

M065670201W000-SEQLIST-JRV
SEQUENCE LISTING

<110> Massachusetts Institute of Technology
AJIKUMAR, Parayil K.
STEPHANOPOULOS, Gregory
PHON, Too Heng

<120> MICROBIAL ENGINEERING FOR THE PRODUCTION OF CHEMICAL AND
PHARMACEUTICAL PRODUCTS FROM THE ISOPRENOID PATHWAY

<130> M0656.70201W000

<150> US 61/280,877
<151> 2009-11-10

<150> US 61/388,543
<151> 2010-09-30

<160> 52

<170> PatentIn version 3.5

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Ala Ala Leu Asp Lys Ala Ile Pro Leu Glu Tyr Pro Glu Lys Ile His
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 Ala Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Ser Gln Asp Leu
 50 55 60
 Ala Met Pro Thr Ala Cys Ala Met Glu Met Ile His Thr Met Ser Leu
 65 70 75 80
 Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Phe Arg Arg Gly
 85 90 95
 Lys Pro Thr Asn His Lys Val Phe Gly Glu Asp Thr Ala Val Leu Ala
 100 105 110
 Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Ile Ala Val Ala Thr
 115 120 125
 Ser Lys Thr Val Pro Ser Asp Arg Thr Leu Arg Val Ile Ser Glu Leu
 130 135 140
 Gly Lys Thr Ile Gly Ser Gln Gly Leu Val Gly Gly Gln Val Val Asp
 145 150 155 160
 Ile Thr Ser Glu Gly Asp Ala Asn Val Asp Leu Lys Thr Leu Glu Trp
 165 170 175
 Ile His Ile His Lys Thr Ala Val Leu Leu Glu Cys Ser Val Val Ser
 180 185 190
 Gly Gly Ile Leu Gly Gly Ala Thr Glu Asp Glu Ile Ala Arg Ile Arg
 195 200 205
 Arg Tyr Ala Arg Cys Val Gly Leu Leu Phe Gln Val Val Asp Asp Ile
 210 215 220
 Leu Asp Val Thr Lys Ser Ser Glu Glu Leu Gly Lys Thr Ala Gly Lys
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 Asp Leu Leu Thr Asp Lys Ala Thr Tyr Pro Lys Leu Met Gly Leu Glu
 245 250 255
 Lys Ala Lys Glu Phe Ala Ala Glu Leu Ala Thr Arg Ala Lys Glu Glu
 260 265 270
 Leu Ser Ser Phe Asp Gln Ile Lys Ala Ala Pro Leu Leu Gly Leu Ala
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 Asp Tyr Ile Ala Phe Arg Gln Asn
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 aaaacggccg tgctgctgga atgtagcgtg gtgtcagggg ggatcttggg gggcgccacg 600
 gaggatgaaa tcgcgcgtat tcgtcgttat gcccgtgtg ttggactgtt atttcaggtg 660
 gtggatgaca tcctggatgt cacaaaatcc agcgaagagc ttggcaagac cgcgggcaaa 720
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 35 40 45

Ser Ser Thr Tyr Gln Glu Arg Ala Asp Glu Leu Val Val Lys Ile Lys
 50 55 60

Asp Met Phe Asn Ala Leu Gly Asp Gly Asp Ile Ser Pro Ser Ala Tyr
 65 70 75 80

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Asp Thr Ala Trp Val₈₅ Ala Arg Leu Ala Thr₉₀ Ile Ser Ser Asp Gly₉₅ Ser
 Glu Lys Pro Arg₁₀₀ Phe Pro Gln Ala Leu₁₀₅ Asn Trp Val Phe Asn₁₁₀ Asn Gln
 Leu Gln Asp₁₁₅ Gly Ser Trp Gly Ile₁₂₀ Glu Ser His Phe Ser₁₂₅ Leu Cys Asp
 Arg Leu₁₃₀ Leu Asn Thr Thr Asn₁₃₅ Ser Val Ile Ala Leu₁₄₀ Ser Val Trp Lys
 Thr₁₄₅ Gly His Ser Gln Val₁₅₀ Gln Gln Gly Ala Glu₁₅₅ Phe Ile Ala Glu Asn₁₆₀
 Leu Arg Leu Leu Asn₁₆₅ Glu Glu Asp Glu Leu₁₇₀ Ser Pro Asp Phe Gln Ile
 Ile Phe Pro Ala₁₈₀ Leu Leu Gln Lys Ala₁₈₅ Lys Ala Leu Gly Ile₁₉₀ Asn Leu
 Pro Tyr Asp₁₉₅ Leu Pro Phe Ile Lys₂₀₀ Tyr Leu Ser Thr Thr₂₀₅ Arg Glu Ala
 Arg Leu₂₁₀ Thr Asp Val Ser Ala₂₁₅ Ala Ala Asp Asn Ile₂₂₀ Pro Ala Asn Met
 Leu Asn Ala Leu Glu Gly₂₃₀ Leu Glu Glu Val Ile₂₃₅ Asp Trp Asn Lys Ile₂₄₀
 Met Arg Phe Gln Ser₂₄₅ Lys Asp Gly Ser Phe₂₅₀ Leu Ser Ser Pro Ala₂₅₅ Ser
 Thr Ala Cys Val₂₆₀ Leu Met Asn Thr Gly₂₆₅ Asp Glu Lys Cys Phe₂₇₀ Thr Phe
 Leu Asn Asn₂₇₅ Leu Leu Asp Lys Phe₂₈₀ Gly Gly Cys Val Pro₂₈₅ Cys Met Tyr
 Ser Ile₂₉₀ Asp Leu Leu Glu Arg₂₉₅ Leu Ser Leu Val Asp₃₀₀ Asn Ile Glu His
 Leu Gly Ile Gly Arg His₃₁₀ Phe Lys Gln Glu Ile₃₁₅ Lys Gly Ala Leu Asp₃₂₀
 Tyr Val Tyr Arg His₃₂₅ Trp Ser Glu Arg Gly₃₃₀ Ile Gly Trp Gly Arg₃₃₅ Asp
 Ser Leu Val Pro₃₄₀ Asp Leu Asn Thr Thr₃₄₅ Ala Leu Gly Leu Arg₃₅₀ Thr Leu

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Arg Met His Gly Tyr Asn Val Ser Ser Asp Val Leu Asn Asn Phe Lys
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 Asp Glu Asn Gly Arg Phe Phe Ser Ser Ala Gly Gln Thr His Val Glu
 370 375 380
 Leu Arg Ser Val Val Asn Leu Phe Arg Ala Ser Asp Leu Ala Phe Pro
 385 390 395 400
 Asp Glu Arg Ala Met Asp Asp Ala Arg Lys Phe Ala Glu Pro Tyr Leu
 405 410 415
 Arg Glu Ala Leu Ala Thr Lys Ile Ser Thr Asn Thr Lys Leu Phe Lys
 420 425 430
 Glu Ile Glu Tyr Val Val Glu Tyr Pro Trp His Met Ser Ile Pro Arg
 435 440 445
 Leu Glu Ala Arg Ser Tyr Ile Asp Ser Tyr Asp Asp Asn Tyr Val Trp
 450 455 460
 Gln Arg Lys Thr Leu Tyr Arg Met Pro Ser Leu Ser Asn Ser Lys Cys
 465 470 475 480
 Leu Glu Leu Ala Lys Leu Asp Phe Asn Ile Val Gln Ser Leu His Gln
 485 490 495
 Glu Glu Leu Lys Leu Leu Thr Arg Trp Trp Lys Glu Ser Gly Met Ala
 500 505 510
 Asp Ile Asn Phe Thr Arg His Arg Val Ala Glu Val Tyr Phe Ser Ser
 515 520 525
 Ala Thr Phe Glu Pro Glu Tyr Ser Ala Thr Arg Ile Ala Phe Thr Lys
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 Thr Leu Asp Glu Leu Lys Ser Phe Thr Glu Gly Val Lys Arg Trp Asp
 565 570 575
 Thr Ser Leu Leu His Glu Ile Pro Glu Cys Met Gln Thr Cys Phe Lys
 580 585 590
 Val Trp Phe Lys Leu Met Glu Glu Val Asn Asn Asp Val Val Lys Val
 595 600 605
 Gln Gly Arg Asp Met Leu Ala His Ile Arg Lys Pro Trp Glu Leu Tyr
 610 615 620

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Phe Asn Cys Tyr Val Gln Glu Arg Glu Trp Leu Glu Ala Gly Tyr Ile
625 630 635 640

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

Gly Pro Cys Thr Leu Gln Pro Ile Leu Leu Met Gly Glu Leu Val Lys
660 665 670

Asp Asp Val Val Glu Lys Val His Tyr Pro Ser Asn Met Phe Glu Leu
675 680 685

Val Ser Leu Ser Trp Arg Leu Thr Asn Asp Thr Lys Thr Tyr Gln Ala
690 695 700

Glu Lys Ala Arg Gly Gln Gln Ala Ser Gly Ile Ala Cys Tyr Met Lys
705 710 715 720

Asp Asn Pro Gly Ala Thr Glu Glu Asp Ala Ile Lys His Ile Cys Arg
725 730 735

Val Val Asp Arg Ala Leu Lys Glu Ala Ser Phe Glu Tyr Phe Lys Pro
740 745 750

Ser Asn Asp Ile Pro Met Gly Cys Lys Ser Phe Ile Phe Asn Leu Arg
755 760 765

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

Ser Leu Lys Leu Pro Pro Gly Lys Leu Gly Ile Pro Phe Ile Gly Glu
50 55 60

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

Phe Asp Glu Arg Val Lys Lys Phe Gly Leu Val Phe Lys Thr Ser Leu
85 90 95

Ile Gly His Pro Thr Val Val Leu Cys Gly Pro Ala Gly Asn Arg Leu
100 105 110

Ile Leu Ser Asn Glu Glu Lys Leu Val Gln Met Ser Trp Pro Ala Gln
115 120 125

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

Asp His Ile Val Met Arg Ser Ala Leu Ala Gly Phe Phe Gly Pro Gly
145 150 155 160

Ala Leu Gln Ser Tyr Ile Gly Lys Met Asn Thr Glu Ile Gln Ser His
165 170 175

Ile Asn Glu Lys Trp Lys Gly Lys Asp Glu Val Asn Val Leu Pro Leu
180 185 190

Val Arg Glu Leu Val Phe Asn Ile Ser Ala Ile Leu Phe Phe Asn Ile
195 200 205

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Tyr Asp Lys Gln Glu Gln Asp Arg Leu His Lys Leu Leu Glu Thr Ile
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 Leu Val Gly Ser Phe Ala Leu Pro Ile Asp Leu Pro Gly Phe Gly Phe
 225 230 235 240
 His Arg Ala Leu Gln Gly Arg Ala Lys Leu Asn Lys Ile Met Leu Ser
 245 250 255
 Leu Ile Lys Lys Arg Lys Glu Asp Leu Gln Ser Gly Ser Ala Thr Ala
 260 265 270
 Thr Gln Asp Leu Leu Ser Val Leu Leu Thr Phe Arg Asp Asp Lys Gly
 275 280 285
 Thr Pro Leu Thr Asn Asp Glu Ile Leu Asp Asn Phe Ser Ser Leu Leu
 290 295 300
 His Ala Ser Tyr Asp Thr Thr Thr Ser Pro Met Ala Leu Ile Phe Lys
 305 310 315 320
 Leu Leu Ser Ser Asn Pro Glu Cys Tyr Gln Lys Val Val Gln Glu Gln
 325 330 335
 Leu Glu Ile Leu Ser Asn Lys Glu Glu Gly Glu Glu Ile Thr Trp Lys
 340 345 350
 Asp Leu Lys Ala Met Lys Tyr Thr Trp Gln Val Ala Gln Glu Thr Leu
 355 360 365
 Arg Met Phe Pro Pro Val Phe Gly Thr Phe Arg Lys Ala Ile Thr Asp
 370 375 380
 Ile Gln Tyr Asp Gly Tyr Thr Ile Pro Lys Gly Trp Lys Leu Leu Trp
 385 390 395 400
 Thr Thr Tyr Ser Thr His Pro Lys Asp Leu Tyr Phe Asn Glu Pro Glu
 405 410 415
 Lys Phe Met Pro Ser Arg Phe Asp Gln Glu Gly Lys His Val Ala Pro
 420 425 430
 Tyr Thr Phe Leu Pro Phe Gly Gly Gly Gln Arg Ser Cys Val Gly Trp
 435 440 445
 Glu Phe Ser Lys Met Glu Ile Leu Leu Phe Val His His Phe Val Lys
 450 455 460
 Thr Phe Ser Ser Tyr Thr Pro Val Asp Pro Asp Glu Lys Ile Ser Gly
 465 470 475 480

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Asp Pro Leu Pro Pro Leu Pro Ser Lys Gly Phe Ser Ile Lys Leu Phe
 485 490 495

Pro Arg Pro

<210> 47
 <211> 1497
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

<400> 47
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 ctgtttcgct cgaaacgtca tagtagcctg aaattacctc cgggcaaact gggcattccg 180
 tttatcgggtg agtcctttat ttttttgcgc gcgctgcgca gcaattctct ggaacagttc 240
 tttgatgaac gtgtgaagaa gttcggcctg gtatttaaaa cgtcccttat cggtcacccg 300
 acggttgtcc tgtgcggggc cgcaggtaat cgccatcc tgagcaacga agaaaagctg 360
 gtacagatgt cctggccggc gcagtttatg aagctgatgg gagagaactc agttgcgacc 420
 cgccgtggtg aagatcacat tgttatgcgc tccgcgttgg caggcttttt cggcccggga 480
 gctctgcaat cctatatcgg caagatgaac acggaaatcc aaagccatat taatgaaaag 540
 tggaaagggg aggacgaggt taatgtctta cccctgggtgc gggaactggt ttttaacatc 600
 agcgctattc tgttctttaa catttacgat aagcaggaac aagaccgtct gcacaagtgt 660
 ttagaaacca ttctggtagg ctgcttgcc ttaccaattg atttaccggg tttcgggttt 720
 caccgcgctt tacaaggctg tgcaaaactc aataaaatca tgttgtcgtt tattaaaaaa 780
 cgtaaagagg acttacagtc gggatcggcc accgcgacgc aggacctgtt gtctgtgctt 840
 ctgactttcc gtgatgataa gggcaccccg ttaaccaatg acgaaatcct ggacaacttt 900
 agctcactgc ttcacgcctc ttacgacacc acgactagtc caatggctct gatattcaaa 960
 ttactgtcaa gtaaccctga atgctatcag aaagtcgtgc aagagcaact cgagattctg 1020
 agcaataagg aagaagggtga agaaattacc tggaaagatc ttaaggccat gaaatacacg 1080
 tggcagggtt cgcaggagac acttcgcatg tttccaccgg tgttcgggac cttccgcaaa 1140
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 actacctata gcactcatcc taaggacctt tacttcaacg aaccggagaa atttatgcct 1260
 agtcgtttcg atcaggaagg caaacatgtt gcgccctata ccttcctgcc ctttggaggc 1320
 ggtcagcgga gttgtgtggg ttgggagttc tctaagatgg agattctcct cttcgtgcat 1380
 catttcgtga aaacattttc gagctatacc ccggtcgtac ccgatgaaaa aatttcgggc 1440
 gatccactgc cgccgttacc gagcaaaggg ttttcaatca aactgttccc tcgtccg 1497

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<210> 48
 <211> 717
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 48

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Leu Leu Asp Ile Ser Arg Leu Asp His Ile Phe Ala Leu Leu Leu Asn
 20 25 30

Gly Lys Gly Gly Asp Leu Gly Ala Met Thr Gly Ser Ala Leu Ile Leu
 35 40 45

Thr Glu Asn Ser Gln Asn Leu Met Ile Leu Thr Thr Ala Leu Ala Val
 50 55 60

Leu Val Ala Cys Val Phe Phe Phe Val Trp Arg Arg Gly Gly Ser Asp
 65 70 75 80

Thr Gln Lys Pro Ala Val Arg Pro Thr Pro Leu Val Lys Glu Glu Asp
 85 90 95

Glu Glu Glu Glu Asp Asp Ser Ala Lys Lys Lys Val Thr Ile Phe Phe
 100 105 110

Gly Thr Gln Thr Gly Thr Ala Glu Gly Phe Ala Lys Ala Leu Ala Glu
 115 120 125

Glu Ala Lys Ala Arg Tyr Glu Lys Ala Val Phe Lys Val Val Asp Leu
 130 135 140

Asp Asn Tyr Ala Ala Asp Asp Glu Gln Tyr Glu Glu Lys Leu Lys Lys
 145 150 155 160

Glu Lys Leu Ala Phe Phe Met Leu Ala Thr Tyr Gly Asp Gly Glu Pro
 165 170 175

Thr Asp Asn Ala Ala Arg Phe Tyr Lys Trp Phe Leu Glu Gly Lys Glu
 180 185 190

Arg Glu Pro Trp Leu Ser Asp Leu Thr Tyr Gly Val Phe Gly Leu Gly
 195 200 205

Asn Arg Gln Tyr Glu His Phe Asn Lys Val Ala Lys Ala Val Asp Glu
 210 215 220

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

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Asp Asp Asp Gln Cys Ile Glu Asp Asp Phe Thr Ala Trp Arg Glu Gln
 245 250 255
 Val Trp Pro Glu Leu Asp Gln Leu Leu Arg Asp Glu Asp Asp Glu Pro
 260 265 270
 Thr Ser Ala Thr Pro Tyr Thr Ala Ala Ile Pro Glu Tyr Arg Val Glu
 275 280 285
 Ile Tyr Asp Ser Val Val Ser Val Tyr Glu Glu Thr His Ala Leu Lys
 290 295 300
 Gln Asn Gly Gln Ala Val Tyr Asp Ile His His Pro Cys Arg Ser Asn
 305 310 315 320
 Val Ala Val Arg Arg Glu Leu His Thr Pro Leu Ser Asp Arg Ser Cys
 325 330 335
 Ile His Leu Glu Phe Asp Ile Ser Asp Thr Gly Leu Ile Tyr Glu Thr
 340 345 350
 Gly Asp His Val Gly Val His Thr Glu Asn Ser Ile Glu Thr Val Glu
 355 360 365
 Glu Ala Ala Lys Leu Leu Gly Tyr Gln Leu Asp Thr Ile Phe Ser Val
 370 375 380
 His Gly Asp Lys Glu Asp Gly Thr Pro Leu Gly Gly Ser Ser Leu Pro
 385 390 395 400
 Pro Pro Phe Pro Gly Pro Cys Thr Leu Arg Thr Ala Leu Ala Arg Tyr
 405 410 415
 Ala Asp Leu Leu Asn Pro Pro Arg Lys Ala Ala Phe Leu Ala Leu Ala
 420 425 430
 Ala His Ala Ser Asp Pro Ala Glu Ala Glu Arg Leu Lys Phe Leu Ser
 435 440 445
 Ser Pro Ala Gly Lys Asp Glu Tyr Ser Gln Trp Val Thr Ala Ser Gln
 450 455 460
 Arg Ser Leu Leu Glu Ile Met Ala Glu Phe Pro Ser Ala Lys Pro Pro
 465 470 475 480
 Leu Gly Val Phe Phe Ala Ala Ile Ala Pro Arg Leu Gln Pro Arg Tyr
 485 490 495
 Tyr Ser Ile Ser Ser Ser Pro Arg Phe Ala Pro Ser Arg Ile His Val
 500 505 510

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Thr Cys Ala Leu Val Tyr Gly Pro Ser Pro Thr Gly Arg Ile His Lys
515 520 525

Gly Val Cys Ser Asn Trp Met Lys Asn Ser Leu Pro Ser Glu Glu Thr
530 535 540

His Asp Cys Ser Trp Ala Pro Val Phe Val Arg Gln Ser Asn Phe Lys
545 550 555 560

Leu Pro Ala Asp Ser Thr Thr Pro Ile Val Met Val Gly Pro Gly Thr
565 570 575

Gly Phe Ala Pro Phe Arg Gly Phe Leu Gln Glu Arg Ala Lys Leu Gln
580 585 590

Glu Ala Gly Glu Lys Leu Gly Pro Ala Val Leu Phe Phe Gly Cys Arg
595 600 605

Asn Arg Gln Met Asp Tyr Ile Tyr Glu Asp Glu Leu Lys Gly Tyr Val
610 615 620

Glu Lys Gly Ile Leu Thr Asn Leu Ile Val Ala Phe Ser Arg Glu Gly
625 630 635 640

Ala Thr Lys Glu Tyr Val Gln His Lys Met Leu Glu Lys Ala Ser Asp
645 650 655

Thr Trp Ser Leu Ile Ala Gln Gly Gly Tyr Leu Tyr Val Cys Gly Asp
660 665 670

Ala Lys Gly Met Ala Arg Asp Val His Arg Thr Leu His Thr Ile Val
675 680 685

Gln Glu Gln Glu Ser Val Asp Ser Ser Lys Ala Glu Phe Leu Val Lys
690 695 700

Lys Leu Gln Met Asp Gly Arg Tyr Leu Arg Asp Ile Trp
705 710 715

<210> 49
<211> 2151
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

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atgaccgggt cggccttaat tctgacggaa aatagccaga acttgatgat tctgaccact 180

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gcgctggccg	ttctggtcgc	ttgcgttttt	tttttcgttt	ggcgccgtgg	tggaagtgat	240
acacagaagc	ccgccgtacg	tcccacacct	cttgttaaag	aagaggacga	agaagaagaa	300
gatgatagcg	ccaagaaaaa	ggtcacaata	ttttttggca	cccagaccgg	caccgccgaa	360
ggtttcgcaa	aggccttagc	tgaggaagca	aaggcacgtt	atgaaaaggc	ggtattttaa	420
gtcgtggatt	tgataacta	tgcagcggat	gacgaacagt	acgaagagaa	gttgaaaaag	480
gaaaagctag	cgttcttcat	gctcgccacc	tacgggtgacg	gcgaaccgac	tgataatgcc	540
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acttatggcg	tgtttggtt	aggtaaccgt	cagtatgaac	actttaacaa	ggtcgcgaaa	660
gcggtggacg	aagtgtcat	tgaacaaggc	gccaaacgtc	tggtaccggt	agggcttggg	720
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gagaattcaa	ttgaaaccgt	ggaagaagca	gctaaactgt	taggttacca	actggataca	1140
atcttcagcg	tgcatgggga	caaggaagat	ggaacaccat	tgggcgggag	tagcctgcc	1200
ccgccgtttc	cggggccctg	cacgctgcgg	acggcgctgg	cacgttacgc	ggacctgctg	1260
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gctgaacgcc	ttaaatttct	cagttctcca	gccggaaaaag	acgaatactc	acagtgggtc	1380
actgcgtccc	aacgcagcct	cctcgagatt	atggccgaat	tccccagcgc	gaaaccgccg	1440
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gcagtgtgt	tttttgggtg	ccgcaaccgc	cagatggatt	acatctatga	agatgagctt	1860
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gccaccaaag	agtatgttca	gcacaagatg	ttagagaaaag	cctccgacac	gtggtcttta	1980
atcgcccagg	gtgggttatct	gtatgtttgc	ggtgatgcga	agggtatggc	cagagacgta	2040
catcgacccc	tgcatacaat	cgttcaggaa	caagaatccg	tagactcgtc	aaaagcggag	2100
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<210> 50
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 50

Gly Ser Thr Gly Ser
 1 5

<210> 51
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 51

Met Ala Leu Leu Leu Ala Val Phe
 1 5

<210> 52
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide

<400> 52
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41