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SEQUENCE LISTING

<110> Statoil Petroleum AS
Kotlar, Hans Kristian (US only)
Berg, Svein (US only)
Lioliou, Maria G (US only)
Wentzel, Alexander (US only)

<120> Novel enzymes for enhanced gas absorption

<130> P61200378PCT00

<160> 32

<170> PatentIn version 3.5

<210> 1

<211> 450

<212> DNA

<213> Unknown

<220>

<223> Unknown

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 ctgtagtgtg aaaaaattat ggttgtggga cacacagatt gtggtatggc ttcagcagat 240
 gctgaattga ttaaaaagaa gataatcgaa agaggcggaa atcctcattt cactcctaac 300
 tttgaatgct ggtaggttaa aatggagtc atagaagata acgtaattga aggagttaat 360
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 attgaaactg gagatcttga aaaatttgtt 450

<210> 2

<211> 150

<212> PRT

<213> unknown

<220>

<223> Unknown

<400> 2

Leu Ser Ser Asp Ala Lys Pro Lys Lys Lys Leu Ala Ile Val Thr Cys
 1 5 10 15

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

Arg Asn Asp Ala Lys Val Ile Lys Asn Ala Gly Asn Ile Val Thr Asp
 35 40 45

Asp Val Ile Arg Ser Leu Val Val Ser Ile Tyr Leu Leu Asp Val Glu
 50 55 60

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Lys Ile Met Val Val Gly His Thr Asp Cys Gly Met Ala Ser Ala Asp
 65 70 75 80

Ala Glu Leu Ile Lys Lys Lys Ile Ile Glu Arg Gly Gly Asn Pro His
 85 90 95

Phe Thr Pro Asn Phe Glu Cys Trp Leu Gly Lys Met Glu Ser Ile Glu
 100 105 110

Asp Asn Val Ile Glu Gly Val Asn Leu Ile Lys Asn His Pro Ala Ile
 115 120 125

Pro Lys Asp Val Thr Val Glu Gly Tyr Leu Ile Asp Ile Glu Thr Gly
 130 135 140

Asp Leu Glu Lys Leu Cys
 145 150

<210> 3
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 <212> DNA
 <213> Artificial

<220>
 <223> Codon optimised for E. coli

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 ctggacgttg aaaaaattat ggctgtgggc catacggatt gcggtatggc gagtgccgac 240
 gcagaactga ttaaaaagaa aattatcgaa cgtggcggta acccgcaatt taccgccaat 300
 ttcgaatgtt ggctgggcaa aatggaaagc attgaagata atgtgatcga aggtgttaac 360
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 attgaaacgg gtgacctgga aaaactgtgt 450

<210> 4
 <211> 149
 <212> PRT
 <213> Artificial

<220>
 <223> Product of codon optimized nucleotide sequence, differs in first amino-acid residue being M instead of L

<400> 4

Met Ser Ser Asp Ala Lys Pro Lys Lys Lys Leu Ala Ile Val Thr Cys
 1 5 10 15

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

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Arg Asn Asp Ala Lys Val Ile Lys Asn Ala Gly Asn Ile Val Thr Asp
 35 40 45

Asp Val Ile Arg Ser Leu Val Val Ser Ile Tyr Leu Leu Asp Val Glu
 50 55 60

Lys Ile Met Val Val Gly His Thr Asp Cys Gly Met Ala Ser Ala Asp
 65 70 75 80

Ala Glu Leu Ile Lys Lys Lys Ile Ile Glu Arg Gly Gly Asn Pro His
 85 90 95

Phe Thr Pro Asn Phe Glu Cys Trp Leu Gly Lys Met Glu Ser Ile Glu
 100 105 110

Asp Asn Val Ile Glu Gly Val Asn Leu Ile Lys Asn His Pro Ala Ile
 115 120 125

Pro Lys Asp Val Thr Val Glu Gly Tyr Leu Ile Asp Ile Glu Thr Gly
 130 135 140

Asp Leu Glu Lys Leu
 145

<210> 5
 <211> 579
 <212> DNA
 <213> Unknown

<220>
 <223> Unknown

<400> 5
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 gctcgtcttg accctgcaaa atatgcaggc ttagcagaag gtgatgcgca tgtcatccgt 180
 aacgctgggtg gaagggcaag tgatgatgct attcgttcac tggttatttc ttataaatta 240
 ctaggaacaa aagagtgggtt tgttatccat catacagatt gcggaatgca aacatttaat 300
 aatgaaatca tgggagaact actatcaaga agtctaaaaa cctcaagtgt agatgcttct 360
 ggttggcatg atagtaatgc tggtggtggt acaactgatg gcaagtttgt tgagtggctt 420
 acaataagtg accaatcaaa aagtgtatta gaagatgtac aaagaattag aaacaactcc 480
 atggttccaa gcgatattcc aatctacgga tatatttatg attgtgcaac aggaaatctt 540
 atagaagttc cagaagcaac agctgcagga aaagcaagc 579

<210> 6
 <211> 193
 <212> PRT
 <213> Unknown

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<220>

<223> Unknown

<400> 6

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

Ser

<210> 7

<211> 579

<212> DNA

<213> Artificial

<220>

<223> Codon optimised for E. coli

<400> 7

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gctcgtcttg acccggcgaa atacgccggt ctggcagaag gcgatgcgca tgtgatccgt      180
aacgctggcg gtcgcgcgag tgatgacgcc attcgcagcc tggtcatttc ttataaactg      240
ctgggtacga aagaatggtt tgtgattcat cacaccgatt gtggtatgca aacgttcaac      300
aatgaaatca tgggcgaact gctgagtcgt tccctgaaaa ccagctctgt tgatgcgtca      360
ggttggcacg actcgaatgc cggcgggtggc accacggatg gcaaattcgt cgaatggctg      420
acgatttctg atcagtcaaa atcggtgctg gaagacgttc aacgtatccg caacaatagt      480
atggttccgt ccgacattcc gatctatggc tacatttatg actgtgcgac gggtaacctg      540
attgaagtgc cggaagcaac ggctgcgggt aaagcatcc      579

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<210> 8
<211> 193
<212> PRT
<213> Artificial

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<220>
<223> Product of codon optimised sequence

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<400> 8

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Met Ser Lys Val Val Glu Glu Val Thr Ser Ala Asn Ala Gln Tyr Ala
1          5          10          15

```

```

Val Asn Phe Gly Asn Lys Gly Glu Leu Pro Met Pro Pro Gly Arg Gln
          20          25          30

```

```

Phe Ala Ile Leu Thr Cys Met Asp Ala Arg Leu Asp Pro Ala Lys Tyr
          35          40          45

```

```

Ala Gly Leu Ala Glu Gly Asp Ala His Val Ile Arg Asn Ala Gly Gly
          50          55          60

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```

Arg Ala Ser Asp Asp Ala Ile Arg Ser Leu Val Ile Ser Tyr Lys Leu
65          70          75          80

```

```

Leu Gly Thr Lys Glu Trp Phe Val Ile His His Thr Asp Cys Gly Met
          85          90          95

```

```

Gln Thr Phe Asn Asn Glu Ile Met Gly Glu Leu Leu Ser Arg Ser Leu
          100          105          110

```

```

Lys Thr Ser Ser Val Asp Ala Ser Gly Trp His Asp Ser Asn Ala Gly
          115          120          125

```

```

Gly Gly Thr Thr Asp Gly Lys Phe Val Glu Trp Leu Thr Ile Ser Asp
          130          135          140

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```

Gln Ser Lys Ser Val Leu Glu Asp Val Gln Arg Ile Arg Asn Asn Ser
145          150          155          160

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Met Val Pro Ser Asp Ile Pro Ile Tyr Gly Tyr Ile Tyr Asp Cys Ala
 165 170 175

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

Ser

<210> 9
 <211> 660
 <212> DNA
 <213> unknown

<220>
 <223> Unknown

<400> 9
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 gcgtgcagcg attcgcggaac cgatccgctc ttcattcatgc agtgcgagcc gggcgacata 180
 ttcgtgggtcc gcaacgtggc caacatcgctc ccgccgtacg agagcgacga ggggtttccac 240
 ggcgtgtcct cggccatcga gtacgcgggtc caggctcctca aggtggagca cctcatcgctg 300
 ctcggccaca gcctgtgctg cggcatagat gcgctgatgc acgatgacaa ggtccggcac 360
 accgagttcc tgcacaagtg gctgtcggtc atgagtcctg tgcgcgacga ggtcgtggac 420
 catttcggcg aggtcaacaa gaagtcctgc accgcctgcg agatggcggg catcctgcgc 480
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 agcctgcacg gctgggtatct cgagatggag tcggggccagt tgctcagcta catgcgcgag 600
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<210> 10
 <211> 220
 <212> PRT
 <213> Unknown

<220>
 <223> Unknown

<400> 10

Met Lys Asp Ile Gln Lys Phe Ile Ala Gly Phe Arg Asn Phe Arg Lys
 1 5 10 15

Glu Tyr Phe Ser Arg Glu Asp Ala Pro Phe Glu Ile Leu Leu Lys Gly
 20 25 30

Gln Asn Pro Thr Thr Met Val Ile Ala Cys Ser Asp Ser Arg Thr Asp
 35 40 45

Pro Ser Phe Ile Met Gln Cys Glu Pro Gly Asp Ile Phe Val Val Arg
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50

55

60

Asn Val Ala Asn Ile Val Pro Pro Tyr Glu Ser Asp Glu Gly Phe His
65 70 75 80

Gly Val Ser Ser Ala Ile Glu Tyr Ala Val Gln Val Leu Lys Val Glu
85 90 95

His Leu Ile Val Leu Gly His Ser Leu Cys Gly Gly Ile Asp Ala Leu
100 105 110

Met His Asp Asp Lys Val Arg His Thr Glu Phe Leu His Lys Trp Leu
115 120 125

Ser Val Met Ser Pro Val Arg Asp Glu Val Val Asp His Phe Gly Glu
130 135 140

Val Asn Lys Lys Ser Cys Thr Ala Cys Glu Met Ala Gly Ile Leu Arg
145 150 155 160

Ser Val Arg Asn Leu Met Thr Phe Pro Trp Ile Arg Glu Arg Val Asp
165 170 175

Gln Gly Lys Leu Ser Leu His Gly Trp Tyr Phe Glu Met Glu Ser Gly
180 185 190

Gln Leu Leu Ser Tyr Met Arg Glu Thr Glu Thr Phe Glu Pro Leu Ser
195 200 205

Lys Cys Cys Pro Val Leu Lys Arg Glu Gln Thr Asp
210 215 220

<210> 11
<211> 663
<212> DNA
<213> Artificial

<220>
<223> Codon optimised for E. coli

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attgctgca gtgattcccc taccgacccg tcatttatta tgcaatgtga accgggtgat 180
atcttcgtgg ttcgcaacgt ggccaatatt gttccgccgt atgaatcgga cgaaggcttt 240
catggtgtta gctctgcgat cgaatacgcc gttcagggtcc tgaaagttga acatctgatt 300
gtcctgggcc acagtctgtg cggcgggtatc gatgcgctga tgcattgatga caaagtcctg 360
catacggaat ttctgcacaa atggctgtca gtcattgtgc cgggtgcgca tgaagtcgtg 420
gaccacttcg gcgaagttaa caaaaaatct tgcaccgcat gtgaaatggc tgggtattctg 480

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cggtccgtgc gcaatctgat gacgtttccg tggattcgtg aacgcgttga tcagggcaaa 540
 ctgtctctgc acggttggtg tttcgaaatg gaaagcggtc aactgctgtc ttacatgcgt 600
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 gat 663

<210> 12
 <211> 221
 <212> PRT
 <213> Artificial

<220>
 <223> Product of codon optimized nucleotide sequence, additional amino acid residue at position #2 (Ser2 between Met1 and Lys3)

<400> 12

Met Ser Lys Asp Ile Gln Lys Phe Ile Ala Gly Phe Arg Asn Phe Arg
 1 5 10 15

Lys Glu Tyr Phe Ser Arg Glu Asp Ala Pro Phe Glu Ile Leu Leu Lys
 20 25 30

Gly Gln Asn Pro Thr Thr Met Val Ile Ala Cys Ser Asp Ser Arg Thr
 35 40 45

Asp Pro Ser Phe Ile Met Gln Cys Glu Pro Gly Asp Ile Phe Val Val
 50 55 60

Arg Asn Val Ala Asn Ile Val Pro Pro Tyr Glu Ser Asp Glu Gly Phe
 65 70 75 80

His Gly Val Ser Ser Ala Ile Glu Tyr Ala Val Gln Val Leu Lys Val
 85 90 95

Glu His Leu Ile Val Leu Gly His Ser Leu Cys Gly Gly Ile Asp Ala
 100 105 110

Leu Met His Asp Asp Lys Val Arg His Thr Glu Phe Leu His Lys Trp
 115 120 125

Leu Ser Val Met Ser Pro Val Arg Asp Glu Val Val Asp His Phe Gly
 130 135 140

Glu Val Asn Lys Lys Ser Cys Thr Ala Cys Glu Met Ala Gly Ile Leu
 145 150 155 160

Arg Ser Val Arg Asn Leu Met Thr Phe Pro Trp Ile Arg Glu Arg Val
 165 170 175

Asp Gln Gly Lys Leu Ser Leu His Gly Trp Tyr Phe Glu Met Glu Ser
 180 185 190

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Gly Gln Leu Leu Ser Tyr Met Arg Glu Thr Glu Thr Phe Glu Pro Leu
 195 200 205

Ser Lys Cys Cys Pro Val Leu Lys Arg Glu Gln Thr Asp
 210 215 220

<210> 13
 <211> 630
 <212> DNA
 <213> Unknown

<220>
 <223> Unknown

<400> 13
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 gcttgtagtg attcaagagt ggatcccggt ttgattacaa attctgatcc tggagattta 180
 tttatttttaa gaaacatagg aaactttggt cctccttttt ctcttgataa tgactatcat 240
 gcaacagcag ctggtattga gtatgctact catattttta aagtaacaga tattattgta 300
 tgtggacatt ctactgtgg agcaattaat agtctttatc aagatgtaag tagtataaat 360
 cttttgcatg taaagaagtg gttagatttg ggattggaag ctaaaaacta ttagagaaat 420
 agtataaaaa ctggtgcaac tcatgaagaa aaactagaat tgacagaaaa agtttcaatt 480
 gttttgcaga tgaaaaattt acctacatat cctgaagttg attccagagt tgattctgga 540
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 gataaagaac gagaattcaa accaatggta 630

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

<220>
 <223> Unknown

<400> 14

Met Lys Val Gln Asp Leu Ile Asp Gly His Glu Asn Phe Lys Asp Lys
 1 5 10 15

Lys Phe Lys Lys Tyr Glu Asn Lys Phe Leu Asp Leu Val Lys Asn Gly
 20 25 30

Gln Lys Ala Lys Val Leu Phe Ile Ala Cys Ser Asp Ser Arg Val Asp
 35 40 45

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

Asn Ile Gly Asn Phe Val Pro Pro Phe Ser Pro Asp Asn Asp Tyr His
 65 70 75 80

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Ala Thr Ala Ala Gly Ile Glu Tyr Ala Thr His Ile Leu Lys Val Thr
85 90 95

Asp Ile Ile Val Cys Gly His Ser His Cys Gly Ala Ile Asn Ser Leu
100 105 110

Tyr Gln Asp Val Ser Ser Ile Asn Leu Leu His Val Lys Lys Trp Leu
115 120 125

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

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

Val Leu Gln Met Lys Asn Leu Leu Thr Tyr Pro Glu Val Asp Ser Arg
165 170 175

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

Thr Gly Glu Leu Glu Tyr Phe Cys Asp Lys Glu Arg Glu Phe Lys Pro
195 200 205

Met Val
210

<210> 15
<211> 648
<212> DNA
<213> Artificial

<220>
<223> Codon optimized for E coli

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attgcttgca gtgattcccg tgtggaccgg gttctgatca ccaattctga tccgggcgac 180
ctgttcattc tgcgcaacat cggtaat tttgtcccgcgt tcagcccgga taacgactat 240
catgcgacgg cgccgggtat tgaatacgcc acccacatcc tgaaagtgc ggatattatc 300
gtttgcggcc attctcactg tgggtgcaatt aacagtcctgt atcaggatgt cagctctatc 360
aatctgctgc atgtgaaaaa atggctggac ctgggcctgg aagcaaaaaa ctacgtggaa 420
aactccatca aaaccggtgc tacgcacgaa gaaaaactgg aactgaccga aaaagtcagc 480
atcgtgctgc aaatgaaaaa tctgctgacg tatccggaag ttgattcacg tgtcgactcg 540
ggcaaactga gcattcgcgg ttggtattac aaactggaaa ccggcgaact ggaatacttc 600
tgtgacaaag aacgcgaatt taaaccgatg gtctcaatca gcgaattt 648

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<210> 16
 <211> 216
 <212> PRT
 <213> Artificial

<220>
 <223> Product of codon optimized nucleotide sequence, additional amino acid residue at position #2(Ser2 between Met1 and Lys3), and in adding the last five amino acid residues.

<400> 16

Met Ser Lys Val Gln Asp Leu Ile Asp Gly His Glu Asn Phe Lys Asp
 1 5 10 15

Lys Lys Phe Lys Lys Tyr Glu Asn Lys Phe Leu Asp Leu Val Lys Asn
 20 25 30

Gly Gln Lys Ala Lys Val Leu Phe Ile Ala Cys Ser Asp Ser Arg Val
 35 40 45

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

Arg Asn Ile Gly Asn Phe Val Pro Pro Phe Ser Pro Asp Asn Asp Tyr
 65 70 75 80

His Ala Thr Ala Ala Gly Ile Glu Tyr Ala Thr His Ile Leu Lys Val
 85 90 95

Thr Asp Ile Ile Val Cys Gly His Ser His Cys Gly Ala Ile Asn Ser
 100 105 110

Leu Tyr Gln Asp Val Ser Ser Ile Asn Leu Leu His Val Lys Lys Trp
 115 120 125

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

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

Ile Val Leu Gln Met Lys Asn Leu Leu Thr Tyr Pro Glu Val Asp Ser
 165 170 175

Arg Val Asp Ser Gly Lys Leu Ser Ile Arg Gly Trp Tyr Tyr Lys Leu
 180 185 190

Glu Thr Gly Glu Leu Glu Tyr Phe Cys Asp Lys Glu Arg Glu Phe Lys
 195 200 205

Pro Met Val Ser Ile Ser Glu Phe
 210 215

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<210> 17
 <211> 606
 <212> DNA
 <213> Unknown

<220>
 <223> Unknown

<400> 17
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 ggtccaaacg ctgttataag gtgtgatgaa cctccaacta aaggatatatt aataaaagaa 180
 ggggcgaata ttcaagatat ggttgtgata cactgtctta gaaatacgtc ggtagttgtt 240
 ggcaagggaag cttcaatcac tcattccacg gtaattcatg gtcctgcaaa aattggagat 300
 aatgcattta ttgggtttaa ttcagttgta tttggagctg aaattggaga taatacaata 360
 gtgggacata actctgttgt agatggagta gggggcgatt taaaaatacc gaatgataaa 420
 tggatcccc caaatacttc catatataag gattcagatg ggataataaa agcatttttg 480
 ccgaatggaa ctattttaac agattttaac aagcttcccc atattccaga atggtataaa 540
 aaggttccag gagatgttgt gaaagtaaata aaagagttga atttgggata tagagaattt 600
 attaaa 606

<210> 18
 <211> 202
 <212> PRT
 <213> Unknown

<220>
 <223> Unknown

<400> 18

Met Glu Lys Asn Ile Leu Pro Asn Ile Glu Gly Lys Thr Pro Asn Ile
 1 5 10 15

Asp Lys Asn Val Phe Ile Asp Lys Ser Ala Val Ile Ile Gly Asp Val
 20 25 30

Ala Ile Gln Lys Asn Val Tyr Ile Gly Pro Asn Ala Val Ile Arg Cys
 35 40 45

Asp Glu Pro Pro Thr Lys Gly Ile Leu Ile Lys Glu Gly Ala Asn Ile
 50 55 60

Gln Asp Met Val Val Ile His Cys Leu Arg Asn Thr Ser Val Val Val
 65 70 75 80

Gly Lys Glu Ala Ser Ile Thr His Ser Thr Val Ile His Gly Pro Ala
 85 90 95

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Lys Ile Gly Asp Asn Ala Phe Ile Gly Phe Asn Ser Val Val Phe Gly
 100 105 110

Ala Glu Ile Gly Asp Asn Thr Ile Val Gly His Asn Ser Val Val Asp
 115 120 125

Gly Val Gly Gly Asp Leu Lys Ile Pro Asn Asp Lys Trp Ile Pro Pro
 130 135 140

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

Pro Asn Gly Thr Ile Leu Thr Asp Phe Asn Lys Leu Pro Asp Ile Pro
 165 170 175

Glu Trp Tyr Lys Lys Val Pro Gly Asp Val Val Lys Val Asn Lys Glu
 180 185 190

Leu Asn Leu Gly Tyr Arg Glu Phe Ile Lys
 195 200

<210> 19
 <211> 609
 <212> DNA
 <213> Artificial

<220>
 <223> Codon optimised for E. coli

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 gaagggtgcga acatccaaga catggtgggtt attcattgtc tgcgcaatac gtctgtcgtg 240
 gttggcaaaag aagccagcat caccatttct acggtgattc acggcccggc gaaaatcggg 300
 gataacgcct ttattgggtt caattcagtc gtgtttggcg cagaaattgg tgacaacacc 360
 atcgtcggcc acaattcggg tgtcgatggg gtgggcggg acctgaaaat cccgaacgat 420
 aaatggattc cgccgaatac gagtatctat aaagattccg acggcattat caaagccttt 480
 ctgccgaacg gtaccattct gacggatttc aataaactgc cggacattcc ggaatgggtac 540
 aaaaaagtgc cgggcgatgt ggtcaaagtg acaaagaac tgaatctggg ctaccgtgaa 600
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<210> 20
 <211> 203
 <212> PRT
 <213> Artificial

<220>
 <223> Product of codon optimized nucleotide sequence, additional amino acid residue at position #2 (Ser2 between Met1 and Glu3)

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<400> 20

Met Ser Glu Lys Asn Ile Leu Pro Asn Ile Glu Gly Lys Thr Pro Asn
 1 5 10 15

Ile Asp Lys Asn Val Phe Ile Asp Lys Ser Ala Val Ile Ile Gly Asp
 20 25 30

Val Ala Ile Gln Lys Asn Val Tyr Ile Gly Pro Asn Ala Val Ile Arg
 35 40 45

Cys Asp Glu Pro Pro Thr Lys Gly Ile Leu Ile Lys Glu Gly Ala Asn
 50 55 60

Ile Gln Asp Met Val Val Ile His Cys Leu Arg Asn Thr Ser Val Val
 65 70 75 80

Val Gly Lys Glu Ala Ser Ile Thr His Ser Thr Val Ile His Gly Pro
 85 90 95

Ala Lys Ile Gly Asp Asn Ala Phe Ile Gly Phe Asn Ser Val Val Phe
 100 105 110

Gly Ala Glu Ile Gly Asp Asn Thr Ile Val Gly His Asn Ser Val Val
 115 120 125

Asp Gly Val Gly Gly Asp Leu Lys Ile Pro Asn Asp Lys Trp Ile Pro
 130 135 140

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

Leu Pro Asn Gly Thr Ile Leu Thr Asp Phe Asn Lys Leu Pro Asp Ile
 165 170 175

Pro Glu Trp Tyr Lys Lys Val Pro Gly Asp Val Val Lys Val Asn Lys
 180 185 190

Glu Leu Asn Leu Gly Tyr Arg Glu Phe Ile Lys
 195 200

<210> 21
 <211> 615
 <212> DNA
 <213> Unknown

<220>
 <223> Unknown

<400> 21
 atgacgcgaaa aaaacgctcgc gaccgatttt tgcagccagg ttccgaacc tgacatcggg 60
 actggaacct atgtgcaccc cttggccgca gttatcggaa atgttattct tggcaaaaac 120

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atcatggtat caccgacggc cgtggtgaga ggcgatgaag gacagcccct ctttgtcggc 180
gacgattcca acattcagga cggggtggtc atccatgctc tggaaacgga aatgaacggc 240
accccggtga gcaaaaatct ttacgaggtt aacggtcggt cgtatggtgc ctatgtcggg 300
tgccgtgttt ctcttgccca tcaggtgcag attcatggtc ctgcggtggt tttggacgac 360
acgttcgtcg gcatgaaatc gttggtgttc aaatccttca tcggaaaaaa atgctgtatc 420
gaacctggag ccacgtcat gggcgtgacg gtggccgatg gtcgatatgt cccggccggc 480
gcgatcattc gcagccagaa agaagccgat gccctgccgg aaatcaccga cgattatccc 540
ttcaaggata tgaacagggg cgtcgtgcat gtcaatacct cgctggccag gcagtacctg 600
gcggcaaaaa aaggc 615

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<210> 22
 <211> 205
 <212> PRT
 <213> Unknown

<220>
 <223> Unknown

<400> 22

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

Pro Asp Ile Gly Thr Gly Thr Tyr Val His Pro Leu Ala Ala Val Ile
20 25 30

Gly Asn Val Ile Leu Gly Lys Asn Ile Met Val Ser Pro Thr Ala Val
35 40 45

Val Arg Gly Asp Glu Gly Gln Pro Leu Phe Val Gly Asp Asp Ser Asn
50 55 60

Ile Gln Asp Gly Val Val Ile His Ala Leu Glu Thr Glu Met Asn Gly
65 70 75 80

Thr Pro Val Ser Lys Asn Leu Tyr Glu Val Asn Gly Arg Ser Tyr Gly
85 90 95

Ala Tyr Val Gly Cys Arg Val Ser Leu Ala His Gln Val Gln Ile His
100 105 110

Gly Pro Ala Val Val Leu Asp Asp Thr Phe Val Gly Met Lys Ser Leu
115 120 125

Val Phe Lys Ser Phe Ile Gly Lys Lys Cys Val Ile Glu Pro Gly Ala
130 135 140

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

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Ala Ile Ile Arg Ser Gln Lys Glu Ala Asp Ala Leu Pro Glu Ile Thr
 165 170 175

Asp Asp Tyr Pro Phe Lys Asp Met Asn Arg Gly Val Val His Val Asn
 180 185 190

Thr Ser Leu Ala Arg Gln Tyr Leu Ala Ala Lys Lys Gly
 195 200 205

<210> 23
 <211> 615
 <212> DNA
 <213> Artificial

<220>
 <223> Codon optimised for E. coli

<400> 23
 atgttgagaga agaatgttgc gaccgacttc tgctctcaag ttagtgaacc ggatattggc 60
 acggggcacct acgtccaccc gctggccgct gtgattggta acgttatcct gggcaaaaat 120
 attatggctc cgccgaccgc agtgggtcgt ggtgatgagg gtcagccgct gtttgtgggt 180
 gatgacagca acattcaaga cggcgtcgtg atccatgcgc tggaaaccga aatgaatggc 240
 acgcctgtga gtaaaaacct gtagaagtt aatggccggt cctatggtgc atacgtcggc 300
 tgccgcgtgt cactggctca tcaggtgcaa attcacggtc cggcggttgt cctggatgac 360
 acgtttgttg gcatgaaaag cctgggtcttc aaatctttca tcggtagaa atgtgtcatt 420
 gaaccgggtg cgatcgtgat gggcgtgacc gttgccgatg gtcgttatgt tccggcgggc 480
 gccattatcc gcagtcagaa agaagcagat gctctgccgg aaatcacgga tgactaccgc 540
 ttcaaagaca tgaaccgtgg cgttgttcat gtcaatacct ccctggctcg tcaatacctg 600
 gcggcgaaaa aaggc 615

<210> 24
 <211> 205
 <212> PRT
 <213> Artificial

<220>
 <223> Product of codon optimized nucleotide sequence, differs in second amino-acid residue being L instead of I.

<400> 24

Met Leu Glu Lys Asn Val Ala Thr Asp Phe Cys Ser Gln Val Ser Glu
 1 5 10 15

Pro Asp Ile Gly Thr Gly Thr Tyr Val His Pro Leu Ala Ala Val Ile
 20 25 30

Gly Asn Val Ile Leu Gly Lys Asn Ile Met Val Ser Pro Thr Ala Val
 35 40 45

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Val Arg Gly Asp Glu Gly Gln Pro Leu Phe Val Gly Asp Asp Ser Asn
50 55 60

Ile Gln Asp Gly Val Val Ile His Ala Leu Glu Thr Glu Met Asn Gly
65 70 75 80

Thr Pro Val Ser Lys Asn Leu Tyr Glu Val Asn Gly Arg Ser Tyr Gly
85 90 95

Ala Tyr Val Gly Cys Arg Val Ser Leu Ala His Gln Val Gln Ile His
100 105 110

Gly Pro Ala Val Val Leu Asp Asp Thr Phe Val Gly Met Lys Ser Leu
115 120 125

Val Phe Lys Ser Phe Ile Gly Lys Lys Cys Val Ile Glu Pro Gly Ala
130 135 140

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

Ala Ile Ile Arg Ser Gln Lys Glu Ala Asp Ala Leu Pro Glu Ile Thr
165 170 175

Asp Asp Tyr Pro Phe Lys Asp Met Asn Arg Gly Val Val His Val Asn
180 185 190

Thr Ser Leu Ala Arg Gln Tyr Leu Ala Ala Lys Lys Gly
195 200 205

<210> 25
<211> 519
<212> DNA
<213> Unknown

<220>
<223> Unknown

<400> 25
atgaaaaacg agcaaaaact gaacaaaaac aaaaaagcga tttttatagc tcacagtgag 60
attcgctcac tacgaatagc aaaaaatgcg gttattgttg gggatgttga attgggtgaa 120
gatgtaagtg tatggtatgg ggcagtttta aggggcgacg ttagtaaaat aacgataaaa 180
aaagggttcaa acatccaaga caactgtgtg atacatggct caaaagattg tccaacgata 240
atcggagagt atgtgtctat aggccatggt gcagttgttc atggctgtaa gatgggagat 300
aatgttttag ttgggatgaa tgccactatt ctaaacggtg caaaaattgg aaacaactgc 360
atcatcggag caaatgcttt ggttactcaa aataaagaaa taccacctaa tagcttagtt 420
ttaggagttc caggaaaggt tgtagggag ctcacagaag aagaaataaa atctataaga 480
gaaaatgcag taaactatat aaaattatca aaagattta 519

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<210> 26
 <211> 173
 <212> PRT
 <213> Unknown

<220>
 <223> Unknown

<400> 26

Met Lys Asn Glu Gln Lys Leu Asn Lys Asn Lys Lys Ala Ile Phe Ile
 1 5 10 15

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

Val Gly Asp Val Glu Leu Gly Glu Asp Val Ser Val Trp Tyr Gly Ala
 35 40 45

Val Leu Arg Gly Asp Val Ser Lys Ile Thr Ile Lys Lys Gly Ser Asn
 50 55 60

Ile Gln Asp Asn Cys Val Ile His Gly Ser Lys Asp Cys Pro Thr Ile
 65 70 75 80

Ile Gly Glu Tyr Val Ser Ile Gly His Gly Ala Val Val His Gly Cys
 85 90 95

Lys Met Gly Asp Asn Val Leu Val Gly Met Asn Ala Thr Ile Leu Asn
 100 105 110

Gly Ala Lys Ile Gly Asn Asn Cys Ile Ile Gly Ala Asn Ala Leu Val
 115 120 125

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

Gly Lys Val Val Arg Glu Leu Thr Glu Glu Glu Ile Lys Ser Ile Arg
 145 150 155 160

Glu Asn Ala Val Asn Tyr Ile Lys Leu Ser Lys Asp Leu
 165 170

<210> 27
 <211> 522
 <212> DNA
 <213> Unknown

<220>
 <223> Unknown

<400> 27

atggcggttt acgaactcaa cggaaaaaga ccaataatcc acgagactgc tttcattgat 60

gagagtgcct cgataatagg agacgttggtg cttgaggaga agacgagcgt ctggccttcg 120

gcggttctca ggggtgatgt ggagcagatt tacgttggct gctgctccaa catccaggac 180

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```

aacgtcagca tacacacttc ccacggtcag cccacgaaaa taggaaaata cgtcacgata      240
ggccacaacg ccgttggtgca cggggccgag ataggggact acaccataat cgggatgggt      300
gccataatcc tcgacggtgc gaagatcgga aagcacgtca tcataggagc gggggcacta      360
gtaccgccgg gcaaggaaat tccagactac agcctcgtcg ttggagttcc aggaaagggt      420
gtcaggcagc tcagcgaaga ggagatagag tggacgagga agaacgccga gatattatg      480
gagctcgccg agatgcacct aaagagcaga aagcccgtta ag                          522

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<210> 28
<211> 174
<212> PRT
<213> Unknown

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<220>
<223> Unknown

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<400> 28

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Met Ala Val Tyr Glu Leu Asn Gly Lys Arg Pro Ile Ile His Glu Thr
1      5      10

```

```

Ala Phe Ile Asp Glu Ser Ala Ser Ile Ile Gly Asp Val Val Leu Glu
      20      25      30

```

```

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

```

```

Gln Ile Tyr Val Gly Cys Cys Ser Asn Ile Gln Asp Asn Val Ser Ile
      50      55      60

```

```

His Thr Ser His Gly Gln Pro Thr Lys Ile Gly Lys Tyr Val Thr Ile
      65      70      75      80

```

```

Gly His Asn Ala Val Val His Gly Ala Glu Ile Gly Asp Tyr Thr Ile
      85      90      95

```

```

Ile Gly Met Gly Ala Ile Ile Leu Asp Gly Ala Lys Ile Gly Lys His
      100      105      110

```

```

Val Ile Ile Gly Ala Gly Ala Leu Val Pro Pro Gly Lys Glu Ile Pro
      115      120      125

```

```

Asp Tyr Ser Leu Val Val Gly Val Pro Gly Lys Val Val Arg Gln Leu
      130      135      140

```

```

Ser Glu Glu Glu Ile Glu Trp Thr Arg Lys Asn Ala Glu Ile Tyr Met
      145      150      155      160

```

```

Glu Leu Ala Glu Met His Leu Lys Ser Arg Lys Pro Val Lys
      165      170

```

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<210> 29
<211> 534
<212> DNA
<213> Unknown

<220>
<223> Unknown

<400> 29
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gttattcgtg gagatattca taagattaaa ataggcaaaa gaacaaatat acaagattta 180
agtatgattc atgtaacaca ctatactaaa aaagacaaga gtgatggcaa tccaactatt 240
ataggtaatg atgtaacagt tggacataaa gttatgctac atggttgcac aattgaaaat 300
gcttgtttga ttggtatgag tgctaccata ctgatgggtg ctgtaatagg gaaagaatca 360
atagtagggag caaatgctct ggtaacaaaa gataaaaaat ttcctccaag atctctaatt 420
atgggaagtc ctgcaaaagc agtgaaagaa ctcaatgacg aagaagtagc tttttgtat 480
aagtctgcta aaaactatgt aaaatttaaa gatagatacc taaaagagat gtta 534

<210> 30
<211> 178
<212> PRT
<213> Unknown

<220>
<223> Unknown

<400> 30

Met Ile Met Lys Phe Lys Lys Asn Ser Pro Lys Ile Lys Lys Arg Val
1 5 10 15
Phe Ile Ala Pro Ser Ala Asp Val Ile Gly Glu Val Lys Ile Gly Asn
20 25 30
Asp Ser Ala Ile Trp Phe Gly Cys Val Ile Arg Gly Asp Ile His Lys
35 40 45
Ile Lys Ile Gly Lys Arg Thr Asn Ile Gln Asp Leu Ser Met Ile His
50 55 60
Val Thr His Tyr Thr Lys Lys Asp Lys Ser Asp Gly Asn Pro Thr Ile
65 70 75 80
Ile Gly Asn Asp Val Thr Val Gly His Lys Val Met Leu His Gly Cys
85 90 95
Thr Ile Glu Asn Ala Cys Leu Ile Gly Met Ser Ala Thr Ile Leu Asp
100 105 110
Gly Ala Val Ile Gly Lys Glu Ser Ile Val Gly Ala Asn Ala Leu Val
115 120 125

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Thr Lys Asp Lys Lys Phe Pro Pro Arg Ser Leu Ile Met Gly Ser Pro
 130 135 140

Ala Lys Ala Val Lys Glu Leu Asn Asp Glu Glu Val Ala Phe Leu Tyr
 145 150 155 160

Lys Ser Ala Lys Asn Tyr Val Lys Phe Lys Asp Arg Tyr Leu Lys Glu
 165 170 175

Met Leu

<210> 31
 <211> 810
 <212> DNA
 <213> Unknown

<220>
 <223> Unknown

<400> 31
 atgtgtactt actacacatt aagagggtgat atattgaaca aaaagattgc agtattgggc 60
 atgttctgta tggcattaac attgctatatt gcaggatgtg tcgataatca aacagcagtt 120
 gatgaatcta ccacaaacga gttaaaatca gaaatatcca acttagaagc agaagtaaatt 180
 aaattgaaat catcccctaa tatgatacca aatgtaaggc agaatttaga aggacattct 240
 ccttcaataa gtaaaatagg tacctatatt gaccccgatg cagtagttat tggaaatgta 300
 aaaatcggag ataacgtata tgtgggccct catgcagttg taagatgcga tgaagttcca 360
 acaaaaggaa tcgtaattgg aaataaggta aatattcaag atggtgttat catacacgcc 420
 ctaaggggaa caaaaataga aattgaagat gaggccttctc ttgcccatgg gagcatagtg 480
 catggacctg ctaaaatagg taaaaatgcc ttgttcgcat ttggtgccgt cgtatttgct 540
 gcggaagtgg gacccggtgc attaatggga cataatgcag ttgtagatgg aattggagta 600
 gaaggaggat tgaaaatacc tgctggaaaa atggttccat caggagctgt tgtaatgaaa 660
 gatgtagacg ggcaggtaaa agcattttta cctgatggca cagtattgac agatttaaatt 720
 gaactgccta atgtggtgga ttggtataaaa cctgtcccag gaaagggtgt agatgtaaatt 780
 attgagttgg cagaaggata tttgaaaaaa 810

<210> 32
 <211> 270
 <212> PRT
 <213> Unknown

<220>
 <223> Unknown

<400> 32

Met Cys Thr Tyr Tyr Thr Leu Arg Gly Asp Ile Leu Asn Lys Lys Ile
 1 5 10 15

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Ala Val Leu Gly Met Phe Cys Met Ala Leu Thr Leu Leu Phe Ala Gly
20 25 30

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

Lys Ser Glu Ile Ser Asn Leu Glu Ala Glu Val Asn Lys Leu Lys Ser
50 55 60

Ser Pro Asn Met Ile Pro Asn Val Arg Gln Asn Leu Glu Gly His Ser
65 70 75 80

Pro Ser Ile Ser Lys Ile Gly Thr Tyr Ile Asp Pro Asp Ala Val Val
85 90 95

Ile Gly Asn Val Lys Ile Gly Asp Asn Val Tyr Val Gly Pro His Ala
100 105 110

Val Val Arg Cys Asp Glu Val Pro Thr Lys Gly Ile Val Ile Gly Asn
115 120 125

Lys Val Asn Ile Gln Asp Gly Val Ile Ile His Ala Leu Arg Gly Thr
130 135 140

Lys Ile Glu Ile Glu Asp Glu Ala Ser Leu Ala His Gly Ser Ile Val
145 150 155 160

His Gly Pro Ala Lys Ile Gly Lys Asn Ala Phe Val Ala Phe Gly Ala
165 170 175

Val Val Phe Ala Ala Glu Val Gly Pro Gly Ala Leu Ile Gly His Asn
180 185 190

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

Gly Lys Met Val Pro Ser Gly Ala Val Val Met Lys Asp Val Asp Gly
210 215 220

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

Glu Leu Pro Asn Val Val Asp Trp Tyr Lys Pro Val Pro Gly Lys Val
245 250 255

Val Asp Val Asn Ile Glu Leu Ala Glu Gly Tyr Leu Lys Lys
260 265 270