thr Phe Tyr Lys Thr Lys Ser Ala Glu Gly Thr Asn Arg Phe Leu
130 135 140

Phe Leu Ile Ile Gly Leu Gly Leu Ala Ser Leu Ile Leu Ser Met Val
145 150 155 160

Leu Ser His Thr Tyr Val His Ile Ile Ala Thr Glu Phe Val Asn Phe
165 170 175

Val Leu Ile Leu Ile Cys Tyr Leu Gln Ala Asn Tyr Tyr Ser Arg Arg
180 185 190

<210> 1202
<211> 197
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1202
Met Val Asn Tyr Thr Lys Asp Lys Val Cys Tyr Met Gly Gly His Leu
1 5 10 15

Leu Asn Gln Ala Met Val Glu Tyr Arg Thr Lys Gln His Glu Gln Val
20 25 30

Glu Gly Ile Val Gly Val Thr Pro Tyr Ser Pro His Gln Asp Lys Ser
35 40 45

Ile Asn Asp Lys Ala Asn Ala Glu Gln Thr Gly Leu Ala Glu Arg Ile
50 55 60

Leu Asn Asn Asp Phe Lys Ala Met Gln Glu Ser Asp Ile Phe Val Phe
65 70 75 80

```
Asp Ile Leu Asn Glu Gly Leu Gly Thr Ile Ala Glu Leu Gly Ile Leu
                85                  90                  95

Leu Gly Met Lys His Gln Ala Gln Lys Ile Ile Asp Lys Tyr Glu Asp
            100                 105                 110

Ile Asp Phe Arg Asp Leu Glu Pro Leu Thr Gln Tyr Asp Ile Leu Glu
        115                 120                 125

Ala Tyr Asn Ile Val Asn Lys Pro Val Leu Ile Tyr Cys Ser Asp Ile
    130                 135                 140

Arg Gln Gly His Gly Lys Gly Tyr Asp Asp Pro Asp Arg Ala Glu Phe
145                 150                 155                 160

Ser Thr Asn Gln Phe Ile Tyr Gly Cys Val Leu Ser Leu Thr Asn Gly
                165                 170                 175

Glu Gly Phe Ile Ser Trp Glu Glu Val Leu Lys Arg Leu Glu Lys Leu
            180                 185                 190

Gly Gly Gln Asp Gly
        195


<210> 1203
<211> 297
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1203
Met Lys Ser Tyr Thr Lys Val Lys Asn Lys Gly Leu Ser Leu Asp Lys
1               5                   10                  15

Phe Lys Asp Arg Gly Phe Val Val Gln Glu Lys Leu Asp Gly Ser Asn
            20                  25                  30

Ala Ser Phe Thr Thr Glu Asn Gly Glu Leu Val Cys Phe Ser Arg Arg
        35                  40                  45

Lys Lys Leu Asn Glu Asn Glu Thr Leu Asn Gly Phe Tyr Asn Trp Val
    50                  55                  60

His Glu Asn Met Thr Asp Lys Leu Asp Leu Ser Ile Leu Glu Gly Ile
65                  70                  75                  80

Ile Ile Phe Gly Glu Trp Leu Val Lys His Lys Val Asn Tyr Lys Glu
                85                  90                  95

Glu Cys Tyr Asn Asn Phe Tyr Val Phe Asp Val Tyr Asp Lys Asp Ser
```

100 105 110

Glu Thr Tyr Leu Pro Tyr Ser Glu Val Ile Ser Leu Ser Glu Thr Leu
115 120 125

Gly Leu Lys Thr Val Lys Thr Leu Met Ile Ile Glu Pro Ser Phe Tyr
130 135 140

Leu Asn Lys Leu Asn Pro Gln Glu Ile Gln Asp Leu Val Gly Lys Ser
145 150 155 160

Asp Met Thr Val Lys Pro Asn Thr Gly Glu Gly Ile Val Ile Lys Tyr
165 170 175

Leu Asp Gly Lys Ser Glu His Asp Asp Tyr Phe Lys Leu Val Ser Lys
180 185 190

Glu Phe Lys Glu Phe Ser Arg Lys Lys Met Lys Ser Glu Val Arg Ser
195 200 205

Asn Asp Ser Val Ala Asp Tyr Ala Ile Thr Lys Ser Arg Met Glu Lys
210 215 220

Met Ile Phe Arg Ala Ile Glu Glu Asn Arg Leu Ser Lys Asp Asp Leu
225 230 235 240

Glu Leu Glu Asn Phe Gly Leu Ile Met Lys Gln Val Gly Gln Asn Phe
245 250 255

Val Asp Asp Ile Met Glu Glu Glu Lys Glu Asn Met Met Lys Ile Ile
260 265 270

Glu Lys Gln Ile Lys Lys Lys Met Pro His Ile Leu Arg Gly Ile Leu
275 280 285

Glu Glu Lys Gly Asp Thr Ile Asp Gly
290 295

<210> 1204
<211> 74
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1204
Met Asn Tyr Leu Ala Lys Val Phe Ile Asn Asn Asn Trp Leu Val Lys
1 5 10 15

Leu Ile Thr Ile Val Leu Leu Thr Leu Leu Leu Gly Gly Leu Val Tyr
20 25 30

Val Ile Ser Ala Val Ala Leu Phe Leu Ser Thr Val Leu Asn Leu Pro
        35   40   45

Gly Leu Val Val Leu Ala Phe Leu Ala Ser Val Ser Leu Ile Leu Phe
    50   55   60

Ser Ile Val His Asn Ser Lys Glu Asp Asn
65   70

<210> 1205
<211> 246
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1205
Met Ala Ile Gln Leu Lys Glu Leu Asp Phe Lys Leu Lys Asp Tyr Pro
1   5   10   15

Asn Val Arg Tyr Asn Met Gly Glu His Leu Val Phe Asn Glu Phe Leu
            20   25   30

Glu Lys Ala Thr Thr Glu Gln Leu Asp Phe Cys Glu Asp Phe Phe Asn
        35   40   45

Asp Asn Val Glu Ile Leu Trp Asn Glu Ser Gln Ala Gly Thr Gly Lys
    50   55   60

Thr Met Cys Ser Val Ala Cys Ala Tyr Ala Asp Tyr Leu Asn Lys Asp
65   70   75   80

Arg Lys Leu Val Phe Ile Ile Ser Pro Val Ser Glu Asp Leu Gly Ser
                85   90   95

Arg Pro Gly Asn Gln Thr Glu Lys Glu Met Ala Tyr Phe Met Gly Leu
            100   105   110

His Asp Ala Leu Ile Glu Leu Asn Met Asn Pro Glu Gln Gln Ile Thr
        115   120   125

Glu Met Leu Met Met Glu Asp Asn Val Lys Glu Asp Lys Leu Gly Asp
    130   135   140

Cys Trp Val Ser Gln Ile Ser His Leu Phe Leu Arg Gly Gly Asn Leu
145   150   155   160

Arg Asp Ser Thr Ile Ile Ile Asn Glu Ala Gln Asn Phe Lys Arg Ser
                165   170   175

Glu Leu Lys Lys Val Leu Thr Arg Val His Thr Lys Asn Ser Thr Val
            180   185   190

Ile Val Glu Gly Asn Phe Lys Gln Ile Asp Leu Lys Asn Glu Ser Lys
195 200 205

Ser Gly Phe Gly Asp Tyr Met Glu Tyr Phe Lys Lys Tyr Asp Gly Ala
210 215 220

Val Phe His Asn Phe Thr Val Asn Phe Arg Ser Lys Leu Ala Gln Tyr
225 230 235 240

Ala Asp Asn Phe Lys Trp
245

<210> 1206
<211> 204
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1206
Met Lys Lys Ile Asn Ser Val Ile Lys Gly Glu Gly Lys Lys Val Gln
1 5 10 15

Thr Thr Asp Val Arg Lys Ile Ser Tyr Tyr Val Lys Asp Tyr Asn Pro
20 25 30

Cys Met Thr Val Asp Asp Ala Asn Asp Tyr Asn Ser Thr Ser Gln Tyr
35 40 45

Leu Val Ser Asp Asn Gly Lys Phe Ile Ala Lys Tyr Asn Lys Asp Met
50 55 60

Asn Ala Val Gly Phe Tyr Glu Glu Ser Gly Asp Thr Val Lys His Leu
65 70 75 80

Thr His Thr Thr Pro Glu Arg Leu Glu Gly Thr Val Phe Thr Ile Glu
85 90 95

Glu Glu Thr Lys Ile Asp Leu Ile Asn Asp Thr Leu Pro Gln Gly Asp
100 105 110

Ile Leu Ile Lys Phe Ser Asp Gly Ser Ile Tyr Leu Pro Asp Asn Glu
115 120 125

Ser Val Leu Asp Ser Val Asn Tyr Leu Ala Asp Asn Asp Trp Asp Ser
130 135 140

Val Asp Asp Ile Ile Tyr Thr Gly Leu Ser Lys Gly Asn Ser Glu Asn
145 150 155 160

Cys Ile Val Asp Phe Asn Tyr Asn Asn Tyr Asp Ile Gly Tyr Asp Asp
165 170 175

Val Glu Asp Glu Glu Val Cys Asp Asn Tyr Pro Glu Cys Glu Cys Ser
180 185 190

Asn Tyr Cys Ser Ser Thr Gly Glu Tyr Ile Gly Asn
195 200

<210> 1207
<211> 141
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1207
Met Gln Asp Ser Val Asn Ile Tyr Thr Asp Gly Ser Ser Ser Tyr Asn
1 5 10 15

Lys Gly Lys Val Gly Ser Gly Ala Val Leu Val Ser Lys Glu Gly Asn
20 25 30

Ile Ile Ala Glu Ile Ser Lys Ser Val Asp Lys Pro Gly Leu Ile Lys
35 40 45

Tyr Asn Asn Val Ala Gly Glu Ile Leu Ala Cys Cys Tyr Gly Ile Glu
50 55 60

Glu Ala Ile Lys Leu Gly Tyr Asn Gln Ala Ile Val Tyr Ile Asp Tyr
65 70 75 80

Ile Gly Leu Ile His Trp Tyr Glu Gly Thr Trp Ser Ala Arg Asn Ile
85 90 95

Leu Ser Lys Thr Tyr Ile Asn Met Ile Arg Glu Tyr Gln Lys Val Ile
100 105 110

Asp Ile Asn Phe Val Lys Val Lys Ser His Ser Asn Asp Lys Trp Asn
115 120 125

Asp Tyr Ala Asp Asn Leu Ala Lys Lys Ser Ile Asp Ile
130 135 140

<210> 1208
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1208
Met Lys Lys Gly Val Phe Thr Val Ile Ala Asp Gly Phe Lys Phe Asn
1 5 10 15

Val Ile Ala Lys Asp Lys Lys Glu Val Gln Glu His Cys Phe Lys Cys
            20   25   30

Phe Asp Phe Asn Tyr Ile Ser Val Ser Phe Cys Arg Glu Val Tyr Ser
        35   40   45

Asp Cys Glu Phe Pro Gln Phe Met Glu Asp Tyr Lys Tyr Ala Gly
    50   55   60

<210> 1209
<211> 213
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1209
Met Glu Asn Asn Asn Leu Val Asn Phe Leu Met Thr Thr Asp Asp Ile
1   5   10   15

Asp Asp Thr Ile Glu Met Val Asp Ser Phe Glu Leu Gln Asp Ile Asn
            20   25   30

Lys Val Leu Gly Glu Asp Thr Phe Leu Thr Ile Met Glu Ile Thr Asp
        35   40   45

Ser Leu Pro Asp Asn Gln Tyr Lys Ile Val Leu Leu Ser Ser Leu Asp
    50   55   60

Lys Leu Leu Asn Thr Asp Arg Lys Glu Leu Val Glu Tyr Asp Glu Glu
65   70   75   80

Phe Pro Thr Ile Arg Lys His Asn Val Ser Glu Leu Lys Arg Asp Thr
                85   90   95

Val Asn Ser Val Ile Asp Ser Tyr Met Asn Thr Asn Val Glu Ile Leu
            100   105   110

Tyr Thr Glu Tyr Pro Thr Ile Ser Asn Tyr Ser Val Val Val Asp Ser
        115   120   125

Val Lys Val Leu Asn Thr Leu Tyr Leu Ile Glu Ser Lys Asn Gly Lys
    130   135   140

Ile Glu Ala Thr Leu Ser Glu Asp Gly Glu Asp Leu His Glu Tyr Ile
145   150   155   160

Ser Glu Glu Gly Tyr Ser Val Thr Asp Ile Leu Asn Lys Phe Asp Asp
                165   170   175

Val Glu Asp Leu Phe Asp Glu Asp Asp Ser Leu Ile Asn Phe Phe Ser
            180   185   190

Asp Ile Asp Glu Gly Lys Asn Lys Thr Ile Lys Ser Phe Ile Glu Leu
195 200 205

Val Ile Asn Leu Lys
210

<210> 1210
<211> 76
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1210
Met Asp Glu Lys Lys Glu Ser Lys Pro Leu Asn Leu Gln Lys Ile Arg
1 5 10 15

Val Glu Lys Gly His Thr Leu Arg Ser Leu Ala Ser Glu Ile Gly Val
20 25 30

His Tyr Ser Leu Ile Ser Tyr Trp Glu Tyr Gly Lys Lys Lys Pro Arg
35 40 45

Ser Ala Asn Leu Met Arg Leu Glu Lys Ala Leu Asn Thr Pro Gly Lys
50 55 60

Glu Leu Phe Lys Glu Leu Glu Glu Asp Asp Gly Glu
65 70 75

<210> 1211
<211> 75
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1211
Met Asn Lys Phe Lys Arg Trp Phe Arg Ile Asn Val Leu Lys Lys Glu
1 5 10 15

Thr Leu Leu Phe Lys Val Tyr Trp Arg Tyr Glu Ser Pro Ser Leu Lys
20 25 30

Lys Pro His Val Phe His Ile Glu Leu Tyr Ala Lys Ser Lys Ala Glu
35 40 45

Ala Arg Asp Lys Ser His Glu Tyr Ile Leu Lys Asn Ala Lys Ala Ser
50 55 60

Glu Asp Phe Lys Phe Leu Lys Val Glu Glu Lys
65 70 75

<210> 1212

<211> 235
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1212
Met Lys Lys Thr Ile Phe Ala Thr Leu Ala Leu Gly Thr Ala Ile Thr
1 5 10 15

Phe Gly Gly Met Ala Thr Asn Glu Ala Ser Ala Asp Glu Ile Asp Tyr
20 25 30

Asn Lys Leu Ala Glu Gln Ala Lys Ser Asn Ser Val Glu Val Asn Thr
35 40 45

Lys Pro Ile Gln Glu Gly Asn Tyr Asp Phe Ser Phe Ser Asp Gly Glu
50 55 60

Phe Thr Tyr His Phe Tyr Asn Tyr Asn Gly Asn Phe Gly Tyr Glu Tyr
65 70 75 80

His Ser Gly Ser Thr Gln Val Asp Asn Thr Val Ser Arg Leu Ala Gly
85 90 95

Glu Glu Gln Thr Pro Glu Gln Lys Val Asp Gln Gln Gln Ala Gln Phe
100 105 110

Asp Thr Gln Asn Lys Ala Val Glu Gln Pro Lys Gln Glu Thr Thr Thr
115 120 125

Gln Glu Ala Pro Lys Ser Val Glu Ala Pro Lys Val Glu Thr Lys Thr
130 135 140

Thr Ala Thr Lys Ser Thr Gly Gly Ser Val Ala Glu Gln Ile Arg Gln
145 150 155 160

Ala Gly Gly Asp Glu Ala Met Ile Glu Ile Ala Met Arg Glu Ser Thr
165 170 175

Leu Asn Pro Asn Ala Val Asn Pro Thr Ser Gly Ala Gln Gly Leu Phe
180 185 190

Gln Gly Leu Gly Lys Ser Trp Ser Gly Gly Ser Ile Ala Glu Gln Thr
195 200 205

Lys Gly Ala Lys Gln Tyr Met Ile Asp Arg Tyr Gly Ser Thr Ser Gly
210 215 220

Ala Leu Asn Phe His Asn Ala Asn Gly Asn Tyr
225 230 235

<210> 1213
<211> 264
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1213
Met Arg Lys Ser Val Val Ile Ser Gly Val Ile Gly Phe Leu Ala Ile
1 5 10 15

Ile Gly Phe Ile Ile Leu Leu Met Cys Ile Thr Lys Ile Pro Gln Gly
20 25 30

His Val Gly Val Val Tyr Ser Val Asn Gly Val Lys Glu Asp Thr Lys
35 40 45

Ser Pro Gly Trp His Leu Thr Ala Pro Phe Asp Lys Val Asn Lys Tyr
50 55 60

Pro Thr Lys Thr Gln Thr His Lys Tyr Lys Asp Leu Asn Val Ala Thr
65 70 75 80

Ser Asp Gly Lys Asn Leu Gln Met Asp Ile Asp Val Ser Tyr Lys Val
85 90 95

Asp Ala Thr Lys Ala Val Asp Leu Phe Asn Arg Phe Gly Ser Ala Asp
100 105 110

Ile Glu Glu Leu Glu Lys Gly Tyr Leu Arg Ser Arg Val Gln Asp Asn
115 120 125

Val Arg Gln Ser Val Ser Lys Tyr Ser Val Ile Asp Ala Phe Gly Val
130 135 140

Lys Thr Gly Gln Ile Lys Lys Asp Thr Leu Asp Ser Leu Asn Asp Asn
145 150 155 160

Leu Glu Lys Gln Gly Phe Val Ile Glu Asp Ile Ala Leu Ser Ser Pro
165 170 175

Lys Ala Asp Lys Asn Thr Gln Lys Ala Ile Asp Glu Arg Val Lys Ala
180 185 190

Asn Gln Glu Leu Glu Arg Thr Lys Val Asp Lys Gln Ile Ala Glu Glu
195 200 205

Asn Ala Lys Lys Lys Glu Val Glu Ala Lys Gly Glu Lys Lys Ala Asn
210 215 220

Asp Ile Arg Ser Glu Ser Leu Thr Asp Glu Val Leu Gln Gln Gln Leu
225 230 235 240

Ile Glu Lys Trp Asp Gly Lys Gln Pro Ile Gln Ile Gly Gly Asp Gly
245 250 255

Thr Ile Val Asp Val Thr Gly Lys
260

<210> 1214
<211> 102
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1214
Met Ala Leu Phe Leu Thr Tyr Phe Ala Ile Phe Ile Val Phe Leu Val
1 5 10 15

Leu Val Gly Phe Gly Met Ser Tyr Val Phe Asp Phe Leu Ser Met Arg
20 25 30

Glu Lys Lys Ser Asn Ile Arg Lys Gln Tyr Arg Glu Leu Val Arg Gln
35 40 45

Gly Thr Leu Glu Glu Tyr Gly Leu Glu Gln Tyr Val Lys Tyr Lys Lys
50 55 60

Gln Phe Leu Asn Asp Arg Arg Gln Ser Leu Val Thr Lys Ala Asp Lys
65 70 75 80

Gln Glu Ile Asp Lys Glu Glu Lys Ala Leu Asn Ser Leu Ile Lys Glu
85 90 95

Ile Glu Lys Gly Glu Met
100

<210> 1215
<211> 206
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1215
Met Glu Asn Ile Ile Gly Lys Lys Ile Glu Lys Leu Phe Val Glu Glu
1 5 10 15

Tyr Val Gly Ser Asp Lys Ile Lys Gly Lys Leu Tyr Leu Cys Leu Cys
20 25 30

Asp Cys Gly Met Asp Arg Val Leu Ser Lys Ser Gln Leu Tyr Tyr Tyr
35 40 45

Lys Ser Cys Gly Cys Met Lys Ser Arg Asn Gly Ser Lys Lys His Pro

50 55 60

Glu Tyr Thr Val Trp Arg Lys Met Lys Glu Arg Cys Tyr Asn Lys Asn
65 70 75 80

Gln Asp Ser Tyr Pro Tyr Tyr Gly Gly Arg Gly Ile Glu Val Cys Asp
85 90 95

Arg Trp Lys Asn Ser Phe Glu Ser Phe Leu Tyr Asp Met Gly Lys Arg
100 105 110

Pro Ser Asp Lys Tyr Gln Leu Asp Arg Lys Asp Asn Asp Gly Asn Tyr
115 120 125

Ser Pro Glu Asn Cys Arg Trp Thr Thr Arg Ser Glu Asn Ile Val Asn
130 135 140

Arg Pro Ser Lys Leu Glu Gly Leu Lys Asn Ile Gln Glu Arg Thr Asn
145 150 155 160

Gly Lys Tyr Arg Val Ser Ile Thr Arg Asn Asn Ile Arg Tyr Gln Ser
165 170 175

Tyr Gln Val Asp Ser Ile Lys Glu Ala Ile Asn Leu Arg Asp Arg Met
180 185 190

Leu Lys Glu Tyr Glu Glu Thr Lys Ser Ile Thr Ile Phe Lys
195 200 205

<210> 1216
<211> 496
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1216
Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr Ala
1 5 10 15

Lys Gly Thr Val Asp Ser Pro Tyr Arg Val Lys Lys Ala Thr Ser Tyr
20 25 30

Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile Asp Ala Asp Gly
35 40 45

Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp
50 55 60

Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile
65 70 75 80

```
Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu Asn Lys Pro Ser
                85                  90                  95

Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr
            100                 105                 110

Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp Gly Gly Asn Thr Ser
        115                 120                 125

Thr Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys
    130                 135                 140

Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu
145                 150                 155                 160

Ile Pro Val Lys Ala Gly Thr Thr Val Lys Lys Glu Thr Ala Lys Lys
                165                 170                 175

Ser Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys Ala Thr Leu Lys Val
            180                 185                 190

Ser Lys Asn His Ile Asn Tyr Thr Met Asp Lys Arg Gly Lys Lys Pro
        195                 200                 205

Glu Gly Met Val Ile His Asn Asp Ala Gly Arg Ser Ser Gly Gln Gln
    210                 215                 220

Tyr Glu Asn Ser Leu Ala Asn Ala Gly Tyr Ala Arg Tyr Ala Asn Gly
225                 230                 235                 240

Ile Ala His Tyr Tyr Gly Ser Glu Gly Tyr Val Trp Glu Ala Ile Asp
                245                 250                 255

Ala Lys Asn Gln Ile Ala Trp His Thr Gly Asp Gly Thr Gly Ala Asn
            260                 265                 270

Ser Gly Asn Phe Arg Phe Ala Gly Ile Glu Val Cys Gln Ser Met Ser
        275                 280                 285

Ala Ser Asp Ala Gln Phe Leu Lys Asn Glu Gln Ala Val Phe Gln Phe
    290                 295                 300

Thr Ala Glu Lys Phe Lys Glu Trp Gly Leu Thr Pro Asn Arg Lys Thr
305                 310                 315                 320

Val Arg Leu His Met Glu Phe Val Pro Thr Ala Cys Pro His Arg Ser
                325                 330                 335

Met Val Leu His Thr Gly Phe Asn Pro Val Thr Gln Gly Arg Pro Ser
            340                 345                 350
```

Gln Ala Ile Met Asn Lys Leu Lys Asp Tyr Phe Ile Lys Gln Ile Lys
355 360 365

Asn Tyr Met Asp Lys Gly Thr Ser Ser Ser Thr Val Val Lys Asp Gly
370 375 380

Lys Thr Ser Ser Ala Ser Thr Pro Ala Thr Arg Pro Val Thr Gly Ser
385 390 395 400

Trp Lys Lys Asn Gln Tyr Gly Thr Trp Tyr Lys Pro Glu Asn Ala Thr
405 410 415

Phe Val Asn Gly Asn Gln Pro Ile Val Thr Arg Ile Gly Ser Pro Phe
420 425 430

Leu Asn Ala Pro Val Gly Gly Asn Leu Pro Ala Gly Ala Thr Ile Val
435 440 445

Tyr Asp Glu Val Cys Ile Gln Ala Gly His Ile Trp Ile Gly Tyr Asn
450 455 460

Ala Tyr Asn Gly Asn Arg Val Tyr Cys Pro Val Arg Thr Cys Gln Gly
465 470 475 480

Val Pro Pro Ser His Val Pro Gly Val Ala Trp Gly Val Phe Lys Gly
485 490 495

<210> 1217
<211> 167
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1217
Met Ala Asn Glu Thr Lys Gln Pro Lys Val Val Gly Gly Ile Asn Leu
1 5 10 15

Ser Thr Arg Thr Lys Ser Lys Thr Phe Trp Val Ala Ile Ile Ser Ala
20 25 30

Val Ala Leu Phe Ala Asn Gln Ile Thr Gly Ala Phe Gly Leu Asp Tyr
35 40 45

Ser Ala Gln Ile Glu Gln Gly Val Asn Ile Val Gly Ser Ile Leu Thr
50 55 60

Leu Leu Ala Gly Leu Gly Ile Ile Val Asp Asn Asn Thr Lys Gly Leu
65 70 75 80

Lys Asp Ser Asp Ile Val Gln Thr Asp Tyr Leu Lys Pro Arg Asp Ser
85 90 95

Lys Asp Pro Asn Glu Phe Val Gln Trp Gln Ala Asn Ala Asn Asn Ala
100 105 110

Ser Thr Phe Glu Ile Asp Ser Tyr Glu Asn Asn Ala Glu Pro Asp Thr
115 120 125

Asp Asp Ser Asp Glu Val Pro Ala Ile Glu Asp Glu Ile Asp Gly Gly
130 135 140

Ser Ala Pro Ser Gln Asp Glu Glu Asp Thr Glu Glu His Gly Lys Val
145 150 155 160

Phe Ala Glu Glu Glu Val Lys
165

<210> 1218
<211> 61
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1218
Met Ala Ser Ala Lys Gln Leu Tyr Tyr Thr Glu Ser Leu Val Gly Lys
1 5 10 15

Ala Ile Ile Asn Asn Lys Val Ser Asn Lys Glu Glu Val Trp Asp Lys
20 25 30

Leu Glu Leu Leu Pro Glu Thr Lys Leu Glu Asp Leu Asp Asn Lys Gln
35 40 45

Met Ser Glu Val Ile Lys Lys Leu Asn Gln Ile Asn Glu
50 55 60

<210> 1219
<211> 72
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1219
acacccuuag uauaauuagu aguacaaggg ucuccaaaac ccuuagucuu ugugcaaauc 60

aaagagggug ug 72

<210> 1220
<211> 73
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1220
gguuucuuag cucagauggu agagcacuag auugaagcuc uaggugucau ugguucaaau 60

ccaauagaaa cca 73

<210> 1221
<211> 74
<212> RNA
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1221
ggcucauugg uguaacuggu uaacacacug cccugucacg gcagagagua cgaguucgag 60

ucucguaugg gucg 74

<210> 1222
<211> 72
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1222
Met Lys Arg Gln Lys Met Phe Tyr Ser Ser Leu Ile Cys Lys Glu Cys
1 5 10 15

Gly Asn Val Phe Lys Val Pro Arg Lys Arg Ala Asn Lys Arg Glu Glu
20 25 30

Gly His Ile Lys Asp Ile Tyr Cys Ile Lys Cys Cys Lys Thr Thr Lys
35 40 45

His Ile Glu Asp Asn Arg Ser Glu Ala Glu Arg Arg Trp Asp Ala Ile
50 55 60

Gln Glu Glu Leu Thr Lys Asp Asn
65 70

<210> 1223
<211> 69
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1223
Met Ser Lys His Ile Glu Ile Thr Met Ser Ser Gly Ala Lys Tyr Phe
1 5 10 15

Leu Val Ser Thr Asp Glu Lys Ser Tyr Asn Arg Gln Asp Ile Asp Tyr
20 25 30

Met Leu Arg Gly Met Asp Glu Thr Ser Ile Lys Val Tyr Thr Glu Ser
35 40 45

Ala Ile Thr Ser Pro Gln Val Tyr Ile Asn Pro Asn Arg Ile Glu Ser
    50   55   60

Phe Lys Ile Val Phe
65

<210> 1224
<211> 110
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1224
Leu Asp Lys Glu Ile Asn Asn Leu Val Ser Gln Val Glu Thr Ile Lys
1   5   10   15

Ser Lys Ile Gln Glu Gly Asn Tyr Ile Asp Arg Gly Thr Phe Lys Asp
            20   25   30

Leu Glu Val Glu Val Ala Glu Leu Arg Lys Met Ile Val Ser Ile Asp
        35   40   45

Lys Asp Val Ala Val Asn Ser Glu Lys Gln Ser Ala Ile Tyr Val Gln
    50   55   60

Leu Glu Arg Leu Asp Glu Lys Ile Ser Glu Leu Ala Glu Ser Thr Lys
65   70   75   80

Thr Lys Asp Thr Lys Lys Lys Asp Thr Thr Glu Lys Val Leu Leu Leu
                85   90   95

Val Leu Gly Ala Ile Leu Ser Phe Val Phe Asn Lys Phe Ala
            100   105   110

<210> 1225
<211> 108
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1225
Leu Thr Lys Tyr Lys Asp Ile Leu Lys Leu Glu Phe Lys Asp Ser Leu
1   5   10   15

Ala His Phe Lys Arg Asp Arg Arg Phe Phe His Met Tyr Arg Ile Asp
            20   25   30

Arg Leu Leu Ile Asn Gly Ser Ile Ile Tyr Phe Asp Tyr Tyr Tyr Leu
        35   40   45

Pro Ser Asp Asp Pro Asn Ile Val Ile Lys Glu Leu Asp Leu Gln Asp
    50   55   60

Phe Gly Lys Leu Arg Phe Glu Ile Asp Thr Lys Thr Ser Tyr Gly Lys
65   70   75   80

Val Val Thr Asp Asn Tyr Met Glu Ile Ile Asn Asp Phe Leu Glu Asn
                85   90   95

Tyr Asp Ile His Ser Glu Ser Glu Thr Val Arg Pro
            100   105

<210> 1226
<211> 128
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1226
Leu Asn Asn Asn Ile Ala Ile Phe Ile Phe Lys Thr Leu Val Ile Ile
1   5   10   15

Ile Phe Leu Leu Leu Phe Leu Ser Val Val Asn Ser Leu Ser Leu Ile
            20   25   30

Tyr Ser Ile Arg Pro Ser Val Val Met Ala Tyr Phe Thr Phe Gly Gly
        35   40   45

Ile Val Ser Asp Val Ala Leu Thr Met Thr Asp Lys Phe Leu Leu Lys
    50   55   60

Lys Glu Asp Pro Leu Pro Glu Tyr Val Leu Lys Lys Val Glu Ile Asn
65   70   75   80

Asp Lys Glu Ile Ser Ile Ile Lys Lys Ile Ile Glu Ser Asn Tyr Asp
                85   90   95

Ile Thr Ser Glu Glu Ile Lys Val Arg Ala Lys Ala Gln Gln Arg Leu
            100   105   110

Glu Glu Asp Ser Lys Glu Glu Asp Asn Asp Glu Asn Glu Glu Arg Asn
        115   120   125

<210> 1227
<211> 92
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1227
Met Lys Thr Lys Lys Glu Ile Lys Glu Gln Arg Lys Glu Leu Lys Asp
1   5   10   15

```
Gly Ala Thr Thr Val Ser Leu Val Lys Lys Gly Asp Lys Arg Ile Ala
            20                  25                  30

Ser Pro Ser Arg Ile Cys Ser Leu Cys Gly Gln Gln Leu Ser Gly Met
        35                  40                  45

Ser Tyr Thr Lys Gly Lys Ala Leu Ser Lys Val Asn His Phe His Leu
    50                  55                  60

Gln Tyr Ser Lys Tyr Ile Tyr Phe Asp Ile Cys Ala Asp Ile Asn Asn
65                  70                  75                  80

Cys Tyr Lys Asn Leu Arg Lys Arg Gly Glu Met Asp
                85                  90

<210> 1228
<211> 136
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1228
Leu Ser Ala Glu Asn Ile Arg Asp Ile Ile Asn Lys Lys Lys Leu Glu
1               5                   10                  15

Glu Glu Asp Thr Arg Lys Tyr Ile Ala Asp Gly Phe Met Asn Gly Ile
            20                  25                  30

Gly Lys Leu Met Tyr Glu Phe Asn Lys Lys Val Asp Asn Lys Glu Ile
        35                  40                  45

Glu Val Lys Asp Pro Asn Asp Leu Tyr Lys Leu Phe Val Ile Phe Ser
    50                  55                  60

Gln Met Gln Asn Met Val Asn Glu Thr Ser Glu Gly Gly Ala Ile Pro
65                  70                  75                  80

Gln Leu Ser Arg Pro Gln Gln Glu Leu Phe Glu Glu Ile Thr Thr Glu
                85                  90                  95

Asp Ser Asn Gly Glu Ser Thr Val Asp Leu Gln Lys Ile Ser Glu Met
            100                 105                 110

Ser Ala Glu Asp Ile Thr Glu Met Ile Ser Glu Lys Glu Lys Val Met
        115                 120                 125

Asn Glu Glu Asn Ser Lys Thr Phe
    130                 135

<210> 1229
```

<211> 79
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1229
Met Asp Gly Lys Glu Leu Ile Lys Ile Ala Gln Glu Thr Phe Gln Thr
1   5   10   15

Glu Lys Ile Thr Arg Glu Gln Ile Asp His Ile Ile Asn Met Leu Asn
            20   25   30

Pro Ser Thr Tyr Met Leu Lys Tyr His Thr Leu Arg Gly His Pro Ile
        35   40   45

Thr Phe Ser Ile Pro Asn Arg Asp Arg Ser Lys Ala Gln Ala His Arg
    50   55   60

Pro Trp Gln Val Arg Lys His Thr Met Arg Thr Ile Asn Leu Phe
65   70   75

<210> 1230
<211> 47
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1230
Met Ile Val Asn Asp Thr His Pro Asn Lys Ala Val Ile Lys Ser Arg
1   5   10   15

Gln Leu Gly Leu Ser Glu Met Gly Val Met Glu Met Val His Phe Ala
            20   25   30

Asp Met His Ser Tyr Ala Asn Ala Lys Cys Leu Tyr Thr Phe Asn
        35   40   45

<210> 1231
<211> 303
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1231
Met Gly Lys Lys Leu Thr Asn Thr Glu Phe Leu Asn Arg Val Phe Gln
1   5   10   15

Leu Val Ser Asp Glu Tyr Ser Phe Leu Glu Glu Tyr Lys Gly Arg His
            20   25   30

Thr Lys Leu Arg Cys Lys His Asn Leu Cys Ser Tyr Glu Trp Asp Val
        35   40   45

```
Glu Pro Gly Ala Phe Leu Gly Asn Lys Asn Lys Ala Gly Ser Arg Cys
    50                  55                  60

Pro Ser Cys Tyr Gly Asn Val Thr Lys Thr Thr Asp Lys Phe Lys Lys
65                  70                  75                  80

Glu Ile Tyr Asn Leu Thr Lys Asp Glu Tyr Arg Leu Leu Ser Glu Tyr
                85                  90                  95

Ile Asn Ala Lys Thr Lys Val Lys Ile Lys His Ser Lys Cys Gly Asn
            100                 105                 110

Thr Phe Ser Met Thr Pro Asn Thr Phe Ile Asn Gly Ser Arg Cys Pro
        115                 120                 125

Glu Cys Asn Pro Gln Lys Pro Tyr Asn Thr Asp Ser Ala Lys Asp Arg
    130                 135                 140

Ile Asn Lys Glu Thr Asn Gly Thr Phe Glu Leu Val Ser Glu Tyr Lys
145                 150                 155                 160

Gly Cys Tyr Glu Leu Met Lys Leu Lys His His Glu Cys Gly Asn Ile
                165                 170                 175

Val Glu Ile Asn Met Gln Ser Ile Asp Ser Asn Arg Leu Asn Cys Pro
            180                 185                 190

Tyr Cys Tyr Asn Arg Ser Arg Gly Glu Leu Leu Val Ser Ser Phe Leu
        195                 200                 205

Leu Ser Lys Asn Ile Pro Phe Glu Val Gln Lys Arg Phe Asp Gly Phe
    210                 215                 220

Lys Lys Tyr Pro Tyr Asp Phe Tyr Ile Ala Asp Tyr Asn Thr Val Ile
225                 230                 235                 240

Glu Tyr His Gly Glu Gln His Tyr Lys Pro Ile Lys Phe Tyr Gly Gly
                245                 250                 255

Glu Asp Arg Leu Val Arg Gln Lys Asn Ile Asp Leu Lys Lys Lys Asn
            260                 265                 270

Phe Val Glu Gly Lys Gly Ile Asn Tyr Leu Glu Ile Pro Tyr Thr Leu
        275                 280                 285

Asn Asn Gln Asn Lys Val Asn Glu Phe Leu Ile Asn Tyr Phe Lys
    290                 295                 300
```

<210> 1232
<211> 486

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1232
Met Lys Lys Phe Val Gln Ser Arg Leu Asn Pro Val Leu Glu Lys Glu
1 5 10 15

Tyr Phe Arg Asp Ile Val Asp Trp Asp Lys Asp Ser Leu Gly Phe Lys
20 25 30

Lys Ile Arg Asn Ser Ser Leu Phe Phe Arg Thr Ser Ser Lys Ala Ser
35 40 45

Thr Val Glu Gly Val Asp Ile Asp Tyr Leu Ser Leu Asp Glu Tyr Asp
50 55 60

Arg Val Asn Leu Leu Ala Glu Ser Ser Ala Leu Glu Ser Met Ser Ser
65 70 75 80

Ser Pro Phe Lys Ile Val Arg Arg Trp Ser Thr Pro Ser Val Pro Gly
85 90 95

Met Gly Ile His Lys Leu Tyr Gln Gln Ser Asp Gln Trp Tyr Tyr Gly
100 105 110

His Arg Cys Gln His Cys Asp Tyr Leu Asn Glu Met Ser Tyr Asn Asp
115 120 125

Tyr Asn Pro Asp Asn Leu Glu Glu Ser Gly Asn Met Leu Cys Val Asn
130 135 140

Pro Glu Gly Val Asp Glu Gln Ala Lys Thr Val Gln Asn Gly Ser Tyr
145 150 155 160

Gln Phe Val Cys Gln Lys Cys Gly Lys Pro Leu Asp Arg Trp Tyr Asn
165 170 175

Gly Glu Trp His Cys Lys Tyr Pro Glu Arg Thr Lys Gly Asn Lys Gly
180 185 190

Val Arg Gly Tyr Leu Ile Thr Gln Met Asn Ala Val Trp Ile Ser Ala
195 200 205

Asp Glu Leu Lys Glu Lys Glu Met Asn Thr Glu Ser Lys Gln Ala Phe
210 215 220

Tyr Asn Tyr Ile Leu Gly Tyr Pro Phe Glu Asp Val Lys Leu Arg Val
225 230 235 240

Asn Glu Glu Asp Val Tyr Gly Asn Lys Ser Pro Ile Ala Glu Thr Gln

245 250 255

Leu Met Lys Arg Asp Arg Tyr Ser His Ile Ala Ile Gly Ile Asp Trp
260 265 270

Gly Asn Thr His Trp Ile Thr Val His Gly Met Leu Pro Asn Gly Lys
275 280 285

Val Asp Leu Ile Arg Leu Phe Ser Val Lys Lys Met Thr Arg Pro Asp
290 295 300

Leu Val Glu Ala Asp Leu Glu Lys Ile Ile Trp Glu Ile Ser Lys Tyr
305 310 315 320

Asp Pro Asp Ile Ile Ile Ala Asp Asn Gly Asp Ser Gly Asn Asn Val
325 330 335

Leu Lys Leu Ile Asn His Phe Gly Lys Asp Lys Val Phe Gly Cys Thr
340 345 350

Tyr Lys Ser Ser Pro Lys Ser Thr Gly Gln Leu Arg Pro Glu Phe Asn
355 360 365

Glu Asn Asn Asn Arg Val Thr Val Asp Lys Leu Met Gln Asn Lys Arg
370 375 380

Tyr Val Gln Ala Leu Lys Thr Lys Asp Ile Ser Val Tyr Ser Thr Val
385 390 395 400

Asp Asp Asp Leu Lys Thr Phe Leu Lys His Trp Gln Asn Val Val Ile
405 410 415

Met Asp Glu Glu Asp Glu Lys Thr Gly Glu Met Tyr Gln Val Ile Lys
420 425 430

Arg Lys Gly Asp Asp His Tyr Ala Gln Ala Ser Val Tyr Ala Tyr Ile
435 440 445

Gly Leu Thr Arg Ile Lys Glu Leu Leu Lys Glu Gly Asn Gly Thr Ser
450 455 460

Phe Gly Ser Thr Phe Val Ser Thr Asp Tyr Asn Gln Glu Gly Asn Lys
465 470 475 480

Gln Phe Tyr Phe Asp Glu
485

<210> 1233
<211> 273
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1233
Met Asn Arg Gly Glu Ile Asp Leu Thr Asp Lys Leu Phe Tyr Gly Thr
1   5   10   15

Ile Ser Asn Glu Glu Ile Asn Lys Ser Val Leu Asn Leu Leu Leu Gly
            20   25   30

Glu Glu Leu Ser Leu Asp Tyr Val Ser Lys Asn Ser Asp Thr Leu Asp
        35   40   45

Val Lys Tyr Glu His Val Tyr Lys Ser Leu Gly Phe Asp Asn Phe Phe
    50   55   60

Asp Cys Phe Leu Tyr Ala Asn Arg Glu Pro Glu Ile Val His Lys Gly
65   70   75   80

Gly Asp Lys Asn Leu Gly Gly Leu Asn Lys Val Lys Arg Thr Val Ile
                85   90   95

Arg Asn Gly Lys Glu Met Glu Met Thr Val Tyr Glu Asp Gly Asn Lys
            100   105   110

Glu Asn Asp Ser Lys Glu Lys Gln Glu Gly Lys Glu Glu Val Ser Arg
        115   120   125

Ser Ala Val Gly Ala Arg Ala Ile Ser Asn Gly Glu Glu Gly Lys Val
    130   135   140

Asn Pro Lys Lys Val Ala Asn Ser Leu Ser Ser Leu Ser Lys Lys Gly
145   150   155   160

Val Asp Val Ser His Ile Asn Thr Asn Leu Ser Leu Tyr Lys Glu Phe
                165   170   175

Val Asp Asp Asn Gly Asp Thr Leu Gly Ile Thr Ser Phe Lys Arg Thr
            180   185   190

Glu Asn Asp Ile Ile Leu Glu Ser Tyr Ala Ser Ser Pro Asp Ser Asp
        195   200   205

Gly Val Gly Ala Arg Ala Ile Met Glu Leu Leu Arg Leu Ser Ile Lys
    210   215   220

Glu Asn Lys Asn Ala Val Val Tyr Asp Ile Glu Leu Pro Glu Ala Val
225   230   235   240

Glu Tyr Leu Lys Thr Leu Gly Phe Lys Pro Asn Lys Asp Gly Tyr Ile
                245   250   255

Leu Arg Lys Lys Asp Val Lys Gln Phe Leu Gly Asp Tyr Ser Asp Phe
260 265 270

Ile

<210> 1234
<211> 60
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1234
Val Ile Ile Val Ile Leu Phe Ser Thr Ile Val Ile Tyr Ser Ile Val
1 5 10 15

Phe Ile Leu Tyr Ile Val Leu Lys Thr Ile Tyr Ile Lys Ser Asn Met
20 25 30

Ser Arg Ile Asp Asn Thr Thr Glu Leu Leu Lys Ile Leu Gln Glu Asp
35 40 45

Ile Glu Gly Lys Ile Lys Lys Glu Gly Arg Asn Lys
50 55 60

<210> 1235
<211> 159
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1235
Met Thr Leu Glu Glu Asn Lys Leu Thr Leu Glu Glu Ser Ile Thr Pro
1 5 10 15

Leu Ser Lys Glu Glu Lys Glu Asp Ser Ile Lys Glu Phe Ser Ser Leu
20 25 30

Leu Cys Glu Met Val Asn Arg Leu Tyr Lys Ser Tyr Asn Val Phe Arg
35 40 45

Gln Asp Pro Met Asp Glu Thr Gln Arg Leu Asp Gly Ser Leu Met Val
50 55 60

Phe Gln Ser Arg Leu Asn Asp Pro Leu Thr Gly Asp Leu His Asp Lys
65 70 75 80

Met Tyr Lys Leu Ala Phe Ser Lys Arg Ile Asp Ile Phe Glu Ala Asn
85 90 95

Lys Gln Phe Arg Lys Asp Val Glu Ala Gly Lys Ala Ile Glu Leu Gly
100 105 110

Asp Val Ala Ile Ile Asp Thr Ala Leu Ser Asn Ile Leu Ser Gly Asn
115 120 125

Glu Phe Gln Gly Ser Ile Ser Phe Met Leu Arg Lys Asp Phe Glu Glu
130 135 140

Lys Glu Arg Ile Arg Lys Glu Glu Glu Glu Lys Leu Asn Asn Leu
145 150 155

<210> 1236
<211> 403
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1236
Leu Lys Lys Lys Pro Gln Gly Asn Glu Val Ile Ile Thr Ile Ile Thr
1 5 10 15

Val Met Ile Ala Val Phe Val Val Ile Met Thr Ile Phe Phe Asn Lys
20 25 30

Tyr Gln Asp Ala Lys Glu Asp Lys Asp Arg Tyr Gln Arg Leu Val Glu
35 40 45

Ile Tyr Lys Lys Ala Asp Asp Asn Asp Gly Glu Thr Lys Lys Lys Tyr
50 55 60

Val Lys Arg Leu Asn Lys Ala Glu Glu Glu Leu Lys Lys Val Lys Lys
65 70 75 80

Glu Thr Asn Tyr Lys Asp Tyr Asn Lys Lys Ser Ser Lys Glu Arg Gln
85 90 95

Lys Glu Asp Lys Glu Thr Arg Glu Lys Ile Tyr Asp Val Thr Gly Asp
100 105 110

Asp Asp Leu Ile Leu Val Lys Asn Asn Ile Asp Phe Ser Asp Lys Val
115 120 125

Asp Lys Pro Glu Ile Leu Ile Ser Glu Asp Gly Ile Gly Thr Ile Thr
130 135 140

Val Pro Val Asp Ser Gly Tyr Glu Lys Gln Thr Val Gly Ser Ile Ile
145 150 155 160

Thr Ser Val Leu Gly Ser Pro Phe Leu Ser Pro Gly Ser Asn Ser Ile
165 170 175

Asp Gly Leu Ser Val Ile Asn Asp Asn Val Tyr Pro Asn Thr Val Asp

180 185 190

Ser Ile Val Glu Asp Thr Lys Pro Ser Ile Asn Leu Pro Met Asp Asn
195 200 205

Pro Ile Ile Thr Asn Pro Val Glu Pro Thr Ile Pro Ser Asp Thr Ile
210 215 220

Pro Pro Ile Asp Asn Pro Ser Val Pro Val Phe Pro Glu Asn Pro Val
225 230 235 240

Asp Asn Asn Gln Gly Asn Thr Asp Asn Pro Asn Pro Pro Pro Pro Gly
245 250 255

Tyr Thr Asp Glu Asp Gly Gly Arg Gly Ser Gly Gly Gly Gly Asn Ser
260 265 270

Glu Pro Pro Ser Thr Glu Glu Pro Ser Asp Asn Gly Asn Thr Gly Gly
275 280 285

Gly Asp Trp Glu Glu Lys Pro Asp Pro Gly Glu Glu Pro Ser Asp Asn
290 295 300

Gly Asn Thr Gly Gly Asn Gly Gly Glu Val Thr Pro Glu Pro Asp Pro
305 310 315 320

Thr Pro Ser Glu Pro Glu Gln Pro Asn Glu Asn Ser Asp Glu Gly Asn
325 330 335

Glu Glu Lys Pro Ser Glu Pro Ser Asp Asn Pro Asp Glu Asn Gly Gly
340 345 350

Trp Glu Thr Glu Pro Thr Glu Pro Glu Ser Pro Ser Glu Pro Asp Asp
355 360 365

Lys Val Asp Glu Glu Asp Lys Asn Glu Asp Thr Thr Asp Asp Lys Gln
370 375 380

Pro Thr Glu Gln Pro Asp Asp Asn Asn Ile Asp Asn Glu Asp Lys Thr
385 390 395 400

Glu Glu Glu

<210> 1237
<211> 94
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1237

Met Ile Phe Val His Ser Lys Phe Ser Ser Lys Asn Val Phe Val Leu
1 5 10 15

Tyr Val Ile Tyr Ala Ile Ile Gly Ile Gly Thr Tyr Ile Val Leu Thr
20 25 30

Met Phe Gln Thr Thr Ser Val Leu Ile Lys Asn Asp Val Ile Asp Ser
35 40 45

Ile Glu Asn Thr Glu His Tyr Ile Gly Phe Asn Asp Pro Ile Ile Ile
50 55 60

Phe Thr Ile Ser Phe Ile Gly Ala Ile Leu Gly Gly Ile Trp Tyr Lys
65 70 75 80

Met Met Lys Ile Ile Lys Lys Ser Asn Phe Lys Asp Lys Lys
85 90

<210> 1238
<211> 126
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1238
Val Asn Arg Leu Ile Phe Ser Lys Asp Lys Lys Trp Asp Glu Ala Lys
1 5 10 15

Asp Phe Ile Lys Gly Gln Gly Met Gln Asp Asn Trp Ile Glu Ile Val
20 25 30

Asp Tyr Tyr Arg Gln Ile Gly Gly Lys His Val Ala Val Phe Ile Ala
35 40 45

Leu Asn Lys Val Lys Tyr Met Ile Leu Glu Ala Thr Lys Asp Asn Lys
50 55 60

Val Ile Leu Val Asp Lys Asp Asn Asn Ile Leu Leu Glu Asp Tyr Asp
65 70 75 80

Ile Val Met Glu Ser Lys Lys Met Phe Tyr Tyr Ile Glu Glu Pro Phe
85 90 95

Glu Val Lys Ile Asn Ile Pro Gln His Ile Arg Asp Val Thr Tyr Asn
100 105 110

Asn Thr Val Val Leu Thr Thr Val Arg Gly Ser Arg Gly Asp
115 120 125

<210> 1239
<211> 566
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1239
Leu Ala Asp Leu Phe Lys Gln Phe Arg Leu Gly Lys Asp Tyr Gly Asn
1   5   10   15

Asn Ser Thr Ile Ala Gln Val Pro Ile Asp Glu Gly Leu Gln Ala Asn
            20   25   30

Ile Lys Lys Ile Glu Gln Asp Asn Lys Glu Tyr Gln Asp Leu Thr Lys
        35   40   45

Ser Leu Tyr Gly Gln Gln Gln Ala Tyr Ala Glu Pro Phe Ile Glu Met
    50   55   60

Met Asp Thr Asn Pro Glu Phe Arg Asp Lys Arg Ser Tyr Met Lys Asn
65   70   75   80

Glu His Asn Leu His Asp Val Leu Lys Lys Phe Gly Asn Asn Pro Ile
                85   90   95

Leu Asn Ala Ile Ile Leu Thr Arg Ser Asn Gln Val Ala Met Tyr Cys
            100   105   110

Gln Pro Ala Arg Tyr Ser Glu Lys Gly Leu Gly Phe Glu Val Arg Leu
        115   120   125

Arg Asp Leu Asp Ala Glu Pro Gly Arg Lys Glu Lys Glu Glu Met Lys
    130   135   140

Arg Ile Glu Asp Phe Ile Val Asn Thr Gly Lys Asp Lys Asp Val Asp
145   150   155   160

Arg Asp Ser Phe Gln Thr Phe Cys Lys Lys Ile Val Arg Asp Thr Tyr
                165   170   175

Ile Tyr Asp Gln Val Asn Phe Glu Lys Val Phe Asn Lys Asn Asn Lys
            180   185   190

Thr Arg Leu Glu Lys Phe Ile Ala Val Asp Pro Ser Thr Ile Phe Tyr
        195   200   205

Ala Thr Asp Lys Lys Gly Lys Ile Ile Lys Gly Gly Lys Arg Phe Val
    210   215   220

Gln Val Val Asp Lys Arg Val Val Ala Ser Phe Thr Ser Arg Glu Leu
225   230   235   240

Ala Met Gly Ile Arg Asn Pro Arg Thr Glu Leu Ser Ser Ser Gly Tyr
                245   250   255

```
Gly Leu Ser Glu Val Glu Ile Ala Met Lys Glu Phe Ile Ala Tyr Asn
            260                 265                 270

Asn Thr Glu Ser Phe Asn Asp Arg Phe Phe Ser His Gly Gly Thr Thr
        275                 280                 285

Arg Gly Ile Leu Gln Ile Arg Ser Asp Gln Gln Gln Ser Gln His Ala
    290                 295                 300

Leu Glu Asn Phe Lys Arg Glu Trp Lys Ser Ser Leu Ser Gly Ile Asn
305                 310                 315                 320

Gly Ser Trp Gln Ile Pro Val Val Met Ala Asp Asp Ile Lys Phe Val
                325                 330                 335

Asn Met Thr Pro Thr Ala Asn Asp Met Gln Phe Glu Lys Trp Leu Asn
            340                 345                 350

Tyr Leu Ile Asn Ile Ile Ser Ala Leu Tyr Gly Ile Asp Pro Ala Glu
        355                 360                 365

Ile Gly Phe Pro Asn Arg Gly Gly Ala Thr Gly Ser Lys Gly Gly Ser
    370                 375                 380

Thr Leu Asn Glu Ala Asp Pro Gly Lys Lys Gln Gln Gln Ser Gln Asn
385                 390                 395                 400

Lys Gly Leu Gln Pro Leu Leu Arg Phe Ile Glu Asp Leu Val Asn Arg
                405                 410                 415

His Ile Ile Ser Glu Tyr Gly Asp Lys Tyr Thr Phe Gln Phe Val Gly
            420                 425                 430

Gly Asp Thr Lys Ser Ala Thr Asp Lys Leu Asn Ile Leu Lys Leu Glu
        435                 440                 445

Thr Gln Ile Phe Lys Thr Val Asn Glu Ala Arg Glu Glu Gln Gly Lys
    450                 455                 460

Lys Pro Ile Glu Gly Gly Asp Ile Ile Leu Asp Ala Ser Phe Leu Gln
465                 470                 475                 480

Gly Thr Ala Gln Leu Gln Gln Asp Lys Gln Tyr Asn Asp Gly Lys Gln
                485                 490                 495

Lys Glu Arg Leu Gln Met Met Met Ser Leu Leu Glu Gly Asp Asn Asp
            500                 505                 510

Asp Ser Glu Glu Gly Gln Ser Ala Asp Ser Ser Asn Asp Asp Lys Ser
        515                 520                 525
```

Asn Pro Glu Val Gly Thr Asp Ser Gln Ile Lys Gly Asp Ser Asn Val
530 535 540

Tyr Arg Thr Glu Thr Ser Asn Lys Gly Gln Gly Lys Lys Gly Glu Lys
545 550 555 560

Ser Ser Asp Phe Lys His
565

<210> 1240
<211> 384
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1240
Met Ser Val Ile Tyr Lys Asp Asn Asn Trp Ile Asp Leu Thr Asn Val
1 5 10 15

Pro Tyr Leu Gln Lys Gly Asp Ser Gly Tyr Arg Lys Asp Ile Pro Arg
20 25 30

Lys Asn Trp Lys Lys Cys Leu Asn Thr Glu Val Ser Phe Ser Tyr Lys
35 40 45

Gly Lys Lys Gly Leu Phe Tyr Val Thr Tyr Arg Lys Glu Asp Lys Gly
50 55 60

Lys Val Lys Val Glu Tyr Asp Lys Tyr Val Lys Ile Ile Asp Pro His
65 70 75 80

Asp Leu Lys Thr Leu Asn Ile Asn Lys Ile Val Asn Pro Pro Asn Lys
85 90 95

Ala Lys Tyr Arg Glu Gln Glu Val Ile Asn Gly Asp Thr Val Arg Asn
100 105 110

Ile Arg Lys Val Lys Asn Thr Gly Ile Val Tyr Thr Met Leu Cys Ser
115 120 125

Glu Tyr Glu Glu Glu Tyr Asp Ile Arg Glu Ser Asp Leu Leu Arg Gly
130 135 140

Arg Gly Ser Pro Tyr Lys Ser Gly Arg Lys Val Cys Tyr Asn Asn Ser
145 150 155 160

Leu Tyr Ser Val Glu Asn Leu Arg Glu Tyr Ile Cys Asp Leu Glu Tyr
165 170 175

Ala Lys Thr Val Thr Lys Phe Ser His Lys Asp Ile Lys Cys Lys Cys

180 185 190

Pro Ile Cys Ser Glu Glu Lys Val Met Lys Val Asn Lys Leu Val Asn
195 200 205

Asn Gly Phe Ser Cys His Arg Cys Ser Ser Thr Ile Thr Tyr Pro Glu
210 215 220

Arg Leu Met Ile Gly Leu Leu Glu Leu Asn Asn Leu Asn Tyr Glu Tyr
225 230 235 240

Gln Lys Val Phe Lys Asp Leu Pro Asn Arg Lys Phe Asp Phe Tyr Leu
245 250 255

Pro Lys Leu Asn Met Val Ile Glu Thr His Gly Leu Gln His Tyr Arg
260 265 270

Glu Leu Asn Gly Tyr Met Asn His Glu Lys Thr Lys Glu Ser Asp Leu
275 280 285

Glu Lys Tyr Asn Tyr Cys Lys Asn Asn Asn Ile Asp Tyr Ile Glu Ile
290 295 300

Asp Cys Ser Tyr Ser Asp Leu Ser Phe Ile Leu Ser Asn Val Glu Asn
305 310 315 320

Ser Lys Leu Asn Ser Ile Leu Lys Asn Lys Asn Tyr Asp Asn Leu Ser
325 330 335

Asn Tyr Ile Ile Arg Ser Lys Asn Asp Asp Val Lys Tyr Asn Ile Tyr
340 345 350

Leu Asp Tyr Cys Lys Gly Leu Ser Lys Lys Glu Leu Lys Asp Lys Tyr
355 360 365

Asn Lys Thr Ser Tyr Tyr Ile Asn Arg Ser Ile Glu Ile Phe Lys His
370 375 380

<210> 1241
<211> 257
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1241
Leu Glu Glu Ile Lys Phe Asn Ala Phe Val Pro Met Asp Leu Lys Lys
1 5 10 15

Ser Val Ser Thr Ala Ser Asp Thr Asn Glu Tyr Ser Ile Val Ser Gly
20 25 30

```
Trp Ala Ser Thr Pro Ser Met Asp Leu Gln Asn Asp Ile Val Asn Pro
        35                  40                  45

Lys Gly Ile Asp Ile Glu Tyr Phe Lys Ser Gln Gly Tyr Ile Asn Tyr
    50                  55                  60

Glu His Gln Ser Asp Lys Val Val Gly Ile Pro Thr Glu Asn Cys Tyr
65                  70                  75                  80

Val Asp Ile Glu Lys Gly Leu Phe Ile Glu Ala Lys Leu Trp Lys Asn
                85                  90                  95

Asp Glu Asn Val Val Lys Met Leu Asp Leu Ala Glu Lys Leu Glu Lys
            100                 105                 110

Ser Gly Ser Gly Arg Arg Leu Gly Phe Ser Ile Glu Gly Ala Val Lys
        115                 120                 125

Lys Arg Asn Ile Asn Asp Asn Arg Val Ile Asp Glu Val Met Ile Thr
    130                 135                 140

Gly Val Ala Leu Val Lys Asn Pro Ala Asn Pro Glu Ala Thr Trp Glu
145                 150                 155                 160

Ser Phe Met Lys Ser Phe Leu Thr Gly His Gly Thr Ser Pro Asp Thr
                165                 170                 175

Gln Val Asp Ala Gly Ala Leu Arg Lys Glu Glu Ile Ala Ser Ser Ile
            180                 185                 190

Thr Asn Leu Ala Tyr Val Thr Lys Ile Lys Asp Leu Lys Glu Phe Asn
        195                 200                 205

Asp Val Trp Asn Gly Val Val Glu Asp Leu Ser Lys Ser Asn Ser Met
    210                 215                 220

Gly Tyr Glu Glu Ser Val Leu Thr Leu Gln Leu Ala Lys Gly Leu Ser
225                 230                 235                 240

Arg Lys Asp Ala Glu Leu Ala Val Met Asp Ile Asn Lys Gln Lys Leu
                245                 250                 255

Glu
```

<210> 1242
<211> 318
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1242
Met Ser Lys Glu Met Gln Asn Ile Leu Glu Glu Tyr Asp Lys Leu Asn
1   5   10   15

Ala Gln Glu Ala Val Ser Lys Ser Val Glu Asp Asp Glu Lys Asn Thr
            20   25   30

Val Glu Ser Thr Glu Glu Gln Val Ala Glu Thr Thr Glu Glu Pro Ala
        35   40   45

Lys Glu Pro Glu Lys Val Ser Glu Glu Asp Ala Lys Glu Ala Gln Glu
    50   55   60

Gln Gly Glu Lys Val Glu Ser Glu Glu Val Ala Glu Asp Asn Glu Asp
65   70   75   80

Glu Glu Val Glu Lys Ser Ala Lys Glu Ser Lys Asp Pro Val Asp Gln
                85   90   95

Lys Asp Thr Lys Thr Glu Asn Lys Asp Asn Glu Lys Arg Lys Asn Lys
            100   105   110

Lys Asp Lys Lys Glu Asp Ser Asp Ser Asp Asp Glu Asp Lys Asp Thr
        115   120   125

Asp Asp Asp Lys Asp Lys Lys Glu Asp Lys Lys Glu Lys Thr Ser Lys
    130   135   140

Ser Ile Ser Asp Glu Asp Ile Thr Thr Val Phe Lys Ser Ile Leu Thr
145   150   155   160

Ser Phe Glu Asn Leu Asn Lys Glu Lys Glu Asn Phe Ala Thr Lys Glu
                165   170   175

Asp Leu Ser Glu Val Ser Lys Ser Ile Asn Glu Leu Ser Ala Lys Ile
            180   185   190

Ser Glu Ile Gln Ala Glu Asp Val Ser Lys Ser Val Asp Thr Asp Glu
        195   200   205

Glu Ala Val Glu Lys Ser Val Thr Ser Thr Asn Gly Glu Gln Glu Lys
    210   215   220

Val Glu Gly Tyr Val Ser Lys Ser Val Asp Thr Glu Glu Gln Ala Glu
225   230   235   240

Thr Gly Glu Ala Lys Ser Glu Glu Ala Glu Glu Val Gln Glu Asp Asn
                245   250   255

Thr Phe Lys Gly Leu Ser Gln Glu Glu Arg Thr Lys Phe Met Asp Ser
            260   265   270

Tyr Lys Ala Gln Ala Lys Asp Pro Arg Ala Ser Lys His Asp Leu Gln
275 280 285

Ser Ala Tyr Gln Ser Tyr Leu Asn Ile Asn Thr Asp Pro Thr Asn Ala
290 295 300

Ser Glu Lys Asp Ile Lys Thr Val Lys Asp Phe Ala Gln Ile
305 310 315

<210> 1243
<211> 463
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1243
Met Thr Ile Glu Lys Asn Leu Ser Asp Val Gln Gln Lys Tyr Ala Asp
1 5 10 15

Gln Phe Gln Glu Asp Val Val Lys Ser Phe Gln Thr Gly Tyr Gly Ile
20 25 30

Thr Pro Asp Thr Gln Ile Asp Ala Gly Ala Leu Arg Arg Glu Ile Leu
35 40 45

Asp Asp Gln Ile Thr Met Leu Thr Trp Thr Asn Glu Asp Leu Ile Phe
50 55 60

Tyr Arg Asp Ile Ser Arg Arg Pro Ala Gln Ser Thr Val Val Lys Tyr
65 70 75 80

Asp Gln Tyr Leu Arg His Gly Asn Val Gly His Ser Arg Phe Val Lys
85 90 95

Glu Ile Gly Val Ala Pro Val Ser Asp Pro Asn Ile Arg Gln Lys Thr
100 105 110

Val Ser Met Lys Tyr Val Ser Asp Thr Lys Asn Met Ser Ile Ala Ser
115 120 125

Gly Leu Val Asn Asn Ile Ala Asp Pro Ser Gln Ile Leu Thr Glu Asp
130 135 140

Ala Ile Ala Val Val Ala Lys Thr Ile Glu Trp Ala Ser Phe Tyr Gly
145 150 155 160

Asp Ala Ser Leu Thr Ser Glu Val Glu Gly Glu Gly Leu Glu Phe Asp
165 170 175

Gly Leu Ala Lys Leu Ile Asp Lys Asn Asn Val Ile Asn Ala Lys Gly
180 185 190

```
Asn Gln Leu Thr Glu Lys His Leu Asn Glu Ala Ala Val Arg Ile Gly
        195                 200                 205

Lys Gly Phe Gly Thr Ala Thr Asp Ala Tyr Met Pro Ile Gly Val His
    210                 215                 220

Ala Asp Phe Val Asn Ser Ile Leu Gly Arg Gln Met Gln Leu Met Gln
225                 230                 235                 240

Asp Asn Ser Gly Asn Val Asn Thr Gly Tyr Ser Val Asn Gly Phe Tyr
                245                 250                 255

Ser Ser Arg Gly Phe Ile Lys Leu His Gly Ser Thr Val Met Glu Asn
            260                 265                 270

Glu Leu Ile Leu Asp Glu Ser Leu Gln Pro Leu Pro Asn Ala Pro Gln
        275                 280                 285

Pro Ala Lys Val Thr Ala Thr Val Glu Thr Lys Gln Lys Gly Ala Phe
    290                 295                 300

Glu Asn Glu Glu Asp Arg Ala Gly Leu Ser Tyr Lys Val Val Val Asn
305                 310                 315                 320

Ser Asp Asp Ala Gln Ser Ala Pro Ser Glu Glu Val Thr Ala Thr Val
                325                 330                 335

Ser Asn Val Asp Asp Gly Val Lys Leu Ser Ile Ser Val Asn Ala Met
            340                 345                 350

Tyr Gln Gln Gln Pro Gln Phe Val Ser Ile Tyr Arg Gln Gly Lys Glu
        355                 360                 365

Thr Gly Met Tyr Phe Leu Ile Lys Arg Val Pro Val Lys Asp Ala Gln
    370                 375                 380

Glu Asp Gly Thr Ile Val Phe Val Asp Lys Asn Glu Thr Leu Pro Glu
385                 390                 395                 400

Thr Ala Asp Val Phe Val Gly Glu Met Ser Pro Gln Val Val His Leu
                405                 410                 415

Phe Glu Leu Leu Pro Met Met Lys Leu Pro Leu Ala Gln Ile Asn Ala
            420                 425                 430

Ser Ile Thr Phe Ala Val Leu Trp Tyr Gly Ala Leu Ala Leu Arg Ala
        435                 440                 445

Pro Lys Lys Trp Ala Arg Ile Lys Asn Val Arg Tyr Ile Ala Val
    450                 455                 460
```

<210> 1244
<211> 98
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1244
Met Leu Tyr Tyr Lys Lys Leu Leu Asp Lys Lys Met Ala Thr Val Tyr
1 5 10 15

Gly Thr Val Glu Ile Asp Lys Asp Gly Val Val Lys Gly Leu Thr Lys
20 25 30

Glu Gln Glu Lys Glu Phe Ala Asn Val Pro Gly Phe Glu Phe Glu Glu
35 40 45

Glu Lys Lys Thr Thr Arg Lys Gln Ser Ala Ser Thr Ser Lys Glu Glu
50 55 60

Glu Pro Lys Glu Glu Glu Lys Lys Ala Ser Thr Arg Lys Thr Thr Ser
65 70 75 80

Thr Thr Arg Lys Ser Thr Ala Arg Lys Thr Thr Ala Lys Lys Asp Glu
85 90 95

Asn Lys

<210> 1245
<211> 302
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1245
Met Val Asn Ser Met Phe Gly Gly Asp Leu Asp Pro Tyr Glu Lys Ser
1 5 10 15

Leu Asn Tyr Glu Tyr Pro Tyr His Pro Ser Gly Asn Pro Lys His Ile
20 25 30

Asp Val Ser Glu Ile Asp Asn Leu Thr Leu Ala Asp Tyr Gly Trp Ser
35 40 45

Pro Asp Ala Val Lys Ala Tyr Met Phe Gly Ile Ile Val Gln Asn Pro
50 55 60

Asp Thr Gly Gln Pro Met Gly Asp Glu Phe Tyr Asn His Ile Leu Glu
65 70 75 80

```
Arg Ala Val Gly Lys Ala Glu Arg Ala Leu Asp Ile Ser Ile Leu Pro
                85                  90                  95

Asp Thr Gln His Glu Met Arg Asp Tyr His Glu Thr Glu Phe Asn Ser
            100                 105                 110

Tyr Met Phe Val His Ala Tyr Arg Lys Pro Ile Leu Gln Val Glu Asn
        115                 120                 125

Leu Gln Leu Gln Phe Asn Gly Arg Pro Ile Tyr Lys Tyr Pro Ala Asn
    130                 135                 140

Trp Trp Lys Val Glu His Leu Ala Gly His Val Gln Leu Phe Pro Thr
145                 150                 155                 160

Ala Leu Met Gln Thr Gly Gln Ser Met Ser Tyr Asp Ala Val Phe Asn
                165                 170                 175

Gly Tyr Pro Gln Leu Ala Gly Val Tyr Pro Pro Ser Gly Ala Thr Phe
            180                 185                 190

Ala Pro Gln Met Ile Arg Leu Glu Tyr Val Ser Gly Met Leu Pro Arg
        195                 200                 205

Lys Lys Ala Gly Arg Asn Lys Pro Trp Glu Met Pro Pro Glu Leu Glu
    210                 215                 220

Gln Leu Val Ile Lys Tyr Ala Leu Lys Glu Ile Tyr Gln Val Trp Gly
225                 230                 235                 240

Asn Leu Ile Ile Gly Ala Gly Ile Ala Asn Lys Thr Leu Glu Val Asp
                245                 250                 255

Gly Ile Thr Glu Thr Ile Gly Thr Thr Gln Ser Ala Met Tyr Gly Gly
            260                 265                 270

Ala Ser Ala Gln Ile Leu Gln Ile Asn Glu Asp Ile Lys Glu Leu Leu
        275                 280                 285

Asp Gly Leu Arg Ala Tyr Phe Gly Tyr Asn Met Ile Gly Leu
    290                 295                 300


<210> 1246
<211> 292
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1246
Met Glu Lys Pro Tyr Met Ile Gly Ala Asn Ser Asn Pro Asn Val Ile
1               5                   10                  15
```

```
Asn Lys Ser Thr Thr Tyr Thr Thr Thr Thr Gln Ala Asp Glu Gln Asp
            20                  25                  30

Lys Pro Lys Tyr Thr Thr Arg Leu Glu Phe Asp Thr Ile Asp Met Ile
        35                  40                  45

Arg Phe Ile Asn Asp Arg Gly Ile Lys Val Leu Trp Glu Glu Ala Tyr
    50                  55                  60

Phe Cys Pro Cys Leu Asn Pro Asp Thr Gly His Pro Arg Val Asp Cys
65                  70                  75                  80

Pro Arg Cys His Gly Lys Gly Ile Ala Tyr Leu Pro Pro Lys Glu Thr
                85                  90                  95

Ile Met Ala Ile Gln Ser Gln Glu Lys Gly Thr Asn Gln Leu Asp Ile
            100                 105                 110

Gly Ile Leu Asp Thr Gly Thr Ala Ile Gly Thr Thr Gln Leu Glu Lys
        115                 120                 125

Arg Ile Ser Tyr Arg Asp Arg Phe Thr Val Pro Glu Val Leu Met Pro
    130                 135                 140

Gln Gln Met Ile Tyr Phe Val Asn Lys Asp Arg Ile Lys Lys Gly Ile
145                 150                 155                 160

Pro Leu Tyr Tyr Asp Val Lys Glu Val Thr Tyr Ile Ala Thr Gln Asp
                165                 170                 175

Gly Thr Val Tyr Glu Glu Asp Tyr Glu Ile Lys Asn Asn Arg Leu Tyr
            180                 185                 190

Leu Asn Glu Lys Tyr Glu Asn His Thr Val Thr Leu Lys Ile Leu Met
        195                 200                 205

Thr Leu Arg Tyr Val Val Ser Asp Ile Leu Lys Glu Ser Arg Tyr Gln
    210                 215                 220

Tyr Thr Lys Phe Asn Gln Pro Lys Ser Lys Phe Glu Asn Leu Pro Gln
225                 230                 235                 240

Lys Leu Leu Leu Lys Arg Glu Asp Val Ile Val Leu Gln Asp Pro Tyr
                245                 250                 255

Lys Val Asn Asp Gly Ile Glu Glu Asp Leu Glu Ile Gln Val Asp Asp
            260                 265                 270

Pro Lys Ala Ser Ala Ser Asn Pro Ser Asn Leu Gly Gly Phe Phe Gly
        275                 280                 285
```

Gly Ala Phe Lys
290

<210> 1247
<211> 206
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1247
Met Pro Val His Gly Lys Arg Pro Asn Leu Phe Lys Asn Lys Asn Tyr
1 5 10 15

Lys Gln Val Gly Lys Arg Thr Ile Asp Gly Met Arg Ser Glu Val Leu
20 25 30

Asp Lys Leu Gln Ala Thr Ala Gln Gln Val Glu Asn Thr Ser Ile Lys
35 40 45

Arg Met Pro Thr Tyr Leu Gln Ile Thr Glu Lys Lys Leu Glu Lys Glu
50 55 60

Gly Val Val Asp Leu Lys Lys Ala Phe Ala His Ser Ser Lys Lys Lys
65 70 75 80

Thr Ser Lys Asp Gly Gly Trp Tyr Leu Thr Val Pro Ile Arg Ile Lys
85 90 95

Thr Ser Arg Met Asn Asn Ser Thr Tyr Gln Asp Met Arg Thr Leu Lys
100 105 110

Val Asp Lys Gly Thr Gly Ser Val Ser Lys Ile Thr Asp Tyr Leu Glu
115 120 125

Gly Arg Arg Lys Asn Val Ser His Pro Ser Met Lys Pro Glu Pro Met
130 135 140

Thr His Asn Met Thr Lys Val Lys Arg Gly Lys Gln Ser Ser Tyr Phe
145 150 155 160

Ile Phe Arg Thr Val Ser Ser Lys Ser Pro Ala Ser Ser Trp Ile Leu
165 170 175

Asn Arg Asp Lys Val Asn Glu Asp Asn Phe Ser Lys Thr Thr Leu Lys
180 185 190

Thr Val Lys Gln Leu Met Asn Trp Lys Met Lys Asn Leu Asn
195 200 205

<210> 1248
<211> 278

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1248
Met Ala Ile Thr Ser Val Asp Ser Tyr Leu Leu Ser Glu Ile Lys Pro
1 5 10 15

Arg Leu Asn Thr Val Leu Glu Asn Cys Tyr Ile Ile Asp Glu Val Leu
20 25 30

Lys Asp Phe Asp Tyr Gln Thr Arg Glu Ser Phe Lys Glu Ala Phe Cys
35 40 45

Gly Lys Asn Ala Gln His Glu Val Thr Val Gly Phe Asn Phe Pro Lys
50 55 60

Phe Lys Asn Asn Tyr Glu Ala His Tyr Leu Ile Gln Leu Gly Gln Gly
65 70 75 80

Gln Glu Thr Lys Asn Ser Leu Gly Ser Ile Gln Ser Ser Tyr Phe Glu
85 90 95

Ala Thr Gly Asp Thr Leu Val Glu Ser Ser Thr Ala Ile Arg Glu Asp
100 105 110

Asp Lys Leu Val Phe Thr Val Ser Lys Pro Ile Gly Glu Leu Ile Lys
115 120 125

Val Glu Asp Ile Glu Phe Ala Lys Tyr Asp Asn Leu Gln Val Glu Gly
130 135 140

Asn Lys Val Ser Phe Lys Tyr Gln Thr Asn Glu Asp Tyr Glu Asn Tyr
145 150 155 160

Asn Ala Asn Ile Ile Phe Thr Glu Lys Lys Asn Asp Ser Lys Gly Leu
165 170 175

Val Lys Gly Phe Thr Val Glu Glu Gln Val Thr Val Val Gly Leu Ser
180 185 190

Phe Asn Val Asp Val Ala Arg Cys Leu Asp Ala Val Leu Lys Met Ile
195 200 205

Leu Ile Ser Met Arg Asp Ser Ile Glu Glu Gln Gln Thr Phe Gln Leu
210 215 220

Gln Asn Leu Ser Phe Gly Asp Ile Ala Pro Ile Ile Glu Asp Gly Asp
225 230 235 240

Ser Met Ile Phe Gly Arg Pro Thr Ile Ile Lys Tyr Thr Ser Ser Leu

245 250 255

Asp Leu Asp Tyr Thr Ile Thr Gln Asp Ile Asn Lys Leu Thr Phe Lys
260 265 270

Glu Arg Lys Asp Trp Lys
275

<210> 1249
<211> 71
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1249
Met Ala Arg Lys Lys Thr Pro Glu Asn Asn Thr Pro Lys Phe Asn Gly
1 5 10 15

Tyr Val His Ile Asp Thr Phe Leu Asp Thr Ala Lys Thr Leu Phe Asn
20 25 30

Met Lys Asp Ser Gln Val Ala Gly Phe Lys Ala Tyr Met Glu Gly Ser
35 40 45

His Tyr Leu Phe Ser Glu Gln Glu Phe Leu Pro Ser Leu Glu Lys Tyr
50 55 60

Leu Gly Arg Lys Leu Asp Ile
65 70

<210> 1250
<211> 587
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1250
Met Ala Val Glu Pro Phe Pro Arg Arg Pro Ile Thr Arg Pro His Ala
1 5 10 15

Ser Ile Glu Val Asp Thr Ser Gly Ile Gly Gly Ser Ala Gly Ser Ser
20 25 30

Glu Lys Val Phe Cys Leu Ile Gly Gln Ala Glu Gly Gly Glu Pro Asn
35 40 45

Thr Val Tyr Glu Leu Arg Asn Tyr Ala Gln Ala Lys Arg Leu Phe Arg
50 55 60

Ser Gly Glu Leu Leu Asp Ala Ile Glu Leu Ala Trp Gly Ser Asn Pro
65 70 75 80

```
Asn Tyr Thr Ala Gly Lys Ile Leu Ala Met Arg Ile Glu Asp Ala Lys
                85                  90                  95

Pro Ala Ser Ala Glu Ile Gly Gly Leu Lys Val Thr Ser Lys Ile Tyr
            100                 105                 110

Gly Asn Val Ala Asn Asn Ile Gln Val Gly Leu Glu Lys Asn Thr Leu
        115                 120                 125

Ser Asp Ser Leu Arg Leu Arg Val Ile Phe Gln Asp Asp Arg Phe Asn
    130                 135                 140

Glu Val Tyr Asp Asn Ile Gly Asn Ile Phe Thr Ile Lys Tyr Lys Gly
145                 150                 155                 160

Glu Glu Ala Asn Ala Thr Phe Ser Val Glu His Asp Glu Glu Thr Gln
                165                 170                 175

Lys Ala Ser Arg Leu Val Leu Lys Val Gly Asp Gln Glu Val Lys Ser
            180                 185                 190

Tyr Asp Leu Thr Gly Gly Ala Tyr Asp Tyr Thr Asn Ala Ile Ile Thr
        195                 200                 205

Asp Ile Asn Gln Leu Pro Asp Phe Glu Ala Lys Leu Ser Pro Phe Gly
    210                 215                 220

Asp Lys Asn Leu Glu Ser Ser Lys Leu Asp Lys Ile Glu Asn Ala Asn
225                 230                 235                 240

Ile Lys Asp Lys Ala Val Tyr Val Lys Ala Val Phe Gly Asp Leu Glu
                245                 250                 255

Lys Gln Thr Ala Tyr Asn Gly Ile Val Ser Phe Glu Gln Leu Asn Ala
            260                 265                 270

Glu Gly Glu Val Pro Ser Asn Val Glu Val Glu Ala Gly Glu Glu Ser
        275                 280                 285

Ala Thr Val Thr Ala Thr Ser Pro Ile Lys Thr Ile Glu Pro Phe Glu
    290                 295                 300

Leu Thr Lys Leu Thr Gly Gly Thr Asn Gly Glu Pro Pro Ala Thr Trp
305                 310                 315                 320

Ala Asp Lys Leu Asp Lys Phe Ala His Glu Gly Gly Tyr Tyr Ile Val
                325                 330                 335

Pro Leu Ser Ser Lys Gln Ser Val His Ala Glu Val Ala Ser Phe Val
            340                 345                 350
```

```
Lys Glu Arg Ser Asp Ala Gly Glu Pro Met Arg Ala Ile Val Gly Gly
        355                 360                 365

Gly Phe Asn Glu Ser Lys Glu Gln Leu Phe Gly Arg Gln Ala Ser Leu
    370                 375                 380

Ser Asn Pro Arg Val Ser Leu Val Ala Asn Ser Gly Thr Phe Val Met
385                 390                 395                 400

Asp Asp Gly Arg Lys Asn His Val Pro Ala Tyr Met Val Ala Val Ala
                405                 410                 415

Leu Gly Gly Leu Ala Ser Gly Leu Glu Ile Gly Glu Ser Ile Thr Phe
            420                 425                 430

Lys Pro Leu Arg Val Ser Ser Leu Asp Gln Ile Tyr Glu Ser Ile Asp
        435                 440                 445

Leu Asp Glu Leu Asn Glu Asn Gly Ile Ile Ser Ile Glu Phe Val Arg
    450                 455                 460

Asn Arg Thr Asn Thr Phe Phe Arg Ile Val Asp Asp Val Thr Thr Phe
465                 470                 475                 480

Asn Asp Lys Ser Asp Pro Val Lys Ala Glu Met Ala Val Gly Glu Ala
                485                 490                 495

Asn Asp Phe Leu Val Ser Glu Leu Lys Val Gln Leu Glu Asp Gln Phe
            500                 505                 510

Ile Gly Thr Arg Thr Ile Asn Thr Ser Ala Ser Ile Ile Lys Asp Phe
        515                 520                 525

Ile Gln Ser Tyr Leu Gly Arg Lys Lys Arg Asp Asn Glu Ile Gln Asp
    530                 535                 540

Phe Pro Ala Glu Asp Val Gln Val Ile Val Glu Gly Asn Glu Ala Arg
545                 550                 555                 560

Ile Ser Met Thr Val Tyr Pro Ile Arg Ser Phe Lys Lys Ile Ser Val
                565                 570                 575

Ser Leu Val Tyr Lys Gln Gln Thr Leu Gln Ala
            580                 585
```

<210> 1251
<211> 134
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1251
Met Ala Ser Glu Ala Lys Gln Thr Val His Thr Gly Asn Thr Val Leu
1 5 10 15

Leu Met Ile Lys Gly Lys Pro Val Gly Arg Ala Gln Ser Ala Ser Gly
20 25 30

Gln Arg Glu Tyr Gly Thr Thr Gly Val Tyr Glu Ile Gly Ser Ile Met
35 40 45

Pro Gln Glu His Val Tyr Leu Arg Tyr Glu Gly Thr Ile Thr Val Glu
50 55 60

Arg Leu Arg Met Lys Lys Glu Asn Phe Ala Asp Leu Gly Tyr Ala Ser
65 70 75 80

Leu Gly Glu Glu Ile Leu Lys Lys Asp Ile Ile Asp Ile Leu Val Val
85 90 95

Asp Asn Leu Thr Lys Gln Val Ile Ile Ser Tyr His Gly Cys Ser Ala
100 105 110

Asn Asn Tyr Asn Glu Thr Trp Gln Thr Asn Glu Ile Val Thr Glu Glu
115 120 125

Ile Glu Phe Ser Tyr Leu
130

<210> 1252
<211> 309
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1252
Met Gly Lys Asn Gln Tyr Thr Phe Asn Ile Lys Glu Asn Lys Asn Lys
1 5 10 15

Trp Tyr Glu Trp Cys Lys Leu Gln Asn Val Lys Pro Leu Val Glu Tyr
20 25 30

Glu Asn Ala Gln Gln Ile Phe Tyr Phe Glu Phe Leu Glu Gly Lys Phe
35 40 45

Lys Gly Leu Ile Gly Lys Thr Tyr Trp Ala Ser Ile Asn Arg Gly Ser
50 55 60

Asn Met Arg Met Ser Cys Leu Thr Ser Glu Ser Lys Asp Lys Tyr Leu
65 70 75 80

Lys Asn Leu Gly Lys Arg Lys Gly Ile Glu Val Val Glu Asp Tyr Lys

85 90 95

Gly Gly Arg Lys Leu Lys His Lys Phe Ile Val Leu Glu Gly Lys Tyr
100 105 110

Gln Gly Cys Glu Gly Tyr Ile Thr Leu Asn Asp Leu Glu Asn Leu Gly
115 120 125

Arg Val Asp Asn Arg Ser Leu Ser Glu Lys Gly Arg Lys Gln Tyr Phe
130 135 140

Asp Lys Gln Ala Arg Leu Arg Asp Cys Ile Ile Leu Glu Tyr Pro Lys
145 150 155 160

Asp Tyr Arg Ile Lys Thr Lys Asp Lys Ile Val Val Lys Asp Lys Glu
165 170 175

Gly His Val His Asn Ile Ile Val Gln Asp Phe Phe Glu Lys Ser Ser
180 185 190

Leu Leu Glu Leu Ser Cys Ala Ser Glu Gly Glu Lys Ile Val Lys Glu
195 200 205

Ile Leu Thr Lys Asn Ser Ile Lys Phe Glu Lys Glu Lys Ser Phe Arg
210 215 220

Asn Lys Glu Gly Lys Val Gln Arg Phe Asp Phe Tyr Ile Asn Glu Asn
225 230 235 240

Asn Lys Glu Tyr Ala Ile Glu Tyr Asn Gly Ala Gln His Tyr Ile Asp
245 250 255

Ser Thr Gly Tyr Leu Lys Asp Thr Leu Glu Thr Thr Gln Lys Arg Asp
260 265 270

Lys Leu Lys Lys Glu Tyr Ser Lys Asp Lys Gly Ile Asn Leu Leu Ile
275 280 285

Ile Pro Tyr Thr Ile Thr Asp Lys Lys Glu Met Glu Lys Ile Ile Leu
290 295 300

Asn Phe Leu Asn Lys
305

<210> 1253
<211> 52
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1253

Met Asn Asn Arg Gln Ala Lys Ile Lys Gly Tyr Asn Gln Phe His Tyr
1   5   10   15

Tyr Asp Phe Pro Thr Thr Lys Gly Lys Phe Lys Asp Ile Met Lys Arg
            20   25   30

Lys Ser Arg Thr Glu Leu Lys Lys Asp Leu Gln Lys Glu Arg Lys Tyr
        35   40   45

Tyr Leu Asp Lys
    50

<210> 1254
<211> 46
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1254
Leu Thr Asn Lys Arg Lys Thr Ile Gly Lys Met Ser Asn Thr Arg Ala
1   5   10   15

Thr Trp Asn Ile Asn Pro Val Thr Lys Val Lys Lys Asp Lys Thr Lys
            20   25   30

Tyr Ser Arg Lys Asn Lys His Lys Gly Leu Asp Asn Tyr Asn
        35   40   45

<210> 1255
<211> 152
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1255
Met Ser Thr Phe Trp Ser Glu Arg Arg Thr Thr Asn Lys Asp Arg Gln
1   5   10   15

Val Lys Lys His Tyr Thr Gln Met Ser Met Tyr Glu Arg Lys Lys Cys
            20   25   30

Val Glu Leu Leu Gln Glu Thr Ile Thr Glu Asn Arg Ile Ile Asn Phe
        35   40   45

Thr Arg His Ser Ala Lys Lys Val Lys Gly Lys Pro Thr Thr Asn Ile
    50   55   60

Pro Lys Leu Ile Gly Phe Ile Phe Lys Asn Lys Phe Ala Tyr Glu Asn
65   70   75   80

Ile Ile Glu Tyr Asn Asn Thr Asp Tyr Asn Gly Asn Ile Glu Arg Arg
                85   90   95

Ile Val Val Lys His Pro Lys Val Ile Thr Val Glu Gly Lys Pro Ser
100 105 110

Tyr Gln Phe Leu Thr Ile Ser Leu Glu Asp Ala Arg Val Ile Thr Val
115 120 125

Trp Tyr Asn Ser Val Asp Asp Thr His Arg Thr Leu Asp Leu Asn Tyr
130 135 140

Tyr Ser Lys Asp Leu Thr Ile Gln
145 150

<210> 1256
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1256
Met Gly Ile Thr Ile Val Asn Ser Tyr Phe Ile Leu Ser Asn Ile Phe
1 5 10 15

Leu Ile Ile Leu Thr Ile Leu Asn Gly Lys Gly Thr Val Thr Arg Glu
20 25 30

Ser Leu Thr Met Ser Lys Ile Leu Val Val Ile Thr Ser Ile Gln Phe
35 40 45

Leu Ala Cys Leu Ile Ile Asn Gly Ile Tyr Trp Ser Leu Lys Phe
50 55 60

<210> 1257
<211> 103
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1257
Met Ser Gln Asp Lys Leu Arg Ala Ile Tyr Thr Glu Met Lys Val Glu
1 5 10 15

Leu His Lys Phe Pro Lys Glu Val Asp Ile Thr Ser Lys Ser Thr Ala
20 25 30

Ile Ala Ile Asn Gln Ile Leu Asp Lys Phe Lys Thr Leu Thr Glu Gln
35 40 45

Ala Gly Lys Ile Thr Arg Lys Tyr Leu Glu Gly Gln Glu Ile Leu Thr
50 55 60

Ile Asp Tyr Glu Tyr Tyr Asp Ser Leu Gln Glu Tyr Tyr Ile Tyr Leu
65 70 75 80

Leu Arg Asn Ser Glu Lys Ile Glu Gln Ser Leu Gln Glu Ile Thr Lys
85 90 95

Arg Thr Gly Glu Tyr Val Lys
100

<210> 1258
<211> 152
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1258
Met Ala Glu Glu Ile Lys Lys Glu Gln Asp Val Gln Glu Thr Thr Lys
1 5 10 15

Glu Glu Lys Lys Asp Val Ser Lys Met Thr Pro Glu Glu Ile Asp Lys
20 25 30

Leu Lys Tyr Gln Asp Lys Gln Glu Lys Glu Gln Val Ile Asn Lys Val
35 40 45

Ile Lys Gly Val Asn Asp Thr Trp Glu Lys Glu Tyr Asn Phe Glu Glu
50 55 60

Leu Asp Leu Arg Phe Lys Val Lys Ile Lys Leu Pro Asn Ala Arg Glu
65 70 75 80

Gln Gly Asn Ile Phe Ala Leu Arg Ser Ala Tyr Leu Gly Gly Met Asp
85 90 95

Met Tyr Gln Thr Asp Gln Val Ile Arg Ala Tyr Gln Met Leu Ala Thr
100 105 110

Leu Gln Glu Val Gly Ile Glu Val Pro Lys Glu Phe Gln Asp Pro Asp
115 120 125

Asp Ile Tyr Asn Leu Tyr Pro Leu Thr Val Met Tyr Glu Asp Trp Leu
130 135 140

Gly Phe Leu Asn Ser Phe Arg Tyr
145 150

<210> 1259
<211> 178
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1259
Met Glu Ser Ile Val Lys Gln Pro Leu Ser Arg Asn Leu Trp Ala Ile
1 5 10 15

Met Lys Glu Phe Asn Val Leu Pro Thr Glu Gln Arg Phe Lys Asp Leu
20 25 30

Asp Asp Tyr Gln Ile Glu Phe Ile Ile Gly Asn Met Asn Arg Asp Val
35 40 45

Tyr Glu His Asn Lys Gln Leu Lys Gln Ala Gln Lys Gly Gly Lys Phe
50 55 60

Asp Ser Gln Phe Glu Asp Asp Asp Ser Ser Trp Trp Asn Glu Ser His
65 70 75 80

Glu Asp Phe Asp Pro Val Pro Asp Phe Leu Asp Ala Asp Asp Leu Ala
85 90 95

Gln Gln Val Glu Ala Lys Leu Ser Asp Arg Asp Lys Glu Glu Arg Ala
100 105 110

Lys Arg Asn Asp Ala Glu Leu Asn Asp Glu Thr Glu Gly Leu Thr Thr
115 120 125

Gln His Leu Ala Met Met Glu Tyr Ile Arg Gln Lys Gln Gln Glu Leu
130 135 140

Asp Asp Glu Val Gly Asn Gly Lys Thr Ser Glu Glu Asp Ala Thr Ile
145 150 155 160

Ser Gln Asp Ser Val Asn Lys Ala Leu Glu Asp Leu Asp Asp Asp Trp
165 170 175

Tyr Met

<210> 1260
<211> 1351
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1260
Met Ala Met Asn Asp Asp Tyr Arg Leu Val Leu Ser Gly Asp Ser Ser
1 5 10 15

Asp Leu Glu Asn Ser Leu Lys Ala Ile Glu Leu Tyr Met Asp Ser Leu
20 25 30

Glu Ser Lys Asn Ile Asp Ala Pro Leu Asp Asn Phe Leu Lys Lys Leu

```
        35                  40                  45

Lys Val Ile Ala Lys Glu Val Lys Asn Val Gln Asn Ala Met Asp Lys
    50                  55                  60

Gln Asp Gly Lys Ser Val Ile Ser Ser Lys Asp Met Asp Glu Ser Ile
65                  70                  75                  80

Lys Ser Thr Gln Ser Ala Thr Lys Asn Ile Asn Glu Leu Lys Lys Ala
                85                  90                  95

Leu Asp Asp Leu Gln Lys Glu Asn Ile Ser Lys Gly Ile Ala Pro Asp
            100                 105                 110

Pro Glu Val Glu Lys Ala Tyr Ala Lys Met Gly Lys Val Val Asp Glu
        115                 120                 125

Thr Gln Glu Lys Leu Glu Lys Met Ser Ser Gln Lys Ile Gly Ser Asp
    130                 135                 140

Ala Ser Ile Gln Asn Arg Ile Lys Glu Met Lys Thr Leu Asn Gln Val
145                 150                 155                 160

Thr Glu Glu Tyr Asn Lys Ile Ser Lys Asp Ser Ser Ala Thr Lys Asp
                165                 170                 175

Tyr Thr Lys Arg Leu Arg Ala Asn Arg Asn Met Thr Arg Gly Tyr Met
            180                 185                 190

Glu Arg Ser Glu Gly Thr Gly Arg Leu Thr Tyr Asp Gln Gly Ala Arg
        195                 200                 205

Val Arg Ser Glu Leu Gly Lys Ile Ser Ser Tyr Glu Ser Gln Arg Lys
    210                 215                 220

Gln Asn Gln Arg Asn Leu Gly Gln Ala Arg Glu Gln Tyr Ser Asn Tyr
225                 230                 235                 240

Arg Asn Gln Gln Gln Asp Leu Thr Lys Arg Arg Ala Ser Gly Gln Ile
                245                 250                 255

Asn Lys Ala Gln Tyr Glu Gln Glu Leu Ala Ser Ile Lys Gln Glu Met
            260                 265                 270

Lys Ala Arg Glu Glu Leu Ile Ser Asn Tyr Glu Lys Leu Gly Ala Glu
        275                 280                 285

Leu Asp Lys Thr Val Gln Tyr Tyr Lys Gly Ser Val Gln Lys Asp Phe
    290                 295                 300

Gln Ser Arg Asp Val Asp Gln Gln Arg Gly Thr Phe Gly Arg Met Val
```

305 310 315 320

Gln Glu Arg Leu Pro Ser Ile Gly Ser His Ala Met Met Gly Thr Thr
325 330 335

Ala Met Ala Thr Gly Leu Tyr Met Lys Gly Ala Ser Leu Ser Glu Thr
340 345 350

Asn Arg Pro Met Val Thr Ser Leu Gly Gln Asn Ser Asp Asn Met Asp
355 360 365

Ile Asp Ser Val Arg Asn Ala Tyr Gly Asp Leu Ser Ile Asp Asn Lys
370 375 380

Leu Gly Tyr Asn Ser Thr Asp Met Leu Lys Met Ala Thr Ser Tyr Glu
385 390 395 400

Ala Ser Val Gly His Lys Ser Asp Glu Asp Thr Met Ala Gly Thr Lys
405 410 415

Gln Leu Ala Ile Gly Gly Arg Ser Leu Gly Ile Arg Asp Gln Glu Ala
420 425 430

Tyr Gln Glu Ser Met Gly Gln Ile Met His Thr Gly Gly Val Asn Ser
435 440 445

Asp Asn Met Lys Glu Met Gln Asp Ala Phe Leu Gly Gly Ile Lys Gln
450 455 460

Ser Gly Met Val Gly Arg Gln Asp Glu Gln Leu Lys Ala Leu Gly Ser
465 470 475 480

Ile Ala Glu Gln Ser Gly Glu Gly Arg Thr Leu Thr Lys Asp Gln Met
485 490 495

Ser Asn Leu Thr Ala Met Gln Ser Thr Phe Ala Glu Ser Gly Ser Lys
500 505 510

Gly Leu Gln Gly Glu Gln Gly Ala Asn Ala Ile Asn Ser Ile Asp Gln
515 520 525

Gly Leu Lys Asn Gly Met Asn Ser Ser Tyr Ala Arg Ile Ala Met Gly
530 535 540

Trp Gly Thr Gln Tyr Gln Gly Leu Glu Gly Gly Tyr Asp Leu Gln Lys
545 550 555 560

Arg Met Asp Glu Gly Ile Ser Asn Pro Glu Asn Leu Thr Asp Met Ala
565 570 575

Asp Met Ala Thr Gln Met Gly Gly Ser Glu Lys Glu Gln Lys Tyr Leu

580 585 590

Phe Asn Arg Ser Met Lys Glu Ile Gly Ala Asn Leu Thr Met Glu Gln
595 600 605

Ser Asp Glu Ile Phe Lys Asp Ala Gln Ser Gly Lys Leu Ser Lys Glu
610 615 620

Glu Leu Ala Lys Lys Ala Lys Lys Met Glu Lys Glu Gly Lys Lys Glu
625 630 635 640

Gly Glu Asp Asn Ala Thr Asp Tyr Lys Glu Ser Lys Ser Gly Lys Asn
645 650 655

Asp Gln Asn Lys Ser Lys Thr Asp Asp Lys Ala Glu Asp Thr Tyr Asp
660 665 670

Met Ala Gln Pro Leu Arg Asp Ala His Ser Ala Leu Ala Gly Leu Pro
675 680 685

Ala Pro Ile Tyr Leu Ala Ile Gly Ala Ile Gly Ala Phe Thr Ala Ser
690 695 700

Leu Ile Ala Ser Ala Ser Gln Phe Gly Ala Gly His Leu Ile Gly Lys
705 710 715 720

Gly Ala Lys Gly Leu Arg Asn Lys Phe Gly Arg Asn Lys Gly Gly Ser
725 730 735

Ser Gly Gly Asn Pro Met Ala Gly Gly Met Pro Ser Gly Gly Gly Ser
740 745 750

Pro Lys Gly Gly Gly Ser Pro Lys Gly Gly Gly Thr Arg Ser Thr Gly
755 760 765

Gly Lys Ile Leu Asp Ser Ala Lys Gly Leu Gly Gly Phe Leu Val Gly
770 775 780

Gly Ala Gly Trp Lys Gly Met Phe Gly Gly Glu Ser Lys Gly Lys Gly
785 790 795 800

Phe Lys Gln Thr Ser Lys Glu Ala Trp Ser Gly Thr Arg Lys Val Phe
805 810 815

Asn Arg Asp Asn Gly Arg Lys Ala Met Asp Lys Ser Lys Asp Ile Ala
820 825 830

Lys Gly Thr Gly Ser Gly Leu Lys Asp Ile Tyr Asn Asp Ser Ile Phe
835 840 845

Gly Lys Glu Arg Arg Gln Asn Leu Gly Glu Lys Ala Lys Gly Phe Gly

```
850                 855                 860

Gly Lys Ala Lys Gly Leu Tyr Gly Lys Phe Ala Asp Lys Phe Gly Asp
865                 870                 875                 880

Gly Gly Lys Asn Gly Ile Leu Ser Gln Ser Pro Lys Ala Gly Gly Ser
                885                 890                 895

Gly Ile Gly Lys Leu Gly Lys Leu Ala Gly Gly Leu Gly Lys Gly Ala
            900                 905                 910

Gly Val Leu Gly Val Ala Thr Ser Ala Leu Ser Leu Ile Pro Ala Leu
        915                 920                 925

Ala Ser Gly Asp Ser Lys Ala Ile Gly Gly Gly Ile Gly Ser Met Gly
    930                 935                 940

Gly Gly Met Ala Gly Ala Ser Ala Gly Ala Ser Ile Gly Ala Leu Phe
945                 950                 955                 960

Gly Gly Val Gly Ala Ile Pro Gly Ala Leu Ile Gly Gly Ala Ile Gly
                965                 970                 975

Ser Phe Gly Gly Gly Ala Val Gly Glu Lys Val Gly Asp Met Ala Lys
            980                 985                 990

Lys Ala Asn Thr Lys Glu Gly Trp  Asn Leu Gly Trp Thr  Asn Gly Asp
        995                 1000                1005

Lys Asp  Gly Lys Asn Lys Phe  Gln Asp Ser Leu Leu  Gly Lys Pro
    1010                1015                1020

Ile Ser  Lys Ala Trp Ser Gly  Ile Thr Gly Leu Phe  Asp Asn Asp
    1025                1030                1035

Ala Glu  Ala Ser Glu Glu Asp  Ser Lys Asp Lys Lys  Lys Gly Val
    1040                1045                1050

Lys Gly  Val Lys Gly Asp Thr  Lys Lys Lys Glu Lys  Met Thr Ala
    1055                1060                1065

Glu Gln  Leu Arg Glu Lys Asn  Asn Gln Ser Glu Thr  Lys Asn Leu
    1070                1075                1080

Lys Ile  Tyr Ser Asp Leu Leu  Asp Arg Ala Gln Lys  Ile Ile Glu
    1085                1090                1095

Ser Ala  Lys Gly Ile Asn Ile  Asp Gly Gly Thr Ser  Asp Ser Gly
    1100                1105                1110

Ser Asp  Ser Gly Gly Ser Ala  Ser Asp Val Gly Gly  Glu Gly Ala
```

1115 1120 1125

Glu Lys Met Tyr Lys Phe Leu Lys Gly Lys Gly Leu Ser Asp Asn
1130 1135 1140

Gln Val Gly Ala Val Met Gly Asn Leu Gln Gln Glu Ser Asn Leu
1145 1150 1155

Asp Pro Asn Ala Lys Asn Ala Ser Ser Gly Ala Phe Gly Ile Ala
1160 1165 1170

Gln Trp Leu Gly Ala Arg Lys Thr Gly Leu Glu Asn Phe Ala Lys
1175 1180 1185

Ser Lys Gly Lys Lys Ser Ser Asp Met Asp Val Gln Leu Asp Tyr
1190 1195 1200

Leu Trp Lys Glu Met Gln Ser Asp Tyr Glu Ser Asn Asn Leu Lys
1205 1210 1215

Asn Ala Gly Trp Ser Lys Gly Gly Ser Leu Glu Gln Asn Thr Lys
1220 1225 1230

Ala Phe Ala Thr Gly Phe Glu Arg Met Gly Ala Asn Glu Ala Met
1235 1240 1245

Met Gly Thr Arg Val Asn Asn Ala Lys Glu Phe Lys Lys Lys Tyr
1250 1255 1260

Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Ala Leu Ser Ser Thr
1265 1270 1275

Tyr Gln Glu Ala Met Ser Asn Pro Val Leu Thr Thr Gly Ser Asn
1280 1285 1290

Tyr Arg Gly Ser Asn Asp Ala Ser Asn Ala Ser Thr Thr Asn Arg
1295 1300 1305

Ile Thr Val Asn Val Asn Val Gln Gly Gly Asn Asn Pro Glu Glu
1310 1315 1320

Thr Gly Asp Ile Ile Gly Gly Arg Ile Arg Glu Val Leu Asp Ser
1325 1330 1335

Asn Met Asp Ile Phe Ala Asn Glu His Lys Arg Ser Tyr
1340 1345 1350

<210> 1261
<211> 808
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1261
Met Arg Arg Ile Arg Arg Pro Lys Val Arg Ile Glu Ile Val Thr Asp
1   5   10   15

Asp Asn Thr Phe Thr Leu Arg Phe Glu Asp Thr Arg Asp Tyr Asn Gly
            20   25   30

Asp Glu Phe Gly Ala Lys Leu Leu Gly Phe Gln Thr Lys Asn Ser Met
        35   40   45

Glu Asp Asp Ser Ser Val Phe Gln Ile Asn Met Ala Gly Asp Thr Tyr
    50   55   60

Trp Asp Lys Leu Val Met Ala Asn Asp Ile Ile Arg Ile Phe Ile Thr
65   70   75   80

Pro Asn Asp Asp Pro Asn Asp Lys Glu Gly Arg Gln Glu Arg Leu Ile
                85   90   95

Gln Val Gly Met Val Ser Gln Val Ser Lys Val Gly Ser Tyr Gly Asn
            100   105   110

Asp Gln Thr Gln Phe Arg Ile Thr Gly Gln Ser Phe Val Lys Pro Phe
        115   120   125

Met Lys Phe Gly Leu Gly Val Ile Gln Glu Val Gln Ala Val Leu Pro
    130   135   140

Glu Val Gly Trp Leu Ile Asp Gly Asp Gly Asp Asn Glu Val Lys Phe
145   150   155   160

Thr Gly Ser Ser Ala His Glu Val Met Thr Gly Ile Ile Arg Arg Phe
                165   170   175

Ile Pro Tyr Met Lys Tyr Asn Tyr Thr Glu Lys Thr Tyr Asn Thr Ile
            180   185   190

Asp Asn Tyr Leu Asp Tyr Asp Asp Leu Ser Ser Trp Asp Glu Phe Glu
        195   200   205

Lys Leu Thr Glu Val Ser Ala Phe Thr Asn Phe Asp Gly Ser Leu Lys
    210   215   220

Gln Leu Met Asp Met Val Thr Ala Arg Pro Phe Asn Glu Leu Phe Phe
225   230   235   240

Lys Asn Ser Glu Lys Thr Pro Gly Lys Ala Gln Leu Val Leu Arg Lys
                245   250   255

```
Thr Pro Phe Asn Pro Thr Glu Trp Arg Ala Leu Asp Met Ile Lys Val
            260                 265                 270

Pro Thr Glu Asp Phe Ile Glu Glu Asp Val Gly Lys Ser Asp Val Glu
        275                 280                 285

Thr Tyr Ser Ile Phe Thr Ala Thr Pro Ala Gly Met Leu Lys Glu Leu
    290                 295                 300

Asn Gly Asp Val Phe Ser Lys Pro Gln Phe His Pro Glu Leu Thr Asp
305                 310                 315                 320

Arg Tyr Gly Tyr Thr Lys Phe Glu Val Glu Asn Ile Tyr Leu Ser Thr
                325                 330                 335

Lys Ser Gly Ser Ala Thr Glu Asp Ser Asp Ser Ser Gly Asp Asp Asn
            340                 345                 350

Gly Thr Glu Arg Gly Thr Tyr Ser Lys Ile Met Lys Asp Leu Ser Asn
        355                 360                 365

Tyr Gly Arg Asp Asn Ile Ser Lys Gly Ile Asp Lys Tyr Thr Ser Lys
    370                 375                 380

Leu Ser Ser Lys Tyr Lys Asn Leu Lys Lys Ala Gln Ala Lys Lys Ile
385                 390                 395                 400

Ile Glu Lys Phe Val Lys Glu Gly Lys Val Thr Glu Lys Glu Tyr Glu
                405                 410                 415

Lys Ile Thr Gly Asn Lys Val Asp Asp Glu Leu Thr Ser Asp Asn Arg
            420                 425                 430

Pro Lys Leu Thr Lys Asp Lys Leu Lys Ser Ile Leu Lys Glu Lys Phe
        435                 440                 445

Lys Thr Gln Asp Asp Phe Asn Asn Ser Lys Lys Lys Lys Lys Ala Lys
    450                 455                 460

Thr Asp Ala Leu Lys Glu Leu Thr Thr Lys Tyr Arg Phe Gly Asn Lys
465                 470                 475                 480

Thr His Ala Thr Thr Leu Leu Asp Glu Tyr Ile Lys Tyr Lys Gly Glu
                485                 490                 495

Pro Pro Asn Asp Glu Ala Phe Asp Lys Tyr Leu Lys Ala Ile Glu Gly
            500                 505                 510

Val Ser Asn Val Ala Thr Asp Thr Gly Ser Asp Ala Ser Asp Ser Pro
        515                 520                 525
```

```
Leu Val Met Phe Ser Arg Met Leu Phe Asn Trp Tyr His Gly Asn Pro
    530                 535                 540

Asn Phe Tyr Ala Gly Asp Ile Ile Val Leu Gly Asp Pro Lys Tyr Asp
545                 550                 555                 560

Leu Gly Lys Arg Leu Phe Ile Glu Asp Lys Gln Arg Gly Asp Thr Trp
                565                 570                 575

Glu Phe Tyr Ile Glu Ser Val Glu His Lys Phe Asp Tyr Lys Gln Gly
            580                 585                 590

Tyr Tyr Thr Thr Val Gly Val Thr Arg Gly Leu Lys Asp Ala Ile Leu
        595                 600                 605

Glu Asp Gly Lys Gly Ser Pro His Arg Phe Ala Gly Leu Trp Asn Gln
    610                 615                 620

Ser Ser Asp Phe Met Gly Gly Leu Met Gly Glu Asp Thr Ser Lys Glu
625                 630                 635                 640

Leu Lys Glu Lys Gly Val Ala Glu Lys Gln Ser Ser Gly Gly Lys Asp
                645                 650                 655

Gly Gly Ser Asp Ser Gly Gly Ala Gln Asp Gly Gly Ser Leu Asp Ser
            660                 665                 670

Leu Lys Lys Tyr Asn Gly Lys Leu Pro Lys His Asp Pro Ser Phe Val
        675                 680                 685

Gln Pro Gly Asn Arg His Tyr Lys Tyr Gln Cys Thr Trp Tyr Ala Tyr
    690                 695                 700

Asn Arg Arg Gly Gln Leu Gly Ile Pro Val Pro Leu Trp Gly Asp Ala
705                 710                 715                 720

Ala Asp Trp Ile Gly Gly Ala Lys Gly Ala Gly Tyr Gly Val Gly Arg
                725                 730                 735

Thr Pro Lys Gln Gly Ala Cys Val Ile Trp Gln Arg Gly Val Gln Gly
            740                 745                 750

Gly Ser Pro Gln Tyr Gly His Val Ala Phe Val Glu Lys Val Leu Asp
        755                 760                 765

Gly Gly Lys Lys Ile Phe Ile Ser Glu His Asn Tyr Ala Thr Pro Asn
    770                 775                 780

Gly Tyr Gly Thr Arg Thr Ile Asp Met Ser Ser Ala Ile Gly Lys Asn
785                 790                 795                 800
```

Ala Gln Phe Ile Tyr Asp Lys Lys
805

<210> 1262
<211> 295
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1262
Met Ala Thr Asp Lys Glu Ala Lys Asp Val Ile Asp Lys Phe Ile Asp
1 5 10 15

Asn Val Phe Asn Phe Asp Val Leu Thr Lys Glu Arg Ile Lys Glu Lys
20 25 30

Asp Glu Glu Ile Lys Lys Ile Thr Thr Asp Asp Met Tyr Glu Lys Val
35 40 45

Val Tyr Ile Arg Pro Tyr Val Gly Val Ile Gln Ser Leu Asn Pro Gln
50 55 60

His Val Gln Tyr Glu Ser Phe Ser Asn Asn Gly Tyr Asp Ile Glu Ala
65 70 75 80

Glu Leu Ser Phe Arg Lys Val Ser Tyr Leu Val Asp Lys Gly Ser Ile
85 90 95

Pro Thr Asp Ser Leu Ser Thr Leu Thr Val His Leu Val Glu Arg Asn
100 105 110

Gln Glu Leu Leu Ile Asp Tyr Phe Asp Glu Ile Gln Asp Val Leu Tyr
115 120 125

Gly Glu Tyr Met Glu Glu Glu Tyr Val Phe Asp Glu Asp Val Pro Leu
130 135 140

Ser Thr Ile Leu Ala Leu Asp Leu Asn Asp Asn Leu Lys Ser Leu Ser
145 150 155 160

Asn Ile Lys Tyr Met Phe Lys Gly Ala Pro Lys Glu Asn Pro Phe Gly
165 170 175

Thr Asp Lys Asp Val Tyr Ile Asp Thr Tyr Asn Leu Leu Tyr Trp Leu
180 185 190

Tyr Leu Gly Glu Asp Glu Glu Leu Ala Tyr Pro Met Asn Ile Asn Tyr
195 200 205

Phe Phe Thr Glu Gly Arg Phe Phe Thr Ile Phe Gly Lys Gly His Lys
210 215 220

```
Tyr Lys Val Asp Val Ser Lys Phe Ile Val Gly Asp Ile Leu Phe Phe
225                 230                 235                 240


Gly Arg Ser Asp Thr Asn Ile Gly Ile Tyr Val Gly Asp Gly Glu Phe
                245                 250                 255


Ile Ser Met Met Gly Lys Phe Pro Lys Asp Glu Thr Pro Ile Gly Lys
            260                 265                 270


Tyr Lys Leu Asp Asp Tyr Trp Asn Glu Phe Asn Gly Arg Val Met Arg
        275                 280                 285


Phe Asp Glu Glu Val Tyr Ile
    290                 295


<210> 1263
<211> 848
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1263
Met Val Val Arg Phe Gln Ser Ser Met Gly Arg Ser Leu Lys Arg Val
1               5                   10                  15


Asp Ser Asp Asp Leu Asn Val Lys Gly Leu Val Leu Ala Thr Val Ser
            20                  25                  30


Lys Ile Asn Tyr Lys Tyr Gln Ser Val Glu Val Lys Val Asn Asn Leu
        35                  40                  45


Thr Leu Gly Ser Arg Ile Gly Asp Asp Gly Ser Leu Ala Val Pro Tyr
    50                  55                  60


Pro Lys Ser Phe Ile Gly Arg Thr Pro Glu Gly Ser Val Phe Gly Thr
65                  70                  75                  80


Lys Pro Leu Ile Thr Glu Gly Ser Val Val Leu Ile Gly Phe Leu Asn
                85                  90                  95


Asp Asp Ile Asn Ser Pro Ile Ile Leu Ser Val Tyr Gly Asp Asn Glu
            100                 105                 110


Gln Asn Lys Met Ile Asn Thr Asn Pro Leu Asp Gly Gly Lys Phe Asp
        115                 120                 125


Thr Glu Ser Val Tyr Lys Tyr Ser Ser Ser Leu Tyr Glu Ile Leu Pro
    130                 135                 140


Ser Leu Asn Tyr Lys Tyr Asp Asp Gly Glu Gly Thr Ser Ile Arg Thr
145                 150                 155                 160
```

```
Tyr Asn Gly Lys Ser Phe Phe Ser Met Thr Ser Gly Glu Glu Glu Lys
                165                 170                 175

Pro Gln Ala Thr Asp Phe Tyr Thr Gly Thr Glu Tyr Gln Asp Leu Phe
            180                 185                 190

Thr Ser Tyr Tyr Gly Asn Lys Thr Leu Ile Glu Pro Arg Ile Gln Lys
        195                 200                 205

Ala Pro Asn Met Leu Phe Lys His Gln Gly Val Phe Tyr Asp Asp Gly
    210                 215                 220

Thr Pro Asp Asn His Ile Thr Thr Leu Phe Ile Ser Glu Arg Gly Asp
225                 230                 235                 240

Ile Arg Ala Ser Val Leu Asn Thr Glu Thr Gln Lys Arg Thr Thr Gln
                245                 250                 255

Glu Met Ser Ser Asp Gly Ser Tyr Arg Val Ile Lys Gln Asp Asp Asp
            260                 265                 270

Leu Met Leu Asp Glu Ala Gln Val Trp Ile Glu Tyr Gly Ile Ser Glu
        275                 280                 285

Asp Asn Lys Phe Tyr Ile Lys Asn Asp Lys His Lys Phe Glu Phe Thr
    290                 295                 300

Asp Glu Gly Ile Tyr Ile Asp Asp Lys Pro Met Leu Glu Asn Leu Asp
305                 310                 315                 320

Glu Ser Ile Ala Glu Ala Met Lys Asn Leu Asn Glu Ile Gln Lys Glu
                325                 330                 335

Leu Asp Asp Ile Asn Tyr Leu Leu Glu Gly Val Gly Lys Asp Asn Leu
            340                 345                 350

Glu Glu Leu Ile Glu Ser Thr Lys Glu Ser Ile Glu Ala Ser Lys Lys
        355                 360                 365

Ala Thr Ser Asp Val Asn Arg Leu Thr Thr Gln Ile Ala Glu Val Ser
    370                 375                 380

Gly Arg Thr Glu Gly Ile Ile Thr Gln Phe Gln Lys Phe Arg Asp Glu
385                 390                 395                 400

Thr Phe Lys Asp Phe Tyr Glu Asp Ala Ser Thr Val Ile Asn Glu Val
                405                 410                 415

Asn Gln Asn Phe Pro Thr Met Lys Thr Asp Val Lys Thr Leu Lys Thr
            420                 425                 430
```

```
Lys Val Asp Asn Leu Glu Lys Thr Glu Ile Pro Asn Ile Lys Thr Arg
        435                 440                 445

Leu Thr Glu Leu Glu Asn Asn Asn Asn Asn Ala Asp Lys Ile Ile Ser
    450                 455                 460

Asp Arg Gly Glu His Ile Gly Ala Met Ile Gln Leu Glu Glu Asn Val
465                 470                 475                 480

Thr Val Pro Met Arg Lys Tyr Met Pro Ile Pro Trp Ser Lys Val Thr
                485                 490                 495

Tyr Asn Asn Ala Glu Phe Trp Asp Ser Asn Asn Pro Thr Arg Leu Val
            500                 505                 510

Val Pro Lys Gly Ile Thr Lys Val Arg Val Ala Gly Asn Val Leu Trp
        515                 520                 525

Asp Ser Asn Ala Thr Gly Gln Arg Met Leu Arg Ile Leu Lys Asn Gly
    530                 535                 540

Thr Tyr Ser Ile Gly Leu Pro Tyr Thr Arg Asp Val Ala Ile Ser Thr
545                 550                 555                 560

Ala Pro Gln Asn Gly Thr Ser Gly Val Ile Pro Val Lys Glu Gly Asp
                565                 570                 575

Tyr Phe Glu Phe Glu Ala Phe Gln Asp Ser Glu Gly Asp Arg Gln Phe
            580                 585                 590

Arg Ala Asp Pro Tyr Thr Trp Phe Ser Ile Glu Ala Ile Glu Leu Glu
        595                 600                 605

Thr Glu Thr Met Glu Lys Asp Phe Met Leu Ile Gly His Arg Gly Ala
    610                 615                 620

Thr Gly Tyr Thr Asp Glu His Thr Ile Lys Gly Tyr Gln Met Ala Leu
625                 630                 635                 640

Asp Lys Gly Ala Asp Tyr Ile Glu Leu Asp Leu Gln Leu Thr Lys Asp
                645                 650                 655

Asn Lys Leu Leu Cys Met His Asp Ser Thr Ile Asp Arg Thr Thr Thr
            660                 665                 670

Gly Thr Gly Lys Val Gly Asp Met Thr Leu Ser Tyr Ile Gln Thr Asn
        675                 680                 685

Phe Thr Ser Leu Asn Gly Glu Pro Ile Pro Ser Leu Asp Asp Val Leu
    690                 695                 700
```

```
Asn His Phe Gly Thr Lys Val Lys Tyr Tyr Ile Glu Thr Lys Arg Pro
705                 710                 715                 720

Phe Asp Ala Asn Met Asp Lys Glu Leu Leu Thr Gln Leu Lys Ala Lys
                725                 730                 735

Gly Leu Ile Gly Ile Gly Ser Glu Arg Phe Gln Val Ile Ile Gln Ser
            740                 745                 750

Phe Ala Arg Glu Ser Leu Ile Asn Ile His Asn Gln Phe Ser Asn Ile
        755                 760                 765

Pro Leu Ala Tyr Leu Thr Ser Thr Phe Ser Glu Ser Glu Met Asp Asp
    770                 775                 780

Cys Leu Ser Tyr Gly Ser Tyr Ala Ile Ala Pro Lys Tyr Thr Thr Ile
785                 790                 795                 800

Thr Lys Glu Leu Val Asp Leu Ala His Ser Lys Gly Leu Lys Val His
                805                 810                 815

Ala Trp Thr Val Asn Thr Lys Glu Glu Met Gln Ser Leu Ile Gln Met
            820                 825                 830

Gly Val Asp Gly Phe Phe Thr Asn Tyr Leu Asp Glu Tyr Lys Lys Ile
        835                 840                 845
```

<210> 1264
<211> 263
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1264

```
Met Pro Gln Ser Asp Gly Ile Ser Asn Leu His Arg Ile Ala Leu Arg
1               5                   10                  15

Phe Pro Lys Glu Gly Gly Gly Tyr Asp Met Tyr Arg Phe Lys Val Asn
            20                  25                  30

Pro Glu Asn Tyr Thr Ile Asp Ser Pro Gln Arg Thr Thr Ala Ile Lys
        35                  40                  45

Thr Lys Ser Asp Ile Val Ile Glu Asp Tyr Gly Lys Asp Ile Glu Val
    50                  55                  60

Ile Asn Phe Thr Gly Thr Thr Gly Phe Arg Pro Val Arg Glu Ala Asp
65                  70                  75                  80

Gly Leu Lys Thr Gly Lys Gln Lys Met Glu Glu Leu Gln Ser Arg Val
```

85 90 95

Ser Glu Tyr Ala Met Gln Gly Gly Ser Gly Asn Val Ser Gly Ser Tyr
100 105 110

Leu Gln Phe Phe Asn Phe Thr Asp Asp Ser Tyr Tyr Lys Val His Leu
115 120 125

Ala Pro Gln Gly Leu Lys Ile Thr Arg Ser Lys Asp Glu Pro Leu Leu
130 135 140

Phe Arg Tyr Glu Ile Thr Leu Val Val Ile Gly Ser Leu Thr Glu Ala
145 150 155 160

Asp Arg Ser Ala Val Thr Thr Glu Glu Phe Gly Asn Val Lys Pro Asn
165 170 175

Ala Ser Gln Arg Val Asp Glu Gly Ile Lys Glu Leu Asp Lys Asn Ala
180 185 190

Arg Lys Thr Arg Asp Arg Asn Asn Gln Glu Ile Ser Arg Arg Glu Asn
195 200 205

Thr Ile Pro Lys Ser Thr Gly Asp Asn Thr Asn Glu Gly Asn Arg Leu
210 215 220

Lys Gln Ser Phe Pro Ser Ser Ser Ile Tyr Asn Pro Arg Gln Ser Thr
225 230 235 240

Asn Gly Leu Lys Gly Asn Ile Asp Asn Met Ala Leu Ile Ile Gly Tyr
245 250 255

Gly Asp Gly Gly Val Ser Ser
260

<210> 1265
<211> 174
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1265
Met Asn Asn Phe Ile Pro Gln Pro Gln Gly Leu Leu Arg Phe Leu Asn
1 5 10 15

Ala Leu Asp Thr Asp Leu Thr Ser Ser His Met Asn Leu Leu Asp Glu
20 25 30

Glu Val Ser Phe Val Ser Lys Phe Tyr Thr Pro Gln Leu Gln Leu Ser
35 40 45

```
Glu Leu Ala Lys Lys Val Leu Thr Asn Ile Lys Thr Asp Asp Ile Pro
    50                  55                  60

Val Leu Glu Arg Glu Phe Asn Asp Asn Thr Ile Ile His Lys Ala Asn
65                  70                  75                  80

Asp Thr Leu Leu Lys Val Gln Ala Pro Arg Met Tyr Met Ile Leu Gln
                85                  90                  95

Ser Ile Val Leu Glu Ala Tyr Ala Ile Val Asn Cys Phe Val Glu Asn
            100                 105                 110

Pro Ser Ser Leu Lys Tyr Leu Thr Glu Glu Asp Val Ser Ile Thr Arg
        115                 120                 125

Glu Asn Leu Asn Tyr Val Ala Asp Tyr Leu Gly Asn Tyr Asp Asp Tyr
    130                 135                 140

Asn Ser Val Val Leu Asp Leu Arg Asp Leu Asp Leu Cys Phe Ser Ala
145                 150                 155                 160

Ile Glu Leu Gln Leu Pro Leu Ile Lys Lys Glu Ala Asn Val
                165                 170


<210> 1266
<211> 234
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1266
Met Arg Phe Lys Lys His Val Val Gln His Glu Glu Thr Met Gln Ala
1               5                   10                  15

Ile Ala Gln Arg Tyr Tyr Gly Asp Val Ser Tyr Trp Ile Asp Leu Val
            20                  25                  30

Glu His Asn Asn Leu Lys Tyr Pro Tyr Leu Val Glu Thr Asp Glu Glu
        35                  40                  45

Lys Met Lys Asp Pro Glu Arg Leu Ala Ser Thr Gly Asp Thr Leu Ile
    50                  55                  60

Ile Pro Ile Glu Ser Asp Leu Thr Asp Val Ser Ala Lys Glu Ile Asn
65                  70                  75                  80

Ser Arg Asp Lys Asp Val Leu Val Glu Leu Ala Leu Gly Arg Asp Leu
                85                  90                  95

Asn Ile Thr Ala Asp Glu Lys Tyr Phe Asn Glu His Gly Thr Ser Asp
            100                 105                 110
```

Asn Ile Leu Ala Phe Ser Thr Asn Gly Asn Gly Asp Leu Asp Thr Val
115 120 125

Lys Gly Ile Asp Asn Met Lys Gln Gln Leu Gln Ala Arg Leu Leu Thr
130 135 140

Pro Arg Gly Ser Leu Met Leu His Pro Asn Tyr Gly Ser Asp Leu His
145 150 155 160

Asn Leu Phe Gly Leu Asn Ile Pro Glu Gln Ala Thr Leu Ile Glu Met
165 170 175

Glu Val Leu Arg Thr Leu Thr Ser Asp Asn Arg Val Lys Ser Ala Asn
180 185 190

Leu Ile Asp Trp Lys Ile Gln Gly Asn Val Tyr Ser Gly Gln Phe Ser
195 200 205

Val Glu Ile Lys Ser Val Glu Glu Ser Ile Asn Phe Val Leu Gly Gln
210 215 220

Asp Glu Glu Gly Ile Phe Ala Leu Phe Glu
225 230

<210> 1267
<211> 348
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1267
Met Lys Thr Arg Lys Leu Thr Asn Ile Leu Ser Lys Leu Ile Asp Lys
1 5 10 15

Thr Met Ala Gly Thr Ser Lys Ile Thr Asp Phe Thr Pro Gly Ser Ala
20 25 30

Ser Arg Ser Leu Leu Glu Ala Val Ser Leu Glu Ile Glu Gln Phe Tyr
35 40 45

Ile Leu Thr Lys Glu Asn Ile Asp Trp Gly Ile Gln Glu Gly Ile Ile
50 55 60

Glu Ala Phe Asp Phe Gln Lys Arg Gln Ser Lys Arg Ala Tyr Gly Asp
65 70 75 80

Val Thr Ile Gln Phe Tyr Gln Pro Leu Asp Met Arg Met Tyr Ile Pro
85 90 95

Ala Gly Thr Thr Phe Thr Ser Thr Arg Gln Glu Tyr Pro Gln Gln Phe
100 105 110

```
Glu Thr Leu Val Asp Tyr Tyr Ala Glu Pro Asp Ser Thr Glu Ile Val
        115                 120                 125

Val Glu Val Tyr Cys Lys Glu Thr Gly Val Ala Gly Asn Val Pro Glu
    130                 135                 140

Gly Thr Ile Asn Thr Ile Ala Ser Gly Ser Ser Leu Ile Arg Ser Val
145                 150                 155                 160

Asn Asn Glu Tyr Ser Phe Asn Thr Gly Thr Lys Glu Glu Ser Gln Glu
                165                 170                 175

Asp Phe Lys Arg Arg Phe His Ser Phe Val Glu Ser Arg Gly Arg Ala
            180                 185                 190

Thr Asn Lys Ser Val Arg Tyr Gly Ala Leu Gln Ile Pro Asp Val Glu
        195                 200                 205

Gly Val Tyr Val Tyr Glu Glu Thr Gly His Ile Thr Val Phe Ala His
    210                 215                 220

Asp Arg Asn Gly Asn Leu Ser Asp Thr Leu Lys Glu Asp Ile Ile Asp
225                 230                 235                 240

Ala Leu Gln Asp Tyr Arg Pro Ser Gly Ile Met Leu Asp Val Thr Gly
                245                 250                 255

Val Glu Lys Glu Glu Val Asn Val Ser Ala Thr Val Thr Ile Ser Asn
            260                 265                 270

Lys Ser Arg Ile Gly Asp Thr Leu Gln Lys His Ile Glu Ser Val Ile
        275                 280                 285

Arg Ser Tyr Leu Asn Asn Leu Lys Thr Ser Asp Asp Leu Ile Ile Thr
    290                 295                 300

Asp Leu Ile Gln Ala Ile Met Asn Ile Asp Asp Val Leu Ile Tyr Asp
305                 310                 315                 320

Val Ser Phe Asp Asn Leu Asp Glu Asn Ile Ile Val Pro Pro Gln Gly
                325                 330                 335

Ile Ile Arg Ala Gly Glu Ile Lys Val Glu Leu Lys
            340                 345
```

<210> 1268
<211> 1019
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: Bacteriophage F125/10

<400> 1268

```
Val Ala Asn Phe Leu Lys Asn Leu His Pro Leu Leu Arg Arg Asp Arg
1               5                  10                  15

Asn Lys Lys Asp Asn Gln Asp Pro Asn Phe Ala Leu Ile Asp Ala Leu
            20                  25                  30

Asn Glu Glu Met Asn Gln Val Glu Lys Asp Ala Ile Glu Ser Lys Leu
        35                  40                  45

Gln Ser Ser Leu Lys Thr Ser Thr Ser Glu Tyr Leu Asp Lys Phe Gly
    50                  55                  60

Asp Trp Phe Gly Val Tyr Arg Lys Thr Asp Glu Asn Asp Asp Val Tyr
65                  70                  75                  80

Arg Ala Arg Ile Ile Lys Tyr Leu Leu Leu Lys Arg Gly Thr Asn Asn
                85                  90                  95

Ala Ile Ile Asp Ala Ile Lys Asp Tyr Leu Gly Arg Asp Asp Ile Asp
            100                 105                 110

Val Ser Val Tyr Glu Pro Phe Thr Asn Ile Phe Tyr Thr Asn Lys Ser
        115                 120                 125

His Leu Asn Gly Glu Asp His Leu Met Gly Tyr Tyr Tyr Arg Phe Ala
    130                 135                 140

Val Ile Asn Val Ser Ile Gly Asp Tyr Phe Pro Val Glu Ile Ile Asp
145                 150                 155                 160

Val Ile Asn Glu Phe Lys Pro Ala Gly Val Thr Leu Tyr Val Thr Tyr
                165                 170                 175

Asp Gly Ala Ser Thr Ile Arg Gly Gly Ala Ile Ile Lys Trp Leu Asp
            180                 185                 190

Gly Leu Pro Lys Ile Glu Thr Tyr Gln Glu Phe Asp Arg Phe Thr Gly
        195                 200                 205

Tyr Asp Asp Thr Phe Tyr Gly His Ile Asn Met Asn Gln Ser Lys Asp
    210                 215                 220

Thr Asp Asn Ser Ser Ser Asp Ile Phe Lys Thr Asn His Ser Leu Ile
225                 230                 235                 240

Asn Ser Leu Asp Val Leu Thr Gly Ser Ser Ser Val Gly Arg Gln Tyr
                245                 250                 255

Ile Asn Tyr Gly Tyr Val Thr Ser Tyr Val Tyr Asn Pro Gly Met Thr
```

260 265 270

Ser Ser Val Asn Gln Ile Ser Ala Ser Thr Glu Gly Arg Gly Gln Glu
275 280 285

Val Pro Thr Asp Tyr Tyr Met Tyr Thr Ser Thr Lys Asn Asn Asn Thr
290 295 300

Val Glu Leu Ser Met Gln Thr Thr Ser Gly Val Ser Tyr Leu Tyr Asn
305 310 315 320

Asn Phe Asn Phe Arg Asp Tyr Met Ser Lys Tyr Arg Pro Gln Val Asp
325 330 335

Leu Gln Ser Asp Glu Ala Arg Arg Ile Val Ser Asp Tyr Ile Lys Glu
340 345 350

Leu Ser Ile Asp Tyr Tyr Leu Ser Ala Val Ile Pro Pro Asp Glu Ser
355 360 365

Ile Glu Ile Lys Leu Gln Val Tyr Asp Phe Ser Ile Asn Arg Trp Leu
370 375 380

Thr Val Ser Ile Asn Asn Leu Ser Phe Tyr Glu Lys Asn Ile Gly Ser
385 390 395 400

Asn Ile Gly Tyr Ile Lys Asp Tyr Leu Asn Ser Glu Leu Asn Met Phe
405 410 415

Thr Arg Leu Glu Ile Asn Ala Gly Lys Arg Asp Ser Val Asp Ile Lys
420 425 430

Val Asn Tyr Leu Asp Leu Met Phe Tyr Tyr Tyr Glu Arg Gly Ile Tyr
435 440 445

Thr Ile Lys Pro Tyr Lys Ala Leu Ile Glu Asn Tyr Leu Asp Ile Ser
450 455 460

Arg Glu Thr Tyr Val Glu Ala Phe Lys Ile Ala Ser Leu Ser Asn Gly
465 470 475 480

Asp Ile Ile Thr Lys Thr Gly Phe Gln Pro Ile Gly Tyr Leu Lys Leu
485 490 495

Val Gly Asn Tyr Glu Asn Thr Arg Pro Ser Thr Ile Asn Ile Val Ala
500 505 510

Lys Asp Thr Asp Asn Asn Pro Ile Glu Ser Asn Glu Leu Asp Val Tyr
515 520 525

Asn Thr Val Glu Asn Arg Asn Leu Leu Gln Ser Tyr Lys Gly Ala Asn

530 535 540

Thr Ile Ala Arg Glu Ile Thr Ser Thr Lys Glu Phe Thr Val Ser Gly
545 550 555 560

Trp Ala Lys Glu Ile Tyr Ser Thr Asn Tyr Leu Ser Lys Val Leu Lys
565 570 575

Pro Gly Lys Val Tyr Thr Leu Ser Phe Asp Ile Glu Ile Thr Gly Asn
580 585 590

Asp Leu Thr Leu Lys Ser Tyr Ser Asp Asn His Gly Ile Tyr Leu Tyr
595 600 605

Ser Asn Thr Lys Gly Ile Val Val Asn Gly Val Lys Ser Met Glu Arg
610 615 620

Thr Ile Gly Asn Lys Val Ser Val Thr Gln Thr Phe Thr Ala Pro Thr
625 630 635 640

Ile Thr Asp His Arg Leu Leu Ile Tyr Thr Gly Arg Tyr Thr Ser Asp
645 650 655

Gly Lys Ala Ser Thr Pro Pro Val Phe Phe Asn Thr Val Lys Ile Thr
660 665 670

Glu Leu Lys Leu Ser Glu Gly Thr Ser Asn Leu Glu Tyr Ser Pro Ala
675 680 685

Pro Glu Asp Lys Pro Asn Val Ile Glu Lys Gly Ile Lys Phe Asn Asn
690 695 700

Ile Leu Thr Asn Ile Gln Thr Leu Ser Ile Asn Ser Asp Thr Ile Leu
705 710 715 720

Lys Asn Val Thr Leu Tyr Tyr Ser Tyr Tyr Gly Asp Asn Trp Val Glu
725 730 735

Leu Lys Thr Leu Gly Asn Ile Ser Thr Gly Glu Thr Thr Glu Thr Asn
740 745 750

Asn Leu Ile Asp Leu Tyr Gly Leu Gln Thr Val Asp Tyr Ser Asn Ile
755 760 765

Asn Pro Met Ser Lys Val Ser Leu Arg Ser Ile Trp Asn Val Lys Leu
770 775 780

Gly Glu Leu Asn Asn Gln Glu Gly Ser Leu Ser Asn Met Pro Asn Asp
785 790 795 800

Tyr Phe Asn Ala Val Trp Gln Asp Ile Asp Lys Leu Ser Asp Ile Glu

805 810 815

Ile Gly Ser Met Arg Met Val Lys Asp Thr Glu Gly Gly Val Phe Asp
820 825 830

Gly Ala Thr Gly Glu Ile Ile Lys Ala Thr Leu Phe Asn Val Gly Ser
835 840 845

Tyr Thr Asp Leu Asp Met Leu Ala Tyr Thr Leu Thr Asn Tyr Thr Glu
850 855 860

Pro Leu Thr Leu Gly Ser Ser Arg Leu Ile Ser Glu Leu Lys Glu Glu
865 870 875 880

Leu Leu Thr Ser Glu Ser Phe Asn Val Asp Asn Arg Ile Lys Val Ile
885 890 895

Asp Ser Ile Tyr Glu Glu Leu Pro Asn Thr Ser Ile Ile Lys Asn Gly
900 905 910

Phe Val Glu Arg Glu Val Thr Gly Ser Lys Tyr Leu Asp Tyr Gly Leu
915 920 925

Tyr Glu Pro Ile Glu Asp Gly Thr Arg Tyr Lys Leu Ile Val Glu Gly
930 935 940

Glu Phe Lys Asp Asn Ile Glu Phe Ile Tyr Leu Tyr Asn Ser Asn Pro
945 950 955 960

Asn Phe Asn Glu Thr Phe Ile Tyr Pro Ser Glu Ile Ile Asn Gly Val
965 970 975

Ala Glu Lys Glu Phe Ile Ala Lys Pro Ser Thr Glu Asp Lys Pro Arg
980 985 990

Leu Asn Thr Asp Val Arg Ile Tyr Ile Arg Pro Tyr Asp Ser Thr Ile
995 1000 1005

Ser Lys Val Arg Arg Val Glu Leu Arg Lys Val
1010 1015

<210> 1269
<211> 173
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1269
Met Ala Ile Ala Thr Tyr Asn Ser His Val Glu Leu Ala Lys Tyr Leu
1 5 10 15

Val Ser Lys Ala Asp Ser Val Tyr Leu Thr Ile Gly Lys Ser Thr Pro
20 25 30

Trp Ser Asn Glu Thr Asn Pro Pro Gln Pro Asp Glu Asn Ala Thr Val
35 40 45

Leu Gln Glu Val Ile Gly Tyr Lys Lys Ala Thr Lys Val Thr Leu Val
50 55 60

Arg Pro Ser Lys Ser Pro Glu Asp Asp Asn Lys Asn Leu Ile Ser Tyr
65 70 75 80

Gly Asn Lys Ser Trp Val Glu Val Thr Pro Glu Asn Ala Lys Ala Glu
85 90 95

Gly Ala Lys Trp Val Tyr Leu Glu Ser Ser Ile Val Gly Asp Glu Leu
100 105 110

Pro Leu Gly Thr Tyr Arg Gln Val Gly Phe Val Met Asp Leu Val Ala
115 120 125

Lys Ser Gly Ile Ser Lys Phe Asn Leu Val Pro Ser Glu Val Glu Ser
130 135 140

Thr Gly Thr Leu Leu Phe Phe Asp Asn Lys Gln Phe Gln Asn Arg Ser
145 150 155 160

Glu Gln Thr Thr Ala Lys Glu Arg Phe Ile Val Glu Val
165 170

<210> 1270
<211> 1152
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1270
Met Ala Ile Asn Phe Lys Gly Ser Pro Tyr Leu Asp Arg Phe Asp Pro
1 5 10 15

Ser Lys Asp Arg Thr Lys Val Leu Phe Asn Pro Asp Arg Pro Leu Gln
20 25 30

Gln Ala Glu Leu Asn Glu Met Gln Ser Ile Asp Gln Tyr Tyr Leu Lys
35 40 45

Asn Leu Gly Asp Ala Ile Phe Lys Asp Gly Asp Lys Gln Ser Gly Leu
50 55 60

Gly Phe Thr Leu Ser Glu Asp Asn Val Leu Thr Val Asn Pro Gly Tyr
65 70 75 80

```
Val Tyr Ile Asn Gly Lys Ile Arg Tyr Tyr Asp Asn Asp Asp Ser Val
                85                  90                  95

Lys Ile Thr Gly Val Gly Lys Glu Thr Ile Gly Ile Lys Leu Thr Glu
            100                 105                 110

Arg Ile Val Thr Pro Asp Glu Asp Ala Ser Leu Leu Asp Gln Thr Ser
        115                 120                 125

Gly Val Pro Ser Tyr Phe Ser Lys Gly Ala Asp Arg Leu Glu Glu Lys
    130                 135                 140

Met Ser Leu Thr Val Asn Asp Pro Thr Ser Ala Thr Ile Tyr Thr Phe
145                 150                 155                 160

Met Asp Gly Asp Leu Tyr Ile Gln Ser Thr Asn Ala Glu Met Asp Lys
                165                 170                 175

Ile Asn Lys Val Leu Ala Glu Arg Thr Tyr Asp Glu Ser Gly Ser Tyr
            180                 185                 190

Lys Val Asn Gly Phe Glu Leu Phe Ser Glu Gly Asn Ala Glu Asp Asp
        195                 200                 205

Asp His Val Ser Val Val Val Asp Ala Gly Lys Ala Tyr Val Lys Gly
    210                 215                 220

Phe Lys Val Asp Lys Pro Val Ser Thr Arg Ile Ser Val Pro Lys Ser
225                 230                 235                 240

Tyr Asp Leu Gly Thr Ala Glu Asn Glu Ser Thr Ile Phe Asn Lys Ser
                245                 250                 255

Asn Asn Ser Ile Ser Leu Ala Asn Ser Pro Val Lys Glu Ile Arg Arg
            260                 265                 270

Val Thr Gly Gln Val Leu Ile Glu Lys Glu Arg Val Thr Arg Gly Ala
        275                 280                 285

Gln Gly Asp Gly Gln Asp Phe Leu Ser Asn Asn Thr Ala Phe Glu Ile
    290                 295                 300

Val Lys Val Trp Thr Glu Thr Ser Pro Gly Val Thr Thr Lys Glu Tyr
305                 310                 315                 320

Lys Gln Gly Glu Asp Phe Arg Leu Thr Asp Gly Gln Thr Ile Asp Trp
                325                 330                 335

Ser Pro Gln Gly Gln Glu Pro Ser Gly Gly Thr Ser Tyr Tyr Val Ser
            340                 345                 350
```

```
Tyr Lys Tyr Asn Lys Arg Met Glu Ala Gly Lys Asp Tyr Glu Val Thr
        355                 360                 365

Thr Gln Gly Glu Gly Leu Ser Lys Lys Trp Tyr Ile Asn Phe Thr Pro
    370                 375                 380

Ser Asn Gly Ala Lys Pro Ile Asp Gln Thr Val Val Leu Val Asp Tyr
385                 390                 395                 400

Thr Tyr Tyr Leu Ala Arg Lys Asp Ser Val Phe Ile Asn Lys Tyr Gly
                405                 410                 415

Asp Ile Ala Ile Leu Pro Gly Glu Pro Asn Ile Met Arg Leu Val Thr
            420                 425                 430

Pro Pro Leu Asn Thr Asp Pro Glu Asn Leu Gln Leu Gly Thr Val Thr
        435                 440                 445

Val Leu Pro Asp Ser Asp Glu Ala Val Cys Ile Ser Phe Ala Ile Thr
    450                 455                 460

Arg Leu Ser Met Glu Asp Leu Gln Lys Val Lys Thr Arg Val Asp Asn
465                 470                 475                 480

Leu Glu Tyr Asn Gln Ala Val Asn Ala Leu Asp Asp Gly Ala Met Glu
                485                 490                 495

Gly Gln Asn Pro Leu Thr Leu Arg Ser Val Phe Ser Glu Gly Phe Ile
            500                 505                 510

Ser Leu Asp Lys Ala Asp Ile Thr His Pro Asp Phe Gly Ile Val Phe
        515                 520                 525

Ser Phe Glu Asp Ala Glu Ala Thr Leu Ala Tyr Thr Glu Ala Val Asn
    530                 535                 540

Gln Pro Lys Ile Ile Pro Gly Asp Thr Thr Ala His Ile Trp Gly Arg
545                 550                 555                 560

Leu Ile Ser Ala Pro Phe Thr Glu Glu Arg Thr Ile Tyr Gln Gly Gln
                565                 570                 575

Ala Ser Glu Thr Leu Asn Val Asn Pro Tyr Asn Ile Pro Asn Lys Gln
            580                 585                 590

Gly Val Leu Lys Leu Thr Pro Ser Glu Asp Asn Trp Ile Asp Thr Glu
        595                 600                 605

Asn Val Thr Ile Thr Glu Gln Lys Thr Lys Lys Val Thr Met Lys Arg
    610                 615                 620
```

```
Phe Trp Arg His Asn Glu Ser Tyr Tyr Gly Glu Thr Glu His Tyr Leu
625                 630                 635                 640

Tyr Ser Asn Leu Gln Leu Asp Ala Gly Gln Lys Trp Lys Gly Glu Thr
                645                 650                 655

Tyr Ala Tyr Asp Arg Glu His Gly Arg Thr Gly Thr Leu Leu Glu Ser
            660                 665                 670

Gly Gly Gln Arg Thr Leu Glu Glu Met Ile Glu Phe Ile Arg Ile Arg
        675                 680                 685

Asp Val Ser Phe Glu Val Lys Gly Leu Asn Pro Asn Asp Asn Asn Leu
    690                 695                 700

Tyr Leu Leu Phe Asp Gly Val Arg Cys Ala Ile Thr Pro Ala Thr Gly
705                 710                 715                 720

Tyr Arg Lys Gly Ser Glu Asp Gly Thr Ile Met Thr Asp Ala Lys Gly
                725                 730                 735

Thr Ala Lys Gly Lys Phe Thr Ile Pro Ala Gly Ile Arg Cys Gly Asn
            740                 745                 750

Arg Glu Val Thr Leu Lys Asn Ala Asn Ser Thr Ser Ala Thr Thr Tyr
        755                 760                 765

Thr Ala Gln Gly Arg Lys Lys Thr Val Gln Asp Ile Ile Ile Arg Thr
    770                 775                 780

Arg Val Thr Val Asn Leu Val Asp Pro Leu Ala Gln Ser Phe Gln Tyr
785                 790                 795                 800

Asp Glu Asn Arg Thr Ile Ser Ser Leu Gly Leu Tyr Phe Ala Ser Lys
                805                 810                 815

Gly Asp Lys Gln Ser Asn Val Val Ile Gln Ile Arg Gly Met Gly Asp
            820                 825                 830

Gln Gly Tyr Pro Asn Lys Thr Ile Tyr Ala Glu Thr Val Met Asn Ala
        835                 840                 845

Asp Asp Ile Lys Val Ser Asn Asn Ala Ser Ala Glu Thr Arg Val Tyr
    850                 855                 860

Phe Asp Asp Pro Met Met Ala Glu Gly Gly Lys Glu Tyr Ala Ile Val
865                 870                 875                 880

Ile Ile Thr Glu Asn Ser Asp Tyr Thr Met Trp Val Gly Thr Arg Thr
                885                 890                 895
```

```
Lys Pro Lys Ile Asp Lys Pro Asn Glu Val Ile Ser Gly Asn Pro Tyr
            900                 905                 910

Leu Gln Gly Val Leu Phe Ser Ser Ser Asn Ala Ser Thr Trp Thr Pro
        915                 920                 925

His Gln Asn Ser Asp Leu Lys Phe Gly Ile Tyr Thr Ser Lys Phe Asn
    930                 935                 940

Glu Thr Ala Thr Ile Glu Phe Glu Pro Ile Lys Asp Val Ser Ala Asp
945                 950                 955                 960

Arg Ile Val Leu Met Ser Thr Tyr Leu Thr Pro Glu Arg Thr Gly Cys
                965                 970                 975

Thr Trp Glu Met Lys Leu Ile Leu Asp Asp Met Ala Ser Ser Thr Thr
            980                 985                 990

Phe Asp Gln Leu Lys Trp Glu Pro  Ile Gly Asn Tyr Gln  Asp Leu Asp
        995                 1000                1005

Val Leu  Gly Leu Ala Arg Gln  Val Lys Leu Arg Ala  Thr Phe Glu
    1010                1015                1020

Ser Asn  Arg Tyr Ile Ser Pro  Leu Met Ser Ser Ser  Asp Leu Thr
    1025                1030                1035

Phe Thr  Thr Phe Leu Thr Glu  Leu Thr Gly Ser Tyr  Val Gly Arg
    1040                1045                1050

Ala Ile  Asp Met Thr Glu Ala  Pro Tyr Asn Thr Val  Arg Phe Ser
    1055                1060                1065

Tyr Glu  Ala Phe Leu Pro Lys  Gly Thr Lys Val Val  Pro Lys Tyr
    1070                1075                1080

Ser Ala  Asp Asp Gly Lys Thr  Trp Lys Thr Phe Thr  Lys Ser Pro
    1085                1090                1095

Thr Thr  Thr Arg Ala Asn Asn  Glu Phe Thr Arg Tyr  Val Ile Asp
    1100                1105                1110

Glu Lys  Val Lys Ser Ser Gly  Thr Asn Thr Lys Leu  Gln Val Arg
    1115                1120                1125

Leu Asp  Leu Ser Thr Glu Asn  Ser Phe Leu Arg Pro  Arg Val Arg
    1130                1135                1140

Arg Leu  Met Val Thr Thr Arg  Asp Glu
    1145                1150
```

<210> 1271
<211> 52
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1271
Met Pro Arg Glu Val Arg Asp Pro Tyr Ser Gln Ala Lys Leu Phe Ile
1 5 10 15

Pro Thr Val Glu Glu Lys Ser Ile Lys Glu Leu Glu Lys Thr Tyr Lys
20 25 30

Glu Lys Ile Asp Glu Ala Thr Lys Leu Ile Asn Glu Leu Lys Lys Glu
35 40 45

Arg Gly Glu Lys
50

<210> 1272
<211> 640
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1272
Met Ala Phe Asn Tyr Thr Pro Leu Thr Glu Thr Gln Lys Leu Lys Asp
1 5 10 15

Met Tyr Pro Lys Val Asn Asp Ile Gly Asn Phe Leu Lys Thr Glu Val
20 25 30

Asn Leu Ser Asp Val Lys Gln Ile Ser Gln Pro Asp Phe Asn Asn Ile
35 40 45

Leu Ala Ser Ile Pro Asp Ser Gly Asn Tyr Tyr Val Thr Asn Ser Lys
50 55 60

Gly Ala Pro Ser Gly Glu Ala Thr Ala Gly Phe Val Arg Leu Asp Lys
65 70 75 80

Arg Asn Val Asn Tyr Tyr Lys Ile Tyr Tyr Ser Pro Tyr Ser Ser Asn
85 90 95

Lys Met Tyr Ile Lys Thr Tyr Ala Asn Gly Thr Val Tyr Asp Trp Ile
100 105 110

Ser Phe Lys Leu Asp Glu Gly Asn Leu Tyr Asn Glu Gly Asn Thr Leu
115 120 125

Asn Val Lys Glu Leu Thr Glu Ser Thr Thr Gln Tyr Ala Thr Leu Val

130 135 140

Asn Pro Pro Lys Glu Asn Leu Asn Thr Gly Trp Val Asn Tyr Lys Glu
145 150 155 160

Ser Lys Asn Gly Val Ser Ser Leu Val Glu Phe Asn Pro Val Asn Ser
165 170 175

Thr Ser Thr Phe Lys Met Ile Arg Lys Leu Pro Val Gln Glu Gln Lys
180 185 190

Pro Asn Leu Leu Lys Asp Ser Leu Phe Val Tyr Pro Glu Thr Ser Tyr
195 200 205

Ser Asn Ile Lys Thr Asp Asn Trp Asp Thr Pro Pro Phe Trp Gly Tyr
210 215 220

Ser Ser Asn Ser Gly Arg Ser Gly Val Arg Phe Arg Gly Glu Asn Thr
225 230 235 240

Val Gln Ile Asp Asp Gly Ser Asn Thr Tyr Pro Leu Val Val Ser Asn
245 250 255

Arg Phe Lys Met Gly Lys Glu Leu Ser Val Gly Asp Thr Val Thr Val
260 265 270

Ser Val Tyr Ala Lys Ile Asn Asp Pro Ala Leu Leu Lys Asp Asn Leu
275 280 285

Val Tyr Phe Glu Leu Ala Gly Tyr Asp Thr Val Asp Asp Thr Ser Lys
290 295 300

Asn Pro Tyr Thr Gly Gly Arg Arg Glu Ile Thr Ala Ser Glu Ile Thr
305 310 315 320

Thr Glu Trp Lys Lys Tyr Ser Phe Thr Phe Thr Ile Pro Glu Asn Thr
325 330 335

Ile Gly Ala Ser Gly Val Lys Val Asn Tyr Val Ser Leu Leu Leu Arg
340 345 350

Met Asn Cys Ser Ser Ser Lys Gly Asn Gly Ala Val Val Tyr Tyr Ala
355 360 365

Leu Pro Lys Leu Glu Lys Ser Pro Lys Val Thr Pro Phe Ile Thr His
370 375 380

Glu Asn Asp Val Arg Lys Tyr Asp Glu Ile Trp Ser Asn Trp Gln Glu
385 390 395 400

Val Ile Ser Lys Asp Glu Leu Lys Gly His Ser Pro Val Asp Ile Glu

405 410 415

Tyr Asn Asp Tyr Phe Lys Tyr Gln Trp Trp Lys Ser Glu Val Asn Glu
420 425 430

Lys Ser Leu Lys Asp Leu Ala Met Thr Val Pro Gln Gly Tyr His Thr
435 440 445

Phe Tyr Cys Gln Gly Ser Ile Ala Gly Thr Pro Lys Gly Arg Ser Ile
450 455 460

Arg Gly Thr Ile Gln Val Asp Tyr Asp Lys Gly Asp Pro Tyr Arg Ala
465 470 475 480

Asn Lys Phe Val Lys Leu Leu Phe Thr Asp Thr Glu Gly Ile Pro Tyr
485 490 495

Thr Leu Tyr Tyr Gly Gly Tyr Asn Gln Gly Trp Lys Leu Leu Lys Gln
500 505 510

Ser Glu Thr Ser Thr Leu Leu Trp Glu Gly Thr Leu Asp Phe Gly Ser
515 520 525

Thr Glu Ala Val Asn Leu Asn Asp Ser Leu Asp Asn Tyr Asp Leu Ile
530 535 540

Glu Val Thr Tyr Trp Thr Arg Ser Ala Gly His Phe Ser Thr Lys Arg
545 550 555 560

Leu Asp Ile Lys Asn Thr Ser Asn Leu Leu Tyr Ile Arg Asp Phe Asn
565 570 575

Ile Ser Asn Asp Ser Thr Gly Ser Ser Val Asp Phe Phe Glu Gly Tyr
580 585 590

Cys Thr Phe Pro Thr Arg Ala Ser Val Gln Pro Gly Met Val Lys Ser
595 600 605

Ile Thr Leu Asp Gly Ser Thr Asn Thr Thr Lys Val Ala Ser Trp Asn
610 615 620

Glu Lys Glu Arg Ile Lys Val Tyr Asn Ile Met Gly Ile Asn Arg Gly
625 630 635 640

<210> 1273
<211> 123
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1273

```
Met Ala Val Lys Tyr Asp Ile Gly Asn Asn Glu Ile Val Leu His Leu
1               5                   10                  15

Arg Glu Gly Lys Tyr Ile Thr Gly Phe Thr Thr Val Gly Gly Tyr Asp
            20                  25                  30

Lys Glu Leu Gly Gln Val Lys Val Asn Arg Glu Ile Leu Pro Ala Tyr
        35                  40                  45

Phe Phe Asp Asn Phe Ala Tyr Glu Arg Tyr Leu Tyr Tyr Ser Lys Pro
    50                  55                  60

Glu Glu Val Ile Glu Asn Lys Asn Tyr Val Pro Pro Gln Ile Asn Asp
65                  70                  75                  80

Asp Glu Glu Ser Gln Gln Ile Thr Val Pro Lys Glu Gln Tyr Asp Ser
                85                  90                  95

Leu Lys Glu Glu Leu Glu Leu Met Arg Lys Gln Gln Glu Ala Met Met
            100                 105                 110

Glu Met Leu Gln Lys Leu Leu Gly Gln Lys Gly
        115                 120


<210> 1274
<211> 458
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1274
Met Ala Leu Asn Phe Thr Thr Ile Thr Glu Asn Asn Val Ile Arg Asp
1               5                   10                  15

Leu Thr Thr Gln Val Asn Asn Ile Gly Glu Glu Leu Thr Lys Glu Arg
            20                  25                  30

Asn Ile Phe Asp Ile Thr Asp Asp Leu Val Tyr Asn Phe Asn Lys Ser
        35                  40                  45

Gln Lys Ile Lys Leu Thr Asp Asp Lys Gly Leu Thr Lys Ser Tyr Gly
    50                  55                  60

Asn Ile Thr Ala Leu Arg Asp Ile Lys Glu Pro Gly Tyr Tyr Tyr Ile
65                  70                  75                  80

Gly Ala Arg Thr Leu Ala Thr Leu Leu Asp Arg Pro Asp Met Glu Ser
                85                  90                  95

Leu Asp Val Val Leu His Val Val Pro Leu Asp Thr Ser Ser Lys Val
            100                 105                 110
```

```
Val Gln His Leu Tyr Thr Leu Ser Thr Asn Asn Asn Gln Ile Lys Met
        115                 120                 125

Leu Tyr Arg Phe Val Ser Gly Asn Ser Ser Ser Glu Trp Gln Phe Ile
    130                 135                 140

Gln Gly Leu Pro Ser Asn Lys Asn Ala Val Ile Ser Gly Thr Asn Ile
145                 150                 155                 160

Leu Asp Ile Ala Ser Pro Gly Val Tyr Phe Val Met Gly Met Thr Gly
                165                 170                 175

Gly Met Pro Ser Gly Val Ser Ser Gly Phe Leu Asp Leu Ser Val Asp
            180                 185                 190

Ala Asn Asp Asn Arg Leu Ala Arg Leu Thr Asp Ala Glu Thr Gly Lys
        195                 200                 205

Glu Tyr Thr Ser Ile Lys Lys Pro Thr Gly Thr Tyr Thr Ser Trp Lys
    210                 215                 220

Lys Glu Phe Glu Pro Lys Asp Met Glu Lys Tyr Leu Leu Ser Ser Ile
225                 230                 235                 240

Arg Asp Asp Gly Ser Ala Ser Phe Pro Leu Leu Val Tyr Thr Ser Asp
                245                 250                 255

Asn Lys Thr Phe Gln Gln Ala Ile Ile Asp His Ile Asp Arg Thr Gly
            260                 265                 270

Gln Thr Thr Phe Thr Phe Tyr Val Gln Gly Gly Val Ser Gly Ser Pro
        275                 280                 285

Met Ser Asn Ser Cys Arg Gly Leu Phe Met Ser Asp Thr Pro Asn Thr
    290                 295                 300

Ser Ser Leu His Gly Val Tyr Asn Ala Ile Gly Thr Asp Gly Arg Asn
305                 310                 315                 320

Val Thr Gly Ser Val Val Gly Gly Asn Trp Thr Ser Pro Lys Thr Ser
                325                 330                 335

Pro Ser His Lys Glu Leu Trp Thr Gly Ala Gln Ser Phe Leu Ser Val
            340                 345                 350

Gly Thr Thr Lys Asn Leu Ala Asp Asp Ile Ser Asn Tyr Ser Tyr Val
        355                 360                 365

Glu Val Tyr Thr Lys His Lys Thr Val Glu Lys Thr Lys Gly Asn Asp
    370                 375                 380
```

```
Asp Ser Gly Thr Ile Cys His Lys Phe Tyr Leu Asp Gly Ser Gly Thr
385                 390                 395                 400


Tyr Val Cys Ser Gly Thr Phe Val Ser Gly Asp Arg Thr Asp Thr Lys
                405                 410                 415


Pro Pro Val Thr Glu Phe Tyr Arg Val Gly Val Ser Phe Lys Gly Ser
            420                 425                 430


Thr Trp Thr Leu Val Asp Ser Ala Val Gln Asn Ser Lys Thr Gln Tyr
        435                 440                 445


Val Thr Arg Ile Ile Gly Ile Asn Met Pro
    450                 455


<210> 1275
<211> 582
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1275
Met Arg Leu Arg Ile Lys Asn Leu Tyr Thr Tyr Val Glu Phe Glu Glu
1               5                   10                  15


Asp Asp Lys Tyr Leu Lys Asp Ile Phe Leu Lys Arg Val His Thr Thr
            20                  25                  30


Ile Gly Ala Arg Gln Glu Gly Phe Gln Tyr Ser Pro Ala Tyr Lys Arg
        35                  40                  45


Gly Ser Trp Asp Gly Tyr Val Asp Phe Tyr Val Tyr Glu Glu Asp Lys
    50                  55                  60


Phe Pro Thr Gly Leu Leu Phe Lys Ile Glu Leu Leu Leu Gly Glu Leu
65                  70                  75                  80


Gln Ser Arg Tyr Asn Phe Gln Phe Glu Thr Ile Asp Glu Arg Asp Glu
                85                  90                  95


Ser Phe Leu Ser Glu Glu Asp Ile Asp Asp Glu Ile Thr Leu Leu Asp
            100                 105                 110


Asn Asn Val Gly Gln Ile Thr Leu Arg Asp Tyr Gln Tyr Glu Ala Val
        115                 120                 125


Tyr Asn Ser Leu Thr Phe Tyr Asn Gly Ile Ala His Leu Ala Thr Asn
    130                 135                 140


Gly Gly Lys Thr Glu Val Ala Ser Gly Ile Ile Asp Gln Leu Leu Pro
145                 150                 155                 160
```

```
Gln Leu Glu Lys Gly Glu Arg Val Ala Phe Phe Thr Gly Ser Thr Glu
                165                 170                 175

Ile Phe His Gln Ser Ala Asp Arg Leu Gln Glu Arg Leu Asn Ile Pro
            180                 185                 190

Ile Gly Lys Val Gly Ala Gly Lys Phe Asp Val Lys Gln Val Thr Val
        195                 200                 205

Val Met Ile Pro Thr Leu Asn Ala Asn Leu Lys Asp Pro Thr Gln Gly
    210                 215                 220

Val Lys Val Thr Pro Lys Gln Asn Ile Ser Lys Lys Ile Ala Gln Glu
225                 230                 235                 240

Ile Leu Pro Lys Phe Glu Gly Gly Thr Asn Gln Lys Lys Leu Leu Lys
                245                 250                 255

Val Leu Leu Asp Asn Thr Thr Pro Lys Thr Lys Val Glu Gln Asn Val
            260                 265                 270

Leu Ser Ala Leu Glu Ile Ile Tyr Gln Asn Ser Lys Thr Asp Ala Glu
        275                 280                 285

Val Leu Leu Asn Leu Arg Asn His Asn Ala His Phe Gln Lys Ile Val
    290                 295                 300

Arg Glu Lys Asn Glu Lys Lys Tyr Asp Lys Tyr Gln Asp Met Arg Asp
305                 310                 315                 320

Phe Leu Asp Ser Val Thr Val Met Ile Val Asp Glu Ala His His Ser
                325                 330                 335

Lys Ser Asp Ser Trp Tyr Asn Asn Leu Met Thr Cys Glu Lys Ala Leu
            340                 345                 350

Tyr Arg Ile Ala Leu Thr Gly Ser Ile Asp Lys Lys Asp Glu Leu Leu
        355                 360                 365

Trp Met Arg Leu Gln Ala Leu Phe Gly Asn Val Ile Ala Arg Thr Thr
    370                 375                 380

Asn Lys Phe Leu Ile Asp Glu Gly His Ser Ala Arg Pro Thr Ile Asn
385                 390                 395                 400

Ile Ile Pro Ile Ala Asn Pro Asn Asp Ile Asp Arg Ile Asp Asp Tyr
                405                 410                 415

Arg Glu Ala Tyr Asp Arg Gly Ile Thr Asn Asn Asp Phe Arg Asn Lys
            420                 425                 430
```

Leu Ile Ala Lys Leu Thr Glu Lys Trp Tyr Asn Gln Asp Lys Gly Thr
435 440 445

Leu Ile Ile Val Asn Phe Ile Glu His Gly Asp Thr Ile Ser Glu Met
450 455 460

Leu Asn Asp Leu Asp Val Glu His Tyr Phe Leu His Gly Glu Ile Asp
465 470 475 480

Ser Glu Thr Arg Arg Glu Lys Leu Asn Asp Met Arg Ser Gly Lys Leu
485 490 495

Lys Val Met Ile Ala Thr Ser Leu Ile Asp Glu Gly Val Asp Ile Ser
500 505 510

Gly Ile Asn Ala Leu Ile Leu Gly Ala Gly Gly Lys Ser Leu Arg Gln
515 520 525

Thr Leu Gln Arg Ile Gly Arg Ala Leu Arg Lys Lys Lys Asp Asp Asn
530 535 540

Thr Thr Gln Ile Phe Asp Phe Asn Asp Met Thr Asn Arg Phe Leu Tyr
545 550 555 560

Thr His Ala Asn Glu Arg Arg Lys Ile Tyr Glu Glu Glu Asp Phe Glu
565 570 575

Ile Lys Asp Leu Gly Lys
580

<210> 1276
<211> 537
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1276
Met Ala Thr Lys Thr Gln Arg Lys Leu Tyr Gln Tyr Leu Glu Glu Asn
1 5 10 15

Ala Thr Glu Asn Lys Phe His Ile Ser Thr Lys Lys Glu Leu Ala Asp
20 25 30

Ser Leu Gly Val Ser Ile Ser Ala Leu Ser Asn Asn Leu Lys Lys Leu
35 40 45

Glu Glu Glu Asn Lys Val Val Thr Val Ser Lys Arg Gly Lys Asn Gly
50 55 60

Gly Val Ile Ile Thr Leu Val Arg Glu Tyr Asp Thr Glu Glu Leu Lys

65 70 75 80

Glu Phe Asn Asn Ser Thr Asp Asn Ile Ile Thr Ser Asp Leu Gln Tyr
85 90 95

Ala Lys Ala Leu Arg Glu Lys His Phe Pro Ser Tyr Arg Tyr Glu Arg
100 105 110

Lys Glu Gln Arg Arg Arg Thr Lys Ile Glu Met Ala Gln Tyr Asn Ala
115 120 125

Ile Lys Asp Glu Lys Arg Arg Ile Ile Ala Asp Met Asn Phe Tyr Ser
130 135 140

Glu Gly Leu Pro Tyr Pro Ser Lys Asp Ile Phe Asn Met Ser Tyr Asp
145 150 155 160

Pro Glu Gly Phe Tyr Lys Ala Tyr Ile Leu Cys Lys Leu Tyr Asp Gln
165 170 175

Tyr Ala Ile Ser His Met Asp Ala Lys His Thr Ser His Leu Lys Ala
180 185 190

Met Ser Lys Ala Thr Thr Lys Asp Glu Tyr Asp Tyr His Gln His Met
195 200 205

Ser Glu Tyr Tyr Arg Asn Lys Met Ile Gln Asn Leu Pro Arg Asn Ser
210 215 220

Val Ser Asp Asn Phe Phe Gly Ser Lys Met Phe Asn Thr Phe Tyr Asn
225 230 235 240

Phe Tyr Leu Lys Ile Lys Asp Lys Asn Ile Asn Val Phe Lys Tyr Met
245 250 255

Gln Asn Val Phe Lys Asn Val Thr Phe Tyr Tyr Glu Asn Gly Met Gln
260 265 270

Pro Asn Pro Ile Pro Ser Pro Asn Phe Phe Ser Ser Asp Lys Tyr Phe
275 280 285

Lys Asn Tyr Asn Asn Tyr Ile Lys Gly Ile Lys Lys Gly Val Asn Ser
290 295 300

Thr Asn Arg His Leu Gly Asp Thr Asp Ser Ile Ile Asn Ser Ser Asp
305 310 315 320

Tyr Val Lys Asn Pro Ala Val Leu His Leu His Gln Leu Tyr Thr Thr
325 330 335

Gly Leu Asn Ser Thr Leu His Asp Ile Asp Thr Met Phe Glu Gln Ala

340 345 350

Leu Asp Leu Glu Asn Ala Ser Tyr Gly Leu Phe Gly Asp Met Lys His
355 360 365

Ile Ile Leu Leu Gln Tyr Asn Ser Met Ile Glu Glu Glu Ile Lys Asn
370 375 380

Leu Pro Arg Glu Glu Lys Asp Ile Ile Asn Lys Tyr Val Lys Gln Cys
385 390 395 400

Ile Ile Asn Asp Tyr Ser Pro Thr Ser Ile Ser Pro Ser Ala Arg Leu
405 410 415

Ser Met Phe Thr Met Gln Lys Glu His Ile Val Tyr Asn Lys Gln Leu
420 425 430

Asn Lys Gly Ile Lys Arg Glu Asp Leu Leu Pro Leu Ser Leu Gly Gly
435 440 445

Ile Val Asn Lys Asp Ser Leu Ser Gly Met Asp Ile Gln Asn Leu Glu
450 455 460

Gln Asn Gly Asn Glu Tyr Leu Tyr Met Arg Gln His Thr Ser Thr Tyr
465 470 475 480

Tyr Ile Leu Arg Met Phe Gly Asp Tyr Leu Gly Tyr Glu Val Asn Leu
485 490 495

Arg Glu Val Lys Tyr Ile Val Glu Lys Tyr Asn Leu Ile Asp Lys Ile
500 505 510

Pro Leu Thr Lys Glu Gly Met Leu Asp Tyr Asn Lys Leu Ile His Leu
515 520 525

Val Glu Glu Glu Val Asn Asn Tyr Glu
530 535

<210> 1277
<211> 480
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1277
Met Ser Lys Lys Ile Lys Glu Leu Ile Leu His Lys Ser Met Lys Asp
1 5 10 15

Ile His Phe Ala Arg Glu Val Leu Asp Asn Leu Pro Lys Asn Leu Phe
20 25 30

```
Ser Ala Glu Ser Glu Asp Met Gly Tyr Leu Phe Thr Ala Ile Lys Arg
        35                  40                  45

Thr Ala His Ile Ser Asp Lys Met Ser Asn Glu Ala Leu Ala Ile Lys
    50                  55                  60

Val Glu Gln Leu Met Gly Asn Asn Lys Glu Asp Glu Glu Lys Val Thr
65                  70                  75                  80

Lys Thr Leu Thr Tyr Leu Glu Asp Leu Tyr Lys Val Asp Val Asn Glu
                85                  90                  95

Lys Asp Glu Ser Val Asn Tyr Glu Ile Glu Lys Tyr Ile Lys Thr Glu
            100                 105                 110

Met Ser Lys Glu Val Leu Val Lys Phe Ile Ala Glu Asn Lys Gln Glu
        115                 120                 125

Asp Ser Asp Asn Leu His Glu Leu Val Asp Lys Leu Lys Gln Ile Glu
    130                 135                 140

Val Ser Asp Ile Ser Gly Gly Asn Gly Glu Phe Ile Asp Phe Phe Glu
145                 150                 155                 160

Asp Thr Glu Lys Lys Gln Glu Leu Leu Ser Asn Leu Ala Thr Asn Lys
                165                 170                 175

Phe Ser Thr Gly Phe Thr Ser Ile Asp Asn His Ile Glu Gly Gly Ile
            180                 185                 190

Ala Arg Gly Glu Val Gly Leu Ile Ile Ala Pro Thr Gly Arg Gly Lys
        195                 200                 205

Ser Leu Met Ala Ser Asn Leu Ala Lys Asn Tyr Val Lys Ser Gly Leu
    210                 215                 220

Ser Val Leu Tyr Ile Ala Leu Glu Glu Lys Met Asp Arg Met Val Leu
225                 230                 235                 240

Arg Ala Glu Gln Gln Met Ala Gly Ala Glu Lys Ser Gln Ile Val Asn
                245                 250                 255

Gln Asp Met Ser Leu Asn Asn Lys Val Tyr Asp Ala Ile Gln Asn His
            260                 265                 270

Tyr Gln Lys Asn Arg Lys Leu Leu Gly Asp Phe Tyr Ile Ser Lys His
        275                 280                 285

Met Pro Gly Glu Val Thr Pro Asn Gln Leu Glu Gln Ile Ile Val Asn
    290                 295                 300
```

Thr Thr Ile Lys Lys Asp Lys Asn Ile Asp Val Val Ile Ile Asp Tyr
305 310 315 320

Pro His Leu Met Arg Asn Pro Tyr Ala Lys Tyr His Ser Glu Ser Asp
325 330 335

Ala Gly Gly Lys Leu Phe Glu Asp Ile Arg Arg Leu Ser Gln Gln Tyr
340 345 350

Gly Phe Val Cys Trp Thr Leu Ala Gln Thr Asn Arg Gly Ala Tyr Gly
355 360 365

Ser Asp Val Ile Thr Ser Glu His Val Glu Gly Ser Arg Lys Ile Val
370 375 380

Asn Ala Val Glu Val Ser Leu Ala Val Asn Gln Lys Asp Glu Glu Phe
385 390 395 400

Lys Ser Gly Phe Leu Arg Leu Tyr Leu Asp Lys Ile Arg Asn Ser Ser
405 410 415

Asn Thr Gly Glu Arg Phe Val Asn Leu Lys Val Glu Pro Thr Lys Met
420 425 430

Ile Val Arg Asp Glu Thr Pro Glu Glu Lys Gln Glu His Ile Gln Leu
435 440 445

Leu Ser Asp Asn Gly Lys Glu Asp Thr Ser Lys Phe Gln Asn Lys Asp
450 455 460

Asn Lys Ile Glu Ala Ile Asn Asn Thr Phe Gly Gly Leu Pro Gly Val
465 470 475 480

<210> 1278
<211> 341
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1278
Met Lys Phe Val Phe Phe Thr Asp Ser His Phe His Leu Phe Thr Asn
1 5 10 15

Tyr Ala Lys Pro Asp Asn Glu Phe Val Asn Asp Arg Phe Lys Glu Gln
20 25 30

Ile Glu Ala Leu Gln Lys Val Phe Asp Ile Ala Lys Lys Glu Glu Ala
35 40 45

Thr Val Ile Phe Gly Gly Asp Leu Phe His Lys Arg Asn Ser Val Asp
50 55 60

```
Thr Arg Val Tyr Asn Lys Val Phe Ser Thr Phe Ala Lys Asn Asp Glu
65                  70                  75                  80

Val Pro Val Leu Leu Leu Arg Gly Asn His Asp Ala Thr Thr Asn Ser
                85                  90                  95

Leu Tyr Thr Asp Ser Ser Ile Asp Thr Phe Glu Tyr Leu Pro Asn Val
            100                 105                 110

Ser Val Ile Lys Ser Leu Asn Thr Ile Leu Lys Asp Asn Val Asn Ile
        115                 120                 125

Val Phe Thr Ala Tyr Gly Asp Glu Thr Lys Glu Ile Lys Thr Tyr Ile
    130                 135                 140

Asn Ser Asn Tyr Asp Lys Asp Met Val Asn Ile Leu Val Gly His Leu
145                 150                 155                 160

Gly Val Glu Gly Ser Leu Thr Gly Lys Gly Ser His Arg Leu Glu Gly
                165                 170                 175

Ala Phe Gly Tyr Gln Asp Leu Leu Pro Asp Lys Tyr Asp Phe Ile Leu
            180                 185                 190

Leu Gly His Tyr His Arg Arg Gln Tyr Phe Gln Asn Pro Asn His Phe
        195                 200                 205

Tyr Gly Gly Ser Leu Met Gln Gln Ser Phe Ser Asp Glu Gln Glu Ala
    210                 215                 220

Asn Gly Val His Leu Ile Asp Thr Glu Lys Met Thr Thr Glu Phe Ile
225                 230                 235                 240

Pro Ile His Thr Arg Arg Phe Ile Thr Ile Gln Gly Glu Asp Ile Pro
                245                 250                 255

Glu Asn Phe Glu Gln Leu Ile Glu Glu Gly Asn Phe Ile Arg Val Ile
            260                 265                 270

Gly Thr Ala Asn His Ala Lys Val Leu Glu Met Asp Asp Ser Met Lys
        275                 280                 285

Asp Lys Asn Val Glu Val Gln Ile Lys Lys Glu Tyr Thr Val Glu Lys
    290                 295                 300

Arg Ile Asp Ser Asp Val Ser Asp Asp Pro Leu Thr Ile Ala Ser Thr
305                 310                 315                 320

Tyr Ala Lys Gln Tyr Ser Pro Glu Ser Glu Gln Glu Ile Leu Glu Cys
                325                 330                 335
```

Leu Lys Glu Val Leu
340

<210> 1279
<211> 125
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1279
Met Lys Lys Tyr Arg Glu Tyr Leu Asn Lys Thr Asp Ala Glu Asn Leu
1 5 10 15

Ala Glu Asp Trp Glu Lys Val Thr Glu Asp Leu Trp Lys Val Phe Lys
20 25 30

Asp Met Lys Pro Lys Ile Asn Thr Leu Asp Ile Ser Asn Val Glu Ser
35 40 45

Lys Asn Leu Asp Lys Ser Lys Pro Ile Leu Gln Phe Gln Asp Ser Asp
50 55 60

Gly Val Ile Glu Asn Ile Cys Asn Val Glu Gly Leu Glu Asp Gly Leu
65 70 75 80

Ser Lys Met Lys Lys Val Phe Asp Asp Ser Asn Phe Glu Lys His Tyr
85 90 95

Tyr Ser Arg Val Val Asp His Asp Glu Tyr Tyr Trp Ile Asp Tyr Gly
100 105 110

Ser His His Cys Phe Phe Arg Val Thr Lys Gly Asp Lys
115 120 125

<210> 1280
<211> 639
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1280
Met Val Val Phe Lys Gln Val Glu Val Asn Asn Phe Leu Ala Ile Lys
1 5 10 15

Glu Ala Thr Leu Glu Leu Asp Asn Arg Gly Leu Ile Leu Ile Glu Gly
20 25 30

Glu Asn Lys Ser Asn Glu Ser Phe His Ser Asn Gly Ser Gly Lys Ser
35 40 45

Thr Leu Ile Ser Ala Ile Thr Tyr Ala Leu Tyr Gly Lys Thr Glu Lys

50 55 60

Gly Leu Lys Ala Asp Asp Val Val Asn Asn Ile Glu Lys Lys Asn Thr
65 70 75 80

Ser Val Lys Leu Lys Phe Asp Ile Gly Glu Asp Ser Tyr Leu Ile Glu
85 90 95

Arg Tyr Arg Lys Asp Lys Glu Asn Lys Asn Lys Val Lys Leu Phe Val
100 105 110

Asn Glu Lys Glu Ile Thr Gly Ser Thr Asn Asp Val Thr Asp Lys Gln
115 120 125

Ile Gln Asp Leu Phe Gly Ile Glu Phe Asn Thr Tyr Val Asn Ala Ile
130 135 140

Met Tyr Gly Gln Gly Asp Ile Pro Met Phe Ser Gln Ala Thr Asp Lys
145 150 155 160

Gly Lys Lys Glu Ile Leu Glu Ser Ile Thr Lys Thr Asp Val Tyr Lys
165 170 175

Gln Ala Gln Asp Val Ala Lys Glu Lys Val Lys Glu Val Glu Glu Gln
180 185 190

Gln Asn Asn Ile Arg Gln Glu Ile Tyr Lys Leu Gly Tyr Gln Leu Ser
195 200 205

Thr Lys Asp Glu Tyr Phe Gln Arg Glu Ile Glu Gln Tyr Asn Gln Tyr
210 215 220

Lys Glu Gln Leu Val Gln Ile Glu Asn Ser Asn Lys Glu Lys Asp Arg
225 230 235 240

Leu Arg Glu Gln Glu Glu Lys Gln Ile Glu Ala Gln Ile Glu Gln Leu
245 250 255

Ala Ser Gln Ile Pro Thr Ile Pro Glu Asp Glu Phe Lys His Ser Glu
260 265 270

Glu Tyr Asn Lys Ala Ser Gln Ser Leu Asp Leu Leu Ser Asn Lys Leu
275 280 285

Thr Glu Leu Asn Gln Val Tyr Ser Glu Tyr Asn Thr Lys Glu Gln Val
290 295 300

Leu Lys Ser Glu Ile Ala Thr Leu Ser Asn Ser Leu Asn Lys Leu Asp
305 310 315 320

Thr Asn Asp His Cys Pro Val Cys Gly Ser Pro Ile Asp Asn Ser His

325 330 335

Lys Leu Lys Glu Gln Glu Asn Ile Asn Asn Gln Ile Glu Asn Lys Lys
340 345 350

Gln Glu Ile Thr Ser Val Leu Glu Met Lys Asp Thr Tyr Lys Glu Ala
355 360 365

Ile Asp Lys Val Lys Asp Lys Ser Gln Glu Ile Lys Asp Lys Met Ser
370 375 380

Gln Glu Asp Gln Gln Glu Arg Glu His Asn Asn Lys Ile Asn Ser Ile
385 390 395 400

Ile Gln Glu Ala Ser Arg Ile Lys Ser Asp Ile Ser Ser Leu Glu Asn
405 410 415

Asn Lys Thr Tyr Leu Lys Val Lys Tyr Gln His Gln Ser Val Gln Gly
420 425 430

Leu Glu Arg Glu Glu Pro Ser Lys Glu Lys His Glu Glu Asp Lys Lys
435 440 445

Glu Leu Gln Glu Ser Ile Asp Lys His Glu Glu Asn Ile Val Gln Leu
450 455 460

Glu Thr Lys Lys Gly Lys Tyr Gln Gln Ala Val Asp Ala Phe Ser Asn
465 470 475 480

Lys Gly Ile Arg Ser Val Val Leu Asp Phe Ile Thr Pro Phe Leu Asn
485 490 495

Glu Lys Ala Asn Glu Tyr Leu Gln Thr Leu Ser Gly Ser Asp Ile Glu
500 505 510

Ile Glu Phe Gln Thr Gln Val Lys Asn Ala Lys Gly Glu Leu Lys Asp
515 520 525

Lys Phe Asp Val Ile Val Lys Asn Ser Lys Gly Gly Gly Ser Tyr Lys
530 535 540

Ser Asn Ser Ala Gly Glu Gln Lys Arg Ile Asp Leu Ala Ile Ser Phe
545 550 555 560

Ala Ile Gln Asp Leu Ile Met Ser Lys Asp Glu Ile Ser Thr Asn Ile
565 570 575

Ala Leu Tyr Asp Glu Cys Phe Asp Gly Leu Asp Thr Ile Gly Cys Glu
580 585 590

Asn Val Ile Lys Leu Leu Lys Asp Arg Leu Asn Thr Val Gly Thr Ile

595 600 605

Phe Val Ile Thr His Asn Thr Glu Leu Lys Pro Leu Phe Glu Gln Thr
610 615 620

Ile Lys Ile Val Lys Glu Asn Gly Val Ser Lys Leu Glu Glu Lys
625 630 635

<210> 1281
<211> 198
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1281
Met Lys Leu Lys Ile Leu Asp Lys Asp Asn Ala Thr Leu Asn Val Phe
1 5 10 15

His Arg Asn Lys Glu His Lys Thr Ile Asp Asn Val Pro Thr Ala Asn
20 25 30

Leu Val Asp Trp Tyr Pro Leu Ser Asn Ala Tyr Glu Tyr Lys Leu Ser
35 40 45

Arg Asn Gly Glu Tyr Leu Glu Leu Lys Arg Leu Arg Ser Thr Leu Pro
50 55 60

Ser Ser Tyr Gly Leu Asp Asp Asn Asn Gln Asp Ile Ile Arg Asp Asn
65 70 75 80

Asn His Arg Cys Lys Ile Gly Tyr Trp Tyr Asn Pro Ala Val Arg Lys
85 90 95

Asp Asn Leu Lys Ile Ile Glu Lys Ala Lys Gln Tyr Gly Leu Pro Val
100 105 110

Ile Thr Glu Glu Tyr Asp Ala Asn Thr Val Glu Gln Gly Phe Arg Asp
115 120 125

Ile Gly Val Ile Phe Gln Ser Leu Lys Thr Ile Val Val Thr Arg Tyr
130 135 140

Leu Glu Gly Lys Thr Glu Glu Glu Leu Arg Ile Phe Asn Met Lys Ser
145 150 155 160

Glu Glu Ser Gln Leu Asn Glu Ala Leu Lys Glu Ser Asp Phe Ser Val
165 170 175

Asp Leu Thr Tyr Ser Asp Leu Gly Gln Ile Tyr Asn Met Leu Leu Leu
180 185 190

Met Lys Lys Ile Ser Lys
195

<210> 1282
<211> 355
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1282
Met Arg Phe Glu Asp Phe Leu Thr Gln Glu Leu Gly Glu Pro Lys Glu
1 5 10 15

Asn Thr Ile Gly Glu Leu Arg Tyr Cys Cys Pro Phe Cys Gly Glu Lys
20 25 30

Ser Tyr Lys Phe Tyr Val Lys Gln Ala Leu Asp Ser Ser Asn Gly Gln
35 40 45

Tyr His Cys Lys Lys Cys Asp Glu Ser Gly Asn Pro Ile Thr Phe Met
50 55 60

Lys Thr Tyr Tyr Asn Ile Thr Gly Lys Gln Ala Phe Asp Leu Leu Glu
65 70 75 80

Ser Lys Asn Ile Asp Ile Glu Arg Ala Pro Leu Leu Thr Thr Asn Asn
85 90 95

Lys Asp Leu Thr Glu Ser Glu Lys Leu Ile Leu Met Leu Arg Gly Val
100 105 110

His Gln Asp Lys Gly Thr Thr Ser Ile Lys Pro Pro Arg Leu Pro Glu
115 120 125

Gly Tyr Lys Leu Leu Lys Asp Asn Leu Asn Asn Lys Glu Ile Ile Pro
130 135 140

Phe Leu Lys Tyr Leu Lys Gly Arg Gly Ile Thr Leu Glu Gln Ile Ile
145 150 155 160

Asn Asn Asn Ile Gly Tyr Val Ile Asn Gly Ser Phe Tyr Lys Val Asp
165 170 175

Gly Glu Ser Lys Val Ser Leu Arg Asn Ser Ile Ile Phe Phe Thr Tyr
180 185 190

Asp Asn Asp Gly Asn Tyr Gln Tyr Trp Asn Thr Arg Ser Ile Glu Lys
195 200 205

Asn Pro Tyr Ile Lys Ser Ile Asn Ala Pro Ala Lys Gln Asp Glu Val
210 215 220

```
Gly Arg Lys Asp Val Ile Phe Asn Leu Asn Ile Ala Arg Lys Lys Lys
225                 230                 235                 240


Phe Leu Val Ile Thr Glu Gly Val Phe Asp Ala Leu Thr Phe His Glu
                245                 250                 255


Tyr Gly Val Ala Thr Leu Gly Lys Gln Val Thr Glu Asn Gln Ile Lys
            260                 265                 270


Lys Ile Ile Asp Tyr Val Ser Ile Asp Thr Ser Ile Tyr Ile Met Leu
        275                 280                 285


Asp Thr Asp Ala Leu Asp Asn Asn Ile Asp Leu Ala Tyr Lys Leu Lys
    290                 295                 300


Thr His Phe Asn Lys Val Tyr Phe Val Pro His Gly Asp Glu Asp Ala
305                 310                 315                 320


Asn Asp Met Gly Thr Arg Lys Ala Phe Glu Leu Leu Lys Gln Asn Arg
                325                 330                 335


Val Leu Val Thr Pro Glu Ser Ile Gln Ser Tyr Lys Ile Gln Gln Lys
            340                 345                 350


Leu Lys Leu
        355


<210> 1283
<211> 112
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1283
Met Ser Asn Asn Lys Lys Asp Ile Leu Glu Phe Val Asp Glu Tyr Ile
1               5                   10                  15


Thr Ala Leu Arg Val Gly Asn Glu Gln Arg Gln His Gln Leu Glu Glu
            20                  25                  30


Met Gly Lys Glu Glu Thr Ala Thr Leu Thr Asp Val Ala Lys Ala Ile
        35                  40                  45


Thr Asn Leu Met Leu Gly Val Asn Glu Gln Met Thr Asp Leu Glu Tyr
    50                  55                  60


Asn Asn Glu Leu Asn Leu Asn Ile Leu Ile Asp Ala Leu Tyr Lys Ala
65                  70                  75                  80


Glu Leu Ile Asn Glu Asp Val Leu Asp Tyr Ile Gln Glu Ser Ile Asp
                85                  90                  95
```

```
Lys Ser Gln Glu Glu Pro Lys Asn Glu Glu Glu Lys Gly Glu Gln Glu
            100                 105                 110


<210> 1284
<211> 150
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1284
Met Glu Lys Asn Ile Ser Thr His Thr Lys Gly Ile Ser Gln Ala Asp
1               5                   10                  15


Met Glu Lys Trp Ile Glu Ala Val Val Gln Gly Thr Val Asp Gly Lys
            20                  25                  30


Gln Val Asp Glu Lys Thr Ala Lys Gln Leu Asp Arg Ile Gly Ser Arg
        35                  40                  45


Ser Val Ser Leu Glu Glu Ala Thr Arg Ile Ala Lys Val Leu Asn Ala
    50                  55                  60


Val Thr Ala Gln Glu Val Thr Gly Asp Phe Asn Asp Ala Phe Asn Ala
65                  70                  75                  80


Ile Asp Leu Met Met Ile Ile Met Glu Asp Glu Leu Gly Val Thr Gln
                85                  90                  95


Glu Lys Val Gly Lys Ala Lys Asp Lys Leu Asn Glu Lys Arg Glu Ala
            100                 105                 110


Tyr Leu Lys Glu Lys Gln Glu Glu Leu Arg Gln Lys Gln Gln Glu Glu
        115                 120                 125


Ala Gln Lys Glu Thr Glu Ser Asp Ser Asn Glu Lys Val Ile Gln Leu
    130                 135                 140


Lys Lys Asn Asp Glu Gln
145                 150


<210> 1285
<211> 202
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1285
Met Thr Asn Ser Lys Lys Lys Gly Asp Thr Phe Glu Arg Lys Ile Ala
1               5                   10                  15
```

```
Lys Glu Leu Thr Ala Trp Trp Gly Tyr Gln Phe Asn Arg Ser Pro Gln
            20                  25                  30

Ser Gly Gly Ala Ser Trp Gly Lys Asp Asn Asn Ala Val Gly Asp Ile
        35                  40                  45

Val Val Pro Gln Glu Ala Asn Phe Pro Leu Val Val Glu Cys Lys His
    50                  55                  60

Arg Glu Glu Trp Thr Ile Asp Asn Val Leu Leu Asn Asn Arg Glu Pro
65                  70                  75                  80

His Thr Trp Trp Glu Gln Val Ile Asn Asp Ser Ser Lys Val Asn Lys
                85                  90                  95

Thr Pro Cys Leu Ile Phe Thr Arg Asn Arg Ala Gln Ser Tyr Val Ala
            100                 105                 110

Leu Pro Tyr Asn Glu Lys Val Tyr Glu Asp Leu Arg Asn Asn Glu Tyr
        115                 120                 125

Pro Val Met Arg Thr Asp Phe Ile Ile Asp Asn Ile Arg Lys Asp Lys
    130                 135                 140

Phe Phe Tyr Asp Val Leu Ile Thr Thr Met Asn Gly Leu Thr Ser Phe
145                 150                 155                 160

Thr Pro Ser Tyr Ile Ile Ser Cys Tyr Asp Lys Lys Asp Ile Lys Pro
                165                 170                 175

Tyr Lys Lys Val Glu Ser Asn Leu Ser Glu Val Ser Lys His Glu Asp
            180                 185                 190

Glu Leu Ile Asn Asp Leu Leu Ser Asp Ile
        195                 200


<210> 1286
<211> 139
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1286
Val Ile Tyr Lys Glu Gly Lys Ile Ser Met Thr Ser Lys Glu Arg Pro
1               5                   10                  15

Leu Ile Val Tyr Phe Ser Gly Thr Gly Gln Thr Glu Arg Leu Val Asn
            20                  25                  30

Lys Ile Asn Ile Asn Asn Ser Phe Glu Thr Phe Arg Val Lys Ser Gly
        35                  40                  45
```

Lys Glu Lys Val Asn Lys Pro Phe Ile Leu Ile Thr Pro Thr Tyr Lys
50 55 60

Lys Gly Ala Ile Pro Lys Gln Ile Glu Arg Phe Leu Glu Ile Asn Gly
65 70 75 80

Ser Pro Lys Glu Val Ile Gly Thr Gly Asn Lys Gln Trp Gly Ser Asn
85 90 95

Phe Cys Gly Ala Ser Lys Lys Ile Ser Glu Met Phe Lys Ile Pro Leu
100 105 110

Ile Ala Lys Val Glu Gln Ser Gly His Phe Asn Glu Ile Gln Pro Ile
115 120 125

Leu Glu His Phe Ser Asn Lys Tyr Lys Val Ala
130 135

<210> 1287
<211> 704
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1287
Met Ala Thr Tyr Gly Lys Trp Ile Glu Leu Asn Asn Glu Ile Thr Gln
1 5 10 15

Leu Asp Asp Asn Gly Lys Asn Lys Leu Tyr Lys Asp Gln Glu Ala Leu
20 25 30

Asp Glu Tyr Leu Lys Tyr Ile Glu Asp Asn Thr Arg Lys Phe Asn Ser
35 40 45

Glu Val Glu Arg Ile Arg Val Leu Thr Lys Glu Gly Thr Tyr Asp Lys
50 55 60

Ile Phe Asp Lys Val Pro Asp Thr Ile Ile Asp Glu Met Thr Lys Leu
65 70 75 80

Ala Tyr Ser Phe Asn Phe Lys Phe Pro Ser Phe Met Ala Gly Gln Lys
85 90 95

Phe Tyr Glu Ser Tyr Ala Ser Lys Gln Tyr Asp Glu Asn Lys Lys Pro
100 105 110

Ile Phe Val Glu Asp Tyr Glu Gln His Asn Val Arg Val Ala Leu Tyr
115 120 125

Leu Phe Gln Asn Asp Tyr Val Lys Ala Arg Glu Leu Leu Val Gln Leu
130 135 140

```
Met Glu Gln Thr Phe Gln Pro Ser Thr Pro Thr Tyr Asn Asn Ser Gly
145                 150                 155                 160

Gln Ala Asn Arg Gly Glu Leu Ser Ser Cys Tyr Leu Phe Val Val Asp
                165                 170                 175

Asp Ser Ile Glu Ser Leu Asn Phe Val Glu Asp Ser Val Ala Asn Ala
            180                 185                 190

Ser Ser Asn Gly Gly Gly Val Ala Ile Asp Leu Thr Arg Ile Arg Pro
        195                 200                 205

Lys Gly Ala Pro Val Arg Asn Arg Pro Asn Ser Ser Lys Gly Val Ile
    210                 215                 220

Ala Phe Ala Lys Ala Ile Glu His Lys Val Ser Ile Tyr Asp Gln Gly
225                 230                 235                 240

Gly Val Arg Gln Gly Ser Gly Ala Val Tyr Leu Asn Ile Phe His Asn
                245                 250                 255

Asp Ile Leu Asp Leu Leu Ser Ser Lys Lys Ile Asn Ala Ser Glu Ser
            260                 265                 270

Val Arg Leu Asp Lys Leu Ser Ile Gly Val Thr Ile Pro Asn Lys Phe
        275                 280                 285

Met Glu Leu Val Lys Glu Gly Arg Pro Phe Tyr Thr Phe Asp Thr Tyr
    290                 295                 300

Asp Ile Asn Lys Val Tyr Gly Lys Tyr Leu Asp Glu Leu Asn Ile Asp
305                 310                 315                 320

Glu Trp Tyr Asp Lys Leu Leu Asp Asn Asp Ser Ile Gly Lys Val Lys
                325                 330                 335

His Asp Ala Arg Glu Val Met Thr Asp Ile Ala Lys Thr Gln Leu Glu
            340                 345                 350

Ser Gly Tyr Pro Tyr Val Phe Tyr Ile Asp Asn Ala Asn Asp Asn His
        355                 360                 365

Pro Leu Lys Asn Leu Gly Lys Val Lys Met Ser Asn Leu Cys Thr Glu
    370                 375                 380

Ile Ser Gln Leu Gln Glu Val Ser Glu Ile Tyr Pro Tyr Ser Tyr Ser
385                 390                 395                 400

Asn Lys Asn Val Ile Asn Arg Asp Val Val Cys Thr Leu Gly Ser Leu
                405                 410                 415
```

```
Asn Leu Val Asn Val Val Glu Lys Gly Leu Leu Asn Glu Ser Val Asp
            420                 425                 430

Ile Gly Thr Arg Ala Leu Thr Lys Val Thr Asp Ile Met Asp Leu Pro
        435                 440                 445

Tyr Leu Pro Ser Val Gln Lys Ala Asn Asp Asp Ile Arg Ala Ile Gly
    450                 455                 460

Leu Gly Ser Met Asn Leu His Gly Leu Leu Ala Lys Asn Met Ile Ser
465                 470                 475                 480

Tyr Gly Ser Arg Glu Ala Leu Asp Leu Val Asn Ser Leu Tyr Ser Ala
                485                 490                 495

Ile Asn Phe Gln Ser Ile Lys Thr Ser Met Leu Met Ala Lys Glu Thr
            500                 505                 510

Gly Lys Pro Phe Lys Gly Phe Glu Lys Ser Asp Tyr Ala Thr Gly Glu
        515                 520                 525

Tyr Phe Val Arg Tyr Ile Arg Glu Ser Asn Gln Pro Lys Thr Asp Lys
    530                 535                 540

Ala Lys Lys Val Leu Asp Lys Val Tyr Ile Pro Thr Gln Asp Asp Trp
545                 550                 555                 560

Asp Glu Leu Ala Lys Ala Val Lys Val His Gly Leu Tyr Asn Gly Tyr
                565                 570                 575

Arg Lys Ala Glu Ala Pro Thr Gln Ser Ile Ser Tyr Val Gln Asn Ala
            580                 585                 590

Thr Ser Ser Ile Met Pro Val Pro Ser Ala Ile Glu Asn Arg Gln Tyr
        595                 600                 605

Gly Asp Met Glu Thr Tyr Tyr Pro Met Pro Tyr Leu Ser Pro Ile Thr
    610                 615                 620

Gln Phe Phe Tyr Glu Gly Glu Thr Ala Tyr Lys Ile Asp Asn Lys Arg
625                 630                 635                 640

Ile Ile Asn Thr Ser Ala Val Val Gln Lys His Thr Asp Gln Ala Val
                645                 650                 655

Ser Thr Ile Leu Tyr Val Glu Ser Glu Ile Pro Thr Asn Lys Leu Val
            660                 665                 670

Ser Leu Tyr Tyr Tyr Ala Trp Glu Gln Gly Leu Lys Ser Leu Tyr Tyr
        675                 680                 685
```

Thr Arg Ser Arg Lys Leu Ser Val Ile Glu Cys Glu Thr Cys Ser Val
690 695 700

<210> 1288
<211> 349
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1288
Met Asp Ile Thr Gln Lys Val Lys Gln His Asn Lys Asn Ala Val Leu
1 5 10 15

Lys Ala Thr Asn Trp Asn Ile Glu Asp Asp Gly Met Ser Asp Ile Tyr
20 25 30

Trp Glu Gln Gly Ile Ser Gln Phe Trp Thr Pro Glu Glu Phe Asp Val
35 40 45

Ser Arg Asp Leu Ser Ser Trp Asn Ser Leu Thr Glu Ser Glu Lys Asn
50 55 60

Thr Tyr Lys Lys Val Leu Ala Gly Leu Thr Gly Leu Asp Thr Lys Gln
65 70 75 80

Gly Gly Glu Gly Met Asn Leu Val Ser Tyr His Glu Pro Arg Pro Lys
85 90 95

Tyr Gln Ala Val Phe Ala Phe Met Gly Gly Met Glu Glu Ile His Ala
100 105 110

Lys Ser Tyr Ser His Ile Phe Thr Thr Leu Leu Ser Asn Lys Glu Thr
115 120 125

Ser Tyr Leu Leu Asp Thr Trp Val Glu Glu Asn Asp Phe Leu Lys Val
130 135 140

Lys Ala Gln Phe Ile Gly Tyr Tyr Tyr Asp Gln Leu Leu Lys Pro Asn
145 150 155 160

Pro Thr Val Phe Asp Arg Tyr Met Ala Lys Val Ala Ser Ala Phe Leu
165 170 175

Glu Ser Ala Leu Phe Tyr Ser Gly Phe Tyr Tyr Pro Leu Leu Leu Ala
180 185 190

Gly Arg Gly Gln Met Thr Gln Ser Gly Ala Ile Ile Tyr Lys Ile Thr
195 200 205

Gln Asp Glu Ala Tyr His Gly Ser Ala Val Gly Leu Thr Ala Gln Tyr

210 215 220

Asp Tyr Asn Leu Leu Thr Glu Glu Glu Lys Lys Gln Ala Asp Lys Glu
225 230 235 240

Thr Tyr Glu Leu Leu Asp Ile Leu Tyr Thr Asn Glu Val Ala Tyr Thr
245 250 255

His Ser Leu Tyr Asp Pro Leu Glu Leu Ser Glu Asp Val Ile Asn Tyr
260 265 270

Val Gln Tyr Asn Phe Asn Arg Ala Leu Gln Asn Leu Gly Arg Glu Asp
275 280 285

Tyr Phe Asn Pro Glu Pro Tyr Asn Pro Ile Val Glu Asn Gln Thr Asn
290 295 300

Val Asp Arg Leu Arg Asn Val Asp Phe Phe Ser Gly Lys Ala Asp Tyr
305 310 315 320

Glu Lys Ser Thr Asn Ile Lys Asp Ile Lys Asp Glu Asp Phe Ser Phe
325 330 335

Leu Asp Ser Lys Glu Tyr Ser Thr Ala Lys Glu Phe Leu
340 345

<210> 1289
<211> 109
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1289
Met Asp Arg Lys Glu Ala Met Asp Leu Leu Ser Lys Ala Glu Ile Leu
1 5 10 15

Phe Lys Lys His Asp Glu Phe Ser Cys Val Ser Asp Ile Asn Asp Pro
20 25 30

Met Lys Leu Phe Ser Asn Ser Lys Asp Ala Lys Ala Asp Asp Thr Ser
35 40 45

Lys Ser Phe Gln Leu Glu Phe Met His Asp Met Thr Met Tyr Thr Leu
50 55 60

Ser Tyr Gly Ser Gly Gln Leu Lys Leu Ile Asp Leu Ala Glu Gly Tyr
65 70 75 80

Glu Ala Gln Lys Ala Thr Val Val Asn Ser Phe Pro Glu Ile Ile Lys
85 90 95

Thr Leu Glu Lys Asp Asp Ser Glu Asp Gly Lys Asn Glu
100 105

<210> 1290
<211> 106
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1290
Met Glu Lys Met Asn Ser Leu Val Asp Leu Asn Thr Ala Ile Arg Gln
1 5 10 15

Lys Lys Asp Val Ile Val Met Ile Thr Gln Asp Asn Cys Gly Lys Cys
20 25 30

Glu Ile Leu Lys Ser Val Ile Pro Met Phe Gln Glu Ser Gly Asp Ile
35 40 45

Lys Lys Pro Ile Leu Thr Leu Asn Leu Asp Ala Glu Asp Val Asp Arg
50 55 60

Glu Lys Ala Val Lys Leu Phe Asp Ile Met Ser Thr Pro Val Leu Ile
65 70 75 80

Gly Tyr Lys Asp Gly Gln Leu Val Lys Lys Tyr Glu Asp Gln Val Thr
85 90 95

Pro Met Gln Leu Gln Glu Leu Glu Ser Leu
100 105

<210> 1291
<211> 198
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1291
Met Asp Glu Leu Ile Ser Lys Ser Arg Arg Tyr Ile Met Arg Asp Glu
1 5 10 15

Asn His Tyr Met Leu Phe Asn Glu Lys Tyr Asn Asn Asp Arg Leu Ile
20 25 30

Glu Lys Val Cys Lys His Gly Gly Lys Val Thr Tyr Tyr Thr Asp Ser
35 40 45

Val Leu Pro Tyr Tyr Val Leu Lys Asp Leu Ser Ser His Pro Asp Ser
50 55 60

Glu Val Val Tyr Arg Met Arg Asn Gly Phe Thr Ala Lys Glu Val Asp
65 70 75 80

```
Asn Ile Ala Leu Ser Phe Met Gly Thr Lys Val Ile Ile Asp Ile Ser
                85                  90                  95

Val Val Phe Pro Tyr Val Asn Pro Tyr Asp Ile Ile Arg Ser Leu His
            100                 105                 110

Asp Ile Lys Thr Asn Val Asp Glu Val His Leu Ser Phe Pro Arg Ile
        115                 120                 125

Leu Glu Val Asp Glu Lys Gln Glu Lys Phe Tyr Phe Phe Asp Gly Glu
    130                 135                 140

Ala Tyr Asp Leu Lys Pro Glu Tyr Lys Val Asp Phe Ala Asp Lys Ile
145                 150                 155                 160

Arg Val Ser Leu Ser Val Trp Lys Met Tyr Ile Tyr Ile Leu Thr Ser
                165                 170                 175

Ser Arg Asp Phe Glu Asp Val Asp Asn Val Ile Thr Lys Leu Lys Gln
            180                 185                 190

Gln Arg Lys Ile Lys Ile
        195


<210> 1292
<211> 101
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1292
Met Ser Thr Ala Asn Arg Arg Asp Ile Ala Arg Lys Ile Ser Glu Asn
1               5                   10                  15

Thr Gly Tyr Tyr Ile Gln Asp Val Glu Glu Ile Leu Ser Ala Glu Thr
            20                  25                  30

Asp Ala Ile Ser Asp Leu Leu Glu Glu Gly Tyr Thr Lys Val Lys Asn
        35                  40                  45

His Lys Phe Met Gln Ile Glu Val Ile Glu Arg Lys Gly Lys Lys Ala
    50                  55                  60

Trp Asp Gly Leu Asn Lys Glu Tyr Phe His Leu Pro Asn Arg Lys Ala
65                  70                  75                  80

Ile Lys Phe Lys Pro Leu Lys Glu Leu Glu Glu Val Ile Asp Arg Leu
                85                  90                  95

Asn Glu Glu Glu Lys
```

100

<210> 1293
<211> 1072
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1293
Met Lys Val Leu Ile Leu Phe Asp His Ile Arg Glu Glu His Phe Ser
1 5 10 15

Val Ser Lys Asp Gly Ser Val Lys Ser Asn Val Leu Asn Thr Pro Asn
20 25 30

Gly Lys Thr Leu Lys Lys Leu Leu Glu Lys Cys Ser Asn Leu Lys Arg
35 40 45

Asp Lys Thr Asn Arg Asp Tyr Asp Ile Asp Phe Leu Tyr Asn Ala Val
50 55 60

Pro Thr Pro Ile Arg Asn Asp Tyr Gly Lys Ile Ile Lys Tyr Gln Asp
65 70 75 80

Val Lys Gln Ala Glu Val Lys Pro Tyr Tyr Glu Arg Met Asn Asn Ile
85 90 95

Ile Ile Asp Asn Ser Tyr Asp Met Ile Ile Pro Val Gly Lys Leu Gly
100 105 110

Val Lys Tyr Leu Leu Asn Val Thr Ala Ile Gly Lys Val Arg Gly Val
115 120 125

Pro Ser Lys Val Thr Ile Glu Asn Gly Thr Ser Ser His Asp Val Trp
130 135 140

Val Leu Pro Thr Tyr Ser Ile Glu Tyr Thr Asn Val Asn Lys Asn Ser
145 150 155 160

Glu Arg His Val Val Ser Asp Leu Gln Thr Val Gly Lys Phe Val Glu
165 170 175

Gln Gly Glu Glu Ala Phe Lys Pro Lys Glu Val Ser Tyr Glu Leu Val
180 185 190

Asp Asn Ile Glu Arg Val Arg Glu Ile Phe Asn Lys Glu Val Lys Asn
195 200 205

Asp Asn Tyr Asp Gly Val Asp Ile Thr Ala Trp Asp Leu Glu Thr Asn
210 215 220

```
Ser Leu Lys Pro Asp Lys Glu Gly Ser Lys Pro Leu Val Leu Ser Leu
225                 230                 235                 240

Ser Trp Arg Asn Gly Gln Gly Val Thr Ile Pro Leu Tyr Lys Ser Asp
                245                 250                 255

Phe Asn Trp Glu Asn Gly Gln Asp Asp Ile Asp Glu Val Leu Glu Leu
            260                 265                 270

Leu Lys Asn Trp Leu Ala Ser Lys Glu Asp Ile Lys Val Ala His Asn
        275                 280                 285

Gly Lys Tyr Asp Ile Lys Phe Leu Met Ser Thr Glu Asn Phe Lys Asp
    290                 295                 300

Phe Glu Ser Ile Gln Asp Thr Lys Val Gly Trp Tyr Leu Ala Val Thr
305                 310                 315                 320

Gln Glu Val Lys Glu Ser Leu Arg Leu Ser Asp Leu Ala Tyr Glu Val
                325                 330                 335

Thr Asp Val Gly Gly Tyr Asp Lys Pro Leu Glu Asp Phe Lys Leu Trp
            340                 345                 350

Phe Val Thr Lys Leu Leu Arg Phe Phe Ser Asp Lys Ile Lys Glu Ile
        355                 360                 365

Gln Lys Glu Asn Lys Lys Ile Ala Lys Lys Glu Tyr Asp Val Lys Ala
    370                 375                 380

Pro Glu Tyr Lys Glu Trp Leu Glu Asn Lys Leu Asn Glu Thr Val Val
385                 390                 395                 400

Glu Leu Asp Asp Thr Glu Lys Lys Phe Arg Val Ser Glu Leu Glu Lys
                405                 410                 415

Lys Tyr Ile Gln Leu Gly Leu Ser Pro Glu Ile Val Asn Met Asn Leu
            420                 425                 430

Val Met Asn Asn Asp Glu Phe Ile Ser Ile Ala Glu Gln Ser Pro Glu
        435                 440                 445

Tyr Met Gly Leu Ser Asp Tyr Ala Lys Ser Tyr Thr Leu Asn Thr Ala
    450                 455                 460

Ile Asn Leu Ile Asn Glu Tyr Arg Asp Val Lys Asp Val Val Asn Asp
465                 470                 475                 480

Ile Asp Gly Gly Asn Phe Asn Tyr Asp Trp Phe Pro Ile Glu Leu Met
                485                 490                 495
```

```
His Pro Tyr Ala Ser Gly Asp Thr Asp Val Cys Arg Arg Ile His Cys
            500                 505                 510

Asp Val Val Lys Lys Leu Lys Glu Gln Asp Arg Pro Lys Ser Met His
        515                 520                 525

Leu Leu Glu Val Asn Tyr Pro Arg Leu Thr Lys Ser Leu Ala Arg Ile
    530                 535                 540

Glu Ser Asn Gly Leu Tyr Cys Asp Leu Asp Tyr Met Lys Glu Asn Asp
545                 550                 555                 560

Glu Ser Tyr Glu Ser Glu Met Ala Lys Asn His Ala Thr Met Arg Glu
                565                 570                 575

His Trp Ala Val Lys Glu Phe Glu Glu Tyr Gln Tyr Asn Leu Tyr Gln
            580                 585                 590

Met Ala Leu Glu Glu His Glu Lys Lys Pro Lys Asp Arg Asp Lys Asp
        595                 600                 605

Ile His Gln Tyr Arg Asp Lys Phe Lys Asp Gly Lys Trp Met Phe Ser
    610                 615                 620

Pro Ser Ser Gly Asp His Lys Gly Arg Val Ile Tyr Asp Ile Leu Gly
625                 630                 635                 640

Ile Gln Leu Pro Tyr Asp Lys Glu Tyr Val Lys Glu Lys Pro Phe Asn
                645                 650                 655

Ala Asn Val Lys Glu Ala Asp Leu Thr Trp Gln Asp Tyr Lys Thr Asp
            660                 665                 670

Lys Lys Ala Ile Gly Tyr Ala Leu Asp Asn Leu Glu Leu Lys Asp Asp
        675                 680                 685

Val Arg Glu Leu Leu Glu Leu Leu Lys Tyr His Ala Ser Met Gln Thr
    690                 695                 700

Lys Arg Asn Ser Phe Thr Lys Lys Leu Pro Asn Met Ile Asn Lys Gln
705                 710                 715                 720

Lys Arg Thr Leu His Gly Ser Phe Ser Glu Thr Gly Thr Glu Thr Ser
                725                 730                 735

Arg Leu Ser Ser Ser Asn Pro Asn Leu Gln Asn Leu Pro Ala His Thr
            740                 745                 750

Ser Asp Val Asn Lys Phe Asp Tyr Lys His Pro Ile Lys Arg Ser Phe
        755                 760                 765
```

```
Val Ser Arg Phe Glu Asn Gly Val Leu Leu Gly Ala Asp Tyr Ser Ala
    770                 775                 780

Leu Glu Met Arg Ile Ile Gly Leu Phe Thr Lys Asp Pro Asp Met Leu
785                 790                 795                 800

Gln Ser Phe Leu Asn Gly Glu Asp Ile His Lys Ala Thr Ala Ser Ile
                805                 810                 815

Val Tyr Asn Lys Pro Val Glu Glu Val Thr Lys Glu Glu Arg Gln Ala
            820                 825                 830

Thr Lys Ala Val Asn Phe Gly Leu Ala Phe Gly Glu Ser Pro Phe Ser
        835                 840                 845

Phe Ala Gly Lys Asn Asn Met Glu Val Ser Glu Ala Glu Glu Ile Phe
    850                 855                 860

Glu Lys Tyr Phe Gln Thr Lys Pro Ser Val Lys Thr Ser Ile Asp Asn
865                 870                 875                 880

Val His Glu Phe Val Gln Gln Tyr Gly Tyr Val Asp Thr Met His Gly
                885                 890                 895

His Arg Arg Phe Ile Arg Ser Ala Gln Ser Thr Asp Lys Lys Ile Lys
            900                 905                 910

Asn Glu Gly Leu Arg Gln Ser Phe Asn Thr Ile Ile Gln Gly Ser Gly
        915                 920                 925

Ser Phe Leu Thr Asn Met Ser Leu Thr Tyr Leu Asp Asp Phe Ile Gln
    930                 935                 940

Ser Arg Asn Leu Lys Ser Lys Val Ile Ala Thr Val His Asp Ser Ile
945                 950                 955                 960

Leu Ile Asp Cys Pro Pro Glu Glu Ala Lys Ile Met Ala Lys Val Thr
                965                 970                 975

Ile His Ile Met Glu Asn Leu Pro Phe Asp Phe Leu Lys Ala Glu Ile
            980                 985                 990

Asp Gly Lys Glu Val Gln Tyr Pro  Ile Glu Ala Asp Met  Glu Ile Gly
        995                 1000                1005

Leu Asn  Tyr Asn Asp Met Val  Glu Tyr Asp Glu Glu  Glu Ile Asp
    1010                1015                1020

Thr Phe  Asn Ser Tyr Gln Gly  Tyr Ile Lys Tyr Met  Met Asn Leu
    1025                1030                1035
```

Gln Thr Leu Glu Asp Tyr Lys Glu Ser Gly Lys Leu Thr Asp Glu
1040 1045 1050

Gln Phe Glu Lys Ala Thr Asn Val Val Lys Ser Glu Lys His Ile
1055 1060 1065

Tyr Gln Glu Ile
1070

<210> 1294
<211> 80
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1294
Val Asn Thr Gly Glu Ile Arg Phe Asn Arg Ser Met Asp Glu Trp Ile
1 5 10 15

Ile Thr Ser Met Tyr Gln Asp Glu Leu Gly Glu Met Asn Ile Val Val
20 25 30

Thr Phe Tyr Asn Arg Glu Glu Asn Lys His Gly Ser Thr Val Leu Pro
35 40 45

Thr Glu Ser Ser Thr Gly Glu Val Ala Glu Glu Leu Ala Ser Leu Glu
50 55 60

Glu Glu Tyr Pro Leu Ala Leu Pro Leu Ser Ser Ile Ser Val Asn Ile
65 70 75 80

<210> 1295
<211> 160
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1295
Met Glu Ile His Ile Asp Ser Leu Asp Phe Thr Asn Phe Thr Ile Lys
1 5 10 15

Asp Arg Asn Gly Asn Ser Gln Glu Phe Asp Ile Thr Asp Glu Leu Arg
20 25 30

Ile Thr Glu Tyr Thr Ile Gln Glu Asp Phe Met Gln Gln Ser Ala Lys
35 40 45

Tyr Ala Phe Trp Ala Ser Ile Leu Glu Lys Val Arg Ala Tyr Ser Glu
50 55 60

Met Glu Gln Arg Asn Leu Glu Thr Ile Gly Ser Lys Leu Asn Leu Thr
65 70 75 80

Ile Arg Gln Glu Tyr Glu Gln Gln Gly Lys Lys Pro Thr Lys Asp Met
85 90 95

Ile Glu Ser Ser Val Tyr Ile His Asp Ser Tyr Gln Gln Gln Leu Lys
100 105 110

Val Val Glu Ala Trp Asn Tyr Lys Val Lys Gln Leu Gln Tyr Val Val
115 120 125

Lys Ala Phe Glu Thr Arg Arg Asp Met Met Ile Gln Leu Gly Ala Glu
130 135 140

Leu Arg Gln Thr Asn Lys Asn Gly Gly Ile Thr Asn Pro Phe Ser His
145 150 155 160

<210> 1296
<211> 423
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1296
Met Asp Phe Asn Gln Phe Ile Asn Asn Glu Ala Ser Lys Leu Glu Ser
1 5 10 15

Asn Asn Ser Ser Phe Asn Asn Asn Val Glu Ser Tyr Lys Pro Lys Asn
20 25 30

Pro Val Leu Arg Leu Gly Asn Ile Lys Asp Ala Asn Gly Asn Lys Val
35 40 45

Val Lys Glu Asn Ala Phe Val Arg Val Leu Pro Pro Ala Gln Gly Thr
50 55 60

Asn Val Phe Phe Lys Glu Phe Arg Thr Thr Gly Ile Asn Tyr Ser Lys
65 70 75 80

Lys Asp Gly Ser Gln Gly Phe Thr Gly Leu Thr Leu Pro Ala Glu Glu
85 90 95

Gly Ser Ser Val Leu Asp Pro Tyr Ile Gln Asp Trp Ile Thr Asn Gly
100 105 110

Val Gln Phe Ser Arg Phe Pro Asn Lys Pro Gly Val Arg Tyr Tyr Ile
115 120 125

His Val Ile Glu Tyr Phe Asn Asn Asn Gly Gln Ile Gln Pro Lys Thr
130 135 140

Asp Ala Gln Gly Asn Val Met Ile Gln Pro Met Glu Leu Ser Asn Thr

145 150 155 160

Gly Tyr Lys Glu Leu Leu Ala Asn Leu Lys Asp Thr Met Leu Lys Pro
165 170 175

Ser Pro Asn Ala Pro His Ser Phe Ile Ser Ala Asn Glu Ala Phe Leu
180 185 190

Val Asn Ile Val Lys Ala Lys Lys Gly Glu Met Ser Trp Lys Val Ser
195 200 205

Val Tyr Pro Asn Ala Pro Leu Gly Ala Leu Pro Gln Gly Trp Glu Gln
210 215 220

Gln Leu Ser Asp Leu Asp Gln Leu Ala Lys Pro Thr Glu Glu Gln Asn
225 230 235 240

Pro Asn Phe Val Asn Phe Leu Ile Asn Asn Val Asn Asn Thr Glu Leu
245 250 255

Ser His Asp Asn Phe Lys Phe Asn Arg Glu Thr Asn Val Leu Gly Glu
260 265 270

Glu Pro Ser Glu Pro Lys Gln Ala Pro Thr Gln Gln Asp Val Asp Ser
275 280 285

Gln Met Pro Ser Asn Met Gly Gly Gln Pro Asn Gln Pro Gln Gln Gly
290 295 300

Gln Val Gly Gln Tyr Ala Gln Gln Gly Gln Ser Asn Gly Gln Gly Gln
305 310 315 320

Gln Leu Gln Gly Thr Gln Gln Pro Ile Asn Asn Thr Gln Phe Gly Gln
325 330 335

Gly Thr Pro Ser Gly Gln Gln Pro Ser Asn Thr Gly Ser Val Asp Trp
340 345 350

Asp Asn Leu Ala Gln Gln Gln Ser Gln Pro Asp Ser Asn Pro Phe Asn
355 360 365

Asp Phe Asp Val Ser Ser Val Asp Asp Ser Gln Val Pro Phe Glu Thr
370 375 380

Gln Pro Gln Asn Thr Gln Gln Ala Pro Glu Pro His Gln Thr Thr Gln
385 390 395 400

Glu Pro Pro Lys Gln Lys Gln Thr Gln Ser Ile Asp Asp Val Leu Gly
405 410 415

Gly Leu Asp Leu Asp Asn Leu

420

<210> 1297
<211> 421
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1297
Met Ala Arg Ala Lys Lys Gly Lys Glu Val Asp Leu Thr Asp Leu Asn
1 5 10 15

Thr Ile Asp Leu Gly Lys Glu Leu Gly Leu Thr Leu Leu Ser Asp Ser
20 25 30

Asn Arg Ala Asp Ile Lys Asn Ile Val Pro Thr Met Val Pro Gln Tyr
35 40 45

Asp Arg Ile Leu Gly Gly Gly Ile Pro Leu Gly Arg Leu Thr Glu Val
50 55 60

Tyr Gly Leu Thr Gly Ser Gly Lys Ser Ser Phe Ala Val His Leu Ser
65 70 75 80

Arg Ile Ser Thr Gln Leu Gly Val Ile Thr Ile Trp Ile Asp Ile Glu
85 90 95

Gly Thr Ala Asp Asn Asn Arg Met Glu Gln Leu Gly Val Asp Val Ser
100 105 110

Lys Leu Phe Ser Ile Gln Ala Gly Glu Gly Arg Leu Lys Asn Thr Val
115 120 125

Glu Leu Ser Val Glu Thr Val Gly Lys Glu Leu Asp Tyr Trp Ile Asp
130 135 140

Thr Phe Asn Glu Lys Ala Pro Gly Val Pro Ile Leu Phe Ile Trp Asp
145 150 155 160

Ser Leu Gly Ala Thr Arg Thr Gln Ala Glu Ile Glu Glu Gly Val Asp
165 170 175

His Arg Lys Leu Gly Thr Lys Ala Thr Ala Thr Gln Lys Val Ile Asn
180 185 190

Ala Val Ser Pro Lys Leu Asn Asp Thr Asn Thr Gly Leu Ile Val Ile
195 200 205

Asn Gln Ala Arg Asp Asn Leu Asn Met Ser Asn Pro Tyr Asp Asp Pro
210 215 220

Ile Lys Ser Thr Gly Gly Arg Ala Phe Glu His Gly Ala Ser Leu Arg
225 230 235 240

Leu Lys Ile Thr Lys Gly Lys Glu Ser Asp Leu Lys Gln Ser Asp Ser
245 250 255

Met Thr Gly Lys Pro Thr Tyr Lys Gly His Val Met Arg Val Glu Thr
260 265 270

Lys Lys Ser Lys Leu Ser Arg Pro Gly Gln Lys Ala Glu Ala Asp Leu
275 280 285

Leu Ser Gly Tyr Glu Val Gly Ser Gly Ser Asp Ile Thr Gln Leu Asn
290 295 300

Gly Ile Asp Pro Tyr His Thr Ile Tyr Lys Glu Ala Val Glu Arg Gly
305 310 315 320

Leu Ile Thr Lys Gly Thr Trp Arg Asn Tyr Ile Thr Leu Asn Gly Glu
325 330 335

Glu Ile Lys Leu Tyr Asp Lys Asp Trp Val Pro Arg Leu Ile Asp Asp
340 345 350

His Glu Leu Tyr Leu Glu Leu Phe Ser Arg Val Tyr Gly Glu His Phe
355 360 365

Pro Asn Gly Tyr Ser Pro Leu Leu Asn Thr Lys Val Ile Val Thr Gln
370 375 380

Leu Glu Glu Tyr Gln Ala Leu Glu Asn Tyr Tyr Glu Glu Trp Ala Lys
385 390 395 400

Asp Asn Lys Gln Glu Glu Gln Glu Glu Glu Ser Lys Gly Glu Ser Gln
405 410 415

Glu Lys Asp Ser Glu
420

<210> 1298
<211> 117
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1298
Met Tyr Asn Leu Ile Asp Lys Asn Met Arg Gln Val Lys Glu Ser Leu
1 5 10 15

Gly Asn Ala Asn Ser Ser Asp Val Leu Pro Leu Pro Tyr Lys Asp Ile
20 25 30

Ala Lys Lys Phe Glu Glu Val Lys Glu Lys Gly Glu Ser Ile Ile Ile
35 40 45

Glu Glu Gly Gly Phe Pro Tyr Thr Asp Ser Thr Val Met Tyr Ile Glu
50 55 60

His Val Thr Asp Arg Trp Ala Gly Gly Tyr Ser Leu Ile Arg His Glu
65 70 75 80

Gly Glu Glu Val Lys Val Pro Lys Thr Ile His Phe Ser Asp Ile Tyr
85 90 95

Val Lys Asp Lys Ser His Lys Val Arg Ile Ile Phe Glu Gly Ala Asn
100 105 110

Pro Tyr Glu Glu Gly
115

<210> 1299
<211> 220
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1299
Met Lys Lys Ala Lys Asn Gly Asn Arg Tyr Val Ile Asp Ile Asp Gly
1 5 10 15

Ile Pro Val Asp Phe Glu Arg Asp Leu Asp Ser Leu Leu Asn Arg Tyr
20 25 30

Lys Asn Leu Arg Trp Ser Leu Tyr His Lys Tyr Ala Gly Ile Leu Ser
35 40 45

Asn Asp Phe Glu Arg Gln Glu Leu Arg Glu Tyr Ile Asp Glu Gln Phe
50 55 60

Ile Lys Leu Val Lys Glu Tyr Asn Ile Arg Ser Lys Val Asp Phe Pro
65 70 75 80

Gly Tyr Ile Lys Ala Lys Leu Thr Leu Arg Val Gln Asn Ser Tyr Val
85 90 95

Lys Lys Asn Glu Lys Tyr Lys Arg Thr Glu Ile Ile Gly Lys Lys Asp
100 105 110

Tyr Thr Val Glu Ser Leu Thr Glu Asp Leu Asn Glu Asp Phe Glu Asp
115 120 125

Asn Gln Ile Met Ser Tyr Val Phe Asp Asp Ile Glu Phe Thr Glu Val
130 135 140

```
Gln Ser Glu Leu Leu Lys Glu Leu Leu Ile Asn Pro Glu Arg Glu Asp
145                 150                 155                 160

Asp Ala Phe Ile Val Ser Gln Val Ala Glu Lys Phe Asp Met Lys Arg
                165                 170                 175

Lys Glu Val Ala Ser Glu Leu Thr Glu Leu Arg Asp Tyr Val Arg Phe
            180                 185                 190

Lys Ile Asn Ala Tyr His Glu Tyr Tyr Ala Lys Lys Glu Leu Asn Asn
        195                 200                 205

His Arg Val Asn Thr Glu Asn His Ile Trp Glu Asn
    210                 215                 220


<210> 1300
<211> 293
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Bacteriophage F125/10

<400> 1300
Val Arg Ile Glu Lys His Lys Ile Lys Asn Asn Lys Val Ile Asn Glu
1               5                   10                  15

Met Ser Ile Thr Ala Asn Asn Leu Tyr Asn His Ala Asn Phe Ile Leu
            20                  25                  30

Arg Gln Asn Phe Phe Asn Asn Lys Thr Asn Lys Gly Tyr Arg Lys Phe
        35                  40                  45

Leu Asn Tyr Asn Thr Ile His Arg Ile Leu Lys Asn Met Asn Glu Glu
    50                  55                  60

Asn Tyr Ile Lys Leu Pro Arg Gln Thr Ser Gln Gln Val Leu Arg Asp
65                  70                  75                  80

Leu Ile Asn Asn Trp Ser Ser Phe Arg Lys Ser Glu Lys Asp Tyr Phe
                85                  90                  95

Lys Asn Pro Asn Lys Tyr Arg Asn Arg Pro Lys Pro Pro Lys Tyr Lys
            100                 105                 110

Ala Lys Gly Gly Lys Gly Thr Ile Lys Phe Thr Asn Gln Gln Cys Arg
        115                 120                 125

Ile His Lys Lys Asp Gly Leu Ile His Leu Pro Thr Pro Leu Gln Asp
    130                 135                 140

Ile Thr Ile Lys Pro Tyr Lys Ala Lys Asn Ile Arg Glu Leu Val Cys
```

```
145                 150                 155                 160

Ile Pro Lys Ser Asp Tyr Phe Glu Val Leu Val Cys Tyr Lys Glu Glu
                165                 170                 175

Asn Ser Asn Lys Thr Leu Asn Asp Asn Glu Asn Ile Ala Ser Ile Asp
            180                 185                 190

Leu Gly Leu Asp Asn Leu Ile Thr Met Val Ser Ile Val Asp Lys Pro
        195                 200                 205

Ile Ile Ile Asn Gly Lys Gly Leu Lys Ser Lys Asn Lys Tyr Phe Asn
    210                 215                 220

Lys Lys Ile Arg Tyr Tyr Gln Ser Leu Leu Gln Asn Asn Ser Tyr Ser
225                 230                 235                 240

Ser Lys Arg Ile Leu Lys Tyr Trp Glu Lys Arg His Asn Ile Ile Leu
                245                 250                 255

Asp Tyr Phe His Lys Ala Thr Asn Glu Val Val Lys Tyr Cys Val Lys
            260                 265                 270

Asn Asp Ile Ser Lys Val Val Ile Gly Tyr Asn Lys Gln Gln Lys Tyr
        275                 280                 285

Lys Ser Lys Leu Lys
    290
```